Role of posttranslational modifications of histone proteins in epigenetics



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Abstract

Nature has evolved an additional level of genetic regulation by-passing direct changes in genetic code through the means of posttranslational modifications (PTMs) of nucleobases and histone proteins. Acetylation, methylation, phosphorylation, *O*-GlcNAcylation, ubiquitination, sumoylation, and ADP ribosylation are few common examples of various histone modifications. Identification of these modifications and subsequent access to homogeneously modified histone proteins are key for understanding the functional consequence of these PTMs. In this doctoral thesis, the role of PTMs of histone proteins in epigenetics was investigated with emphasis on understanding the role of *O*-GlcNAcylation in particular.

In the second chapter, the functional consequence of *O*-GlcNAcylation at histone protein, H2B-Ser112 was explored. Homogeneously GlcNAcylated histones and nucleosomes were synthesized using protein chemical reactions. Mass Spectrometry (MS) based quantitative interaction proteomics revealed a direct interaction between GlcNAcylated nucleosomes and the Facilitates Chromatin Transcription (FACT) complex. Preferential binding of FACT to GlcNAcylated nucleosomes provides a molecular mechanism for FACT-driven transcriptional control.

In the third chapter, the physical effect of *O*-GlcNAcylation on the nucleosome structure is described. Homogeneously GlcNAcylated histone protein, H2A-Thr101 was synthesized. The modified protein was used to reconstitute histone sub-complexes and nucleosomes. Various biophysical studies involving circular dichroism and native mass spectrometry revealed that H2A-T101 GlcNAcylation regulates the stability of the nucleosome structure, suggesting a role in transcriptional activation.

In the fourth chapter, we discuss an interesting scenario where two PTMs – *O*-GlcNAcylation and phosphorylation – can compete for the same modification site of histone protein, H2B-Ser36. The resulting outcome is possibly a competitive antagonism or cross-talk, which can modulate the overall control of chromatin regulation. Using a “Tag-and-modify” approach, modified histone proteins bearing both modifications was synthesized, and was later used for nucleosome reconstitution. Quantitative interaction proteomics experiments with the modified nucleosome revealed key interacting protein partners for both the modifications.

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Declaration

I declare the work presented in this thesis was carried out at the Chemistry Research Laboratory and Department of Biochemistry, University of Oxford, UK. All the work is my own, except where otherwise stated, and has not been submitted for any other degree at this or any other university.



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Abbreviations

°C	degree Celsius
Amp	ampicillin
aq.	aqueous
Ac	acetyl
ACN	acetonitrileAmmonium persulfate
BSA	Bovine Serum Albumin
calc.	calculated
CD	Circular dichroism
Da	Dalton
DNA	2'-deoxyribose nucleic acid
eq.	equivalent
et al.	et alia
ESI	Electrospray ionization
FA	formic acid
FPLC	Fast protein liquid chromatography
g	gram
GlcNAc	*N*-acetylglucosamine
IPTG	Isopropyl thiogalactoside
kbp	kilo-base pair
kDa	kilodalton
LC-MS	liquid chromatography-mass spectrometry
m	milli
M	molarity
m/z	mass to charge ratio
min	minute
mL	milliliter
mol	mole
MES	2-(*N*-morpholino)ethanesulfonic acid
MS	Mass spectrometry
OD	optical density
PBS	phosphate buffered saline
PCR	Polymerase chain reaction
pH	$-\log_{10}[H^+]$
PVDF	polyvinylidene fluoride
rt	room temperature

SDS-PAGE	sodium dodecyl sulfate polyacrylamide gel electrophoresis
soln.	solution
SUMO	Small ubiquitin-related modifier protein
TB	terrific broth
β-GlcNAc-thiol	2-acetamido-2-deoxy-1-thio-β-D-glucopyranose

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1. Introduction

The elucidation of the double helical DNA structure stands as one of the biggest discoveries in modern science. This seminal discovery along with findings of Avery[1] and Hershey-Chase[2] confirmed the role of DNA as the genetic material of life. Based on this and other scientific findings of the time, Crick introduced the idea of the "central dogma of molecular biology" to explain the flow of information in biological systems.[3] According to the central dogma, genetic information is maintained through semi-conservative replication of DNA and is sequentially propagated by two templated processes, the transcription of DNA to RNA, followed by translation of RNA to produce proteins. The dogma allows the possibility of feedback from the RNA to the DNA level, but discards such a transfer from protein to DNA or protein to protein. In some way, it emphasizes most of the genetic regulation to occur at the DNA level, which holds true to explain many biological situations.

However, it is not always possible to explain the genetic complexity observed in biological systems using the mere genetic code of DNA, encoded by 4 letters (A, T, G, C). One of the simplest and straight-forward example to illustrate this complexity is the phenomenon of cell differentiation and development. As one moves from simple unicellular organisms to multicellular organisms, like human, one observes that despite identical genome sequence, the cells differentiate into over 200 distinct cells types. The DNA sequence alone cannot explain this phenomenon, since all cells contain nearly identical genomic information, and suggests a regulation of gene expression without alterations in the DNA sequence. The discovery of prions[4] and certain non-Mendelian inheritance patterns further corroborated the idea of an additional layer of regulation above the genetic level (*'Epigenetics'*).

Indeed, there exist many regulatory mechanisms which provide multidimensional layers of regulation for genomic sequences without physically changing them. This epigenetic regulation occurs through modulation of the chromatin template, the physiological form of genomic DNA.

1.1 The chromatin template

In eukaryotes, the chromosomal DNA is packaged in a dynamic polymeric complex called chromatin. The fundamental unit of chromatin is the nucleosome, composed of an octameric protein core around which ~ 150 base pairs of DNA is spooled in a left-handed spiral **(Figure 1)**. This wrapping of DNA around histone octamer constitutes the first level of genomic compaction. Although the composition of the nucleosome was known for a while, the first insight into the nucleosome structure was provided via 2.8 Å crystal structure solved by Luger *et al.*[5] in 1997. The octameric protein core is made up of two copies of four relatively small (10-20 kDa), highly basic histone proteins – H2A, H2B, H3, and H4. The canonical histone proteins contain a histone-fold motif, made up of three α helices with one central helix connected to two other small helices through two loops, along with flexible *N*-terminal tails. Histone protein, H2A has an additional *C*-terminal tail. The histone-fold motifs of distinct histone proteins complement each other to form a handshake motif leading to assembly of histone heterodimers (H2A/H2B and H3/H4). For octamer constitution, two H3/H4 heterodimers come together to form a central $(H3/H4)_2$ tetramer with two binding surfaces for H2A/H2B heterodimers on opposite faces. The DNA is wrapped around the octamer in a bent duplex conformation, an energetically unfavorable conformation owing to phosphate backbone interactions of DNA.[6] However, this energetically unfavorable situation is compensated by highly favorable histone-DNA interactions of the nucleosome leading to very efficient packaging of the DNA. These favorable interactions between histone and DNA stem from ionic interactions, water-mediated hydrogen bonds, non-ionic interactions, and dipole interaction between histone-fold helices and phosphate backbone.[7,8]

The next level of genomic compaction occurs through self-assembly of nucleosomes into higher-order chromatin structures. Initially, individual nucleosome core particles (NCPs) thread together with adjacent nucleosome core particles through a linker DNA to form the 11-nm 'bead on a string' template.[9] The 11-nm chromatin template is further compacted into a 30-nm higher-order structure through recruitment of an additional histone protein, H1.[10] The

H1 protein promotes genomic compaction by interactions between its central globular domain (gH1) and nucleosome core particles. There are currently two different models explaining the interaction between gH1 and NCP. First, the symmetric model, which assumes gH1 to bind at the NCP dyad and interact with linker DNA extending from both side of NCP.[11,12] The second model considers gH1 to bind near the dyad and interact with 10-20 bp of linker DNA extending from one side of NCP.[11,13,14]

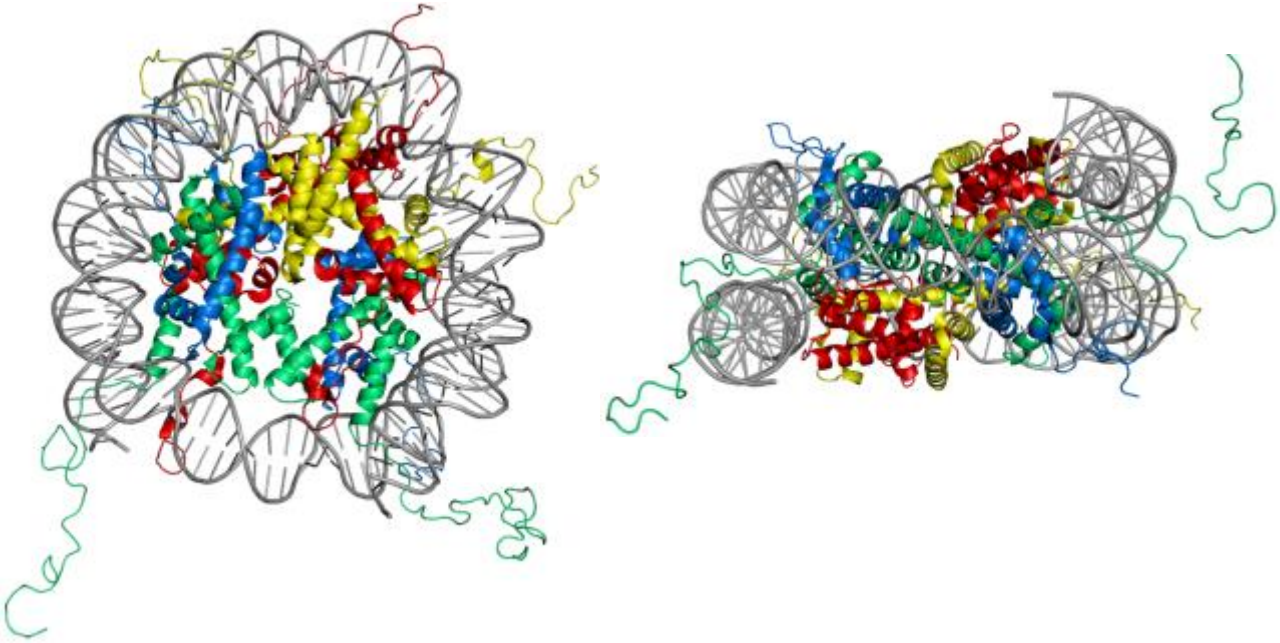


Figure 1. Structure of the nucleosome core particle. The figure on the right shows the top view and on the left shows the side view of nucleosome structure. The histone proteins H2A, H2B, H3, and H4 are shown in red, yellow, green and blue whereas DNA is shown in grey. Adapted from PDB structure: 1KX5.[15]

Despite recent studies having questioned the prevalence of the 30-nm chromatin fiber, structural details regarding the organization of the 30 nm fiber have been one of the most debated topics in chromatin biology.[16,17] Two models have been suggested – the solenoid (one-start) model, wherein sequential nucleosomes are coiled around a helical axis, or the zig-zag (two-start) model, wherein sequential nucleosomes are separated by a zig-zag pattern of straight linker DNA.[18,19] A recent cryo-EM structure of 30 nm fibers shows a left-handed parallel double helix supporting the two-start model proposed by Richmond and colleagues.[20] It is worth-noting that the DNA is compacted only approximately 50-fold by 30 nm fiber and

higher-order re-organization exists for further compaction which are yet to be resolved. The efficiency of DNA packaging in nucleosome can be gauged by the fact that human genomic DNA which spans over a length of two meters is compacted 10000-20000 fold to fit in the cell nucleus.[21]

1.2 Epigenetic mechanisms

The tight compaction of the eukaryotic genomic DNA into chromatin leads to a condensed DNA structure which occludes DNA-binding proteins. However, a rigid chromatin structure can only block DNA-templated processes rather than regulate it. Indeed, chromatin is dynamic in nature and allows DNA-binding proteins selective access to the nucleosomal DNA via different epigenetic mechanisms. These comprise mainly of: 1) Modification of DNA bases,[22,23] 2) Post-translational modification of histone proteins,[24] 3) Introduction of histone variants,[25-28] 4) Nucleosome positioning,[29-32] 5) Non-coding RNA based mechanism.[33-35] In this thesis, we focus on the role of the post-translational modification of histone protein in epigenetics.

1.3 Post-translational modifications (PTMs) of histone proteins

Histone proteins were first found to be acetylated by Allfrey in 1964.[36] Since then a large number of histone protein modifications have been identified using western blotting and mass spectrometry based methods.[37] These include lysine acetylation, acylation with longer chain length acids,[38,39] formylation,[40] methylation,[41,42] sumoylation, and ubiquitination;[43] arginine methylation and citrullination;[44] serine and threonine phosphorylation and GlcNAcylation;[45-47] histidine phosphorylation;[48] glutamine methylation;[49] glutamate and arginine mono- and poly-ADP ribosylation,[24] and tyrosine hydroxylation. The chemical structure of few important and frequently studied histone modifications are shown in **Figure 2**.

Histone PTMs are highly dynamic in nature and are regulated by the opposing catalytic

activity of enzymes. Histone proteins are modified by transferase 'writers' whereas the reverse reaction is catalysed by a variety of 'eraser' enzymes. For example, in the case of histone acetylation, histone acetyltransferases (HATs) 'writers' catalyse acetylation of lysine residues whereas histone deacetylases (HDACs) erase this modification by hydrolysis. It is striking to note the diverse chemical space of the PTMs. PTMs size varies vastly from small modification such as a methyl group to the addition of a whole protein via ubiquitination/sumoylation. PTMs can modulate electrostatics properties of proteins by removing or adding charges as in acetylation or phosphorylation, or they can add hydrogen bonding donors/acceptors such as *O*-GlcNAc. Indeed, these diverse modifications play an important and context-dependent role in epigenetic regulation.

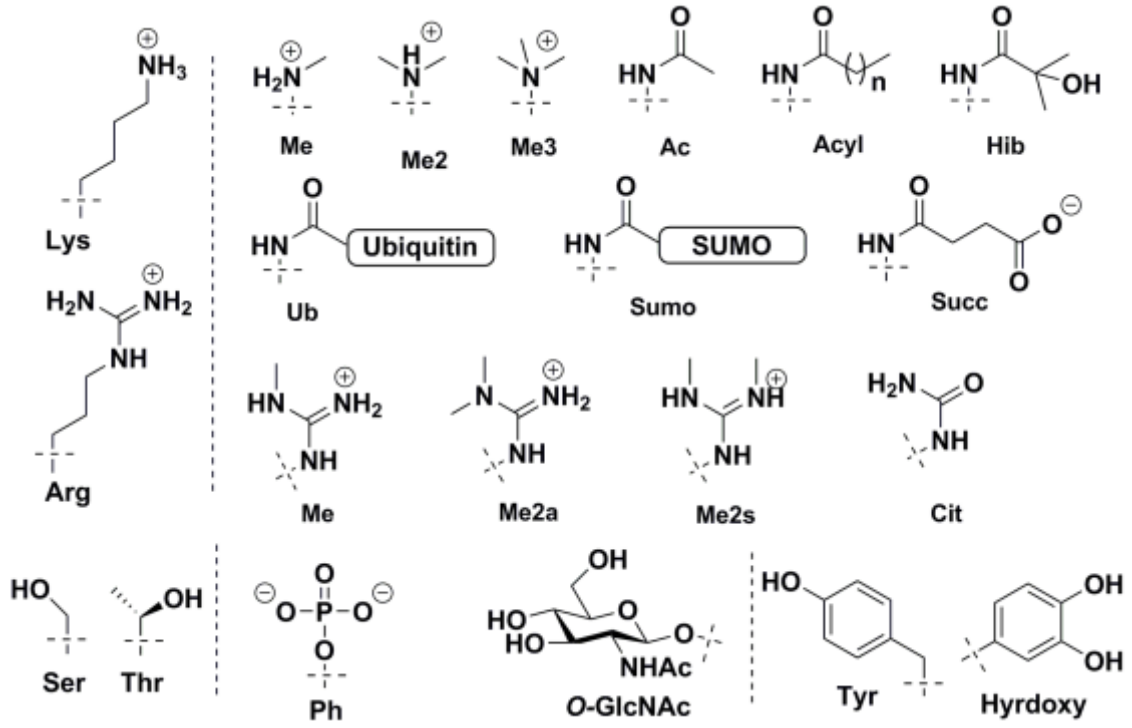


Figure 2. Chemical Structure of commonly observed histone PTMs.

1.3 Role of Histone PTMs in epigenetics

The epigenetic regulation by histone protein modifications, in their own capacity, occurs through two main mechanisms.[50,51] The first mechanism involves modulation of

nucleosome structure/stability upon histone modification.[52] This structure modulation can stem from the changes in histone-fold or histone-DNA interactions. The second and widely prevalent mechanism involves the recruitment of specific reader or effector proteins to the site of modification which either catalyze the functional output of the modification or recruit additional chromatin remodelers.[53,54] Interestingly, different histone protein modifications can also enhance or interfere with their respective signal output (histone cross-talk) to provide an additional layer of complexity to transcriptional regulation.

1.3.1 Nucleosome structural modulation

Histone PTMs can directly modulate the nucleosome structure to a subtle or drastic extent either through electrostatic interactions or via sterics depending on the modification and site **(Figure 3)**.[52] For long, histone acetylation has been associated with a relaxed chromatin state, facilitating transcription, although the extent of this 'relaxation' has just started to be understood.[55] In a simple mechanism, acetylation of lysine residue inhibits the salt-bridge interaction between positively-charged lysine and negatively-charged nucleosomal DNA leading to a less tightly packed chromatin. A more open chromatin environment provides RNA polymerases easy access to the DNA template for transcription. Indeed, in line with this simple mechanism, histone acetylation marks are found to be enriched at enhancer and promoter regions.[56,57] In a recent study, details at the molecular level linking H3K56 acetylation to chromatin accessibility were provided.[58] Separate experiments based on mutational analysis and synthetic nucleosome construct bearing homogeneous acetylation revealed that although acetylation does not affect the nucleosome structure substantially, it does promotes DNA unwrapping leading to nucleosome-free chromatin regions.[58-60] Consistent with this a fluorescence resonance energy transfer (FRET)-based study revealed destabilization of nucleosome structure upon H3K64 acetylation leading to enrichment of the mark at active genes. The destabilization was attributed to reduced histone-DNA interaction.[61] In a slightly different mechanism, acetylation of H4-K91 was shown to destabilize the nucleosome structure by modulating the H2A/B dimer-H3/H4 tetramer interface. This is of special interest

since here it's the steric of the modification rather than electrostatic effect, usually associated with acetylation, which is responsible for the functional output.[62]

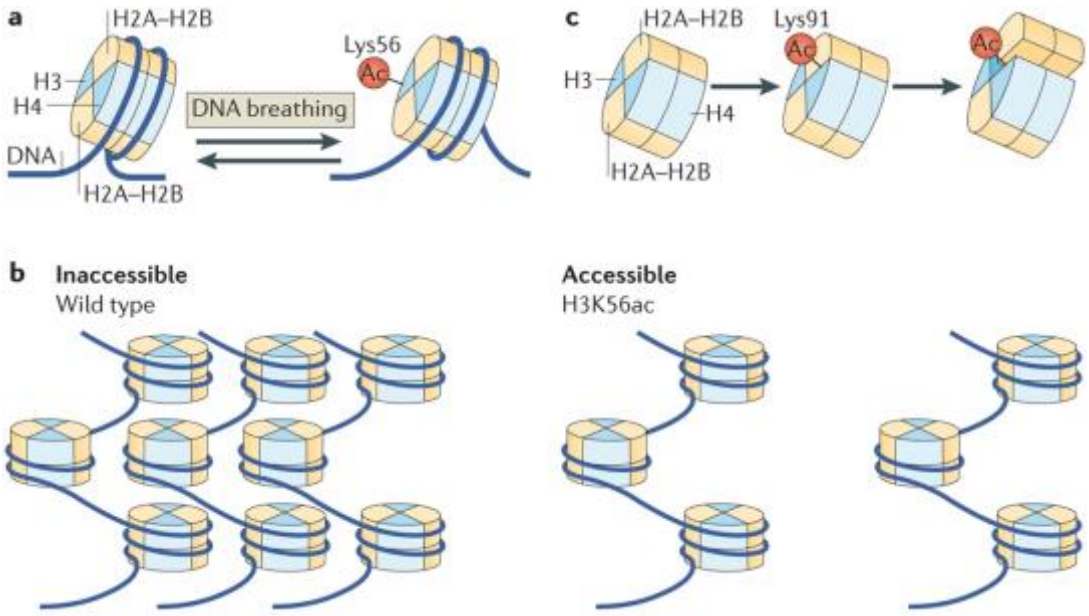


Figure 3. Regulation of nucleosome structure by histone PTMs through histone-histone and histone-DNA interactions. (a) H3K56-acetylation enhances DNA unwrapping by regulating histone-DNA interactions. (b) H3K56-acetylation promotes nucleosome-free higher order chromatin structure. (c) H4K91-acetylation destabilizes the nucleosome structure. (Reproduced from Tessarz et al.[52])

There lies a potential that negative charge introduced on histone protein through modifications such as phosphorylation and ADP-ribosylation can affect histone-DNA interactions mediated by electrostatic repulsion, and thus regulate nucleosome structure. Indeed, phosphorylation of H3T118 site, located in vicinity of nucleosomal dyad (within 3 Å), destabilizes the nucleosome structure.[63] In a study based on *in vitro* nucleosome reconstitutions, North *et al.* reported dramatically reduced DNA-histone binding free energy and decreased nucleosome stability upon phosphorylation of H3T118. In line with destabilized nucleosome structure, a significant increase in DNA accessibility near the nucleosome dyad was found. It is worth-noting that the H3(T118E) substitution, a mutation widely used to mimic phosphates, did not affect the DNA-histone binding free energy or nucleosome mobility.

Interestingly, a separate report from the same group reported formation of an alternative nucleosome structure upon H3T118 phosphorylation highlighting significant structure distortion.[64]

In contrast to these histone PTMs which modulate the charge of amino acids, there are neutral modifications which can modulate nucleosome structure based on their steric properties. Certainly modifications such as ubiquitination and sumoylation can affect histone-histone or histone-DNA leading to conformational change of the nucleosome. In a previous report, it has been speculated that ubiquitin modification of H4K91 likely alters the nucleosome structure by destabilizing the histone dimer-tetramer interface.[65]

Intriguingly, contrary to earlier belief that histone methylation cannot directly perturb nucleosome structure,[50] recent results have shown otherwise. Asymmetric dimethylation of H3R42 residue supposedly affects the histone-DNA interaction by blocking hydrogen bonding. The reduced histone-DNA interaction lowers the overall nucleosome stability and promotes transcription.[66] Similarly, for H3K79 methylation, a subtle reorganization around the modification occurs because of a loss of a hydrogen bond to histone protein, H4.[67]

1.3.2 Recruitment of effector proteins

The second mechanism by which histone PTMs exert their function is by acting as a docking site for numerous chromatin-associated protein complexes.[50,53] These nucleosome-binding complexes contain distinct domains which can recognize specific histone modifications. Often, these protein complexes are multivalent and have more than one domain through which they can recognize several distinct modifications.[68] Once localized to a genomic region by the PTM, these chromatin-associated proteins can recruit other nuclear signaling machinery to catalyze DNA-templated processes.

Of all the histone modifications, protein domains recognizing lysine methylation are best understood and include PHD (plant homeodomain) fingers, ADD (ATRX-DNMT3-DNMT3L), BAH (bromo-adjacent homology), chromodomain and Tudor domains.[69-71] Lysine methylation marks can activate or repress transcription, depending on methylation state and

site of modification. Interestingly, different domains recognizing the same modification can be found in transcription activating or repressing complexes, which suggests a context-dependent readout for the PTMs.[72] For example, H3K4me3, considered to be a gene-activation mark, binds to TFIID through its PHD finger, implicating it in transcriptional activation.[73] However, recognition of the same mark by PHD finger of ING2 links the modification to gene repression.[74] In separate studies, the same modification has also been shown to bind to the tandem chromodomains within CHD1, a chromatin remodeler and to the tandem Tudor domains within JMJD2A, a histone demethylase.[75,76] The recruitment of effector proteins to other methylation marks has been linked to chromatin compaction. In a relevant example, binding of HP1 protein through its chormodomain to H3K9me3 modification, a repressive mark, has been found to affect the heterochromatin structure.[77,78]

Histone acetylation can be recognized by three different reader domains: the bromodomain[79,80], the double PHD finger (DPF) of DPF3b protein and the double pleckstrin homology (PH) domain of the histone chaperone Rtt106 can also specifically recognize acetylated histones.[81-83] Similarly, there are reader domains such as 14-3-3 and BRCT for phosphorylated histone proteins.[84,85]

1.3.3 Histone Cross-talk

In a biologically-relevant context, nucleosomes are decorated with different histone modifications at multiple sites, rather than bearing a single histone modification.[86] Given the number of possible histone modifications and modification sites available on nucleosome, the number of potential combinations is astronomical. These modification combinations can potentially act as a mechanism for tighter control of chromatin regulation, where a *'codon'* of modifications can translate a certain epigenetic state. Different modifications can work in a cohort and interact with each other ('*cross-talk*') to provide an extra-layer of genomic regulation.[87]

There are various mechanisms possible for this histone cross-talk.[50,51,88-90] In one of the simplest mechanisms, two or more different histone modifications can compete for the

same modification site leading to a competitive antagonism to define the epigenetic state. This kind of cross-talk can operate for histone residues which are capable of different modifications such as lysine which can undergo different modifications such as acetylation, (mono, di-, and tri-) methylation, ubiquitination, various acylations, and sumoylation in a context-dependent manner.

In a different mechanism, the state of modification at one site can promote or inhibit modification at other site. Previous studies have shown that ubiquitination of H2BK123 by Rad6 enzyme is a necessary condition for H3K4 methylation catalyzed by the COMPASS sub-complex and H3K79 methylation mediated by the Dot1 methyltransferase.[91,92] In a similar fashion, H3S10 phosphorylation mediated by the Snf1 kinase is known to promote H3K14 acetylation by the Gcn5 acetyltransferase, enhancing gene activation.[93] Daujat *et al.* have previously shown that acetylation at H3K18 and H3K23 induces the methylation of H3R17 residue by the CARM1 methyltransferase, resulting in activation of estrogen responsive genes.[94] Note that in the last two examples, histone modification of one site promote other modification on the same histone protein (*cis*-histone effect), whereas in the first example, the modification of one histone proteins affects modification of a different histone protein (*trans*-histone effect). However, the modifications can also be negatively cooperative. In one of the classical examples of histone cross-talk, H3S10 phosphorylation inhibits binding of HP1 protein to di- and tri-methylated H3K9 during mitosis.[95] Similarly, H3K4 acetylation inhibits binding of Chp1 protein to di- and tri-methylated H3K9 in yeast to regulate heterochromatin assembly.[96]

Alternatively, different histone modifications can jointly amplify the binding efficiency of effector proteins. Using MS-based quantitative interaction proteomics, Vermeulen *et al.* showed that the binding of PHF8 to H3K4me3 is stronger in presence of acetylated H3K9 and H3K14.[97] Apart from cross-talk between histone proteins, there can be a cross-talk between modifications of histone protein and nucleosomal DNA. In an earlier report from the Kouzarides group, the binding of UHRF1 protein to methylated nucleosome was shown to be significantly enhanced upon CpG methylation of nucleosomal DNA.[98]

1.4 Research goals of this thesis

The overall goal of my doctoral work was to use the tools of chemical biology to decipher how different posttranslational modifications of histone proteins function in epigenetic regulation. Special emphasis was given to understand the role of *O*-GlcNAcylation in transcriptional regulation; since not much is known about the functional consequence of this recently discovered histone modification.[46,47,99] In the past, most chromatin research to understand the role of histone PTMs has relied on the use of synthetic histone peptides. However, these peptides are mere fragments of the physiologically-relevant substrate, the nucleosome, and cannot be used to investigate epigenetic processes which rely on the multivalency arising from histone-histone and histone-DNA interactions.[100,101] Thus, emphasis has been placed on developing new chemical methods that can lead to ready synthesis of modified histone proteins in useful quantities, which in turn can be assembled into designer nucleosomes. Currently, the generation of modified histone proteins relies on three different approaches: 1) Nonsense-suppression mutagenesis, 2) Chemical ligation based protein synthesis, and 3) Post-translational protein chemical modification.

Histone PTMs can be site-selectively installed in form of '*unnatural amino acids*' (UAAs; natural amino acids with desired modification) during translation using nonsense-suppression mutagenesis.[102] The approach involves engineering an evolved orthogonal tRNA/tRNA synthetase pair into the expression system (*E.coli*, yeast, human). This engineered pair recognizes the desired UAA, and incorporates it into the recombinant protein in place of nonsense codon. Chin and co-workers have extensively used this technique to incorporate various lysine PTMs in histone proteins.[103-105] Although, the technique is simple and often scalable in moderate yields, the limitation lies in the fact that for each PTM, a new pair of tRNA/tRNA synthetase needs to be evolved, which can be time consuming if not impossible.

Native chemical ligation based protein (semi- and total) synthesis methods have been the workhorse for generation of modified histone proteins required to study chromatin

biology.[101,106,107] Total synthesis of a protein relies on assembling the different peptide fragments of the protein by the ligation reaction between thioester on the *C*-terminal of one peptide with cysteine on the *N*-terminal of second peptide. These peptide fragments are synthesized using standard solid-phase synthesis, and in principle can be decorated by any number of desired PTMs leading to synthesis of multiply modified histone proteins. However, despite the control and flexibility provided by this approach, the method is marred due to the difficulty in accessing long peptide fragments which leads to time consuming, low yielding multiple ligation reactions between smaller peptide fragments. To overcome this limitation, semi-synthesis of protein was envisaged. In this approach, a small synthetic peptide bearing the desired histone PTM is ligated with a recombinantly expressed protein fragment. The protein semi-synthesis approach is well-suited to study histone PTMs occurring on either the *N*- or *C*- terminal of the protein. As would be expected, the downfall of this approach lies in the generation of histone protein wherein the modification lies far-away from either terminus.

The post-translational protein chemical modification strategy to generate modified histone protein depends on the presence of a 'tag' with unique reactivity. Usually, this unique reactivity is provided by a cysteine residue due to its inherent nucleophilicity and redox behavior. Note that the only cysteine residue found in histone protein family is the highly conserved Cys110 in histone protein H3, which is usually mutated to alanine for most chromatin research. In such a scenario, a cysteine residue is often incorporated as a 'tag' at the desired site of modification, and is later reacted to synthesize modified protein. The promise of this method was first demonstrated by Shokat and co-workers who used the alkylation reactions of cysteine residue to produce mimics of methylated lysines.[108] Work from different groups also exploited the ability of cysteine residue to undergo the thiol-ene reaction to install mimic of acetylated lysine and methylated arginine.[109,110] It is worth-noting that all these analogues bear an unnatural thioether linkage, however, despite that these analogues have proved extremely valuable to reveal the functional outcome of various histone PTMs.[111-113] However, the reactions of cysteine discussed earlier cannot be used for synthesis of GlcNAcylated or phosphorylated histone proteins. Previous work in Davis group has overcome

this limitation by ready synthesis of dehydroalanine (Dha) 'tag' starting from a cysteine residue.[114-116] Dha 'tag' can undergo Thia-michael reaction to generate differently modified histone proteins including the GlcNAcylated and phosphorylated proteins.

In this thesis, we applied protein chemical reactions to synthesize homogeneously modified histone proteins, which were then used to study the effect of PTMs on nucleosome biophysics and the nucleosome interactome. For the study of histone *O*-GlcNAcylation, three different modification sites were chosen (Chapter 2, 3, 4). All three sites were situated on distinct nucleosome surfaces, raising the possibility of context-dependent functional outcome. The effect of the modifications on the nucleosome structure was probed using different biophysical methods, including circular dichroism spectroscopy and native mass spectrometry.

Recent advances in quantitative mass spectrometry has made it the method of choice for studying the 'reader/effector' proteins for modified nucleosome, over traditional western-blotting based methods.[37,117] We applied MS-based affinity proteomics to identify putative interaction partners for modified nucleosomes based on which we could propose a molecular mechanism for the functional output.

In the last chapter, we envisioned to study the cross-talk between *O*-GlcNAcylation and phosphorylation. Use of dehydroalanine as a chemical handle to readily install different chemical modifications proved effective, and could potentially be used for study of any such cross-talk.

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2. Synthetic nucleosome construction reveals interaction of FACT modulated by histone H2B-Ser112 GlcNAcylation1†

2.1 Introduction

As previously discussed, the chromatin dynamics of eukaryotes is regulated, in parts, by post-translational modifications (PTMs) of histone proteins.[2-4] One of such histone PTM is *O*-GlcNAcylation, the addition of *O*-linked β-*N*-acetylglucosamine (*O*-GlcNAc) to serine and threonine residues. Although this modification has been observed on all canonical histone proteins[5-7], comprehensive details of its effect on chromatin reorganisation remain elusive. O-GlcNAcylation is catalysed by a single *O*-GlcNAc transferase (OGT) enzyme and is removed by one *O*-GlcNAcase (OGA) enzyme. This single set of enzymes (OGT and OGA) is also responsible for the *O*-GlcNAc modification of all cytosolic and nuclear proteins.[8] The modification has been shown to be nutrient sensitive; with level of modification fluctuating in response to extracellular glucose.[7] Deregulation of O-GlcNAc has been linked to neurodegenerative diseases, cancer and diabetes.[9,10] In this chapter, we describe our study on the effect of *O*-GlcNAcylation on a known histone modification site, H2B-Ser112. We show that GlcNAcylation at H2B-Ser112 leads to preferential binding of FACT (Facilitates Chromatin Transcription) complex to GlcNAcylated nucleosome providing a plausible molecular mechanism for its role in transcriptional activation.

2.1.1 H2B-Ser112: Proximity to Acidic Patch

H2B-Ser112 was described as an *O*-GlcNAc modification sites by Fujiki *et al.*[7] along with Ser-91 and Ser-123 on H2B. H2B-Ser112 resides on the disk face of the histone octamer being located on the αC helix of H2B. This residue is in close proximity of the nucleosome 'acidic patch' **(Figure 1)**. The 'acidic patch' is a negatively-charged region of the nucleosome surface, comprising of eight acidic residues (E56, E61, E64, D90, E91, E92 of H2A and E102,

† The results described in this chapter has been published at the mentioned citation.

E110 of H2B).[11] The 'patch' forms a groove, large enough to accommodate a range of protein binding motifs. With the highest negative charge density of the solvent-accessible octamer disk face along with hydrophobic features along the bottom of the groove, the acidic patch presents an ideal interface for possible docking of chromatin remodeling factors. Indeed, a large number of nucleosome-binding proteins such as LANA[12], IL-33[13], RCC1[14], Sir3[15], CENP-C[16], HMGN2[17], RNF168[18] and RING1B/BMI1[18] as well as the H4 tail[19] are known to interact competitively with the 'acidic patch' leading to remodeling of chromatin structure. From earlier work, H2B-Ser112-*O*-GlcNAc has been linked to transcriptional activation *via* promotion of H2B-Lys120 ubiquitination.[7] We wondered if the *O*-GlcNAcylation modification in the vicinity of acidic patch could possibly modulate binding of certain chromatin remodeling factors leading to the earlier observation.

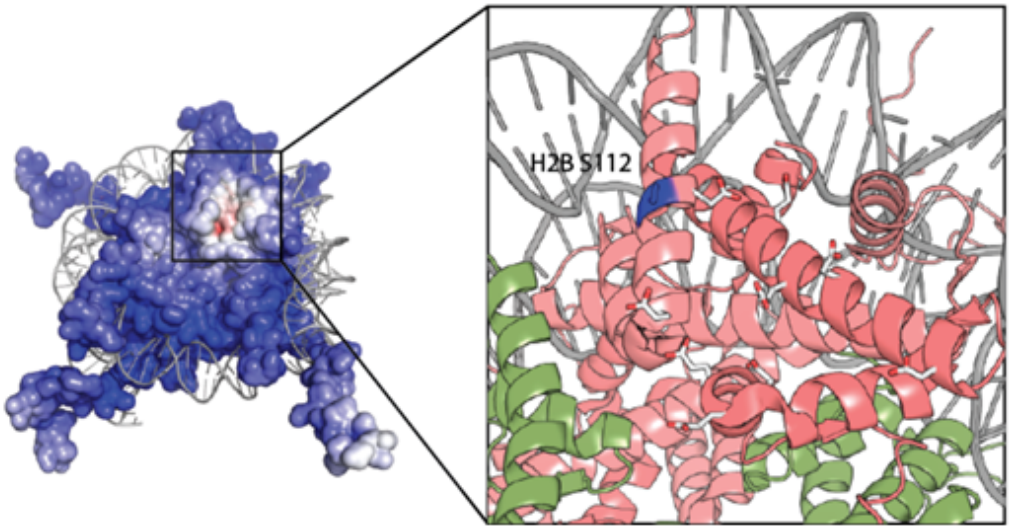


Figure 1. The nucleosome acidic patch. Electrostatic potential view of the nucleosome was generated using ABPS tools in PyMol. Blue denotes positively charged octamer surface, whereas red denotes negatively charged octamer surface; inset shows the location of H2B-S112 residue along with other acidic residues comprising the acidic patch. (Reproduced from Raj *et al.*[1])

Histone PTMs usually establish their functional consequence mainly either through direct modulation of nucleosome structure or via recruitment of chromatin 'reader'/ interactor proteins identifying the modification.[3] Given the location of H2B-Ser112 residue on the disk face of the nucleosome, it seems highly unlikely that the *O*-GlcNAc modification at the site will

perturb the nucleosome structure significantly, suggesting protein recruitment as it's likely consequence. We confirmed this hypothesis through step-wise creation and characterization of synthetic nucleosome GlcNAcylated at site H2B-Ser112. Traditionally, identification of nucleosome-binding protein partners has relied heavily on Western blotting approaches, however Mass spectrometry (MS)-based proteomics provides a powerful and unbiased alternative.[20-22] In this chapter, we report our results of an interaction proteomics approach **(Figure 2)** towards identification of H2B-S112 GlcNAc interactor proteins. Based on the proteins identified, we propose a molecular mechanism linking the modification to transcriptional activation.

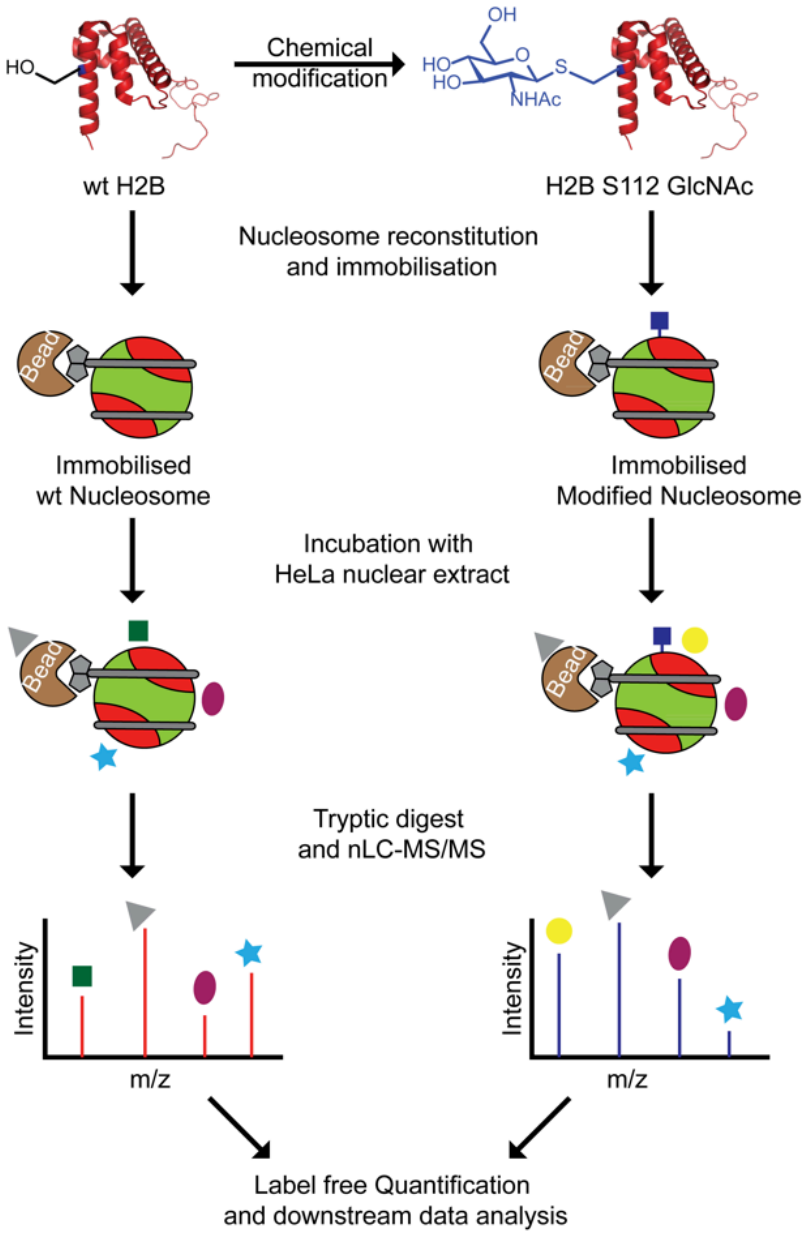


Figure 2. Interaction proteomics approach for identification of H2B-S112 GlcNAc interactor proteins. H2B-S112 GlcNAc protein was synthesized using a "tag-and-modify" approach. The modified histone protein (along with other canonical histone proteins and biotinylated DNA (shown in grey)) were used for nucleosome reconstitution. Wildtype (wt) and GlcNAcylated nucleosome (modified) were immobilized on magnetic beads (brown) *via* streptavidin-biotin affinity to enrich nucleosome binding proteins. Pooled proteins from each sample were separately digested and identified by nanoLC-MS/MS. MS-based Label-free Quantification (LFQ) was applied for relative quantification. H2A/B dimers shown in red, H3/H4 tetramer shown in green, GlcNAc shown as a blue square. (Reproduced from Raj *et al.*[1])

2.2 Results and Discussion

2.2.1 Synthesis of H2B-Ser112 GlcNAc

Accessibility to homogeneous, site-specifically modified histone proteins is central to the identification and characterization of nucleosome-binding proteins. Enzymatic reactions can be used for synthesis of modified histone proteins, however the difficulty in scale-up poses a serious limitation. Chemo-enzymatic synthesis of GlcNAcylated histones is also hindered due to the promiscuous nature of OGT.[7] In general, despite advances in chemical as well as chemo-enzymatic syntheses access to homogeneous glycoproteins still remains a bottleneck.[23-26] Currently, three approaches have been routinely used for syntheses of modified histone proteins: 1) non-sense suppression mutagenesis, 2) semi-synthetic approaches, and 3) reactions at site-selectively installed cysteine residue.[27] Unfortunately, there is currently no method for the synthesis of *O*-GlcNAcylated histone proteins using non-sense suppression mutagenesis.[28] While chemical ligation based semi-synthetic approaches e.g. Native Chemical Ligation (NCL) and Expressed Protein Ligation (EPL), can be used for precise installation of the desired modification, these methods demand synthesis and purification of the required peptide/protein fragments that may prove challenging. The utility of semi-synthesis methods are often limited in cases where modifications lie far-way from either protein terminals. However, total protein synthesis methods can overcome these limitations, and can be potentially used for synthesis of modified proteins. Previous work in the Davis group has used the inherent reactivity of cysteine residue for site-selective chemical protein

modification. A large number of differently modified functional proteins, including GlcNAcylated histones have been generated using the "tag-and-modify" approach.[29-31] "Tag-and-Modify" approach is a two-step protein modification method relying on installing a uniquely reactive chemical species ("tag") followed by site-selective modification of the "tag". These "tags" can be any chemical residue possessing biorthogonal reactivity varying from natural amino acid such as cysteine; genetically encoded unnatural amino acids such as azidohomoalanine (Aha), homoallylglycine (Hag) or homopropargylglycine (Hpg); or a chemically derived amino acid such as dehydroalanine (Dha). In this work, we have used dehydroalanine (Dha) as a "tag" which can be readily synthesized starting from a cysteine residue on the protein. Installation of Dha moiety on the protein surface proceeds through bis-alkylation of cysteine residue followed by subsequent elimination. Dha, being nucleophilic in nature, can be selectively modified using a Thia-michael addition of an appropriate thiol resulting in the synthesis of modified proteins. While direct alkylation or radical reactions of cysteine has been used to install PTMs like lysine methylation and acetylation, this two-step approach provides new routes for modifications such as glycosylation and phosphorylation.[32-36] This approach was used to synthesize H2B-S112-GlcNAc protein which was later utilized for the reconstitution of site-specifically GlcNAcylated nucleosomes **(Figure 3)**.

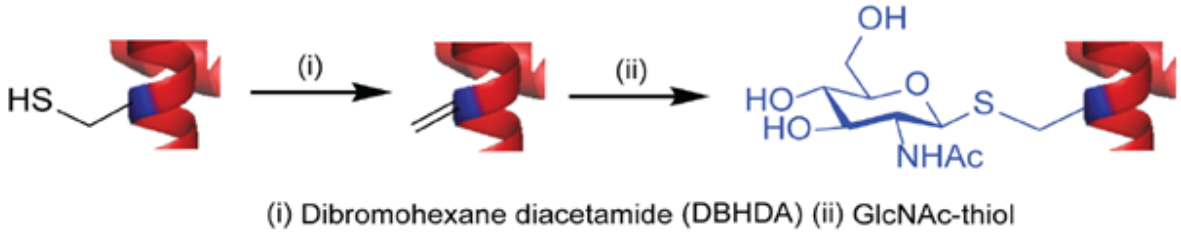


Figure 3. Scheme for synthesis of GlcNAcylated-H2B-S112 using "Tag-and-Modify" approach. (Reproduced from Raj *et al.*[1])

Towards site-selective synthesis of GlcNAcylated H2B, a Ser112Cys (S112C) mutant of the *Xenopus laevis* H2B protein was designed.[37] The protein was expressed in *E. coli* in good yield as inclusion bodies. It was purified by Size-exclusion and Ion-Exchange chromatography. Dha "tag" was site-selectively installed at Cys112 by treating H2B-S112C

protein with 90 equivalents of 2,5-dibromohexanediamide (DBHDA)[30] under denaturing conditions. Initially the reaction was incubated at room temperature for half an hour leading to mono- and bis-alkylation of cysteine. Later the reaction was incubated at 37 °C to facilitate the elimination of cyclic intermediate leading to formation of H2B-S112Dha intermediate protein. The resulting intermediate protein was reacted with 400 equivalents GlcNAc-thiol under denaturing conditions to yield H2B with a GlcNAc mimic installed at S112 **(Figure 4)**.

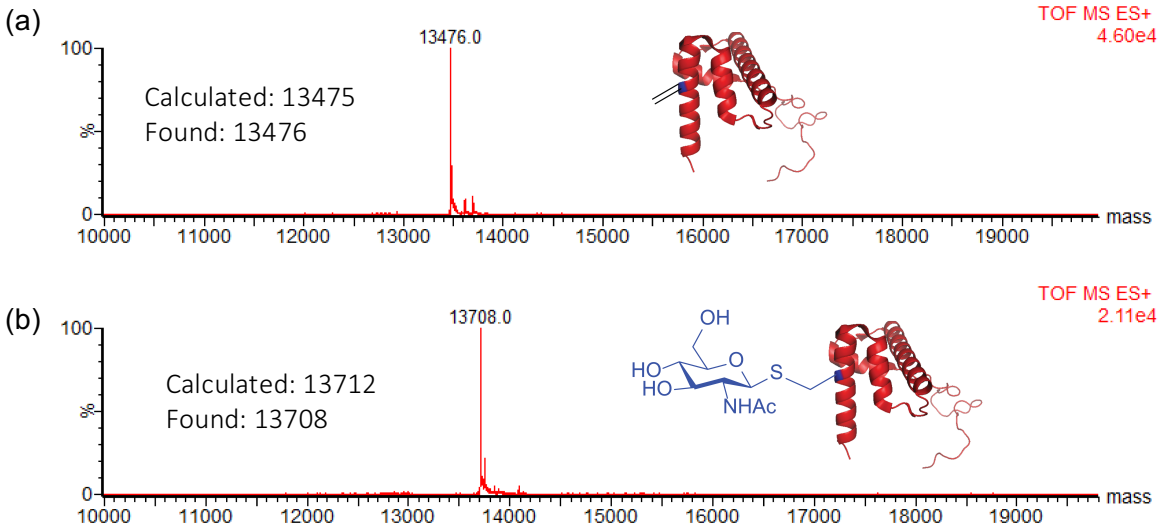


Figure 4. Step-wise synthesis of H2B-S112 GlcNAc protein. (a) LC-MS spectrum of H2B-S112Dha protein. (b) LC-MS spectrum for H2B-S112 GlcNAc protein. (Reproduced from Raj *et al.*[1])

The approach used here is simple and elegant, however, not without limitations. Since the reaction proceeds through a planar Dha intermediate, the Thia-michael addition can occur from either faces of Dha resulting in likely epimeric mixtures. Although, it can be speculated that inherent chirality of the protein can promote one stereochemistry over the other.[38] In the present case as the reaction is done under denaturing conditions, it is most likely that the modified protein consists of equimolar mixture of D- and L- isomers at the site of modification. Secondly, the modified protein bears a thioether linkage instead of the natural ether linkage. Earlier works have shown that despite the replacement of oxygen atom by a larger sulphur atom, the conformation of the glycosidic bond remains similar.[39,40] The unnatural linkage also enhances stability, since it is not processed easily by natural enzymes (here, OGA), thus

increasing the over-all efficacy of it as an affinity probe in enzymatically-active systems.

With the modified protein in hand, the site-specific, homogeneous nature of modification was verified by LC-MS/MS analysis. The modified protein was proteolytically digested using trypsin. The resulting peptide mixture was separated and analyzed on an UHPLC (Ultra-high performance liquid chromatography) coupled to a hybrid Ion Trap-Orbitrap mass spectrometer. MS/MS analysis of intact glycopeptide is challenging owing to the labile nature of the glycosidic bond during commonly used collision-based fragmentation methods (Collision-induced dissociation (CID) & Higher-energy collisional dissociation (HCD)).[41] The loss of glycan information during MS2 fragmentation hinders the simultaneous site-localization and glycan identification of glycopeptides. Electron-transfer dissociation (ETD) fragmentation can be the method of choice for glycopeptide analysis as it fragments only the peptide backbone leaving the glycan on side-chain intact. However, data acquisition based solely on ETD provides lower sequence coverage and is not ideal for complex samples.[42] Hence, a hybrid method combining HCD and ETD was optimized for glycopeptide analysis, which confirmed the site-selective nature of the modification **(Figure 5)**.[43,44] In this *HCD-PD-ETD* (PD: Product dependent) method, glycan signature peaks arising from HCD fragmentation are specified for triggering ETD fragmentation of precursor ion, thus allowing ETD fragmentation of only glycopeptides. By doing so, the method improves the dynamic range of analysis as well as decreases the rate of false positives.

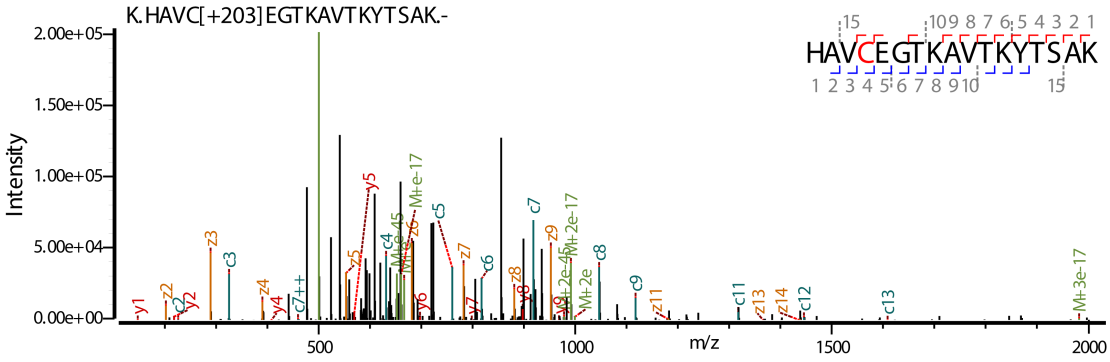


Figure 5. ETD MS/MS Spectrum of H2B-S112 GlcNAc peptide confirming site-selective nature of modification. (Reproduced from Raj *et al.*[1])

To investigate the effect of GlcNAcylation on protein structure, circular dichroism (CD) spectra of wild-type and GlcNAc modified protein was recorded. The proteins were refolded by dialysis against low-salt buffer. CD spectra of refolded H2B-S112 GlcNAc protein displayed similar ellipticity at *'signature'* wavelengths (208 and 222 nm) as compared to wt H2B protein indicative of no gross change in secondary structure of protein upon modification **(Figure 6)**.

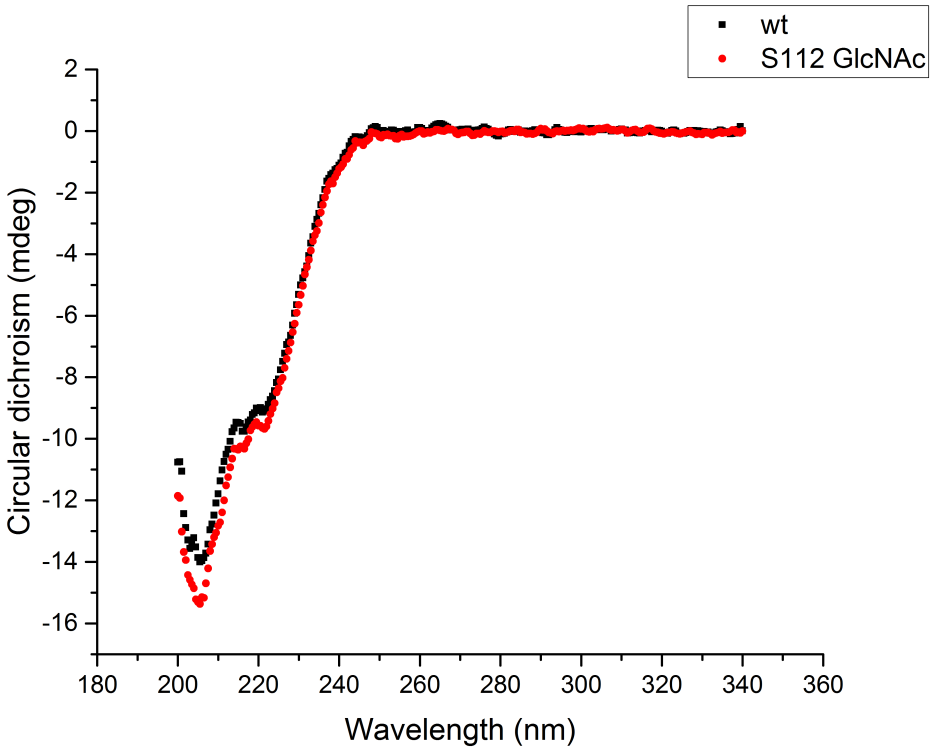


Figure 6. CD spectra of refolded wt H2B monomer (black) and H2B-S112 GlcNAc monomer (red). (Reproduced from Raj *et al.*[1])

2.2.2 Formation and Stability Assessment of Histone Sub-complexes

In an effort to understand the effect of GlcNAcylation on the nucleosome structure, we synthesized modified nucleosome in a step-wise manner.[37] First, H2B-S112 GlcNAc protein was mixed with wt histone protein H2A in equimolar ratio under denaturing condition. The proteins were refolded by dialyzing against high-salt buffer to form GlcNAc-modified H2A/H2B heterodimers. High ionic strength (2M NaCl) in the refolding buffer neutralizes the highly positively charged individual histone proteins and facilitates histone sub-complex formation.[45] In a similar fashion, GlcNAc-modified octamers were refolded by assembling modified H2B

protein with other wt canonical histone proteins H2A, H3, and H4. The resulting histone sub-complexes were purified from higher-order aggregates and residual histone proteins by size-exclusion chromatography (SEC). SEC is routinely used to analyze histone sub-complexe formation. Similar retention volume and overlapping SEC traces for both modified dimer and octamer when compared to the wt species suggested that the structure of dimer and octamer were not disrupted upon introduction of GlcNAcylation at H2B-S112 **(Figure 7)**.

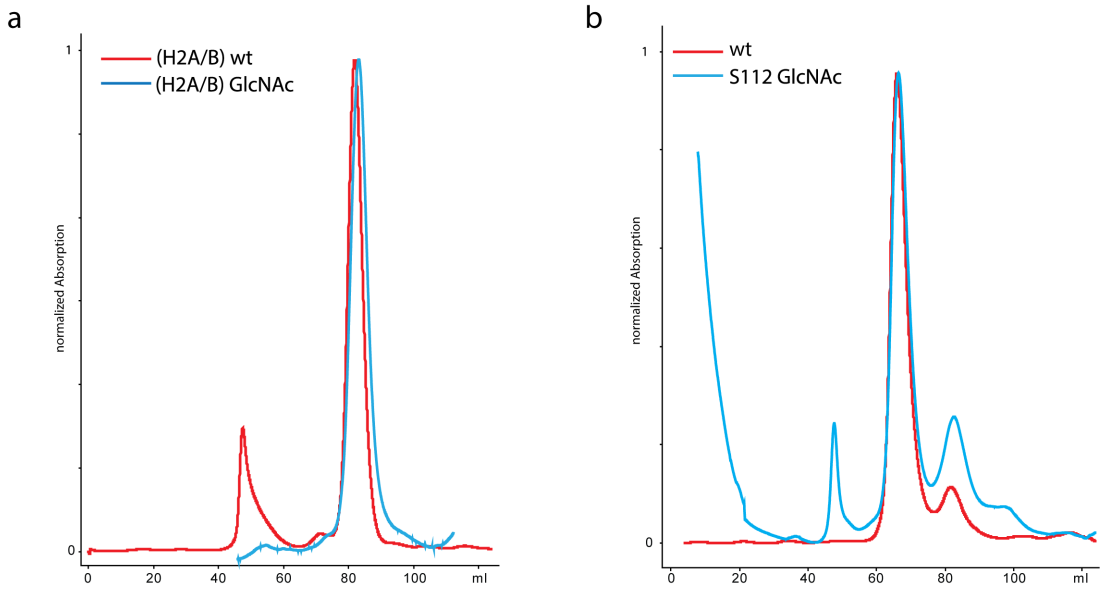


Figure 7. Reconstitution of wt and H2B-S112 GlcNAc modified histone complexes. (a) Overlapped size exclusion traces of wild type (red) and H2B-S112 GlcNAc modified dimer (blue). (b) Overlapped size exclusion traces of wild type (red) and H2B-S112 GlcNAc modified octamer (blue). (Reproduced from Raj *et al.*[1])

The structure of reconstituted dimers was also examined by CD experiments. Similar CD spectra of wt and GlcNAcylated species confirmed that the histone-fold remains identical despite the modification at H2B-S112 **(Figure 8)**. The melting temperature, measured by variable temperature CD analysis, of the GlcNAcylated H2A/H2B dimer was similar to that of the wt dimer (H2B-S112 GlcNAc dimer, T_m = 50.73 ± 0.27 °C; wt dimer, T_m = 52.9 ± 0.1 °C).[46] Based on SEC and CD results, it can be concluded that GlcNAcylation at H2B-S112 has little or no influence on the structure and stability of histone sub-complexes **(Figure 9)**.

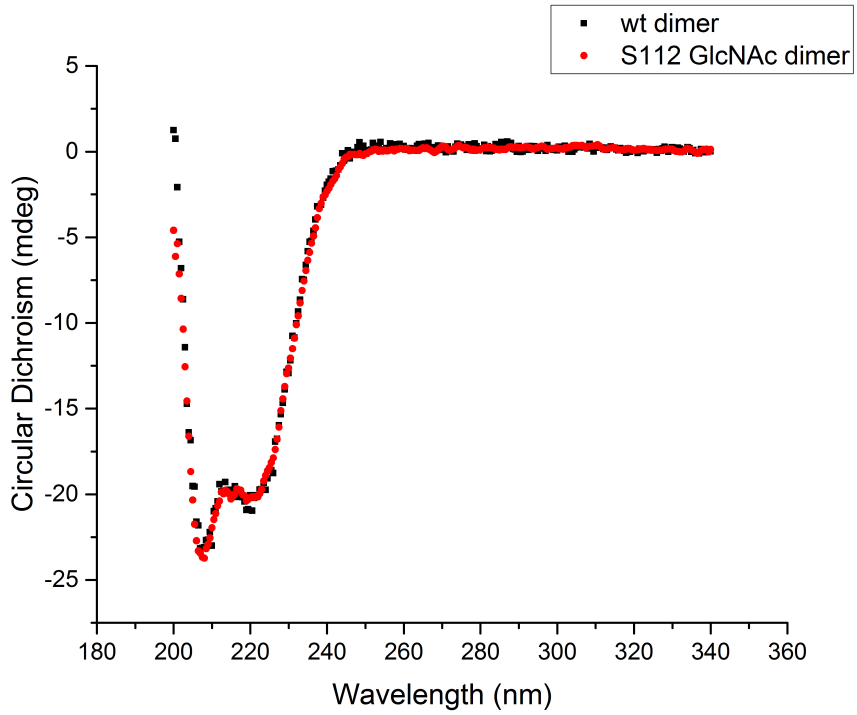


Figure 8. CD spectra of refolded wt H2A/B dimer (black) and S112 GlcNAc modified dimer (red). (Reproduced from Raj *et al.*[1])

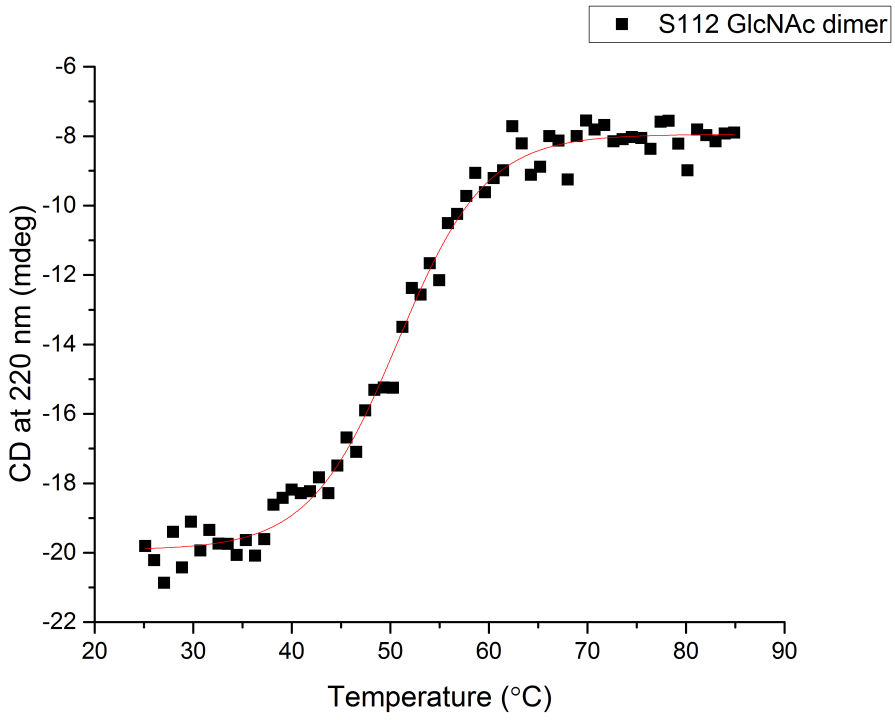


Figure 9. Melting curve for H2B-S112 GlcNAc dimer measured by variable-temperature CD analysis. The melting temperature was extracted by monitoring the CD at 220 nm. (Reproduced from Raj *et al.*[1])

2.2.3 Reconstitution of nucleosome and its stability

With access to wt and modified octamers, nucleosome were reconstituted by the salt-gradient dialysis method using 145 bp DNA fragment containing the strong '601' nucleosome positioning sequence.[21,47] The '601' sequence is a synthetic DNA sequence discovered by Lowary and Widom with high affinity for the histone octamer. The high affinity of the octamer for the 601 sequence results in high yields and homogeneous nucleosome reconstitutions. The 601 DNA was expressed in *E.Coli* cells and purified by alkaline lysis method. To improve the overall DNA yield, a plasmid containing multiple repeats of 601 sequence was used.[48] Nucleosome were reconstituted by mixing the purified DNA with earlier refolded octamer in a buffer with high ionic strength (2M NaCl) and subsequently dialyzing the mixture against a buffer with lower ionic strength. Initially, titration experiments were performed to determine the correct DNA : octamer ratio for reconstitution purposes. Excess octamer can lead to unnatural higher-order structures whereas too little octamer can lead to lower reconstitution yields. The reconstitution of nucleosomes were monitored using SDS-PAGE and native PAGE gels **(Figure 10)**.

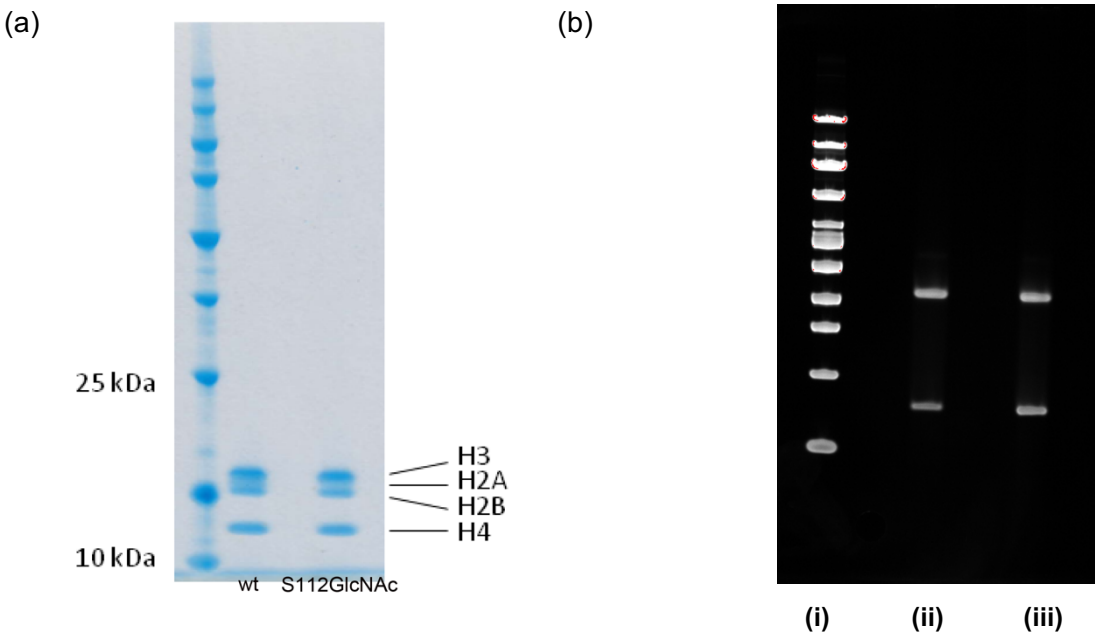
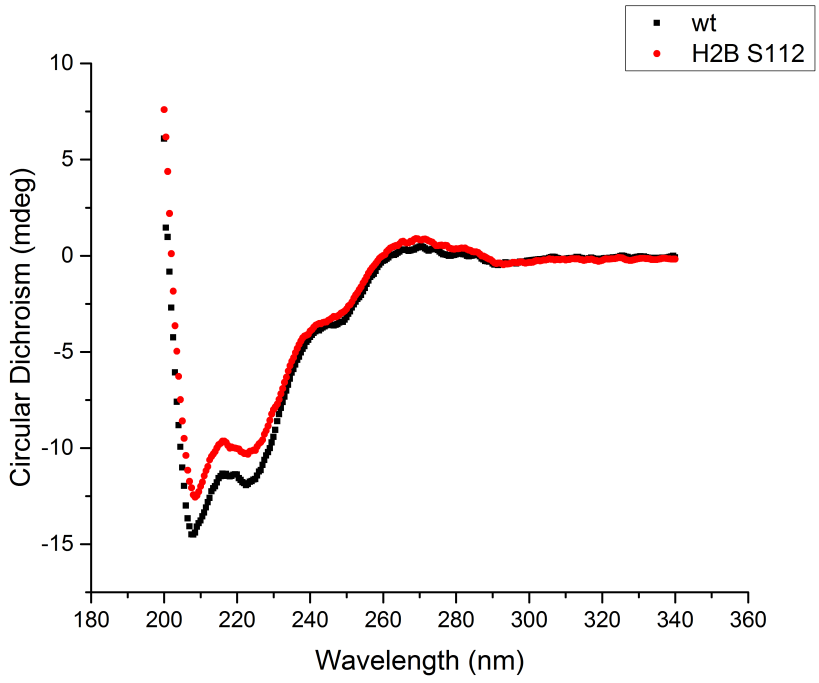


Figure 10. PAGE analysis of nucleosome reconstitution using 145 bp DNA. (a) SDS-PAGE analysis of reconstituted nucleosomes showing stoichiometry of the constituent histone proteins. (b) Native-PAGE analysis of reconstituted nucleosomes. The gel on left has been

stained by SYBR Gold and on right by Coomassie Brilliant Blue. Lane (i) shows 100 bp DNA ladder, lane (ii) shows wt nucleosome, and lane (iii) shows GlcNAc-modified nucleosome. (Reproduced from Raj *et al.*[1])

Similar reconstitution yield and mobility on the PAGE gel was observed for reconstituted nucleosomes indicating no major structural changes upon introduction of the modification, as would be expected for a surface-exposed site. Wt and modified nucleosomes were further analyzed by CD spectroscopy to asses structure and stability. Using CD-based variable-temperature analysis one can simultaneously follow both protein and DNA melting by measuring ellipticity at 220 and 260 nm respectively. For CD studies, nucleosomes were freshly reconstituted using 145 bp DNA. The CD spectra for both the reconstituted nucleosomes were similar suggesting no significant change in structure upon modification **(Figure 11)**. The melting temperatures measured by variable temperature CD analysis were similar (at 220 nm: wt nucleosome, T_m = 73.25 ± 0.61 °C, GlcNAcylated nucleosome, T_m = 74.63 ± 1.16 °C; at 260 nm: wt nucleosome, T_m = 71.86 ± 0.25 °C, GlcNAcylated nucleosome, T_m = 70.63 ± 0.36 °C) suggesting that the modification does not influences the stability of the nucleosome **(Figure 11)**. These combined data confirm that the functional outcome of the modification at this site is not governed by the structure modulation of the nucleosome.

(a)



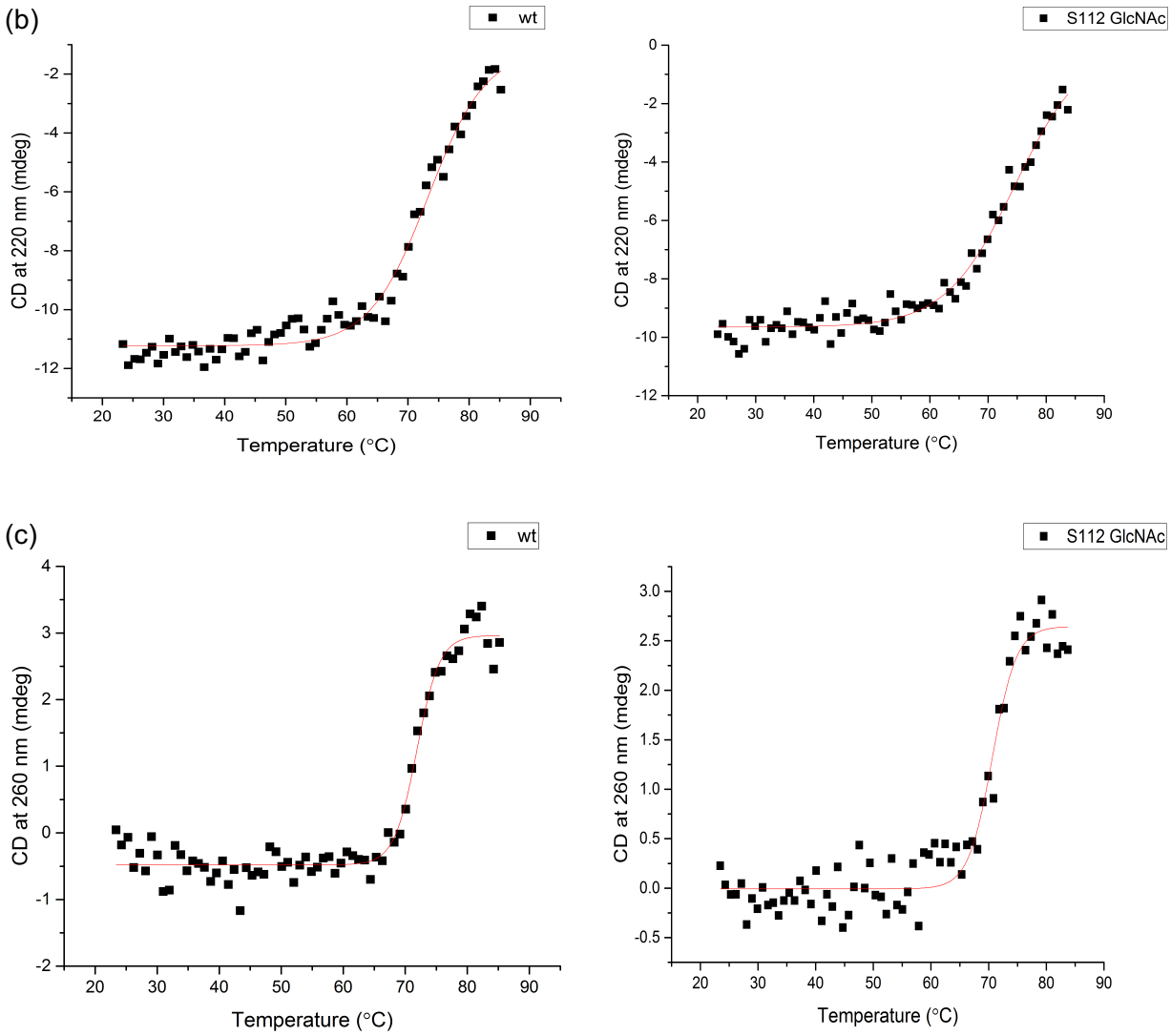


Figure 11. Structure and stability assessment of reconstituted wt and modified nucleosomes by CD analyses. (a) CD spectra of wt nucleosome (black) and H2B-S112 GlcNAc modified nucleosome (red). (b) Melting profile of wt and modified nucleosome monitored at 220 nm. (c) Melting profile of wt and modified nucleosome monitored at 260 nm. (Reproduced from Raj *et al.*[1])

2.2.4 Affinity Enrichment MS-based Proteomics with GlcNAcylated Nucleosome

MS-based techniques have been elegantly used to study protein-protein interactions. However, there has been a paradigm shift in the identification of interacting protein partners using MS over time.[22] Rather than using protein of interest to affinity purify few interacting protein partners, focus has shifted to affinity enrich the interacting proteins. Affinity enrichment approach coupled with advanced quantitative mass spectrometry leads to more precise

determination of interacting partners as well as retains protein partners with lower binding affinity which would have been lost otherwise in affinity purification method.

Here, a similar approach was used to affinity enrich interacting protein partners for GlcNAcylated nucleosomes followed by identification and quantification by MS-based proteomics. As illustrated in Figure 2, biotinylated DNA was used to reconstitute and immobilize the H2B-S112-GlcNAc-modified nucleosome (bait) and wt nucleosome (control). The biotinylated DNA fragment used is a 186 bp long DNA sequence containing the '601' sequence. The DNA was synthesized starting from a plasmid encoding 16 repeats of DNA sequences ligated between EcoRI and EcoRV restriction sites.[21] The DNA was excised and purified from plasmid DNA similar to the 145 bp DNA. The DNA was then digested with EcoRI to generate overhangs, which were then filled in with biotin-11-dUTP using Klenow (3´ to 5´ exo$^-$) polymerase, yielding biotinylated DNA fragments. Nucleosome reconstitution was accomplished as earlier using the salt-gradient dialysis method. Similar reconstitution yield and mobility was observed for wild-type and GlcNAc modified nucleosomes **(Figure 12a)**.

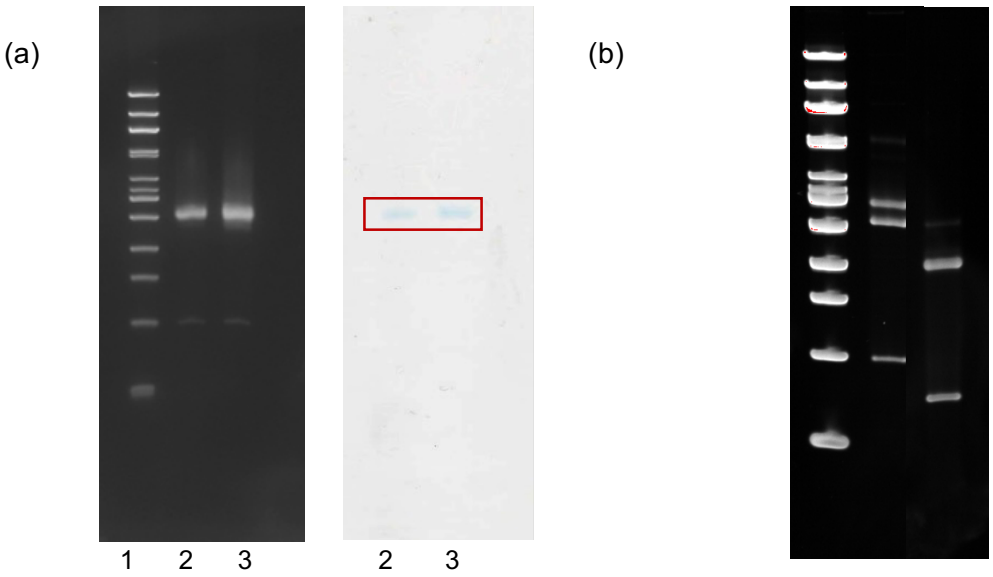


Figure 12. PAGE analysis of nucleosome reconstitution using biotinylated 186 bp DNA. (a) Native-PAGE (left) and SDS-PAGE (right) analysis of 'properly' reconstituted nucleosomes. The gel on left has been stained by SYBR Gold and on right by Coomassie Brilliant Blue. Lane (1) shows 100 bp DNA ladder, lane (2) shows wt nucleosome, and lane (3) shows GlcNAc-modified nucleosome. (b) Native-PAGE analysis of reconstituted nucleosome using

'corrupted' biotinylated DNA. The lanes represent (from left to right) 100 bp DNA ladder, nucleosome reconstituted using 186 bp DNA, and nucleosome reconstituted 145 bp DNA (Reproduced from Raj *et al.*[1])

However, an unexpected complication arose with nucleosome reconstitution in the latter part of this study. During nucleosome reconstitution, instead of a single nucleosome band, two bands corresponding to DNA-histone complexes were observed upon Native-PAGE analysis **(Figure 12b)**. Initially, it was thought that this was due to deteriorated octamers, since of the two components used for nucleosome reconstitution – octamer and DNA – the latter is much more stable. To address this potential reason, fresh octamers were refolded and nucleosome reconstitution was tried, but with no success. Next, contribution of biotinylated DNA to this abnormality in nucleosome reconstitution was probed. Fresh batch of biotinylated DNA was prepared as before. Titration experiments were performed between DNA and octamer, but still it was not possible to reconstitute homogeneous nucleosomes. To confirm the efficacy of the reconstitution method, nucleosome reconstitution using both 145 bp DNA and 186 bp biotinylated DNA was performed. Native-PAGE analysis revealed properly reconstituted nucleosome for 145 bp DNA but not for 186 bp biotinylated DNA. In order to understand this observed *anomaly*, the two bands observed upon reconstitution were investigated in details. Thermal shift and salt-dissociation assays were performed along with Native MS analysis **(Figure 13)**. Despite use of strong positioning DNA sequence (like 601 sequence used here), at times reconstitution of nucleosome can lead to heterogeneous population of nucleosome with respect to the position of DNA fragment on the histone octamer.[37] This heterogeneous population usually results in multiple bands being observed on Native-PAGE analysis. However, by incubating the heterogeneous population of reconstituted nucleosome at an elevated temperature, the nucleosomes can be brought to a single energetically-favorable DNA-octamer position, thus yielding a homogeneous nucleosome population. Freshly reconstituted nucleosomes were incubated at 37 °C and 55 °C. Thermal incubation at 37 °C did not reposition the bands indicating the two bands belonged to two

different species with only one of them corresponding to proper nucleosome. Thermal incubation at 55 °C led to melting of band at lower molecular weight with release of DNA **(Figure 13a)**. In addition, the structure of reconstituted nucleosomes was probed by salt-dissociation assay. It has been proposed that at elevated ionic strength, reconstitution artefacts arising from weaker non-canonical histone-DNA interactions dissociate.[49,50] Nucleosomes were incubated at higher salt concentration, however there was no effect on the observed bands indicating that these structures were indeed based on canonical histone-DNA interactions **(Figure 13a)**. Native MS analysis was performed for structural assignment of the observed bands (Performed by Dr. Nisha Patel, Carol Robinson Group, Oxford). Native MS analysis confirmed the presence of two species, and assigned them to be nucleosome and hexasome **(Figure 13b)**.

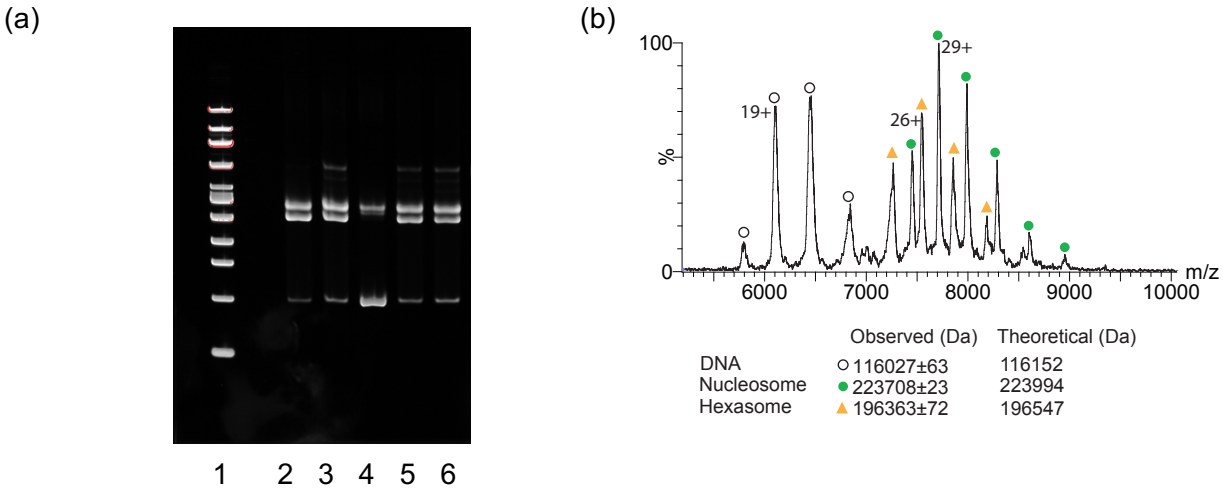


Figure 13. Analysis of reconstituted 'nucleosome-hexasome'. (a) Native-PAGE analysis of thermal and salt-dissociation assay. The lanes show (1) 100 bp DNA ladder, (2) control reconstituted 'nucleosome' sample, (3), (4) thermal shift assay results with nucleosome samples incubated at 37 °C and 55 °C respectively, (5), (6) salt-dissociation assay result with nucleosome samples incubated with 0.4 and 0.6 M KCl respectively. (b) Native MS analysis of reconstituted nucleosome reveals formation of nucleosome and hexasome.

Based on these results, it was concluded that this batch of biotinylated DNA was leading to formation of hexasome and nucleosome. It is interesting to note that the DNA precursor is being excised from a 16-mer repeat, so there lies a possibility of mutation or

recombination of the DNA sequence. Sequencing of the entire construct was tried but the data obtained was not very useful due to long, repeating sequences. In order to overcome possible recombination/mutation problem, biotinylated DNA synthesis was performed using a plasmid coding for single copy of 186 bp DNA. Plasmid DNA was isolated and further biotinylated as before. It was possible to reconstitute 'proper' nucleosome with this new batch of biotinylated DNA.

With homogeneous nucleosome preperations in hand, focus was shifted on the affinity enrichment of interacting protein partners for biotinylated nucleosomes. Equal amount of each nucleosome (wt and GlcNAcylated) were immobilized separately on streptavidin coated magnetic beads. These immobilized nucleosomes were incubated with HeLa cell nuclear extract under gentle rotation for affinity enrichment of nucleosome-binding protein partners. After four hours of incubation, the beads were washed to remove non-specifically bound proteins. The enriched nucleosome-binding proteins were released from the magnetic beads under high-salt, chaotropic conditions. The pooled protein partners were digested proteolytically using Filter-aided sample preparation (FASP) protocol to avoid down-stream MS complications arising from residual detergent in the sample.[51] The resulting peptide mixtures were separated by UHPLC and sprayed directly into a hybrid quadrupole-orbitrap (Q-Exactive) mass spectrometer for analysis. All the experiments were performed as three independent biological replicates, using three different batches of nuclear extract. Proteome quantification was done using MaxLFQ,[52] a MS-based label free quantitation (LFQ) algorithm. The label free quantification relies on high-resolution MS data with peptide peaks clearly resolved. The peak areas of the same/similar peptide across samples can be calculated and compared to report a relative quantification. As different samples (here, modified and wt) are analyzed separately, it is imperative that the peptides from one sample do not 'contaminate' other sample, leading to false quantification. We optimized sample loading and ran digested BSA between each sample runs to avoid such 'contamination'. The reproducibility of LFQ intensities within group and across replicates were visualized using Pearson correlation

coefficients **(Figure 14)**. The average Pearson correlation coefficient was found to be 0.795, indicative of reproducible experimental procedure.

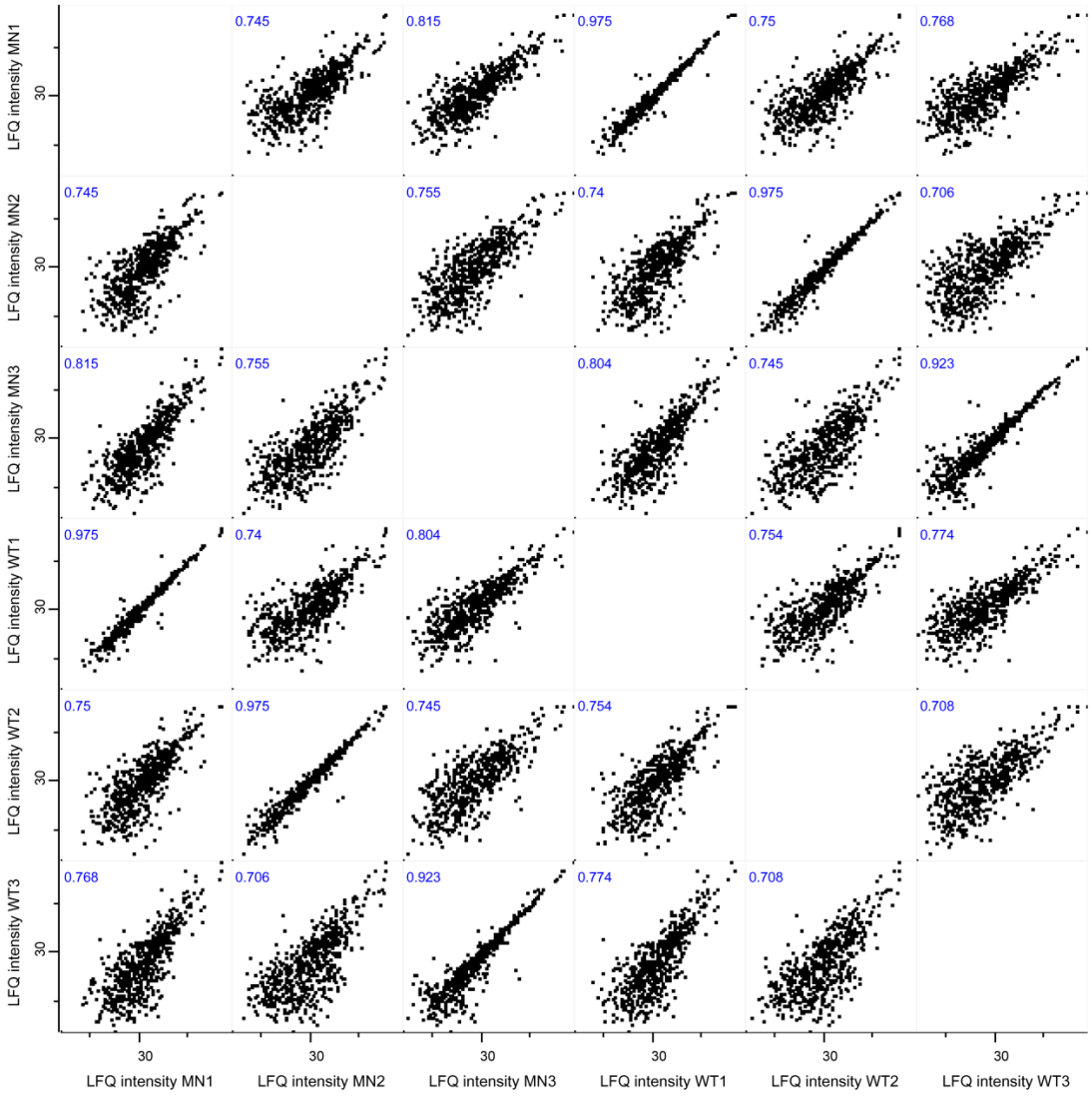


Figure 14. Experimental reproducibility of LFQ protein intensities among group and replicates. Scatterplots of logarithmized protein intensities among experiments and corresponding Pearson correlation coefficients have been shown. WT, MN indicates wild-type and modified nucleosome sample respectively; numbers (1, 2, 3) denote the replicate number. (Reproduced from Raj *et al.*[1])

MS-based LFQ analyses allowed us to identify and quantify 584 nucleosome-interacting protein groups **(Appendix 1)**. LFQ data were analyzed further using Perseus to generate *p* value and log-fold change among two samples for each protein group based on False discovery rate (FDR) based t-test.[53] The proteomics analyses revealed FACT sub-units,

Suppressor of Ty (SPT16) and Structure Specific Recognition Protein 1 (SSRP1), as being both the statistically most significant and the most enriched interacting protein partners for H2B-S112 GlcNAc modified nucleosome. The quantitative data has been represented using volcano and scatter plot respectively **(Figure 15, 16)**. The proteomics results were validated by western blotting of nucleosome-binding proteins from both samples against anti-SUPT16H and anti-SSRP1 antibodies **(Figure 17)**. It is worth-noting that validation by western blotting is not an orthogonal method. Given the advancement in the data quality of quantitative mass spectrometry and ease of reproducing the results in different laboratory conditions, validation by western blotting is becoming a redundant exercise.[20]

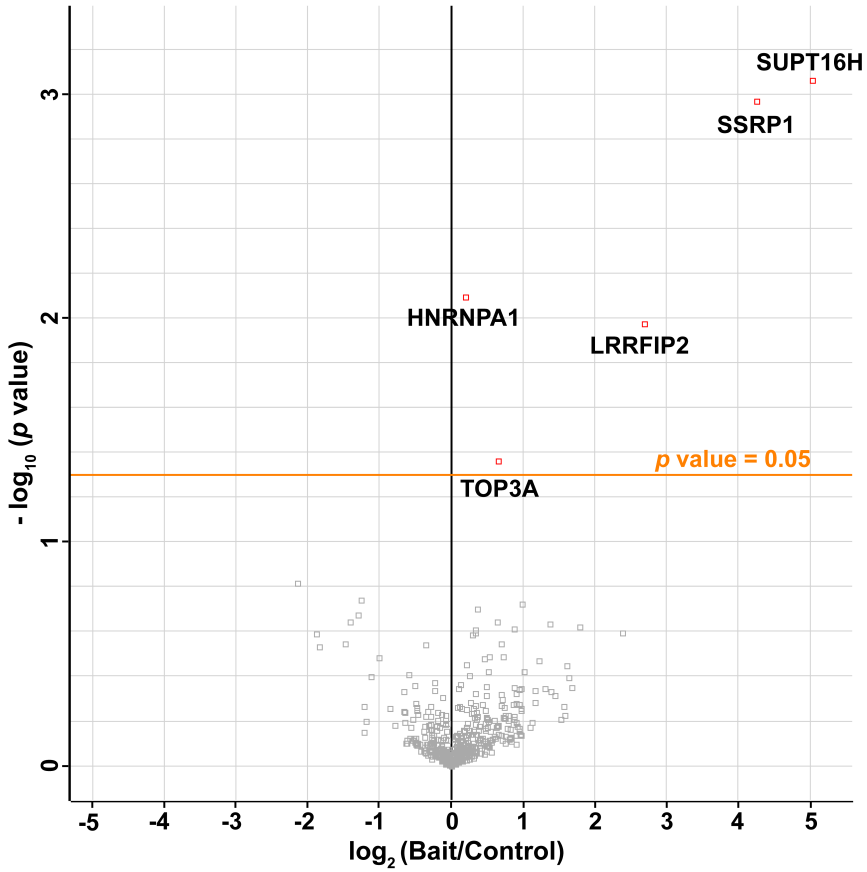


Figure 15. H2B-S112 GlcNAcylation modulates binding of FACT sub-units to nucleosome. Ratio of logarithmized LFQ intensity of protein groups identified in H2B-S112 GlcNAc nucleosome sample (Bait) and wt nucleosome sample (Control) have been plotted against logarithmized *p* value of the FDR based t-test in a volcano plot. Each hollow square represents an identified protein group. Threshold for *p* value (< 0.05) is denoted by orange line.

Statistically significant proteins are denoted in red by their gene names. (Reproduced from Raj *et al.*[1])

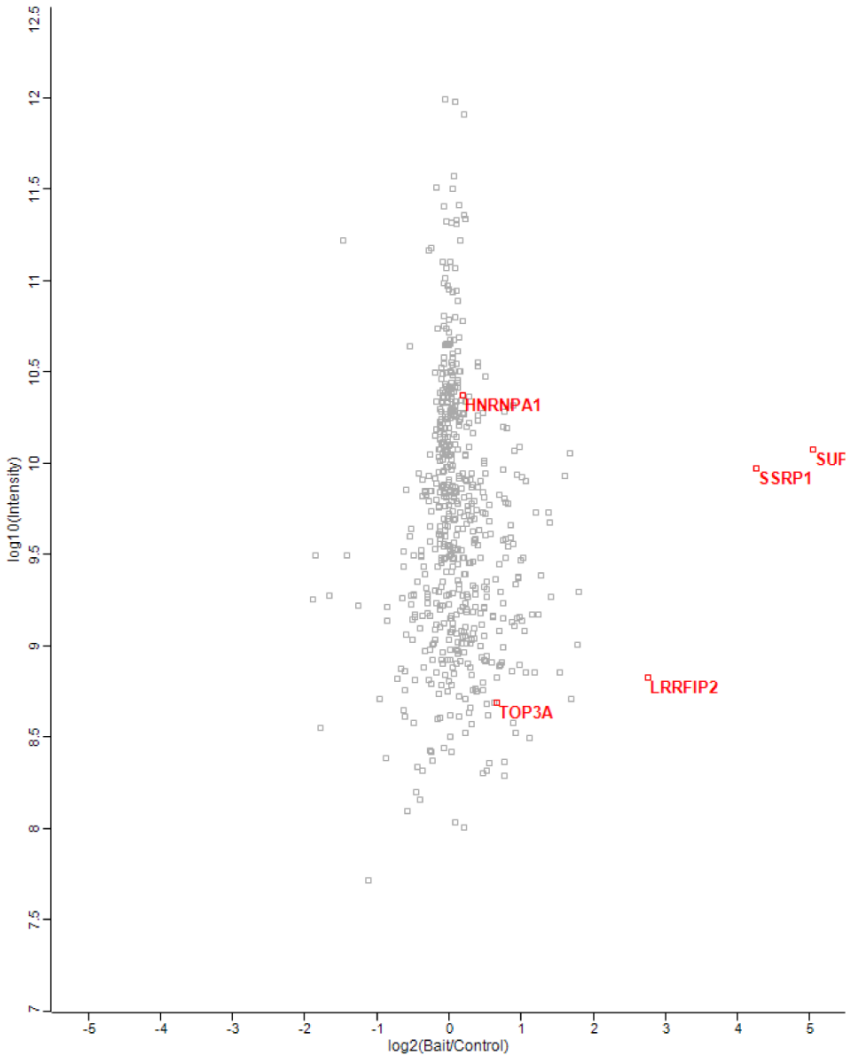


Figure 16. Scatter plot for the interacting protein partners for H2B-S112 GlcNAc nucleosome (bait) over wild-type nucleosome (control) among 584 identified proteins. x axis, logarithmized ratio of average LFQ intensities of protein groups in the bait over control pulldown experiment; y axis, log10-transformed summed up intensity of protein groups. Each hollow square represents an identified protein group. Five significant proteins identified using t-test have been highlighted in red with their gene names. The log fold change for most significant interactors, SUPT16H and SSRP1 are significantly higher than the variance for the non-interacting protein partners. (Reproduced from Raj *et al.*[1])

2.2.5 FACT – Facilitates Chromatin Transcription

FACT is a histone chaperone involved in numerous DNA templated processes such as DNA damage repair,[54] replication,[55] and transcription[56] leading to nucleosome reorganization.[57] Human FACT complex is comprised of two sub-units - SSRP1 & SPT16. These two sub-units contain a dimerization domain which facilitates their heterodimer formation.[58] Whilst the role of FACT in modulating nucleosome structure and promoting transcription is well established, its exact mode of action is often debated. There exists two major model: *'dimer eviction model'* and *'global accessibility/non-eviction model'*. According to former, FACT complex chaperones to displace a single H2A/B dimer from nucleosome to culminate in a hexasome structure with rather loosely bound DNA which eases transcriptional activation. The latter model supports the hypothesis where loss of dimer is not essential; it suggests that binding of FACT complex to nucleosome loosens the 'rigid' structure of nucleosome just enough to allow productive transcriptional elongation.[58-61]

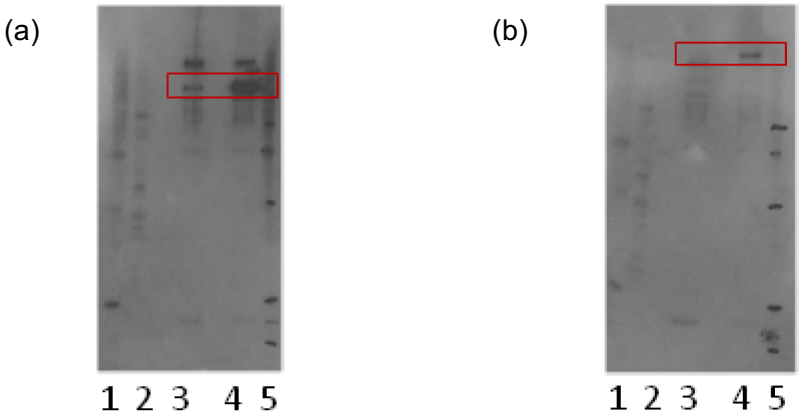


Figure 17. Validation of proteomics result by Western blotting. (a) Western blot analysis against anti-SUPT16H antibody. (b) Western blot analysis against anti-SSRP antibody. Lanes are as follows: 1,5: 10-225 kDa Protein Ladders, 2: Nuclear extract as positive control, 3: Interacting protein partners from control experiment (wt nucleosome), 4: Interacting protein partners from bait experiment (H2B-S112 GlcNAc nucleosome). The red boxes enclose the expected proteins. (Reproduced from Raj *et al.*[1])

2.2.6 Interplay between H2B-Ser112 GlcNAc, FACT, and H2B-Lys120 Ubiquitination

Previous results from Fujiki *et al.*[7] has linked H2B-S112 GlcNAc modification to H2B-K120 monoubiquitination (H2B-K120 ub), a known epigenetic mark involved in transcriptional elongation. In their studies, they postulated GlcNAc moiety at Ser112 of monomeric H2B protein to be the anchor for H2B-K120 monoubiquitination ligase, BRE1A/B. However, we did not observe BRE1A/B in our pulldown studies with GlcNAcylated nucleosome. To confirm that absence of ligase was not a mass spectrometry artefact, nucleosome-binding proteins from pulldown experiments as well as nuclear extract as a positive control were analyzed by mass spectrometric and western blotting methods. Both methods confirmed the presence of BRE1A/B in nuclear extract but not amongst nucleosome-binding proteins **(Figure 18)**. (The results describing identified proteins in nuclear extract by mass spectrometry has not been included in this thesis.) The absence of BRE1A/B in our data might suggest a weaker interaction, or maybe it to be a secondary interaction, between ligase and the GlcNAcylated nucleosome. Interestingly, earlier studies have revealed a direct cooperative linkage between FACT and H2B-K120 monoubiquitination in promoting transcription activation.[62] FACT-nucleosome interaction is intriguing; its sub-complexes can interact independently with free histones, histone sub-complexes, nucleosomal DNA, and intact nucleosomes.[63] For precise assessment of how different nucleosome components influence the GlcNAcylated nucleosome-FACT interaction, interactome of modified histone protein (H2B) and histone dimer (H2A/B) were respectively probed.

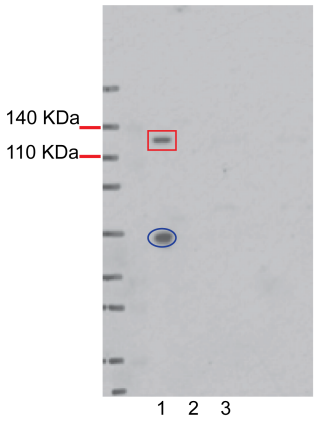


Figure 18. Western blot analysis for detection of BRE1A protein. The membrane was probed against Anti-BRE1A antibody. Lanes are as follows: 1: Nuclear extract as positive control, 2: Nucleosome-binding proteins from control experiment, 3: Nucleosome-binding proteins from bait experiment. The red box encloses detected BRE1A in positive control; blue oval indicates antibody cross-reactivity. (Reproduced from Raj *et al.*[1])

2.2.7 Synthesis of FLAG-tagged-H2B-Ser112 GlcNAc

To investigate the interacting protein partners for histone monomers and dimers, a similar strategy as used for the identification of nucleosome binding partners was envisaged **(Figure 19)**. The monomer and dimer were immobilized on a solid support for efficient affinity enrichment of their respective interacting protein partners. For this, FLAG tagged wt-H2B (FLAG-H2B) and corresponding S112C mutant (FLAG-H2B-S112C) were designed. The FLAG tag is an eight amino acid (Asp-Tyr-Lys-Asp-Asp-Asp-Asp-Lys) long protein fusion tag commonly used for protein purification.[64,65] FLAG-tagged proteins can be easily immobilized on Anti-FLAG antibodies for affinity enrichment purposes.

Starting from plasmids encoding wt and S112C mutant of H2B protein, a FLAG tag was introduced on their *N*-terminal using standard molecular biology techniques to generate desired gene constructs. The proteins were expressed and purified similar to that used for other histone proteins. With FLAG-H2B-S112C protein in hand, we employed a "Tag-and-Modify" approach to synthesize FLAG-H2B-S112-GlcNAc. In two steps (Figure 3), FLAG-H2B-S112C was treated with DBHDA under denaturing condition to yield FLAG-H2B-S112Dha intermediate. The Dha intermediate was then reacted with GlcNAc-thiol to generate FLAG-H2B-S112-GlcNAc **(Figure 20)**.

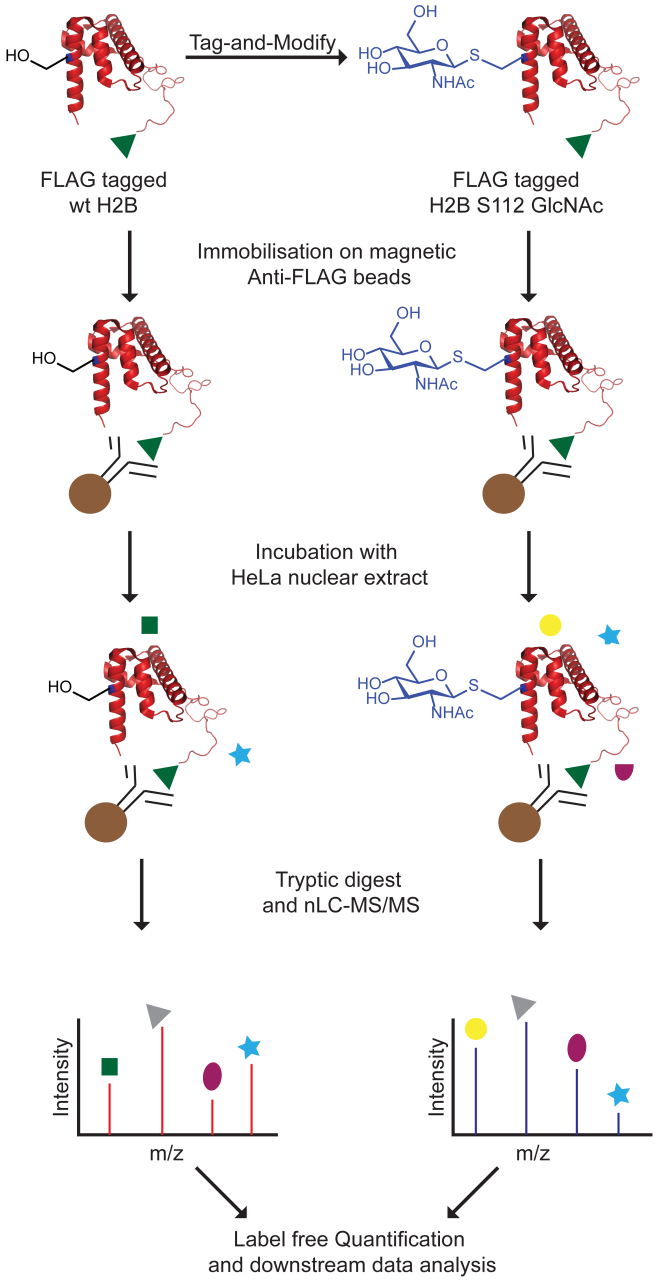


Figure 19. Schematic for interactome mining of GlcNAcylated histone monomer and dimer. FLAG-tagged wt and modified histone monomer (or dimer) were immobilized on magnetic Anti-FLAG beads to affinity enrich interacting protein partners from nuclear extract. The proteomics analysis for pooled proteins from each sample were done similarly as that for the nucleosome samples. Green triangle represents the FLAG tag and magnetic Anti-FLAG antibody has been shown as brown cartoon. (Reproduced from Raj *et al.*[1])

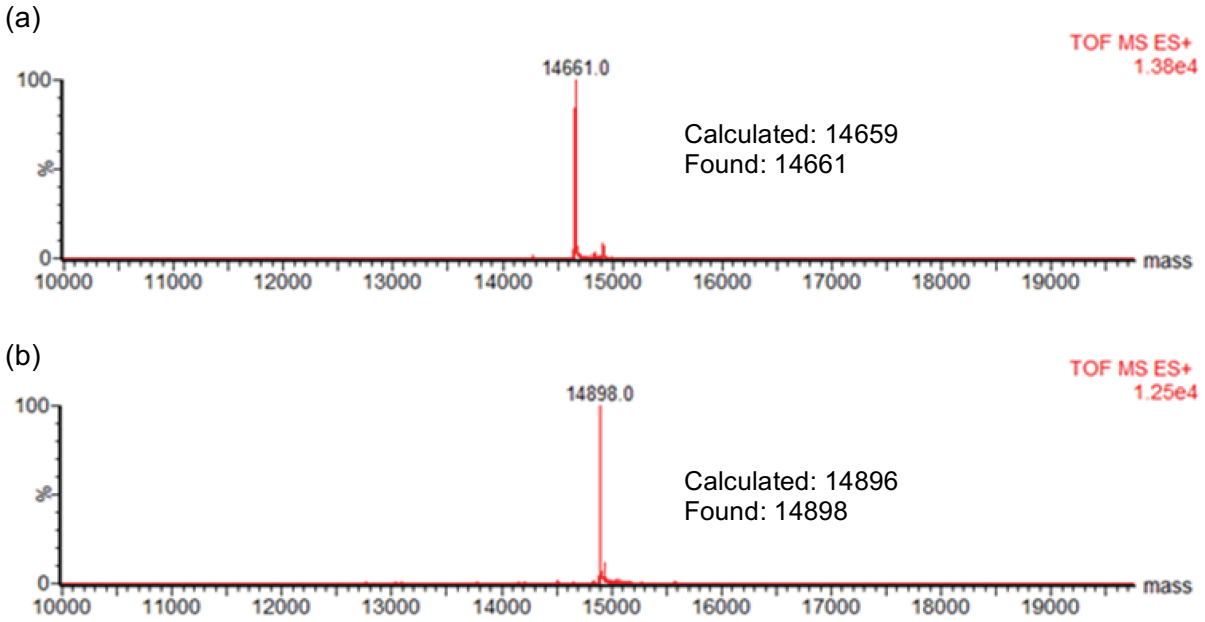


Figure 20. Synthesis of FLAG-H2B-S112 GlcNAc protein using "Tag-and-Modify" approach. (a), (b) LC-MS spectra for FLAG-H2B-S112Dha and FLAG-H2B-S112 GlcNAc proteins respectively. (Reproduced from Raj *et al.*[1])

2.2.8 Monomer and Dimer refolding

Since the protein chemical reactions are done under denaturing conditions, the modified protein cannot be used directly for pulldown purposes. Wild-type and modified monomer proteins were refolded by dialysis against low-salt buffer. Their structural integrity was confirmed by CD analyses. Similar CD spectra for wt and modified protein indicated no major structural changes upon modification **(Figure 21)**. For dimer refolding, each FLAG-tagged H2B protein (wt and modified) was mixed in equimolar ratio with wt H2A protein under denaturing condition. The protein mixture was dialyzed against high-salt buffer, as before, to allow for heterodimer formation. The resulting complexes were purified by Size-exclusion chromatography. Similar retention volume of wt and modified FLAG-tagged histone heterodimer point to same degree of reconstitution for both heterodimers despite the modification **(Figure 22)**.

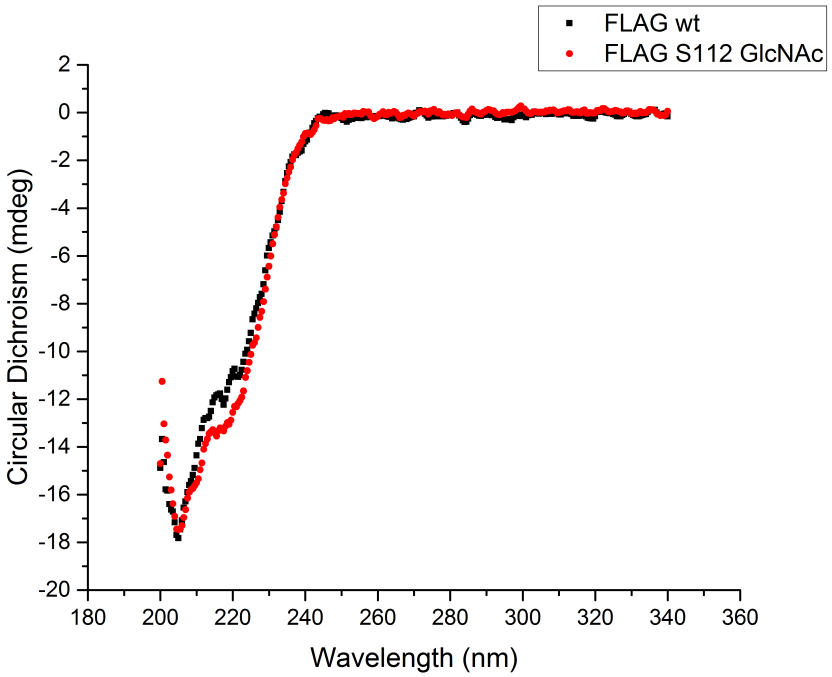


Figure 21. CD spectra of refolded FLAG-H2B protein (black) and FLAG-H2B-S112 GlcNAc protein (red). (Reproduced from Raj *et al.*[1])

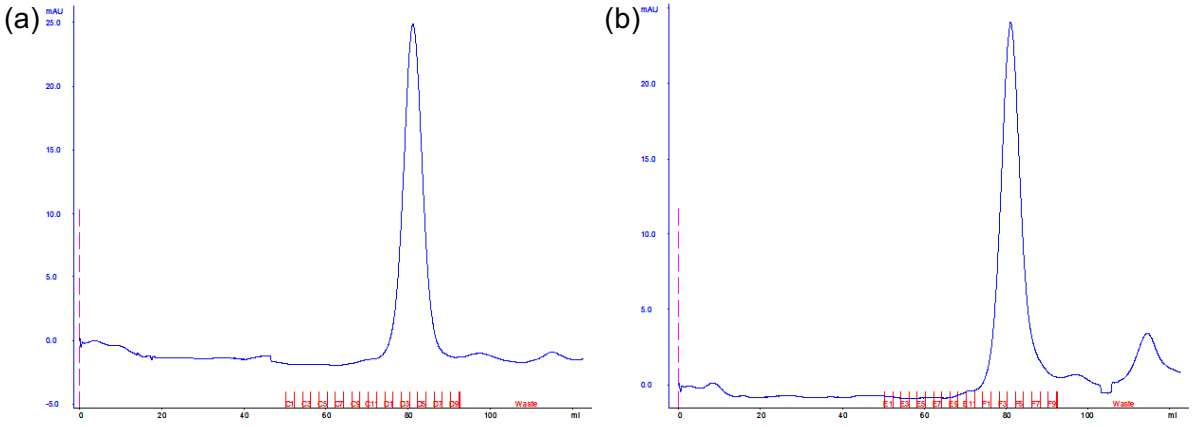


Figure 22. Size-exclusion chromatography (SEC) traces of FLAG-tagged histone heterodimers. (a) SEC trace of FLAG-tagged wt H2A/B dimer. (b) SEC trace of FLAG-tagged GlcNAc modified H2A/B dimer.

2.2.9 Interactome for wt and GlcNAc modified FLAG-H2B monomer and heterodimer

Access to refolded FLAG-tagged monomers and dimers (wt and S112 GlcNAc modified) allowed us to perform pull-downs to enrich interacting protein partners from nuclear extract. Anti-FLAG magnetic beads (M2 magnetic beads from Sigma-Aldrich) were used to

immobilize the protein species. These magnetic beads greatly enhance the isolation of interacting protein partners from non-specifically bound proteins. However, these beads are antibodies-based which make them susceptible to reducing conditions. Under reducing conditions, the disulfide bonds essential for antibody integrity can be reduced destroying its ability to bind the FLAG epitope. To overcome this problem, new batches of nuclear extract were prepared under non-reducing conditions.

For the analysis of the monomer interactome, wt and modified FLAG-tagged H2B proteins were immobilized on magnetic beads and incubated with nuclear extract for four hours. The interacting protein partners were eluted with commercially available IgG elution buffer with low pH. The protein partners were analysed using quantitative MS as earlier. To get a robust data-set, pull-down experiments were performed in duplicate. Quantitative MS analyses revealed 948 interacting protein partners, amongst which FANCI, INF2 and COAX6A1 were most significant interaction partners of GlcNAcylated H2B when compared to wt H2B **(Appendix 2, Figure 23)**. Interestingly, we did observe FACT in both the samples; with slight enrichment (not statistically significant) in the GlcNAcylated sample. However, as with the nucleosome samples, we did not observe BRE1A/B in these experiments. As earlier, we confirmed the absence of BRE1A/B not to be a mass spectrometric artefact by analysing the nuclear extract.

The same approach was used to identify 886 interacting protein groups for FLAG-tagged dimers from a single experiment **(Appendix 3, Figure 24)**. FACT was observed in both the samples but with slight enrichment (although not statistically significant) in GlcNAcylated sample. The presence of FACT in both monomer and dimer interactome is not surprising as it is known to interact with free histone monomers and dimers.[59,63] BRE1A/B protein, again, was not observed in the dimer interactome.

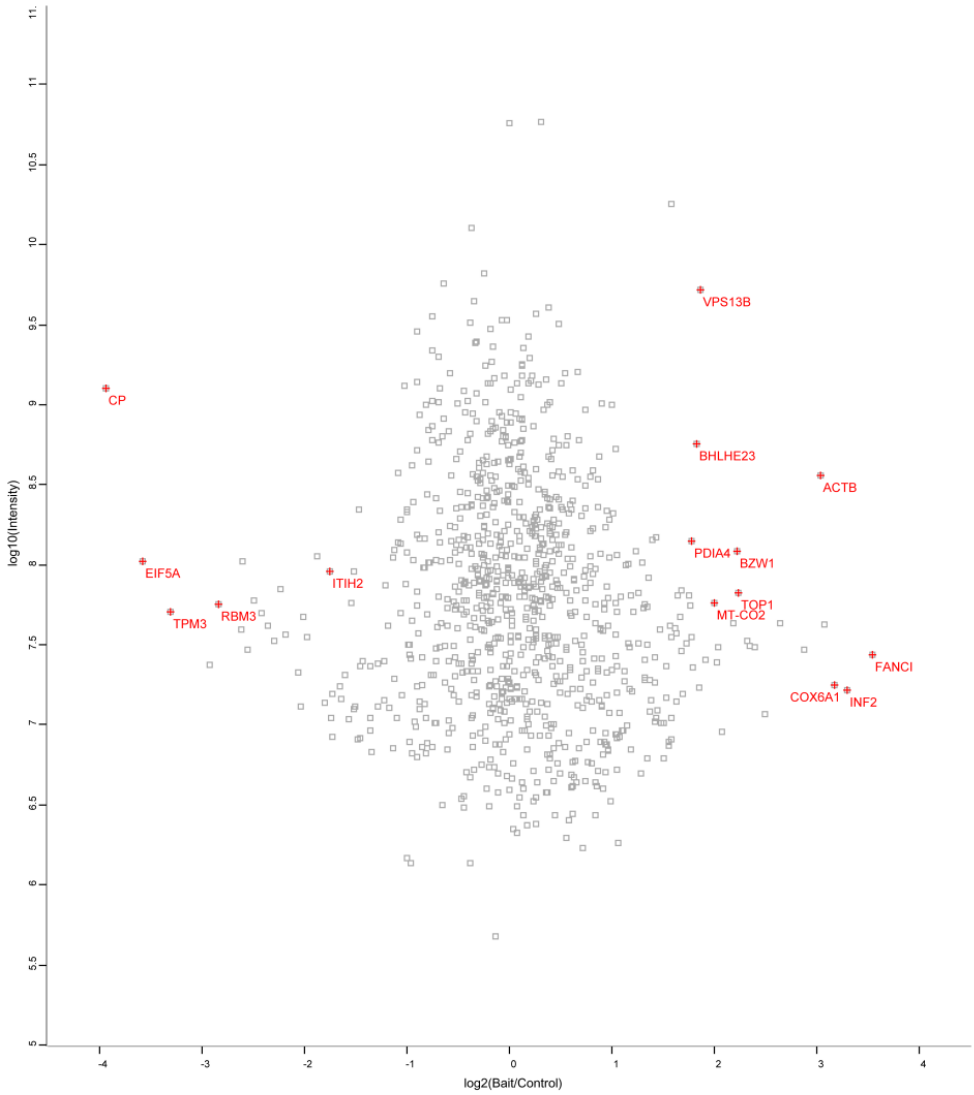


Figure 23. Interactome for FLAG-tagged wt and modified H2B protein. 948 interacting protein groups from two biological replicate experiments have been represented by hollow squares in a scatter plot. x axis: logarithmized ratio of average LFQ intensities of protein groups in the bait (H2B-S112 GlcNAc) over control (wt) pulldown experiments; y axis: log10-transformed summed up intensity of protein groups. Top 15 significant interacting protein partners (denoted by gene name) identified by Label free quantification (LFQ) on Significance B analysis are shown in red in a scatter plot. (Reproduced from Raj *et al.*[1])

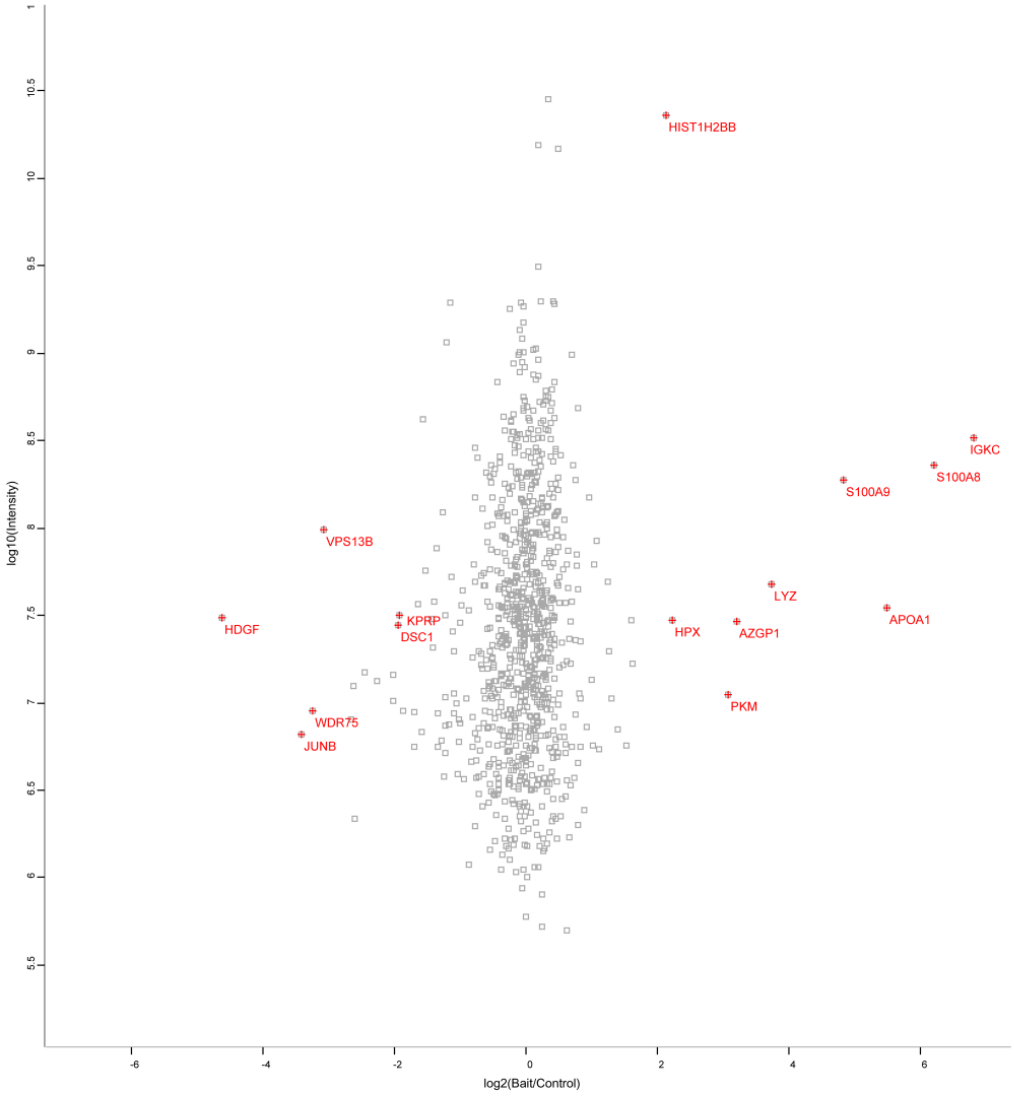


Figure 24. Interactome for FLAG-tagged wt and modified H2A/B histone dimer. 886 interacting protein groups from a single experiment has been represented by hollow squares in a scatter plot. x axis: logarithmized ratio of average LFQ intensities of protein groups in the bait (modified dimer) over control (wt dimer) pulldown experiment; y axis: log10-transformed summed up intensity of protein groups. Top 15 significant interacting protein partners (denoted by gene name) identified by Label free quantification (LFQ) on Significance B analysis are shown in red in a scatter plot. (Reproduced from Raj *et al.*[1])

2.2.10 Proposed molecular mechanism for H2B-Ser112 GlcNAc promoted ubiquitination

The results obtained here by analyzing the interactome of pure, homogeneously GlcNAcylated nucleosomes and its constituents provided a basis to update the molecular mechanism linking H2B-S112 GlcNAcylation and H2B-K120 monoubiquitination, and the role of *O*-GlcNAc modification leading to transcriptional activation **(Figure 25)**. In a mechanism consistent with present data and reported literature,[7,62] it was proposed that GlcNAcylation of nucleosome at H2B-Ser112 by OGT leads to significantly enhanced interaction with FACT complex. FACT being a chromatin remodeler alters the nucleosome architecture leading to a more accessible H2A/B dimer for ubiquitination. FACT itself can enhance H2B-K120 ubiquitination by directly or indirectly recruiting BRE1A complex (RNF20/40).[62,66] In support of our claim, it was earlier reported that FACT plays a crucial role in chromatin remodeling by directly recruiting RNF20 in case of DNA damage repair.[66] Residues on the acidic patch have been found to be essential for H2B ubiquitination as they anchor the ligase. A possible modulation in the enzymatic activity of ligase upon modification of an amino acid residue in close proximity to acidic patch cannot be ruled out.[67] In light of earlier result, it was expected to detect BRE1A/B in the pulldown experiments, as GlcNAc moiety supposedly acts as an anchor for the ligase.[7] However, the absence of BRE1A/B can be attributed to two possible reasons. First, differences in enrichment protocol or use of a different bait, might be responsible for these discrepancies. The pulldown reported here used a homogeneously GlcNAcylated histone protein/nucleosome as compared to earlier assays which used partially modified heterogeneous protein sample. Second, active transcription is required for H2B-K120 ubiquitination,[62] and as such even a FACT-bound nucleosome might not be sufficient for BRE1A/B association. Preferential binding of FACT to GlcNAcylated nucleosomes may also point towards the modification as a trigger for FACT-driven transcriptional activation or generation of a ‘relaxed’ chromatin state facilitating transcription elongation.

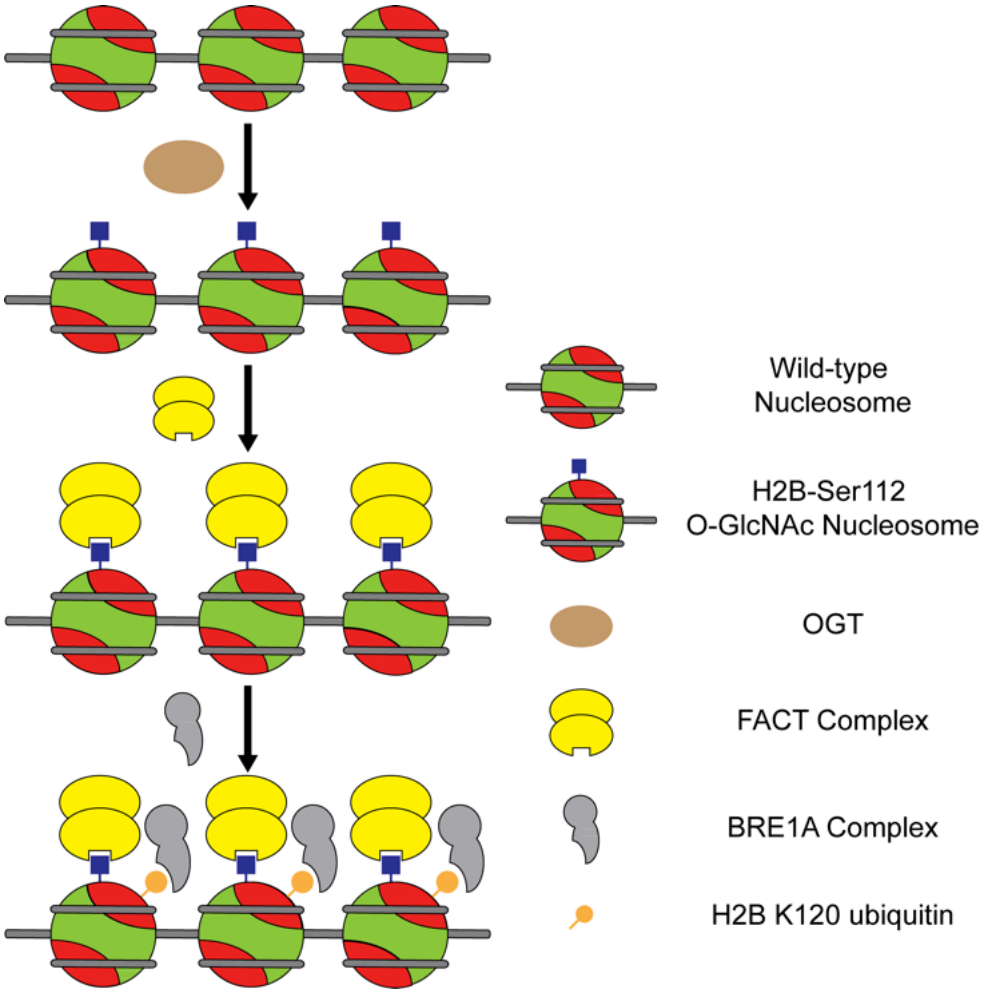


Figure 25. An updated plausible molecular mechanism for FACT-mediated H2B-Lys120 ubiquitination upon H2B-Ser112 *O*-GlcNAcylation. (Reproduced from Raj *et al.*[1])

2.3 Conclusion and Outlook

In summary, GlcNAcylated histone proteins and corresponding nucleosomes were synthesized using post-translational chemical modification. The chemical approach used here can be translated to other histone proteins as well for installation of different PTMs. The chemical method used here can complement ligation-based approaches, for example, expressed protein ligation[68] or native chemical ligation[69] for access to pure, homogeneously modified protein and can serve as an excellent alternative to traditional enzymatic approaches. The synthesized protein allowed construction of homogeneously modified nucleosomes and aided the investigation regarding the effect of the modification on the nucleosome structure. Synthetic nucleosomes (and modified proteins) coupled with interaction proteomic analyses

allowed us the exploration of the mechanistic details of a transcriptionally relevant mechanism involving *O*-GlcNAcylation. It is worth-noting that the interaction proteomics experiment only reveals the global change in the affinity of an interacting protein partner towards modified nucleosome rather than pin-pointing the molecular details of any interaction. Indeed, to validate that whether the enhanced interaction between GlcNAcylated nucleosome and FACT stemmed due to GlcNAc moiety alone, we did perform pulldown experiments with GlcNAcylated monomer and dimer. However, the results of those experiments do not support this hypothesis. Interestingly, the *N*-terminal tail of histone protein H4 tail is known to interact with the acidic patch of the nucleosome.[19] In a separate experiment, Luger and co-workers have shown the importance of H3-H4 tails to promote binding between FACT and nucleosome.[63] It may be reasoned that *O*-GlcNAcylation modification at the acidic patch disrupts the interaction of H4 tail with acidic patch. Thus, 'released' H4 tail can interact with FACT complex, in turn promoting interaction with GlcNAcylated nucleosome. To validate this hypothesis, it is envisaged to perform similar interaction proteomics experiments but with a GlcNAcylated nucleosome assembled without H4 tail. A variant of histone protein H4 without a tail was designed and expressed in *E.coli*. The 'release' of H4 upon GlcNAcylation might also be monitored by further NMR experiments.

The affinity enrichment proteomics approach used here with synthetic nucleosomes can potentially be used to elucidate the role of various PTMs as well as revealing 'cross-talk' between PTMs. We anticipate that this approach will allow discovery of key players in PTM mediated transcriptional regulation to create a precise mechanistic picture of this fundamental process at the molecular level. The field of chromatin biology has relied heavily on short peptides and isolated proteins constituting only a fragment of the biologically relevant interaction environment; the work presented here and other reports[70] suggests that use of less reductionist probes which provide a more relevant context may prove vital for detailed mechanistic investigation.

2.4 Experimental Section

2.4.1 General Considerations

All molecular biology related experiments were performed in sterile condition inside a HERAsafe KS-12 Class II biological safety cabinet (Thermo Fischer Scientific). Media, glass and plastic equipment used for these experiments were either bought sterile or were sterilized using an autoclave. Autoclaving was performed at 121 °C for 20 min in either a Falcon LTE tabletop autoclave or a LTE Scientific Touchclave-R autoclave. LB, 2xYT medium were bought as pre-formulated dry granules and diluted according to the manufacturer's specifications. All buffers were prepared using Milli-Q water and sterile-filtered using 0.22 µm filter prior to use. pH of the buffers was measured using Jenway 3510 pH meter. Bacterial cultures were incubated in New Brunswick incubator shakers (Innova 44/44R, Excella E25/25R). Optical density was measured using either a SPECTROstar Nano (BMG Labtech) or NovaSpec III (Amersham Biosciences) spectrophotometer. Centrifugation was performed in a Beckman Coulter Avanti J-25 Centrifuge (using F10BA-6x500y and JA-25.50 rotors) or Beckman Coulter Allegra X-12R Centrifuge. Microcentrifugation was performed either on an accuSpin micro17 or Heraeus Fresco 17 centrifuge (Thermo Fischer Scientific). Protein purifications were performed using an ÄKTA-FPLC (GE Healthcare Life Sciences) in a cold-room maintained at 4 °C. Pre-packed columns for FPLC and G-25 desalting columns (SpinTrap™, MiniTrap™, and MidiTrap™) were purchased (GE Healthcare Life Sciences). Heating baths used were Grant JB Series. Polymerase chain reaction was performed using an Applied Biosystems 2720 Thermal Cycler (Thermo Fischer Scientific). DNA concentration was determined using a NanoDrop Spectrophotometer ND-1000 (Thermo Fischer Scientific). Electrophoretic analysis of DNA was done on 1% Agarose gel using TAE buffer using the following equipment: BioRad Power Pack Basic (at 110 V), Bio-Rad Mini-sub Cell GT, visualized using an UVP Mini Benchtop UV Transilluminator TM-10E, and imaged using a Bio-Rad Gel Doc XR system. Protein concentration was measured either by NanoDrop or by BCA assay. Protein analysis used the following equipment: Invitrogen XCell *Sure*Lock™ and

BioRad Power Pack Basic (at 200 V). Pre-cast NuPAGE Novex Bis-Tris protein gels (Life Technologies, using MES or MOPS buffer) were used for protein SDS-PAGE analysis. Protein samples were boiled for 5 min at 95% in Laemmli loading buffer (6x concentrate; 0.375M Tris pH 6.8, 12% SDS, 60% glycerol, 0.6M DTT, 0.06% bromophenol blue) before being loaded on the gel for analysis. The gel was stained using InstantBlue protein stain (Expedeon).

2.4.2 Expression and purification of wt Histone proteins

pET3 bacterial plasmids encoding canonical *Xenopus laevis* wild-type histone proteins were kindly donated by Prof. Rob Klose, University of Oxford, Oxford. The histone proteins were expressed in *E.coli* BL21(DE3)pLysS cells and purified by size-exclusion (HiLoad 26/600 Superdex 200, GE Healthcare Life Sciences) followed by ion-exchange (HiTrap SP HP 5 mL, GE Healthcare Life Sciences) chromatography.[31,37] Gene sequence and corresponding amino acid sequence for wt histone proteins used throughout this thesis are given below:

(i) wild-type H2A

DNA sequence:

ATGTCAGGAAGAGGCAAACAAGGCGGTAAAACCCGCGCTAAGGCCAAGACTCGCTCAT
CTCGGGCTGGGCTACAGTTCCCTGTTGGCCGTGTTCACCGGCTGTTAAGGAAAGGCAA
TTATGCAGAGCGGGTGGGAGCTGGAGCTCCAGTCTATCTGGCTGCAGTGTTGGAGTAT
CTGACCGCTGAGATTTTGGAATTGGCCGGGAATGCGGCCCGTGATAACAAGAAGACTC
GCATTATCCCCAGACACCTGCAGCTCGCTGTGCGCAACGATGAGGAACTGAACAAACT
GCTCGGAAGAGTCACTATCGCTCAGGGCGGGGTCCTGCCCAACATCCAGTCCGTGCT
GCTGCCCAAGAAAACCGAGAGTTCCAAGTCGGCCAAGAGCAAGTGATCGGATCCGGC
TGCTAACAAAGCCCGAAAGGAAGCTGAGTTGGCTGCTGCCACCGCTGAGCAATAACTA
GCATAACCCCTTGGGGCCTCTAAACGGGTCTTGAGGGGTTTTTTGCTGAAAGGAGGAA
CTATATCCGGATATCCACAGGACGGGTGTGGTCGCCATGATCGCGTAGTCGATAGTGG
CTCCAAGTAGCGAAGCGAGCAGGACTGGGCGGCGGCCAAAGCGGTCGGACAGTGCT
CCGAGAACGGGTGCGCATAGAAATTGCATCAACGCATATAG

Translated Amino Acid Sequence:

MSGRGKQGGK TRAKAKTRSS RAGLQFPVGR VHRLLRKGNY AERVGAGAPV
YLAAVLEYLT AEILELAGNA ARDNKKTRII PRHLQLAVRN DEELNKLLGR

VTIAQGGVLP NIQSVLLPKK TESSKSAKSK

(ii) wild-type H2B

DNA sequence:

ATGGCCAAGTCCGCTCCAGCCCCGAAGAAAGGCTCCAAGAAAGCGGTGACCAAGACT
CAGAAGAAAGACGGGAAAAAGCGCAGGAAGACAAGGAAGGAGAGTTATGCCATTTACG
TGTACAAGGTGCTGAAGCAGGTGCACCCCGATACCGGCATCTCGTCCAAGGCCATGAG
CATCATGAACTCCTTTGTCAACGATGTGTTTGAGCGCATCGCAGGGGAAGCCTCCCGC
CTGGCTCATTACAACAAGCGCTCCACCATCACCTCCCGGGAGATCCAGACCGCGGTCC
GACTGCTGCTGCCTGGGGAGTTGGCCAAACACGCCGTGTCCGAGGGCACCAAGGCTG
TCACCAAGTACACCAGCGCCAAGTAACTGCTGCTGCCGGATCCGGCTGCTAACAAAGC
CCGAAAGGAAGCTGAGTTGGCTGCTGCCACCGCTGAGCAATAACTAG

Translated Amino Acid Sequence:

MAKSAPAPKK GSKKAVTKTQ KKDGKKRRKT RKESYAIYVY KVLKQVHPDT
GISSKAMSIM NSFVNDVFER IAGEASRLAH YNKRSTITSR EIQTAVRLLL
PGELAKHAVS EGTKAVTKYT SAK

(iii) wild-type H3

DNA sequence:

ATGGCCCGTACCAAGCAGACCGCCCGTAAATCCACCGGAGGGAAGGCTCCCCGCAAG
CAGCTGGCCACCAAGGCAGCCAGGAAGTCCGCTCCTGCTACCGGCGGAGTCAAGAAA
CCTCACCGTTACCGGCCCGGCACAGTCGCTCTCCGCGAGATCCGCCGCTACCAGAAA
TCCACCGAGCTGCTCATCCGCAAACTGCCTTTCCAGCGCCTGGTCCGGGAGATCGCTC
AGGACTTCAAGACCGACCTGCGCTTCCAGAGCTCGGCCGTTATGGCTCTGCAGGAGG
CCAGCGAGGCTTATCTGGTCGCTCTCTTTGAGGACACCAACCTGGCCGCCATCCACGC
CAAGAGGGTCACCATCATGCCCAAGGACATCCAGCTGGCCCGCAGAATCCGAGGCGA
GAGGGCTTAGATCCGGCTGCTAACAAAGCCCGAAAGGAAGCTGAGTTGGCTGCTGCC
ACCGCTGAGCAATAACTAGCATAACCCCTTGGGGCCTCTAAACGGGTCTTGAGGGGTT
TTTTGCTGAAAGGAGGAACTATATCCGGATATCCACAGGACGGGTGTGGTCGCCATGA
TCGCGTAGTCGATAGTGGCTCCAAGTAG

Translated Amino Acid Sequence:

MARTKQTARK STGGKAPRKQ LATKAARKSA PATGGVKKPH RYRPGTVALR
EIRRYQKSTEL LIRKLPFQRL VREIAQDFKT DLRFQSSAVM ALQEASEAYL
VALFEDTNLA AIHAKRVTIM PKDIQLARRI RGERA

(iv) wild-type H4

DNA sequence:

ATGTCTGGTCGTGGTAAAGGTGGTAAAGGTCTGGGTAAAGGTGGTGCTAAACGTCACC
GTAAAGTTCTGCGTGACAACATCCAGGGTATCACCAAGCCGGCTATCCGTCGTCTGGC
TCGTCGTGGTGGTGTTAAACGTATCTCCGGTCTGATCTACGAAGAAACCCGCGGTGTT
CTGAAAGTTTTCCTGGAAAACGTTATCCGTGACGCTGTTACCTACACCGAACACGCTAA
ACGTAAAACCGTTACCGCTATGGACGTTGTTTACGCTCTGAAACGTCAGGGTCGTACCC
TGTACGGTTTCGGTGGTTAAAGATCCGGCTGCTAACAAAGCCCGAAAGGAAGCTGAGT
TGGCTGCTGCCACCGCTGAGCAATAACTAG

Translated Amino Acid Sequence:

MSGRGKGGKG LGKGGAKRHR KVLRDNIQGI TKPAIRRLAR RGGVKRISGL
IYEETRGVLK VFLENVIRDA VTYTEHAKRK TVTAMDVVYA LKRQGRTLYG
FGG

Bacterial Transformation

The required histone encoding plasmid was transformed in XL10-gold ultracompetent cells (Agilent). Briefly, 45 µL of XL10-gold cells were aliquoted in a prechilled 14 mL BD Falcon polypropylene round-bottom tube. 2 µL of β-mercaptoethanol was added to the cells. The content of the tube was swirled gently and left to incubate on ice for 10 minutes. (In case of transformation in BL21(DE3)pLysS cells, addition of β-mercaptoethanol is not required.) 1 µL (50 ng/µL) of plasmid DNA was added to the cells and swirled gently. The cells were incubated on ice for 30 minutes on ice, followed by heat-shock at 42 °C for approximately 40 seconds. The transformed mixture was immediately cooled by incubating it on ice for 2 minutes. 300 µL of pre-warmed SOC medium was then added and the cells were incubated at 37 °C with shaking for 60 minutes. The transformed cells were subsequently plated on freshly prepared LB/Agar plates containing appropriate antibiotics and incubated overnight at 37 °C. The plates containing transformed cells were stored at 4 °C for short-term use.

A single colony of transformed cell was used to inoculate 10 mL of LB media containing appropriate antibiotics (10 µL of 100 mg/mL Ampicillin stock solution or/and 10 µL of 33 mg/mL Chloramphenicol stock solution) in a 50 mL falcon tube. The falcon tube was incubated for 16

hours at 37 °C. The plasmid DNA was isolated by performing a QIAprep Spin Miniprep protocol (Qiagen). The concentration of plasmid DNA was determined by NanoDrop. The sequence of plasmid DNA was confirmed by sequencing.

Expression and Purification of Histone Proteins

pET3 plasmid encoding for required histone protein was transformed into BL21(DE3)pLysS cells on freshly prepared LB-Agar plate containing ampicillin and chloramphenicol. A single transformed colony was used to inoculate 50 mL of LB media containing the same antibiotics. This starter culture was grown at 37 °C either overnight or until slightly turbid (approximately 4-5 hours). 10 mL of starter culture was used to inoculate 800 mL of freshly prepared 2xYT medium containing the same antibiotics. The culture was incubated at 37 °C. OD_{600} of the culture was checked occasionally and was allowed to grow at 37 °C until OD_{600} reached ~ 0.4-0.6 (approximately 4 hours). Protein expression was induced by addition of IPTG to a final concentration of 0.5 mM (400 µL of 1 M stock solution). The cells were further incubated at 37 °C for 2 hours (3 hours in case of histone protein H4). Longer expression time proves detrimental for protein yield. Cells were harvested by centrifugation (8000 rpm; 8 min; F10BA-6x500y rotor). The cell pellet (from 2.4 L of cell culture) was suspended in 35 mL of lysis buffer (50 mM Tris pH 7.5, 100mM NaCl, 1 mM EDTA, 5 mM β-ME) supplemented with protease inhibitor tablet (cOmplete, EDTA-free (Roche Life Sciences)). The resuspended cell pellet was frozen and stored at -80 °C.

For purification, frozen cells were thawed in a water bath at room temperature. ~ 5 mg of DNase I (Roche Life Sciences) was added and the mixture was incubated at 4 °C with gentle rotation. The mixture was subjected to sonication (5 cycles of 30 seconds sonication pulses (0.5 second on, 0.5 second off, 60% Amplitude) with 1 min interval in between) followed by centrifugation at 20k rpm for 20 min. The supernatant was discarded and the pellet was resuspended in 40 mL TW buffer (lysis buffer + 1% Triton X-100). The resulting suspension was sonicated once more for 30 seconds at 60% amplitude, followed by centrifugation at 20k rpm for 10 min. The pellet was washed two more times with TW buffer and once with lysis

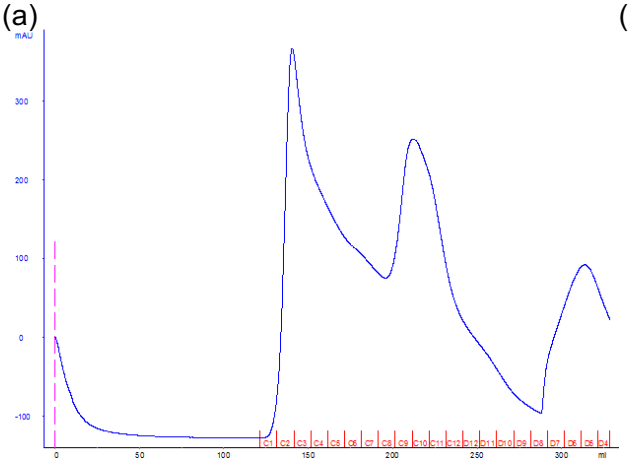
buffer. 0.2-0.3 mL of DMSO was added to the pellet. The pellet was minced with a spatula and left at room temperature for 10 minutes. 7-15 mL of unfolding buffer (7 M Guanidinum hydrochloride, 10 mM Tris pH 7.5, 1 mM EDTA, 10 mM DTT, 1 mM Benzamidine) was added to the minced pellet and the mixture was gently rotated for 1 hour at room temperature. The mixture was centrifuged for 10 min at 20k rpm at room temperature. The supernatant was decanted, filtered and loaded onto a size-exclusion column (HiLoad 26/60 Superdex 200, GE Healthcare Life Sciences) pre-equilibrated with 1 CV SAU-1000 buffer (7 M Urea, 20 mM NaOAc pH 5.2, 1 M NaCl, 1 mM EDTA, 5 mM β-ME). The histone was eluted with SAU-1000 buffer, and analyzed by SDS-PAGE. Fractions containing purified histones were pooled together and dialyzed against IEX binding buffer (7 M Urea, 10 mM Tris pH 7.5, 100 mM NaCl, 1mM EDTA, 5 mM β-ME).

Histones were further purified by Ion-exchange chromatography using a HiTrap SP HP column (GE Healthcare Life Sciences). The proteins were loaded onto the column using IEX binding buffer (7 M Urea, 10 mM Tris pH 7.5, 100 mM NaCl, 1mM EDTA, 5 mM β-ME). Non-binding proteins were washed out using 12 CV of binding buffer. The protein was eluted using a linear gradient from 0 to 100% of elution buffer (7 M Urea, 10 mM Tris pH 7.5, 1 M NaCl, 1mM EDTA, 5 mM β-ME) over 15 CV. Eluted fractions were analyzed by SDS-PAGE. Fractions containing purified histones were pooled together and dialyzed against water containing 2 mM β-ME. Purified histone proteins were checked by LC-MS. They were later lyophilized and stored at -80 °C.

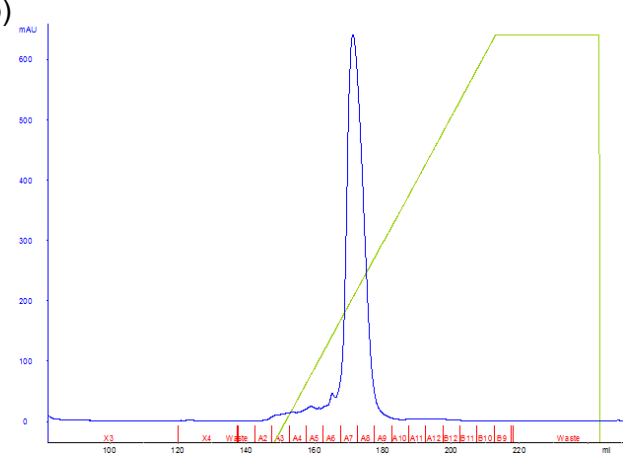
FPLC traces, SDS-PAGE gels and MS spectra for purified wt histone proteins are shown below **(Figure 26-29)**.

(i) wt H2A protein

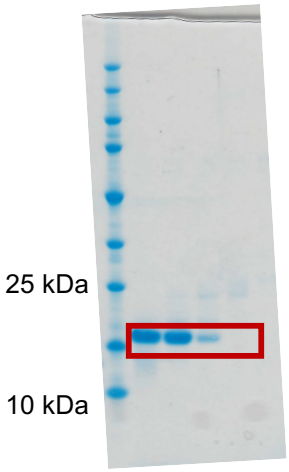
(a)



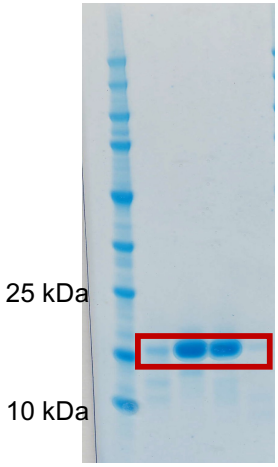
(b)



(c)



(d)



(e)

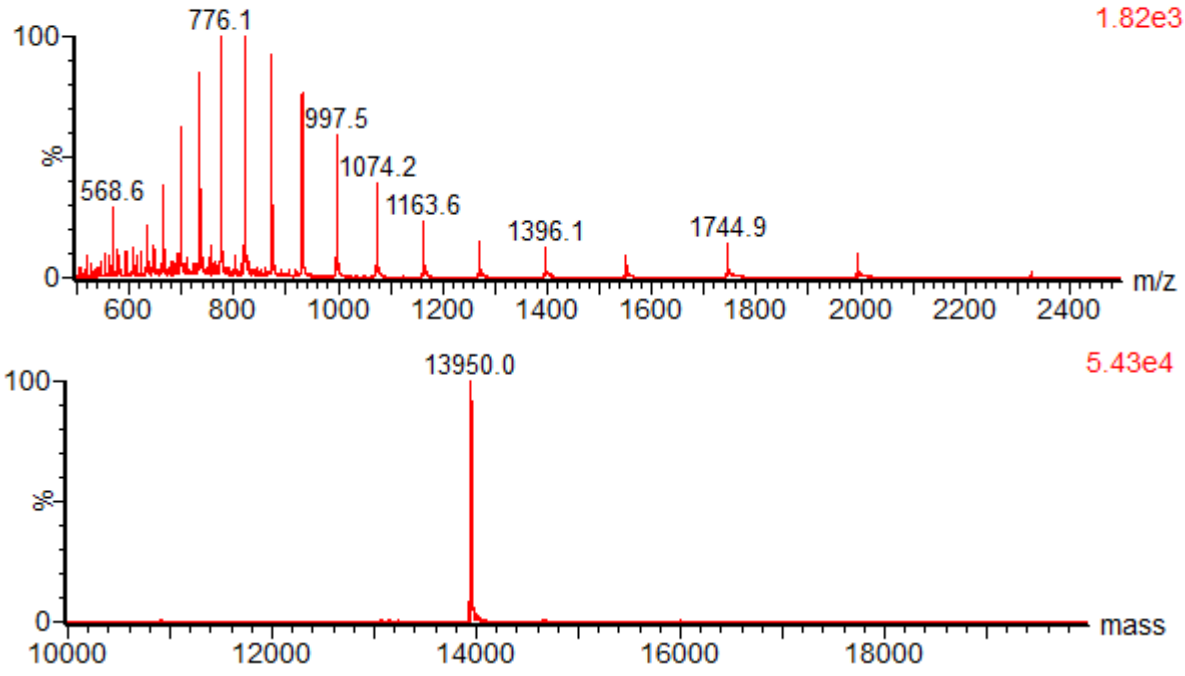
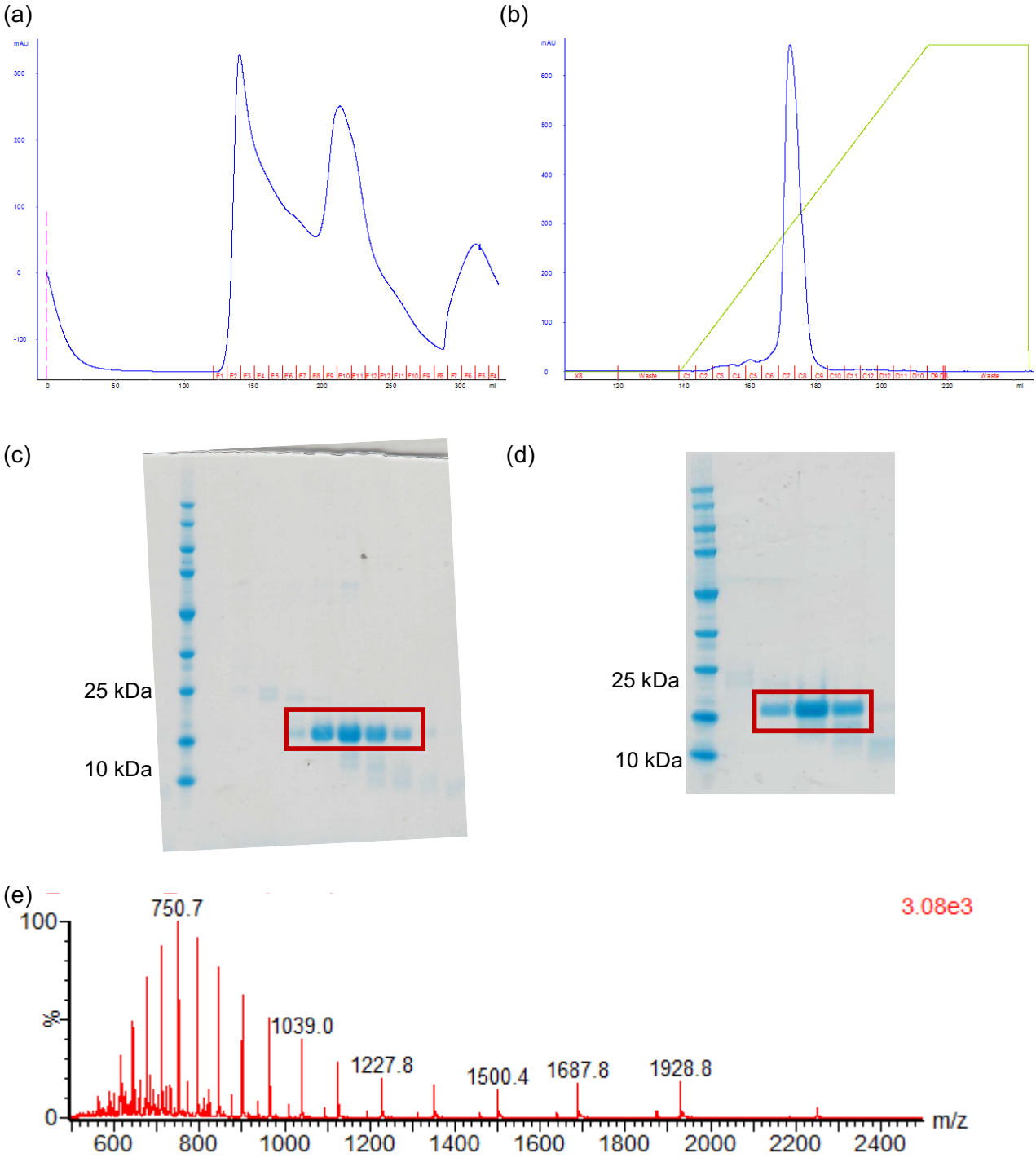


Figure 26. Expression and purification of wt histone protein H2A. (a), (b) FPLC traces for SEC and SCX purification. (c), (d) SDS-PAGE analysis for purified protein after SEC and SCX purification. (e) LC-MS spectrum for purified protein.

(ii) wt H2B protein



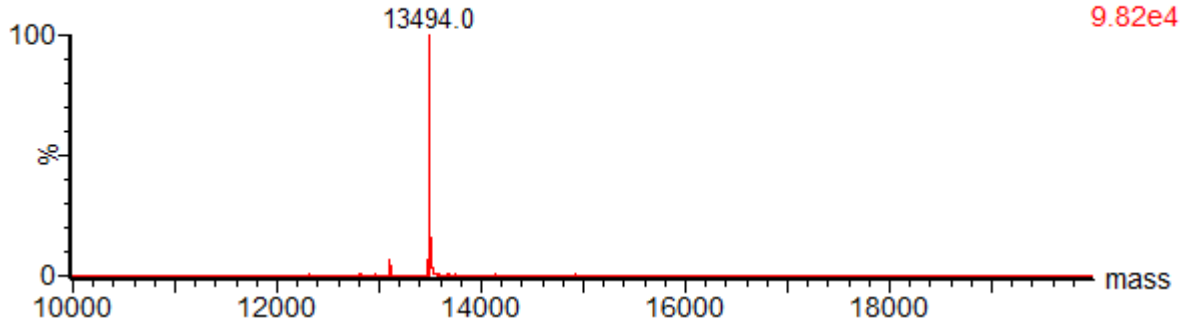
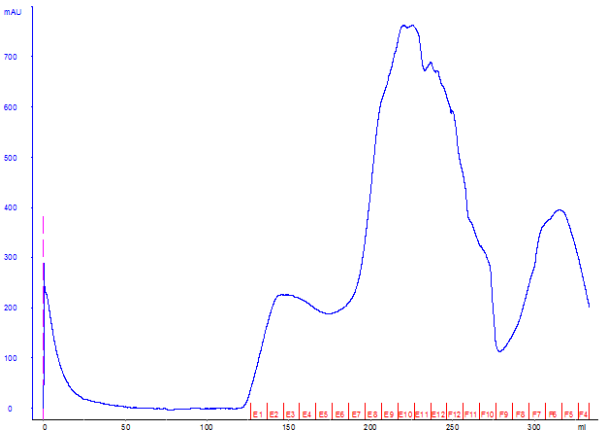


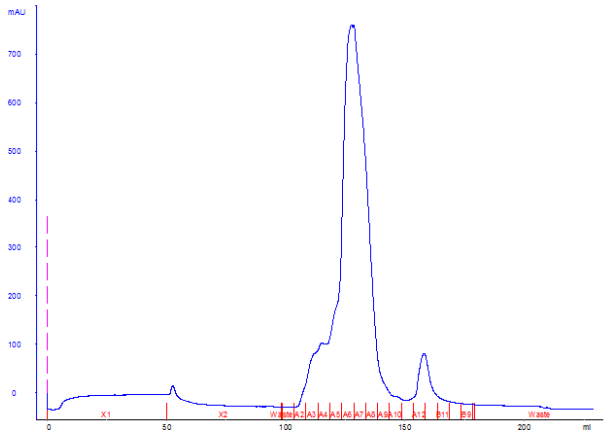
Figure 27. Expression and purification of wt histone protein H2B. (a), (b) FPLC traces for SEC and SCX purification. (c), (d) SDS-PAGE analysis for purified protein after SEC and SCX purification. (e) LC-MS spectrum for purified protein.

(iii) wt H3 protein

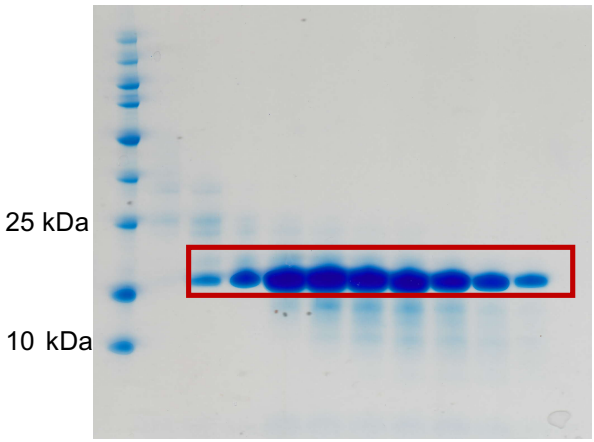
(a)



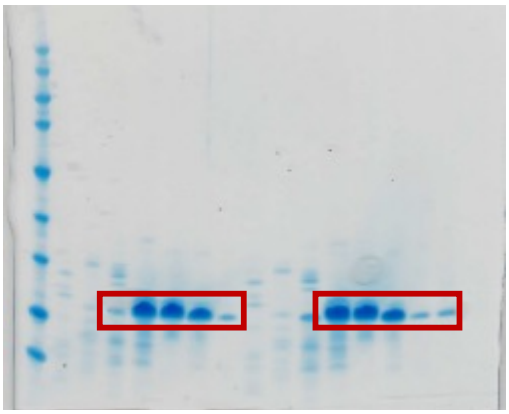
(b)



(c)



(d)



(e)

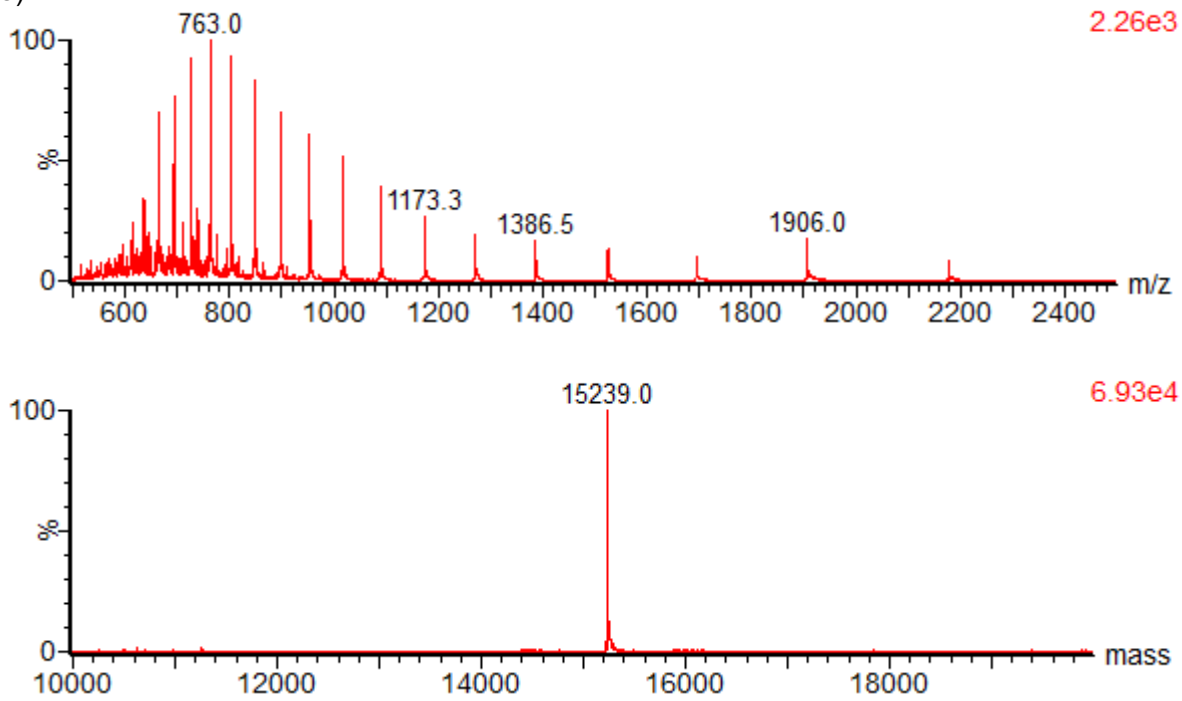
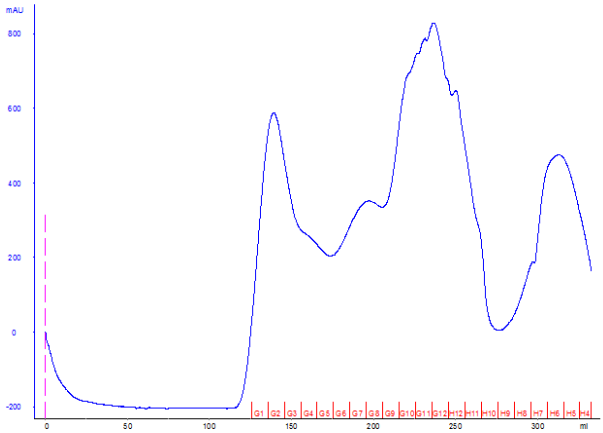


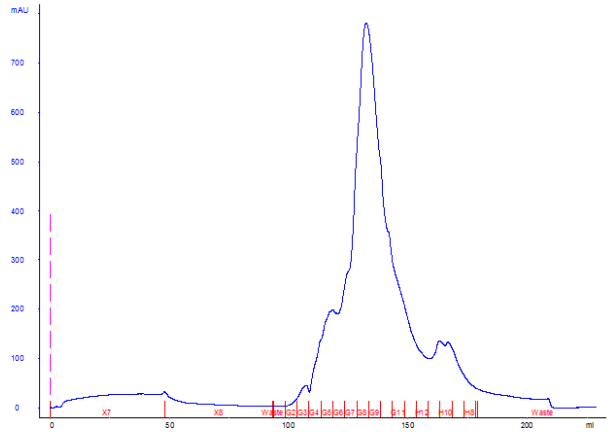
Figure 28. Expression and purification of wt histone protein H3. (a), (b) FPLC traces for SEC and SCX purification. (c), (d) SDS-PAGE analysis for purified protein after SEC and SCX purification. (e) LC-MS spectrum for purified protein.

(iv) wt H4

(a)



(b)



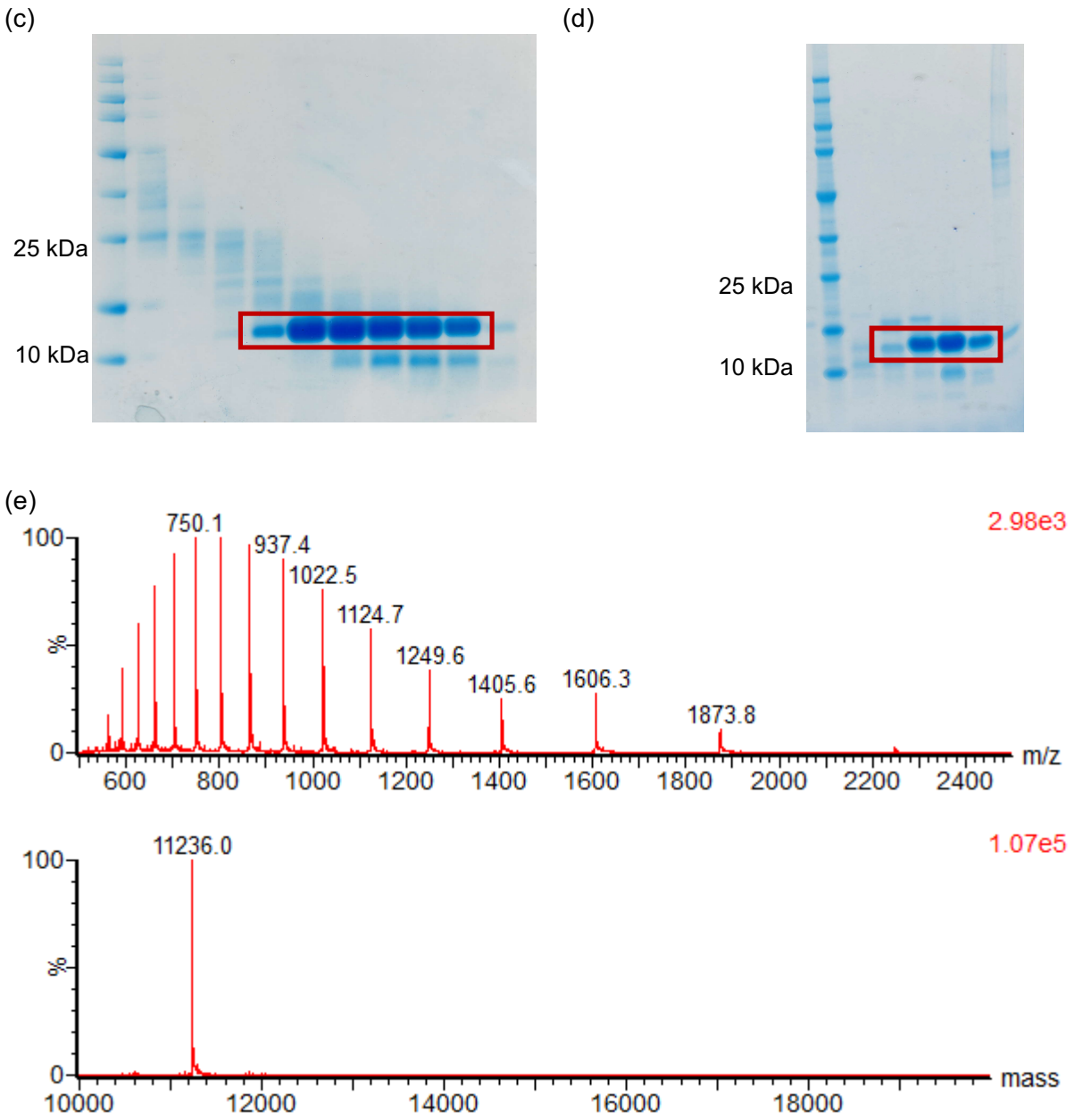


Figure 29. Expression and purification of wt histone protein H4. (a), (b) FPLC traces for SEC and SCX purification. (c), (d) SDS-PAGE analysis for purified protein after SEC and SCX purification. (e) LC-MS spectrum for purified protein.

2.4.3 Expression and purification of Histone protein variants

Four different histone variants were designed for study in this chapter. They are as follows:

(i) H2B-S112C protein: Plasmid encoding H2B-S112C protein was designed by Dr. Lukas Lercher using side-directed mutagenesis. The gene sequence and corresponding amino acid sequence for the protein is given below.

DNA sequence:

ATGGCCAAGTCCGCTCCAGCCCCGAAGAAAGGCTCCAAGAAAGCGGTGACCAAGACT
CAGAAGAAAGACGGGAAAAAGCGCAGGAAGACAAGGAAGGAGAGTTATGCCATTTACG
TGTACAAGGTGCTGAAGCAGGTGCACCCCGATACCGGCATCTCGTCCAAGGCCATGAG
CATCATGAACTCCTTTGTCAACGATGTGTTTGAGCGCATCGCAGGGGAAGCCTCCCGC
CTGGCTCATTACAACAAGCGCTCCACCATCACCTCCCGGGAGATCCAGACCGCGGTCC
GACTGCTGCTGCCTGGGGAGTTGGCCAAACACGCCGTGTGCGAGGGCACCAAGGCTG
TCACCAAGTACACCAGCGCCAAGTAACTGCTGCTGCCGGATCCGGCTGCTAACAAAGC
CCGAAAGGAAGCTGAGTTGGCTGCTGCCACCGCTGAGCAATAACTAG

Translated Amino Acid Sequence:

MAKSAPAPKK GSKKAVTKTQ KKDGKKRRKT RKESYAIYVY KVLKQVHPDT
GISSKAMSIM NSFVNDVFER IAGEASRLAH YNKRSTITSR EIQTAVRLLL
PGELAKHAV**C** EGTKAVTKYT SAK

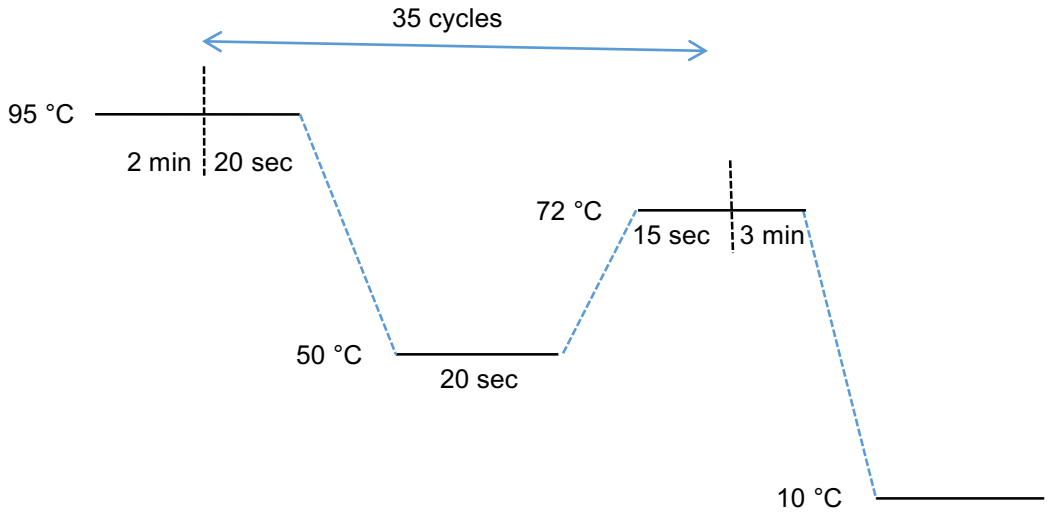
H2B S112C protein was expressed and purified using same protocol as for wt proteins.

(ii) FLAG-tagged wt H2B and H2B S112C proteins: Starting from wt H2B and H2B S112C plasmids, FLAG-tag was introduced on their *N*-terminal using sub-cloning. The following primers were designed and obtained commercially.

Forward Primer: acgtac CATATG GACTACAAAGACGACGACGACAAA GGC GCC AAG TCC GCT CCA GCC

Reverse primer: acgtac GGATCC TTA CTT GGC GCT GGT GTA CTT GGT G

The primers were obtained commercially and were diluted to a final concentration of 100 pmol/µL. In a typical PCR reaction set-up, 5 µL of *Pfu* DNAP 10x buffer, 1 µL of dNTP mix (10 mM), 1 µL of DNA template (100 ng/µL), 1 µL of both primers (10 pmol/µL), and 1 µL of *Pfu* DNA polymerase were taken in a PCR tube. The volume was made up to 50 µL using water. The tubes were placed in a thermal cycler programmed to run the cycle shown below:



The PCR reaction mixture was checked on 1% Agarose gel. The PCR product was extracted using the QIAquick® gel extraction kit protocol (Qiagen). The PCR products and pET3 vector were digested using the restriction enzymes NdeI & BamHI HF. The digested PCR product and vector were checked on Agarose gel and extracted as before. Thereafter, the digested vector and PCR product was ligated. In a typical ligation experiment, 50 ng of digested vector was combined with a 3-fold molar excess of PCR product in an eppendorf tube. 1 µL of T4 DNA ligase, 2 µL of 2x Quick ligation buffer were added to the tube. Water was added to adjust the volume to 20 µL. Reaction mixture was centrifuged briefly and was incubated at room temperature for 20 minutes. The ligated product was used for transformation in XL10-gold cells. Starting from the transformed cells, plasmid DNA was isolated and sequenced. The gene sequence and corresponding amino acid sequence for the constructs are given below:

DNA sequence for FLAG-tagged H2B:

ATGGACTACAAAGACGACGACGACAAAGGCGCCAAGTCCGCTCCAGCCCCGAAGAAA
GGCTCCAAGAAAGCGGTGACCAAGACTCAGAAGAAAGACGGGAAAAAGCGCAGGAAG
ACAAGGAAGGAGAGTTATGCCATTTACGTGTACAAGGTGCTGAAGCAGGTGCACCCCG
ATACCGGCATCTCGTCCAAGGCCATGAGCATCATGAACTCCTTTGTCAACGATGTGTTT
GAGCGCATCGCAGGGGAAGCCTCCCGCCTGGCTCATTACAACAAGCGCTCCACCATC

ACCTCCCGGGAGATCCAGACCGCGGTCCGACTGCTGCTGCCTGGGGAGTTGGCCAAA
CACGCCGTGTCCGAGGGCACCAAGGCTGTCACCAAGTACACCAGCGCCAAGTAAGGA
TCCGGCTGCTAACAAAGCCCGAAAGGAAGCTGAGTTGGCTGCTGCCACCGCTGAGCA
ATAACTAG

Corresponding Amino Acid Sequence:

MDYKDDDDKG AKSAPAPKK GSKKAVTKTQ KKDGKKRRKT RKESYAIYVY
KVLKQVHPDT GISSKAMSIM NSFVNDVFER IAGEASRLAH YNKRSTITSR
EIQTAVRLLL PGELAKHAVS EGTKAVTKYT SAK

DNA sequence for FLAG-tagged H2B-S112C:

ATGGACTACAAAGACGACGACGACAAAGGCGCCAAGTCCGCTCCAGCCCCGAAGAAA
GGCTCCAAGAAAGCGGTGACCAAGACTCAGAAGAAAGACGGGAAAAAGCGCAGGAAG
ACAAGGAAGGAGAGTTATGCCATTTACGTGTACAAGGTGCTGAAGCAGGTGCACCCCG
ATACCGGCATCTCGTCCAAGGCCATGAGCATCATGAACTCCTTTGTCAACGATGTGTTT
GAGCGCATCGCAGGGGAAGCCTCCCGCCTGGCTCATTACAACAAGCGCTCCACCATC
ACCTCCCGGGAGATCCAGACCGCGGTCCGACTGCTGCTGCCTGGGGAGTTGGCCAAA
CACGCCGTGTGCGAGGGCACCAAGGCTGTCACCAAGTACACCAGCGCCAAGTAAGGA
TCCGGCTGCTAACAAAGCCCGAAAGGAAGCTGAGTTGGCTGCTGCCACCGCTGAGCA
ATAACTAG

Corresponding Amino Acid Sequence:

MDYKDDDDKG AKSAPAPKK GSKKAVTKTQ KKDGKKRRKT RKESYAIYVY
KVLKQVHPDT GISSKAMSIM NSFVNDVFER IAGEASRLAH YNKRSTITSR
EIQTAVRLLL PGELAKHAVC EGTKAVTKYT SAK

FLAG-tagged proteins were expressed and purified using same protocol as for wt proteins.

FPLC traces and SDS-PAGE gels for purification are shown below **(Figure 30,31)**.

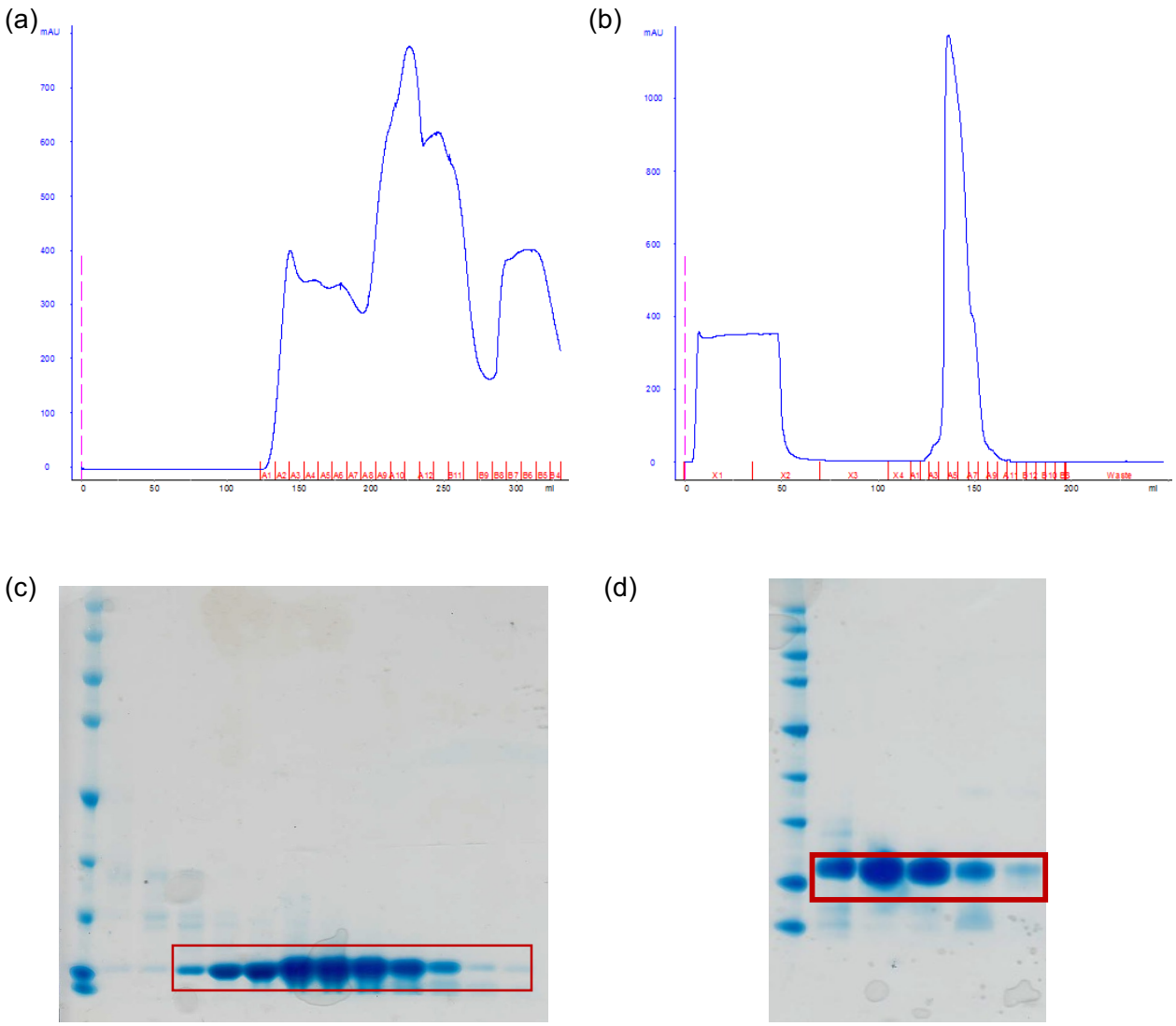
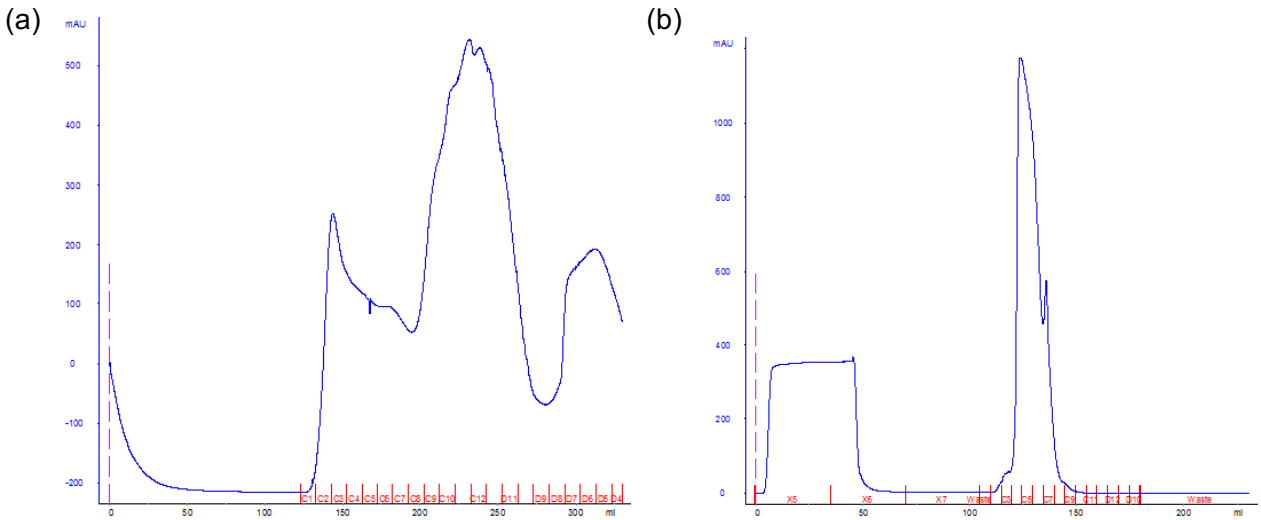
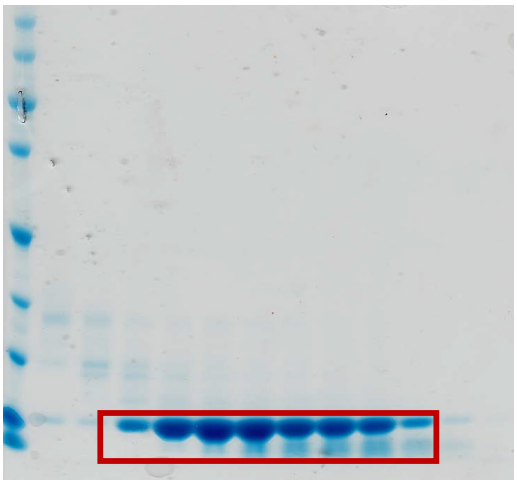


Figure 30. Expression and purification of FLAG-tagged H2B protein. (a), (b) FPLC traces for SEC and SCX purification. (c), (d) SDS-PAGE analysis for purified protein after SEC and SCX purification.



(c)



(d)

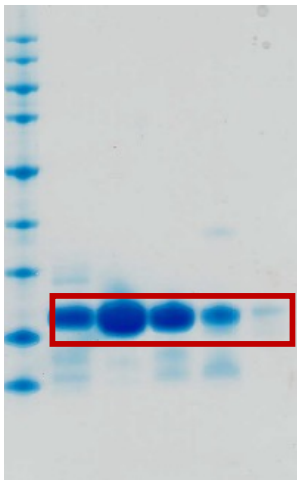


Figure 31. Expression and purification of FLAG-tagged H2B-S112C protein. (a), (b) FPLC traces for SEC and SCX purification. (c), (d) SDS-PAGE analysis for purified protein after SEC and SCX purification.

(iii) Tailless H4 protein: Plasmid encoding for Taillless H4 protein was designed starting for wt H4 plasmid through sub-cloning. The following primers were used for sub-cloning:

Forward Primer: agtcat CAT ATG AAA GTT CTG CGT GAC AAC ATC C

Reverse Primer: ATT AAT GGA TCC TTA ACC ACC GAA ACC GTA CAG G

Sub-cloning was done as before except for the annealing temperature which was kept at 54 °C in this case. The success of sub-cloning was checked by sequencing. The gene sequence and the corresponding amino acid sequence are given below:

DNA sequence for tailless H4:

ATGAAAGTTCTGCGTGACAACATCCAGGGTATCACCAAGCCGGCTATCCGTCGTCTGG
CTCGTCGTGGTGGTGTTAAACGTATCTCCGGTCTGATCTACGAAGAAACCCGCGGTGT
TCTGAAAGTTTTCCTGGAAAACGTTATCCGTGACGCTGTTACCTACACCGAACACGCTA
AACGTAAAACCGTTACCGCTATGGACGTTGTTTACGCTCTGAAACGTCAGGGTCGTACC
CTGTACGGTTTCGGTGGTTAAGGATCCGGCTGCTAACAAAGCCCGAAAGGAAGCTGAG
TTGGCTGCTGCCACCGCTGAGCAATAACTAG

Corresponding Amino Acid Sequence:

MKVLRDNIQG ITKPAIRRLA RRGGVKRISG LIYEETRGVL KVFLENVIRD
AVTYTEHAKR KTVTAMDVVY ALKRQGRTLY GFGG

The protein was expressed as described earlier. The cells were resuspended in the lysis buffer and stored at -20 °C waiting purification.

2.4.4 Site-selective chemical protein modification

Synthesis of DBHDA and GlcNAc-thiol has been previously described.[31] DBHDA and GlcNAc-thiol were kindly provided by Dr. Phin Chooi and Dr. Arghya Modak respectively.

(i) Synthesis of H2B-Ser112 Dha protein

5.10 mg (0.37 μmol) of H2B-S112C protein was weighed in an eppendorf tube. 500 μL of freshly prepared reaction buffer (5 M Gd.HCl, 300 mM HEPES pH 7.5) was added to it and the mixture was vortexed gently. 6 mg of DTT was added to the protein solution. The protein solution was reduced at 37 °C for 30 minutes. The sample was desalted using a pre-equilibrated PD minitrap G-25 column (GE Healthcare Life Sciences). Desalted protein was eluted in 1 mL of reaction buffer.

100 equivalents of DBHDA solution (35 μmol, 0.50 M in DMF, 70 μL) was added to 950 μL (0.35 μmol) of reduced protein sample. The reaction mixture was incubated at room temperature for 30 minutes and then at 37 °C. The progress of reaction was monitored by LC-MS.

LC-MS analysis was performed using a Prominence HPLC system (Shimadzu) connected to an ESI-TOF Micromass LCT Classic (Waters) mass spectrometer. The protein sample was loaded onto a Chromolith® FastGradient RP-18 column (Merck) with solvent A (0.1 % Formic Acid in water). The protein sample was analyzed using a gradient from 20 % to 60 % solvent B (0.1 % Acetonitrile) in 4.5 minutes at a flow rate of 0.4 mL /minute. The capillary and cone voltage for the electrospray source was kept at 3000 V and 25 V respectively. The raw MS data was processed using MassLynx software (Waters, version 4.1). Myoglobin protein was used for creating calibration file. Deconvolution of spectra was done using in-built MaxEnt algorithm.

The reaction reached completion after 3 hours yielding H2B Ser112Dha **(Figure 32)**. The reaction mixture was desalted using a pre-equilibrated PD miditrap G-25 column (GE Healthcare Life Sciences). Protein sample was eluted in 1.5 mL of reaction buffer.

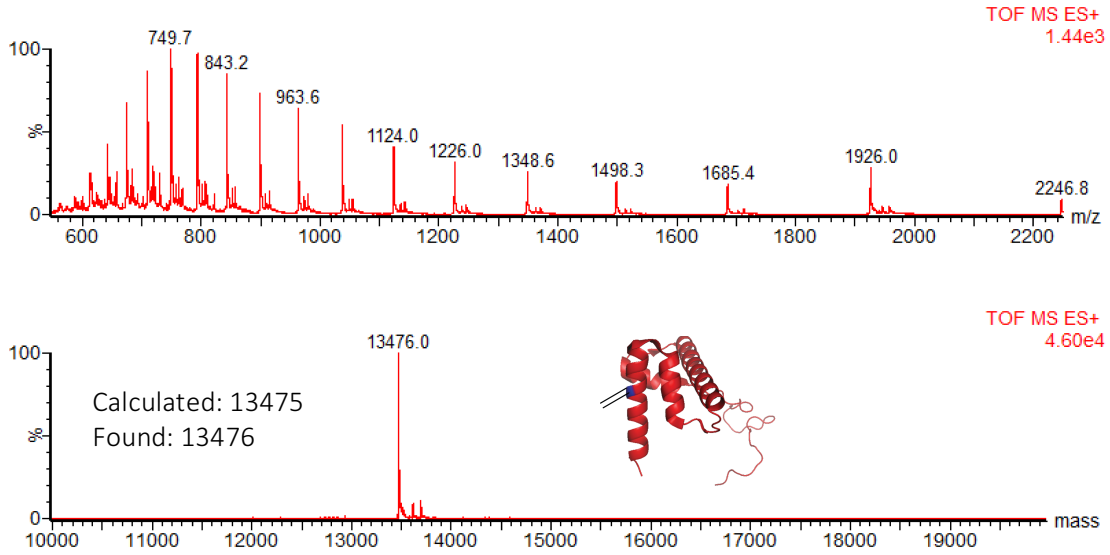


Figure 32. LC-MS Spectrum of H2B-S112-Dha protein. (Reproduced from Raj *et al.*[1])

(ii) Synthesis of H2B Ser112 GlcNAc

1 mL of desalted H2B S112Dha (2.50 mg, 0.185 µmol) in reaction buffer was transferred to an eppendorf tube. 400 equivalent of GlcNAc-thiol (17.55 mg, 74 µmol) was added to the protein sample as solid. The reaction mixture was incubated at room temperature for 30 minutes and then at 37 °C. The progress of reaction was monitored by LC-MS as described earlier. The reaction reached completion in 3 hours resulting in first homogeneous synthesis of H2B S112 GlcNAc **(Figure 33)**. The reaction mixture was desalted using a pre-equilibrated PD miditrap G-25 column (GE Healthcare Life Sciences). Protein sample was eluted in 1.5 mL of unfolding buffer (7 M Gd.HCl, 10 mM Tris pH 7.5, 1 mM DTT, 1 mm EDTA) and stored at -20 °C till further manipulation.

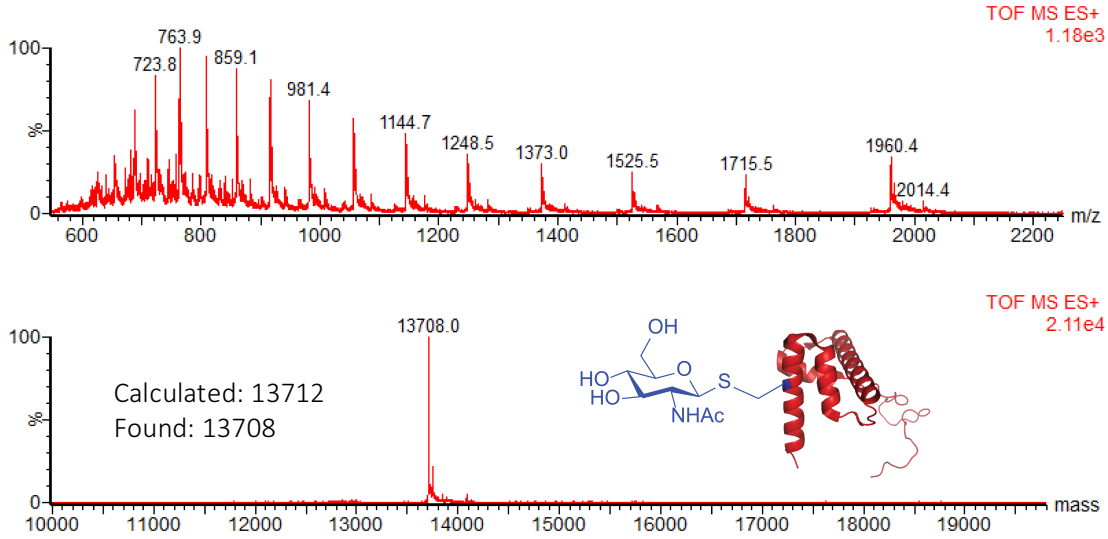


Figure 33. LC-MS Spectrum of H2B-S112-GlcNAc protein. (Reproduced from Raj *et al.*[1])

(iii) Synthesis of FLAG-tagged H2B-Ser112 Dha protein

3.10 mg (0.21 µmol) of FLAG-tagged H2B-S112C protein was transferred to an eppendorf tube. 500 µL of freshly prepared reaction buffer (5 M Gd.HCl, 300 mM HEPES pH 7.5) was added and the mixture was vortexed gently. Then, 10 mg of DTT was added to the protein solution. The protein mixture was incubated at 37 °C for 30 minutes. The sample was desalted using a pre-equilibrated PD minitrap G-25 column (GE Healthcare Life Sciences) and eluted in 1 mL of reaction buffer.

100 equivalents of DBHDA solution (21 µmol, 0.50 M in DMF, 42 µL) was added to 1000 µL (0.21 µmol) of reduced protein sample. The reaction mixture was incubated at 25 °C for 30 minutes and then at 37 °C for 2 hours. LC-MS analysis revealed completion of reaction after 2 hours **(Figure 34)**. The reaction mixture was desalted using a pre-equilibrated PD miditrap G-25 column (GE Healthcare Life Sciences). Protein sample was eluted in 1.5 mL of reaction buffer.

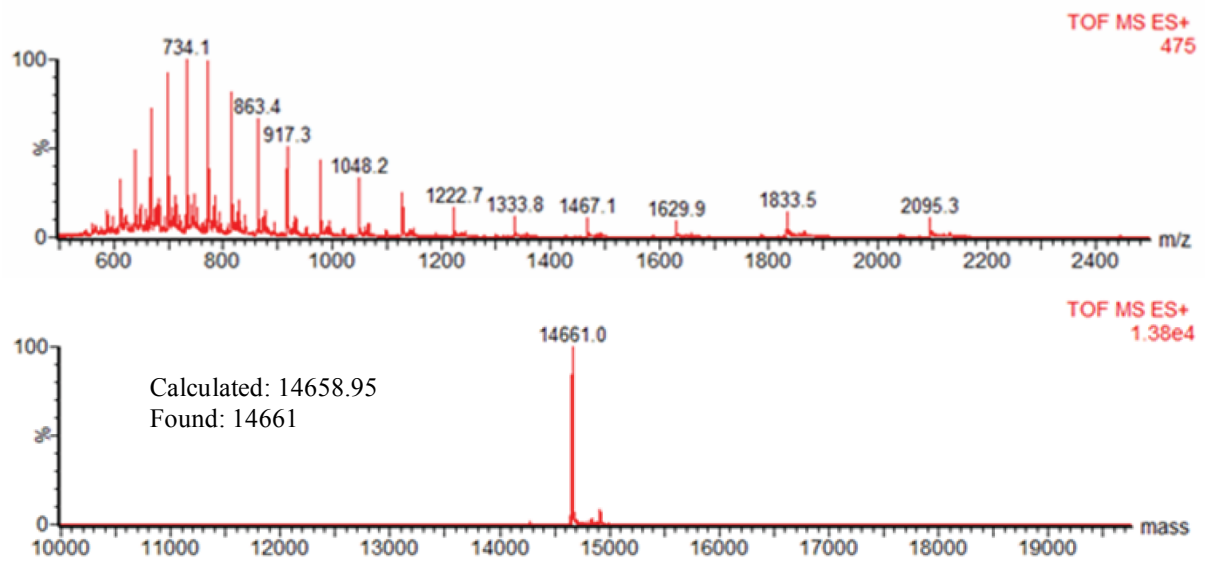


Figure 34. LC-MS Spectrum of FLAG-tagged H2B-S112-Dha protein. (Reproduced from Raj *et al.*[1])

(iv) Synthesis of FLAG-tagged H2B-Ser112-GlcNAc protein

1 mL of desalted FLAG-tagged H2B-S112 Dha protein (2.09 mg, 0.14 µmol) in reaction buffer was transferred to an eppendorf tube. 500 equivalent of GlcNAc-thiol (16.66 mg, 70 µmol) was added to the protein sample as solid. The reaction mixture was incubated at 37 °C with shaking and monitored by LC-MS. The reaction reached completion in 90 minutes **(Figure 35)**. The reaction mixture was desalted using a pre-equilibrated PD miditrap G-25 column (GE Healthcare Life Sciences). Protein sample was eluted in 1.5 mL of reaction buffer (5 M Gd.HCl, 300 mM HEPES pH 7.5) and stored at -20 °C till further manipulation.

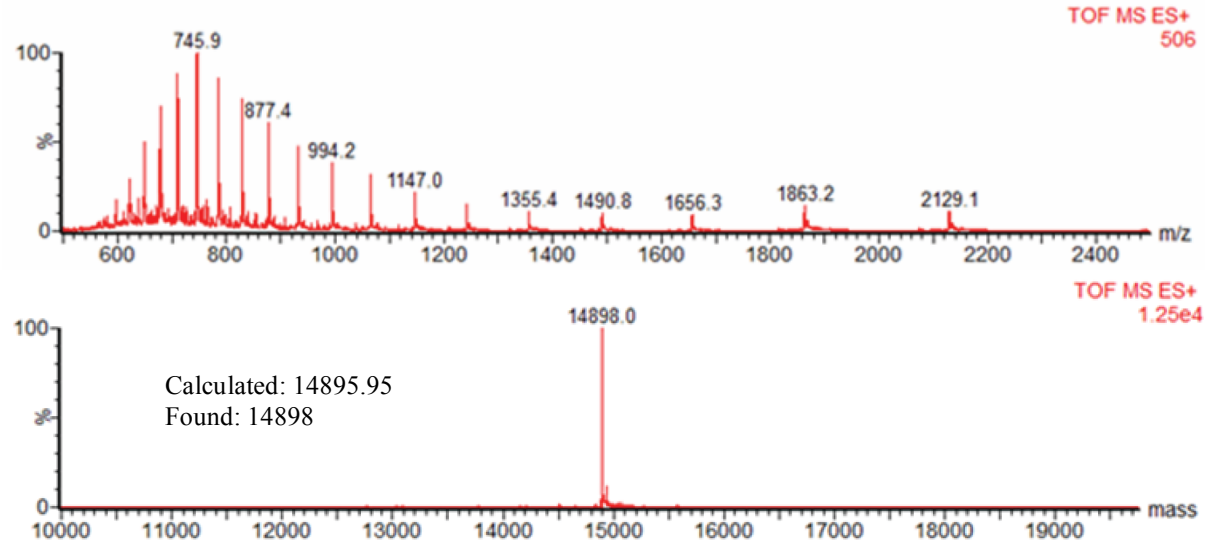


Figure 35. LC-MS Spectrum of FLAG-tagged H2B-S112-GlcNAc protein. (Reproduced from Raj *et al.*[1])

2.4.5 LC-MS/MS analysis for H2B-S112 GlcNAc

Site-selective installation of GlcNAc at H2B-S112 was verified by LC-MS/MS analysis. 25 µg of synthesized GlcNAcylated H2B protein was buffer exchanged against 100 µL of denaturing buffer (2 M Urea, 50 mM Ammonium Bicarbonate). The sample was reduced with DTT (2 µL of 200 mM solution in denaturing buffer) at 56 °C for 20 minutes, followed by alkylation with iodoacetamide (4 µL of 200 mM solution in denaturing buffer) at room temperature for 30 minutes. Alkylation was quenched by further addition of 2 µL of DTT solution. Trypsin was added to the sample in 1:50 (Enzyme: Protein (w/w)) ratio. The sample was incubated at 37 °C for 16 hours. The digested sample was diluted to a final concentration of 100 fmol/ µL using 10 % Formic Acid solution.

Resulting tryptic peptides were analyzed on an EASY-nLC 1000 UHPLC system (Proxeon) connected to an Orbitrap Elite mass spectrometer (Thermo Fischer Scientific) possessing an EASY-Spray nano-electrospray ion source (Thermo Fischer Scientific). The peptides were trapped on an in-house packed guard column (75 µm i.d. x 20 mm, reprosil C18, 3µm, 120 Å) using solvent A (0.1% Formic Acid, 5 % DMSO in water) at a pressure of 500 bar. The peptides were separated on an EASY-spray Acclaim PepMap® analytical column (75 µm i.d. × 500 mm, RSLC C18, 2 µm, 100 Å) using a linear gradient (length: 58 minutes, 8 % to 30 % solvent B (0.1% formic acid, 5 % DMSO in acetonitrile), flow rate: 200 nL/min). The separated peptides were electrosprayed directly into the mass spectrometer operating in a data-dependent mode using a HCD/ETD based method.[43,44] Full scan MS spectra (scan range 350-1500 m/z, resolution 30000, AGC target 1e6, maximum injection time 250 ms) and sub-sequent HCD MS/MS spectra (resolution 15000, AGC target 3e4, maximum injection time 500 ms) of 5 most intense peaks were acquired in the Orbitrap. HCD fragmentation was performed at 30 % of normalized collision energy and the signal intensity threshold was kept at 500 counts. If peaks at any of *m/z* 138.0546, 168.0563 or 204.0867

were detected among top 20 most intense peak of a HCD spectrum, an ETD MS/MS spectrum of the precursor was triggered. ETD spectra (AGC cation target 5e4, AGC anion target 2e5, cation maximum injection time 100 ms) were acquired in the Iontrap.

The raw data was processed using Byonic™ software (Protein Metrics, version 2.0-3). The raw MS file was searched against H2B-S112C sequence as well as list of common contaminants. Trypsin with a maximum number of 2 missed cleavages was selected as the protease. Carbamidomethylation (Cysteine) and GlcNAc (Cysteine) were set as variable modifications. Precursor mass tolerance was set as 10 ppm. Fragment mass tolerances for HCD and ETD were set to 50 ppm and 0.8 Da respectively. LC-MS/MS analysis revealed 82.92% sequence coverage for H2B protein along with GlcNAc modification at S112 site **(Figure 36)**. All glyco-peptide spectra were manually validated.

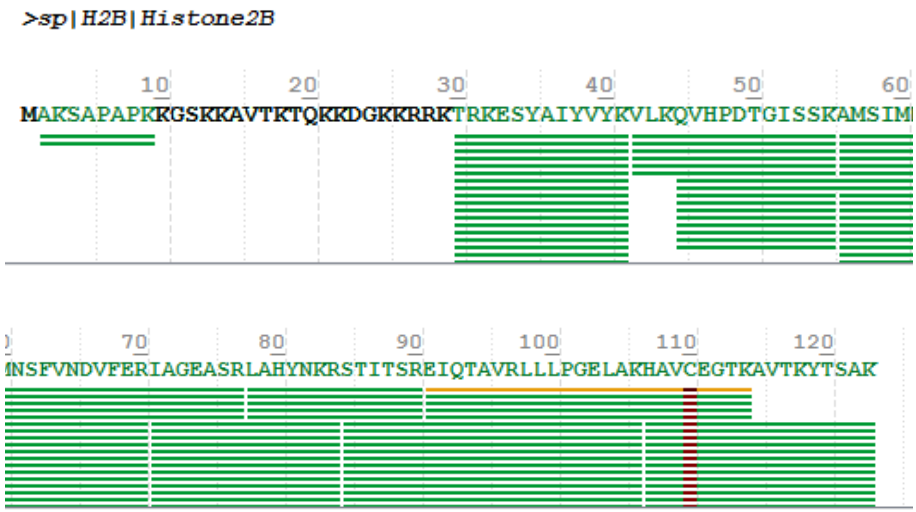


Figure 36. Sequence coverage obtained for GlcNAcylated H2B protein after LC-MS/MS analysis. S112 modification is underlined in red. Section of protein sequence highlighted in green have peptide matches from the MS/MS data.

2.4.6 Histone complex reconstitution

Histone complexes were refolded as described earlier.[37,71,72] For reconstitution purpose, all canonical histone were dissolved in unfolding buffer (7 M Gd.HCl, 10 mM Tris pH 7.5, 1 mM DTT, 1 mm EDTA); H2B-S112 GlcNAc modified protein was desalted in unfolding

buffer during synthesis itself. The exact concentration of each protein sample was measured using Nanodrop based on their molecular weight and extinction co-efficient. For dimer reconstitution, equal amount of H2A and H2B/H2B S112 GlcNAc proteins were mixed to a final protein concentration of 1-1.5 mg/mL. The protein mixture was loaded on a dialysis cassette (MWCO 3500). The sample was dialyzed thrice against 2 L of refolding buffer (2 M NaCl, 10 mM Tris pH 7.5, 1 mM DTT, 5 mM β-ME) for at least 4 hours each, with one dialysis being overnight. After this, the sample was centrifuged to remove precipitate, if any, and refolded histone dimers were purified by gel filtration chromatography (HiLoad 16/60 Superdex 200 column, (GE Healthcare Life Sciences)) in refolding buffer. The purified dimers were concentrated and stored in 50% glycerol at -20 °C for further use.

Wt or H2B S112 GlcNAc modified octamers were reconstituted by mixing H2B or H2B S112 GlcNAc proteins with H2A, H3 and H4 proteins in a ratio of 1, 0.9 and 0.9 respectively to a final protein concentration of 1-1.5 mg/mL. The protein mixture was loaded on a dialysis cassette (MWCO 3500). The sample was dialyzed thrice against refolding buffer for at least 4 hours each. Octamer was purified by gel filtration chromatography as described earlier. The purified octamers were concentrated and stored in 50% glycerol at -20 °C for further use.

As discuss earlier, the synthesized H2B-GlcNAc protein in all likelihood is an epimeric mixture comprising of D- and L-amino acid at the site of modification. In order to investigate whether the epimeric nature of the modification has any influence on the octamer reconstitution, a titration experiment between modified protein and rest of constituent histone proteins was performed. Two octamer reconstitution reaction were set-up. In the first reconstitution experiment, usual amount of proteins as mentioned above were added and in the second reconstitution, twice the amount of modified protein was added. SEC analysis revealed similar reconstitution yield in both the cases with excess of modified protein eluting as monomer in the latter case **(Figure 37)**. The SEC result indicated that epimeric nature of the modification had no effect on octamer reconstitution in this case.

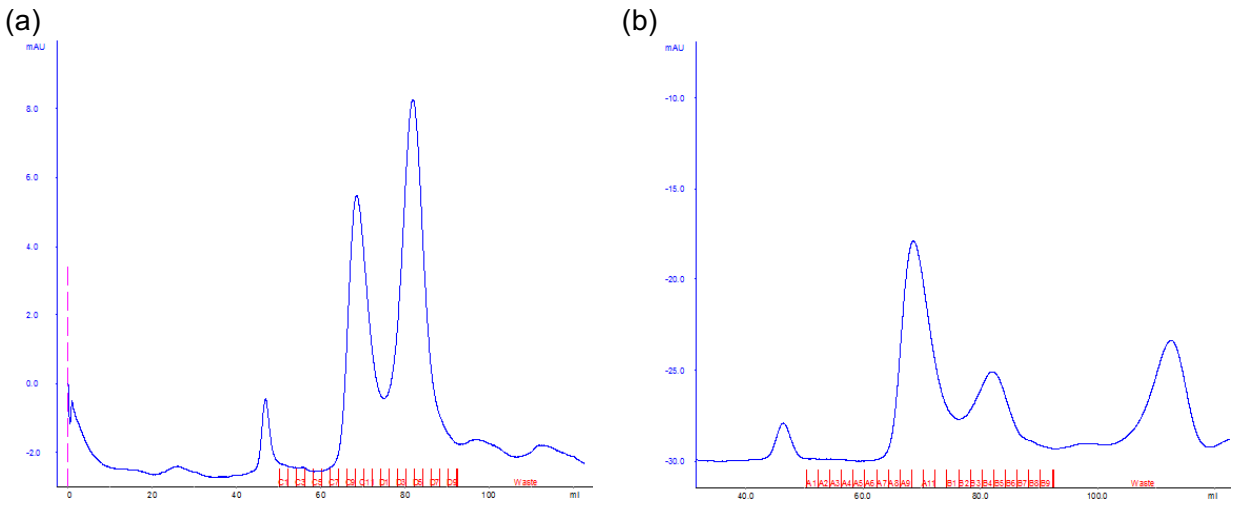


Figure 37. SEC traces for titration experiment for octamer reconstitution.

2.4.7 Large scale DNA preparation for nucleosome reconstitution

(i) 145 bp '601' DNA

Large scale expression and purification of 145 bp '601' DNA was performed as described.[37] The pUC57 plasmid encoding 145 bp '601' DNA was transformed into XL10-gold cells. The transformed cells were plated on freshly prepared LB-Agar/Amp plates. The plates were incubated overnight at 37 °C. A single colony of transformed cells was used to inoculate 100 mL of starter culture (2xYT media containing 100 µg/mL ampicillin). The starter culture was incubated at 37 °C either overnight or until slightly turbid (4-5 hours). These where then used to inoculate six large cultures (800 mL TB media containing 100 µg/mL ampicillin). The large cultures were incubated at 37 °C for 20-22 hours. The cells were then harvested (8000 rpm; 8 min) and re-suspended in a total of 60 mL alkaline lysis buffer 1 (50 mM glucose, 25 mM Tris pH 8.0, 10 mM EDTA) per litre of culture. 120 mL Alkaline lysis buffer 2 (0.2 M NaOH, 1% (w/v) sodium dodecyl sulfate (SDS)) was added and the mixture was shaken vigorously to break down the cellular clumps. The mixture was incubated on ice for 10-20 minutes. Then 210 mL of cold Alkaline lysis buffer 3 (4 M sodium acetate, 2 N acetic acid) was poured down gently down the side of flask. The mixture was shaken well and left to incubate on ice for 20 min. Subsequently, the mixture was centrifuged (10000 g, 20 minutes, 4 °C) and filtered through miracloth. 0.52 volume of isopropanol was added to the DNA containing filtrate and

the mixture was left to stand at room temperature for 15 minutes. The mixture was then centrifuged (10000 g, 30 minutes, 20 °C). The supernatant was decanted and the pellet was air-dried at room temperature for 60 minutes. The pellet was transferred to a 50 mL Falcon tube and was dissolved in 20 mL TE 10/50 buffer (10 mM Tris, 50 mM EDTA pH 8.0). 60 µL RNase A (20mg/mL, PureLink™ ((Thermo Fischer Scientific)) was added and the mixture incubated at 37 °C overnight. Next day, the mixture was centrifuged (JA25.50, 20k rpm, 15 min) to remove particulates. The supernatant was decanted to fresh falcon tubes. The plasmid DNA was precipitated from the supernatant by adding one-fifth of original volume of 4 M NaCl and two-fifth of 40% Peg 6000. The mixture was shaken at 37 °C for 5 min followed by incubation on ice for 30 min. The mixture was centrifuged at 3750 rpm for 20 min. The supernatant was decanted. The pellet was dissolved in 15 mL TE 10/0.1 buffer (10 mM Tris, 0.1 mM EDTA pH 8.0) by incubation at 37 °C overnight. The supernatant and dissolved pellet were checked on Agarose gel to ensure no contamination of DNA by RNA.

The concentration of the plasmid DNA was determined using Nanodrop. The 145 bp DNA fragment was excised from the plasmid DNA by restriction digestion of plasmid DNA using EcoRV enzyme. 30 units of EcoRV-HF (NEB) per nmol of restriction site was added to plasmid DNA dissolved in 1x CutSmart buffer (NEB). The restriction digestion was performed at 37 °C for 16 hours. The extent of the reaction was checked using 1% Agarose gel. Once the reaction was complete, the insert was precipitated by addition of 0.192 volume of 4 M NaCl and 0.346 volume of 40% PEG 6000. The mixture was incubated on ice for 1 hour followed by centrifugation (27000 g, JA25.50, 20 minutes, 4 °C). The supernatant containing the insert was transferred to fresh tubes. The partition of plasmid DNA and insert was checked by Agarose gel. The insert was precipitated by addition of 3 volumes of ice-cold ethanol. The mixture was incubated on ice for 1 hour followed by centrifugation (27000 g, JA25.50, 20 minutes, 4 °C). The insert was dissolved in TE 10/0.1 and further purified by phenol extraction and ethanol precipitation. The DNA was stored at -20 °C for further use.

The sequence of 145 bp ‘601’ DNA is given below:

ATCAGAATCCCGGTGCCGAGGCCGCTCAATTGGTCGTAGACAGCTCTAGCACCGCTTA
AACGCACGTACGCGCTGTCCCCCGCGTTTTAACCGCCAAGGGGATTACTCCCTAGTCT
CCAGGCACGTGTCAGATATATACATCGAT

(ii) 186 bp biotinylated '601' DNA

The bacterial plasmid encoding single and sixteen repeat of 186 bp '601' DNA was a kindly donated by Prof. Till Bartke, Imperial College, London. The insert DNA was excised and biotinylated as described earlier.[21,37] Plasmid DNA was extracted in a similar protocol as that used for 145 bp DNA.

The 186 bp insert was excised from the plasmid DNA by restriction digestion using EcoRV enzyme. In a typical digestion reaction, plasmid (1 mg/mL) was taken in 1x CutSmart buffer (NEB) and EcoRV (~ 130 u/mg DNA) was added to it. The digestion was performed for 16 hours at 37 °C. The digested fragment was separated from the vector DNA by PEG precipitation. The final concentrations of NaCl and PEG-6000 in the digestion reaction were adjusted to 0.5 M and 7% respectively using 4 M NaCl and 40% PEG-6000 solutions. The mixture was incubated on ice for 1 hour followed by centrifugation (27000 g, 20 minutes, 4 °C). The supernatant containing the EcoRV digested insert was decanted to fresh falcon tubes. The fragment was precipitated by addition of 2.5 volumes of ice-cold ethanol. The precipitated fragment was dissolved in milli-Q water. The EcoRV fragment was further digested by EcoRI (1 mg/mL EcoRV fragment; 300 u EcorI/mg DNA). The digest was performed at 37 °C for 16 hours. The digested fragment was ethanol precipitated as before. The EcoRI digested fragment was dissolved in water and was biotinylated. In a typical biotinylation reaction, 4 mg of DNA (0.407 mg/mL DNA) was taken in 1x NEBuffer 2. 100 µM dATP (NEB), 40 µM Biotin-11-dUTP (York Biosciences) and 33.3 u/mL Klenow 3` to 5` exo (NEB) was added to the reaction mixture. The reaction mixture was incubated at 25 °C for 2 hours and the reaction was quenched by addition of EDTA to a final concentration of 20 mM. The biotinylated reaction product was then phenol extracted, ethanol precipitated and re-suspended in water. The biotinylated DNA was stored at -20 °C for further use. While preparing

the DNA starting from plasmid encoding single copy of 186 bp DNA, as was done to avoid possible recombination/mutation problem, double restriction digest using EcoRV and EcoRI was done in a single step.

The sequence of 186 bp '601' DNA is given below:

ATCGGATCTTACATGCACAGGATGTATATATCTGACACGTGCCTGGAGACTAGG
GAGTAATCCCCTTGGCGGTTAAAACGCGGGGGACAGCGCGTACGTGCGTTTAA
GCGGTGCTAGAGCTGTCTACGACCAATTGAGCGGCCTCGGCACCGGGATTCTC
CAGGGCGGCCGCGTAGTACTGAA**U(Biotin)U(Biotin)**

2.4.8 Nucleosome reconstitution

The nucleosome were reconstituted as described earlier.[37,72] Nucleosomes were reconstituted using 145 bp DNA for stability assessment and using 186 bp biotinylated DNA for immobilization/pulldown purposes. The correct ratio of DNA to octamer for nucleosome reconstitution was found by performing titration experiment on small scale (~ 10-20 µg). The titration experiment was performed by mixing wt/modified octamer with DNA in a molar ratio of 1:0.85, 1:1, and 1:1.15. The mixing was done in high-salt buffer (2 M KCl, 10 mM Tris pH 7.5, 1 mM EDTA, 1 mM DTT) and the mixture was transferred to a 100 µL dialysis cup (3500 or 10000 MWCO). The mixture was dialyzed sequentially against buffer with lower-salt concentrations (0.85 M KCl, 0.65 M KCl, and 0.25 M KCl). Each dialysis step was done for at least 2 hours. The octamer-DNA ratio of 1:0.85 was found to be optimal for nucleosome reconstitution. Small-scale reconstitutions (up to 100 µg) were done using the protocol as described above.

For large scale reconstitution, DNA and octamer were combined using high-salt buffer in the ratio described above and transferred to a 6-8 kda MWCO dialysis tube. The tube was transferred to a 500 mL beaker containing 400 mL of high-salt buffer. 2 L of low-salt buffer (250 mM KCl, 10 mM Tris pH 7.5, 1 mM EDTA, 1 mM DTT) was prepared. Low-salt buffer was added slowly (at rate of 0.8 mL/min) to the beaker using a peristaltic pump. Simultaneously, buffer was being removed from the beaker at the same rate using another

peristaltic pump keeping the total volume in the beaker constant. This method leads to a slow-salt gradient over 36 hours and results in efficient nucleosome reconstitution.

After dialysis, the samples were transferred to eppendorf tubes and centrifuged to remove any precipitation, if any. The reconstituted nucleosomes were analyzed by Native-PAGE using Novex TBE Gels (6%, Invitrogen). The TBE gel was pre-run in 0.5 % TBE buffer at 150 V for 90 minutes at 4 °C. 0.5-1 µg (1 µL) of nucleosome samples along with 5 µL of 6 % sucrose solution were loaded per well. 100 bp DNA ladder was also added. The gel was run at 150 V for 90 minutes. The gel was stained with SYBR® Gold nucleic acid gel stain (Invitrogen) followed by Coomassie Brilliant Blue stain.

2.4.9 Circular Dichroism Analysis

(i) CD analysis of the H2B monomers

Wild-type H2B protein and H2B-S112 GlcNAc protein were buffer exchanged into 20 mM $NaHPO_4$ pH 7.2, 200 mM KCl, 0.1 mM EDTA by dialysis. CD spectra were recorded using a Chirascan CD-spectrophotometer (Applied Photophysics). For the measurement, 200 µL of 10 µM protein samples were taken in a micro-cuvette (1 mm path length). CD spectra were recorded from 200–340 nm with a step size of 0.5 nm and 1 second per point. The initial spectra were recorded in triplicates. The three traces were averaged and smoothed using in-built savitzky-golay function (window size 4). The raw data were imported from the Pro-data as CSV and further processed using OriginPro. Prior to plotting the spectra, background for the buffer was subtracted.

(ii) CD analysis of the H2A/B dimers

Wild-type H2A/B dimer and H2B-S112 GlcNAc modified dimer were buffer exchanged into 20 mM $NaHPO_4$ pH 6.7, 1 mM EDTA, 150 mM NaCl by dialysis. CD spectra were recorded using a Chirascan CD-spectrophotometer (Applied Photophysics). For the measurement, 200 µL of 6.2 µM protein samples were taken in a micro-cuvette (1 mm path length). CD spectra were recorded from 200–340 nm with a step size of 0.5 nm and 0.5 second per point. The

initial spectra were recorded in triplicates. The three traces were averaged and smoothed using in-built savitzky-golay function (window size 4). The raw data were imported from the Pro-data as CSV and further processed using OriginPro. Prior to plotting the spectra, background for the buffer was subtracted.

For melting curves, the temperature was increased stepwise from 25–90 °C in 1 °C steps with a hold time of 60 seconds. The temperature of the sample as measured by a sample probe was recorded for each step. The raw data were exported from the Pro-data as CSV and further processed using OriginPro. The melting temperature was extracted by plotting the CD at 220 nm against temperature and fitting using a Boltzmann sigmoidal function. Reported are the fitted parameters including the standard error.

(iii) CD analysis of the nucleosome

Nucleosomes (1 µM) were buffer exchanged into 10 mM $NaHPO_4$ pH 7.5, 1 mM EDTA, 150 mM NaCl. For the measurement, 200 µl of nucleosome solution in a micro cuvette (1 mm path length) was used. CD spectra were recorded from 200–340 nm with a step size of 0.5 nm and 1 second measurement per point. For melting curves, temperature was ramped stepwise from 25–90 °C in 1 °C steps with 120 seconds at each temperature. The melting temperature was extracted by plotting the CD at 220 and 260 nm against temperature and fitting using a Boltzmann sigmoidal function. Reported are the fitted parameters including the standard error.

(iv) CD analysis of the FLAG tagged H2B monomers

FLAG tagged Wild-type H2B protein and FLAG tagged H2B-S112 GlcNAc protein were buffer exchanged into 10 mM Tris pH 7.5, 250 mM KCl, 1 mM EDTA by dialysis. CD analysis was done as earlier for the H2B monomers.

2.4.10 Nuclear extract preparation

HeLa cell tissue culture were performed in sterile condition inside a HERAsafe KS-12 Class II biological safety cabinet (Thermo Fischer Scientific). For biological replicates, HeLa cells from different batches were grown. The cells were grown to near-confluency in a HYPERFlask™ cell culture vessel (Corning Life Sciences) containing 500 mL DMEM medium supplemented with 10 % FBS and 1 % Pen-Strep. Cells were trypsinized and were washed with 10 mL of ice-cold PBS buffer by centrifugation at 300g for 5 minutes at 4 °C.

The HeLa nuclear extract was prepared using an adapted protocol as previously described [http://www.cyclex.co.jp/resource/protocol/classical_biochemical/preparation_of_nuclear_extracts.pdf]. For nuclear extract preparation, following buffers were freshly prepared: (a) Lysis Buffer (10 mM Tris pH 7.5, 10 mM NaCl, 15 mM $MgCl_2$, 250 mM Sucrose, 0.1 mM EGTA, 0.5% NP-40); (b) Sucrose Cushion (30% Sucrose, 10 mM Tris pH 7.5, 10 mM NaCl, 3 mM $MgCl_2$); (c) Wash buffer (10 mM Tris pH 7.5, 10 mM NaCl); and (d) Extraction buffer (50 mM HEPES, 420 mM NaCl, 0.5 mM EDTA, 0.1 mM EGTA, 10 % Glycerol, 0.1 % NP-40). All buffers were supplemented with complete protease and phophatase inhibitors.

Cells were re-suspended in 10 mL of lysis buffer and vortexed for 10 seconds. Cells were incubated on ice for 15 minutes followed by being spun through 40 mL of sucrose cushion at 1300g for 10 minutes at 4 °C. The supernatant was discarded. The isolated nuclei were washed with 10 mL of ice-cold wash buffer. Nuclei were re-suspended in 1 mL of extraction buffer and sonicated for 30 seconds. The ruptured nuclei were incubated on ice for 30 minutes followed by centrifugation at 13000g for 10 minutes at 4 °C. The supernatant, nuclear extract, was collected. The concentration of nuclear extract was checked using a BCA assay. The nuclear extract was diluted using a buffer such that final concentration was 0.5 mg/mL and buffer conditions were: 20 mM HEPES pH 7.9, 150 mM NaCl, 0.2 mM EDTA, 20 % glycerol, 0.1% DTT with complete protease and phosphatase inhibitors (Binding Buffer). The nuclear extract aliquots were flash frozen in liquid nitrogen and stored at -80 °C.

For pulldown experiments with FLAG-tagged protein, separate batches of nuclear extract were prepared under non-reducing conditions without the use of DDT following earlier mentioned protocol.

2.4.11. Interaction proteomics experiments

(i) Interaction Proteomics experiment with nucleosomes

Interaction proteomics experiment was performed as previously described.[21] Briefly, 20 µg of each nucleosome were immobilized separately on 100 µL Dynabeads® Streptavidin MyOne™ T1 (Life Technologies) in the reconstitution buffer (10 mM Tris pH 7.5, 250 mM KCl, 1 mM EDTA, 1 mM DTT with 0.1% NP-40). The immobilization efficiency was monitored by measuring the absorption value at 260 nm of the supernatant. Immobilized nucleosomes were washed with the binding buffer (20 mM HEPES pH 7.9, 150 mM NaCl, 0.2 mM EDTA, 20% Glycerol, 0.1% NP-40, 1 mM DTT supplemented with complete protease and phosphatase inhibitors) and then incubated with 1 mL of nuclear extract (0.5 mg/mL in binding buffer) for 4 hours at 4 °C. After 4 hours, non-specifically bound proteins were removed by washing with binding buffer (1 mL X 5 times). The interacting partners were eluted in 100 µL of 8 M Urea, 2 M NaCl.

Pooled interacting partners from each nucleosome sample were digested by Trypsin using the Filter-Aided Sample Preparation (FASP) protocol[51] using 10 kDa Microcon filtration devices (Millipore). Protein samples were loaded onto the filtration device and centrifuged at 14000 g for 15 minutes. The flow-through was discarded. The concentrate was washed twice by centrifuging 200 µL of 8 M Urea, 50 mM Ambic solution at 14000 g for 15 minutes. The concentrate was reduced in the filtration device by adding DTT (100 µL of a 30 mg/mL solution in 8 M Urea, 50 mM ammonium bicarbonate buffer) at 50 °C for 20 min, followed by centrifugation (14000 g, 15 min). The sample was alkylated with iodoacetamide (100 µL of a 36 mg/mL solution in 8 M Urea, 50 mM ammonium bicarbonate buffer) for 25 min in the dark. Excess alkylating agent was removed by centrifugation (14000 g, 15 min), followed by washes of the centrifugal unit with 8 M Urea, 50 mM ammonium bicarbonate buffer (3 times 200 µL).

The collection tubes of the filtration units were changed. Lys-C enzyme was added to the resulting concentrate (final enzyme:protein ratio: 1:50 (w/w) in 35 µL of 8 M Urea, 50 mM ammonium bicarbonate buffer). The sample was incubated at 37 °C for four hours. After four hours, trypsin enzyme was added (final enzyme:protein ratio: 1:25 (w/w) in 120 µL of 50 mM ammonium bicarbonate buffer) and the samples were incubated at 37 °C overnight. Following overnight digestion, peptides were eluted to a fresh Eppendorf tube by centrifugation. 10% Formic acid solution (50 µL) was added to the centrifugal unit and centrifuged again to elute the remaining peptides.

Resulting tryptic peptides were analyzed on an EASY-nLC 1000 UHPLC system (Proxeon) connected to a Q Exactive mass spectrometer (Thermo Fischer Scientific) through an EASY-Spray nano-electrospray ion source (Thermo Fischer Scientific). The peptides were trapped on an in-house packed trap column (75 µm i.d. x 20 mm, reprosil C18, 3µm, 120 Å) using solvent A (0.1% Formic Acid, 5 % DMSO in water) at a pressure of 500 bar. The peptides were separated on an EASY-spray Acclaim PepMap® analytical column (75 µm i.d. × 500 mm, RSLC C18, 2 µm, 100 Å) using a linear gradient (length: 120 minutes, 8 % to 28 % solvent B (0.1% formic acid, 5 % DMSO in acetonitrile), flow rate: 200 nL/min). The separated peptides were electrosprayed directly into the mass spectrometer operating in a data-dependent mode. Full scan MS spectra were acquired in the Orbitrap (scan range 350-1500 m/z, resolution 70000, AGC target 3e6, maximum injection time 100 ms). After the MS scans, the 20 most intense peaks were selected for HCD fragmentation at 30 % of normalized collision energy. HCD spectra were also acquired in the Orbitrap (resolution 17500, AGC target 5e4, maximum injection time 120 ms).

The raw data files generated were processed using MaxQuant software (Version 1.4.3.17), integrated with Andromeda search engine as previously described.[73,74] Raw MS data were searched against human database (Swiss-Prot, version 04/13) as well as list of common contaminants by Andromeda. Trypsin with a maximum number of 2 missed cleavages was selected as the protease. Acetylation (Protein N-term) and Oxidation (Methionine) were used as variable modifications while Carbamidomethylation (Cysteine) was

set as a fixed modification. Protein and PSM false discovery rate (FDR) were set at 0.01. Label free quantification (LFQ) was performed using the in-built algorithm in the MaxQuant.[52] Further downstream data analysis was performed using Perseus software (Version 1.4.2.27). LFQ intensity of all identified protein groups was exported; reverse and protein groups only identified by site were removed. Protein groups identified in all three replicate experiments of either bait or control samples were considered for analysis. LFQ intensities were logaritmized and missing LFQ intensities were added. False discovery rate (FDR) based two-sample t-test was used to generate fold-change difference as well as a *p* value. Protein groups with corresponding *p* value lower than 0.05 were considered as significant. The data was visualized in a volcano plot of ratio change versus log (*p* value).

(ii) Interaction Proteomics experiment with FLAG-tagged proteins

20 µg of each monomer/dimer were immobilized separately on 70 µL of Anti-FLAG® M2 magnetic beads (M8823, Sigma-Aldrich) in reconstitution buffer (10 mM Tris pH 7.5, 20 mM KCl, 1 mM EDTA with 0.1% NP-40). The immobilization efficiency was monitored by measuring the absorption value at 280 nm of the supernatant. The immobilized proteins were washed with the binding buffer (20 mM HEPES pH 7.9, 150 mM NaCl, 0.2 mM EDTA, 20% Glycerol, 0.1% NP-40 with complete protease and phosphatase inhibitors) and then incubated with 1 mL of nuclear extract (0.5 mg/mL in binding buffer) for 4 hours at 4 °C. After stringent washes with binding buffer, the beads were incubated with 250 µL of IgG elution buffer (21004, Thermo Fisher Scientific) for 5 minutes at room temperature with gentle rotation. The supernatant was collected in an eppendorf tube containing 50 µL of 1 M Tris pH 9.0 buffer solution. The elution step was repeated once more.

Tryptic digestion and nLC-MS/MS analysis for the interacting protein partners were performed in a similar way as for interacting protein partners from nucleosome samples. The data analysis was performed in a similar way as that for nucleosome samples. The results for interaction study with monomer were visualized by importing the LFQ intensities into Perseus software (Version 1.4.2.27). Contaminant, reverse and protein groups only identified by site

were removed. Protein groups identified in at least one of bait and control samples in either replicate were used. Their LFQ intensities were logarithmized, missing LFQ intensities were added and mean intensity values were calculated. The difference between the average LFQ intensities of protein groups between bait and control samples alongside total intensity were evaluated by Significance B using Benjamini-Hochberg FDR (threshold value = 0.05) in order to generate a p-value.

The LFQ intensities of the interacting protein partner for dimer pulldown were imported into Perseus. Contaminant, reverse and protein groups only identified by site were removed. Only protein groups identified in each sample were considered for analysis. The LFQ intensities were logarithmized and a difference between bait and control sample was calculated. The difference between the intensities was plotted against total intensity. Significance B analysis was used to generate a p-value.

2.4.12. Western blot experiments

8 µL aliquots of nuclear extract (as positive control), interacting partners from control experiment and interacting partners from bait experiment were subjected to SDS-PAGE analysis. Pre-stained protein standards were also added. The SDS-PAGE analysis was performed using 4-12 % Bis-Tris gel (Novex). The gel was run in 1x MOPS buffer at 200 V for 50 minutes. The proteins were transferred to PVDF membrane using iBlot dry blotting system (Life Technologies). The membrane was blocked using 50 mL 5 % BSA solution in 1x TBST buffer by gentle rocking at room temperature for 1 hour. After blocking, the membrane was washed with TBST buffer (2 X 30 mL, 5 minutes each). The membrane was probed by primary antibody in 50 mL of 5 % BSA solution in TBST buffer by gentle rocking at room temperature for 1 hour. The membrane was extensively washed by TBST buffer (6 X 40 mL, 10 minutes each). The membrane was probed by secondary antibody (Goat anti-rabbit antibody conjugated with HRP, Bio-Rad) at 1: 10000 dilutions in 50 mL of 5 % BSA solution in TBST buffer by gentle rocking at room temperature for 1 hour. After that, the membrane

was extensively washed by TBST buffer (6 X 40 mL, 10 minutes each). The membrane was then developed using 1 mL of Clarity™ Western ECL substrate (Bio-Rad). Excess of ECL reagent was removed and the blot was developed on X-ray film.

Antibodies used in this study:

(i) against BRE1A (anti-RNF20 antibody, (ab181032, [EPR13563(B)], Abcam)

(ii) against SUPT16H (anti-SUPT16H antibody (ab108960, [EPR3685], Abcam)

(iii) against SSRP1 (anti-SSRP1 antibody (ab129109, [EPR7894], Abcam)

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3. GlcNAcylation of Histone Protein H2A Regulates Nucleosome Stability[1‡]

3.1 Introduction

In the previous chapter, it was shown how *O*-GlcNAcylation modification of histone H2B, leads to recruitment of the FACT protein complex without significantly altering the nucleosome structure.[2] The results described there illustrate one of the two main mechanisms used by histone PTMs to regulate chromatin dynamics, wherein the modification promotes binding of effector proteins.[3] However, *O*-GlcNAc rather than being just utilized as an epitope for promoting protein binding, also has potential to modulate nucleosome structure directly. This structural modulation could be either steric promoted owing to moderate size of the modification or through hydrogen bond promoted interactions. Earlier studies based on model peptides derived from the repeating *C*-terminal domain of RNA polymerase II, murine estrogen receptor β (mER-β), and mucosal addressin cell adhesion molecule-1 (MadCAM-1) have shown that *O*-GlcNAc modification alters the peptide backbone conformation leading to turn-like structures.[4-6] In the context of nucleosome, *O*-GlcNAcylation, in principle, can modulate histone protein-protein or DNA-histone protein interactions due to its size or non-bonding interactions leading to re-organization of nucleosome structure, and thus invoke the *'direct structural perturbation'* mechanism.[3] Indeed, we demonstrate that GlcNAcylation of histone protein, H2A, at the site, Thr101, destabilizes the nucleosome structure. Herein, we generate homogeneously GlcNAcylated histones and nucleosomes to study the effect of the modification on the structure/stability of histone sub-complexes and nucleosome using various biophysical methods. Nucleosome-binding protein groups for destabilized nucleosome has been explored using MS-based proteomics. A destabilized nucleosome state generated as an outcome of *O*-GlcNAcylation can plausibly enforce transcription by providing direct access to RNA polymerase.

‡ The results described in this chapter have been based on initial experiments performed by Dr. Lukas Lercher.

3.1.1 Site of modification: H2A-Thr101

Histone proteins were first identified to be *O*-GlcNAcylated by Sakabe *et al.* using immunological and chemoenzymatic methods.[7] Mass spectrometry based MS/MS analyses helped them localize the modification to three sites – Thr101 of H2A, Ser36 of H2B, and Ser47 of H4. To confirm these sites, histone variants bearing an Alanine mutation at the reported sites were expressed in mammalian cells and probed with anti-*O*-GlcNAc antibody. A decrease in modification was observed for the mutants. This result not only confirmed the sites of modification, but also suggested more possible sites of modification. Interestingly, in a separate *in vitro* investigation, it was shown that OGT can transfer an *O*-GlcNAc moiety to Thr101 site of free H2A protein but not when it is in the context of a histone octamer.[8] H2A-Thr101 residue is located on the *C*-terminal tail domain of H2A **(Figure 1)**.[9] The aforementioned domain is at the interface of the H2A/B dimer and the H3/H4 tetramer. It is structurally significant because it stabilizes the histone-fold domains of the histone octamer. In such structural setting, modulation of nucleosome stability by *O*-GlcNAc modification at Thr101 seemed highly likely and we tested it through step-wise creation and characterization of a synthetic nucleosome bearing a GlcNAc mimic at the modification site.

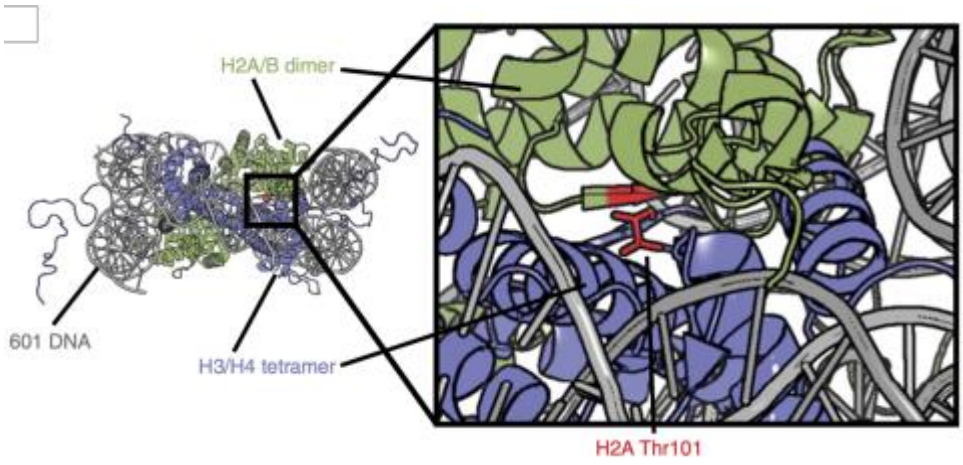
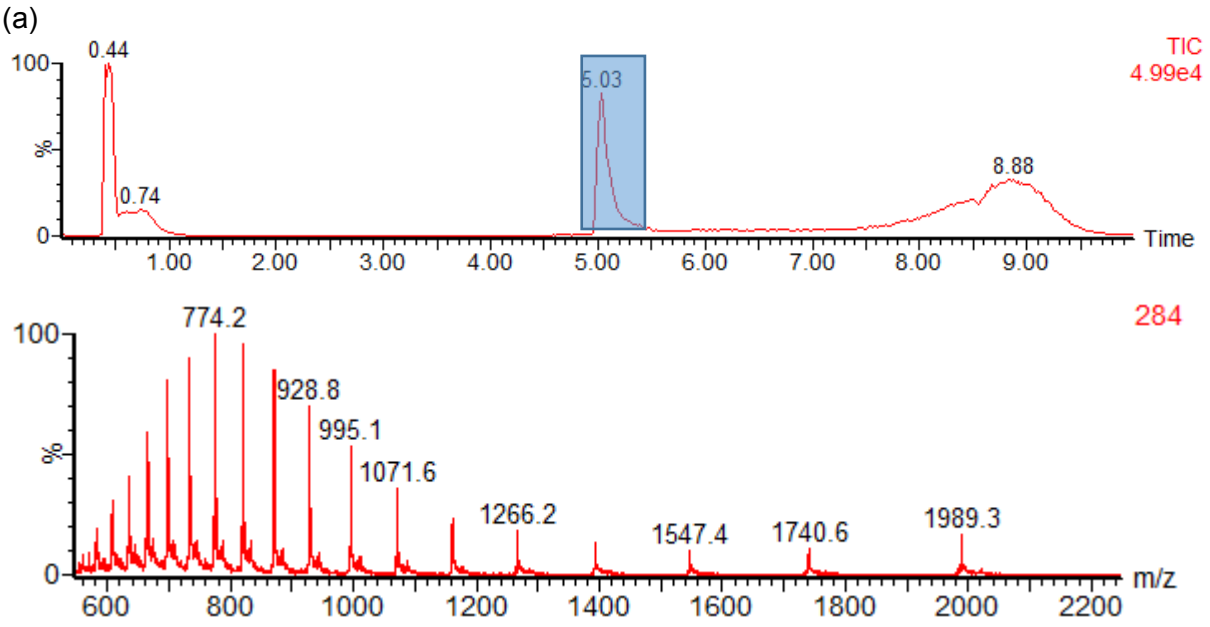


Figure 1. Nucleosome structure showing the modification site, H2A-Thr101. The site has been shown in red, H2A/B dimer in green, and H3/H4 tetramer in blue. (Reproduced from Lercher *et al.*[1])

3.2 Results and Discussion

3.2.1 Synthesis of H2A-Thr101 GlcNAc

As discussed previously, enzymatic synthesis of GlcNAcylated histone protein is not attainable.[8] As such, a "Tag-and-Modify" approach was employed to access site-specific, homogeneously GlcNAcylated protein.[2,10,11] A gene construct encoding *Xenopus laevis* histone protein H2A bearing a cysteine mutation at site Thr101 was designed.[12] The protein was expressed in *E.Coli* cells in the insoluble fraction. It was later purified under denaturing condition by size-exclusion and strong cation exchange chromatography. With the protein in hand, the Dha "tag" was installed, by treatment with 2,5-dibromohexanediamide (DBHDA) under denaturing conditions. The reaction was initially incubated at room temperature for 30 minutes, followed by incubation at 37 °C. The progress of the reaction was monitored by LC-MS analysis which revealed the completion of reaction after 2 hours. The H2A-T101 Dha protein, thus synthesized, was reacted with GlcNAc-thiol to yield homogeneous H2A-T101 GlcNAc protein **(Figure 2)**.



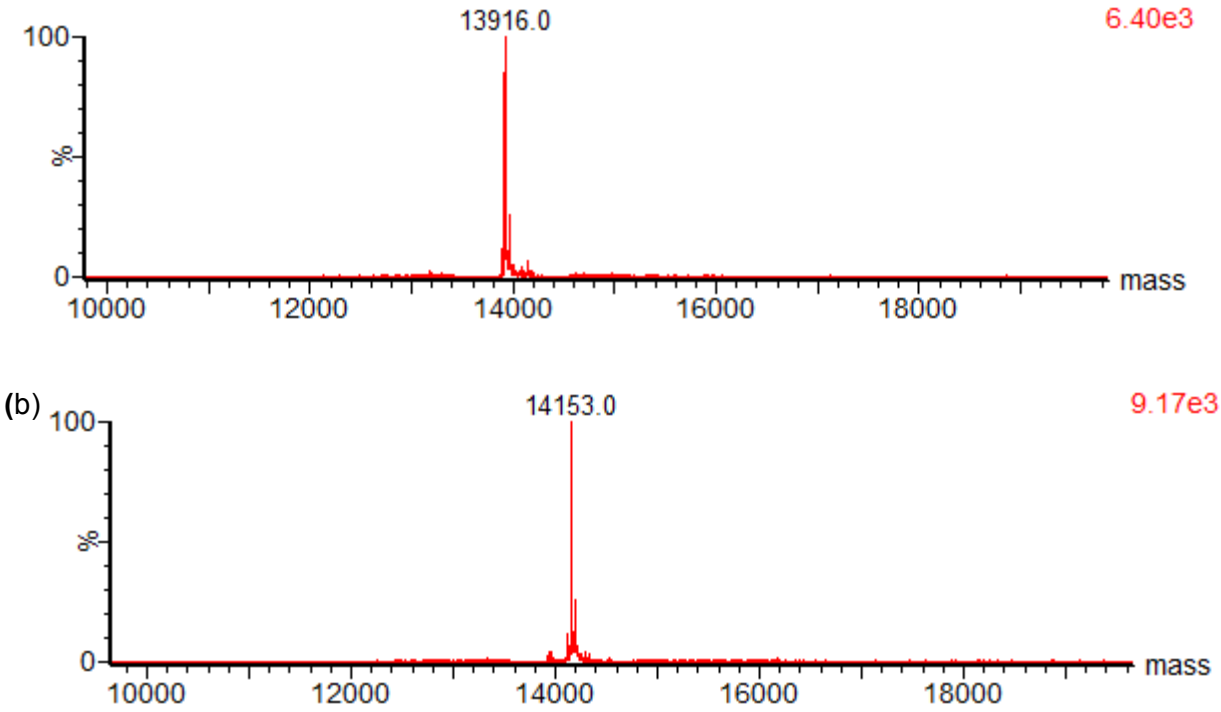


Figure 2. Synthesis of H2A-T101 GlcNAc protein using "Tag-and-Modify" approach. (a) LC-MS spectrum of H2A-T101 Dha protein. Note that the protein LC-MS analysis described in this thesis was used for separation of small molecules from the protein mixture to increase its ionization rather than separation of starting or intermediate material from final protein product. In a representative example shown in (a), the entire peak (enclosed by blue box) in the protein region of LC spectrum was integrated to produce the corresponding ion-series spectrum, which was later de-convoluted to corresponding MS spectrum. (b) LC-MS spectrum for H2A-T101 GlcNAc protein.

3.2.2 Effect of the modification on Histone Sub-complexes stability

In previous studies carried out by Dr. Lukas Lercher (Ben Davis Group), it was shown that the GlcNAc modification at H2A-T101 does not affects the H2A/B dimer structure, however it does inhibit the histone octamer formation. In these experiments, modified octamers were refolded by mixing, the modified H2A/B dimer with wt H3/H4 tetramer in a 1.1: 1.0 ratio. The mixture was incubated for 1 hour at 4 °C and later purified by Size-exclusion chromatography (SEC). The SEC trace revealed two separately eluting peaks, one at 71 mL corresponding to tetramer species and other at 81 mL corresponding to dimer species. The SEC results indicated that the modification hinders the octamer formation, possibly due to destabilization of the histone-fold at dimer/tetramer interface. However, it is worth-noting that

proper folding of histone sub-complexes usually depends highly on the correct stoichiometric use of constituent histone proteins. As discussed in the previous chapter, the "Tag-and-Modify" approach, used here for synthesis of GlcNAcylated histone protein, will in most likelihood under the used reaction condition lead to an epimeric mixture of products. In such a situation, the refolded modified H2A/B dimer will consist of an equivalent mixture of physiologically relevant L-species and unnatural D-species. If during the histone octamer formation, the refolding process only selects H2A/B dimer with L-epimeric modification, it would mean an incorrect input of dimer as compared to tetramer and would provide an alternative explanation for the observed SEC result. To confirm that the octamer destabilization was indeed an outcome of H2A-T101 GlcNAcylation and not an artefact arising from the potentially wrong stoichiometric use of modified protein, octamer formation using different equivalents of H2A/B was tried.

In order to perform titration experiments for octamer refolding, access to modified dimer and wt tetramer was required. Synthetic GlcNAcylated H2A protein was mixed in an equimolar ratio with canonical wt histone protein H2B and dialyzed against high-salt buffer to induce dimer formation. The refolded modified dimer was purified and analyzed by Size-exclusion chromatography.[12] As shown in previous work, the modified dimer eluted at same retention volume as that for wt dimer, indicating no structural change upon modification. In a separate experiment, wt histone proteins H3 and H4 were refolded in similar manner to constitute H3/H4 tetramer **(Figure 3)**.

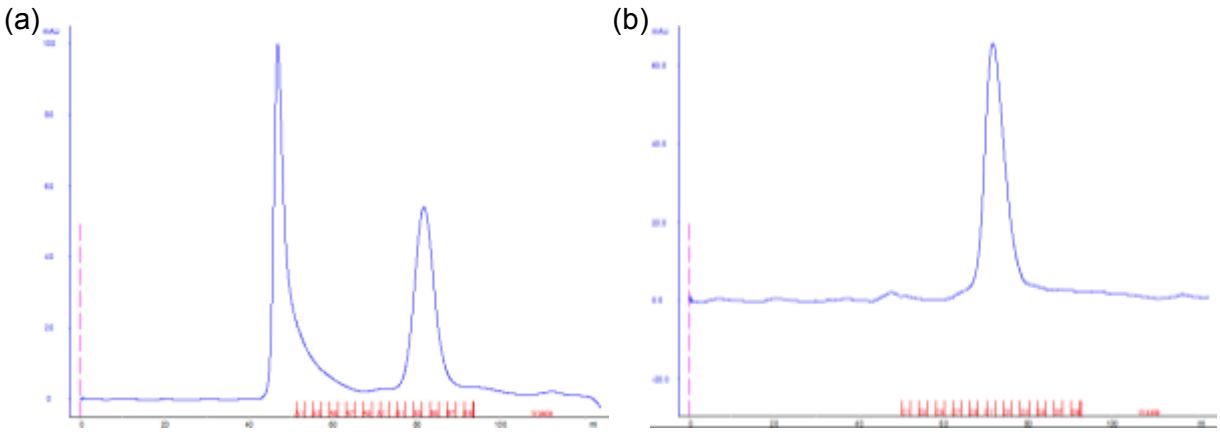


Figure 3. Reconstitution of histone sub-complexes. (a) SEC trace for H2A-T101 GlcNAc modified H2A/B dimer (b) SEC trace for wt H3/H4 tetramer.

With modified dimer and wt tetramer in hand, analytical octamer refolding was performed. The dimer was mixed in excess (3- and 4-fold) with tetramer and incubated at 4 °C, before being purified by analytical SEC column. Previously purified H2A-T101 GlcNAc modified dimer and wt tetramer were also analyzed by analytical SEC as reference. However, again rather than an octamer peak, two separately eluting peaks corresponding to dimer and tetramer were observed. This result confirmed our initial hypothesis that the destabilization of the octameric histone core was indeed due to the GlcNAcylation modification rather than artefact arising due to epimeric nature of modification.

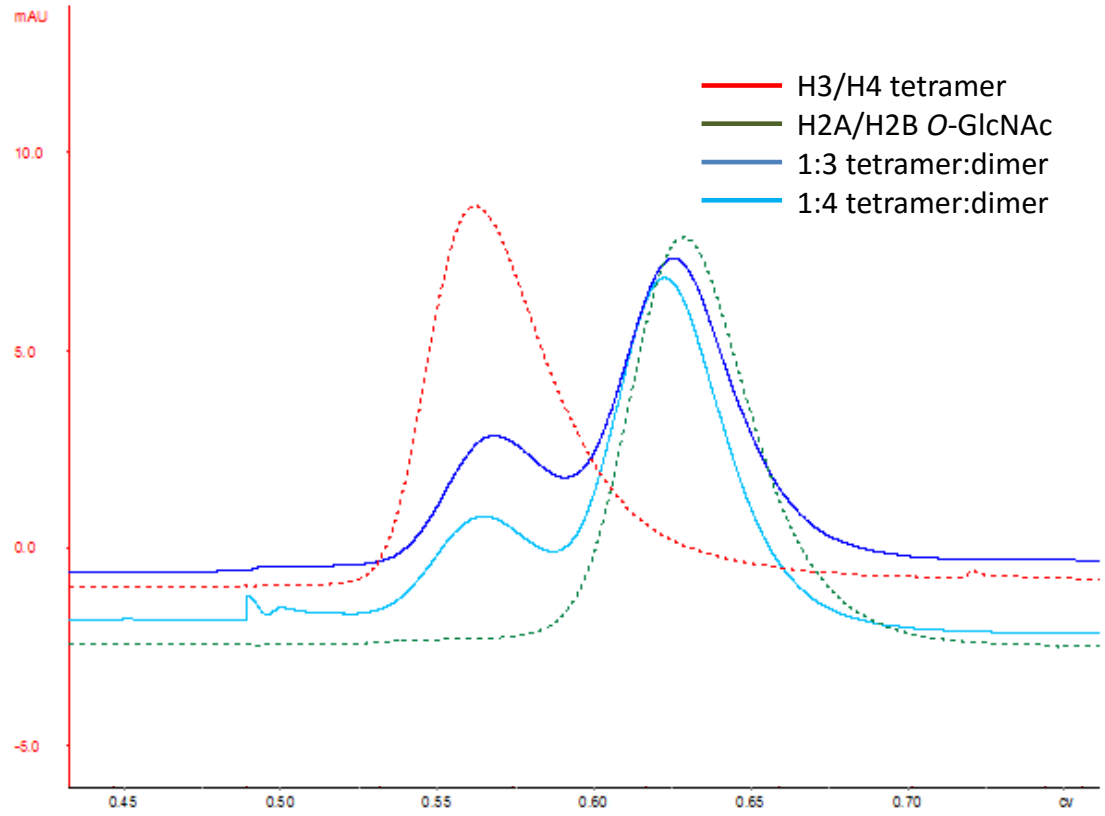


Figure 4. Analytical octamer refolding using different ratios of modified H2A/B dimer and wt H3/H4 tetramer. (Reproduced from Lercher *et al.*[1])

3.2.3 H2A-Thr101 GlcNAcylation destabilizes nucleosome structure

Destabilization of octamer core upon GlcNAcylation of H2A-T101 did suggest a

possible structural modulation of nucleosomes. However, unlike histone octamers, stability of nucleosome is not entirely governed by protein interactions. Nucleosome structure is additionally influenced by interactions stemming from DNA-protein interactions, association with chaperones and chromatin-associated proteins.[13] In earlier studies, the effect of GlcNAcylation on the nucleosome structure was investigated. Since access to GlcNAc modified octamer was not possible, GlcNAcylated nucleosomes were reconstituted by mixing the modified dimer, wt tetramer, and DNA in contrast to using wt octamer and DNA for wt nucleosome reconstitution.[12,14] Native-PAGE analysis revealed a diffused band for reconstituted GlcNAcylated nucleosome as compared to that for wt nucleosome, indicative of a destabilized nucleosome structure. Apart from modification at H2A-T101, two other plausible reasons for the observed result could be: 1) Nucleosome refolding only selects physiologically relevant H2A/B dimer with L-amino acid at site of modification, and 2) The use of different reconstitution methods for wt and modified nucleosome. Indeed, if only H2A/B dimer bearing L-amino acid is selected during nucleosome reconstitution, it would mean a depleted dimer condition (roughly 50% input of required value). As discussed earlier, proper folding of histone sub-complexes and nucleosomes are highly sensitive to the correct input of constituent species. Incorrect ratio of dimer to tetramer is known to induce formation of tetrasomes and hexasomes.[15] Although, the second reason – use of different reconstitution method – seemed less likely to effect the observed result, additional set of experiments were performed to address both concerns regarding nucleosome reconstitution.

Nucleosomes were refolded using 145 bp '601' DNA construct following salt-gradient dialysis method.[12] The '601' DNA sequence binds tightly to histone octamer and is regularly used for homogeneous *in vitro* nucleosome reconstitution. The sequence was discovered by Lowary and Widom through SELEX experiments.[16] The DNA was expressed on a large-scale in *E. Coli* starting from a plasmid encoding multiple copies of the DNA fragment inserted between EcoRV restriction sites.[17] DNA was excised and purified as described earlier.[12] With DNA in hand, nucleosome reconstitution was performed. To address the concern regarding the stoichiometry of H2A/B dimer during nucleosome reconstitution, nucleosomes were

refolded with different tetramer/dimer ratios (1.5–5 eq dimer). Wt tetramer, DNA and different equivalents of modified dimer were mixed together in a high-salt buffer and were dialyzed sequentially against buffer with lower salt-concentrations. The reconstituted nucleosomes were analyzed using native-PAGE **(Figure 5)** which revealed similar migrating bands for each reconstitution in spite of different equivalents of dimer used for refolding. PAGE analysis confirmed the initial hypothesis that destabilized nucleosome was indeed an outcome of the modification at H2A-Thr101, rather than an artefact arising due to epimeric nature of modified dimer used for nucleosome reconstitution.

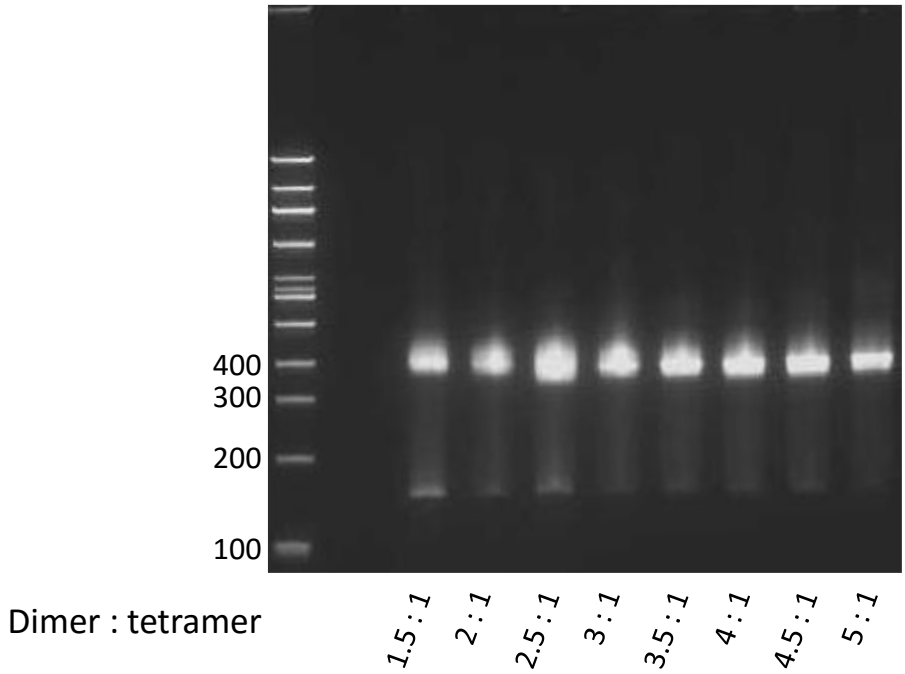


Figure 5. Native-PAGE analysis of nucleosome reconstitutions using different ratio of H2A/B GlcNAc dimer and wt H3/H4 tetramer. (Reproduced from Lercher *et al.*[1])

To address the second concern regarding, that different reconstitution methods were contributing to a destabilized nucleosome structure, wild-type nucleosomes were refolded using both methods. Nucleosome reconstitution were performed by mixing wt octamer with DNA as well as by mixing wt dimer, wt tetramer and DNA. The nucleosome refolding was performed as before by salt-gradient dialysis. The reconstituted nucleosomes were analyzed by native-PAGE gels **(Figure 6)**. As expected, PAGE analysis revealed similar mobility and

reconstitution yield for both batches of wt nucleosome irrespective of reconstitution method. In light of this result, it was unequivocally confirmed that destabilization of the modified nucleosome was definitely due to the GlcNAc modification at H2A-Thr101.

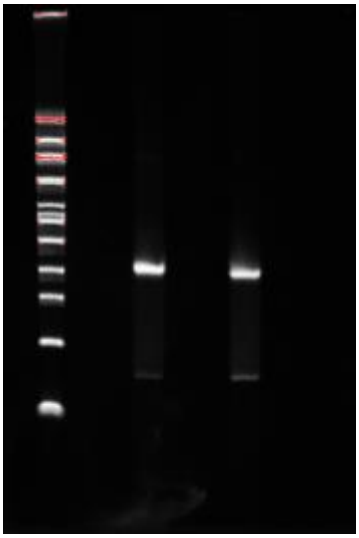


Figure 6. Native-PAGE analysis of wild-type nucleosome reconstituted using different methods. The lane on the left represents 100 bp DNA ladder, the central lane represents nucleosome reconstituted using wt dimer and tetramer, and the lane on the right represents nucleosome reconstituted using wt octamer.

3.2.4 Nucleosome structure and stability assessment

In earlier studies, it has been shown that histone sub-complexes can bind to the DNA through weak electrostatic interactions leading to formation of non-native structures such as tetrasomes where just two dimers are bound to DNA.[18] Since the nucleosomes were reconstituted starting from H2A/B dimers and H3/H4 tetramers, there was a possibility of formation of non-native species during refolding. Reconstituted nucleosomes were probed for non-native structures by incubating them with elevated salt-concentrations. Previous studies have demonstrated the dissociation of non-native complexes, stemming from unspecific electrostatic interactions between histones and the DNA, at elevated salt-concentrations.[19] Reconstituted nucleosomes were incubated in the presence of 200, 400 or 600 mM KCl at 37 °C for 1 hour. They were later analyzed by native-PAGE **(Figure 7)**. Native-PAGE analysis

indicated nucleosomes to be stable even at elevated ionic strength, with only small amounts of DNA being liberated during salt-based disassembly assay. It was thus concluded that both nucleosome species, wt and GlcNAcylated, formed similar native nucleosome core particles stabilized by interactions as found in canonical nucleosomes.

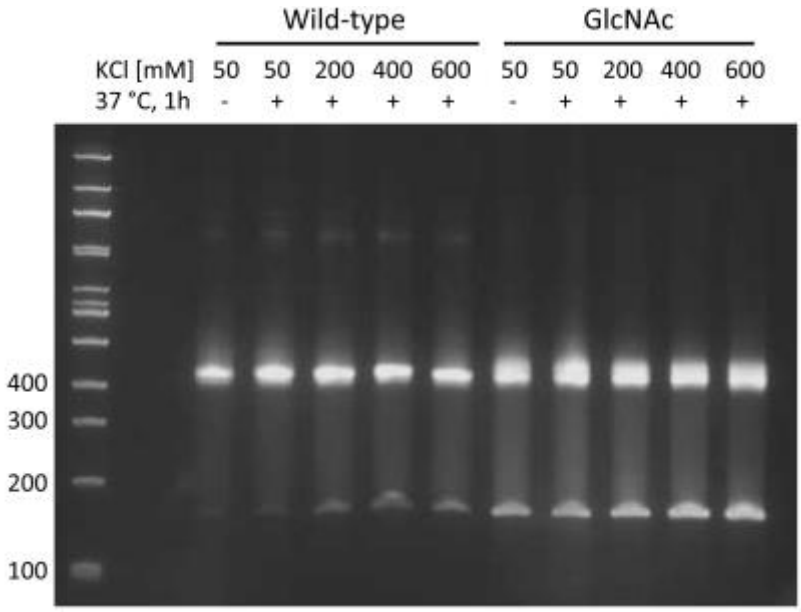
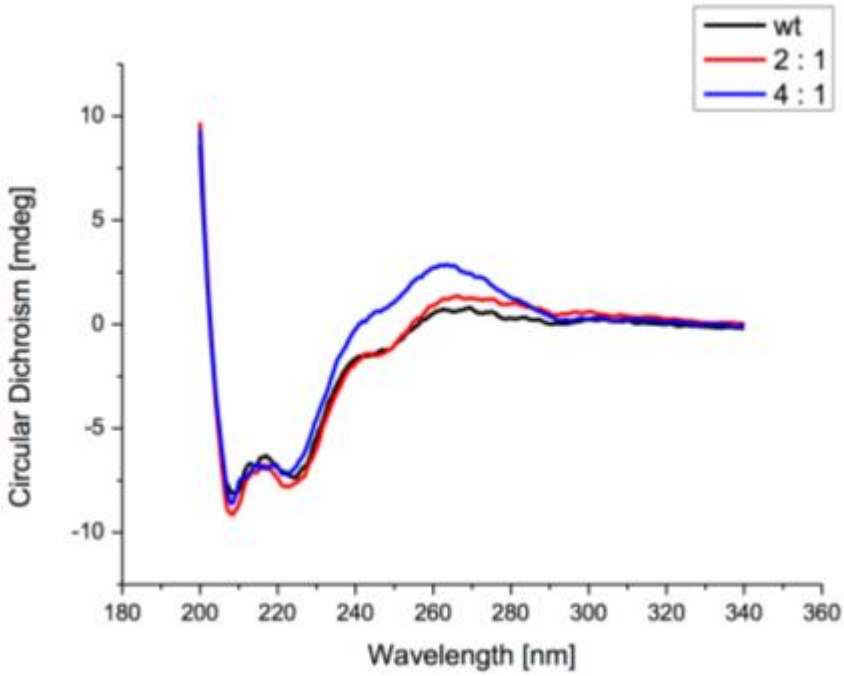


Figure 7. Salt-based disassembly of nucleosomes. wt and GlcNAcylated nucleosomes were incubated with varying concentrations of KCl for 1 h at 37 °C. (Reproduced from Lercher *et al.*[1])

The structural details of reconstituted nucleosomes were further examined by circular dichroism (CD) spectroscopy. Wt and GlcNAcylated nucleosomes (reconstituted using 2:1 and 4:1 dimer to tetramer ratio) were refolded as before and CD spectra were compared **(Figure 8)**. The spectra for the wt and the modified nucleosome reconstituted using 2:1 dimer to tetramer ratio looked identical with slight increase in the positive band around 260 nm. However, the nucleosome reconstituted using higher dimer to tetramer ratio (4:1) revealed significantly increased positive band around 260 nm, a characteristic wavelength for CD emanating from DNA motif. Earlier works have suggested a positive correlation between the increased intensity of this band around 260 nm and unwinding of DNA duplex.[20,21] Based on CD spectra, it was thus concluded that the extent of DNA wrapping around octamer in wt nucleosome and GlcNAcylated nucleosome constituted using 2:1 dimer to tetramer ratio was

almost identical, however the nucleosome reconstituted using higher equivalents of dimer seemed to had a more relaxed wrapping of DNA around octamer. To exclude that the observed results were an artifact arising from different assembly methods used for wt and GlcNAcylated nucleosome, CD spectra for wt nucleosome reconstituted using both methods were recorded. As expected, the CD spectra for two samples were near-identical **(Figure 8)**.

(a)



(b)

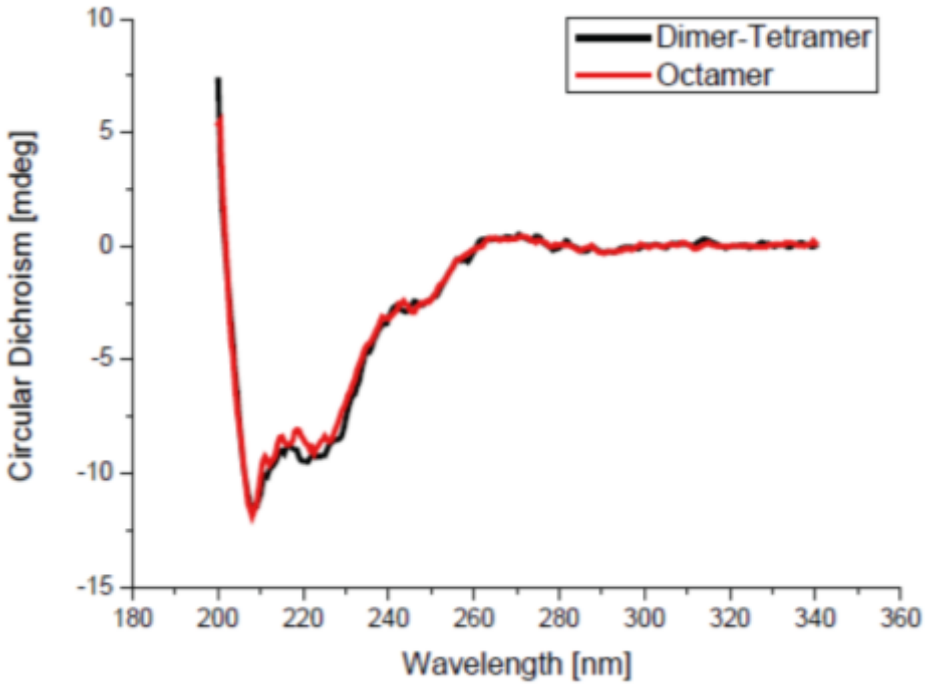


Figure 8. CD analysis of reconstituted nucleosomes. (a) CD spectra for wt nucleosome (black) and GlcNAc modified nucleosomes reconstituted with different GlcNAc dimer: tetramer ratios (2:1, red; 4:1 blue). (b) CD spectra for wt nucleosomes reconstituted using different assembly methods. (Reproduced from Lercher *et al.*[1])

Next, the extent of destabilization was explored through CD monitored melting experiments. The unfolding dynamics as well as unfolding intermediates of biomolecules can potentially be investigated by analyzing their temperature-dependent CD spectra.[22] In case of nucleosomes, CD-based melting experiments prove even more useful as they can be used to simultaneously follow the melting of both protein and DNA by measuring their ellipticity at their 'signature' wavelengths (220 and 260 nm).[23] To realize the thermal stability of reconstituted nucleosomes their CD spectra were monitored as a function of temperature at both these wavelengths **(Figure 9)**.

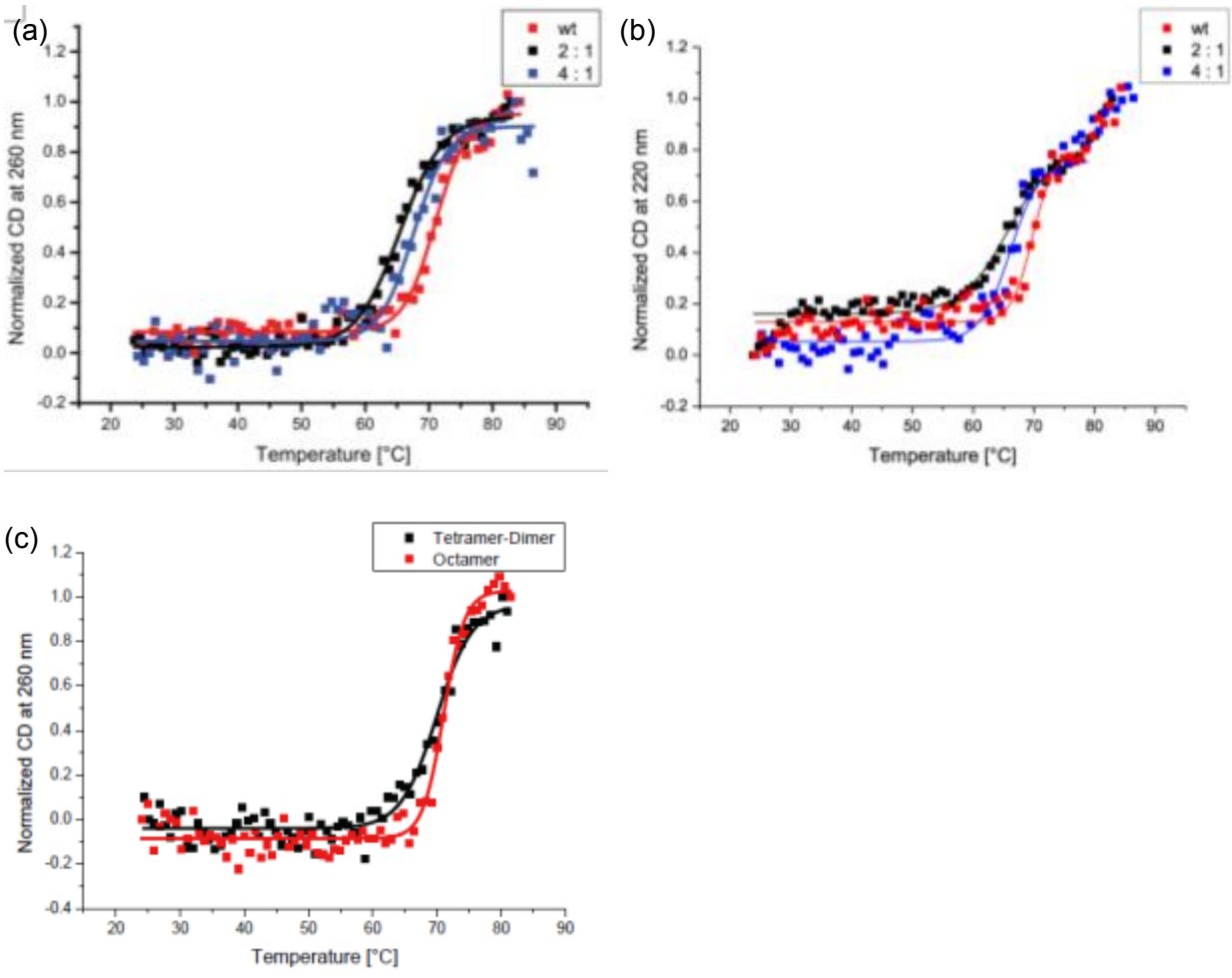


Figure 9. Stability assessment of reconstituted wt and modified nucleosomes by CD analyses. (a) Thermal profile of nucleosome monitored by CD at 260 nm. Red curve denotes profile for wt nucleosome whereas black and blue curves denote profile for GlcNAcylated nucleosome reconstituted with different dimer to tetramer ratio. (b) Thermal profile of nucleosome monitored by CD at 220 nm. Red curve denotes profile for wt nucleosome whereas black and blue curves denote profile for GlcNAcylated nucleosome reconstituted with different dimer to tetramer ratio. (c) Thermal profile of wt nucleosomes reconstituted using different assembly methods monitored by CD at 260 nm. (Reproduced from Lercher *et al.*[1])

The melting profile measured by variable-temperature CD analysis at 260 nm revealed a single transition for wt and modified nucleosomes. The melting temperature for modified nucleosomes (T_m 2:1 = 65.5±0.2 °C, T_m 4:1 = 67.6±0.4 °C) were significantly lower as compared to that of wt nucleosome (T_m wt = 71.0±0.3 °C), confirming the destabilized status of modified nucleosome **(Figure 9a)**. However, the melting profile at 220 nm revealed a biphasic melting of nucleosomes indicative of an existing intermediate state **(Figure 9b)**. The observed first transition state for modified nucleosomes corresponded to a lower melting temperature (T_m 2:1 = 65.8±0.9 °C; T_m 4:1 = 66.1±0.4 °C) when compared to the wt nucleosome (T_m wt = 69.7±0.3 °C). After the first transition, CD profile for the nucleosomes behaved similarly irrespective of the modification. These observations indicate a nucleosome melting model where H2A/B dimer dissociates first from the nucleosome, followed by dissociation of H3/H4 tetramer. This is in agreement with GlcNAc modification at H2A-T101 lowering the activation energy for first transition leading to lower melting temperature, and overall destabilizing the nucleosome structure. The results obtained here by CD-based melting experiments corroborate the earlier observations made by Dr. Lercher. In these earlier experiments, a significant difference in melting temperature for wt and modified nucleosome based on differential scanning fluorimetry (DSF)-based melting experiments was observed.[1] Again as earlier, to confirm that these observations were not an artifact arising due to different assembly methods used for wt and GlcNAcylated nucleosome, melting profile for wt nucleosomes reconstituted using both methods were examined **(Figure 9c)**. As expected, the

melting temperature for nucleosome belonging to either batches were found to be near-identical (T_m di-tet = 70.0±0.4 °C; T_m oct = 71.0±0.2 °C).

The nucleosome melting model was further substantiated by results obtained from nucleosome thermal-incubation experiment. Wt and GlcNAcylated nucleosomes were incubated at elevated temperature around observed melting temperature for 30 minutes and were analyzed by native-PAGE and SDS-PAGE **(Figure 10)**. The native-PAGE analysis of nucleosomes revealed liberation of DNA and higher migrating bands for both nucleosomes at elevated temperature indicative of nucleosome disassembly, although the high migrating bands appear at a lower temperature for GlcNAcylated nucleosome as was expected **(Figure 10a)**. In line with biphasic melting model, SDS-PAGE analysis of the soluble fractions revealed selective loss of H2A and H2B proteins at lower temperature as compared to that for H3 and H4 proteins **(Figure 10b)**.

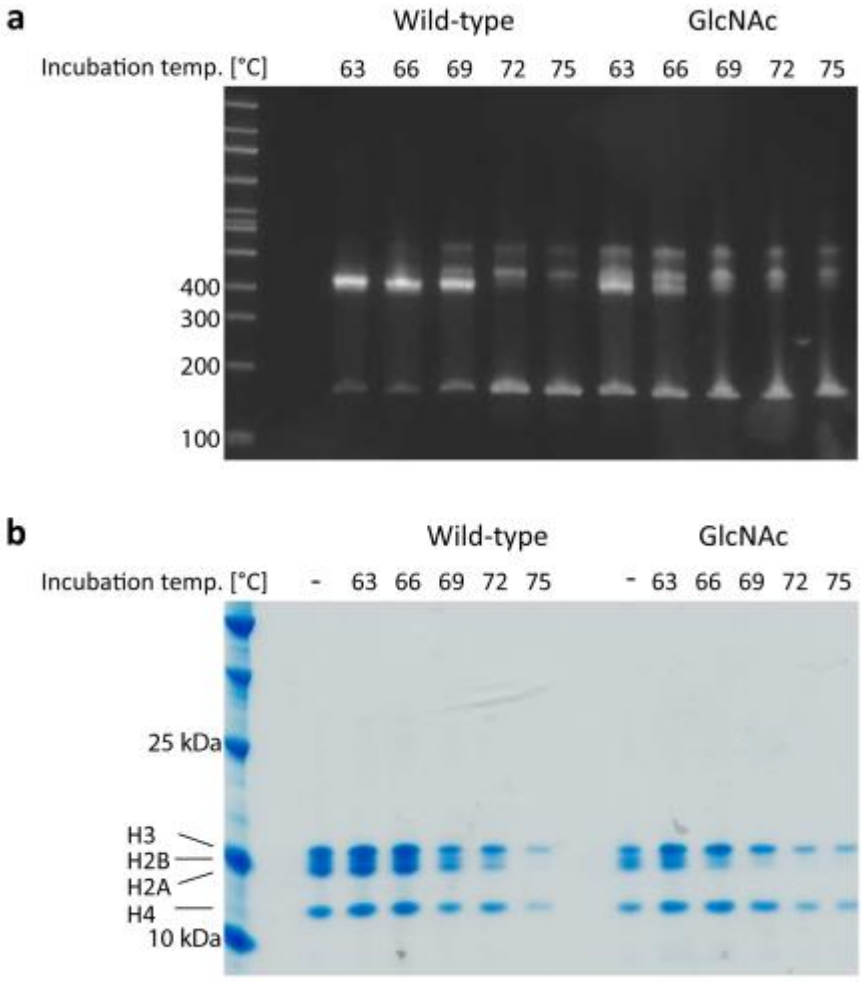


Figure 10. Thermal denaturation of wt and GlcNAcylated nucleosomes confirming the biphasic nucleosome-melting model. (a) Native-PAGE analysis of nucleosomes incubated at the indicated temperature for 30 minute. (b) SDS-PAGE analysis of the soluble fraction of nucleosomes after 30-minute incubation at the indicated temperature. (Reproduced from Lercher *et al.*[1])

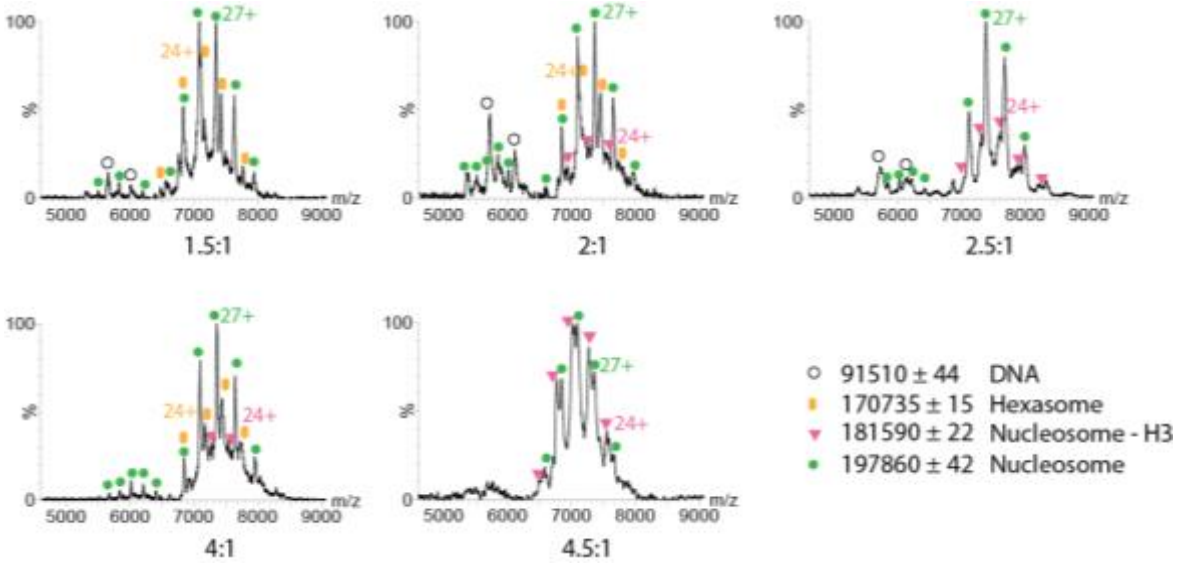
3.2.5 Native-MS analysis of GlcNAcylated Nucleosomes[§]

The reconstituted nucleosomes were further examined by non-denaturing native mass spectrometry (nMS) in order to investigate their assembly at the molecular level. nMS exploits 'soft' ionization conditions which preserve non-covalent interactions and thus allows the study of biomolecular assemblies.[24-27] This relatively new technique is routinely used for analyzing exact mass, accurate stoichiometry, and intramolecular interactions of biomolecular assemblies. In addition, nMS combined with ion-mobility allows conformational details of biomolecules, making the technique ideal for study of complex, dynamic biomolecular systems such as nucleosome.[28-30] In earlier studies by Dr. Lercher, it was shown that nMS spectra of wt nucleosomes consisted of one major species corresponding to intact nucleosomes whereas spectra of GlcNAcylated nucleosomes (assembled using dimer to teramer ratio of 2:1) consisted of at least three different species.[1] The three observed ion-series corresponded to a heterogeneous population comprised of intact nucleosome, a hexasome lacking a H2A/B dimer and a nucleosome species lacking one H3 sub-unit. To exclude that these observed results were an artefact arising due to potential loss of stereochemistry at GlcNAcylation site, nucleosomes assembled earlier using different ratio of dimer to tetramer were analyzed by native-MS **(Figure 11)**. nMS spectra revealed mixed population of species (intact nucleosome, hexasome, and nucleosome-H3) for all GlcNAcylated nucleosomes although the relative amount of each species in the population varied among different samples. Each GlcNAcylated nucleosome sample showed decreased amount of intact particles as compared to wt nucleosome. As before to rule out the possibility of these results arising due to the use of

[§] Native-MS experiments were performed by Dr. Nisha Patel, Carol Robinson Group, Oxford.

different assembly method for nucleosome reconstitution, wt nucleosomes assembled using both the methods were analyzed by nMS **(Figure 11)**. Their nMS spectra looked identical, thus providing additional evidence that indeed the destabilization of nucleosome was caused by GlcNAcylation of H2A-Thr101.

(a)



(b)

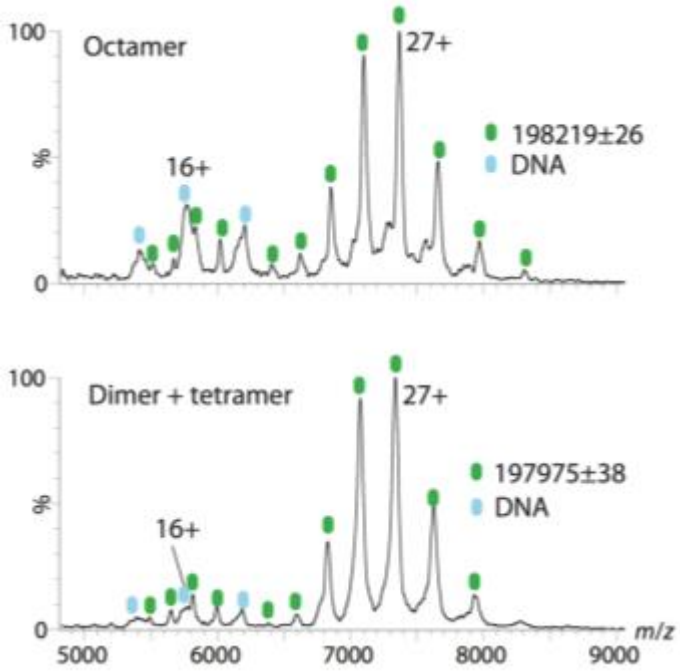


Figure 11. Native-MS analysis of reconstituted nucleosomes. (a) nMS spectra of GlcNAcylated nucleosomes reconstituted with different dimer to tetramer ratio. The ratio is given below each spectra. (b) nMS spectra of wt nucleosomes reconstituted using different

assembly methods. On the top is the spectra of wt nucleosome assembled using wt octamer whereas the bottom spectrum is of wt nucleosome assembled using wt dimer and tetramer. (Reproduced from Lercher *et al.*[1])

3.2.6 MS-based Interaction Proteomics with GlcNAcylated Nucleosome

Having defined the physical effect of H2A-T101 GlcNAcylation modification on nucleosome structure, it was envisaged to understand its potential *in vivo* implications. Earlier studies have shown that various chromatin-assembly proteins can modulate nucleosome stability and help in epigenetic regulation.[31,32] It was speculated whether the destabilized nucleosome leads to recruitment of certain chromatin remodelers, which upon identification would potentially explain *'nascent'* protein-protein interactions upon modification. For this purpose, interacting protein partners of GlcNAcylated nucleosome were analyzed using MS-based quantitative proteomics, a robust technique commonly used for identification of 'effector' proteins for various chromatin marks.[33]

To identify selective interactors for GlcNAcylated nucleosomes interacting protein partner were affinity enriched using immobilized GlcNAcylated nucleosomes. To this end, nucleosome reconstitution using a 186 bp biotinylated DNA fragment based on '601' sequence was required.[34] Starting from a bacterial plasmid encoding multiple copies of required DNA fragment, plasmid DNA was isolated on a large-scale.[12,34] The desired DNA fragment was released from the plasmid DNA by the action of restriction enzymes and were further biotinylated by *Klenow*-catalyzed enzymatic reaction. Wt and modified nucleosomes were assembled using the biotinylated DNA as before based on salt-dialysis method **(Figure 12)**. The reconstituted nucleosomes were then immobilized on magnetic beads exploiting the biotin-streptavidin interaction. These immobilized nucleosomes were incubated with HeLa cell nuclear extract to affinity enrich respective nucleosome-binding proteins. To obtain a robust data-set, the experiments were performed as two independent biological replicates. The enriched nucleosome-binding proteins for each sample were pooled separately and were enzymatically-digested using Filter-aided sample preparation (FASP) protocol.[35] The resulting

peptide mixtures were analyzed on an UHPLC coupled to a hybrid quadrupole-orbitrap (Q-Exactive) mass spectrometer.

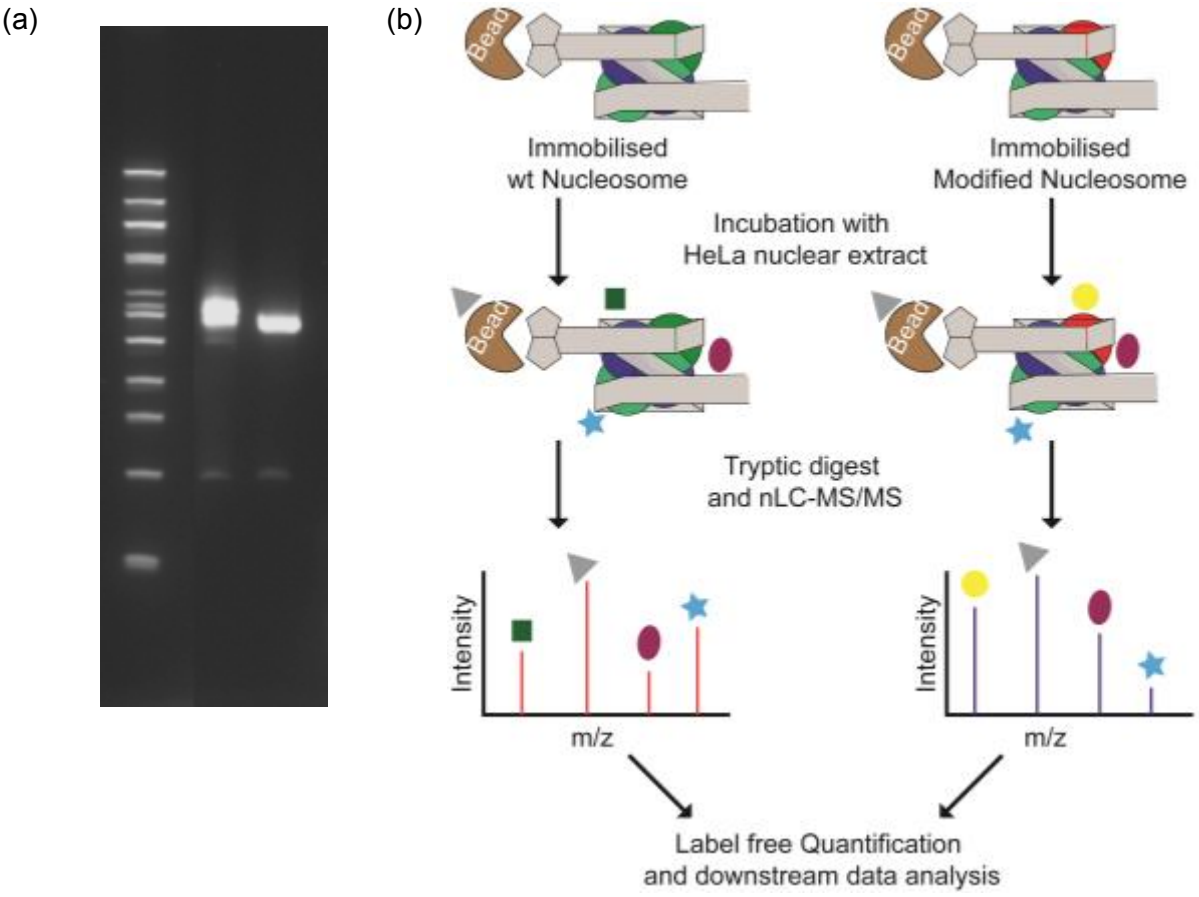


Figure 12. MS-based quantitative proteomics approach for interactome mining of H2A-T101 GlcNAc interactor proteins. (a) wt and GlcNAcylated nucleosome were reconstituted using 186 bp biotinylated DNA. The lane on the left represents 100 bp DNA ladder, the one in middle GlcNAcylated nucleosome, and on the right wt nucleosome. (b) Reconstituted nucleosomes were immobilized on magnetic beads (brown) *via* streptavidin-biotin affinity to enrich nucleosome binding proteins. Interacting protein partners were enzymatically-digested and analyzed by nanoLC-MS/MS. MS-based Label-free Quantification (LFQ) was applied for relative quantification.

The acquired proteome data was processed and quantified using MaxQuant and its in-built MaxLFQ computational proteomics platforms.[36-38] MaxLFQ is a MS-based label-free quantification algorithm with precision on par with isotope-based quantification methods. Label-free quantification followed by a statistical analysis (significance B with Benjamini-Hochberg[39] FDR) enabled identification of 20 proteins, among 720 quantified nucleosome-

binding proteins **(Appendix 4)**, which were over threefold enriched in the GlcNAcylated nucleosome sample **(Figure 13)**. Interestingly, 12 out of these 20 proteins are DNA-binding proteins including USF1 and USF2 proteins. This suggests an increased accessibility to certain regions of nucleosomal DNA which is line with the *in vitro* biophysical results obtained earlier. USF1 and USF2 proteins have been earlier shown to bind an E-Box DNA sequence, part of '601' DNA sequence, which complexes H2A/B dimer in the nucleosome structure.[17,40] Among the highly enriched interacting protein partners for modified nucleosomes were two DNA mismatch repair (MMR) proteins – Msh3 (MutS Homolog 3) being the most enriched, and Msh2 (MutS Homolog 2). In an earlier report, Msh2-Msh6 heterodimer has been identified as a nucleosome remodeler catalyzing the disassembly of the nucleosome.[41] The presence of Msh3 and Msh2 among enriched protein partners might suggest a role for these proteins in additional destabilization of the nucleosome upon modification.

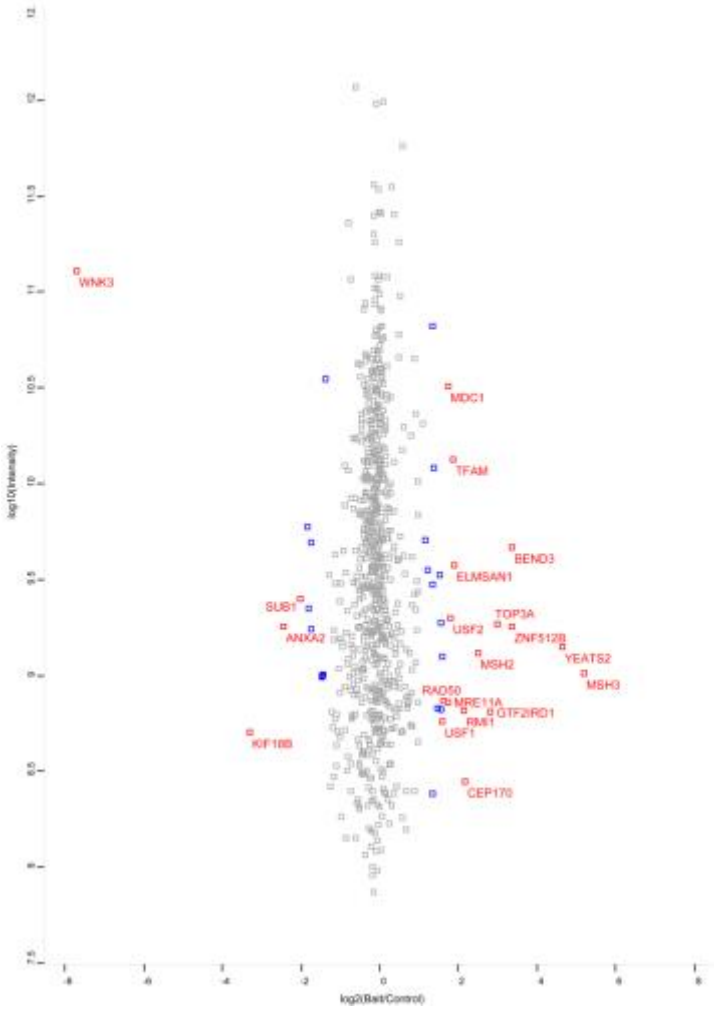


Figure 13. MS-based proteomics allowed identification of preferential interacting partners for H2A-T101 GlcNAc nucleosome (bait) over wild-type nucleosome (control). Significant protein partners identified by Label free quantification (LFQ) on Significance B analysis with a Benjamini-Hochberg FDR of 1% are shown in blue in a scatter plot. Top 20 significant interactors among them are denoted in red with their gene name. Scatter plot: x axis, logarithmized ratio of average LFQ intensities of protein groups in the bait over control pulldown experiment from two independent replicates; y axis, log10-transformed summed up intensity of protein groups. (Reproduced from Lercher *et al.*[1])

3.2.7 Plausible mechanism for H2A-T101 GlcNAc promoted transcription

Based on the results obtained here, a speculative mechanism linking H2A-T101 *O*-GlcNAcylation to transcriptional activation was proposed **(Figure 14)**. According to proposed mechanism, under normal conditions H2A/B dimers are in rapid equilibrium with a free H2A/B dimer pool maintaining the nucleosome structure and limiting the accessibility of DNA for transcription. However, upon recruitment of OGT, free H2A/B dimers get modified and exchange with nucleosomal H2A/B dimer. The incorporation of modified dimer decreases the nucleosome stability and direct the chromatin towards an open state. The open chromatin state lowers the barrier for RNA polymerase passage and enhances transcription. In addition, the exposed nucleosomal DNA as a result modification at H2A-Thr101 promotes binding of chromatin remodelers and transcription factors (such as those identified by interaction proteomics experiment). The H2A/B dimer destabilization model leading to transcriptional activation has been observed previously as well.[42,43] As compared to OGT-mediated posttranslational modification leading to labile H2A/B dimer in this case, earlier studies have shown modulation of H2A/B dimer stability in nucleosome structure through incorporation of labile H2A variants.[44] H2A variants, such as H2A.Z.2.2 and H2A.Bbd, also do not form stable histone octamer but do form a slightly less stable nucleosome in presence of DNA and promote transcription by structure modulation of nucleosomes.[14,18,45] The mechanism proposed here is the simplest that is consistent with the biophysical data gathered here, although, the role of H2A-T101 *O*-GlcNAcylation in other cellular processes such as histone processing, recycling and localization cannot be ruled out.

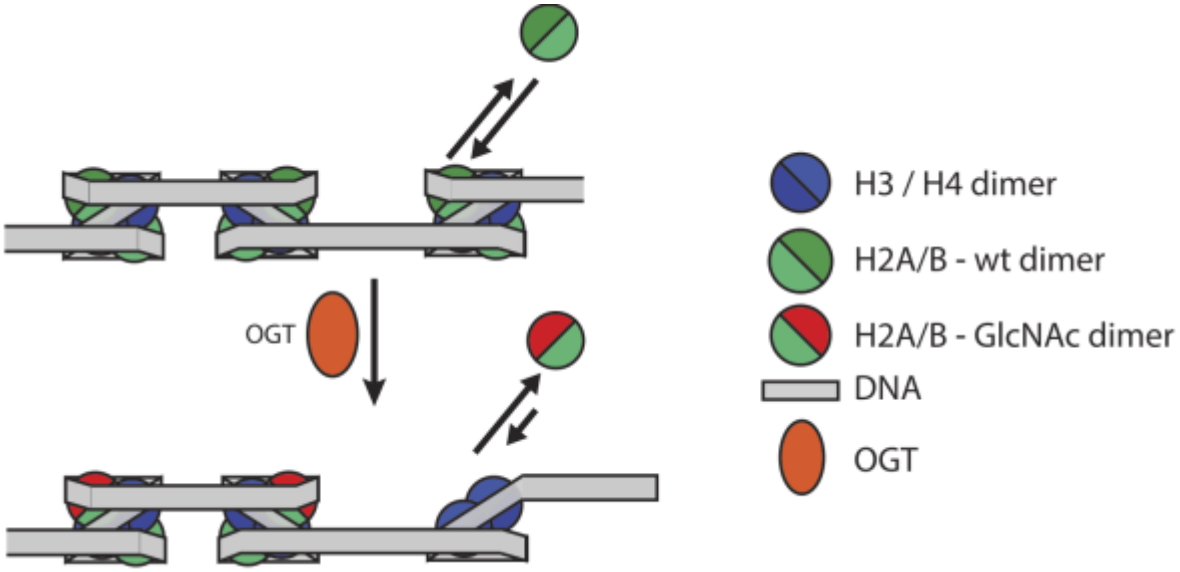


Figure 14. A proposed model for H2A-T101 *O*-GlcNAcylation promoted transcriptional activation. OGT-mediated GlcNAcylated H2A/B dimer upon incorporation in nucleosome destabilizes the structure and promotes an open chromatin state. (Reproduced from Lercher *et al.*[1])

3.3 Conclusion and Outlook

In this chapter, GlcNAcylated histone protein H2A was synthesized using "tag-and-modify" chemical approach. The modified histone protein was used for refolding of modified histone sub-complexes and nucleosomes. The structure and stability of these refolded biomolecules were studied by an array of biophysical tools which revealed a modulation in their structure and stability upon modification. Further examination of reconstituted nucleosomes by native mass spectrometry allowed a deeper insight into the biomolecule assembly at a molecular level. It would have been of interest to validate the proteomics experiments results using an orthogonal, independent experiment such as electrophoretic mobility shift assay (EMSA). In contrast to H2B-S112 *O*-GlcNAcylation (studied in previous chapter), H2A-T101 GlcNAcylation directly affects the nucleosome structure by destabilizing it. The destabilized nucleosome structure can plausibly promote transcription by lowering the barrier for RNA polymerase passage. The study described here taken together with results described in previous chapter highlights contrasting mechanisms for epigenetic regulation by histone *O*-GlcNAcylation. It is worth-noting that a large knowledge-set on chromatin research

has been derived by use of modified peptides.[46] However, the structural details obtained here and elsewhere[2,47] by using 'designer' nucleosome would not have been possible by study based on modified peptides, highlighting the need of using 'proper' models for future chromatin research.

3.4 Experimental Section

For general consideration, details of expression and purification of histone proteins please see section 2.4.1 and 2.4.2 of Chapter 2. Native-MS analysis was performed by Nisha Patel (Carol Robinson group).

3.4.1 Expression and purification of Histone protein H2A-T101C

Starting from the pET3 bacterial plasmid encoding wt *Xenopus laevis* histone protein H2A, desired mutation was introduced by Dr. Lukas Lercher by site-directed mutagenesis. The primers used for mutagenesis are as follows:

Forward Primer: CTG CTC GGA AGA GTC TGT ATC GCT CAG GGC GG

Reverse Primer: CCG CCC TGA GCG ATA CAG ACT CTT CCG AGC AG

The protein was expressed in *E.coli* BL21(DE3)pLysS competent cell and purified by size-exclusion (HiLoad 26/600 Superdex 200, GE Healthcare Life Sciences) followed by ion-exchange (HiTrap SP HP 5 mL, GE Healthcare Life Sciences) chromatography as described previously.[12] The purified histone protein was lyophilized and stored at -80 °C. FPLC traces, SDS-PAGE gels and MS spectra for purified histone protein has are shown below

been shown below **(Figure 15)**:

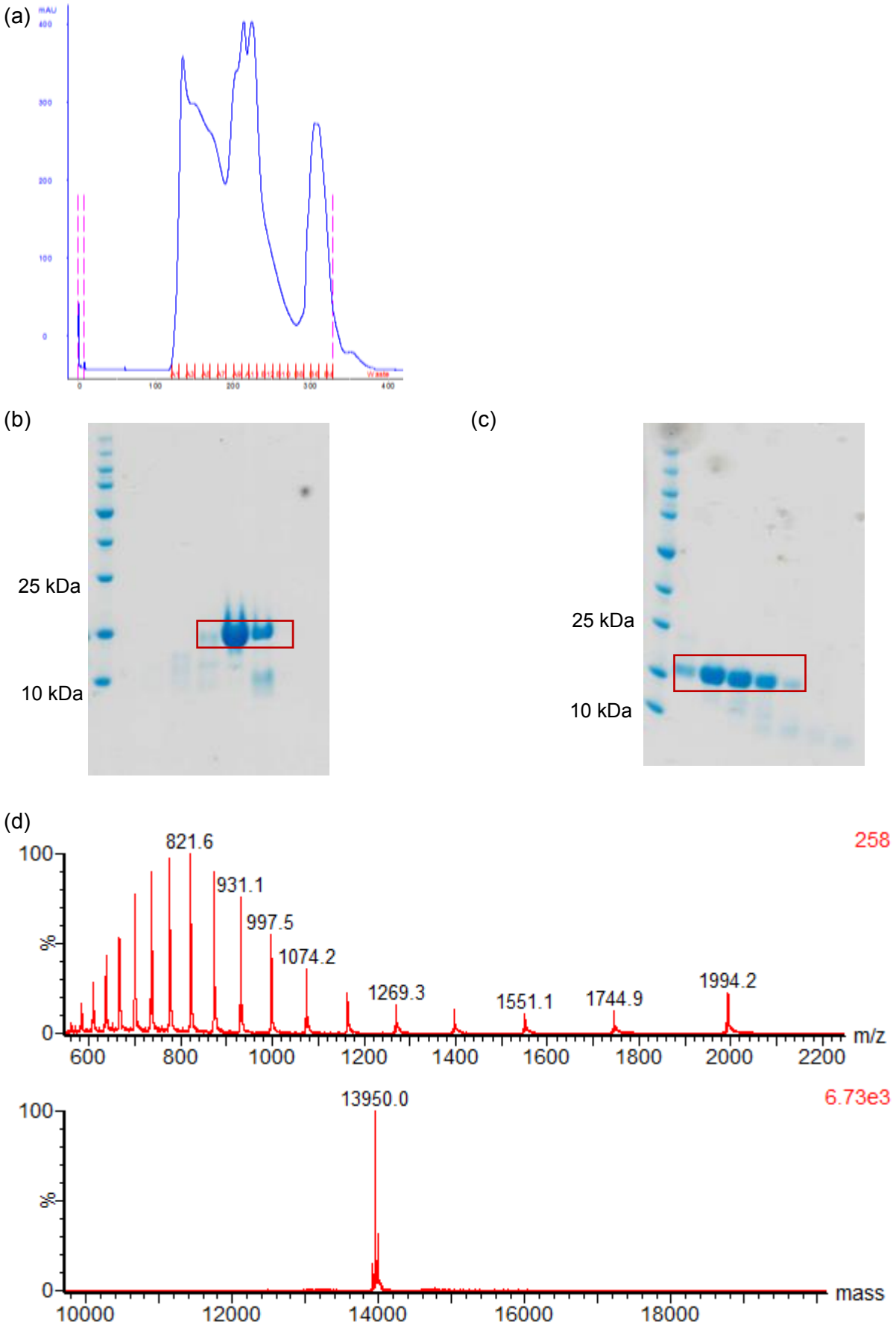


Figure 15. Expression and purification of histone protein H2A-T101C. (a) FPLC traces for

SEC purification. (b), (c) SDS-PAGE analysis for purified protein after SEC and SCX purification. (d) LC-MS spectrum for purified protein.

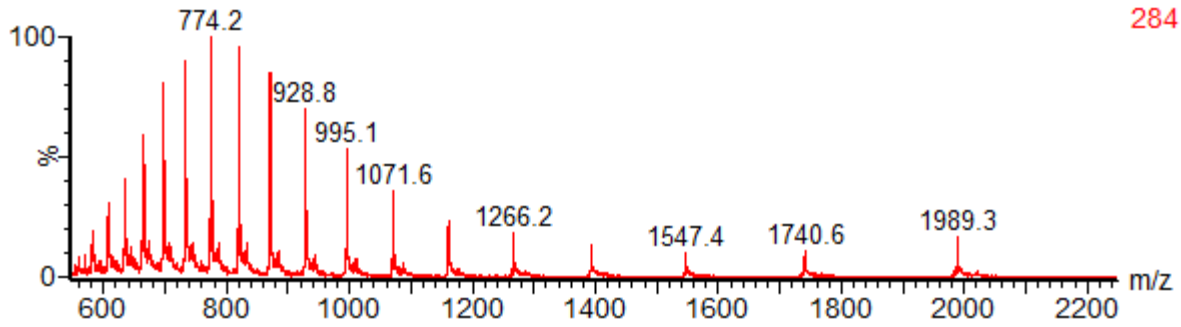
3.4.2 Site-selective chemical protein modification

Synthesis of DBHDA and GlcNAc-thiol has been previously described.[48] DBHDA and GlcNAc-thiol were kindly provided by Dr. Phin Chooi and Dr. Arghya Modak respectively.

(i) Synthesis of H2A-Thr101 Dha

9.40 mg of H2A-T101C protein (0.6 µmol) was taken in 500 µL of freshly prepared reaction buffer (5 M Gd.HCl, 50 mM Tris pH 8.0). ~ 10 mg of DTT was added to the protein solution. The resulting mixture was reduced at 37 °C for 30 minutes. The protein solution was desalted using a pre-equilibrated PD minitrap G-25 column (GE Healthcare Life Sciences) eluting with 1 mL of reaction buffer.

100 µL of DBHDA solution (in DMF, 90 equivalents, 54 µmol) was added to 900 µL of reduced protein sample. 100 equivalents of DBHDA solution (35 µmol, 0.50 M in DMF, 70 µL) was added to 950 µL (0.35 µmol) of reduced protein sample. The reaction mixture was incubated at 37 °C. The progress of reaction was monitored by LC-MS (see section 2.4.4). LC-MS analysis revealed completion of reaction after 2 hours **(Figure 16)**. The reaction mixture was desalted using a pre-equilibrated PD miditrap G-25 column (GE Healthcare Life Sciences) eluting with 1.5 mL of reaction buffer. The modified protein was stored at -20 °C waiting further manipulation.



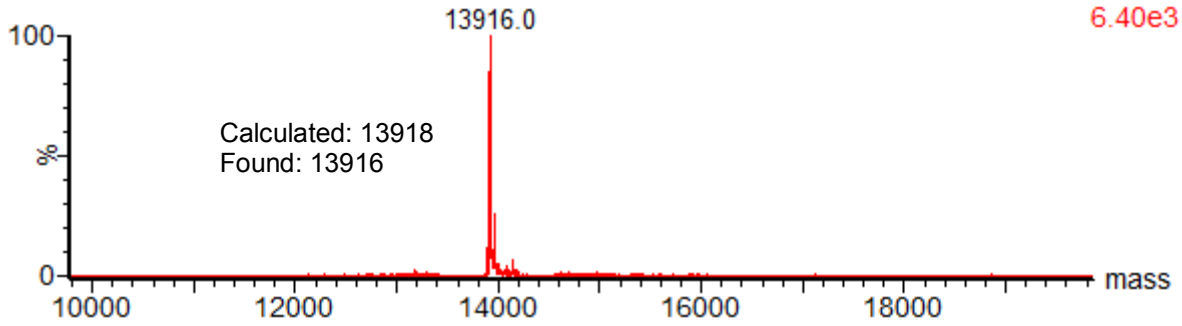


Figure 16. LC-MS Spectrum for synthesis of H2A-T101 Dha protein.

(ii) Synthesis of H2A-Thr101 GlcNAc

1 mL of earlier synthesized H2A-T101 Dha protein (1.90 mg, 0.136 µmol) in reaction buffer was transferred to an eppendorf tube. 1000 equivalent of GlcNAc-thiol (32.48 mg, 136 µmol) was added to the protein sample as a solid (though such high equivalents of GlcNAc-thiol are not necessary). The reaction mixture was incubated at 37 °C. The progress of reaction was monitored by LC-MS. The reaction reached completion in 3 hours resulting in synthesis of H2A-T101 GlcNAc protein **(Figure 17)**. The reaction mixture was desalted using a pre-equilibrated PD miditrap G-25 column (GE Healthcare Life Sciences) and was stored at -20 °C till further manipulation.

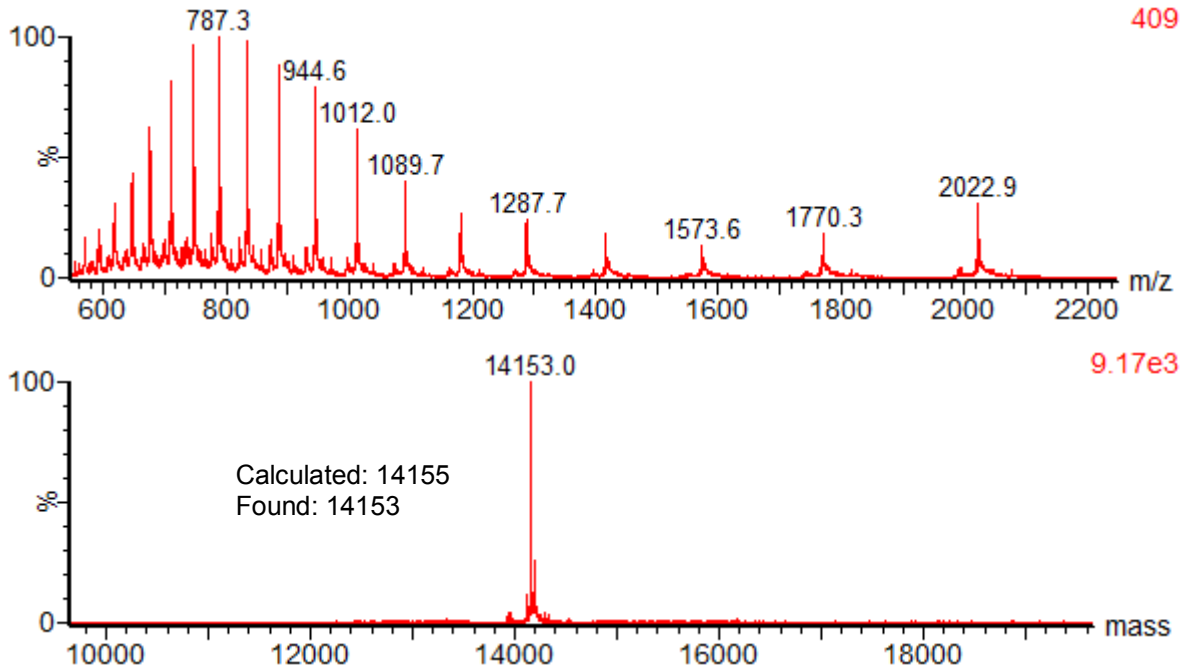


Figure 17. LC-MS Spectrum of H2A T101 GlcNAc

3.4.3 Histone complex reconstitution

Histone sub-complexes were refolded as described earlier (see section 2.4.6).[12,49,50] For octamer reconstitution starting from dimers and tetramers, the two species were mixed in 1.1:1 ratio in refolding buffer (2 M NaCl, 10 mM Tris pH 7.5, 1mm EDTA, 1 mM DTT). The mixture was incubated on ice for 1 hour and subsequently purified by gel filtration. The titration experiment for octamer reconstitution was done by mixing dimer and tetramer in earlier mentioned ratios in refolding buffer. The mixture was incubated on ice for 1 hour followed by size-exclusion analysis using a Superdex S200 10/300 GL column (GE Healthcare Life Sciences) in refolding buffer.

3.4.4 Nucleosome reconstitution

Nucleosomes were reconstituted using two different DNA fragments – 145 bp '601' DNA and 186 bp biotinylated '601' DNA. DNA was prepared as detailed in section 2.4.7. Wt nucleosomes were assembled by combining wt octamers and DNA in a 1: 0.9 molar ratio in high-salt buffer (2 M KCl, 10 mM Tris pH 7.5, 1 mM EDTA, 1 mM DDT). The DNA-protein mixture was then transferred to a 3500 MWCO dialysis tubing and was dialyzed against a series of low-salt step-gradient buffers (0.85 M KCl, 0.65 M KCl, 0.25 M KCl) for at least 2 hours.[12] GlcNAcylated nucleosomes were reconstituted by combining dimer: tetramer: DNA in a 2: 1: 0.9 ratio in high-salt buffer followed by dialysis against low-salt step-gradient buffers. Titration experiment for nucleosome reconstitution by varying the dimer equivalent were done by keeping the tetramer and DNA amount constant. After dialysis, the samples were transferred to eppendorf tubes and centrifuged to remove any precipitation, if any. The reconstituted nucleosomes were analyzed by Native PAGE using Novex TBE Gels (6%, Invitrogen). The TBE gel was pre-run in 0.5 % TBE buffer at 150 V for 90 minutes at 4 °C. 0.5-1 µg (1 µL) of nucleosome samples along with 5 µL of 6 % sucrose solution were loaded per

well. 100 bp DNA ladder was also added. The gel was run at 150 V for 90 minutes. The gel was stained with SYBR® Gold nucleic acid gel stain (Invitrogen) followed by Coomassie Brilliant Blue stain.

3.4.5 CD analysis of the nucleosomes

CD analysis of nucleosome was done exactly as described in section 2.4.9. For CD analysis, 180 µL of 0.62 µM nucleosome solution was used.

3.4.6 Native-MS analysis of the nucleosomes

Nucleosomes were buffer exchanged using Micro Bio-Spin chromatography columns (Bio-Rad) equilibrated with 50 mM ammonium acetate pH 7.5. Spectra were acquired on a QToF II MS (Waters) modified for high mass analysis and preservation of non-covalent interactions.[51] Aliquots (3 µl) diluted to 1-2.5 µM were introduced into the mass spectrometer from gold-plated capillary needles (Harvard Apparatus). Capillary voltages were kept at 1.4-1.6 kV, cone voltages at 80-100 V and collision voltage at 10 eV. ToF pressure $2.05X10^{-6}$ bar, analyzer pressure $1.54X10^{-4}$ bar and backing pressure $4.26X10^{-3}$ bar. The recorded mass spectra were calibrated externally using caesium iodide in water. Data were acquired and processed with Mass Lynx V4.1 software (Waters) with minimal smoothing and no background subtraction.

3.4.6 Salt-based disassembly of the nucleosomes

Salt based disassembly was performed as previously described.[18,52] To 5 µL of each nucleosome (4 µM in 10 mM Tris pH 7.5, 1mM EDTA) was added 1 µL of a KCl stock solution to give the final salt concentration as indicated. The samples were then incubated at 37 °C for 60 minutes and analyzed by Native PAGE.

3.4.7 Thermal disassembly of the nucleosome

10 µL of each nucleosome (4 µM in 10 mM Tris pH 7.5, 20 mM KCl, 1 mM EDTA) were incubated at 63 °C, 66 °C, 69 °C, 72 °C or 75 °C in a PCR machine for 30 minutes. The samples were centrifuged and the supernatant was analyzed using Native PAGE and SDS-PAGE. SDS-PAGE analysis was performed using 12 % Bis-Tris gel (Novex). The gel was run in 1x MOPS buffer at 200 V for 50 minutes. The gel was stained with InstantBlue (Expedeon).

3.4.8 MS-based interaction proteomics experiment with H2A-T101 GlcNAc modified nucleosome

For affinity enrichment of nucleosome-binding proteins, wt and H2A-T101 GlcNAc modified nucleosomes were reconstituted using 186 bp biotinylated '601' DNA as described earlier. The nuclear extracts were prepared as described in the section 2.4.10. Interaction studies between the nucleosome and the nuclear extract were performed in a similar manner as described in the section 2.4.11. The nucleosome-binding proteins for each nucleosome were digested enzymatically using FASP protocol and resulting peptide mixtures were analyzed on mass spectrometer. For details on digestion and mass spectrometric data acquisition, please refer to section 2.4.11.

The raw data files generated were processed using MaxQuant software (Version 1.4.3.17), integrated with Andromeda search engine as previously described.[37,38] For protein groups identification, peak lists were searched against human database (Swiss-Prot, version 04/13) as well as list of common contaminants by Andromeda. Trypsin with a maximum number of missed cleavages of 2 was chosen. Acetylation (Protein N-term) and Oxidation (Methionine) were used as variable modifications while Carbamidomethylation (Cysteine) was set as a fixed modification. Protein and PSM false discovery rate (FDR) were set at 0.01. Label free quantification (LFQ) was performed using the in-built algorithm in the MaxQuant.[36] LFQ intensities were imported into Perseus software (Version 1.4.2.27)[53] for down-stream analysis. Contaminant, reverse and protein groups only indentified by site were filtered off. Only protein groups identified in both bait and control samples and each replicates were considered for

further analysis. Their LFQ intensities were logarithmized and a mean value was calculated. The difference between the average LFQ intensities of protein groups between bait and control samples alongside total intensity were evaluated by Significance B in order to generate a p-value.

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4. Probing the competitive antagonism between O-GlcNAcylation and phosphorylation modifications of the nucleosome at H2B-Ser36

4.1 Introduction

In the previous chapters, potential regulation of chromatin dynamics as a consequence of *O*-GlcNAcylation of nucleosomes was described.[1,2] These studies focused on nucleosomes having a single histone modification at a single site. However, in a biologically-relevant context, nucleosomes are decorated with different modifications at multiple sites.[3] These multiple modifications can establish a 'cross-talk' to act in a concerted manner, providing an extra layer of complexity in chromatin regulation as compared to a 'two-state (on/off)' regulation afforded by a single modification.[4] The cross-talk between different histone modifications can occur through various mechanisms.[5,6] In one of the simplest mechanisms, two or more different histone modifications can compete for the same modification site leading to different epigenetic states. Earlier studies have shown that for example the role of histone H3 lysine 9 in the regulation of chromatin dynamics depends upon its modification state; with acetylated H3-Lys9 being associated with transcriptional activation whereas trimethylation modification of the same residue being linked to heterochromatin domains.[7,8]

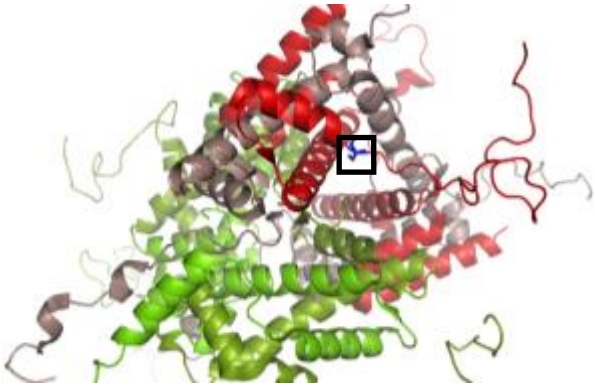
A similar interplay can occur on serine or threonine residues with *O*-GlcNAcylation and phosphorylation.[9,10] Earlier studies have established a competitive behavior between these two modifications to occupy same sites on many different protein such as c-Myc oncogene protein, estrogen receptor β protein, RNA polymerase II protein, endothelial nitric oxide synthase protein as well as histone protein H2B in a context-dependent manner.[11-17] Like *O*-GlcNAcylation, phosphorylation is also a dynamic protein modification being regulated in response to cellular stimuli; which modulates the structure as well as interacting protein partners of the target proteins.[18] Intriguingly, the regulatory roles of these two modifications are often supposed to be intertwined and to some extent reciprocal in nature. In this chapter, initial results describing such an interplay between *O*-GlcNAcylation and phosphorylation

modifications of histone protein H2B on a commonly occupied Serine residue (H2B-Ser36) are reported.

4.1.1 Site of modification: H2B-Ser36

H2B-Ser36 was shown to be a site for *O*-GlcNAcylation or phosphorylation modifications in two independent reports.[16,17] The site of modification is located on the lateral surface of histone octamer in close proximity to nucleosomal DNA. The serine residue serves to delineate the protruding *N*-terminal tail of H2B from the nucleosome core **(Figure 1)**.[19] HBR (Histone H2B repression) domain; a highly basic, conserved domain comprised of residues 30-37 in yeast H2B, encompasses the modification site.[20] The HBR domain has been previously implicated in DNA-templated processes such as gene expression and DNA repair.[21]

(a)



(b)

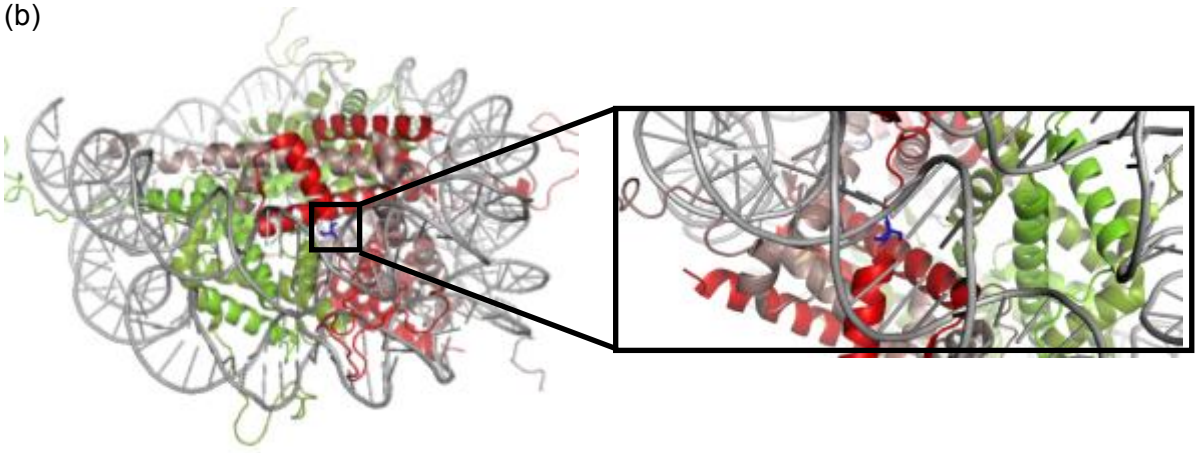


Figure 1. Histone octamer and nucleosome structure showing the modification site, H2B-Ser36. The site has been enclosed in black box. H2A and H2B proteins are shown in different shades of red, H3 and H4 proteins in different shades of green, and DNA in grey.

Bungard *et al.* previously found histone protein H2B to be phosphorylated at Ser-36 residue.[16] The phosphorylation was catalyzed by adenosine monophosphate-activated kinase (AMPK). AMPK is central for the energy regulation in eukaryotic cells. The energy regulation by AMPK is, in parts, performed by modulation of gene expression through phosphorylation of various transcription factors and coactivators.[22] The modification at H2B-Ser36 was found to facilitate transcription with the modified protein being associated with the promoter as well as transcribed regions of p53 target genes. Phosphorylation of H2B-Ser36 was found to be nutrient-sensitive as would be expected for a modification that is catalyzed by AMPK, with the amount of modification decreasing in response to increased glucose level.

In a separate study, Sakabe *et al.* reported H2B-Ser36 as one of the modification sites for *O*-GlcNAcylation, although no functional consequence of the modification has been established to date.[17] Interestingly, Fujiki *et al.* have earlier demonstrated a positive correlation between *O*-GlcNAcylation modification of histone protein and elevated amount of glucose level.[23] In light of such results, a possible competition between these two modifications to occupy the same site in a nutrient-dependent manner seems plausible.

As discussed in earlier chapters, histone modifications usually achieve their functional outcome either through modulating nucleosome structure or by promoting preferential binding of interactor proteins.[5] In this case, the modification site lies in a loop protruding away from histone octamer, as such H2B-Ser36 modification will in most likelihood not destabilize the octamer structure **(Figure 1)**. However, the same cannot be said for physical effects of the modification on the nucleosome structure. H2B-Ser36 is known to interact with nucleosomal DNA, and modifications such as phosphorylation or *O*-GlcNAcylation on this site can potentially modulate the octamer-DNA interactions. The structural modulation can result either from charge repulsion (introduced by phosphate groups) or by steric repulsion (introduced by *O*-GlcNAc moiety). In order to understand the physical effects of the modification on the nucleosome structure, assembly of synthetic nucleosomes bearing modifications were attempted **(Figure 2)**. These modified nucleosomes were later used in conjugation with quantitative MS to analyze interacting protein partners for each nucleosome in order to reveal

potential effector proteins which could provide a molecular basis for functional output of these modifications.

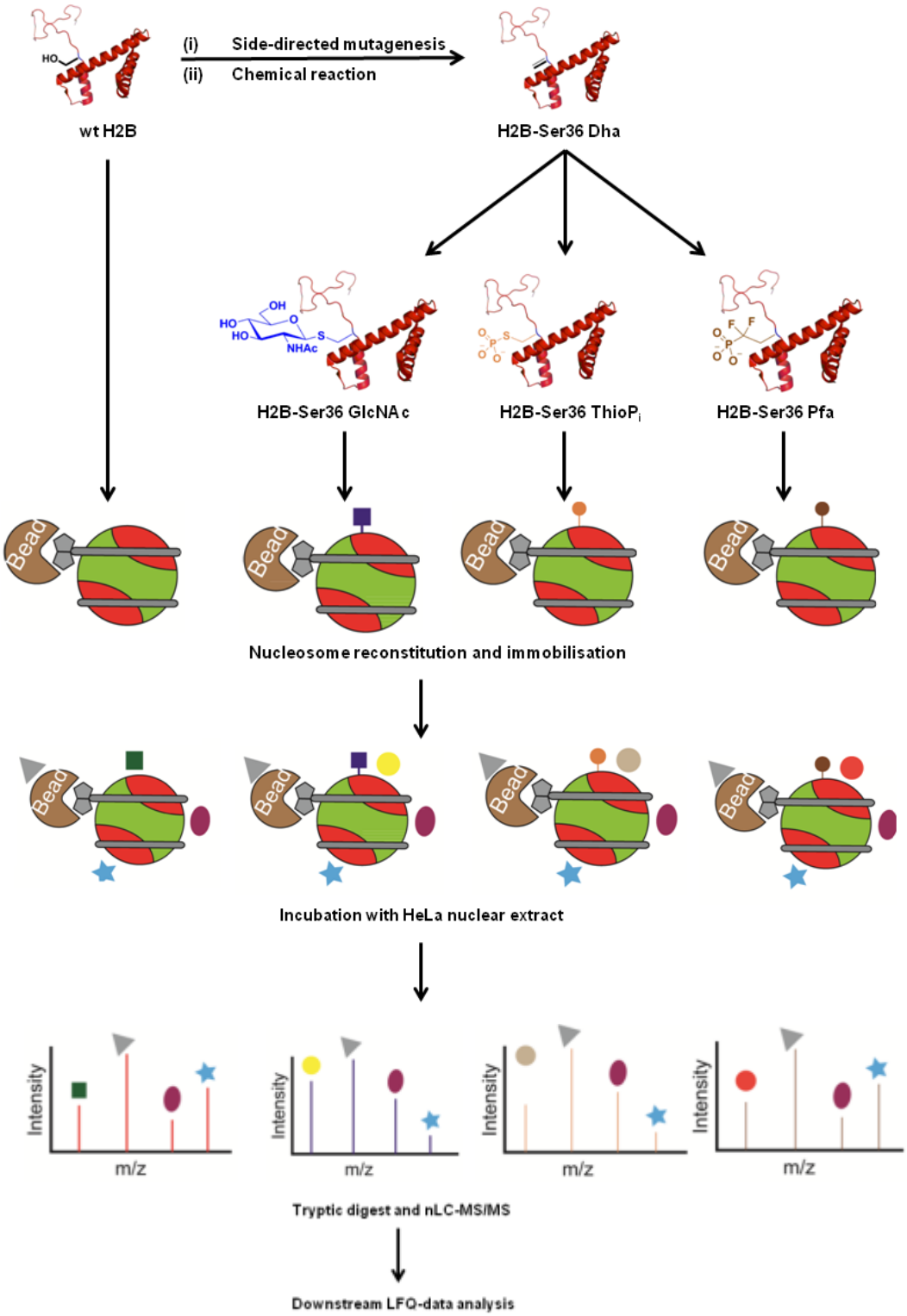


Figure 2. Schematic for probing the potential competitive antagonism of histone modifications at H2B-Ser36. Starting from wt H2B protein, H2B-S36Dha protein (precursor protein) was synthesized which was later reacted to yield differently modified histone proteins. The modified

histone protein (along with other canonical histone proteins and biotinylated DNA (shown in grey)) were used to assemble nucleosome in step-wise manner. Wildtype and modified nucleosomes were immobilized on magnetic beads (light brown) *via* streptavidin-biotin affinity to enrich nucleosome binding proteins. Pooled proteins from each sample were separately digested and identified by nanoLC-MS/MS. The identified protein partners were quantified against each other using MS-based Label-free Quantification (LFQ). H2A/B dimers shown in red, H3/H4 tetramer shown in green, GlcNAc shown as a blue square, Thiophosphate shown as orange circle, Phosphofluoroalanine shown as dark brown circle.

4.2 Results and Discussion

4.2.1 Synthesis of modified H2B-Ser36 proteins

The study of various cross-talk mechanisms of nucleosome have been impeded by a lack of suitable methods for easy access to differently modified nucleosomes.[24] Although, protein semi-synthesis based methods have been regularly used to assemble designer nucleosomes[25], the low throughput and time constraints have curbed its potential as a method of choice for assembly of differently modified nucleosomes. To overcome these limitations, it was decided to install a chemical handle at the site of modification which can be used to readily generate differently modified proteins **(Figure 2)**. Earlier work in our group has established the versatility of dehyrdoalanine 'tag' for synthesis of acetylated, methylated, GlcNAcylated, and phosphorylated functional proteins using a 'tag-and-modify' approach.[1,2,26,27]

In order to synthesize modified proteins, a mutant of histone protein H2B bearing a cysteine residue at site 36 was designed. The protein was produced in *E. coli* cells and later purified by standard chromatography techniques.[28] The purified protein was characterized by SDS-PAGE and LC-MS analysis. It is worth-mentioning that sometimes protein degradation (cleavage of the last four amino acid residues) was observed during few expression-purification trials and on long-term storage at -20 °C, although the exact reason for this observation was not clear. With purified protein in hand, Dha "tag" was site-selectively installed by treating the protein with ninety equivalents of 2,5-dibromohexanediamide (DBHDA) under denaturing conditions. The reaction was initially incubated at room temperature for 30 minutes,

followed by incubation at 37 °C. The reaction progress was monitored by LC-MS analysis which revealed completion after 2-3 hours. The reaction mixture was purified by desalting to yield H2B-S36 Dha protein **(Figure 3)**.

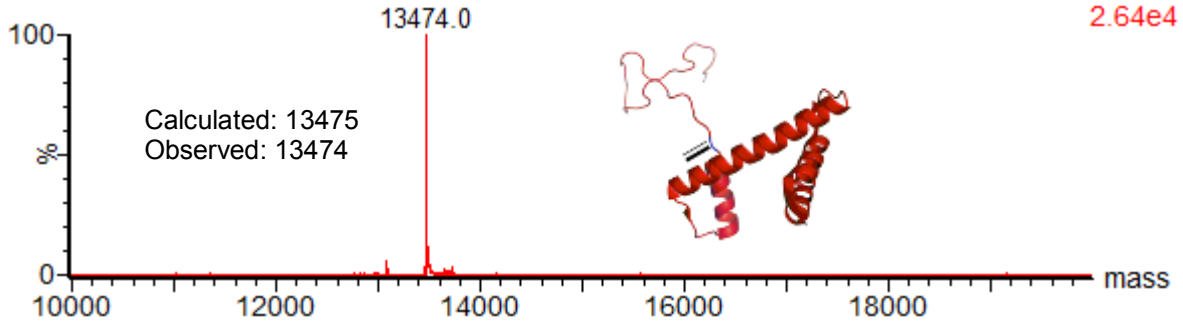


Figure 3. LC-MS spectrum of H2B-Ser36 Dha protein.

Next, to access the GlcNAcylated histone protein, the Dha bearing precursor protein was reacted with 400 equivalents of GlcNAc-thiol under denaturing conditions. The reaction mixture was incubated at 37 °C and its progress was analyzed by LC-MS. Full conversion to the desired product was observed after 2 hours of incubation **(Figure 4)**. The protein was purified as before by desalting.

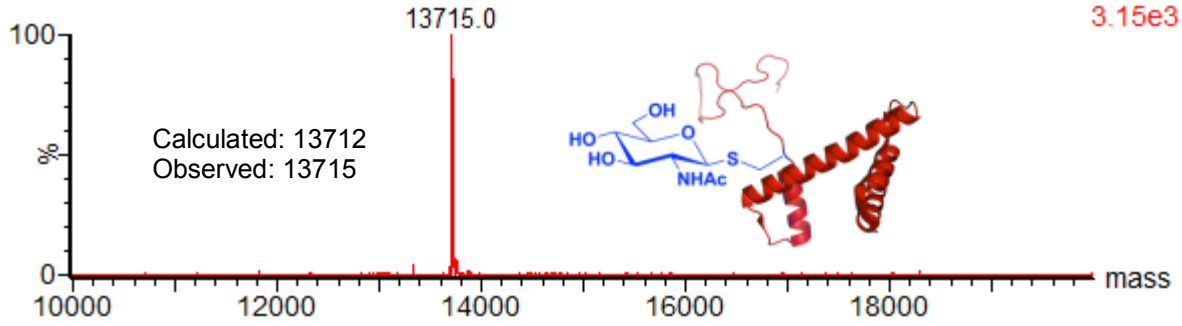


Figure 4. LC-MS spectrum for synthesis of H2B-Ser36 GlcNAc protein.

With GlcNAcylated histone protein in hand, the focus was shifted towards the synthesis of phosphorylated proteins. The elucidation of various kinase-dependent signaling pathways has been hampered by limited access to pure, homogeneously modified phosphoproteins. Phosphoproteins isolated from biological samples and *in vitro* enzymatic reactions are often heterogeneous mixtures.[29] Native chemical ligation based semisynthetic approaches provide

a route to phosphorylated proteins but their utility is often limited in cases where the modification sites are away from either protein terminals. In such cases, total chemical synthesis of modified proteins can provide a possible route. Indeed, Jbara *et al.* used a similar approach to synthesize histone protein H2A phosphorylated at site Tyr-57 to study its role in regulation of H2B deubiquitination.[30] Recent developments have made the incorporation of phosphoserine into protein possible using amber codon suppression, however low expression yields of the modified protein remain a concern.[31] In order to overcome these limitations, it was envisioned to synthesize the phosphorylated histone protein using protein chemical modification methods developed in our group, starting from the same Dha intermediate.[26,27]

In order to generate a histone protein modified with phosphoserine mimic, previously synthesized H2B-S36 Dha protein was treated with a buffered solution of sodium thiophosphate. In initial trial experiment, the reaction was incubated at 37 °C and was found to reach 100% conversion after 1 hour. Unfortunately, this result was not reproducible in later trials. The reactions were found not to be complete after 1 hour and longer incubation time led to the appearance of an additional +32 peak along with the desired product. The outcome of the reaction was found to be dependent upon the batch of sodium thiophosphate. (NMR investigation of commercial batches of sodium thiophosphate bought from Sigma-Aldrich and Alfa Aesar were performed by co-workers in Ben Davis group. An additional 'impurity' peak was found in Sigma-Aldrich batch). Later, the reactions were performed using sodium thiophosphate bought from Alfa Aesar. Different reaction conditions were screened for optimal conversion by varying the reaction time, incubation temperature, and salt concentration. Longer incubation time (overnight) at 25 °C was found to be the reproducible condition for > 90% conversion **(Figure 5)**.

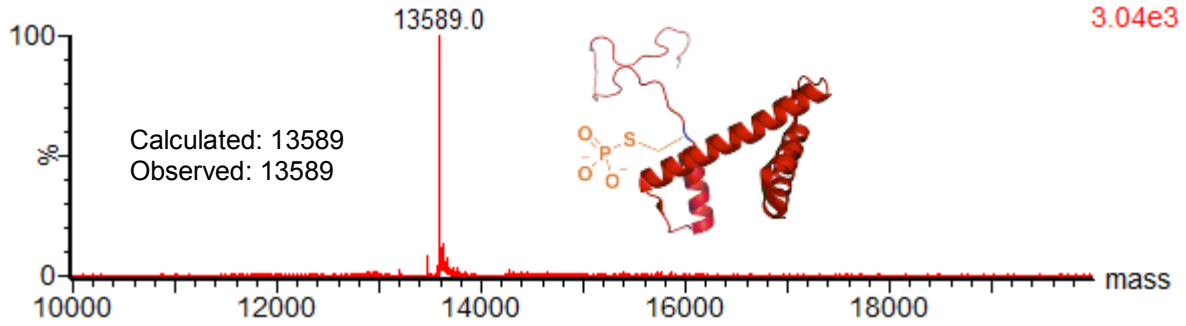
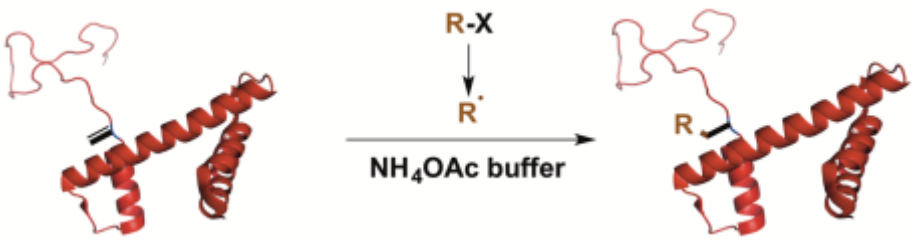


Figure 5. LC-MS spectrum for synthesis of H2B-Ser36 thiophosphate protein.

Apart from behaving like an electrophile in Thia-micheal reactions, dehydroalanine has the potential to function as a radical acceptor. Recent works in our group and other labs have exploited this possible reactivity to enable carbon-carbon bond formation on protein motifs to introduce various posttranslational modifications **(Figure 6)**.[32,33] In earlier work, this C-C bond formation strategy was used to install a Phosphonodifluoromethylene alanine (Pfa) residue on serine-10 site of histone H3 to create a functional mimic of a phosphorylated histone protein. This fluorinated residue has been suggested to be a more suitable alternative to phosphoserine residue based on its better mimicry of p*K*a, polarity and shape.[34,35] While struggling to find reproducible reaction conditions for the synthesis of the thiophosphate mimic, it was thought to use this radical route for the synthesis of fluorinated mimic of phosphoserine.

The modified protein was synthesized by treating the H2B-S36 Dha protein with (Bromodifluoromethyl)phosphonic acid in presence of sodium borohydride inside a glove box. The reaction was incubated at 4 °C for 30 minutes. The progress of reaction was monitored by LC-MS analysis which confirmed 100% conversion for the reaction **(Figure 6)**.

(a)



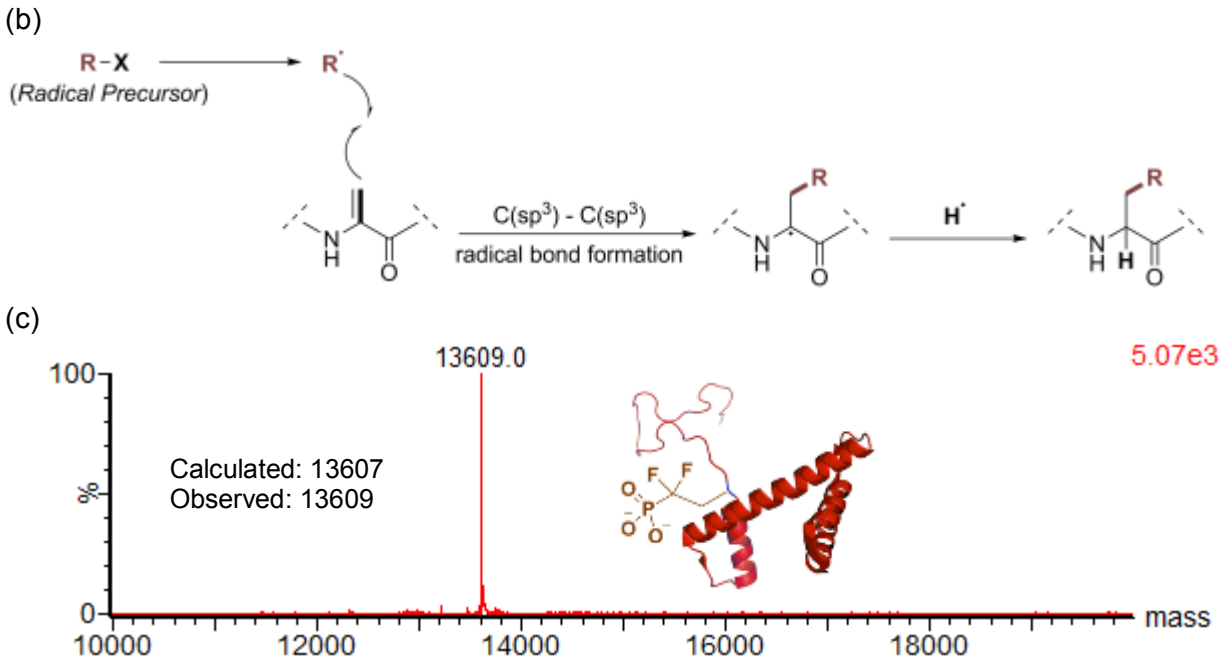


Figure 6. Synthesis of Phosphoserine mimic of H2B protein. (a) General scheme for C-C bond formation on protein using Dha residue. (b) Radical protein reaction for generation of C(sp^3)-C(sp^3) bond leading to installation of phosphate mimic. (c) LC-MS spectrum for H2B-Ser36 Pfa protein.

4.2.2 LC-MS/MS analysis of modified proteins

The synthesized proteins were later characterized by LC-MS/MS analysis to confirm the site-specific installation of different modifications. As discussed in chapter 2, the commonly used fragmentation technique, collision-induced dissociation (CID), is not suitable for the analysis of labile posttranslational modifications such as glycosylation and phosphorylation.[36] The glycosylated sample was analyzed by the earlier optimized HCD-PD-ETD hybrid acquisition method (for more details, please see chapter 2).[37,38] For the analysis of phosphoproteins, another hybrid method based on CID and ETD fragmentation techniques was optimized. Since, both these fragmentation techniques are complementary in nature (for e.g. their speed, preference for peptide charge state), a data-dependent decision tree algorithm was designed and optimized to increase the overall sequencing rate.[39]

The modified proteins were digested enzymatically and analyzed on an UHPLC (Ultra-high performance liquid chromatography) coupled to a hybrid Ion Trap-Orbitrap mass

spectrometer using above-mentioned data-acquisition methods. LC-MS/MS analysis confirmed the homogeneous and site-specific nature of the protein chemical modification **(Figure 7)**.

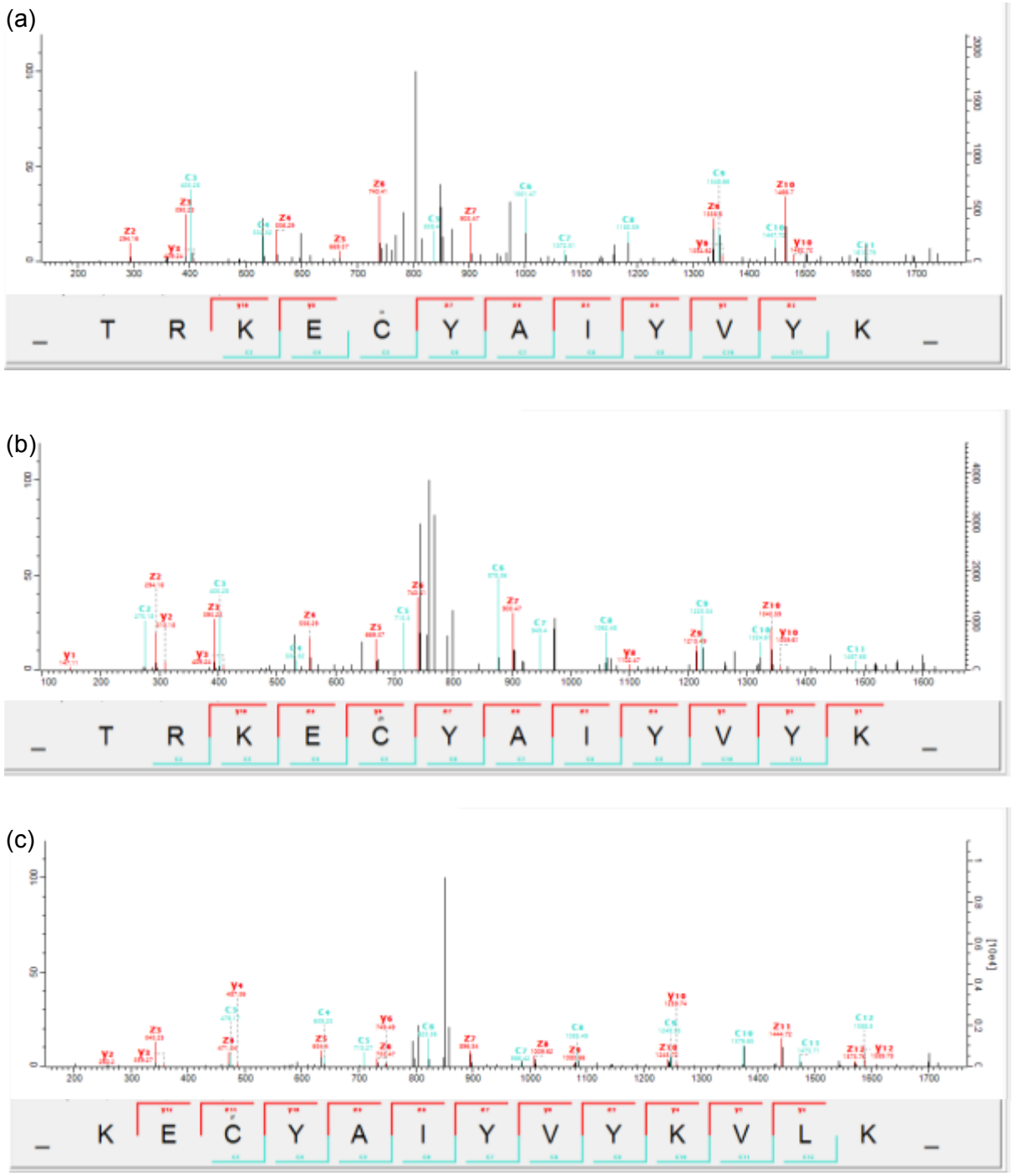


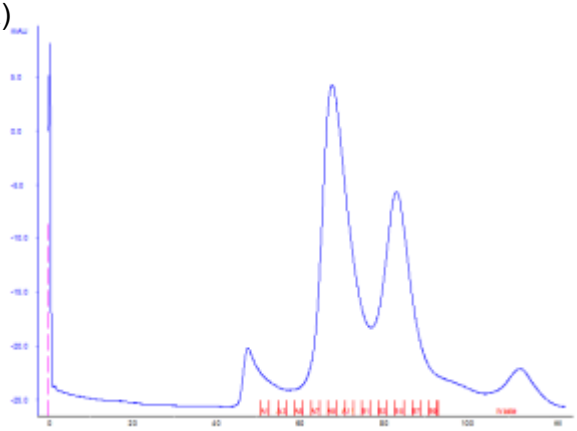
Figure 7. LC-MS/MS analysis of synthesized proteins. (a) ETD LC-MS/MS spectrum confirming the site-specific installation of thio-GlcNAc on H2B-Ser36. (b) ETD LC-MS/MS spectrum confirming the site-specific installation of thio-phosphate on H2B-Ser36. (c) ETD

LC-MS/MS spectrum confirming the site-specific installation of Pfa residue on H2B-Ser36.

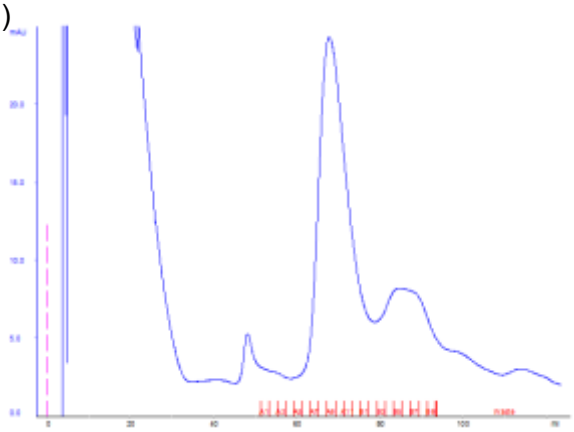
4.2.3 Reconstitution of Histone Octamers

With modified proteins in hand, assembly of wt and modified histone octamers was performed. The wt and modified H2B proteins were mixed with other canonical wt histone proteins (H2A, H3 and H4) under denaturing condition and dialyzed against high-salt buffer (2 M NaCl) to allow for histone octamer formation. The resulting histone sub-complexes were purified and analyzed by Size-exclusion chromatography (SEC). All refolded octamers had similar looking SEC trace suggesting no major disruption of histone-folds upon modification, as would be expected given the location of modification site **(Figure 8)**. However, the retention volume for Pfa modified octamer was slightly higher as compared to other octamers (retention volumes, wt octamer: 67.88 mL, GlcNAc modified octamer: 67.83 mL, thiophosphate modified octamer: 66 mL, and Pfa modified octamer: 70.15 mL). To find if the Pfa octamer had correct stoichiometry of constituent proteins, SDS-PAGE analysis was performed **(Figure 8e)**. However, result from the SDS-PAGE analysis were not very conclusive and further refolding experiment needs to be performed to confirm whether the observed result was due to the modification or a systematic purification artefact.

(a)



(b)



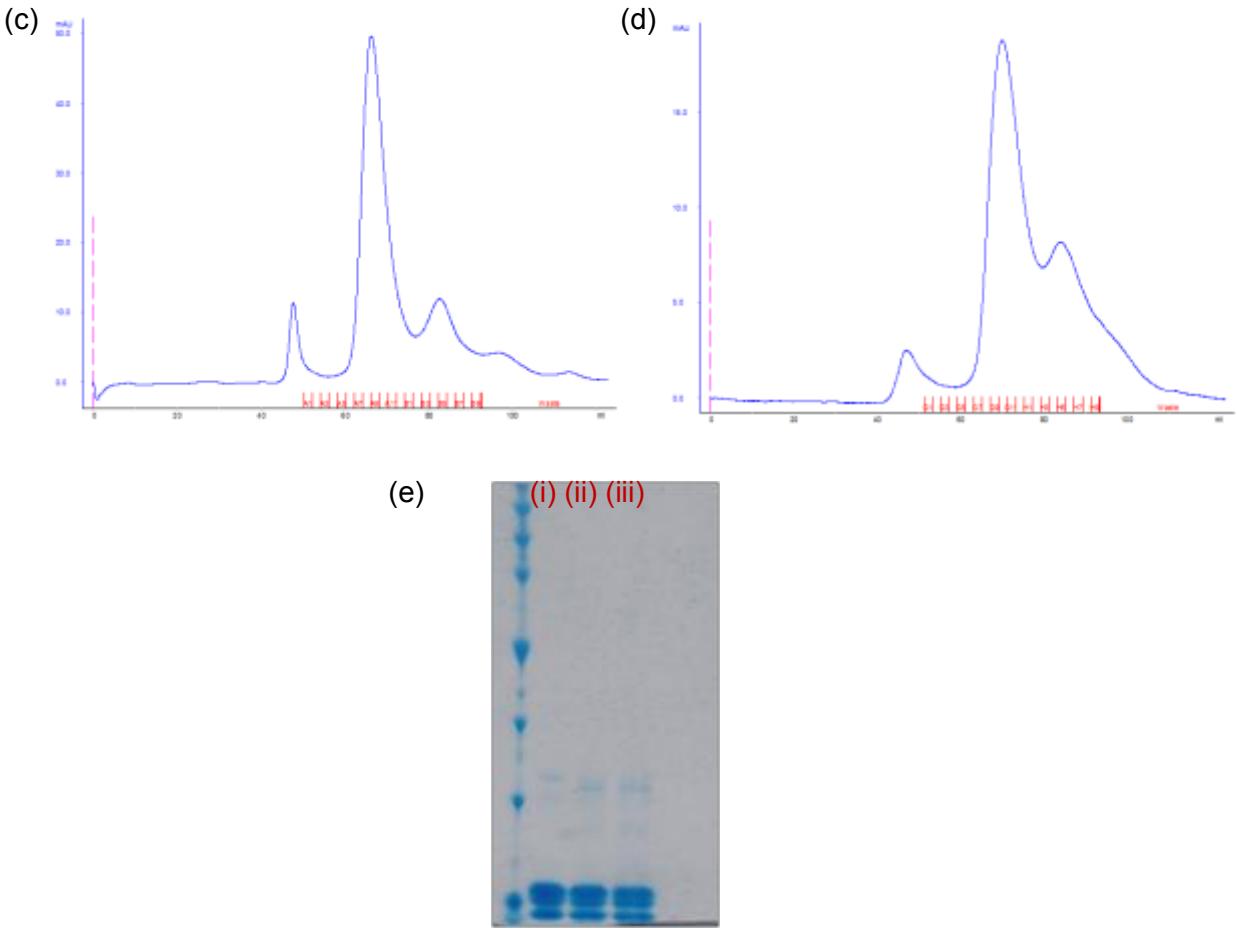


Figure 8. Reconstitution of histone octamer complexes. (a) SEC trace for wt octamer. (b) SEC trace for H2B-S36 GlcNAc modified octamer. (c) SEC trace for H2B-S36 thiophosphate modified octamer. (d) SEC trace for H2B-S36 Pfa modified octamer. (e) SDS-PAGE analysis of refolded octamers. The lanes are as follows: (i) wt octamer, (ii) H2B-S36 GlcNAc modified octamer, (iii) H2B-S36 Pfa modified octamer.

4.2.4 Nucleosome reconstitution

Nucleosomes were reconstituted by the salt-gradient dialysis method using a 186 bp biotinylated DNA fragment containing the strong '601' nucleosome positioning sequence.[28] In salt-gradient dialysis method, the octamer and DNA are mixed together in a high-salt buffer (2 M KCl) and are dialyzed against a series of buffers with decreasing salt-concentrations (0.85 M KCl, 0.65 M KCl, 0.25 M KCl). The salt-gradient dialysis based nucleosome reconstitution relies on the sequential binding of H3/H4 tetramer to DNA at higher salt concentration (~ 0.85 M KCl) followed by deposition of H2A/B dimers onto the DNA at lower

salt concentration (~ 0.65 M KCl). The nucleosome reconstitutions were performed in two separate batches. In the first batch, refolding of wt, H2B-S36 GlcNAc modified, and H2B-S36 thiophosphate modified nucleosomes was attempted. The reconstituted nucleosomes were analyzed using native-PAGE **(Figure 9)** which revealed similar mobility and reconstitution yield for the modified nucleosomes whereas for the wt nucleosome reconstitution, an additional minor band was observed. The appearance of this band was attributed to deteriorated batch of wt octamer.

In a separate experiment, reconstitution of wt, H2B-S36 GlcNAc modified, and H2B-S36 Pfa modified nucleosomes were accomplished. In this attempt, the reconstitution of wt nucleosome was done starting from a freshly folded wt octamer. The reconstituted nucleosomes were again analyzed by native-PAGE gels which revealed similar mobility and reconstitution yield for all the nucleosomes. Based on native-PAGE results, it seems that neither GlcNAcylation nor phosphorylation modification of H2B-Ser36 has substantial effect on nucleosome structure. However, it is of interest to further probe the reconstituted nucleosomes by CD spectroscopy (as done in earlier chapters) to reveal finer details regarding the effect of the modifications on structure and stability of the assembled biomolecules.

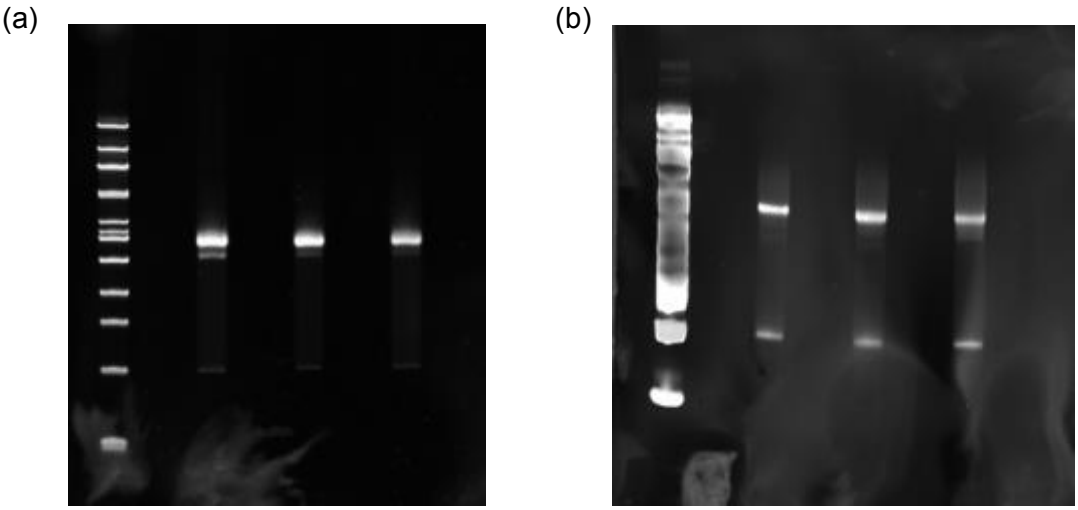


Figure 9. Native-PAGE analysis of reconstituted nucleosomes. The nucleosomes were reconstituted in two different batches. (a) The lanes represent: (i) 100 bp DNA ladder, (ii) wt

nucleosome, (iii) H2B-S36 GlcNAc modified nucleosome, (iv) H2B-S36 thiophosphate modified nucleosome. (b) The lanes represent: (v) 100 bp DNA ladder, (vi) wt nucleosome, (vii) H2B-S36 GlcNAc modified nucleosome, (viii) H2B-S36 pfa modified nucleosome.

4.2.5 MS-based Interaction Proteomics with Modified Nucleosomes

Since no direct structural perturbation of the modified nucleosomes was observed, it was envisioned to probe their interacting protein partners to understand the role of these modifications on DNA-templated processes. As before, a MS-based interaction proteomics approach was used to identify and quantify nucleosome-binding proteins **(Figure 2)**.[40] Wt, H2B-S36 GlcNAc modified, and H2B-S36 thiophosphate modified nucleosomes were immobilized on streptavidin-coated magnetic beads. These immobilized nucleosomes were incubated with HeLa cell nuclear extract for 4 hours to interrogate their putative interacting protein partners. After incubation, the beads were washed extensively to remove non-specific protein binders. The interacting protein partners for each modified nucleosome were eluted separately and were digested by Lys-C/trypsin proteases using the filter-aided sample preparation (FASP) protocol.[41] The resulting peptide mixtures from each sample were separated on an UHPLC and sprayed directly into a hybrid quadrupole-orbitrap (Q-Exactive) mass spectrometer operating under a data-dependent method.

The acquired mass spectrometry data were processed in pairs using MaxQuant software (e.g. GlcNAc modified nucleosome vs wt nucleosome). The relative quantification was done as in earlier chapters using the MaxLFQ algorithm (included in MaxQuant).[42-44] Since, the proteomics data was from a single pulldown experiment to avoid complications related to data-analysis, only protein groups identified in both the samples were used for analysis. Note that by doing so, information regarding the proteins which selectively bind to only one of two samples will be lost. Statistically significant protein partners for each batch were determined by significance B analysis based on Benjamini-Hochberg[45] FDR. The list of all identified proteins for each batch and their ratios are given in **(Appendix 5-7)**.

False discovery rate (FDR) based Significance B statistics revealed Serine/Threonine Protein Kinase WNK3 protein (*WNK3*) as the statistically most significant and most enriched interacting protein partner for GlcNAcylated nucleosome compared to wt nucleosome **(Figure 10)**. In case of phosphorylated nucleosome versus wt nucleosome, DNA topoisomerase 2 protein (*TOP2B*), Transformer-2 protein homolog alpha protein (*TRA2A*), 60S ribosomal protein L22-like 1 protein (*RPL22L1*), Serine/Threonine protein phosphatase PPP1CC protein (*PPP1CC*) and Transcription factor AP-2-alpha/epsilon protein (*TFAP2A*) were among the significantly enriched protein partner for modified nucleosome **(Figure 11)**.

The sub-family of WNK protein kinases is composed of four human genes coding for WNK1, WNK2, WNK3, and WNK4 and is characterized by lack of highly conserved catalytic lysine in subdomain II, leading to their name, **W**ith **N**o **K** [Lysine].[46] These kinases have been implicated in regulation of different ion transporters in both the kidneys and extrarenal tissues. Recently, there has been growing evidence for additional roles of WNK kinases in signalling cascades related to cancer. WNK3 has been suggested to be involved in the evasion of the apoptosis and thus promote cell survival in a procaspase-3-dependent pathway.[47] Interestingly, phosphorylation of H2B at Serine-14 promotes apoptosis in a caspase dependent manner.[48] An interplay between these two modifications of H2B at Ser14 and Ser36 as a 'control' mechanism leading to eventual apoptosis state cannot be ruled out and requires further examination.

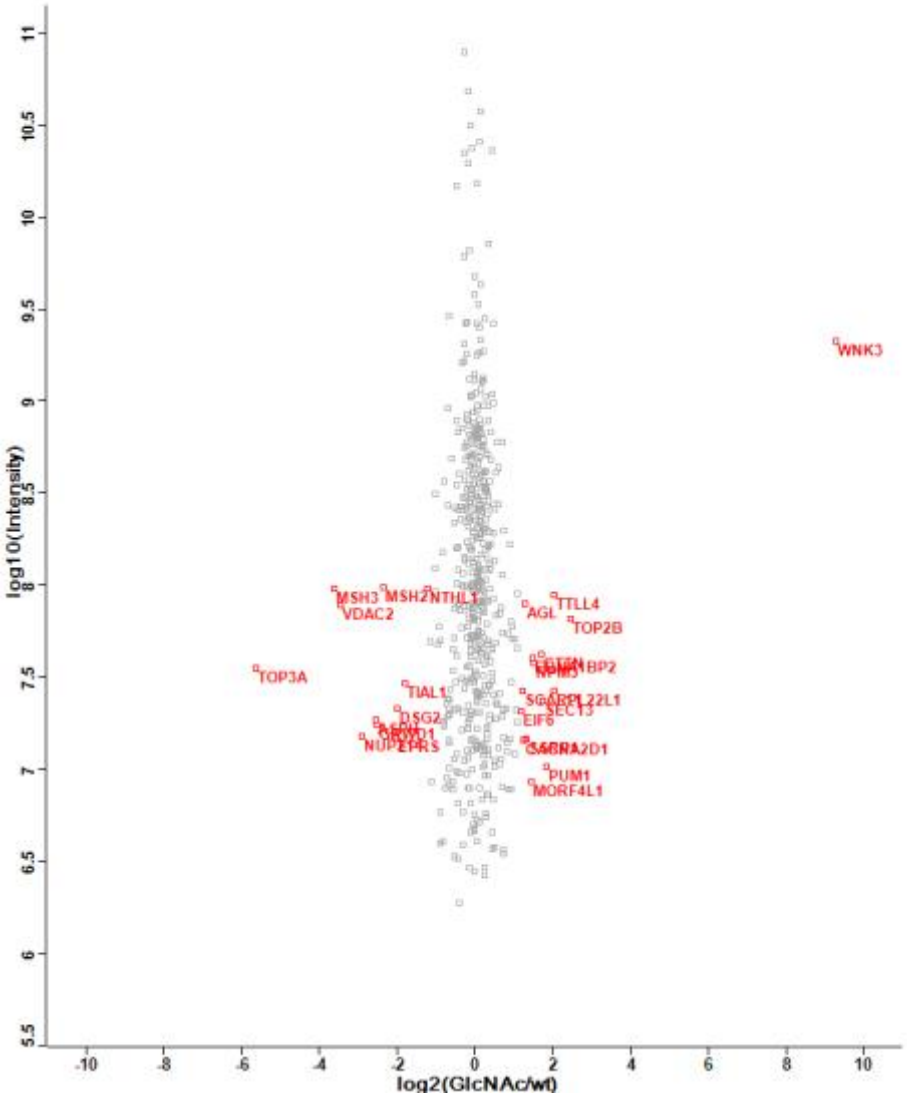


Figure 10. Quantitative MS-based proteomics allowed identification of nucleosome-binding protein partners for H2B-Ser36 GlcNAc nucleosome over wild-type nucleosome. The proteins identified in both the samples have been shown as a square in a scatter plot. x axis, logarithmized ratio of LFQ intensity of protein groups in the bait over control pulldown experiment; y axis, log10-transformed summed up intensity of protein groups. Significant protein partners identified by Significance B analysis are shown in red with their gene name.

Interestingly, for phosphorylated nucleosome, PPP1CA, a phosphatase, was observed amongst the significant protein partners **(Figure 11)**. It needs to be investigated if it is indeed the 'eraser' protein for this histone mark. Two proteins – DNA topoisomerase 2 protein (most enriched protein partner) and TFAP2A protein (a transcription factor) – previously linked to

active transcription were found to be the amongst significant interacting protein partners for phosphorylated nucleosome.[49,50] TOP2B protein is assumed to remove excessive DNA supercoils during elongation and in turn promote transcription. The observation of these nucleosome-binding proteins which promote active transcription might provide a molecular basis for earlier observed H2B-Ser36 phosphorylation promoted transcription.[16]

Next, the interacting protein partners for the GlcNAcylated nucleosome and the phosphorylated nucleosome were compared **(Figure 12)**. Certain proteins such as serine/threonine-protein kinase WNK3 protein, mortality factor 4-like protein, 5'-3' exoribonuclease 2 protein and interleukin enhancer-binding factor 2 were amongst proteins significantly enriched for GlcNAcylated nucleosome as compared to phosphorylated nucleosome. Intriguingly, previous studies have found association between 5'-3' exoribonuclease 2 protein and transcription termination.[51-53] Proteins coded by genes VPS13B, TMPO, PA2G4 and KTN1 were among the proteins that were selectively enriched for phosphorylated nucleosome as compared to GlcNAcylated nucleosome.

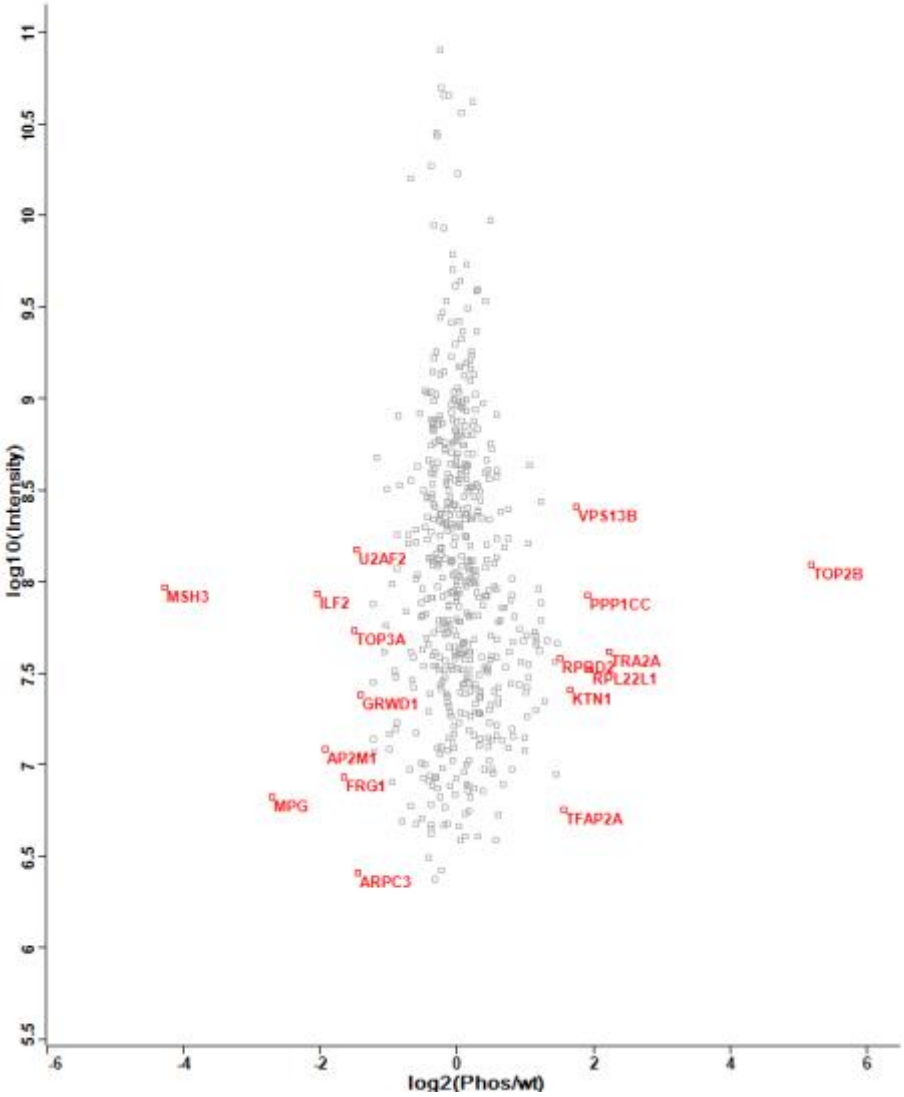


Figure 11. Quantitative MS-based proteomics allowed identification of nucleosome-binding protein partners for H2B-Ser36 thiophosphate nucleosome over wild-type nucleosome. The proteins identified in both the samples have been shown as a square in a scatter plot. x axis, logarithmized ratio of LFQ intensity of protein groups in the bait over control pulldown experiment; y axis, log10-transformed summed up intensity of protein groups. Significant protein partners identified by Significance B analysis are shown in red with their gene name.

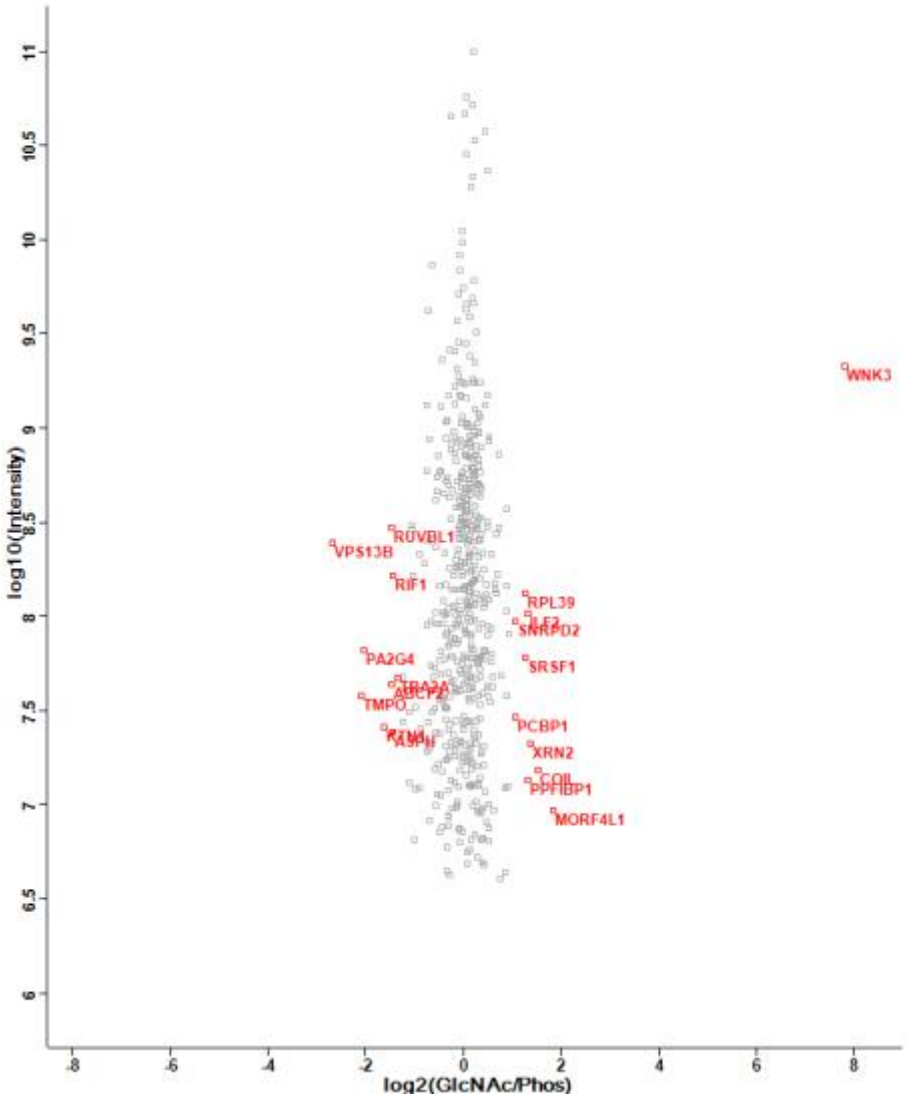


Figure 12. Quantitative MS-based proteomics allowed identification of nucleosome-binding protein partners for H2B-Ser36 GlcNAc modified nucleosome over H2B-Ser36 thiophosphate nucleosome. The proteins identified in both the samples have been shown as a square in a scatter plot. x axis, logarithmized ratio of LFQ intensity of protein groups in the GlcNAc modified nucleosome sample over thiophosphate modified nucleosome sample; y axis, log10-transformed summed up intensity of protein groups. Significant protein partners identified by Significance B analysis are shown in red with their gene name.

4.3 Conclusion and Outlook

The work described in this chapter shows the versatility of the Dha based chemical protein modification method to readily install different posttranslational modifications starting

from a single precursor. The synthesized proteins were used to reconstitute modified nucleosomes for the study of potential histone modifications cross-talk. However, to expedite the synthesis of differently modified nucleosomes even further, we envision to perform these mild, bioorthogonal protein chemical reactions at a later stage (at histone sub-complex or even at nucleosome stage) to introduce the desired modification. If possible, this would save precious starting material as well as time during assembly/purification of histone sub-complexes or/and nucleosome reconstitution. As such, in a proof-of-principle experiment, we have assembled and purified a histone octamer complex with Dha as an auxiliary 'tag' for late-stage functionalization. Although, the modifications did not seem to affect the nucleosome structure substantially, it would be ideal to further characterize the finer details of nucleosome structure and stability by circular dichroism spectrometry. Synthetic nucleosomes coupled with MS-based proteomics revealed interacting protein partners based on which a molecular mechanism for H2B-Ser36 phosphorylation mediated transcription could be proposed. However, no replicates have yet been performed for the pulldown experiment described in this chapter, and more biological replicates are needed for a robust and confident dataset. In conclusion, the multiplex approach used here provides a simple yet powerful route to study of histone modification 'crosstalk' which has previously lagged behind due to the low throughput and time constraints of methods for accessing modified histone proteins.

4.4 Experimental Section

For general consideration, details of expression and purification of histone proteins please see section 2.4.1 and 2.4.2 of Chapter 2.

4.4.1 Expression and purification of Histone protein H2B-S36C

H2B-S36C protein was expressed in *E.coli* BL21(DE3)pLysS cells starting from a pET3 bacterial plasmid encoding the desired protein. Side-directed mutagenesis to introduce the

mutation was performed by Dr. Lukas Lercher. The gene sequence and amino acid sequence of the mutant protein are given below:

DNA sequence:

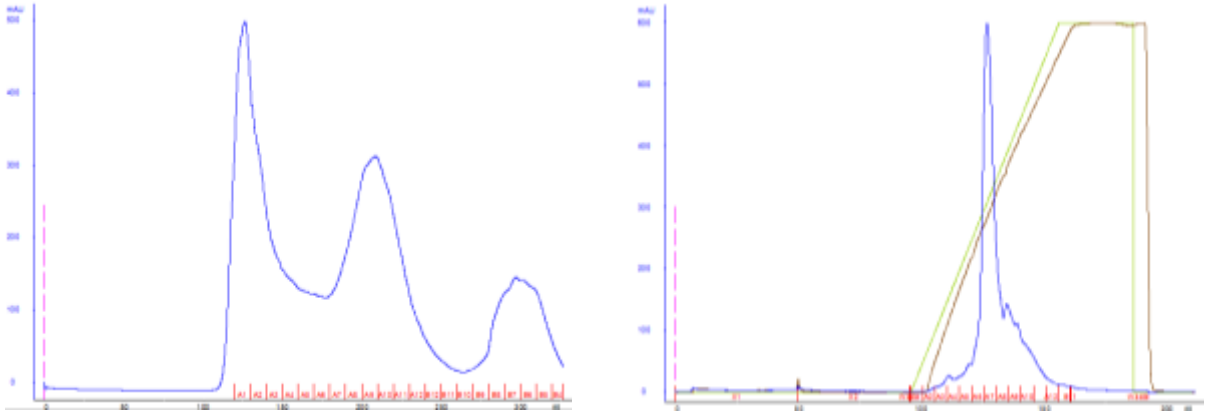
ATGGCCAAGTCCGCTCCAGCCCCGAAGAAAGGCTCCAAGAAAGCGGTGACCAAGACT
CAGAAGAAAGACGGGAAAAAGCGCAGGAAGACAAGGAAGGAGTGTTATGCCATTTACG
TGTACAAGGTGCTGAAGCAGGTGCACCCCGATACCGGCATCTCGTCCAAGGCCATGAG
CATCATGAACTCCTTTGTCAACGATGTGTTTGAGCGCATCGCAGGGGAAGCCTCCCGC
CTGGCTCATTACAACAAGCGCTCCACCATCACCTCCCGGGAGATCCAGACCGCGGTCC
GACTGCTGCTGCCTGGGGAGTTGGCCAAACACGCCGTGTCCGAGGGCACCAAGGCTG
TCACCAAGTACACCAGCGCCAAGTAACTGCTGCTGCCGGATCCGGCTGCTAACAAAGC
CCGAAAGGAAGCTGAGTTGGCTGCTGCCACCGCTGAGCAATAACTAG

Corresponding Amino Acid Sequence:

MAKSAPAPKK GSKKAVTKTQ KKDGKKRRKT RKE**C**YAIYVY KVLKQVHPDT
GISSKAMSIM NSFVNDVFER IAGEASRLAH YNKRSTITSR EIQTAVRLLL
PGELAKHAVS EGTKAVTKYT SAK

The protein was purified under denaturing condition from the inclusion bodies by size-exclusion (HiLoad 26/600 Superdex 200, GE Healthcare Life Sciences) followed by ion-exchange (HiTrap SP HP 5 mL, GE Healthcare Life Sciences) chromatography as described previously.[28] For more details of protein expression and purification, please refer to section 2.4.2. The purified histone protein was lyophilized and stored at -80 °C. The characterization details of protein expression and purification are shown below **(Figure 13)**:

(a) (b)



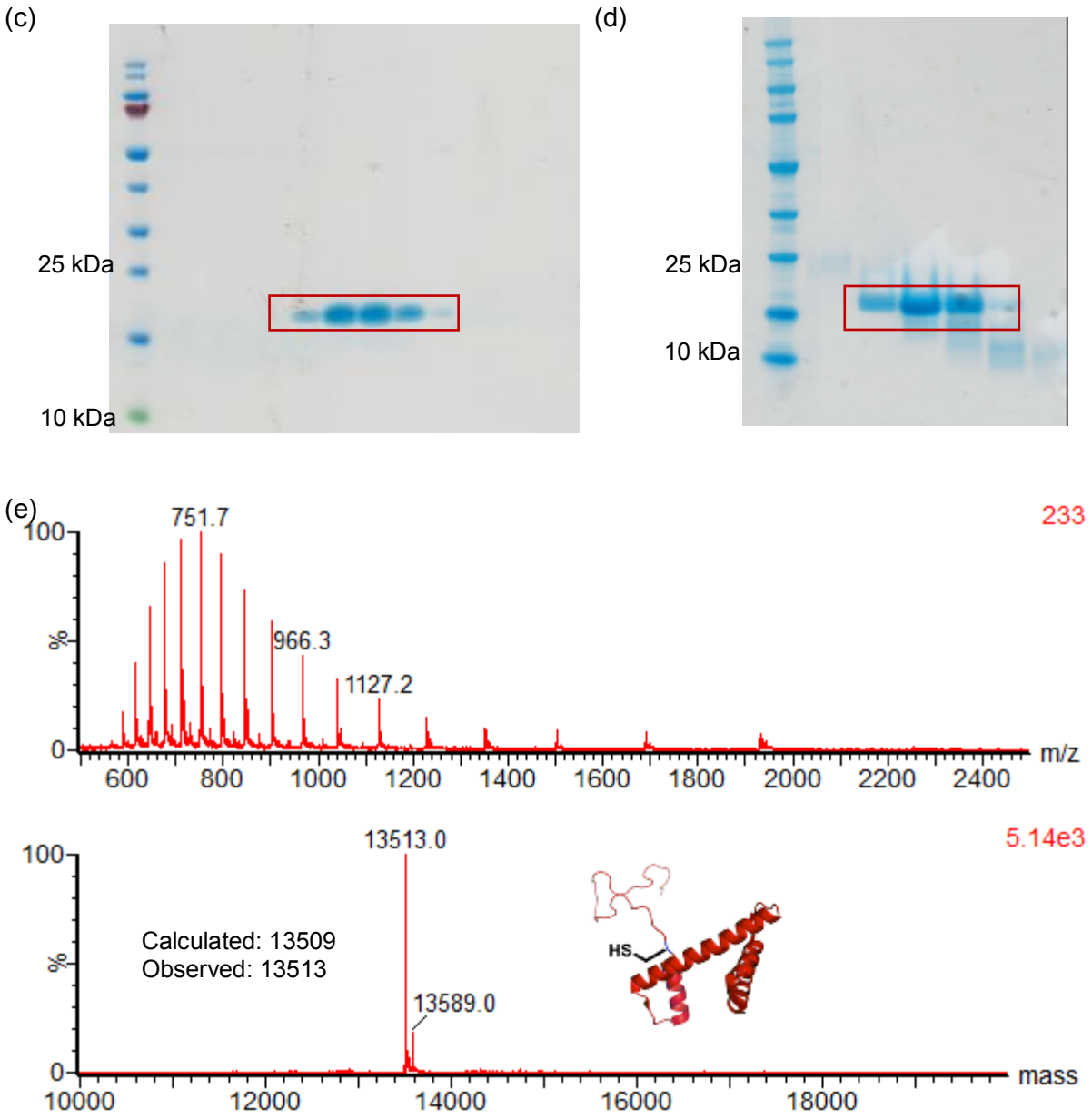


Figure 13. Expression and purification of histone protein H2B-S36C. (a), (b) FPLC traces for SEC and SCX purification respectively. (c), (d) SDS-PAGE analyses for purified protein fractions after SEC and SCX purification respectively. (e) LC-MS spectrum for purified protein. Note that minor peak at 13589 is the β-mercaptoethanol adduct peak.

4.4.2 Site-selective chemical protein modification

Synthesis of DBHDA and GlcNAc-thiol has been previously described.[26] DBHDA and GlcNAc-thiol were kindly provided by Dr. Phin Chooi and Dr. Mylène Richard respectively.

(i) Synthesis of H2B-Ser36 Dha protein

In a representative reaction, 5.41 mg of H2B-S36C protein (0.4 µmol) along with ~ 10 mg of DTT were weighed in an eppendorf tube. The mixture was dissolved in 500 µL of freshly prepared reaction buffer (5 M Gd.HCl, 50 mM Tris pH 8.0). The resulting protein solution was reduced at 37 °C for 30 minutes. After reduction, DTT was removed by desalting the protein mixture using a pre-equilibrated PD minitrap G-25 column (GE Healthcare Life Sciences) eluting in 1 mL of reaction buffer.

72 µL of DBHDA solution (in DMF, 90 equivalents, 36 µmol) was added to 1000 µL of reduced protein sample. The reaction mixture was initially incubated at 25 °C for 30 minutes, followed by incubation at 37 °C. The progress of the reaction was monitored by LC-MS. LC-MS analysis revealed completion of the reaction after 2 hours **(Figure 14)**. The reaction mixture was purified from the small molecules by desalting using a pre-equilibrated PD miditrap G-25 column (GE Healthcare Life Sciences) eluting in 1.5 mL of reaction buffer. The modified protein was stored at -20 °C.

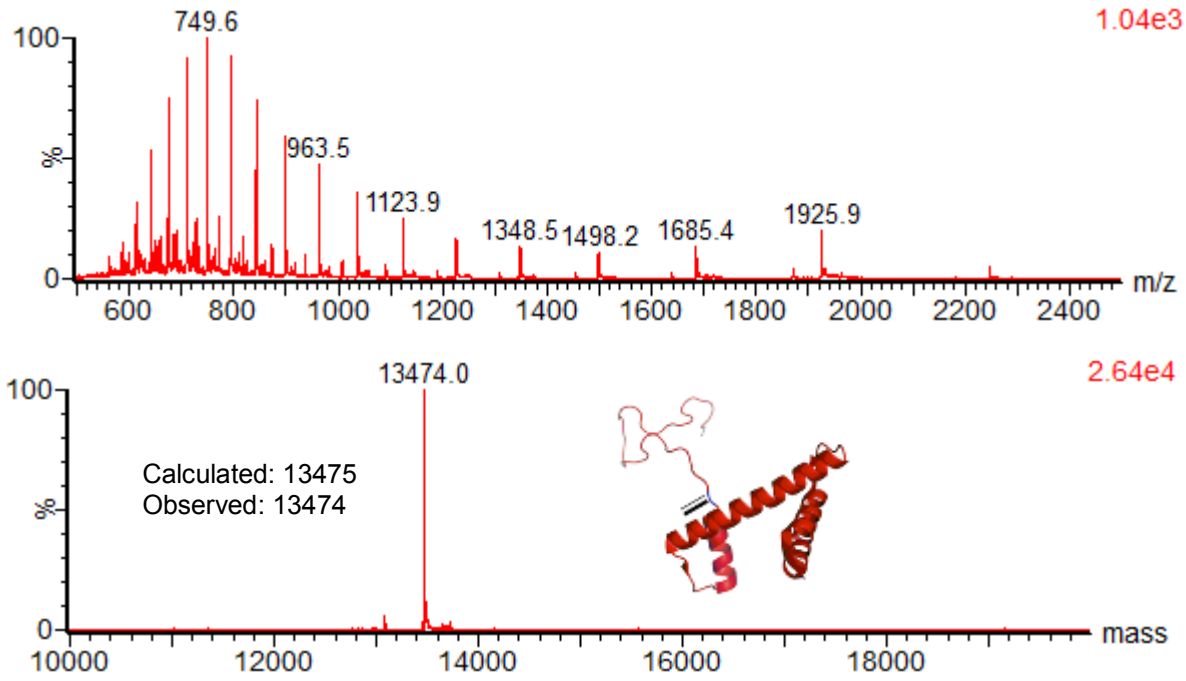


Figure 14. LC-MS Spectrum for synthesis of H2B-S36 Dha protein.

(ii) Synthesis of H2B-Ser36 GlcNAc protein

In a representative reaction, 2 mg (8 mg/mL, 250 µL, 0.148 µmol) of previously synthesized H2B-S36 Dha protein (in reaction buffer) was transferred to an eppendorf tube. 400 equivalents of GlcNAc-thiol (14.12 mg, 59.2 µmol) was added to the protein solution as a solid. The reaction mixture was incubated at 37 °C. The reaction progress was monitored by LC-MS. The reaction reached completion in 2 hours resulting in synthesis of the H2B-S36 GlcNAc protein **(Figure 15)**. Excess of GlcNAc-thiol was removed by desalted using a pre-equilibrated PD miditrap G-25 column (GE Healthcare Life Sciences) and was stored at -20 °C .

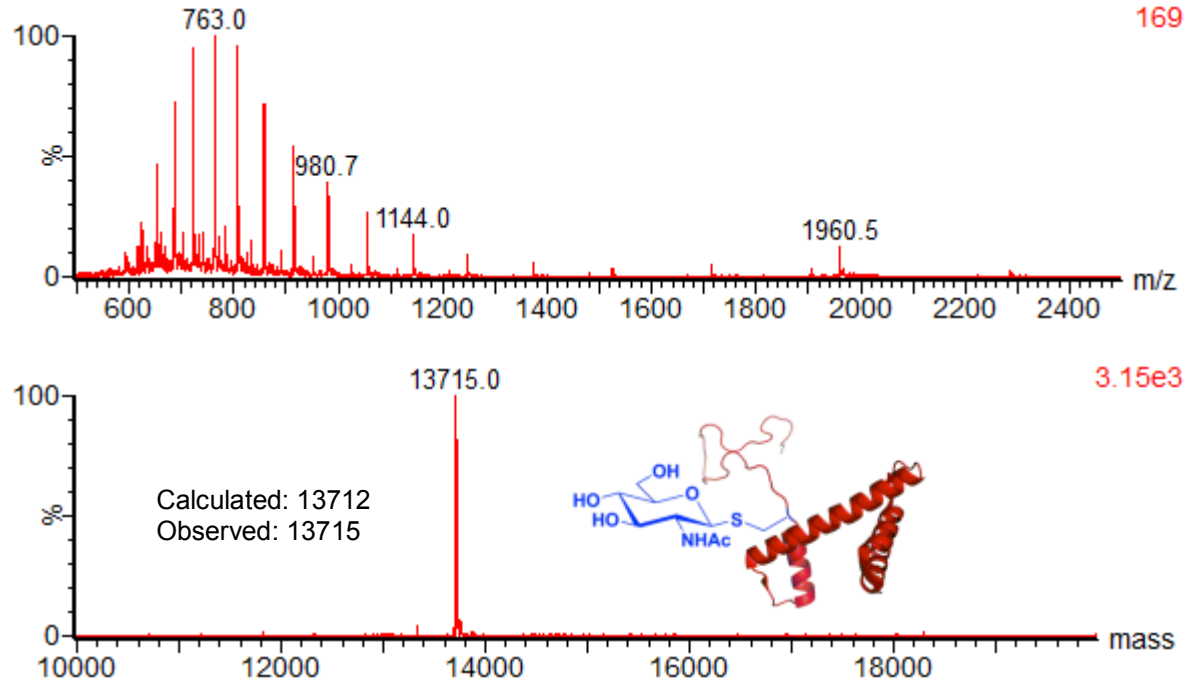


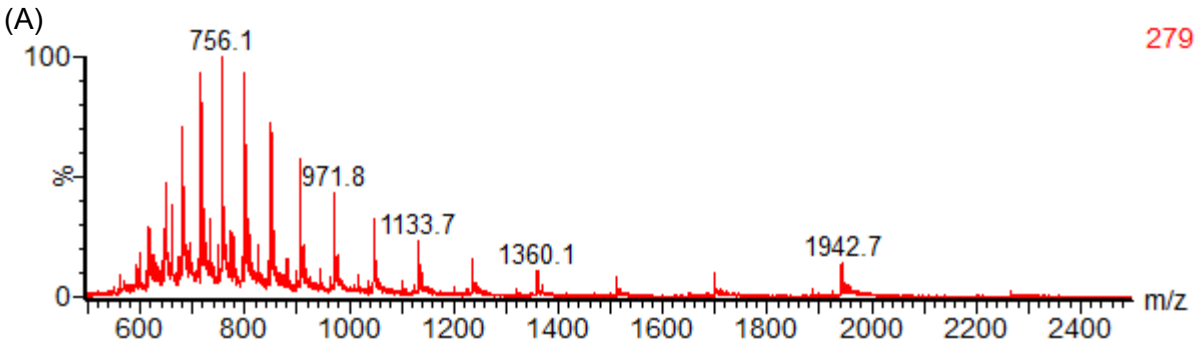
Figure 15. LC-MS spectrum for synthesis H2B-S36 GlcNAc protein.

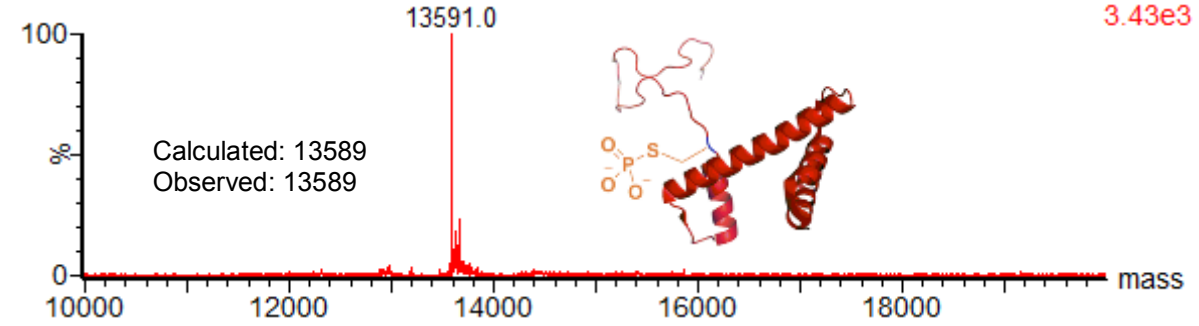
(iii) Optimization of the reaction conditions for the synthesis of H2B-Ser36 thiophosphate protein

A stock solution of sodium thiophosphate (Alfa Aesar) was prepared by dissolving 148 mg in 60 µL H_2O and 60 µL of 5 M HCl. The final pH of this stock solution was found to be around 8. 25 µL of H2B-S36 Dha protein (8 mg/mL) was transferred to two separate eppendorf tubes. 50 µL of sodium thiophosphate stock solution was added to each tubes. One of the

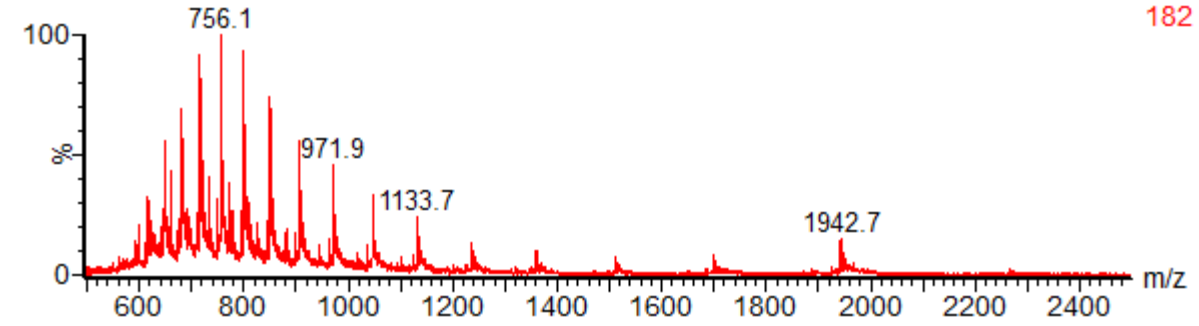
tube was incubated at 25 °C (Reaction condition A) and the other one at 37 °C (Reaction Condition B). After 2 hours, an extra portion of sodium thiophosphate stock solution (50 µL) was added to each tubes. The progress of reactions was monitored by LC-MS which revealed incomplete reactions after 4 hours. The reactions were then incubated overnight. The extent of the reaction after overnight incubation was again monitored by LC-MS analysis **(Figure 16)**, which revealed better reactivity at 25 °C.

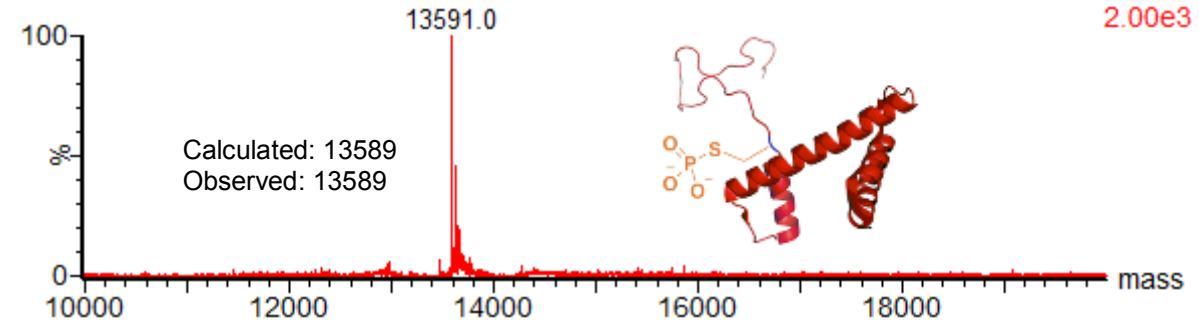
Next, the effect of salt-concentration on the reaction was probed. Two different stock solutions of sodium thiophosphate (Alfa Aesar) were prepared by dissolving (a) 254 mg in 102.9 µL of 200 mM NaCl and 84.25 µL of 5 M HCl and (b) 206 mg in 83.45 µL water and 68.28 µL of 5 M HCl. Again, 25 µL of H2B-S36 Dha protein (8 mg/mL) was transferred to two separate eppendorf tubes. 50 µL of sodium thiophosphate stock solution containing the salt was added to one of the tube (Reaction condition C) and 50 µL of sodium thiophosphate stock solution without the salt was added to another tube (Reaction condition D). Thiophosphate stock solution were added in two extra batches after 1 hour and 3 hours. The reactions were incubated at 25 °C overnight. LC-MS analysis revealed slightly better reactivity for sample without the salt **(Figure 16)**. Of all the reaction conditions tried, reaction condition A was found to be best-suited, but the conversion was not 100%. In order to push the conversion, an additional batch of freshly prepared sodium thiophosphate was added after 17 hours of reactions (Reaction condition E) **(Figure 16)**. The modified protein was desalted using pre-equilibrated PD SpinTrap G-25 columns (GE Healthcare Life Sciences).



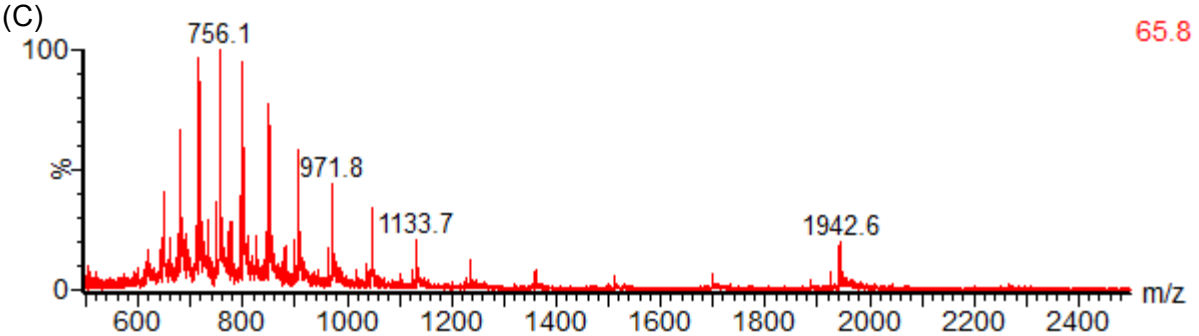

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3.43e3
100
%
0
Calculated: 13589
Observed: 13589
mass
10000
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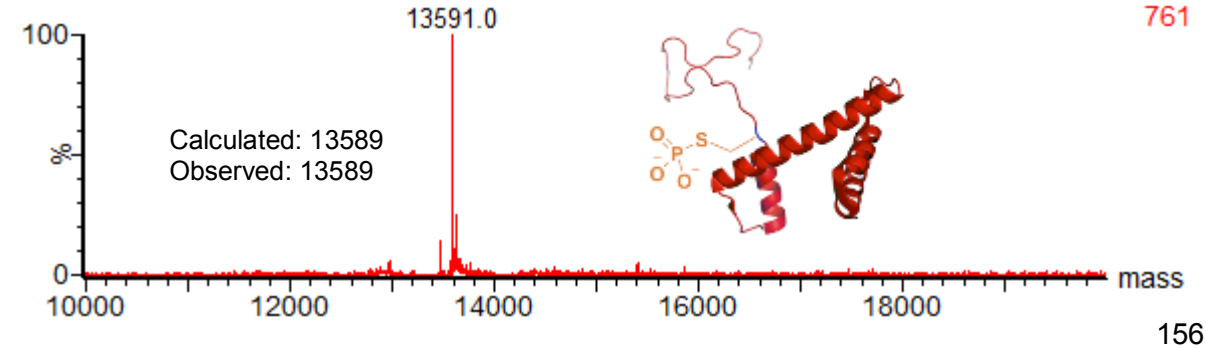
(B)


756.1
182
100
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m/z
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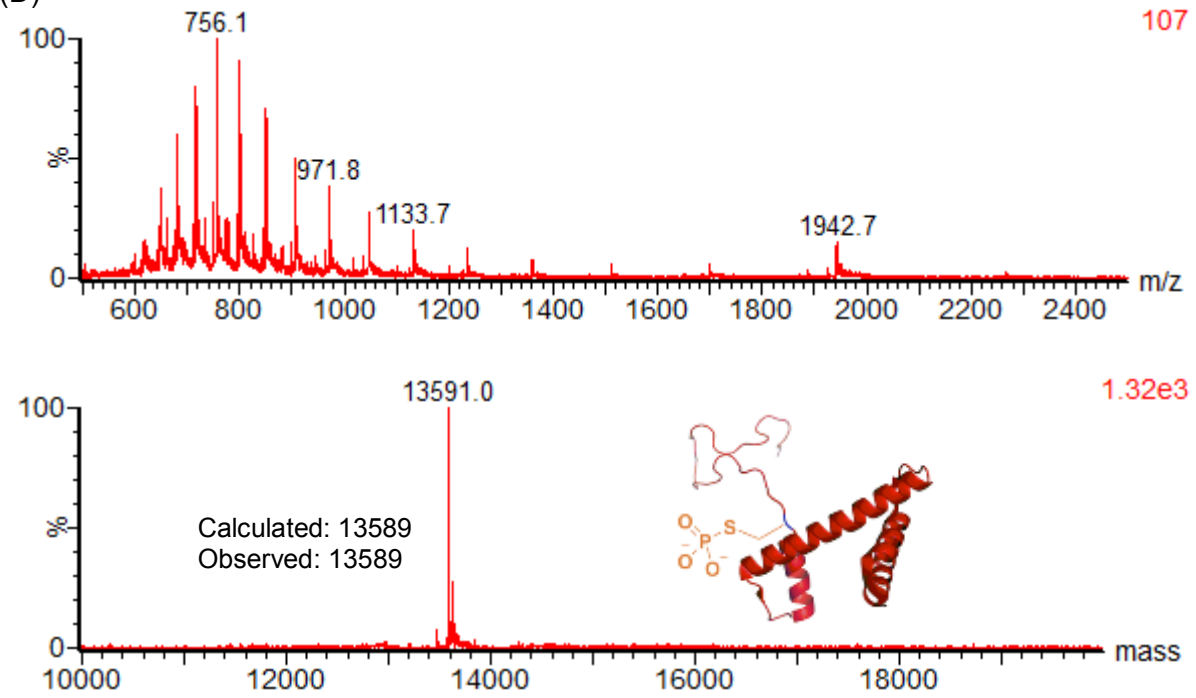

13591.0
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Calculated: 13589
Observed: 13589
mass
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14000
16000
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(C)

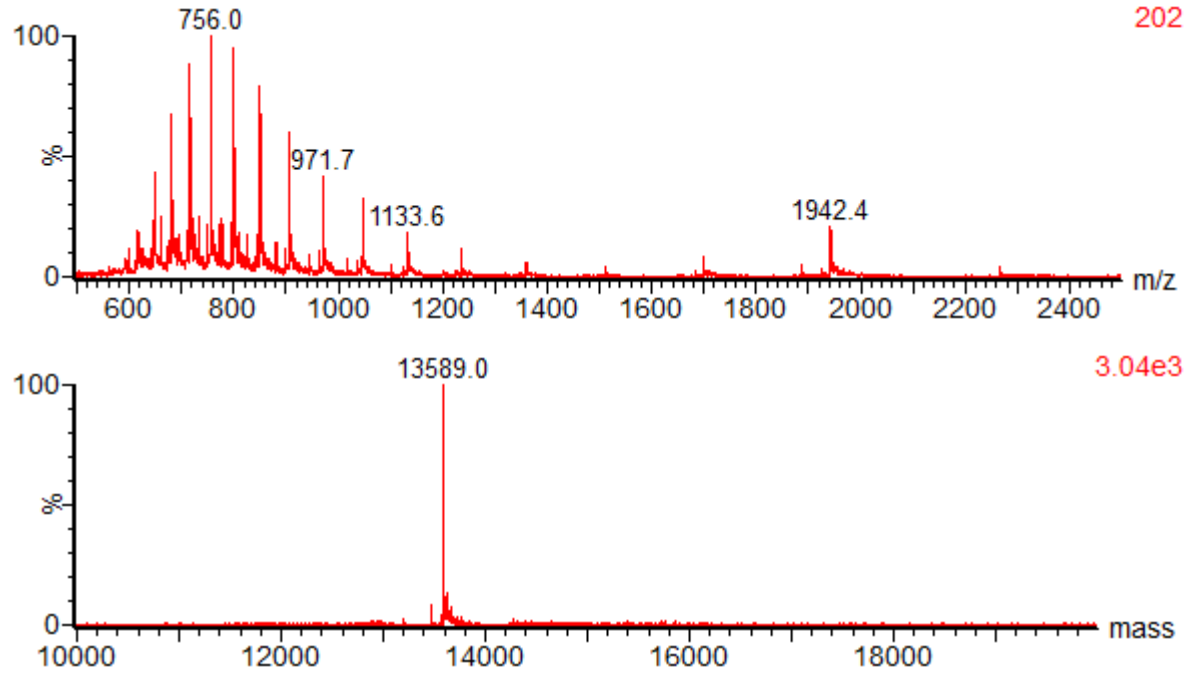

756.1
65.8
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971.8
1133.7
1942.6
m/z
600
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1000
1200
1400
1600
1800
2000
2200
2400


13591.0
761
100
%
0
Calculated: 13589
Observed: 13589
mass
10000
12000
14000
16000
18000

(D)


756.1
107
100
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971.8
1133.7
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m/z
13591.0
1.32e3
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Calculated: 13589
Observed: 13589
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(E)


756.0
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100
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971.7
1133.6
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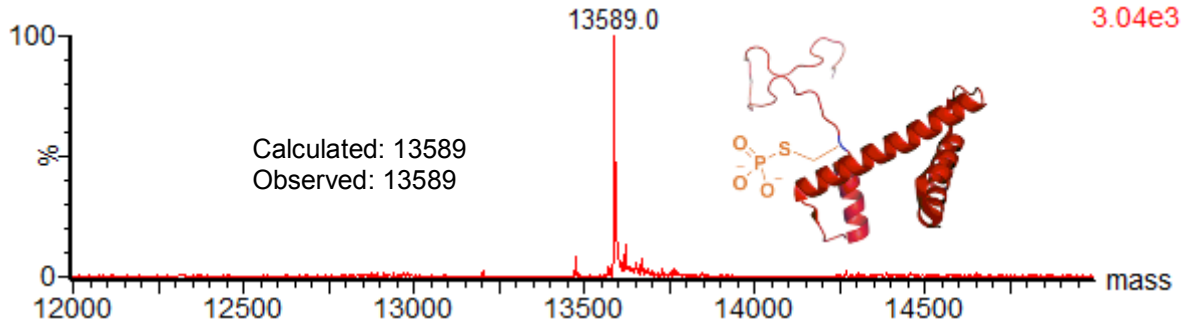


Figure 16. LC-MS spectra for optimization of reaction conditions for synthesis of H2B-S36 thiophosphate protein.

(iv) Synthesis of H2B-Ser36 Pfa protein

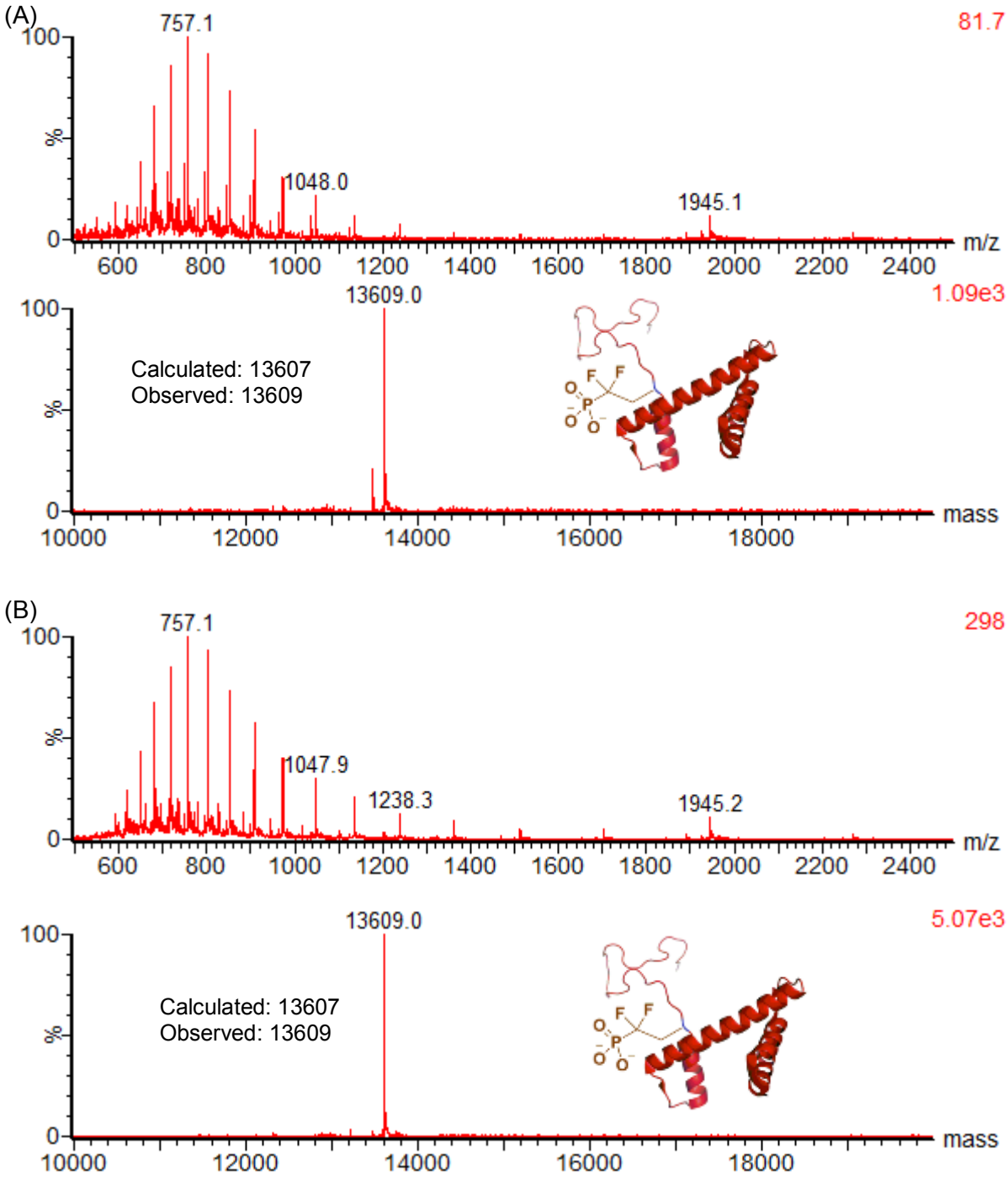
Previously synthesized H2B-S36 Dha protein was buffer exchanged into ammonium acetate buffer (5 M Gd.HCl, 500 mM NH_4OAc pH 6.0). The protein solution was diluted using the same buffer to a final concentration of 1 mg/mL and was incubated inside an anaerobic glovebox overnight.

On the day of the reaction, a fresh stock solution of (Bromodifluoromethyl)phosphonic acid (Pfa-Br) was prepared (by dissolving 16 mg of it in 80 µL of water) and its pH was adjusted to 6.0. The bromide stock solution was ported into the glovebox. The reaction conditions were optimized by varying the amount of Pfa-Br as shown in the table below:

	1 mg/mL Protein (µL)	**$NaBH_4$ (mg)**	**Pfa-Br stock solution (µL)**
A	200	0.8	2
B	200	0.8	4
C	200	0.8	6

The Pfa-Br stock solution was added to the buffered protein solution, which was then pipetted into a separate eppendorf tube containing solid $NaBH_4$ and kept at 4°C. The reaction

was shaken gently and was incubated at 4°C for 30 minutes. The reaction mixture was desalted using pre-equilibrated PD SpinTrap G-25 columns (GE Healthcare Life Sciences). The progress of the reaction was checked by LC-MS **(Figure 17)**. LC-MS analysis revealed reaction conditions B and C to be optimal for 100% conversion. For synthesis of modified on large-scale, reaction condition B was used.



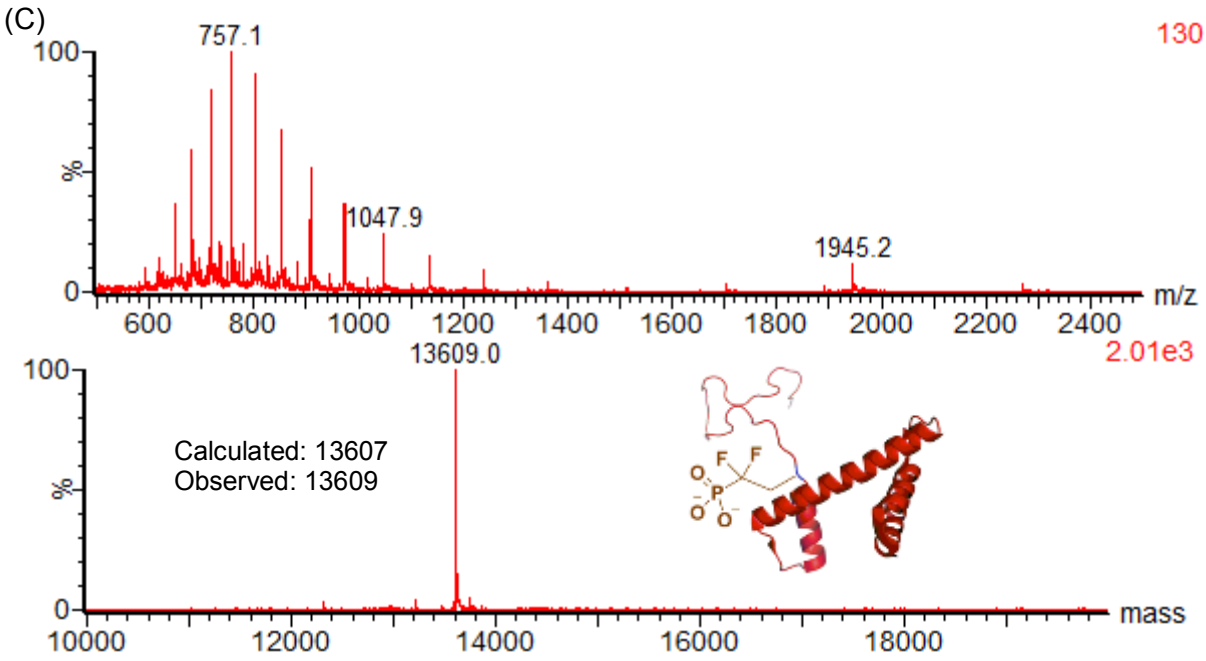


Figure 17. LC-MS spectra for optimization of reaction conditions for synthesis of H2B-S36 Pfa protein.

4.4.3 LC-MS/MS analysis of modified histone proteins

The proteolytic digestion and data-acquisition for this section was done by Ms. Svenja Hester, Shabaz Mohammed Group. Briefly, the modified proteins (~ 20 µg in reaction buffer i.e. 5 M Gd.HCl) were diluted 5-fold by 50 mM ammonium bicarbonate buffer. Trypsin was added to the samples in 1:40 (Enzyme: Protein (w/w)) ratio. The samples were incubated at 37 °C for 16 hours. The digested samples were diluted using water before injecting it to the mass spectrometer.

The digested peptides were separated by reverse phase chromatography on a UHPLC system. For chromatography details, please see section 2.4.5. The data acquisition for glycosylated sample was performed using an optimized HCD-PD-ETD method (described earlier in 2.4.5). The data acquisition for phosphorylated samples were done using a CID-ETD based Data-dependent decision tree (DDDT) method.[27] Full scan MS spectra were acquired in the Orbitrap (350-1500 m/z, resolution 120 000, AGC target 1×10^6, maximum injection time 250 ms). CID and ETD spectra were acquired in Ion Trap (resolution 7500, AGC cation target 3×10^4, AGC Anion target 2×10^5, maximum injection time 100 ms). After the MS scans,

the 5 most intense peaks were selected for fragmentation based on a data-dependent decision tree (DDDT). The signal threshold for fragmentation of the parent ion was set to 500 ion counts. For CID fragmentation, the normalized collision energy and default charge state was set to 35% and 2 respectively. For ETD fragmentation, reaction time was set to 50 ms and supplemental activation was enabled. Charge state screening was enabled; parent ions with an unassigned charge state or charge state 1 were rejected. Dynamic exclusion was enabled (exclusion size list 75, exclusion duration 5 s). For the DDDT, ETD fragmentation was followed for charge states 3, 4 and 5 with m/z less than 750. For charge states greater than 5, ETD fragmentation was always performed. In all other cases, CID activation was performed.

The raw data was processed using the MaxQuant software (Version1.4.3.17), integrated with the Andromeda search engine.[43,44] For identification of modified peptides, Andromeda searched peak lists against the sequence of H2B-S36C as well as against a list of common contaminants. Trypsin was selected as specific digestion mode with maximum number of missed cleavages set to be 2. Carbamidomethylation (Cysteine), GlcNAc (Cysteine), Thiophosphate (Cysteine), Pfa (Cysteine) along with acetylation (N-term) and oxidation (M) were set as variable modifications. All MS/MS spectra were manually validated.

4.4.4 Histone octamer reconstitution

Histone octamers were refolded and purified as described earlier in chapter 2 (section 2.4.6). It is worth-noting that proper removal of thiophosphate by desalting using PD-10 columns can be difficult, owing to high equivalent of sodium thiophosphate used in the reactions. This can lead to wrong measurement of protein concentration and thus be a problem for histone octamer reconstitution. For proper desalting, an overnight dialysis step was performed.

4.4.5 Nucleosome reconstitution

Nucleosomes were reconstituted by the salt-gradient dialysis method using a 186 bp biotinylated DNA. For reconstitution purpose, the ratio of protein octamer to DNA was kept at 1:0.9. Reconstitutions were performed as previously described in section 2.4.7.

4.4.6 MS-based interaction proteomics experiment with modified nucleosomes

Affinity-enrichment experiments between the nucleosome and the nuclear extract were performed as described in the section 2.4.11. The nucleosome-binding proteins for each nucleosome were digested separately using FASP protocol and resulting peptide mixtures were analyzed on mass spectrometer. For details on digestion and mass spectrometric data acquisition, please refer to section 2.4.11.

The mass spectrometry data was processed using MaxQuant software (Version 1.4.3.17), integrated with Andromeda search engine.[43,44] The protein groups were identified by the search engine using a human database (Swiss-Prot, version 04/13) as well as a list of common contaminants. Trypsin with a maximum number of missed cleavages of 2 was chosen. Acetylation (Protein N-term) and Oxidation (Methionine) were used as variable modifications while Carbamidomethylation (Cysteine) was set as a fixed modification. Protein and PSM false discovery rate (FDR) were set at 0.01. Label free quantification (LFQ) was performed using the in-built algorithm in the MaxQuant.[42] The downstream data analysis and visualization was done using the Perseus software (Version 1.4.2.27)[54]. Contaminant, reverse and protein groups only identified by site were filtered off. Only Protein groups identified in both samples were considered for analysis. Their LFQ intensities were logarithmized. The difference between the LFQ intensities of protein groups between two samples alongside total intensity were evaluated by Significance B in order to generate a p-value.

4.5 References

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Appendix 1 (Chapter 2)

Identification and quantification of interacting protein groups for bait (H2B S112 GlcNAc nucleosome) versus control (wt) samples. Statistically significant interacting partners (*p* value < 0.05) are denoted with a '+'

Majority Protein Ids	Gene names	log2(Bait/Control)	log10(p value)	Statistically Significant Interactor	PEP
Q9Y5B9	SUPT16H	5.038078944	3.061507507	+	0
Q08945	SSRP1	4.251744588	2.968569012	+	0
P09651;P09651-3;F8VXY0;F8\	HNRNPA1;HNRNPA1	0.198673248	2.09455328	+	0
Q9Y608-2;Q9Y608-4;Q9Y608;	LRRFIP2	2.689150492	1.974461635	+	3.96E-136
Q13472;B4DK80;Q13472-2;B4	TOP3A	0.659311295	1.360955022	+	8.27E-46
Q96HA7;Q96HA7-2	TONSL	-2.148585002	0.813891982		0.0025564
F5GWP8	JUP	-1.249556859	0.740439051		3.71E-183
Q96E14;I3L2E0	RMI2	0.985944748	0.720380047		8.14E-39
Q13151	HNRNPA0	0.362734477	0.701840918		6.96E-102
O14974-3;O14974-4;F8VZN8	PPP1R12A	-1.294486364	0.674819984		0
P48668;CON__P48668	KRT6C	-1.409152985	0.642325754		1.12E-304
Q15637-6;Q15637-2;Q15637-	SF1	0.64846611	0.640353254		5.76E-72
P53999	SUB1	1.380776087	0.631082405		2.34E-14
Q9ULW0;Q96RR5	TPX2;HCA90	1.795644124	0.620288916		2.16E-141
P35251;P35251-2	RFC1	0.881896973	0.611342878		0
Q15427	SF3B4	0.337552389	0.608670209		3.69E-80
P27694	RPA1	2.389371872	0.593162448		2.65E-233
P31943;G8JLB6;E9PCY7;D6RII	HNRNPH1	0.330139796	0.592388256		0
P35659;P35659-2;B4DFG0;D6	DEK	-1.881011963	0.589908866		2.67E-82
Q6I9Y2	THOC7	0.29744784	0.584337699		1.81E-131
P38919	EIF4A3	0.699170431	0.545048404		1.33E-118
Q8IUE6	HIST2H2AB	-1.474319458	0.543799059		5.00E-138
M0QZM1	HNRNPM	-0.352521261	0.539989717		2.10E-161
P08779;CON__P08779	KRT16	-1.842549006	0.530661051		0
Q9Y2S0	POLR1D	0.535025915	0.488518186		2.71E-64
P41208	CETN2	0.721959432	0.487406039		2.10E-125
P02533;CON__P02533;CON_	KRT14	-1.000313441	0.481790332		1.02E-212
Q9BQ04;E9PLB0;E9PM61	RBM4B	0.459698995	0.477326723		7.36E-89
P62841;K7EM56;K7ELC2;K7EJ	RPS15	1.222133001	0.46908449		3.62E-23
P62805	HIST1H4A	0.21070226	0.452649414		0
P35249;C9JZI1;C9J8M3;C9JTT	RFC4	1.614082972	0.447245625		0
Q9NUW8;Q86TV8;G3V2F4;E7	TDP1	0.520119985	0.419889768		1.23E-17
P35250;P35250-2;H7C5P4	RFC2	1.011479696	0.418357593		0
Q9UII2	ATPIF1	-0.590906143	0.407960103		1.10E-06
Q96KR1	ZFR	0.254386902	0.404218832		0
Q9NUK0;Q9NUK0-2;B1AKI6	MBNL3	-1.111483256	0.397996501		1.81E-18
Q9UNL2;C9JA28;B4E2P2	SSR3	1.639628092	0.394513594		6.14E-15
P62306;F8W0W6	SNRPF	-0.231740316	0.372402552		5.30E-22
Q5M775;Q5M775-4;Q5M775	SPECC1	0.129275004	0.364275713		2.23E-269
P35580;P35580-2;F8W6L6;P3	MYH10	-0.507511139	0.357291105		0
P50402;Q5HY57	EMD	0.484237671	0.351980254		7.41E-160
Q12904;Q12904-2	AIMP1	0.882725398	0.348019465		2.96E-196
P40938;P40938-2	RFC3	1.682502111	0.347867729		0
Q14011;K7EMY9;K7EPM4;K7I	CIRBP	1.312144597	0.343152371		6.08E-60
P05787;CON__P05787;P0578	KRT8	0.096977234	0.342957126		0
Q9ULV0	MYO5B	0.972047806	0.342476917		7.19E-35
P40937;P40937-2;F8W9B4	RFC5	0.949289958	0.340766737		0
Q86XZ4	SPATS2	1.166576385	0.335598594		3.52E-149
P15328	FOLR1	-0.231505712	0.334229184		9.69E-101
P13647;CON__P13647;F8W0	KRT5	-0.664825439	0.33262993		9.40E-243
Q9UKF6;G5E9W3	CPSF3	1.385275523	0.330879965		1.14E-161
P63173;J3KT73;J3QL01;J3KSP	RPL38	0.334237417	0.322421622		2.84E-16
P56182	RRP1	0.910595576	0.320776341		4.06E-21
P62873;B3KVK2	GNB1	0.700613022	0.318089115		1.06E-73
Q9H307;Q9H307-2	PNN	0.495153427	0.314424009		6.64E-124
Q9P2J5;F5H698;B4DJ10;B4DE	LARS	1.438474655	0.312061811		8.53E-70
G5E9M5;Q12906-4;Q12906-6	ILF3	-0.114262899	0.305783365		0
P47755;F8W9N7	CAPZA2	0.711062749	0.293689324		6.83E-90
P08729;CON__Q3KNV1;F8VZ	KRT7	0.272989909	0.282669348		0
Q9HC52	CBX8	1.167825063	0.280525126		6.32E-60
Q9P035;B4DRF4;H3BS72;H3B	PTPLAD1	0.910380046	0.277353553		6.65E-85

P62273;P62273-2	RPS29	-0.497578939	0.276189419	6.06E-20
Q9Y3B4	SF3B14	0.947014491	0.274286213	1.19E-22
Q86XK2;Q86XK2-5;Q86XK2-6	FBXO11	0.86783282	0.273025699	1.88E-83
Q9H7E2;Q9H7E2-3;Q9H7E2-2	TDRD3	0.430744171	0.272482783	6.19E-59
P17480;P17480-2;E9PKP7	UBTF	0.333123525	0.267464829	0
Q12926;Q12926-2;B1AM49;E	ELAVL2;ELAVL4	0.702601751	0.267226027	4.18E-91
Q96CW1;Q96CW1-2;E9PFW3	AP2M1	-1.218945821	0.266732592	2.87E-114
P16403;P16402	HIST1H1C;HIST1H1D	-0.284726461	0.266580802	1.69E-38
Q15287;H3BV80;Q15287-3;Q	RNPS1	0.120931625	0.26435906	1.50E-30
Q96DI7;B4DQJ1	SNRNP40	1.575176875	0.26340872	5.51E-252
P51114;B4DXZ6;P51114-2;P5	FXR1	0.085731506	0.26159061	0
Q13045;J3QLG3;Q13045-2	FLII	-0.480203629	0.261370147	1.62E-299
P27105;B4E2V5	STOM	0.745147069	0.260115799	1.38E-50
Q6P5R6;C9JYQ9;H0Y8C2	RPL22L1	0.311777751	0.256257337	8.24E-107
Q9NYL9;H0YNJ8	TMOD3	0.13660876	0.255274788	0
Q6NZI2;Q6NZI2-2	PTRF	-0.849328359	0.255220508	3.42E-74
P62847;P62847-2;E7ETK0;P6	RPS24	0.976221085	0.254890641	3.63E-17
P42167;G5E972;P42167-2;H0	TMPO	0.213640849	0.250682074	1.36E-180
P49207	RPL34	0.473462423	0.248722194	3.02E-13
Q12800;F8VX55;Q12800-3;Q	TFCP2	0.97723643	0.24842123	2.80E-231
Q14134;Q14134-2;B7Z8U9;E	TRIM29	-0.486513138	0.245107986	2.88E-28
Q9Y4P3;E9PF19	TBL2	-0.329182307	0.2406	3.43E-238
P60468	SEC61B	-0.666510264	0.240323845	2.15E-05
Q9BWJ5	SF3B5	-0.191724141	0.238121442	2.49E-14
Q9NRC1;B7Z4U3;Q9NRC1-4;E	ST7;ST7L	-0.646879196	0.237425658	1.23E-06
P18077;C9K025;F8WBS5;F8W	RPL35A	0.35761706	0.236900686	1.18E-15
O75531	BANF1	0.28351593	0.232152398	3.55E-18
P61513;C9J4Z3;Q6P4E4;E9PE	RPL37A	0.315478007	0.232067988	2.14E-36
Q7Z2E3;Q7Z2E3-7;Q7Z2E3-8;	APTX	-0.134639104	0.231204974	9.91E-145
P61619;B4DR61;P61619-3	SEC61A1	-0.464300791	0.229743817	1.39E-28
Q9Y3A4	RRP7A	0.750528971	0.22677029	8.88E-76
Q96HS1;Q96HS1-2;F5GXG4	PGAM5	0.788026174	0.226390393	5.55E-137
Q71U36;G3V1U9;Q9BQE3;F5	TUBA1A;TUBA1C;TU	1.583175659	0.223523119	3.86E-299
Q01844;Q01844-6;B0QYK0;Q	EWSR1	-0.082613627	0.223279646	1.35E-177
Q86U38;A8MY76	NOP9	-0.285728455	0.220283318	4.49E-115
Q8N3X1;Q8N3X1-2	FNBP4	0.361172994	0.220226401	0
Q9UHB7;Q9UHB7-2	AFF4	0.87548701	0.220058374	6.37E-76
O43823	AKAP8	-0.357156118	0.218005793	2.40E-150
Q8N684;Q8N684-2;Q8N684-3	CPSF7	0.720559438	0.216646566	2.68E-116
O95425;O95425-2;F5H2Q5	SVIL	0.318286896	0.21502921	2.14E-171
Q12905	ILF2	0.49299113	0.214753924	0
Q5BKZ1;Q5BKZ1-3	ZNF326	0.743563334	0.211638274	7.49E-69
Q9Y3T9	NOC2L	0.751158396	0.211458966	1.05E-45
Q29RF7	PDS5A	0.492919922	0.209806009	3.95E-195
P14866;M0QXS5;P14866-2	HNRNPL	0.503950119	0.208714954	0
P55265;P55265-5;P55265-4;E	ADAR	1.533538183	0.208155294	0
Q9H583;Q5T3Q7	HEATR1	0.880447388	0.20745311	6.04E-150
Q13148;Q13148-2;B1AKP7;G	TARDBP	0.356906255	0.206529765	7.28E-70
P16401	HIST1H1B	-0.532803853	0.20620755	1.39E-40
P62854;Q5JNZ5;F8VZW7	RPS26;RPS26P11	0.796175639	0.204174215	1.93E-50
P38159;P38159-2;H0Y6E7;H3	RBMX;RBMXL1	-0.076836904	0.201628903	1.24E-180
Q9P0K7;Q9P0K7-4;Q9P0K7-3	RAI14	-0.188624064	0.201515667	0
Q14671;Q14671-2;H0YEH2;E	PUM1	0.602442424	0.200834837	2.43E-105
Q01081;Q01081-2;Q01081-4	U2AF1	0.516981761	0.198832036	5.35E-64
Q9NX63;C9JRZ6;G3V1K1;F8W	CHCHD3	-1.189995448	0.196037814	1.51E-66
Q9Y2R4;A8MTP9	DDX52	1.130537669	0.194322716	1.07E-194
Q96I24;Q96I24-2	FUBP3	-0.64308993	0.194071205	7.78E-151
O95831;O95831-3;Q1L6K4;O	AIFM1	0.900039673	0.192599762	1.18E-48
E7EWI9;P51991-2	HNRNPA3	0.223924637	0.190719298	0
Q9NY12;Q9NY12-2	GAR1	0.4815286	0.190536548	6.30E-128
Q86W92;Q86W92-2;Q86W92	PPFIBP1	0.230793635	0.18996197	9.90E-97
P62891;Q59GN2	RPL39;RPL39P5	-0.122477849	0.189746899	7.20E-10
P35637;P35637-2;H3BPE7	FUS	-0.053173065	0.189571008	0
Q86UE4	MTDH	-0.116986593	0.188252848	0
P26368;P26368-2;K7ENG2	U2AF2	0.856957118	0.185521197	1.05E-106
P05783;F8VZY9	KRT18	-0.076917013	0.18533237	0
Q13595;Q13595-2;B4DQI6;B4	TRA2A	-0.284554164	0.184329218	5.43E-23
O15145;C9JZD1;F8VR50	ARPC3	0.331354777	0.184328035	4.89E-19

Q9NVN8	GNL3L	-0.784830729	0.182116139	5.43E-78
Q6ZNB6;Q6ZNB6-2	NFXL1	0.660271962	0.17992998	3.47E-123
Q7RTV0	PHF5A	-0.308056513	0.178402527	1.36E-76
Q15629;G3XAN4;B4E0K2	TRAM1	-0.202694575	0.177912759	1.27E-173
O43290	SART1	0.918571472	0.177715326	2.34E-259
Q9UPQ9;Q9UPQ9-1;H0Y720	TNRC6B	0.643892288	0.177356345	5.15E-193
P62314;J3QLI9	SNRPD1	0.651203156	0.177299261	2.86E-86
Q8NCA5;Q8NCA5-2;E9PH82;I	FAM98A	0.386144002	0.17567217	0
P11021	HSPA5	0.409109751	0.175293604	5.86E-169
Q9NR56;C9JP00;Q9NR56-3;Q	MBNL1	-0.363865534	0.173674514	2.08E-17
Q96EY1;Q96EY1-2;E7ES32	DNAJA3	0.507000605	0.173034138	4.42E-176
P24928	POLR2A	-0.560366313	0.172113246	8.94E-128
P14373;P14373-2;B0V297	TRIM27	0.205828985	0.170162913	8.90E-155
Q9NW13;Q9NW13-2	RBM28	0.626188914	0.169785871	4.77E-38
Q9UNQ0;Q9UNQ0-2	ABCG2	-0.166984558	0.169273721	1.80E-12
Q99700;H0YH87;Q99700-2;Q	ATXN2	1.103461583	0.169090907	1.17E-196
P61313;E7EQV9;E7EX53;E7EI	RPL15	0.774974187	0.166924361	4.46E-87
Q15269	PWP2	0.951863607	0.165617953	0
Q12872;Q12872-2;F5H5X1	SFSWAP	0.472863515	0.164897006	2.33E-42
Q9BUT9	FAM195A	-0.290112178	0.16351826	3.64E-148
O95782;O95782-2	AP2A1	0.817335765	0.162315816	5.52E-176
O95816;B4DXE2	BAG2	-0.307242076	0.161369171	0
P60842;J3QLN6;J3KS25;J3QR	EIF4A1;EIF4A2	0.372303009	0.159739214	5.20E-55
Q9UBB4;Q9UBB4-2	ATXN10	0.477761587	0.157376366	3.76E-45
Q92522	H1FX	-0.197905858	0.157251741	7.97E-49
Q15366-4;Q15366-6;Q15366	PCBP2	-0.269107183	0.156921698	1.16E-109
Q15393	SF3B3	0.257021586	0.156651002	0
Q99933;Q99933-4;Q99933-3;	BAG1	0.169298172	0.155946435	1.22E-14
Q8WYP5;Q8WYP5-2;Q8WYP5	AHCTF1	-0.379303614	0.154767144	3.65E-238
P46783;F6U211	RPS10	0.95215416	0.154484272	3.40E-68
Q02543;M0R1A7;M0R3D6;M	RPL18A	0.185241699	0.153504094	2.77E-208
P62979;P0CG47;J3QS39;J3QT	RPS27A;UBB;UBC;U	-0.0658741	0.153116411	2.78E-207
Q9BRJ6;H7C0T1;H7C2R9;C9J	C7orf50	0.541238785	0.152504371	6.41E-16
P62318;B4DJP7	SNRPD3	0.310180664	0.15141752	2.64E-166
Q07157;Q07157-2;G5E9E7;G	TJP1	-1.217394511	0.148998556	0
Q14103;Q14103-3;H0YA96;H	HNRNPD	0.114749908	0.145104978	5.57E-56
Q7Z7K6;Q7Z7K6-3;Q7Z7K6-2	CENPV	0.654734929	0.142059391	4.69E-44
P62995;P62995-3	TRA2B	0.240797679	0.141842293	5.00E-118
Q13428-6;J3KQ96;Q13428-7;	TCOF1	-0.269649506	0.140757857	1.33E-210
Q7Z2W4;C9J6P4;Q7Z2W4-2;(	ZC3HAV1	0.34281985	0.140638185	0
Q14498;Q14498-2;Q14498-3;	RBM39	0.355051041	0.140426194	2.87E-272
E7ERS3;Q86VM9;Q86VM9-2	ZC3H18	0.298557281	0.139594271	2.80E-82
Q9H9Y6;F5GZX4;Q9H9Y6-2;F	POLR1B	0.955305735	0.138780055	5.14E-103
Q9P2I0	CPSF2	0.698778788	0.137786343	1.37E-109
CON__Streptavidin		0.092631658	0.137631475	1.23E-246
Q96AG4	LRRC59	0.218009949	0.137022576	0
P51116	FXR2	0.07637914	0.136813322	0
P04908;P0C0S8;Q99878;Q93	HIST1H2AB;HIST1H2	-0.238797506	0.135991587	1.95E-86
Q96EP5;Q96EP5-2;K7EQ02;K	DAZAP1	0.904953003	0.135131912	1.09E-91
Q8IWR0;I3L2K5	ZC3H7A	0.979173024	0.135126917	0
P48634	PRRC2A	0.062806447	0.132684516	1.92E-255
O60563	CCNT1	0.599611282	0.13158414	2.86E-151
Q14684;Q14684-2	RRP1B	0.749744415	0.129634665	0
Q96PK6	RBM14	0.137941996	0.128570308	3.18E-188
Q9BZK7	TBL1XR1	0.091720581	0.128496153	2.30E-40
P46776;E9PJD9;E9PLL6	RPL27A	-0.10433197	0.127110629	5.23E-97
Q5UIP0;Q5UIP0-2	RIF1	0.197634379	0.126350045	3.41E-284
Q8TDD1;Q8TDD1-2	DDX54	0.828330358	0.125860164	1.86E-108
Q9NPE3	NOP10	-0.365484238	0.125310231	2.57E-138
O15143	ARPC1B	-0.269436518	0.124686599	3.01E-71
P31689;B7Z5C0	DNAJA1	0.439849854	0.123342321	1.87E-104
Q9NUL3;Q9NUL3-2;E9PH62;(	STAU2	-0.572971344	0.122894449	2.26E-148
Q9UHB9;F5H5Y3;G3V1U4;Q9	SRP68	0.611813863	0.121805884	3.84E-107
Q14676;Q14676-2;E9PGY5;Q	MDC1	0.828233083	0.121606135	0
Q9UKV8;Q9UKV8-2	AGO2	-0.527801514	0.120807156	2.33E-204
Q9BYJ9;F8W840	YTHDF1	-0.496463776	0.120804016	4.01E-86
Q6UN15;Q6UN15-5;Q6UN15	FIP1L1	0.412851334	0.11978872	9.18E-121
P49458;E9PE20;P49458-2	SRP9	-0.183481216	0.118756164	4.74E-40

P63010;P63010-2;Q7Z451;K7	AP2B1	0.802996953	0.118365899	4.00E-216
P39656;E7EWT1	DDOST	0.361787796	0.117910755	6.06E-35
P20042	EIF2S2	0.578777949	0.11737932	1.58E-203
P46779;P46779-2;P46779-3;I	RPL28	-0.073652903	0.116304636	1.67E-39
O15446;O15446-2	CD3EAP	-0.537755966	0.115728047	1.58E-180
Q7Z6E9;Q7Z6E9-2;Q7Z6E9-4	RBBP6	0.717622121	0.115464492	3.57E-232
Q9NQG5	RPRD1B	0.230208715	0.115274147	5.05E-48
P05386	RPLP1	0.399029414	0.11496863	8.61E-158
Q9P275;Q9P275-2;E9PEW0	USP36	0.550163905	0.114546753	0
Q16637;Q16637-4;Q16637-2;	SMN1	-0.143174489	0.114459314	4.21E-198
P07910;P07910-4;P07910-2;(	HNRNPC	0.137295405	0.114066067	3.48E-85
P18887;F5H8D7	XRCC1	-0.057131449	0.113512728	0
Q9Y3Y2;Q9Y3Y2-4;Q9Y3Y2-3;	CHTOP	-0.246803284	0.113385253	1.02E-33
Q9H2Y7;E9PE29	ZNF106	-0.62471962	0.112709791	0
P61978;P61978-2;Q5T6W1	HNRNPK	0.440475464	0.112523146	0
P51571;H7C1C6;A6NLM8	SSR4	0.535345713	0.11195644	6.23E-84
P61158;F5H3P5;B4DXW1	ACTR3	0.130383174	0.111787975	6.03E-54
O60506;O60506-2	SYNCRIP	0.126490911	0.110470857	0
Q53GS9;B9A018;B8ZZD1;G5E	USP39	0.830551147	0.107925422	2.24E-270
Q13769	THOC5	0.477025986	0.107911745	8.89E-136
CON__Q8VED5		0.231921514	0.106406353	7.52E-76
O00571;O00571-2;O15523;B4	DDX3X;DDX3Y	0.089059194	0.10596625	0
Q9NR30;Q9NR30-2	DDX21	0.404545466	0.10506887	0
P04843;B7Z4L4	RPN1	0.372299194	0.105054069	1.00E-118
P62857	RPS28	0.56444931	0.103081757	8.25E-43
Q9H089	LSG1	-0.504476547	0.102496895	3.80E-35
P04844;P04844-2	RPN2	0.201605479	0.102393853	3.42E-55
P26038	MSN	-0.462253571	0.102159432	6.84E-42
P62244;I3L3P7;I3L246;H3BN9	RPS15A	0.306032181	0.101794211	7.61E-118
P07437;Q5JP53;F8VYX6;F8VV	TUBB;TUBB2B;TUBB	-0.633658091	0.100886966	6.86E-148
C9JKI3;Q03135-2;P56539;E9P	CAV1;CAV3	0.469692866	0.100877903	8.92E-07
O43707;D6PXK4;F5GXS2	ACTN4	-0.620875676	0.100788434	1.58E-293
Q14807;B7Z265;H3BRB3	KIF22	-0.467016856	0.100660384	2.47E-89
Q9NSU2;Q9NSU2-2;Q9NSU2-	TREX1	0.757205327	0.099657717	1.47E-142
Q9BPX5	ARPC5L	-0.280153275	0.099490505	0.00071224
Q9Y446	PKP3	0.049195608	0.09884952	1.99E-84
P55769;B1AHD1	NHP2L1	-0.24163119	0.098186081	3.09E-70
Q8IVT2	MISP	-0.274806976	0.097920765	3.73E-290
Q9BUQ8	DDX23	0.902580897	0.09734573	0
Q8IWX8;J3QK89	CHERP	0.167039235	0.097287232	1.05E-117
P62249;M0R210;M0R3H0	RPS16	-0.194525401	0.097152543	4.56E-51
P06753-2;Q5VU66;P06753-3;	TPM3	-0.29712232	0.096502596	5.51E-107
P47756-2;B1AK87;B1AK88;P4	CAPZB	0.039557139	0.095964671	3.91E-205
P56537;B7ZBG9	EIF6	-0.338989894	0.095955493	4.03E-263
P08621;P08621-2;P08621-3	SNRNP70	-0.441486359	0.095720615	1.18E-71
Q9BX40;Q5TBP9;Q9BX40-2	LSM14B	0.126488368	0.095672071	1.11E-05
Q9BVJ6;F8WD00;E9PEL7;Q9B	UTP14A	-0.487159729	0.095468878	4.36E-203
Q3B726	TWISTNB	-0.334627787	0.095225752	1.64E-187
P16989;P16989-3;P16989-2	YBX3	-0.129456202	0.093825788	3.37E-220
Q9BVP2;Q9BVP2-2	GNL3	-0.480167389	0.093465851	1.13E-121
P62861;E9PR30	FAU	-0.128075918	0.093317641	6.51E-14
P67809;H0Y449	YBX1	0.150520325	0.093275167	0
Q9NZ01;B3KSQ1;M0R3C3	TECR	0.124434153	0.092498749	7.42E-99
Q9UNX4	WDR3	0.495845159	0.09217351	0
O94905;E5RHW4	ERLIN2	0.48789533	0.091890298	4.75E-93
E7EUE1;P28288;F5GYC1;P282	ABCD3	-0.269155502	0.091565116	5.16E-245
O76021;J3QSV6;I3L3U9	RSL1D1	0.504037221	0.091113671	3.89E-292
Q9Y4A5;H0Y4W2;Q9Y4A5-2;F	TRRAP	-0.466222127	0.09038134	9.90E-157
Q99459	CDC5L	0.402372996	0.089980535	0
P18124;A8MUD9	RPL7	-0.200439453	0.089825947	1.88E-242
P57678;I3L2C7	GEMIN4	0.236846924	0.089757059	6.90E-206
P13010	XRCC5	0.224533081	0.089399889	0
Q7LGA3;Q7LGA3-2;A6ND99;(	HS2ST1	0.227979024	0.088076856	2.71E-51
P43243;A8MXP9;D6REM6;D6	MATR3	0.076528549	0.088063706	0
P56192;A6NC17;B3KVK7	MARS	0.296885173	0.087757908	0
P21796;C9JI87	VDAC1	-0.13344574	0.085867723	4.13E-19
P62241;Q5JR95	RPS8	0.075837453	0.084973255	0
Q8NI36;D6R922	WDR36	0.510762533	0.084776027	0

Q92576;Q92576-2;E7EVH3	PHF3	-0.369639079	0.084662186	0
P62879;E7EP32;C9JXA5;C9JIS	GNB2	0.193232218	0.083365127	3.21E-113
Q5JTH9;Q5JTH9-2;Q5JTH9-3;I	RRP12	0.279253006	0.082954242	0
P52597	HNRNPF	0.120400747	0.082752812	7.10E-251
Q9BYG3;C9J808;C9J6C5	MKI67IP	0.527893066	0.081968606	9.16E-143
P54132;H0YNU5	BLM	0.240589778	0.080340173	7.10E-220
P78406;E9PQ57;E9PPG9	RAE1	0.33769544	0.07997101	8.16E-245
Q9UMS4;F5GY56	PRPF19	0.396805445	0.079836447	0
P68431;P84243;K7EK07;K7EN	HIST1H3A;H3F3A;H3	0.076531728	0.079631996	1.80E-114
Q5SW79;H0Y2V6;Q5SW79-2;	CEP170	0.241763433	0.078720707	1.11E-42
Q9BV38;K7EIR0;K7EML4	WDR18	0.230246226	0.077749925	1.36E-49
Q14966;Q14966-3;Q14966-4	ZNF638	-0.144885381	0.077051751	0
Q12788;J3KNP2	TBL3	0.218910853	0.076574437	0
Q9HAV0;C9JD14	GNB4	-0.165062586	0.075404791	7.12E-96
P49454	CENPF	0.116288503	0.075365798	0
P49916;P49916-2;K7ERZ5	LIG3	-0.043404897	0.074516811	0
P38646	HSPA9	0.173075994	0.073971001	3.41E-64
O43293	DAPK3	0.277876536	0.073849599	2.72E-53
Q9H0D6;Q9H0D6-2;B4DZC3	XRN2	0.107152303	0.07372706	3.13E-148
P25398	RPS12	-0.145244598	0.07360775	3.76E-164
P48651;B4DE85;Q9BUQ5	PTDSS1	0.232301076	0.073297923	3.26E-102
P08590;P05976;P05976-2	MYL3;MYL1	0.131204605	0.073105744	0.0011525
P02545;P02545-2;Q6UYC3;PC	LMNA	-0.07038943	0.072050727	4.03E-77
P62266;D6RD47	RPS23	0.190172831	0.072001629	1.96E-43
Q15070;E7EVY0;Q15070-2;J3	OXA1L	-0.188414892	0.071812898	8.66E-16
P60866;P60866-2;E5RJX2	RPS20	-0.267499924	0.071734764	4.75E-35
Q86UP2;Q86UP2-2;Q86UP2-3	KTN1	-0.178264618	0.071673839	0
P41252;J3KR24	IARS	-0.170585632	0.070917803	0
O60287	URB1	0.300289154	0.070874016	0
P62913;P62913-2;Q5VVC8	RPL11	-0.118606567	0.070514981	1.37E-64
P12956;B1AHC8;B1AHC9;F5H	XRCC6	0.204321543	0.070135025	0
Q9BY89	KIAA1671	-0.381790161	0.070104095	2.25E-156
Q9H0H5	RACGAP1	-0.29189237	0.070041408	1.13E-151
Q9P1U0	ZNRD1	-0.270434062	0.069865681	3.46E-39
CON__P08729		0.092525482	0.069725168	0
O15160;O15160-2;E7EQB9;D	POLR1C	0.244497935	0.06900627	2.02E-110
Q14157-1;Q14157;Q14157-4;	UBAP2L	0.12935257	0.068914402	0
Q14254;J3QLD9;E7EMK3	FLOT2	0.189719518	0.068327525	8.67E-148
Q9H2U1;Q9H2U1-3;Q9H2U1-	DHX36	0.256106695	0.067880546	1.91E-271
Q16698;B7Z6B8;E5RFV2;E5RJ	DECR1	0.356396993	0.066587015	1.41E-257
Q13523;F5H2U2;H0YDJ3	PRPF4B	-0.276676814	0.06615252	4.35E-60
O43795;E9PDF6;O43795-2	MYO1B	-0.420419693	0.065692175	0
P29558;P29558-2;B4DN88;E7	RBMS1	0.210026423	0.065556253	2.36E-88
P54136;P54136-2;F5H3T8	RARS	-0.134105682	0.06546227	1.15E-194
Q86TG7	PEG10	0.184673309	0.065264811	2.29E-121
Q86V48;Q86V48-2;Q86V48-3	LUZP1	-0.074485779	0.065071805	0
H9KV59;O43663;O43663-2;F8	PRC1	0.154167175	0.065033251	8.23E-110
P12236;I7HJJ0	SLC25A6	-0.127056758	0.064649728	4.44E-173
Q14527;Q14527-2	HLTF	0.115907669	0.064167816	0
P80723;P80723-2	BASP1	0.483149211	0.063617273	3.94E-126
Q6PKG0;Q6PKG0-3	LARP1	0.241060893	0.063572577	0
P26373;J3QSB4;P26373-2	RPL13	0.131276449	0.06349933	1.26E-154
Q96IZ0	PAWR	0.190090179	0.063269575	1.65E-98
Q03701	CEBPZ	0.292724609	0.06326656	0
P14868;Q68CR9	DARS;DKFZp781B11	0.351195653	0.062440767	1.02E-145
Q5T6F2;F5H2U4;E7EWG4;A6I	UBAP2	-0.173709234	0.062190309	2.05E-235
Q9BY77;B4DMM2	POLDIP3	0.232696533	0.062116874	2.39E-245
P14678;P63162;P14678-2;B3	SNRPB;SNRPN	-0.292150497	0.061461108	8.14E-36
P36578;H3BM89	RPL4	0.117121379	0.0613138	0
P08107;P08107-2;F8VZJ4;E7E	HSPA1A	-0.019503911	0.061302754	0
P16615;P16615-5;P16615-2;F	ATP2A2	0.219546	0.061231733	1.33E-75
Q12797;F5H667	ASPH	0.090648651	0.061175829	0
P62701	RPS4X	-0.155138016	0.060893353	1.05E-207
O14974;O14974-5;O14974-2	PPP1R12A	-0.060338338	0.060828995	0
Q9UM00;J3QQY2;Q9UM00-2	TMCO1	-0.177295685	0.06072748	5.35E-25
P07814	EPRS	-0.172912598	0.060678567	0
P42677;Q5T4L4	RPS27	-0.090937297	0.060561366	5.25E-48
O75477;B0QZ43	ERLIN1	0.321115494	0.060282197	7.38E-40

Q9NVP1	DDX18	0.562267303	0.059971732	1.59E-142
P46782;M0R0F0;M0QZN2;M(	RPS5	0.104817708	0.059963393	1.47E-96
P47897;B4DWJ2;H7C0R3	QARS	-0.367730459	0.059907632	1.13E-202
O75152;E9PQ61;E9PBY7	ZC3H11A	-0.293258667	0.059899764	9.14E-257
Q969Q0;P83881;H7BZ11;H0Y	RPL36AL;RPL36A	-0.124975204	0.059621374	3.57E-22
P46778;M0R181;G3V1B3	RPL21	0.142843246	0.059089025	4.27E-78
Q07666;Q07666-3;Q07666-2	KHDRBS1	-0.098495483	0.059004907	3.21E-255
Q06787-6;Q06787-4;Q06787-	FMR1	0.026473999	0.058918829	0
Q92499	DDX1	0.153116226	0.058659003	0
P09234	SNRPC	0.225678126	0.05861328	1.29E-67
Q15046;Q15046-2	KARS	0.347000122	0.058340312	3.39E-240
Q9Y4W2;Q9Y4W2-2;Q9Y4W2	LAS1L	0.137249629	0.057631722	1.14E-66
P11142;E9PKE3;P11142-2;E9I	HSPA8	-0.061753591	0.057630338	0
Q7L2E3-2;Q7L2E3-3;H7BXY3	DHX30	0.208616257	0.057407115	0
P15880;H0YEN5;E9PQD7;I3L4	RPS2	-0.112714767	0.057059432	9.72E-104
Q14690	PDCD11	0.409331004	0.056909987	0
Q16666;Q16666-2;Q16666-3;	IFI16	-0.351898829	0.056611018	2.32E-199
P62753;A2A3R5	RPS6	0.098481496	0.056411252	2.57E-98
P62277;J3KMX5	RPS13	0.226308187	0.055497162	3.88E-138
Q8IY81	FTSJ3	0.389081319	0.055350241	1.31E-285
P52272-2;P52272	HNRNPM	0.056627909	0.054978692	0
Q6SPF0;E9PIW9	SAMD1	0.144804001	0.054724327	5.33E-131
Q9Y3F4;B4DNJ6;B0AZV0	STRAP	0.238067627	0.054343552	2.00E-73
P49750;P49750-4;P49750-3;F	YLPM1	0.092388153	0.054211526	2.52E-239
Q96SB3	PPP1R9B	0.035043081	0.053538294	1.80E-09
CON__P02769		0.464349747	0.053191397	0
P98175-2;P98175;P98175-3;F	RBM10	-0.146750768	0.05255712	0
P62899;C9JU56;B7Z4E3;P628	RPL31	0.067014058	0.052467288	4.39E-53
P52907	CAPZA1	0.031592051	0.052283959	9.68E-150
P06748;P06748-2;P06748-3	NPM1	0.139532725	0.052228292	0
P63261;I3L3I4;I3L3I0;I3L1U9;	ACTG1	-0.052032471	0.052074056	0
Q00059;H7BYN3;A8MRB2	TFAM	0.166582108	0.051469217	2.89E-120
P61254;J3QRI7;J3QQQ9;J3QC	RPL26;KRBA2;RPL26	-0.027118047	0.051442207	8.99E-60
P46777	RPL5	-0.088989894	0.051275101	1.07E-168
P05141	SLC25A5	-0.044323603	0.050959593	6.99E-115
Q16629;Q16629-3;Q16629-2;	SRSF7	-0.28404808	0.050932038	7.84E-153
Q9UHI6	DDX20	-0.19775327	0.050313978	0
P13645;CON__P13645	KRT10	-0.105246226	0.050153275	0
O15226;G3V1N1	NKRF	0.071233114	0.049957332	0
P08754	GNAI3	-0.096733729	0.049325273	2.32E-165
P62750;H7BY10;K7EJV9;K7ER	RPL23A	-0.038513184	0.049272637	6.04E-70
O95602;B9ZVN9	POLR1A	-0.237196604	0.048719437	0
Q8IX01;M0R2Z9;M0R3F6;Q8I	SUGP2	0.327231725	0.048588623	2.01E-52
Q7Z417	NUFIP2	-0.124330521	0.048579117	0
P40429;M0QYS1	RPL13A	-0.097590764	0.048370349	4.17E-84
O75643	SNRNP200	0.283317566	0.048095688	0
P42766;H0Y3A0;F2Z388	RPL35	-0.070740382	0.046446129	1.14E-158
O43143	DHX15	-0.054734548	0.046340307	2.17E-194
Q15029;Q15029-2;K7EJ81	EFTUD2	0.278768539	0.046262586	0
P78527;E7EUY0;P78527-2	PRKDC	-0.062975566	0.045865634	0
Q9NYF8;Q9NYF8-2;Q9NYF8-4	BCLAF1	0.145033518	0.045339884	0
P04003	C4BPA	-0.326857249	0.045149884	0
P41091;Q2VIR3;Q2VIR3-2;F8\	EIF2S3;EIF2S3L	-0.169295629	0.045083383	1.02E-140
Q92804;Q92804-2;K7EPT6	TAF15	-0.091424306	0.045053095	0
P27635;F8W7C6;Q96L21;B8A	RPL10;RPL10L	0.116713206	0.045039108	8.73E-262
Q9Y3U8;J3QSB5	RPL36	-0.076628367	0.044846976	2.09E-108
P22087;M0QXL5;M0R2Q4;M(	FBL	-0.126659393	0.04463292	9.26E-237
Q13283;F5H4D6	G3BP1	0.190055847	0.044492027	0
Q09161	NCBP1	-0.252756119	0.044286917	1.79E-128
P37108;H0YLA2	SRP14	0.124384562	0.043658721	1.67E-50
Q9UHB6;Q9UHB6-4;Q9UHB6	LIMA1	-0.039580027	0.043347445	0
P39880;P39880-2;P39880-3;F	CUX1	0.12167867	0.043251936	3.28E-142
P09874	PARP1	0.094080607	0.043210667	0
P11387	TOP1	0.097653707	0.042752421	0
Q14126	DSG2	-0.084225337	0.042592805	4.26E-113
Q86Y07;Q86Y07-3;Q86Y07-4;	VRK2	0.184058507	0.042459441	2.35E-30
Q04837;E7EUY5;C9K0U8	SSBP1	-0.086399078	0.042044644	1.69E-224
Q00839;Q00839-2	HNRNPU	0.112108866	0.042025213	1.37E-265

P62304;A6NHK2	SNRPE	-0.172011058	0.041716357	2.62E-40
Q5T3I0;Q5T3I0-3;E9PAV9;F8\	GPATCH4	-0.103925069	0.04167613	0
Q13813;Q13813-3;Q13813-2;	SPTAN1	0.143533707	0.041307538	0
O75533	SF3B1	0.285294215	0.040907601	0
P46013-2	MKI67	-0.120347341	0.040557404	0
CON__P15636		-0.177829742	0.039917673	0
P05388;Q3B7A4;F8VWS0;F8V	RPLP0;RPLP0P6	0.107060115	0.039801675	4.12E-199
P62424;Q5T8U2;Q5T8U3	RPL7A	-0.063568115	0.039763549	0
Q07020;J3QQ67;F8VWC5;G3\	RPL18	0.090079625	0.039753322	5.35E-135
Q14980;Q14980-2;Q14980-4;	NUMA1	0.170436223	0.039750458	0
Q08211	DHX9	0.1681633	0.039690463	0
Q6WCQ1;Q6WCQ1-2;Q6WCC	MPRIP	0.029628118	0.039524542	0
Q96I25;Q5W011;Q5W010	RBM17	-0.124991099	0.03919017	1.40E-146
P83111;P83111-2	LACTB	0.103129705	0.039059723	0
P18621;J3QQT2;J3KRX5;J3QL	RPL17	-0.052298228	0.038079295	5.97E-82
Q9Y230;B3KQ59;M0R0Y3	RUVBL2	-0.149974187	0.038029565	9.65E-114
P08865;C9J9K3;A6NE09	RPSA;RPSAP58	-0.162754695	0.037365085	2.98E-71
P46781;B5MCT8;C9JM19	RPS9	-0.092318853	0.037054917	5.53E-91
Q8NI27	THOC2	0.205177943	0.037007899	0
P61247;D6RG13;D6RAT0;F5H	RPS3A	0.042772929	0.036307748	0
P19338;H7BY16	NCL	-0.106084824	0.035660141	0
Q69YQ0;F5H1H6;F8WAN1;C9	SPECC1L	-0.10425059	0.035453985	0
P62280;M0QZC5	RPS11	0.044268926	0.03539309	1.12E-131
P11940;P11940-2;E7EQV3;E7	PABPC1	0.090333303	0.03518215	0
Q9NVI7-2;Q9NVI7;H0Y2W2;C	ATAD3A	-0.034694672	0.03492067	0
Q13310-3;Q13310;Q13310-2;	PABPC4	-0.102282842	0.034406957	0
Q8NC51;Q8NC51-3;Q8NC51-:	SERBP1	0.310577393	0.034223507	0
Q9BZF9;H0YNH8;G3XAG2;F5I	UACA	0.133086522	0.034093588	4.45E-125
Q9NZI8;Q9NZI8-2	IGF2BP1	-0.091298421	0.033985463	4.79E-226
Q14677-2;Q14677-3;Q14677	CLINT1	-0.132141113	0.032943454	1.65E-105
P84090;G3V279	ERH	0.07371521	0.032912371	2.09E-128
Q3MHD2;Q3MHD2-2;K7ELG9	LSM12	0.109951019	0.031386841	7.44E-14
Q9UDY2;Q9UDY2-3;Q9UDY2-	TJP2	-0.275241852	0.031149573	7.89E-50
O14979-3;O14979-2;O14979	HNRPDL	-0.082021713	0.030887359	4.27E-219
Q00325-2;F8VVM2;Q00325	SLC25A3	0.047609329	0.030803835	3.75E-161
P39019;M0R2L9;M0QXK4;M(	RPS19	-0.055765152	0.030719497	4.81E-103
P49790;F6QR24	NUP153	0.051777522	0.029820068	0
Q9Y2W1	THRAP3	0.10243543	0.029746322	0
O94906;O94906-2	PRPF6	0.252869288	0.029230009	0
Q9UN86	G3BP2	-0.06293869	0.028927703	0
P83731;C9JXB8;C9JNW5	RPL24	0.035640717	0.028719316	4.71E-41
P35527;CON__P35527	KRT9	-0.046009064	0.02839055	0
Q9GZS1-2;Q9GZS1;E7EX70	POLR1E	-0.081334432	0.02813142	3.77E-62
P68133;P68032;P63267;P627	ACTA1;ACTC1;ACTG	-0.038832347	0.028047643	0
P62917;E9PKZ0;E9PKU4;G3V:	RPL8	0.060602824	0.027858603	3.04E-288
P62906	RPL10A	0.046988169	0.02781219	2.46E-130
Q15233;Q15233-2;H7C367;C:	NONO	0.156016032	0.027261674	0
Q01082	SPTBN1	-0.115846634	0.027185306	0
O75955;B4DVY7;B0V109;A2A	FLOT1	0.075298945	0.02710247	5.73E-133
Q00610;Q00610-2	CLTC	0.209073385	0.026700985	0
Q12965	MYO1E	-0.130340576	0.02623282	0
Q9NZB2;Q9NZB2-4;Q9NZB2-(	FAM120A	0.088909785	0.026118948	0
Q08J23;Q08J23-2;G3V1R4	NSUN2	-0.117675781	0.026001056	1.02E-152
P46940;H0YLE8	IQGAP1	0.093566895	0.025967663	2.49E-286
Q92841;Q92841-1;Q92841-2;	DDX17	0.012505849	0.025602894	0
Q10570	CPSF1	-0.11953481	0.024838079	0
O43390;Q2L7G6	HNRNPR	0.013704936	0.024611271	1.81E-256
Q02880-2;Q02880;E9PCY5	TOP2B	0.112443924	0.024292897	0
P26599;P26599-2;P26599-3;A	PTBP1	0.049533844	0.024091264	0
Q8TEQ6	GEMIN5	0.147439957	0.024079321	0
Q86V81	ALYREF	0.032365163	0.023726366	0
Q9BZI7;Q9BZI7-2	UPF3B	0.098591487	0.023197851	1.02E-46
O60832;O60832-2;C9IYT0;H7	DKC1	-0.068130493	0.023118875	0
Q09028;Q09028-3;Q09028-4;	RBBP4	-0.085817973	0.022979261	6.56E-198
O14950;P19105;J3QRS3;P24	MYL12B;MYL12A;M	0.018238068	0.022752378	2.31E-156
P46013	MKI67	0.053525289	0.022636114	0
P45880;P45880-2;P45880-1;E	VDAC2	0.055490494	0.022492731	2.61E-43
Q9Y2X3	NOP58	0.086426417	0.02249155	0

Q16643;A8MV58;D6R9W4	DBN1	0.049020767	0.022351962	0
P62910;D3YTB1;F8W727	RPL32	0.030359268	0.022339743	7.74E-82
O00425	IGF2BP3	-0.040712357	0.022050892	3.38E-228
P08708;P0CW22;H0YN88;H0	RPS17;RPS17L	0.03704071	0.022026852	1.75E-166
P36873;F8VYE8;P36873-2;F8	PPP1CC	-0.10174942	0.021889434	0
P42285;F5H7E2	SKIV2L2	-0.138899485	0.021787051	7.42E-137
Q86SQ0;Q86SQ0-2;Q86SQ0-3	PHLDB2	-0.058052699	0.021669738	8.60E-117
P32969;D6RAN4;H0Y9V9;E7E	RPL9	-0.050457001	0.021517006	2.25E-121
Q9P0L0;Q9P0L0-2	VAPA	-0.112434387	0.021158437	4.70E-84
P84098;J3QR09;J3KTE4	RPL19	-0.027706782	0.021113515	1.64E-87
Q13247;Q13247-3	SRSF6	-0.07492129	0.020918845	1.77E-46
Q96C57;E7ENF1;G5EA44;F5H	C12orf43	-0.093044281	0.020617655	1.83E-119
P23246;P23246-2	SFPQ	0.112603505	0.02045868	0
O00567;Q5JXT2	NOP56	-0.078982671	0.020373389	0
P08174;P08174-2;H3BLV0;Q1	CD55	0.031395594	0.020185969	1.82E-184
P06746;E7EW18;B7Z1W5;H0	POLB	0.047376633	0.020001195	4.08E-191
O00159-2	MYO1C	0.026741028	0.019770608	0
O75475;O75475-2;O75475-3	PSIP1	-0.048936844	0.019753458	0
P84103;B4E241	SRSF3;SFRS3	-0.079807281	0.019563664	5.66E-116
Q9Y224;G3V4C6	C14orf166	0.051845551	0.01946659	3.18E-257
P60660;P60660-2;F8W1R7;G	MYL6	-0.027866364	0.019336904	8.17E-176
Q9BWF3;E9PB51;Q9BWF3-4;	RBM4	0.046536128	0.019287549	3.33E-128
Q9UG63;Q75MJ1	ABCF2	0.154354731	0.019261694	1.91E-246
Q9Y3I0	C22orf28	-0.045758565	0.01864441	2.30E-252
Q9BQG0;Q9BQG0-2;I3L1L3	MYBBP1A	0.064024607	0.018545225	0
Q96DH6;Q96DH6-2;B4DHE8;J	MSI2	-0.035651525	0.01792137	9.60E-78
Q07065	CKAP4	0.047580083	0.017839696	1.60E-166
P08670;B0YJC4;B0YJC5	VIM	-0.084545771	0.017821409	0
P30050;P30050-2	RPL12	0.02988561	0.017550266	3.54E-171
P62140;E7ETD8;C9J9S3;C9JP4	PPP1CB	-0.025916417	0.017010013	0
P17844;J3KTA4;B4DLW8	DDX5	-0.01370875	0.016998363	0
Q5T5U3;E7ESW5;Q5T5U3-3;F	ARHGAP21	0.015026093	0.016585183	4.68E-165
Q1ED39	KNOP1	-0.072722117	0.016397207	0
P63208;E5RJR5;E7ERH2;F8W	SKP1	0.052379608	0.015557886	4.85E-51
Q8WYQ5;Q8WYQ5-3	DGCR8	-0.079186757	0.015409681	2.93E-90
O76094;O76094-2	SRP72	0.072907766	0.015132131	1.90E-232
Q9H6R0;I3L1L6;Q9H6R0-2;Q	DHX33	-0.074112574	0.015036975	9.81E-188
Q9HCE1;Q5JR04;Q9HCE1-2	MOV10	0.057825724	0.015006591	0
Q9Y5S9;Q9Y5S9-2	RBM8A	0.008385976	0.014787975	9.49E-168
P60709	ACTB	-0.042658488	0.014671459	0
P62158;H0Y7A7;E7ETZ0;E7EM	CALM1;CALM2	0.008892059	0.014290161	7.50E-87
Q13155;A8MU58;F8W950	AIMP2	0.096893311	0.014243557	5.68E-53
Q14444;Q14444-2;G3V153;E	CAPRIN1	-0.050722758	0.013855391	0
Q8N8A6	DDX51	0.079984665	0.013648501	1.39E-52
P23396;J3KN86;E9PL09;F2Z2	RPS3	0.029817581	0.013317315	3.28E-301
Q99729-3;D6R9P3;D6RD18;D	HNRNPAB	0.042352676	0.013258325	3.42E-19
Q99590;Q99590-2;F8VXG7;F	SCAF11	-0.045466105	0.013066882	0
P62851	RPS25	0.021113714	0.012943191	6.88E-24
Q9Y265;Q9Y265-2;E7ETR0	RUVBL1	0.061347961	0.012914809	5.32E-302
Q99877;Q93079;P58876;O60	HIST1H2BN;HIST1H2	0.032132467	0.012658906	0
Q02241;Q02241-2;H7BYN4;B	KIF23	-0.045483907	0.012348276	1.02E-219
Q96C19;H0Y4Y4	EFHD2	-0.073593775	0.012339224	6.57E-106
P62316;P62316-2	SNRPD2	-0.048912048	0.01216884	1.52E-69
P61353;K7ELC7;K7EQQ9	RPL27	-0.009798686	0.012150409	5.73E-143
P13987;E9PNW4;E9PR17;H0Y	CD59	-0.011289597	0.01186574	4.67E-37
Q9H0A0;E7ESU4	NAT10	-0.06768163	0.011420948	0
Q13435;E9PPJ0	SF3B2	-0.031016032	0.011380386	0
P05187;P10696	ALPP;ALPPL2	-0.006908417	0.011168014	1.99E-262
P35268;K7ERI7;K7ELC4;K7EM	RPL22	0.016244253	0.01094712	2.06E-177
P05387;H0YDD8	RPLP2	-0.012053172	0.010858969	3.11E-269
P61160;P61160-2;F5H6T1	ACTR2	0.038699468	0.01049076	1.76E-56
O96019;O96019-2;H7C5S0	ACTL6A	0.028393428	0.010456256	1.26E-229
Q9NX58	LYAR	-0.025905609	0.010378283	0
P62888;E5RI99	RPL30	0.024414063	0.009821911	2.02E-272
P07355;H0YN42;A6NMY6;P0	ANXA2;ANXA2P2	0.045404434	0.009324299	2.81E-48
Q09666	AHNAK	0.009531021	0.009295634	1.23E-65
P50914;E7EPB3	RPL14	-0.013216019	0.00927096	7.91E-88
Q8NE71;Q8NE71-2;H0YGW7	ABCF1	-0.038746516	0.009203026	1.46E-211

P46087;P46087-2;P46087-4;F	NOP2	0.042083104	0.009175416	4.44E-241
Q9H6R4;Q9H6R4-4;Q9H6R4-2	NOL6	-0.07366689	0.008872482	0
O60841	EIF5B	0.030753454	0.007608074	4.81E-30
P22626;P22626-2	HNRNPA2B1	0.016864777	0.007449645	0
E9PMS6	LMO7	-0.0133063	0.007420123	0
Q9Y520;Q9Y520-4;E7EPN9;Q	PRRC2C	0.014044444	0.007331856	0
CON__P35908;P35908	KRT2	0.006359736	0.007261109	2.90E-270
Q6ZRS2;Q6ZRS2-3;Q6ZRS2-2	SRCAP	0.044411977	0.007126348	2.56E-160
Q9UBI6	GNG12	-0.014805476	0.006971416	2.14E-23
Q15149;Q15149-6;Q15149-7;	PLEC	-0.027557373	0.006818576	0
P62081;B5MCP9	RPS7	-0.028418223	0.006747345	1.37E-189
P62136;P62136-2;A6NNR3;E	PPP1CA	0.009897868	0.006680097	3.13E-304
Q9P2E9;Q9P2E9-2;Q9P2E9-3;	RRBP1	-0.006429672	0.006647698	0
P26196	DDX6	-0.022424698	0.006592557	1.53E-298
P62269	RPS18	0.008849462	0.006473844	8.08E-298
Q04637;Q04637-3;Q04637-5;	EIF4G1	0.062699	0.006314078	0
P49756;P49756-2;P49756-3;E	RBM25	0.037248611	0.006142721	4.69E-198
Q9HBH0;Q9HBH0-2	RHOF	0.009188334	0.00584693	2.73E-14
Q6P2Q9	PRPF8	0.044700623	0.005506048	0
O75691	UTP20	0.026435852	0.005458572	0
Q02878;F8W181	RPL6	0.00935936	0.005433983	4.52E-179
Q9Y5A9;Q9Y5A9-2	YTHDF2	-0.013853709	0.005360107	1.56E-133
Q76FK4;Q76FK4-4;F5H101;Q	NOL8	0.022940318	0.004938881	1.32E-279
O15042;O15042-2;E7ET15;O	U2SURP	0.009204865	0.004908572	4.70E-239
Q14247;Q14247-3;Q14247-2	CTTN	0.020079295	0.004886976	1.33E-161
P47914	RPL29	-0.006610235	0.004759672	1.07E-20
Q8TDN6	BRIX1	-0.024536133	0.003825724	0
P11388;P11388-2;P11388-3;F	TOP2A	-0.009558996	0.003772896	0
P14923	JUP	-0.002857844	0.003673412	5.70E-223
P62263;E5RH77	RPS14	-0.005116145	0.00354246	4.74E-248
P62829;J3KT29;C9JD32;B9ZVI	RPL23	-0.006421407	0.003461222	2.63E-195
Q71RC2;Q71RC2-3;Q71RC2-4	LARP4	-0.016270955	0.003272712	0
P19388	POLR2E	-0.010197957	0.003129321	2.91E-70
P21333;P21333-2;Q5HY54	FLNA	-0.016258876	0.003042645	0
Q9NX24;D6RC52;D6RCB9;J3C	NHP2	0.006680171	0.002886594	1.27E-278
Q9BUJ2;Q9BUJ2-4;B7Z4B8;Q	HNRNPUL1	-0.004414241	0.002633105	4.54E-294
Q99848;H7C2Q8	EBNA1BP2	0.007567724	0.002557492	7.16E-78
Q15058	KIF14	-0.006120046	0.002419134	0
P04264;CON__P04264	KRT1	-0.00206248	0.002267379	0
Q15717;B4DVB8;M0QZR9	ELAVL1	0.003926595	0.001454258	5.54E-224
P35579;P35579-2	MYH9	-0.001059214	0.000776695	0
Q14978-2;Q14978	NOLC1	-0.002361298	0.000565002	1.26E-266
P38432	COIL	0.003501892	0.000560628	1.76E-109
Q8WWM7;Q8WWM7-6;Q8W	ATXN2L	-0.001240412	0.000461766	0
P39023;G5E9G0;H7C422;B5M	RPL3	-0.000403086	0.000334238	1.60E-264
Q92900;Q92900-2	UPF1	0.000610352	0.000262629	0
Q9H0S4	DDX47	-0.00098292	0.000139688	0

Appendix 2 (Chapter 2)

Identification and quantification of interacting protein groups for bait (H2B S112 GlcNAc monomer) versus control (wt H2B monomer) samples. Statistically significant interacting partners are denoted with a '+'

Majority Protein Ids	Gene names	log2(Bait/Control)	Significance B value	Statistically Significant Interactor	PEP
P00450;E9PFZ2;H7C5R1	CP	-3.933731	1.35E-15	+	8.79E-159
P63241;I3L397;I3L504;P6324	EIF5A;EIF5AL1	-3.576971	3.74E-13	+	3.73E-92
P60709	ACTB	3.030903	2.17E-08	+	6.00E-273
P32969;D6RAN4;E7ESE0;H0Y	RPL9	-2.60548	1.22E-07	+	7.62E-50
Q7Z401;H3BTW5;Q7Z401-2	DENND4A	-2.494539	4.08E-07	+	0.007715
P43487;C9JJ34;C9JXG8;C9JG	RANBP1	-2.230852	5.91E-06	+	9.97E-67
P11387	TOP1	2.230305	3.79E-05	+	6.75E-66
Q7L1Q6;Q7L1Q6-4;Q7L1Q6-3	BZW1	2.216646	4.22E-05	+	2.01E-101
P06753-2;P06753-3;Q5VU59;	TPM3	-3.30904	5.64E-05	+	1.27E-43
Q9NVI1;F8W7R3;Q9NVI1-2;Q	FANCI	3.539764	0.000123629	+	2.41E-72
Q14624;Q14624-2;H7C0L5;Q	ITIH4	-1.878428	0.000137014	+	6.58E-86
P00403	MT-CO2	1.993118	0.000231137	+	4.50E-38
P62495;Q96CG1;B7Z7P8	ETF1	-2.920744	0.000347697	+	7.41E-32
P19823;Q5T985	ITIH2	-1.754955	0.000367166	+	1.57E-51
Q27J81;Q27J81-2	INF2	3.28673	0.000383421	+	3.16E-32
P98179	RBM3	-2.840151	0.000495113	+	3.63E-19
Q7Z7G8;Q7Z7G8-4;Q7Z7G8-3	VPS13B	1.8582	0.000596431	+	4.18E-05
P12074;Q5T8I0;H0YIV9	COX6A1;COX6A1P2	3.171822	0.000624728	+	0.0022159
Q8NDY6	BHLHE23	1.823597	0.000753451	+	0.0041677
Q15125;C9J719;C9JJ78	EBP	3.06864	0.000955277	+	4.80E-08
P13667	PDIA4	1.772488	0.00105662	+	9.23E-133
Q9H4A6	GOLPH3	1.748428	0.001235374		4.25E-19
Q96EP5;K7EQ02;Q96EP5-2	DAZAP1	-2.608852	0.001304372		1.00E-78
P09496-2;P09496;F5H6N3;P0	CLTA	-2.551218	0.001643107		4.36E-82
Q6UXN9	WDR82	1.670712	0.00202111		1.01E-60
P82979;Q567R9;H0YHG0;F8V	SARNP;CIP29	-1.516016	0.002089947		9.72E-103
Q08211	DHX9	2.869242	0.002092643		8.80E-78
P78527;E7EUY0;P78527-2	PRKDC	1.641226	0.002423928		1.93E-199
P33240;P33240-2;E7EWR4;E9	CSTF2;CSTF2T	-2.422033	0.002715313		1.56E-28
P16403;P10412;P16402	HIST1H1C;HIST1H1E	-1.46331	0.002977465		3.27E-13
P55060;B4DUC5;P55060-3;F8	CSE1L	1.582863	0.003445264		1.58E-45
P18846;B4DRF9	ATF1	-2.349073	0.003572872		1.81E-16
P51858;A8K8G0;P51858-2;Q5	HDGF	-2.292467	0.004400584		9.90E-96
P10606	COX5B	2.636181	0.004925247		4.03E-16
Q05519;Q5T760;Q05519-2	SRSF11	-2.178993	0.006602409		1.32E-27
O14787-2;O14787	TNPO2	2.490864	0.008127471		3.11E-35
P18124;A8MUD9	RPL7	1.43066	0.008194288		4.92E-35
Q2TAY7;B4E3L0	SMU1	-2.06321	0.009825279		3.37E-99
P14625	HSP90B1	1.387947	0.010314439		1.41E-107
Q9UJU6;Q9UJU6-2;Q9UJU6-3	DBNL	-2.033878	0.010837785		1.33E-28
Q9Y3B3;Q6JUT2;Q9Y3B3-2	TMED7;TICAM2	2.396786	0.011091364		1.15E-09
P19827;F5H7E1;P19827-2;P1	ITIH1	-2.007128	0.01184099		8.05E-157
P36578;H3BM89	RPL4	1.351997	0.012463591		3.22E-55
Q9HCG8;B7WP27;B7WP74	CWC22	2.346035	0.013060028		8.03E-85
P04792;F8WE04	HSPB1	-1.96756	0.013475911		1.42E-48
P84103;B4E241	SRSF3;SFRS3	-1.205643	0.014424212		1.57E-29
P21796;C9JI87	VDAC1	2.314293	0.01444298		5.03E-60
P17844;B4DLW8;J3KTA4	DDX5	1.298483	0.016397436		1.14E-169
P61313;E7EQV9;E7ENU7	RPL15	1.255165	0.020342019		9.58E-17
P61964	WDR5	2.185143	0.021489505		7.69E-24
P38159;Q96E39;P38159-2;H0	RBMX;RBMXL1	-1.13059	0.02178882		3.42E-78
Q9NYL9;H0YNJ8	TMOD3	-1.123825	0.022590895		1.21E-209
P14927;P14927-2;B7Z2R2	UQCRB	-1.799099	0.022877348		1.34E-17
P12236;I7HJJ0	SLC25A6	1.229916	0.02300412		1.42E-67
P62158;H0Y7A7;E7ETZ0;E7EN	CALM1;CALM2	-1.089409	0.027080476		9.19E-58
Q96BP2;A6NJX6	CHCHD1	-1.736664	0.027592311		1.33E-10
Q14011;K7ELV6;K7ENX8;K7EJ	CIRBP	-1.081627	0.028196304		7.46E-115
P14854	COX6B1	1.186441	0.028299512		3.06E-43
Q9Y570;F5H2D4;J3QT22	PPME1	-1.726671	0.028419938		5.06E-05

Q96B54;M0QXZ5	ZNF428	-1.724455	0.028606375	1.09E-07
O14980;C9IZS4;C9JQ02;C9JV9	XPO1	2.074486	0.029742018	1.29E-27
Q14103;Q14103-3;H0YA96;H	HNRNPD	-1.066395	0.030495408	5.92E-55
P39023;H7C422;G5E9G0;H7C	RPL3	1.159866	0.032028935	3.48E-53
Q9UHB6;Q9UHB6-4;F8VQE1;	LIMA1	-1.055786	0.032190217	9.11E-244
P21127;P21127-12;P21127-4	CDK11B;CDK11A	2.040298	0.032789217	9.36E-29
O00571;O00571-2;O15523;B	DDX3X;DDX3Y	2.02795	0.033953713	8.58E-63
P36954;K7EKS1	POLR2I	-1.65325	0.035182552	4.98E-170
Q86VP6;Q86VP6-2	CAND1	1.13509	0.035877778	2.08E-130
O43324;D6RCQ0;H0YAL7;O43	EEF1E1;hCG_20432	-1.645809	0.035938912	5.08E-08
P35637;P35637-2;H3BPE7	FUS	-1.028553	0.036914549	3.96E-49
P52298;E9PAR5;C9JQX9;B3KS	NCBP2	-1.016911	0.039107637	6.49E-19
P41236;E7EMN6;E7EUI7;Q6N	PPP1R2;PPP1R2P3	-1.602255	0.040649954	5.89E-13
O43809;H3BND3;H3BV41	NUDT21	-0.9989548	0.042706438	5.84E-37
Q9NY12;Q9NY12-2	GAR1	-0.9979153	0.042923088	1.84E-35
Q6FI13;P0C0S8;Q9BTM1;Q16	HIST2H2AA3;HIST1H	-0.9937096	0.043809136	3.15E-68
Q04637;Q04637-3;Q04637-5;	EIF4G1	1.087231	0.044435652	2.90E-49
Q9UBS4	DNAJB11	-1.562435	0.045405228	1.65E-105
Q6ZW49;Q6ZW49-4;Q6ZW49	PAXIP1	1.909166	0.047075365	3.50E-52
P17096;P17096-3;H7BYM6	HMGA1	-1.544928	0.047639829	1.51E-13
Q9NXL6;Q9NXL6-2;J3KPQ7	SIDT1	-1.517628	0.051308352	0.0023186
Q7KZ85	SUPT6H	1.049192	0.052411784	3.05E-208
P16220;P16220-3;P16220-2;C	CREB1;CREM	-1.506956	0.052805303	2.32E-09
Q01844;Q01844-6;B0QYK0;Q	EWSR1	-0.9484062	0.054371595	5.60E-139
Q8N1F7;H3BVG0;Q8N1F7-2	NUP93	1.846777	0.055528827	4.59E-17
Q9Y5B9	SUPT16H	1.035215	0.055628694	4.08E-189
Q9UHA3;H3BMQ2	RSL24D1	-1.4828	0.056329025	0.00043987
Q86T24	ZBTB33	1.031662	0.056472261	9.29E-105
P62857	RPS28	-0.9378338	0.057121094	2.05E-42
Q9UHX1-4;Q9UHX1-6;Q9UHX	PUF60	-0.9366798	0.057428073	6.70E-111
P60903	S100A10	-1.450411	0.061358738	0.0025205
P08195;P08195-3;P08195-2;F	SLC3A2	1.011839	0.061375827	2.47E-211
P52907	CAPZA1	-1.449451	0.06151322	1.24E-25
P25440;H0Y6K2;H0Y5T9;P254	BRD2;DKFZp313H13	1.004726	0.063219025	6.45E-243
A6NHQ2	FBLL1	-1.429802	0.064748672	5.01E-07
Q8NE71;H0YGW7;Q8NE71-2	ABCF1	1.785368	0.065048719	5.08E-56
Q07065	CKAP4	1.780746	0.06581659	1.33E-84
Q86V81	ALYREF	-0.9056301	0.066217118	5.23E-188
Q9P013	CWC15	-0.9047966	0.06646754	1.38E-70
Q92979	EMG1	-0.9008656	0.067659127	3.98E-64
P01617;P01614;P06309;P0631	0	-0.8989601	0.068243001	1.37E-27
P26599;P26599-2;P26599-3;I	PTBP1	-0.8989182	0.068255905	5.50E-211
P13073;Q86WV2;H3BN72;H3	COX4I1	1.764494	0.068576525	2.00E-09
O00203;E5RJ68	AP3B1	0.9780369	0.070547867	7.25E-69
Q96ST2;Q96ST2-2;Q96ST2-3	IWS1	0.968874	0.073219287	5.50E-106
Q86VM9;E7ERS3;Q86VM9-2	ZC3H18	1.730736	0.074613487	2.71E-17
P16401	HIST1H1B	-0.8787842	0.074683194	2.18E-18
Q15165;Q15165-3;J3QT77;Q1	PON2	0.9634438	0.074841131	4.30E-81
P61978-2;P61978;P61978-3;C	HNRNPK	-0.8761673	0.075553748	3.68E-245
Q9UFW8;C9JUJ0	CGGBP1	-1.360332	0.077331191	2.18E-15
P62979;P0CG47;J3QS39;J3QT	RPS27A;UBB;UBC;U	0.9548283	0.077474437	9.38E-202
Q8N1G0;Q8N1G0-2;A2A3Q2;	ZNF687	-1.355858	0.078205623	1.08E-58
Q9Y3Y2;Q9Y3Y2-4;Q9Y3Y2-3	CHTOP	-1.353992	0.078572525	1.34E-31
Q9NR30;Q9NR30-2	DDX21	0.9456711	0.080355543	1.01E-113
P20290;P20290-2;H0Y9Y1;D6	BTF3	-1.342087	0.080947371	2.40E-47
P62241;Q5JR95	RPS8	0.9427147	0.081304081	1.48E-99
P42568;B7Z755;B1APT5	MLLT3	1.686241	0.083226514	6.08E-11
Q9BXW9;Q9BXW9-2;Q9BXW9	FANCD2	1.673532	0.085829352	7.24E-95
Q7RTV0	PHF5A	1.661978	0.088252538	5.12E-28
Q99729-3;D6R9P3;D6RD18;D	HNRNPAB	-0.83811	0.089175635	8.73E-46
Q96C19;H0Y4Y4	EFHD2	-1.286554	0.092805225	5.42E-28
P12273	PIP	-1.282055	0.093824092	1.99E-28
Q8WYQ3;B5MBW9	CHCHD10	1.632891	0.094597166	1.31E-14
Q16698;B7Z6B8;E5RJG7;E5RF	DECR1	-0.8234806	0.094911806	2.02E-101
P35613;P35613-2;P35613-4;I	BSG	0.9027824	0.095028102	1.33E-145
P63104;E7EX29;E7ESK7;B0AZ	YWHAZ	-0.8206635	0.096049644	7.84E-114

Q15269	PWP2	1.62429	0.096541563	4.71E-39
P53985;Q5T8R3;Q49A45;Q5T	SLC16A1	1.614723	0.098742019	2.92E-21
P09651;P09651-3;F8VXY0;F8\	HNRNPA1;HNRNPA1	-0.8130856	0.099164563	1.45E-166
P23284	PPIB	-0.807251	0.101617394	1.56E-72
P43246;P43246-2;E9PHA6	MSH2	0.8848152	0.101780653	1.13E-121
P39656;E7EWT1	DDOST	0.8815002	0.103067275	1.30E-66
P49792;E9PGT0	RANBP2	1.579988	0.107069328	1.38E-34
Q07955;Q07955-3;J3KTL2;Q0	SRSF1	-0.794241	0.107260695	5.61E-64
Q15427;Q5SZ64	SF3B4	-0.7939243	0.107401067	1.56E-130
Q9C0C2;Q9C0C2-2	TNKS1BP1	1.577923	0.107581567	2.43E-77
P23634;P23634-2;P23634-6;F	ATP2B4	-1.223873	0.107823218	1.96E-176
Q4G0J3;H0YA82;Q4G0J3-2	LARP7	1.576897	0.107836752	8.35E-52
Q9BRT6	LLPH	-1.221218	0.108499517	2.82E-12
Q9NQC3;Q9NQC3-2;Q9NQC3	RTN4	0.8659935	0.109258432	2.09E-68
P08240;P08240-2	SRPR	1.56946	0.109700478	5.08E-75
Q9UQ35	SRRM2	0.862793	0.110572153	3.25E-162
P22626;P22626-2	HNRNPA2B1	-0.7856712	0.111111628	1.97E-180
P05556;P05556-5;P05556-2;F	ITGB1	1.551567	0.114288972	9.44E-24
Q12872;Q12872-2;F5H1A5	SFSWAP	1.549686	0.114779893	4.16E-07
P27348	YWHAQ	-0.7720566	0.11745308	6.07E-179
Q9BVK6	TMED9	0.8432579	0.118863119	6.11E-45
O43681	ASNA1	1.532795	0.119263928	2.34E-16
P05114;A6NL93;A6NEL0	HMGN1	-1.180307	0.119350362	2.29E-15
Q13838;Q13838-2;F8VQ10;Q	DDX39B	-1.177315	0.120176338	6.26E-77
Q9UNP9;Q9UNP9-2;Q5TGA3;	PPIE	1.524946	0.121393641	3.74E-15
O76071	CIAO1	1.507164	0.126328731	1.64E-12
P05783;F8VZY9	KRT18	-0.7534924	0.12655354	0
P02545-2;Q5TCI8;Q6UYC3	LMNA	1.50248	0.127654462	1.45E-185
Q8NC51;Q8NC51-2	SERBP1	-0.7511635	0.127732928	3.81E-225
P30050;P30050-2	RPL12	-0.7505875	0.128025951	2.87E-186
P35659;P35659-2;B4DFG0	DEK	-0.7484283	0.129128953	3.06E-147
P01024	C3	-0.7468452	0.129942371	0
Q9H3P2;B3KSP0;H0Y3X6;C9JI	NELFA;WHSC2	-1.138828	0.131201986	1.87E-09
O60220	TIMM8A	0.8098373	0.134168027	6.96E-49
Q8TED0;B4DXK8;H0Y8P4	UTP15	1.478029	0.134750428	7.82E-10
O43719	HTATSF1	0.8083916	0.134862998	2.03E-292
Q00325-2;F8VVM2;Q00325;F	SLC25A3	0.8080387	0.135033036	1.01E-24
Q92804;K7EPT6;Q92804-2	TAF15	-1.123322	0.135859984	7.68E-44
Q9Y3T9	NOC2L	1.469315	0.137352031	9.37E-36
Q7Z5K2;Q7Z5K2-2;Q7Z5K2-3	WAPAL	0.7896538	0.144123705	0
Q9Y421;Q9Y421-3;K7EIY1	FAM32A	-1.09433	0.144909925	5.25E-13
Q9Y224;G3V4C6	C14orf166	-0.7178173	0.145572459	4.17E-117
P52272;P52272-2;M0R019	HNRNPM	0.7863464	0.145807739	4.89E-80
Q5C9Z4	NOM1	1.441277	0.145985441	3.21E-08
P16615;P16615-5;P16615-2;F	ATP2A2	0.7846775	0.146663223	3.19E-257
Q13151	HNRNPA0	0.7846584	0.146673022	1.21E-130
P05141	SLC25A5	0.7832069	0.147420205	1.27E-30
P60510;H3BTA2	PPP4C	1.435974	0.147663878	1.65E-23
Q9NX58	LYAR	-0.7133617	0.148093956	3.76E-223
Q15363;E7EQ72;F5GX39	TMED2	1.420635	0.152602324	1.51E-29
O43172;O43172-2	PRPF4	1.414017	0.154771603	9.51E-35
Q5JPE7;P69849;Q4G177;F5H	NOMO2;NOMO3;NO	1.41325	0.15502442	2.87E-54
Q96PK6	RBM14	-1.058926	0.156579547	1.25E-50
P11940;E7EQV3;P11940-2;E7	PABPC1	-0.6948586	0.158923369	1.29E-264
Q9Y3F4;B4DNJ6;B0AZV0	STRAP	-0.6946583	0.159043777	1.13E-197
E7EWI9;P51991-2;P51991	HNRNPA3	-0.6928463	0.160136315	4.71E-56
P13639	EEF2	-1.04324	0.161972142	9.80E-49
P08670;B0YJC4;B0YJC5	VIM	-0.6893673	0.16224988	0
P67809;H0Y449	YBX1	-0.6866112	0.163939191	6.31E-168
P02790	HPX	-0.6840897	0.165496262	1.67E-138
Q5T8D3-3;Q5T8D3-4;Q5T8D3	ACBD5	1.376125	0.167644033	1.26E-19
Q9Y5L4	TIMM13	0.7458038	0.167692937	3.41E-66
O15042;O15042-2;E7ET15;O1	U2SURP	0.7448521	0.168234838	6.56E-82
Q86TC9;F5GWA6;Q86TC9-3;C	MYPN	1.370214	0.169722547	1.26E-13
O95373	IPO7	0.741684	0.170048111	3.57E-151
Q9NX24;D6RC52;D6RCB9;J3C	NHP2	-0.6767082	0.170118365	1.64E-93

Q9UQ80;F8VTY8	PA2G4	-0.6761093	0.17049759	2.88E-59
Q06546	GABPA	0.7395515	0.171276827	8.15E-112
P52294	KPNA1	1.363966	0.171940721	1.72E-114
P01011;G3V5I3;G3V3A0	SERPINA3	-0.6718903	0.173187039	9.75E-159
Q92973;Q92973-2;Q92973-3	TNPO1	0.7355995	0.173571575	2.00E-201
O14773;O14773-2	TPP1	0.735302	0.173745272	1.65E-36
Q7Z5J4;A8MXE8;Q7Z5J4-4;Q	RAI1	-1.003994	0.17607685	2.86E-05
Q8N2W9	PIAS4	0.7290764	0.177409374	6.00E-105
P56192;A6NC17;B3KVK7	MARS	1.347237	0.177986258	2.33E-92
Q9H8H0;J3QKS9;J3QLQ6;J3Q	NOL11	1.345476	0.178631537	3.73E-47
O96008;K7EJ57;O96008-2;K7	TOMM40	1.34371	0.179280662	7.69E-05
O00425	IGF2BP3	-0.9852905	0.183112562	8.00E-70
O15160;O15160-2;E7EQB9;D	POLR1C	-0.9794407	0.185355319	4.32E-48
Q96B01;Q96B01-2;B4DUS5;C	RAD51AP1	-0.97509	0.187036437	6.08E-15
Q09666	AHNAK	-0.9733982	0.187693197	3.70E-30
P05023;P05023-3;F5H3A1;P0	ATP1A1	1.32111	0.187742172	5.43E-113
O00148;Q8N5M0;B1Q2N1;K7	DDX39A;DDX39	-0.6487179	0.188525912	2.77E-123
Q14331;E9PRR7;Q9BZ01;H0Y	FRG1;FRG1B	1.31744	0.189143492	4.52E-23
Q8NFC6	BOD1L1	1.315765	0.189785528	1.80E-86
Q96IZ7;H7C5Q0;Q96IZ7-2;C9	RSRC1	-0.966444	0.190410679	6.44E-39
P11717	IGF2R	1.313587	0.190623015	6.20E-29
O14617;O14617-5;O14617-4;	AP3D1	1.311699	0.191351231	2.17E-84
Q9Y5J9;G3XAN8	TIMM8B	0.7051792	0.192009183	1.24E-21
O60828;O60828-5;O60828-4;	PQBP1	-0.643364	0.192208295	3.78E-62
Q9UJZ1;B4E1K7	STOML2	-0.9564457	0.194368322	1.90E-05
P05387;H0YDD8	RPLP2	-0.6367264	0.196846635	1.34E-120
P50991;B7Z9L0;P50991-2;B7	CCT4	-0.9479904	0.197762017	2.30E-16
P62805	HIST1H4A	-0.9470921	0.198125125	1.84E-19
Q9BVP2;Q9BVP2-2	GNL3	1.284174	0.202199607	5.97E-27
P04844;P04844-2	RPN2	0.6804771	0.208009987	3.78E-287
Q13868;B4DKK6;A3KFL5;A3K	EXOSC2	-0.9228096	0.208125295	1.51E-20
Q6P2E9	EDC4	-0.9091492	0.213909391	6.86E-12
P17480;P17480-2;E9PKP7	UBTF	0.6696663	0.215308991	2.15E-291
P20674;H3BNX8;H3BRI0	COX5A	1.252178	0.215365416	2.45E-09
Q8N9E0;G3XAI9;Q5BKY9	FAM133A;FAM133B	-0.9023952	0.216811597	0.00021616
Q15054;Q32N00;Q32MZ9	POLD3	-0.9023285	0.216840423	4.04E-34
E9PLD3;E9PRG8	C11orf48	-0.6082382	0.217685798	4.10E-12
Q96FJ2;P63167	DYNLL2;DYNLL1	-0.8974438	0.218957206	2.40E-15
P24534	EEF1B2	-0.892601	0.221070413	2.81E-61
Q68E01;Q68E01-2;Q68E01-3	INTS3	0.6611786	0.22116749	9.02E-257
Q6NZI2;Q6NZI2-2	PTRF	0.6542358	0.226043885	3.03E-88
Q9NUP9;G3V1D4	LIN7C	-0.8725281	0.229985358	3.57E-16
P25311;C9JEV0	AZGP1	-0.8717022	0.230357554	6.61E-16
P23246;P23246-2	SFPQ	-0.5917969	0.230411577	9.23E-84
P20645;F5GXE0;H0YGE9;F5G	M6PR	1.209211	0.234001657	2.16E-25
O95816;B4DXE2	BAG2	-0.8563042	0.237375453	1.71E-62
Q6W2J9;H7C2V9;A6NE70;Q6	BCOR	1.196232	0.239849734	1.46E-36
Q9ULC4;Q9ULC4-3;Q9ULC4-2	MCTS1	-0.8495369	0.240507046	2.74E-48
P62861;E9PR30	FAU	-0.5790882	0.240604327	7.12E-09
P14923	JUP	0.6328068	0.241577561	4.78E-90
Q07666;Q07666-3;Q07666-2	KHDRBS1	-0.5775585	0.241852279	9.50E-41
Q07157;Q07157-2;G5E9E7;G	TJP1	-0.8445377	0.242839051	1.49E-09
P84090;G3V279	ERH	-0.5755482	0.243499272	1.35E-126
Q13601;Q13601-2	KRR1	1.18199	0.246384426	7.41E-14
F8W9Q2;Q8N7H5-2;M0QX35	PAF1	0.6245766	0.247738782	4.47E-71
P52701;F5H2F9;B4DF41;P527	MSH6	0.6217022	0.249916263	9.07E-294
Q09161	NCBP1	1.173248	0.250456462	1.84E-37
Q99547;H3BSB3;H3BNT4	MPHOSPH6	-0.8280296	0.250652492	1.90E-26
Q9H089	LSG1	0.6178684	0.252841291	2.77E-84
P20020;P20020-6;P20020-3;F	ATP2B1	1.165148	0.254271697	2.63E-196
Q9BTT0;Q5TB20;Q5TB19;E9P	ANP32E	0.6158257	0.254409554	1.98E-273
O14950;P19105;J3QRS3;P248	MYL12B;MYL12A;M	-0.5622501	0.254592329	1.27E-106
P62913;P62913-2;Q5VVC9;Q	RPL11	-0.5619736	0.254826709	1.22E-24
P30153;B3KQV6;F5H3X9;P30	PPP2R1A;PPP2R1B	-0.818697	0.25514658	1.88E-30
Q7Z6E9;Q7Z6E9-2;Q7Z6E9-4;	RBBP6	-0.8164215	0.256250761	1.80E-36
Q6PD62	CTR9	1.158545	0.257411515	1.18E-68

P10620;F5H7F6;F5H6X2;P10(	MGST1	-0.8069878	0.260863913	7.36E-08
Q9UG63;Q75MJ1	ABCF2	1.151205	0.260932861	1.23E-17
P16435;H0Y4R2;F5H468;E7E\	POR	0.6039505	0.263660249	1.72E-117
P09429;Q5T7C4;Q5T7C6;Q5T	HMGB1	-0.8007622	0.263939536	1.71E-19
O00264;B7Z1L3	PGRMC1	0.6030293	0.264387476	4.94E-42
Q13310;Q13310-2;B1ANR0;Q	PABPC4	-0.5432625	0.271033202	4.84E-198
O00410;O00410-3;O00410-2;	IPO5	0.593029	0.272370583	1.19E-144
P31943;G8JLB6;E9PCY7;D6RI	HNRNPH1	0.5920258	0.273180492	5.05E-233
P40937;P40937-2;F8W9B4;F5	RFC5	1.124424	0.274063781	8.33E-36
Q93009;F5H8E5;B7Z815;H3B	USP7	1.123348	0.274600493	4.74E-32
Q9UKL0;J3KN32	RCOR1	0.5889282	0.275691433	1.79E-34
Q9BXP5;Q9BXP5-4;Q9BXP5-2	SRRT	-0.5357056	0.277774614	6.56E-76
P54727;P54727-2;H0Y579	RAD23B	-0.7698994	0.279555368	7.58E-33
P56537;B7ZBG9	EIF6	-0.5329723	0.280240769	4.72E-96
Q12797;F5H667	ASPH	0.5816422	0.281659637	2.76E-86
Q8IZL8;F8WDZ1;I3L3A8;C9JF\	PELP1	1.106958	0.282866564	5.80E-06
P62875	POLR2L	1.097439	0.287744323	1.05E-07
Q9UKS6;E9PIY1	PACSIN3	-0.5242805	0.288181887	0
Q9Y4Z0	LSM4	-0.7480011	0.29100905	5.92E-08
P55769;B1AHD1	NHP2L1	-0.5206718	0.291523077	1.56E-30
P55010;H0YLZ1;H0YN40	EIF5	0.5691071	0.292131252	2.47E-160
Q9BQ61	C19orf43	-0.5197258	0.292403283	1.16E-07
Q9BY44;B4DQ14;F8WAE5;B4	EIF2A	-0.7438602	0.293209872	9.98E-44
Q9Y3E5;J3KQ48	PTRH2	0.5674992	0.293493147	8.17E-218
P46937;P46937-2;E9PRV2;P4	YAP1	-0.7329617	0.29905563	1.24E-71
P48681	NES	1.075415	0.299245729	3.39E-16
Q9Y3U8;J3QSB5	RPL36	-0.5117264	0.299917305	3.25E-37
P78344;D3DQV9;P78344-2;H	EIF4G2	0.5580158	0.301612139	1.10E-231
P46977;E9PIJ8;E9PN73;E9PI3	STT3A	1.068916	0.302697094	1.13E-07
Q9BRP8;Q9BRP8-2	WIBG	-0.7211151	0.305497495	7.18E-13
P68366;A8MUB1	TUBA4A	0.5521507	0.30670758	2.98E-228
Q92791;K7ERA3	LEPREL4	0.5498943	0.308682977	1.21E-234
O75521;O75521-2;F1LLU7;C9	ECI2	-0.7152481	0.30872166	1.95E-40
Q9HAF1;Q9HAF1-2;B1AK64;C	MEAF6	-0.7138901	0.309471151	2.13E-11
Q8WWC4;H7C0V0	C2orf47	1.055689	0.309803882	0.00037694
P35268;K7ELC4;K7EMH1;K7E	RPL22	-0.5013695	0.30983543	1.67E-53
Q00341;C9J5E5;C9JIZ1;C9JM(	HDLBP	1.052677	0.311437275	4.26E-15
Q9UBQ5;K7ES31;K7EMQ9;K7	EIF3K	1.050003	0.312892323	1.74E-25
Q07020;F8VUA6;F8VWC5;G3	RPL18	1.049175	0.31334365	7.19E-48
Q9HD45	TM9SF3	1.048832	0.313530962	0.00041671
A6NKV8;Q9H074;D6REB4;Q9	PAIP1	1.046799	0.314641776	2.56E-34
Q9Y5M8;H7C4H2	SRPRB	0.5418205	0.31582009	1.49E-193
Q06830	PRDX1	-0.494791	0.316246421	2.71E-22
Q14919;E9PQX9;Q14919-2;C	DRAP1	-0.6998138	0.317310509	1.04E-26
P27797;K7EJB9	CALR	0.5401497	0.317310509	8.11E-93
P62258;P62258-2;K7EM20	YWHAE	-0.4937077	0.317310509	4.73E-144
Q9P0L0;Q9P0L0-2	VAPA	1.041933	0.317310509	8.71E-17
Q9H1C3	GLT8D2	1.040302	0.318208279	8.27E-11
P40429;M0QYS1;Q6NVV1	RPL13A	1.037668	0.319661874	4.44E-09
Q13243;Q13243-3;B4DJK0;B4	SRSF5	-0.4900379	0.320932343	3.96E-32
Q01650	SLC7A5	1.032709	0.322410316	5.29E-15
P07910-4;P07910-2;G3V4W0	HNRNPC;HNRNPCL1	-0.4838104	0.327140116	7.36E-89
Q5F1R6;Q5F1R6-3;Q5F1R6-2	DNAJC21	-0.6802845	0.328400606	1.35E-42
Q03111	MLLT1	0.5243511	0.331630705	6.16E-31
P46783;F6U211	RPS10	-0.4780521	0.33294907	7.29E-87
Q16629;Q16629-3;Q16629-2;	SRSF7	-0.4777489	0.333256842	6.85E-42
Q96AG4	LRRC59	0.5220642	0.333737704	1.68E-147
P14866;P14866-2;M0QXS5;M	HNRNPL	-0.4758148	0.335223931	1.94E-137
Q68CQ4	DIEXF	0.5179729	0.337528598	5.15E-240
P62633;P62633-2;P62633-4;E	CNBP	-0.6608543	0.33968081	7.71E-83
O15446;O15446-2	CD3EAP	-0.4714394	0.339701666	9.28E-131
P07355;H0YN42;P07355-2;HC	ANXA2;ANXA2P2	-0.4691162	0.342094635	6.97E-133
P08651-4;P08651-3;P08651-2	NFIC	0.9978409	0.342168822	2.75E-18
Q9H1E3	NUCKS1	0.5103111	0.344702027	9.92E-146
Q9NTK5;C9JTK6;Q9NTK5-3;J3	OLA1	-0.6510372	0.345473517	9.15E-12
Q8TDN6	BRIX1	0.9896526	0.346918786	1.78E-13

P63173;J3KT73;J3QL01	RPL38	-0.4629269	0.348522475	1.39E-19
Q9UGP8	SEC63	0.5051899	0.34955064	0
Q9UNF0;Q9UNF0-2	PACSIN2	0.5045853	0.350125927	4.78E-157
Q13247;Q13247-3;Q13247-2	SRSF6	-0.6330833	0.356229229	1.33E-19
O60884	DNAJA2	0.496727	0.357657411	8.91E-78
P45880;B4DKM5;P45880-2;P	VDAC2	0.97118	0.357787989	4.76E-15
P38919	EIF4A3	-0.6271172	0.359849655	7.14E-29
P62750;H7BY10;K7EJV9;K7ER	RPL23A	-0.4493904	0.362845997	1.05E-71
Q4LE39;Q4LE39-2;Q4LE39-3	ARID4B	0.9613914	0.363633419	3.28E-47
P14618;P14618-2;H3BT25;H3	PKM	0.9611187	0.363797149	1.80E-10
Q9NZN4;B4DNU6	EHD2	0.9607162	0.364038821	2.39E-15
Q9Y333	LSM2	0.9554672	0.367200052	2.72E-11
P09874	PARP1	0.4866123	0.367500338	3.74E-148
P60468	SEC61B	0.4865551	0.367556497	0.00010624
P27824;B4DGP8;B4E2T8	CANX	0.4850349	0.369050408	0
Q92945	KHSRP	-0.6098442	0.370460997	5.59E-55
O60763;O60763-2;F5H4X1;F5	USO1	0.4835014	0.370561261	3.13E-164
Q9H4L7;Q9H4L7-2;Q9H4L7-3	SMARCAD1	-0.6094246	0.370721176	1.35E-25
Q9H936;E9PJH7	SLC25A22	0.9485207	0.37140984	1.26E-18
Q05682;Q05682-3;Q05682-2;	CALD1	-0.6071911	0.372107945	1.54E-124
Q9UDW1	UQCR10	0.9468384	0.37243383	9.25E-09
Q9NPE3	NOP10	-0.4402905	0.372679216	7.05E-29
Q92522	H1FX	-0.4402027	0.372774821	3.18E-48
J3KN66;Q5JTV8;H0Y4R4;Q5JT	TOR1AIP1	0.4800835	0.373942529	4.87E-225
Q9BQG0;Q9BQG0-2;I3L1L3	MYBBP1A	0.9430122	0.374769275	1.63E-28
Q13445	TMED1	-0.4383488	0.374798533	6.47E-26
Q16531;F5GY55	DDB1	0.4786434	0.375372812	4.69E-136
P62277;J3KMX5	RPS13	-0.4377956	0.375403628	2.32E-20
Q9UHB9;F5H5Y3;G3V1U4;Q9	SRP68	0.478426	0.375589069	5.75E-268
Q9BWJ5	SF3B5	-0.4361324	0.377226719	8.90E-44
Q96A26;F8W7Q4;E9PH05	FAM162A	0.9371452	0.378367985	1.73E-05
Q13509;A8K854	TUBB3	-0.5957375	0.379269847	2.14E-228
Q8IX15;F8WCA3	HOMEZ	0.4724464	0.381566244	1.47E-38
Q8IVT2	MISP	-0.5918903	0.381694334	1.12E-22
Q15291;Q15291-2	RBBP5	0.9316864	0.38173537	1.78E-06
P63220;Q8WVC2;Q9BYK1	RPS21	-0.432003	0.381776633	4.58E-36
Q9Y2T2	AP3M1	0.470665	0.383358228	1.31E-150
Q9UMS4;F5GY56	PRPF19	0.9290352	0.383377435	1.12E-94
Q7Z7H5;Q7Z7H5-3;Q7Z7H5-2	TMED4	0.9278946	0.384085206	4.25E-41
P01834	IGKC	-0.5874672	0.384493554	3.14E-267
P39019	RPS19	-0.4280357	0.386179477	2.48E-23
O00566;C9JX83	MPHOSPH10	0.9241447	0.386417722	1.14E-09
P52739;P52739-2;D6RJH2;D6	ZNF131	0.9146271	0.392376701	1.59E-37
P15880;H0YEN5;E9PQD7	RPS2	0.9111252	0.394583172	2.26E-13
Q15910;Q15910-2;G3XAL2;Q	EZH2	0.9099083	0.395351662	2.24E-08
P16989;P16989-2;P16989-3	YBX3	-0.4192944	0.395989363	2.22E-127
Q9Y6E2;E7ETZ4;B5MCH7;B5M	BZW2	0.4572716	0.396995122	4.50E-66
P62701	RPS4X	0.457098	0.397173746	6.32E-125
Q96DH6;Q96DH6-2;B4DHE8;(	MSI2	-0.4179974	0.397457615	2.65E-69
Q9NWS0;M0QYF4;M0QXD5;M	PIH1D1	-0.5664558	0.397961446	4.05E-42
P49755;G3V2K7	TMED10	0.4547882	0.399555425	3.85E-53
Q9Y230;B3KQ59;M0R0Y3	RUVBL2	0.4530697	0.401332987	1.39E-97
P61619;B4DR61;P61619-3	SEC61A1	0.8999443	0.401678092	2.00E-10
Q9UBV2	SEL1L	0.8952789	0.40466104	5.58E-22
Q9H501	ESF1	0.8941994	0.405353172	4.13E-24
P0DI83	RAB34	-0.5548496	0.405521189	1.43E-19
P62304;A6NHK2	SNRPE	-0.4107704	0.405698732	3.21E-75
Q9Y6M0;Q9Y6M0-2;I3L3C7;C	PRSS21	0.88974	0.408219678	2.99E-69
P35251;P35251-2	RFC1	0.8888206	0.408812132	1.85E-45
O43660;O43660-2;A8MW61	PLRG1	0.8876152	0.409589735	1.83E-47
P26368;K7ENG2;P26368-2	U2AF2	-0.4044495	0.412989731	3.61E-96
O75459	PAGE1	-0.5426102	0.413585636	2.67E-20
Q9NYF8-3;E9PK91;E9PK09;E9	BCLAF1	0.8786106	0.415426152	1.35E-241
P07919	UQCRH	-0.4022636	0.415528952	4.79E-120
P98175-2;P98175	RBM10	-0.4015675	0.416339623	0
Q9Y2S0	POLR1D	-0.5375919	0.416919351	6.23E-55

P13984	GTF2F2	-0.4009914	0.417011076	2.53E-162
P45973;G3V1X9	CBX5	-0.5337429	0.419487045	9.14E-38
Q9H2H8;B8ZZ77;Q9H2H8-2;H	PPIL3	-0.3977547	0.420795964	2.36E-31
Q9Y3I0	C22orf28	-0.5301704	0.421878541	7.09E-94
Q14165	MLEC	0.8665981	0.42328817	6.22E-142
P52655;J3KNC0	GTF2A1	-0.5241508	0.425926237	5.20E-25
Q16576;Q16576-2;E9PC52	RBBP7	0.4290676	0.42665242	9.71E-49
Q969V3;K7EQ66;K7ELZ9;K7EI	NCLN	0.8612061	0.426845348	4.06E-06
Q92688;Q92688-2;Q5T6W8	ANP32B	0.4269829	0.42889468	1.15E-162
Q02878;F8W181	RPL6	0.8576031	0.429231933	1.69E-11
Q9BRJ6;C9JQV0;H7C0T1;H7C	C7orf50	-0.5190125	0.429399259	2.57E-32
O94992	HEXIM1	0.8549156	0.43101712	2.89E-18
Q9NR50;H0Y580;Q9NR50-3;C	EIF2B3	0.4244461	0.431632359	5.07E-48
Q14318;Q14318-2;J3KQ73	FKBP8	0.4223328	0.433920786	5.58E-118
O15355	PPM1G	0.4207573	0.435631332	2.94E-192
Q9BQ15;C9JT95;C9JMP5	NABP2	-0.5084991	0.436556224	2.79E-39
P14678;P63162;P14678-2;B3	SNRPB;SNRPN	-0.3835716	0.437616893	1.61E-82
Q16181;H0Y3Y4;H0YFF6;Q16	SEPT7	-0.3825188	0.438880807	3.10E-53
O60885;O60885-2;Q4G0X8;M	BRD4	0.4170704	0.439649513	3.46E-167
P62910;D3YTB1;F8W727	RPL32	-0.3802052	0.441665569	8.29E-104
Q99590;F8W028;Q99590-2;F	SCAF11	0.4150658	0.441843151	1.12E-49
D6R9B1;Q15723-4;E9PCX3;Q	ELF2	0.8386917	0.441885205	1.15E-07
P08238	HSP90AB1	0.8369141	0.443085479	2.41E-128
F5GWP8	JUP	0.4138069	0.443223893	2.84E-100
P04843;B7Z4L4	RPN1	0.4133644	0.44370983	3.07E-248
Q8WXG6;Q8WXG6-3;Q8WXG	MADD	0.8355446	0.444011423	1.29E-11
O94874;O94874-3;O94874-2	UFL1	0.8340244	0.445040539	2.99E-47
Q92733;A6NG79	PRCC	0.4116173	0.445631414	3.65E-138
Q9BQE9;Q9BQE9-4;Q9BQE9-	BCL7B	-0.4938641	0.446632624	1.49E-09
P63261;I3L3I4;I3L4N8;I3L3I0;	ACTG1	-0.3759995	0.446753554	0
P62899;H7C2W9;C9JU56;B7Z	RPL31	-0.3748627	0.448134514	3.54E-22
Q9UPP1;Q9UPP1-2;Q9UPP1-4	PHF8	0.8272991	0.449609727	4.62E-37
P60660;P60660-2;F8VZV5;F8	MYL6	-0.373642	0.44962012	5.67E-26
Q15370;B8ZZU8;Q15370-2;I3	TCEB2	-0.4883766	0.450444631	1.36E-08
Q9UHD8;Q9UHD8-2;Q9UHD8	SEPT9	-0.3710365	0.452800282	7.21E-261
P46776;E9PJD9;E9PLL6	RPL27A	-0.3694305	0.45476684	1.30E-19
Q15517;Q2L6G8;G8JLG2	CDSN	0.8160229	0.457330193	0.0016978
Q13724;F5H6D0;C9J8D4	MOGS	0.3996849	0.458881342	2.23E-190
Q96JB5;F5H3I5;J3QQY1;Q96J	CDK5RAP3	0.3983498	0.460377523	1.02E-63
O75643	SNRNP200	0.398016	0.460751994	5.95E-137
Q14676;Q14676-2;E9PGY5;Q	MDC1	0.3967876	0.462131513	6.00E-105
Q14974;B7ZAV6;F5H4R7;J3K1	KPNB1	0.3964272	0.462536809	0
Q13416	ORC2	-0.4710064	0.462632074	4.26E-157
Q9NX40;D6RG39;D6RIT9;Q9N	OCIAD1	0.8075581	0.463174349	6.92E-49
Q08945	SSRP1	0.3946247	0.46456626	2.63E-186
Q9BUA3	C11orf84	-0.4675407	0.465085497	2.57E-45
Q14151	SAFB2	-0.4664345	0.465870169	5.03E-49
P25490;H0YJV7	YY1	0.393362	0.465990896	5.71E-62
P33993;P33993-3	MCM7	0.3927002	0.466738614	2.46E-138
P49411	TUFM	0.3921509	0.467359704	4.41E-124
O75179;O75179-5;O75179-3;	ANKRD17	0.7980881	0.469761528	3.31E-34
Q96N66;Q96N66-3;Q96N66-2	MBOAT7	0.7973404	0.470283799	4.65E-14
O75400;O75400-2;O75400-3	PRPF40A	-0.4599838	0.47046023	8.34E-22
Q96RE7	NACC1	0.3889961	0.470935514	2.38E-105
Q13185	CBX3	-0.3555202	0.472000151	1.27E-108
Q86XP3;Q86XP3-2	DDX42	0.3857613	0.474617748	3.56E-226
P26373;J3QSB4;P26373-2	RPL13	-0.3520393	0.476368235	8.82E-39
P62318;B4DJP7;H3BT13	SNRPD3	-0.3506012	0.478179357	7.47E-79
P68363	TUBA1B	0.3816471	0.479323626	2.17E-292
P16070;H0YE40;H0YD13;H0Y	CD44	-0.4464474	0.480172978	6.32E-31
P27816;P27816-6;E7EVA0;P2	MAP4	-0.3485279	0.480796961	1.24E-60
P42704	LRPPRC	0.3777676	0.483784384	2.28E-186
P55081	MFAP1	0.3760948	0.485714656	2.29E-87
P55199	ELL	0.7749596	0.486064876	2.98E-40
O43290	SART1	-0.4379101	0.486354471	5.29E-94
Q04917;A2IDB2	YWHAH	-0.4377747	0.486452869	1.19E-31

P40939	HADHA	0.3736839	0.488504029	0
P55209;F8VUX1;F8VY35;B3KI	NAP1L1	0.3735828	0.488621177	6.97E-227
P08574	CYC1	0.3722477	0.490169832	2.73E-44
Q6P1N0;Q6P1N0-2;K7EJY5;K7	CC2D1A	0.7605152	0.496399933	1.95E-10
Q15428;K7EP23;K7EMT0;K7E	SF3A2	-0.4230423	0.497221518	1.97E-54
Q16649	NFIL3	-0.4200172	0.499448298	3.34E-23
Q03701	CEBPZ	0.7559433	0.499695426	5.46E-58
O43395;E7EVD1	PRPF3	0.7552013	0.500231332	1.07E-49
P68133;P68032;P63267;P627	ACTA1;ACTC1;ACTG	-0.3328114	0.500891196	3.95E-86
Q8IWA0	WDR75	0.7537346	0.501291642	4.72E-113
Q5VT52;Q5VT52-3;Q5VT52-2	RPRD2	0.3625031	0.501552315	5.14E-160
P98175-3;P98175-4	RBM10	-0.4162312	0.502242727	2.86E-151
Q96EY4;D6RA57;H0Y9X1	TMA16	0.7494965	0.50436205	7.15E-72
P84098;J3QL15;J3QR09;J3KTI	RPL19	0.3595467	0.505033069	3.38E-29
Q15366;Q15366-4;Q15366-5;	PCBP2;PCBP3	-0.3295708	0.505089072	7.48E-40
Q9H4L4;J3KNH7	SENP3	0.7462769	0.506701178	2.26E-09
Q9UHB7;Q9UHB7-2	AFF4	0.3565254	0.508603282	2.93E-114
Q8IYB3;A9Z1X7;Q8IYB3-2;E9I	SRRM1	-0.3244514	0.511758259	2.23E-66
P62888;E5RI99	RPL30	-0.3233414	0.513210448	1.35E-97
P09234	SNRPC	-0.3232555	0.51332282	2.65E-66
O75607	NPM3	0.3525333	0.513340954	4.58E-225
P51648;P51648-2;J3QRD1;J3(	ALDH3A2	0.7362061	0.514054535	1.55E-19
Q92841;Q92841-3;Q92841-1;	DDX17	0.7335491	0.516003752	1.26E-81
P22695;H3BRG4;H3BSJ9;H3B	UQCRC2	0.3493214	0.517169438	1.96E-119
O00483	NDUFA4	0.3478298	0.518952287	3.15E-08
Q15061	WDR43	0.3454933	0.52175148	7.67E-97
Q99714;Q99714-2;Q5H928	HSD17B10	-0.3165398	0.522154863	1.06E-255
Q9Y265;Q9Y265-2;E7ETR0;H7	RUVBL1	0.3441086	0.523414088	2.13E-135
Q9P287;Q9P287-3;Q9P287-2;	BCCIP	-0.3863468	0.524586765	2.67E-84
P30419;O60551;B4DXS1;P30	NMT1;NMT2	-0.3860359	0.524821866	2.26E-05
P55039;A8MZF9;J3QR71;J3QI	DRG2	0.7204056	0.525702381	4.09E-16
P62273;P62273-2	RPS29	-0.384407	0.526054502	3.53E-07
Q14247;Q14247-3;Q14247-2	CTTN	-0.3134727	0.526214182	3.71E-62
Q99613;H3BRV0;B5ME19	EIF3C;EIF3CL	0.7196941	0.526230001	5.34E-144
Q96JJ7	TMX3	0.718668	0.526991495	2.33E-15
Q99848;H7C2Q8	EBNA1BP2	-0.3105545	0.53009151	5.30E-58
P82673;P82673-2;H0YG82	MRPS35	-0.3765926	0.531988488	3.63E-22
Q15424;B7ZLP6;A0AV56;Q15	SAFB	-0.3079376	0.533580734	0
Q66PJ3;Q66PJ3-2;Q66PJ3-3;F	ARL6IP4	-0.3078003	0.533764162	4.60E-114
Q86X53;E5RHA3;H0YB25;H0Y	ERICH1	0.7090263	0.534173785	1.57E-28
Q9Y6A4	C16orf80	0.3348827	0.534560239	2.85E-147
J3KPD9;P22392-2;Q32Q12;P2	NME2;NME1-NME2	-0.3067551	0.535161297	8.59E-55
P08708;P0CW22;H0YN88;H0\	RPS17;RPS17L	-0.3061371	0.535988206	1.49E-29
O43670;J3KS31;O43670-3;O4	ZNF207	-0.3709793	0.53627188	2.11E-07
Q8IXQ4;Q8IXQ4-3;Q8IXQ4-4;	KIAA1704	-0.3670559	0.539276013	1.26E-05
O60832;H7C2Q9;H7C0M1;C9	DKC1	0.7021179	0.539350247	2.74E-22
P20042	EIF2S2	-0.3030014	0.540193894	1.21E-137
Q8IWX8;J3QK89	CHERP	0.7009811	0.540204435	2.53E-45
P50454;E9PKH2;E9PR70;E9PI	SERPINH1	-0.365778	0.540256328	1.79E-14
Q12888;C9JXV0;A6NNK5;F8V	TP53BP1	0.3294125	0.541225223	4.98E-165
P06493;P06493-2	CDK1	-0.3642673	0.541416296	2.43E-21
O76094;O76094-2	SRP72	0.3285542	0.542274738	0
Q7L0Y3;C9JVB6	TRMT10C	-0.301384	0.542369687	4.07E-170
O43852;O43852-3;O43852-6;	CALU	-0.3013496	0.542415918	3.00E-153
P17028;K7EQP8;K7EPZ8;K7EI	ZNF24	-0.3621178	0.543069048	4.13E-12
P37108;H0YLA2	SRP14	-0.2991829	0.545337614	4.99E-123
Q99933;Q99933-4;Q99933-3;	BAG1	-0.3583069	0.54600529	1.21E-12
Q8WXI9	GATAD2B	-0.3568726	0.547112457	1.65E-19
P13861;Q9BUB1;H7C1L0	PRKAR2A	0.6916752	0.54722237	1.36E-52
Q13112	CHAF1B	-0.3565826	0.547336381	2.72E-56
P41208	CETN2	-0.3559799	0.547802052	7.85E-13
P06730;D6RBW1;P06730-3;P	EIF4E	0.3235378	0.548428799	7.92E-24
Q9NXS2	QPCTL	0.3232746	0.548752661	1.21E-78
Q13547;F5GXM1	HDAC1	-0.2959213	0.549750265	1.08E-119
Q15365	PCBP1	-0.2950459	0.550937702	9.94E-46
Q8WX92	NELFB	-0.3504009	0.552121733	3.41E-29

P50402;Q5HY57	EMD	-0.3500404	0.552401425	6.21E-73
O14979;O14979-3;O14979-2	HNRPDL	-0.2936497	0.552833999	9.40E-53
O15427	SLC16A3	0.6812973	0.555101522	0.00033088
O00629	KPNA4	0.315279	0.558635321	2.96E-53
Q9C005;B4DIS3	DPY30;LOC84661	-0.3407822	0.559608356	0.0016526
P22087;M0R299;M0QXL5;M(	FBL	-0.2877579	0.560871346	1.21E-57
P19388	POLR2E	-0.2854652	0.564014077	2.81E-154
P61981	YWHAG	-0.3345909	0.564453138	2.32E-107
P53618;E9PP73	COPB1	0.6672325	0.565867561	3.86E-35
P08865;C9J9K3;A6NE09	RPSA;RPSAP58	-0.2835312	0.566671845	5.91E-81
P06748;P06748-2;P06748-3	NPM1	0.3060036	0.570207127	0
P62851	RPS25	-0.2807751	0.570469642	1.80E-11
Q15554;H3BR06;H3BTA7;Q1!	TERF2	-0.3266506	0.570695974	1.16E-57
P38432	COIL	0.3051357	0.571295649	9.16E-65
P55084;B4E2W0;B5MD38;F5(	HADHB	0.3046761	0.571872605	1.55E-103
P50914;E7EPB3	RPL14	0.3044128	0.572203103	2.63E-24
Q8WVV9;Q8WVV9-4;D6W59:	HNRNPLL;HNRPLL	-0.3237057	0.573019687	1.45E-28
Q9BQE3;F5H5D3	TUBA1C	0.3028107	0.574216786	5.84E-259
P31930	UQCRC1	0.3006477	0.576940567	4.55E-255
Q9NQW6;Q9NQW6-2	ANLN	-0.3178024	0.577691118	3.76E-56
Q9Y6N8	CDH10	0.6515903	0.577957521	0.0012038
P55072	VCP	-0.2740707	0.579758167	2.24E-219
O15533;O15533-2;D3YTI9;A8	TAPBP	0.298233	0.579988577	2.00E-14
C9J3L7;C9JZE3;C9JYJ8;Q9BWI	REPIN1	-0.3142948	0.580475271	2.67E-22
P55347;P55347-2;E7EPN6;H0	PKNOX1	0.2976341	0.580745727	7.97E-21
Q14694;Q14694-3;Q14694-2	USP10	0.2975636	0.580834976	7.50E-65
Q13144;E9PC74	EIF2B5	0.6450272	0.583066204	9.50E-150
P46100;P46100-5;P46100-3;F	ATRX	0.6423302	0.585171587	1.82E-37
Q12899;A2AE48	TRIM26	0.293005	0.586613522	1.72E-75
Q9NRP0;D6RH22	OSTC	0.6395111	0.587376032	0.00023698
Q9BZZ5;Q9BZZ5-2;Q9BZZ5-3;	API5	-0.3026924	0.589729118	1.19E-46
O43143	DHX15	0.6309528	0.594091849	9.46E-11
P30508;P30505;E7ERM2;B0S'	HLA-C	0.2860069	0.595535907	2.59E-205
O75475;O75475-2;O75475-3	PSIP1	-0.2615509	0.597291143	1.44E-180
Q9NP74;Q9NP74-2;Q9NP74-3	PALMD	-0.2601852	0.599218133	7.52E-74
P49321;P49321-2;P49321-3;(	NASP	0.2830181	0.599365359	1.32E-103
Q969S3	ZNF622	-0.2596645	0.599953607	1.21E-82
Q9BT78;Q9BT78-2;D6RAX7;D	COPS4	0.6225662	0.600706821	2.06E-42
P34932	HSPA4	0.6216927	0.601397759	2.31E-22
P51571;H7C1C6;A6NLM8	SSR4	0.2799664	0.603286924	6.55E-127
P49643	PRIM2	0.6169701	0.605139244	4.55E-11
Q8N4Q1;Q8N4Q1-2	CHCHD4	-0.2542915	0.607566452	2.83E-76
P53999	SUB1	-0.2538223	0.6082333	3.67E-38
Q01130;J3QL05;J3KP15;B4DN	SRSF2;SFRS2	-0.2533836	0.608857071	3.45E-26
Q9BUF5;K7ESM5	TUBB6	-0.2774086	0.610126878	9.56E-83
O43847;O43847-2;B1AKJ5;H(	NRD1	0.6105423	0.610248342	3.04E-21
Q8WU90;B4DMW2	ZC3H15	-0.2766457	0.610747224	1.36E-51
Q01658	DR1	-0.2511501	0.612037283	6.63E-17
Q99832;F8WAM2;Q99832-3	CCT7	0.6055107	0.614261	2.86E-17
P46781;B5MCT8;C9JM19	RPS9	0.6046066	0.614983231	5.68E-20
Q9Y5U2;E9PL88;C9JDU0;A6N	TSSC4	-0.271431	0.614994757	0.0025834
Q9BUL8;C9J5C3;C9J363;C9J6I	PDCD10	-0.2481594	0.616307137	3.01E-58
P62753;A2A3R7;A2A3R5	RPS6	0.2696705	0.616601605	2.10E-13
Q9NPA8;G3V117;E5RHX8	ENY2	-0.2478867	0.616697193	2.20E-40
P63000;P15153;P60763;P630	RAC1;RAC2;RAC3	0.6013947	0.617552147	0.00035271
P52434;C9JBJ6;C9JLU1;C9JCU	POLR2H	-0.2678013	0.6179589	1.17E-39
Q8WYP5;Q8WYP5-2;Q8WYP5	AHCTF1	0.2663021	0.620985427	1.14E-119
P10599;P10599-2	TXN	-0.2633133	0.621632583	8.70E-10
P19338;H7BY16	NCL	-0.2440872	0.622141914	0
Q8NI22;Q8NI22-2;Q8NI22-3	MCFD2	0.2642956	0.623603278	1.97E-90
P61513;C9J4Z3;M0R0A1;Q6P	RPL37A	-0.2425632	0.624331661	1.96E-77
P31689;B7Z5C0	DNAJA1	0.2633743	0.624806798	3.60E-46
P63010;Q7Z451;P63010-2;K7	AP2B1;AP1B1	-0.2421265	0.624959874	6.28E-93
Q99583	MNT	-0.2591152	0.625077511	2.78E-58
Q9ULU4;B7ZM62;H7C4X9;Q9	ZMYND8	0.5884628	0.627942089	2.70E-89
Q9H211;H3BSY1	CDT1	0.587925	0.628375858	3.84E-23

Q3ZCQ8;Q3ZCQ8-2;M0R0C3;I	TIMM50	0.5865345	0.62949779	2.06E-14
Q8IVL5;D3DNV8	LEPREL1	0.2583141	0.631435219	7.59E-97
P62316;P62316-2	SNRPD2	-0.2375717	0.631527018	7.85E-110
P40855;B7Z6I5;Q5QNY5;P40	PEX19;DCAF8	-0.2511101	0.631669208	3.57E-287
Q9H334;G5E965;H0Y882;Q9H	FOXP1	0.5824089	0.63283168	7.87E-67
P62263	RPS14	-0.2366066	0.632922314	3.61E-66
Q9Y2X3	NOP58	0.2551498	0.635595326	4.58E-37
Q8N556;Q8N556-2	AFAP1	0.2540302	0.637070054	2.11E-99
Q9NS69	TOMM22	0.2538223	0.637344055	1.08E-86
P02545;P02545-3;D6RAQ3;P(	LMNA	0.2534008	0.63789975	9.65E-238
P68371	TUBB4B	0.2533207	0.63800538	0
Q5SSJ5;B0QZK4;Q5SSJ5-3;Q5	HP1BP3	0.5759315	0.638081087	7.45E-08
P32519;P32519-2	ELF1	0.2514782	0.640436899	2.09E-89
Q9UKV3;E7EQT4;Q9UKV3-5	ACIN1	0.2511253	0.640903005	0
P49959;P49959-2;F8W7U8;B:	MRE11A	-0.2394028	0.641362232	3.90E-24
Q9UNF1;Q5H909;Q9UNF1-2;I	MAGED2	0.5713787	0.641781732	1.47E-86
P46782;M0R0F0;M0QZN2;M(	RPS5	-0.228199	0.64513223	5.39E-128
P46778;G3V1B3;M0R181	RPL21	-0.2274857	0.646172667	1.21E-33
P05089;P05089-2;P05089-3	ARG1	-0.2327805	0.646872488	1.60E-25
E5RGW4	NPM1	0.2464828	0.647048574	1.46E-47
Q13435;E9PPJ0;E9PJ04;H0YC	SF3B2	0.2462597	0.647344597	4.12E-149
Q9GZS3;H0YL19;H0YN81;H3B	WDR61	0.2449188	0.649124438	6.05E-103
Q92667;I3L0W0;Q92667-2	AKAP1	0.5609322	0.650306486	4.28E-08
Q8TBX8;Q8TBX8-2;Q8TBX8-3	PIP4K2C	-0.2270107	0.651689179	0.0004405
Q9Y3A6;M0R072;B1AKT3;B1/	TMED5	0.5584869	0.652308554	9.08E-31
Q9BRK5;Q9BRK5-6;Q9BRK5-2	SDF4	-0.2229691	0.652776249	1.52E-37
E9PAV3;F8VZJ2;F8W0W4;H0\	NACA	-0.2249374	0.653423572	2.70E-39
Q8WWI1-3;E9PMS6;Q8WWI1	LMO7	-0.2218475	0.654420242	1.40E-265
Q15233;C9JYS8;Q15233-2;C9	NONO	-0.2210045	0.655657137	1.05E-51
P35606;B4DZI8	COPB2	0.5526848	0.657069184	3.33E-29
P60866;P60866-2;G3XAN0	RPS20	-0.219162	0.658363683	4.17E-20
Q16656;Q96AN2;Q16656-2;C	NRF1	-0.219101	0.658453417	7.63E-26
Q15185;B4DP11;B4DP21	PTGES3	0.2375221	0.658978495	6.43E-52
O43707;D6PXK4;F5GXS2	ACTN4	0.2371426	0.659485776	2.96E-214
Q14157;Q14157-1;Q14157-4;	UBAP2L	-0.2177773	0.660400748	0
Q15029;Q15029-2;K7EJ81	EFTUD2	0.2361412	0.660824832	4.62E-152
Q15019;B5MCX3;Q15019-2;C	SEPT2	-0.2141933	0.662441309	6.66E-48
Q8NAV1	PRPF38A	-0.2161255	0.662833929	1.16E-134
Q16643-2;Q16643;A8MV58;D	DBN1	-0.2109184	0.665199852	1.68E-44
Q9H2P0	ADNP	-0.2140694	0.665867738	2.33E-77
Q12906;Q12906-4;Q12906-5;	ILF3	-0.2121696	0.668675645	3.03E-168
Q5XKP0;K7EIR2;K7EKR0	QIL1;C19orf70	0.5382748	0.66895253	1.83E-20
P62847;P62847-2;E7ETK0;P6	RPS24	-0.2118568	0.669138437	3.37E-17
O15391	YY2	0.5378208	0.669328253	6.29E-29
P25705;K7ERX7;P25705-2;K7	ATP5A1	0.2291451	0.670210479	1.89E-89
O14579;O14579-2;M0QXB4;M	COPE	0.2265778	0.673667664	2.89E-75
Q15293;B7Z1M1	RCN1	-0.2082138	0.67453749	9.32E-253
P19387	POLR2C	-0.1997509	0.674640469	3.12E-24
Q8N6N3;Q8N6N3-2	C1orf52	-0.1992683	0.675049577	3.64E-83
Q9Y3B4	SF3B14	-0.1990223	0.67525821	1.07E-26
O60684;F5H4G7;F5GYL8;O15	KPNA6;KPNA5	0.2253799	0.675283041	1.20E-125
P63208;E5RJR5;E5RGM3;E7EI	SKP1	-0.2073841	0.675769475	1.28E-89
Q9NVA2;D6RGI3;D6RER5;Q9I	SEPT11	-0.1964149	0.677470609	5.18E-42
P07437;Q5JP53;F8VYX6;F8VV	TUBB	0.2233543	0.67801818	0
P26196	DDX6	-0.194397	0.679184824	2.45E-78
P62306;F8W0W6	SNRPF	-0.2042351	0.68045324	1.66E-50
P32119;A6NIW5	PRDX2	-0.1914654	0.681678092	1.08E-14
Q14966;Q14966-3;Q14966-5;	ZNF638	0.2198544	0.682754148	2.13E-154
P42677;Q5T4L4	RPS27	-0.1899223	0.682991823	1.23E-15
O60341;O60341-2;F6S0T5	KDM1A	-0.1889305	0.683836757	6.32E-107
Q9NZI7;Q9NZI7-4	UBP1	-0.185009	0.687181362	6.98E-44
Q92541	RTF1	-0.1844826	0.687630814	9.76E-27
Q9HC35;B5MCW9;B5MBZ0;F	EML4	-0.1841965	0.687875128	1.03E-17
Q15459;E9PAW1	SF3A1	-0.183754	0.688253064	1.00E-67
Q9NWV8;M0QY17;Q9NWV8-	BABAM1	-0.1826572	0.689190095	6.66E-62
Q9Y232;Q9Y232-2;Q9Y232-3;	CDYL	-0.1813889	0.690274387	1.17E-27

Q13428;Q13428-3;Q13428-2;	TCOF1	0.2136574	0.691170133	2.11E-284
O15156;O15156-2	ZBTB7B	-0.179287	0.692072612	2.41E-12
P29692;E9PK01;P29692-2;P2	EEF1D	-0.1943417	0.695248035	3.58E-112
P62879;C9JIS1;C9JXA5;C9JZN	GNB2	-0.1683807	0.701430845	1.35E-26
Q07021;I3L3Q7;I3L3B0	C1QBP	-0.1900749	0.701664989	1.01E-231
Q9UI10;E7ERK9;F8W8L6	EIF2B4	0.4988422	0.701889949	8.36E-58
O95365	ZBTB7A	0.4979591	0.702634327	3.46E-74
O95049;F5H2X0;K7ESC0;F5H4	TJP3	0.4961472	0.704162562	0.0012097
Q12800;Q12800-4;F8VWL0;C	TFCP2	-0.1879387	0.704885813	1.86E-60
P41091;Q2VIR3;Q2VIR3-2;F8\	EIF2S3;EIF2S3L	0.2022114	0.706814808	1.71E-33
O60841	EIF5B	0.2020473	0.707039932	0
Q9NQZ2	UTP3	0.4919624	0.707696539	1.54E-119
O43447;C9JQD4;A6NM32;H0	PPIH	-0.1581135	0.710282421	6.60E-07
Q01664;I3L254	TFAP4	-0.183712	0.711274009	0
Q96RL1;Q96RL1-3;F8VQY2;Q	UIMC1	-0.15555	0.712498604	6.82E-50
Q96D15	RCN3	-0.182869	0.712550634	1.66E-169
P11021	HSPA5	-0.1811752	0.715117872	0
Q96QA5;J3KRG2	GSDMA	-0.1520653	0.715515122	5.90E-28
O43823	AKAP8	0.4812832	0.716743533	4.39E-21
P09661;H0YMA0;H0YLR3	SNRPA1	-0.1797256	0.717317621	1.78E-144
O43491;E9PHY5;E9PPD9;O43	EPB41L2	0.1933327	0.719036732	4.72E-100
P01040;C9J0E4	CSTA	-0.1468849	0.720007658	1.01E-36
O43865;O43865-2;Q96HN2;C	AHCYL1;AHCYL2	-0.1448536	0.721771927	1.51E-11
Q13283;F5H4D6	G3BP1	-0.1731148	0.72737914	4.72E-194
Q15059;Q15059-2	BRD3	0.1854286	0.729977901	0
Q01105-2;Q01105-3;Q5VXV2	SET	-0.1351833	0.730191004	0
Q92896;Q92896-2;H3BM42;C	GLG1	0.4648018	0.730783804	4.22E-28
P13010	XRCC5	0.464716	0.730857164	1.51E-54
Q9H0E9-2;Q9H0E9;H7C128;H	BRD8	0.4645233	0.731021823	2.46E-56
Q9NYF8;Q9NYF8-2;Q9NYF8-4	BCLAF1	-0.170372	0.73156749	4.46E-247
O00303;H0YDT6;B4DEW9;B3	EIF3F	-0.1333313	0.731807168	9.97E-13
P11142;E9PKE3;P11142-2;E9I	HSPA8	-0.1691494	0.73343707	2.81E-235
Q13263;Q13263-2;M0R0K9	TRIM28	-0.1307793	0.734036128	8.18E-59
Q8N9T8;H0YFD2;D3YTE0;Q8N	KRI1	-0.1306553	0.734144468	3.43E-94
P39687;H0YN26	ANP32A	0.1798382	0.737749929	1.06E-182
Q9BUJ2;Q9BUJ2-4;B7Z4B8;Q9	HNRNPUL1	0.179718	0.737917282	1.85E-215
P25398	RPS12	-0.1661968	0.737958567	3.57E-65
P15924;P15924-2	DSP	0.1795502	0.738151065	1.77E-227
O75925;B3KSY9	PIAS1	0.4558144	0.738478594	6.88E-29
P52597	HNRNPF	0.1790733	0.738815355	2.38E-218
Q9Y605	MRFAP1	-0.1652622	0.73939169	2.74E-91
P31151;Q86SG5	S100A7;S100A7A	-0.1234493	0.740450558	1.26E-08
Q92572;F5H459	AP3S1	-0.1640377	0.741270743	1.68E-79
P23497;P23497-4;P23497-2;F	SP100	0.4514961	0.742185143	3.55E-98
P17693;Q5RJ85	HLA-G	0.4498177	0.743627473	1.26E-09
Q6QNY0	BLOC1S3	-0.1163673	0.746665195	4.09E-20
Q9Y2D5-4;C9JVY5;Q9Y2D5;Q	AKAP2	-0.1162395	0.746777489	1.73E-80
O14929;O14929-2	HAT1	0.4433899	0.749159221	0.00014558
P12956;B1AHC9;B1AHC8;F5H	XRCC6	0.1704025	0.750928353	1.40E-99
Q9Y2W2;F5H721	WBP11	-0.1571178	0.751918159	0
P14316;D6RB34;D6R9N5;D6R	IRF2;IRF1	-0.1070766	0.754843025	6.84E-25
P06702	S100A9	0.4365559	0.755054784	2.64E-25
Q9Y295	DRG1	-0.1546211	0.755771541	3.27E-179
Q53F19;Q53F19-2	C17orf85	-0.1058178	0.755953227	1.50E-30
P22415;E9PME6;Q7Z5Y1;B1A	USF1;usf1-bd	0.4351463	0.756272544	1.82E-23
P14635;H0YA62;Q5TZP9;E9P	CCNB1	-0.105402	0.756320041	8.17E-06
P15170;H3BR35;P15170-2;J3	GSPT1	-0.1045055	0.757111065	4.52E-11
Q04837;C9K0U8;E7EUY5	SSBP1	-0.1027813	0.758633239	4.53E-22
O00472;B4DNK7	ELL2	0.4317207	0.759234598	2.35E-23
P49458;E9PE20;P49458-2	SRP9	-0.1518097	0.760117922	2.41E-46
P62891;Q59GN2	RPL39;RPL39P5	-0.1513119	0.760888327	4.99E-05
P62834;P61224;P61224-2;P6	RAP1A;RAP1B	0.4290524	0.761544353	8.18E-18
P09012;M0R268;M0QZG7	SNRPA	-0.1497078	0.763372351	1.57E-148
Q6UX04;Q6UX04-2	CWC27	0.4198265	0.769546524	1.03E-77
P42167;G5E972;P42167-2;H0	TMPO	0.1557102	0.771592665	1.92E-88
P12270	TPR	0.4158363	0.773015132	3.44E-09

P21333;Q5HY54;P21333-2	FLNA	-0.1433678	0.773213938	0
Q9UFC0;H7C5S6	LRWD1	-0.08474731	0.774608806	4.44E-38
O95831;O95831-3;O95831-2	AIFM1	0.1535683	0.774619235	2.51E-109
P38646	HSPA9	-0.1422997	0.774875611	7.68E-281
P62854;Q5JNZ5;F8VZW7	RPS26;RPS26P11	0.1528549	0.775627956	7.28E-35
Q9UBI6	GNG12	-0.08359718	0.775630985	5.12E-11
O43818	RRP9	0.1526604	0.775903128	1.64E-219
P63272;D3DTZ5;J3QSB9	SUPT4H1	-0.1409073	0.777043267	2.19E-08
P29084;E5RH41	GTF2E2	-0.1407013	0.77736411	1.53E-163
Q96DI7;B4DQJ1	SNRNP40	0.1508312	0.778491652	9.66E-88
O14974;O14974-4;O14974-3;	PPP1R12A	-0.1394272	0.779349421	0
Q2KHR3;Q2KHR3-2;H0YCQ7	QSER1	0.4085445	0.77936548	7.60E-29
Q13427;C9JN15;Q13427-2;C9	PPIG	-0.07910538	0.779626787	1.95E-18
P55735;P55735-2;B4DXJ1	SEC13	0.405098	0.782372232	4.64E-11
Q9H6Y2;G3V1J0	WDR55	0.1477699	0.782829344	4.89E-86
P62829;J3KT29;C9JD32;B9ZVI	RPL23	-0.1369247	0.783252896	1.23E-69
P26641;B4DTG2;E7EMT2	EEF1G	0.4038734	0.783441272	1.08E-81
O75821;K7EL20;K7EP16;K7EN	EIF3G	-0.07070732	0.787113059	6.78E-61
P18583-6;P18583;P18583-3;F	SON	0.1444874	0.787488048	1.40E-50
P35250;P35250-2;H7C5Q7;F8	RFC2	-0.07006073	0.787690276	3.86E-12
Q76FK4;F8WE42;Q76FK4-3;F!	NOL8	0.3980503	0.788530603	5.82E-37
O00505	KPNA3	0.1403503	0.793370307	5.73E-99
Q12948;Q99958;O43638	FOXC1;FOXC2;FOXS1	0.3907738	0.794902868	8.26E-12
Q92879;Q92879-2;Q92879-3;	CELF1	-0.06196213	0.794929736	2.98E-36
P62081;B5MCP9	RPS7	-0.1286793	0.796152878	1.89E-36
Q14160;Q14160-3;Q14160-2	SCRIB	0.3885307	0.796869946	2.74E-84
Q9NW82;D6RIW8	WDR70	0.137352	0.7976409	3.61E-72
Q96AQ6;B4E1J0;F5H2F6;Q96	PBXIP1	-0.0588131	0.797749515	4.03E-21
Q9BW71;Q9BW71-2	HIRIP3	0.1361847	0.799305145	1.48E-251
P36873;F8VYE8;P36873-2;F8\	PPP1CC	-0.05666733	0.799672443	0
Q15393;Q15393-3	SF3B3	0.3845291	0.80038244	1.18E-56
P37275;G3V1R3;F5H4I8;Q5V2	ZEB1	0.3845177	0.800392491	9.72E-68
Q9UI10-2;Q9UI10-3	EIF2B4	0.383419	0.801357549	7.26E-31
Q9GZL7	WDR12	-0.05452156	0.801596586	1.40E-23
Q14697;Q14697-2;F5H6X6;E9	GANAB	-0.1250935	0.801780519	1.49E-153
Q8NEM2	SHCBP1	0.3827801	0.801918964	9.00E-58
P32322;B4DMU0;E2QRB3;P3	PYCR1	-0.053339	0.802657518	6.45E-28
Q9GZT3;H0YJ40;G3V4X6;J3KN	SLIRP	-0.1238022	0.803809606	4.24E-31
Q99873;E9PKG1;Q99873-3;Q	PRMT1	-0.1236191	0.804097442	2.12E-65
Q96A33;Q96A33-2	CCDC47	0.132534	0.804515842	0
Q96C57;E7ENF1;F5H7W8;F5H	C12orf43	-0.1226463	0.805627016	1.51E-112
Q92769;B3KRS5;J3KPW7	HDAC2	0.3769188	0.807073635	8.66E-41
Q09028;Q09028-3;Q09028-4;	RBBP4	0.1303215	0.807678088	1.28E-54
Q9H3Q1;B3KUS7;J3KRZ9	CDC42EP4	-0.1209011	0.808373113	1.84E-178
Q15904;H7C2Y8;A6QRJ1;A6N	ATP6AP1	0.3735142	0.810071673	5.59E-63
O00267;O00267-2	SUPT5H	0.12784	0.811228451	0
Q7Z4V5;Q7Z4V5-2;K7EQZ6;I3	HDGFRP2	0.1271782	0.812176056	1.54E-111
P46777	RPL5	0.1246338	0.815821559	7.05E-142
P46060;F8W7I9	RANGAP1	0.1243114	0.816283682	0
P09543;P09543-2	CNP	0.36549	0.817148595	2.44E-20
Q12874;E7EUT8	SF3A3	0.3649082	0.817662246	6.05E-40
O00193;E9PRZ9;E3W975;E9P	SMAP;C11orf58	-0.03643036	0.817866019	3.32E-297
P24752;G3XAB4;H0YEL7;E9PI	ACAT1	0.3641987	0.818288839	6.38E-29
Q13148;Q13148-2;B1AKP7;G	TARDBP	0.1227188	0.818567888	2.52E-48
Q14978-3;Q14978	NOLC1	0.1224747	0.818918178	1.97E-122
Q9NRY2;Q9NRY2-2	INIP	-0.03475189	0.819379566	0.00033232
Q15007;Q15007-2	WTAP	-0.03290367	0.821046967	8.90E-65
Q96QC0;F5H5K4	PPP1R10	-0.0323391	0.821556468	1.74E-35
Q9H814	PHAX	0.3592911	0.822625929	1.78E-08
P43307;C9J3L8;C9J5W0;E9PA	SSR1	0.1195011	0.823187486	1.94E-71
Q9BSD7;Q5TDF0	NTPCR	-0.03030396	0.823393708	3.65E-11
O43852-4;O43852-2;O43852-	CALU	-0.02959633	0.82403275	1.79E-124
P51148;P51148-2;K7ENY4;K7	RAB5C	-0.02935982	0.824246365	6.08E-12
Q9NPL8;C9JU35	TIMMDC1	0.3566208	0.824988079	2.42E-07
Q9UN86;Q9UN86-2;D6RAC7;	G3BP2	-0.1085281	0.82790774	7.64E-87
P10809	HSPD1	-0.107933	0.828850074	1.66E-108

Q6SPF0;E9PIW9	SAMD1	-0.02071953	0.832058982	1.41E-42
Q06587;Q06587-2	RING1	0.1131725	0.832291089	2.05E-59
P18621;J3QQT2;J3KRX5;J3QL	RPL17	0.1131077	0.832384494	2.67E-78
P23258;Q9NRH3;K7EKE5;K7E	TUBG1;TUBG2	0.3478889	0.83272327	8.13E-23
P05388;Q3B7A4;F8VWS0;F8V	RPLP0;RPLP0P6	0.1113586	0.83490456	7.95E-122
P35269;M0R0R9;E7EUG6;M0	GTF2F1	-0.1036682	0.835610594	1.15E-245
Q7Z6M4;B4DKD5;H7C316;C9	MTERFD2	0.3444862	0.835742031	7.62E-08
P61353;K7ELC7;K7EQQ9	RPL27	-0.1033344	0.836140224	2.20E-17
Q9BVI4;F5H303	NOC4L	0.3437958	0.836354879	1.37E-32
P30101;G5EA52	PDIA3	0.1095219	0.837552868	3.38E-133
P19784;H3BSA1	CSNK2A2	0.1088867	0.838469068	0
P17544;P17544-2;P17544-4;F	ATF7	-0.01325798	0.838819179	1.77E-15
O94776	MTA2	0.3406811	0.839120697	8.01E-71
P04406;E7EUT4;E7EUT5	GAPDH	0.1074505	0.840541641	6.88E-101
Q00610;Q00610-2	CLTC	0.1071053	0.841039994	2.53E-271
P62249;M0R3H0;M0R210;Q6	RPS16	-0.09998703	0.841455728	2.51E-15
P40425;F8VSK3;F8VNW9;F8V	PBX2	-0.00717926	0.844335356	7.44E-56
P49770	EIF2B2	-0.00576973	0.845615546	1.68E-34
P40938;P40938-2	RFC3	-0.004699707	0.846587655	2.96E-15
Q9P289;Q8NBY1;B4E0Y9;Q9F	MST4	0.1014442	0.849220837	3.89E-153
P31944	CASP14	-0.00179863	0.849224434	1.21E-39
P60842;J3KT12;P60842-2;J3K	EIF4A1	0.09967422	0.851782108	2.49E-102
Q8IXH7;Q8IXH7-4	NELFCD	0.001096725	0.851857696	4.82E-27
Q9NQG5	RPRD1B	0.3263531	0.851868894	8.98E-111
Q9BQ70;H3BS87;H3BMJ8;H3	TCF25	0.001382828	0.85211799	8.49E-07
P33991;J3KPV4	MCM4	0.0986557	0.853256654	9.22E-136
Q86UE4;E5RJU9	MTDH	0.09711838	0.855483248	2.09E-168
P06454;P06454-2;B8ZZQ6	PTMA	0.09698486	0.855676679	2.73E-05
Q53EL6;Q53EL6-2	PDCD4	0.09594154	0.857188504	4.46E-102
Q00839;Q00839-2	HNRNPU	0.09564781	0.857614232	3.11E-264
P14406;D6RIE3;D6RGV5;H0U	COX7A2	0.009567261	0.859570844	2.99E-46
Q02413	DSG1	-0.08828735	0.860089546	1.69E-38
Q5QJE6;J3KP30	DNTTIP2	0.09380341	0.86028841	1.08E-152
Q9BPZ3;D6RA77	PAIP2	0.01086807	0.860756552	6.17E-18
P09132;P09132-2	SRP19	0.01092911	0.860812194	8.40E-50
O95218;O95218-2	ZRANB2	0.09309387	0.861317581	5.56E-160
P52292	KPNA2	-0.08735085	0.861584619	1.13E-227
Q9Y6E0-2;B4DR80;Q9Y6E0;H	STK24	0.0125618	0.862300876	8.46E-101
Q969G3;K7EMQ8;C0IMW7;C	SMARCE1	0.01316643	0.8628523	1.00E-41
Q9BRX2	PELO	-0.08617401	0.86346406	1.19E-242
Q92499	DDX1	0.01477242	0.864317288	1.45E-43
P55795	HNRNPH2	0.01706314	0.866407704	4.41E-95
Q6P1J9	CDC73	0.08864784	0.867771796	4.19E-52
O95400	CD2BP2	0.02024269	0.869310768	1.00E-58
Q6P5R6;C9JYQ9;H0Y8C2	RPL22L1	0.02033997	0.869399612	8.38E-16
O94842;B4DPY8	TOX4	0.0225029	0.871375508	7.02E-63
Q9NYB0	TERF2IP	0.08602524	0.871583145	3.22E-43
P17987;E7EQR6;F5H282;E7EF	TCP1	0.3034401	0.87233481	3.87E-37
P08107;P08107-2;F8VZJ4;E7E	HSPA1A	-0.07895279	0.875013107	4.14E-113
P05198;H0YJS4;G3V4T5	EIF2S1	0.2996445	0.875733718	7.69E-49
Q9HCY8	S100A14	0.02786446	0.876276867	3.33E-96
P62314;J3QLI9	SNRPD1	-0.07797623	0.876577046	3.16E-227
P78347;P78347-2;P78347-4;F	GTF2I	0.08144569	0.878245556	1.05E-175
Q08554;Q08554-2	DSC1	0.03006172	0.878286918	1.52E-45
P40424-2;P40424;H0YLF5;P4(	PBX1	-0.07606888	0.879632997	7.99E-105
P18887;F5H8D7	XRCC1	-0.07545853	0.880611283	2.62E-68
O60237;F8W8M3;H7C4R6;O6	PPP1R12B	0.03292274	0.880905346	3.38E-19
P05455;E9PFH8;E7ERC4;E9P(	SSB	-0.07467461	0.881868036	7.74E-176
Q6ZRS2;Q6ZRS2-3;Q6ZRS2-2	SRCAP	0.03495979	0.882770462	0.0012458
P61254;Q9UNX3;J3KTJ8;J3QR	RPL26;RPL26L1;KRB	0.07590866	0.886312428	2.57E-11
Q8WYA6;B4DE16;Q8WYA6-3;	CTNNBL1	0.0737381	0.889477974	0
P17275	JUNB	0.2828369	0.890811275	3.21E-51
P43243;A8MXP9;D6REM6;D6	MATR3	-0.06845856	0.891843658	9.40E-84
P78316;E9PFK5;P78316-2	NOP14	0.2797012	0.893628745	2.15E-29
P47712;E7EU42	PLA2G4A	0.2795887	0.893729884	5.53E-51
O95782;O95782-2	AP2A1	0.04842377	0.89511391	4.05E-50

Q99614;H0YB37	TTC1	0.275526	0.897382309	4.16E-24
Q5SRQ6;P67870;Q5SRQ3	CSNK2B;CSNK2B-LY(	0.06723976	0.898965481	1.30E-105
O96019;O96019-2;H7C5S0	ACTL6A	-0.06315994	0.900360563	1.17E-52
P14314;P14314-2;K7ELL7;K7E	PRKCSH	-0.06185532	0.902459397	5.31E-138
Q14839;F5GWX5;Q14839-2	CHD4	0.2682076	0.903967257	1.05E-73
Q96RT1;B4DIP2;Q96RT1-7;Q9	ERBB2IP	0.2647552	0.907075848	0.00093425
P62906	RPL10A	-0.05830574	0.908173233	1.49E-113
P35221;G3XAM7;P35221-2;F(	CTNNA1	0.2627373	0.908893577	1.78E-78
Q6UN15;Q6UN15-4;Q6UN15·	FIP1L1	0.06359482	0.909052708	4.70E-120
P39880;P39880-6;P39880-4;F	CUX1	0.258194	0.912987776	3.02E-48
Q9H8N7;E5RH90;E5RG59;E5F	ZNF395	0.2578506	0.913297256	2.00E-07
Q969X6;Q969X6-2;H3BSH7;Q	CIRH1A	0.2563629	0.91463849	1.04E-50
P61247;D6RG13;D6RAT0;D6R	RPS3A	-0.05405235	0.915026249	5.74E-44
Q9NS91;F8WE49	RAD18	0.2557278	0.915211168	2.04E-31
O60506;O60506-4;O60506-3;	SYNCRIP	0.05546951	0.916185819	7.21E-104
P61201;B4DIH5;P61201-2	COPS2	0.2543106	0.916489103	2.16E-53
Q8TAQ2;Q8TAQ2-2;F8VZW6;	SMARCC2	0.07325935	0.917947149	3.64E-64
Q9HAV0	GNB4	0.07330322	0.917987547	2.17E-18
Q96EY1;Q96EY1-2;E7ES32	DNAJA3	0.07332039	0.918003355	5.92E-40
Q9H307;Q9H307-2	PNN	0.0536499	0.918851701	2.87E-74
P49790;F6QR24	NUP153	0.2513924	0.919121328	3.18E-105
Q9NV56	MRGBP	0.07480431	0.919369978	6.89E-21
Q5T749	KPRP	0.2488518	0.921413635	3.00E-25
P55036;Q5VWC4;P55036-2;A	PSMD4	0.07765198	0.921993223	4.63E-56
P62826;B5MDF5;F5H018;J3K(	RAN	0.05109787	0.922592175	4.30E-32
P68104;Q5VTE0	EEF1A1;EEF1A1P5	0.0483284	0.926653278	1.71E-50
P80303;P80303-2;J3KQU0;H0	NUCB2	0.2430058	0.926690799	5.40E-49
Q12905	ILF2	-0.04460144	0.930275356	1.68E-39
Q9Y2W1	THRAP3	-0.04390144	0.931405894	3.96E-216
P62136;P62136-2;A6NNR3;E9	PPP1CA	0.23773	0.931455937	0
Q9UBU8;H0YMJ0;H0YLJ3;Q9(	MORF4L1	0.08799934	0.931532044	2.43E-19
Q71UM5;C9JLI6;H0YMV8	RPS27L	0.044981	0.931564386	5.16E-19
P10155;Q5LJA0;P10155-3;P1(	TROVE2	0.2369499	0.932160756	1.14E-33
O95251;O95251-4;E7EUP3;G:	KAT7	0.08899307	0.932448663	4.49E-43
Q9UBD5;Q9UBD5-2;Q9UBD5·	ORC3	0.2353077	0.933644668	2.35E-60
Q9H1E5;E9PIN7	TMX4	0.233326	0.935435665	2.31E-16
Q8IWS0;E9PC97;B4E0G4;Q5J(	PHF6	-0.04107285	0.93597564	1.53E-163
Q8WWY3;E7EVX8;Q8WWY3-:	PRPF31	0.2314587	0.937123536	1.81E-33
Q5JRA6;Q5JRA6-3;Q5JRA6-2;(	MIA3	0.2309189	0.937611502	3.27E-05
Q14257;F8WCY5;A8MXP8	RCN2	0.09555626	0.938504759	9.75E-22
O43684;J3QT28;O43684-2;B4	BUB3	-0.03789139	0.941117962	4.30E-47
Q92542;Q5T205;H0Y6T7;H0Y	NCSTN	0.09945869	0.94210739	0.00038474
P07237;H7BZ94;I3L2P8;F5H8.	P4HB	-0.03500938	0.945778391	1.85E-86
P08579	SNRPB2	-0.03443909	0.946700832	4.84E-60
Q9UJX3;Q9UJX3-2;F8VZ62	ANAPC7	0.2172699	0.949957625	8.53E-31
Q15853;M0QXT0;Q6YI47;Q1!	USF2	0.2171116	0.9501009	1.12E-12
P62424;Q5T8U2	RPL7A	-0.03158188	0.951323343	5.17E-100
Q08J23;Q08J23-2;G3V1R4	NSUN2	0.1108513	0.95263126	2.35E-53
O75534;E9PLT0;O75534-2;O7	CSDE1	0.2128601	0.953949192	7.39E-08
Q14444;G3V153;Q14444-2;E!	CAPRIN1	0.02790451	0.956654631	1.69E-59
O43390;O43390-2;E7ETM7;Q	HNRNPR	0.1181087	0.959339741	1.51E-35
Q01105	SET	-0.02621078	0.960017234	0
Q9P258	RCC2	0.02509117	0.960793023	1.33E-146
P80723	BASP1	0.1992073	0.966314048	1.30E-06
Q9Y657	SPIN1	0.1258678	0.966515084	2.14E-18
Q9UHR5;J3QQJ0;Q9UHR5-2;J	SAP30BP	-0.02173996	0.967257583	2.13E-83
Q14119;J9JIC7;J3QSH4	VEZF1	0.1971569	0.968171795	3.14E-14
Q9BUQ8	DDX23	0.1279831	0.968471689	3.27E-05
P29083	GTF2E1	-0.02049637	0.969272042	2.58E-191
P05386	RPLP1	-0.019701	0.970560535	5.25E-40
Q6UWP8	SBSN	0.1303902	0.970698461	1.75E-19
Q9ULX3;H3BUR4	NOB1	0.131197	0.971444888	1.04E-85
Q9H2K8;G3V1Q8	TAOK3	0.1923866	0.972494515	1.08E-31
P49736;H0Y8E6	MCM2	0.1908379	0.973898154	1.10E-67
P62140;E7ETD8	PPP1CB	0.01555634	0.974825863	0
Q96CB9;Q96CB9-4	NSUN4	0.1359119	0.975807463	3.24E-23

Q02543;M0R0P7;M0R3D6;M	RPL18A	-0.01609612	0.976401378	9.44E-14
P60059	SEC61G	0.1872177	0.977179379	1.95E-05
P62269;J3JS69	RPS18	-0.01545906	0.97743371	6.71E-26
P61011;P61011-2;G3V4F7	SRP54	0.01377869	0.977443101	5.85E-231
Q96HY6;Q96HY6-2	DDRGK1	0.1384392	0.978146123	1.84E-48
Q14566	MCM6	-0.01407623	0.979674678	8.70E-93
P68400;E7EU96;P68400-2	CSNK2A1	0.011343	0.981029554	0
P11532;P11532-3;P11532-2;F	DMD	-0.01256561	0.982122925	0.0010488
Q9Y4X5;H3BSK4;H3BNB9	ARIH1	0.145916	0.985066052	3.35E-46
P12004	PCNA	0.1782207	0.985335591	1.18E-22
Q99733;F5HFY4;C9JZI7;H0YCI	NAP1L4;NAP1L4b	0.00838089	0.985391662	5.72E-126
Q96B36;Q96B36-2;J3KPM3	AKT1S1	0.1772156	0.986246943	5.78E-12
Q7L014	DDX46	0.007551193	0.986613586	2.39E-203
Q9Y305;C9J7L8;Q9Y305-3;Q9	ACOT9	0.176527	0.986871238	1.18E-09
Q15287;H3BV80;H3BMM9;H:	RNPS1	-0.009506226	0.987081736	1.66E-34
Q9Y6H1;Q5T1J5	CHCHD2;CHCHD2P9	-0.009208679	0.987564044	4.54E-81
P0C0S5;Q71UI9;Q71UI9-3;Q7	H2AFZ;H2AFV	-0.009002686	0.987897952	1.03E-13
P62917;E9PKZ0;G3V1A1;E9PI	RPL8	-0.008401871	0.988871863	3.54E-89
H7BZJ3	PDIA3	-0.008041382	0.989456217	4.47E-27
Q9H3P7	ACBD3	0.173336	0.989764539	2.23E-52
P62308;Q49AN9;F5H013;A8M	SNRPG	-0.007591248	0.990185895	1.00E-32
P23396;J3KN86;E9PPU1;E9PL	RPS3	-0.00718689	0.990841376	2.15E-87
P62280;M0QZC5;M0R1H5	RPS11	0.004558563	0.991021179	1.80E-42
O75128;O75128-2;H7C1N2;O	COBL	0.1715088	0.991421375	3.53E-17
Q9H0A0;E7ESU4	NAT10	0.1534367	0.992027714	1.29E-87
P33778;Q16778;Q99877;Q93	HIST1H2BB;HIST2H2	-0.004795074	0.994718717	1.27E-70
P06576;F8VPV9;H0YH81;F8W	ATP5B	0.1674309	0.995119114	5.32E-143
P62995;P62995-3;H7BXF3	TRA2B	0.1653748	0.996983594	1.95E-18
O75152;E9PQ61	ZC3H11A	0.1645851	0.997699642	2.98E-12
P83731;C9JXB8;C9JNW5	RPL24	-0.001537323	1	1.39E-43
P62244;I3L3P7;I3L246;H3BN9	RPS15A	0.1620483	1	6.31E-19

Appendix 3 (Chapter 2)

Identification and quantification of interacting protein groups for bait (H2A/B S112 GlcNAc dimer) versus control (wt H2A/B dimer) samples. Statistically significant interacting partners are denoted with a '+'

Majority Protein Ids	Gene names	log2(Bait/Control)	Significance B value	Statistically Significant Interactor	PEP
P01834	IGKC	6.802614	5.06E-80	+	0
P05109	S100A8	6.20429	7.85E-67	+	4.87E-28
P02647;F8W696	APOA1	5.482416	1.58E-52	+	3.34E-92
P06702	S100A9	4.830589	3.99E-41	+	5.18E-63
P51858;A8K8G0;P51858-2;Q5	HDGF	-4.617218	2.85E-40	+	4.42E-91
P61626;F8VV32	LYZ	3.742329	2.78E-25	+	2.66E-22
Q7Z7G8;Q7Z7G8-4;Q7Z7G8-3	VPS13B	-3.079212	6.48E-19	+	0.0010471
P25311;C9JEV0	AZGP1	3.200577	7.01E-19	+	7.20E-40
P14618;P14618-2;H3BQ34;H3	PKM;PKM2	3.066269	1.46E-15	+	1.10E-18
P17275	JUNB	-3.41736	1.38E-11	+	1.79E-58
Q8IWA0	WDR75	-3.254229	1.25E-10	+	4.37E-59
P02790	HPX	2.225679	7.75E-10	+	1.07E-36
P33778;Q16778;Q99877;Q93	HIST1H2BB;HIST2H2	2.122673	4.57E-09	+	1.83E-60
Q08554;Q08554-2	DSC1	-1.945415	1.71E-08	+	2.32E-38
Q5T749	KPRP	-1.922817	2.48E-08	+	3.95E-52
Q00341;Q00341-2;H7C0A4;H	HDLBP	-2.654352	1.67E-07	+	6.15E-32
P40424-2;P40424;H0YKH1;HC	PBX1	-2.627068	2.24E-07	+	2.20E-22
Q9Y2Z9;G3V2L5;G3V2W8;G3	COQ6	-2.59762	3.06E-07	+	0.010186
Q99583	MNT	-2.459705	1.27E-06	+	1.15E-31
Q02413	DSG1	-1.635183	2.02E-06	+	2.31E-87
P61978;P61978-2;Q5T6W5;P	HNRNPK	-1.573532	4.76E-06	+	8.40E-204
Q14151	SAFB2	-2.271959	7.89E-06	+	6.33E-67
O00148;Q13838;Q8N5M0;Q1	DDX39A;DDX39B	-1.527676	8.83E-06	+	8.86E-60
P31151;Q86SG5	S100A7;S100A7A	1.595768	1.14E-05	+	4.11E-19
P12273	PIP	1.627232	1.85E-05	+	3.89E-22
Q05519;Q05519-2;Q5T760;Q	SRSF11	-1.435543	2.91E-05	+	3.66E-15
Q14247;Q14247-3;Q14247-2	CTTN	-1.395098	4.81E-05	+	1.15E-27
Q9UI10-2;Q9UI10-3;Q9UI10;E	EIF2B4	1.532175	5.40E-05	+	1.55E-41
Q13247;Q13247-3	SRSF6	-2.023279	7.17E-05	+	8.21E-16
Q8N684;F5H669;Q8N684-2;C	CPSF7	-2.014002	7.75E-05	+	1.05E-09
Q9UHX1-4;Q9UHX1-6;Q9UHX	PUF60	-1.355198	7.80E-05	+	1.13E-100
O43809;H3BND3;H3BV41	NUDT21	-1.269453	0.000211246	+	2.59E-44
Q92979	EMG1	1.391155	0.000237676	+	9.29E-13
Q9H2K8	TAOK3	-1.866413	0.000255536	+	8.70E-24
P63167;Q96FJ2	DYNLL1;DYNLL2	-1.228333	0.000333847	+	2.61E-73
P01617;P01614;P06309;P063	10	-1.200989	0.000449334	+	3.86E-46
P35321	SPRR1A	1.307377	0.000540413	+	6.04E-36
P61981	YWHAG	1.250254	0.000618282	+	1.17E-114
P35908	KRT2	-1.142862	0.000828924	+	0
P04792;F8WE04	HSPB1	1.258228	0.00085738	+	1.18E-07
Q9Y450;B7Z524;H0YDX7;J3Q	HBS1L	-1.693838	0.000928501	+	2.71E-48
Q15517;Q2L6G8;G8JLG2	CDSN	-1.689846	0.000955361	+	0.00025876
P14923	JUP	-1.128023	0.000965157	+	1.03E-76
P27816;P27816-6;E7EVA0;P2	MAP4	-1.11367	0.001116392	+	4.84E-30
Q09161	NCBP1	-1.590069	0.001911121		1.49E-13
P0C0L5;P0C0L4;P0C0L4-2;F8V	C4B;C4A	1.120478	0.002886583		1.71E-34
P18124;A8MUD9	RPL7	1.070112	0.003500857		3.35E-34
Q9BUL8;C9J363;C9J5C3;C9J6I	PDCD10	-0.9940052	0.003533966		9.19E-46
F5GWP8	JUP	-0.9869232	0.003770468		1.14E-104
Q9UKS6;E9PIY1	PACSIN3	-0.9711704	0.00434891		8.48E-114
P45880;B4DKM5;P45880-2;P4	VDAC2	1.033531	0.004836838		1.06E-06
Q14697;Q14697-2;F5H6X6;E9	GANAB	-1.406168	0.006224038		7.21E-80
E9PLD3;E9PRG8	C11orf48	1.021023	0.006450178		3.55E-05
P05114;A6NL93;A6NEL0	HMGN1	0.9899445	0.008190749		1.02E-07
P01024	C3	0.96171	0.008871764		7.83E-138
P24752;G3XAB4;H0YEL7;E9PI	ACAT1	-1.344604	0.008986795		1.85E-38
Q9Y3F4;B0AZV0;B4DNJ6;H0Y	STRAP	-1.334658	0.00952387		3.22E-31
P63272;J3QR04;J3KSQ6	SUPT4H1	-0.8622074	0.011088568		1.30E-16
P53985;Q5T8R3;Q49A45;Q5T	SLC16A1	0.9318581	0.012601883		0.012637
P40855;B7Z6I5;Q5QNY5;P40	PEX19;DCAF8	-1.284887	0.012664478		1.55E-108
P49959;P49959-2;F8W7U8;B	MRE11A	-1.238564	0.016378155		2.18E-21

Q9NVI1;F8W7R3;Q9NVI1-2;Q	FANCI	-1.234787	0.01671938	4.16E-09
Q8WVV9;Q5JB52;B7WPG3;Q	HNRNPLL;HNRPLL	-1.230684	0.017097134	4.65E-41
Q9NZT1	CALML5	-1.229403	0.017216674	1.57E-34
P63244;D6RFX4;H0YAF8;D6R	GNB2L1	0.8806419	0.018117663	1.30E-07
P43243;A8MXP9;D6REM6;D6	MATR3	-0.7845535	0.020465681	1.48E-64
P31943;E9PCY7;G8JLB6;D6RI	HNRNPH1	-0.7810822	0.021012143	1.37E-87
P07237;H7BZ94;I3L2P8;F5H8	P4HB	-0.7779045	0.021523468	3.53E-149
P62308;Q49AN9;F5H013;A8N	SNRPG	-0.7723751	0.022439077	4.75E-58
P62937;F8WE65;C9J5S7;Q56	PPIA	0.8372536	0.024341255	1.33E-27
Q8N108;Q8N108-17;Q8N108	MIER1	-1.163668	0.024416075	9.84E-09
P62805	HIST1H4A	0.8337688	0.024913313	7.27E-14
Q9H875;B4DGM2	PRKRIP1	0.8318329	0.025236125	1.41E-22
Q9Y5L4	TIMM13	-0.7391167	0.028692361	2.53E-63
P63010;P63010-2;Q7Z451;K7	AP2B1;AP1B1	0.8072548	0.029659722	6.72E-36
P62263	RPS14	0.7913342	0.032295079	3.88E-32
Q9NRY2;Q9NRY2-2	INIP	-1.101973	0.033414111	2.42E-05
P46779;C9JB50;G5E9L2;H0YL	RPL28	0.785675	0.034078068	0.0090483
P46782;M0R0F0;M0QZN2;M	RPS5	0.7828064	0.034268061	6.54E-109
Q5T750	XP32	-1.09687	0.034271482	0.00011919
P04908;P0C0S8;Q99878;Q93	HIST1H2AB;HIST1H2	0.7815151	0.034575613	9.67E-96
Q9H4L7;Q9H4L7-2	SMARCAD1	0.7828312	0.034700326	0.014817
Q7L0Y3	TRMT10C	-1.093466	0.034853997	8.40E-30
Q01844;Q01844-6;B0QYK0;Q	EWSR1	0.7670536	0.038184135	7.81E-118
P23528;Q9Y281;E9PQB7;G3V	CFL1;CFL2	0.7588654	0.040340251	4.73E-09
Q9P289;Q8NBY1;B4E0Y9;Q9F	MST4	-0.6872673	0.041417334	5.52E-122
Q15269	PWP2	-1.055935	0.041855426	4.93E-18
P37108;H0YLA2	SRP14	0.7517033	0.042359903	5.12E-97
Q92499	DDX1	-1.046686	0.043753057	5.75E-08
Q6SPF0;E9PIW9	SAMD1	0.7455177	0.04380568	2.58E-15
P55735;A8MXL6;P55735-2;B4	SEC13	0.7304955	0.048003292	0.00023769
P41236;E7EUI7;E7EMN6;Q6N	PPP1R2;PPP1R2P3	-1.014549	0.050920891	2.62E-15
Q9ULX3;H3BUR4	NOB1	-1.011868	0.051561122	4.64E-45
P04843;B7Z4L4	RPN1	-0.6537666	0.051959394	8.66E-155
P68133;P68032;P63267;P627	ACTA1;ACTC1;ACTG	0.7140121	0.054277354	2.47E-60
P06753-2;P06753-3;Q5VU59;	TPM3;TPM1;TPM4	-0.9992027	0.054676402	2.69E-10
P16435;H0Y4R2;F5H468;E7E\	POR	-0.6405392	0.056699339	3.93E-158
Q9BQ61;K7ELS0;K7ERU7;K7E	C19orf43	-0.6403637	0.05676456	5.70E-08
Q14978-3;Q14978	NOLC1	0.702528	0.058422106	2.01E-93
F5H6N3;P09496-2	CLTA	0.6964779	0.058769099	8.21E-09
P18583-6;P18583;P18583-3;F	SON	-0.6318398	0.060008759	8.54E-40
Q01658	DR1	0.6938705	0.061717662	4.45E-15
P62854;Q5JNZ5;F8VZW7	RPS26;RPS26P11	0.6867352	0.064548174	5.13E-30
Q04917;A2IDB2	YWHAH	0.6782703	0.065310815	7.49E-51
Q8NC51-3;Q8NC51-4	SERBP1	0.6749668	0.066559815	1.51E-152
P78347;P78347-2;P78347-4;F	GTF2I	-0.6116371	0.068315191	4.32E-165
P26232;P26232-3;P26232-2;F	CTNNA2	-0.9425907	0.070581067	2.48E-40
P20042	EIF2S2	0.6641407	0.070791513	9.37E-42
Q9H0A0;E7ESU4	NAT10	0.6531391	0.075315322	1.80E-30
P15924;P15924-2	DSP	-0.5929489	0.07681908	0
Q8WWY3;E7EVX8;Q8WWY3-	PRPF31	-0.5857601	0.080312017	2.25E-27
Q99590;Q99590-2;F8VXG7;F8	SCAF11	-0.5835876	0.081392618	4.01E-83
P26368;K7ENG2;P26368-2	U2AF2	-0.5782566	0.084094405	5.79E-109
O43290	SART1	-0.9014835	0.08436333	2.37E-16
Q15020;Q15020-2;F8VV04;B7	SART3	0.6255627	0.087697653	5.43E-14
P63104;E7EX29;E7ESK7;B0AZ	YWHAZ	0.6347122	0.088574591	3.78E-114
Q6P5R6;C9JYQ9;H0Y8C2	RPL22L1	0.6236839	0.088597742	2.63E-22
P61254;J3KTJ8;J3QRI7;J3QQC	RPL26;KRBA2;RPL26	0.6343174	0.088781319	4.53E-08
Q12996	CSTF3	0.620615	0.090084041	5.20E-16
Q96QA5;J3KRG2	GSDMA	-0.8755455	0.094128248	0.0036793
Q15014;Q5JXX1;Q5JXX2;Q5J	MORF4L2	0.609705	0.095530988	3.99E-07
Q53EL6;Q53EL6-2	PDCD4	-0.5557899	0.096287856	8.83E-68
Q15427;Q5SZ64	SF3B4	0.6182461	0.097531468	2.73E-97
P13674;P13674-2;P13674-3	P4HA1	-0.5497017	0.099825109	4.43E-68
Q02878;F8W181;F8VR69;F8V	RPL6	0.5948429	0.103371834	1.34E-06
Q86X53;E5RHA3;H0YBT6;H0Y	ERICH1	0.5946102	0.103498548	1.00E-36
O15533;O15533-2;D3YTI9;A8	TAPBP	0.6070328	0.104035115	2.96E-10
Q8IVL5;D3DNV8	LEPREL1	-0.5419388	0.10448479	3.00E-46
P60660;P60660-2;G3V1Y7;F8	MYL6	0.5900936	0.105982603	1.19E-06

O00267;O00267-2	SUPT5H	-0.5386772	0.106493366	2.51E-237
Q15428	SF3A2	-0.5380955	0.106854816	7.86E-31
P22695;H3BSJ9;H3BRG4;H3B	UQCRC2	-0.5344582	0.10913686	2.96E-112
P31930	UQCRC1	-0.533308	0.109866416	1.56E-270
O14519;F5GZF0;F5GYA4	CDK2AP1	0.5925159	0.112961267	1.63E-26
P80303;E9PKG6;J3KQU0;P80	NUCB2	-0.8259182	0.115322887	8.49E-43
Q16643;Q16643-2;A8MV58;[	DBN1	-0.8208332	0.117691363	1.20E-22
Q9P013	CWC15	-0.5133743	0.123132852	1.30E-39
Q9UQ80;F8VTY8	PA2G4	0.5602798	0.123585297	8.63E-20
P62913;P62913-2;Q5VVC9;Q	RPL11	-0.5126534	0.123635153	9.18E-32
Q9Y6E2;E7ETZ4;B5MCE7;Q75	BZW2	-0.8081074	0.123786123	6.71E-10
Q32P28;Q32P28-3;H7C0D1;H	LEPRE1	-0.8064232	0.124610861	5.97E-51
P55039;A8MZF9;J3QRI9;J3QK	DRG2	0.5557995	0.126417351	1.02E-26
P36578;H3BM89	RPL4	0.5719357	0.12663712	2.54E-42
Q96AG4	LRRC59	0.5635548	0.132562567	6.99E-89
P07919	UQCRH	-0.4973087	0.134709254	1.32E-44
P17987;F5GZ03;F5H282;E7EC	TCP1	0.5385094	0.137822396	2.78E-06
P15880;H0YEN5;E9PQD7	RPS2	0.5377808	0.138319877	7.26E-23
Q6QNY0	BLOC1S3	0.5338001	0.141062251	1.45E-23
P82979;Q567R9;H0YHG0	SARNP;CIP29	-0.7739182	0.141381739	4.18E-20
Q9Y5V0;E5RHV4;H0YAP1;E5R	ZNF706	-0.7673836	0.144953614	6.12E-06
P02545;P02545-3;D6RAQ3;P(	LMNA	-0.4789753	0.148928084	5.30E-278
Q8WUA2	PPIL4	-0.7601166	0.149006581	2.70E-12
Q15054;Q32N00;Q32MZ9	POLD3	-0.7472363	0.156401967	3.53E-20
Q92841;Q92841-3;Q92841-1;	DDX17	-0.7445545	0.157976149	5.26E-23
Q07020;F8VUA6;F8VWC5;G3	RPL18	0.510294	0.158115587	5.53E-32
P16989;P16989-3;P16989-2	YBX3	0.5282612	0.159895239	1.28E-121
Q9UNP9;Q9UNP9-2;Q5TGA3;	PPIE	0.5017776	0.164665154	9.45E-08
Q8N488	RYBP	0.5004368	0.16571471	1.04E-18
Q92905;E5RHF2;E5RHH5	COPS5	-0.7260017	0.169196993	2.76E-27
Q6NZI2;Q6NZI2-2	PTRF	-0.724184	0.170327719	4.63E-88
Q86WB0;Q86WB0-3;C9J0I9;C	ZC3HC1	-0.7241821	0.170328908	2.50E-13
Q9NX58	LYAR	0.5143147	0.171800277	5.26E-89
Q9H0G5;K7ERM9	NSRP1	-0.72052	0.172624163	9.17E-07
K7ER90	EIF3G	0.4895287	0.174440715	6.15E-50
P39023;H7C422;G5E9G0;H7C	RPL3	0.5058022	0.179385744	1.13E-35
P17096;P17096-3;H7BYM6	HMGA1	0.4828777	0.179926941	0.00021461
Q9UH99;J3KQE0;Q9UH99-2;E	SUN2	0.4796028	0.182675015	2.55E-06
Q969S3	ZNF622	-0.4380245	0.184789059	4.48E-50
P62241;Q5JR95	RPS8	0.4988155	0.185795326	1.93E-77
O60841	EIF5B	-0.4366341	0.186110121	5.90E-238
P16401	HIST1H1B	0.4982052	0.186363209	6.14E-10
Q9BQE3;F5H5D3	TUBA1C	-0.4358768	0.186832476	2.58E-276
Q96NB3	ZNF830	-0.6963692	0.188343063	5.29E-21
P35250;P35250-2	RFC2	0.4723473	0.188873969	1.41E-05
P67809;H0Y449	YBX1	0.4954891	0.188905847	7.14E-115
P62857	RPS28	-0.4268742	0.195579893	5.10E-68
Q9UKL0;J3KN32	RCOR1	-0.6846733	0.196324507	1.21E-25
Q8WWM7;H3BSK9;Q8WWM	ATXN2L	0.4635525	0.196594276	0.00039853
P14625	HSP90B1	-0.4249687	0.197469195	1.66E-97
P84103;B4E241	SRSF3;SFRS3	-0.4239712	0.1984636	1.66E-33
P62310	LSM3	0.4605885	0.199247556	0.0023264
P08670;B0YJC4	VIM	0.4845448	0.199410737	3.68E-247
Q8IUE6	HIST2H2AB	0.4830246	0.200902967	3.41E-160
P61619;P61619-3;B4DR61	SEC61A1	0.4576988	0.201859345	1.34E-05
P61247;D6RG13;D6RAT0;F5H	RPS3A	0.4811516	0.202752758	8.13E-67
Q9P287;Q9P287-3;Q9P287-2	BCCIP	-0.4192715	0.203197805	4.09E-85
Q12800;Q12800-4;F8VWL0;F	TFCP2	-0.6719646	0.205274963	1.35E-65
Q9UBS4	DNAJB11	0.4530163	0.206144496	2.06E-24
Q9P258	RCC2	-0.4151173	0.20745052	4.09E-82
P46778;G3V1B3;M0R181	RPL21	0.4760036	0.207900705	8.37E-17
Q13151	HNRNPA0	0.4755096	0.208399649	4.93E-75
O43823	AKAP8	-0.6625824	0.212070476	3.38E-06
Q07065	CKAP4	0.4463921	0.21231883	4.35E-63
P49411	TUFM	-0.6588707	0.214803231	1.36E-29
Q9NQG5	RPRD1B	-0.4071712	0.215764109	5.32E-146
P60709	ACTB	0.467411	0.216703331	1.63E-229
Q92522	H1FX	0.440897	0.217541199	1.32E-26

J3KN66;Q5JTV8;Q5JTV8-2;H0	TOR1AIP1	0.4659004	0.218278194	1.05E-113
C9J3L7;C9JZE3;C9JYJ8;Q9BW	REPIN1	-0.6502972	0.221212349	3.74E-12
Q15424;B7ZLP6;A0AV56;Q15	SAFB	-0.4018555	0.221458126	4.89E-275
P05783;F8VZY9	KRT18	0.4608212	0.223633748	3.70E-154
P62633;P62633-2;B4DP17;P6	CNBP	0.4329948	0.225212137	3.77E-63
Q14865;Q14865-3	ARID5B	-0.637907	0.230714944	1.10E-15
Q99714;Q99714-2;Q5H928	HSD17B10	-0.3933125	0.230833189	2.97E-194
P26373;J3QSB4;P26373-2	RPL13	0.4532719	0.231766271	1.94E-22
Q9UNF0;Q9UNF0-2;B0QYG7;	PACSIN2	-0.3918037	0.232517723	1.52E-112
Q14444;Q14444-2;G3V153;E	CAPRIN1	-0.3912373	0.233152486	1.05E-77
Q8IWS0;E9PC97;B4E0G4;Q5J	PHF6	0.4244614	0.233710796	1.80E-42
Q9H0E9-2;Q9H0E9;H7C128;H	BRD8	-0.6337299	0.23398304	7.88E-21
Q5VT52;Q5VT52-3;Q5VT52-2	RPRD2	-0.3904381	0.234050056	2.94E-155
P40429;M0QYS1;Q6NVV1	RPL13A	0.4234924	0.234689956	3.20E-11
P08238;P07900;P07900-2	HSP90AB1;HSP90AA	-0.6322613	0.235139848	7.79E-34
P49756;E9PQU5;P49756-2;P4	RBM25	0.4212399	0.236977531	2.09E-05
Q9Y3B3;Q6JUT2;Q9Y3B3-2	TMED7;TICAM2	0.4472485	0.23840402	4.34E-59
Q8TF01	PNISR	-0.6281147	0.238427788	0.0088198
P05198;H0YJS4;G3V4T5	EIF2S1	0.4196358	0.238616109	2.29E-33
P62249;M0R3H0;M0R210;Q6	RPS16	0.4451256	0.240775087	9.58E-15
P35637;P35637-2;H3BPE7	FUS	0.4446545	0.241303524	3.30E-47
Q7L014	DDX46	-0.3833199	0.242152779	9.32E-92
Q99873;E9PKG1;Q99873-3;Q	PRMT1	-0.3828239	0.242724542	2.11E-24
Q9NQT4;M0R050	EXOSC5	0.4136143	0.244838398	9.68E-05
Q8N9T8;H0YFD2;D3YTE0;Q8N	KRI1	0.412693	0.24580032	5.23E-39
Q9Y2X3	NOP58	0.4120502	0.246473042	4.60E-23
P63261;I3L3I4;I3L4N8;I3L3I0;	ACTG1	0.439436	0.247211646	2.91E-282
Q07955;J3KTL2;Q07955-3;Q0	SRSF1	0.4385777	0.248192995	3.10E-113
P31689;B7Z5C0	DNAJA1	-0.3728123	0.254470983	3.04E-51
Q92733;A6NG79	PRCC	-0.371582	0.255941223	7.94E-60
O76094;O76094-2	SRP72	0.4318199	0.256014731	0
P62258;P62258-2	YWHAE	0.4310131	0.256959889	2.14E-186
Q8N2W9	PIAS4	0.4283409	0.26010759	1.88E-80
P52298;E9PAR5;C9JQX9;B3KS	NCBP2	0.4282856	0.260173027	4.27E-19
P84090;G3V279	ERH	0.4273643	0.261264559	5.40E-90
P54727;H0Y579;P54727-2	RAD23B	0.3981953	0.261287863	4.60E-07
Q8N4Q1;Q8N4Q1-2	CHCHD4	-0.366991	0.261479897	5.16E-81
Q15293;B7Z1M1;E9PJD5;E9P	RCN1	-0.3663731	0.262231723	2.94E-115
P35221;G3XAM7;P35221-2;E	CTNNA1	-0.5972214	0.263946889	1.22E-42
O00139;O00139-2;O00139-1;	KIF2A	-0.59408	0.266643558	2.16E-26
Q5T8D3-3;Q5T8D3-4;Q5T8D3	ACBD5	-0.5909882	0.269316106	1.39E-11
O95400	CD2BP2	0.3878021	0.272797576	3.94E-23
Q9NY12;Q9NY12-2	GAR1	0.4174175	0.273251705	3.87E-21
P14635;H0YA62;Q5TZP9;E9P	CCNB1	0.3862495	0.274546286	0.0010346
P49321;P49321-2;P49321-3;E	NASP	0.4151039	0.276092971	7.06E-64
O60884	DNAJA2	0.3835926	0.277556584	1.45E-54
Q96IZ0	PAWR	0.412981	0.278717668	4.90E-22
O95831;O95831-3;O95831-2	AIFM1	-0.3529091	0.278983098	1.08E-86
Q13445	TMED1	0.3818378	0.279557003	1.25E-55
P62314;J3QLI9	SNRPD1	0.4118462	0.280127749	1.33E-86
P41208	CETN2	0.3791542	0.282635254	1.46E-12
O43865;O43865-2;Q96HN2;C	AHCYL1;AHCYL2	0.3787689	0.28307907	6.02E-11
Q9BW71;Q9BW71-2	HIRIP3	0.4087849	0.283955553	7.05E-149
P10412;P16403;P16402	HIST1H1E;HIST1H1C	0.4067669	0.28649808	2.94E-11
P55081	MFAP1	-0.3461151	0.287706448	8.04E-85
Q14181;E9PIQ6;B4DNB4	POLA2	-0.5695744	0.288330209	0.00071899
P55072	VCP	-0.3447132	0.289529124	0
P02545-2;Q6UYC3;Q5TCI8	LMNA	-0.5677166	0.29002143	1.55E-224
P60842;J3KSZ0;J3KT12;P6084	EIF4A1	-0.5673256	0.290378234	4.62E-70
Q9Y2D5-4;C9JVY5;Q9Y2D5;Q	AKAP2	-0.5632477	0.294117042	1.79E-37
P06576;H0YH81;F8VPV9	ATP5B	0.3691788	0.294278391	2.91E-42
P25440;H0Y6K2;H0Y5T9;P25	BRD2;DKFZp313H13	0.4006195	0.294337948	2.72E-234
Q92541	RTF1	0.3685131	0.295066626	1.09E-15
P62266	RPS23	-0.5622082	0.295075246	1.04E-08
Q15059;Q15059-2	BRD3	0.3979549	0.297780384	4.78E-162
P21127;Q9UQ88;P21127-12;(	CDK11B;CDK11A	0.3654671	0.298691568	3.21E-07
P36873;F8VYE8;P36873-2;F8	PPP1CC	-0.5580387	0.298939609	2.34E-191
Q13206;E9PIF2	DDX10	0.3647537	0.299544768	0.0044254

Q9Y305;C9J7L8;Q9Y305-3;Q9	ACOT9	-0.556572	0.300307026	5.82E-06
P12956;B1AHC9;F5H1I8;B1A	XRCC6	0.3941078	0.302797884	6.92E-64
P60866;P60866-2;E5RIP1;E5R	RPS20	0.3931141	0.30410301	1.01E-28
Q14011;K7ELV6;K7ENX8;K7EJ	CIRBP	0.391613	0.306081551	2.78E-126
Q9NWH9;H0YL55;H7BXE3;H0	SLTM	-0.5493584	0.307092684	6.21E-82
Q03111	MLLT1	0.3902416	0.307896581	5.79E-29
Q9BRX2	PELO	-0.330658	0.308232428	4.25E-178
P50914;E7EPB3	RPL14	0.3882675	0.310521796	1.95E-22
P17028	ZNF24	-0.545742	0.310532403	3.45E-07
Q06546	GABPA	-0.5438976	0.312296488	4.13E-66
P52597	HNRNPF	-0.5437832	0.312406162	1.86E-126
Q15363;F5GX39;E7EQ72	TMED2	0.385397	0.314365422	4.44E-49
Q2KHR3;Q2KHR3-2;H0YCQ7	QSER1	0.3521557	0.314880435	3.91E-104
Q15287;H3BV80;H3BMM9;H	RNPS1	0.3848248	0.315135317	1.90E-41
P51571	SSR4	0.3846321	0.315394793	6.69E-99
Q9BZZ5;Q9BZZ5-2;Q9BZZ5-1;	API5	-0.5386925	0.317310509	9.74E-20
Q92804;K7EPT6;Q92804-2	TAF15	0.3501968	0.317310509	1.72E-51
O60220	TIMM8A	-0.3240395	0.317310509	7.23E-34
O60885;O60885-2;Q4G0X8;M	BRD4	0.383213	0.317310509	1.58E-121
O00193;E9PM92;E9PRZ9;E3V	SMAP;C11orf58	0.3500328	0.317514557	5.91E-79
P40938;P40938-2	RFC3	-0.5384102	0.317583931	4.14E-16
Q9Y6A4	C16orf80	0.382988	0.317615045	8.06E-86
Q86XP3;Q86XP3-2	DDX42	-0.3236046	0.31791307	5.59E-295
P31944	CASP14	-0.5374527	0.318512501	7.60E-20
P78344;P78344-2;H0Y3P2;D3	EIF4G2	-0.3211098	0.321384348	3.41E-232
Q96JB5;J3QQY1;F5H3I5;J3QS	CDK5RAP3	-0.3206539	0.322021291	1.17E-39
P23396;J3KN86;E9PPU1;E9PL	RPS3	0.3797054	0.322078392	7.50E-126
P05386	RPLP1	0.378643	0.323531687	1.39E-19
P62424;Q5T8U2;Q5T8U3	RPL7A	0.3773212	0.325345768	1.50E-96
P29084	GTF2E2	0.3770981	0.325652692	1.71E-78
Q16576;E9PC52;Q16576-2	RBBP7	-0.3180161	0.325723206	6.02E-44
O14579;O14579-2;M0QXB4;M	COPE	-0.3176956	0.326174772	1.26E-96
P49736;H0Y8E6	MCM2	-0.3170433	0.327095289	2.51E-103
P27635;B8A6G2;F8W7C6;A6(	RPL10	0.3377075	0.333092636	1.64E-21
P04217;P04217-2;M0R009	A1BG	0.3370037	0.333996838	9.48E-25
Q13148;Q13148-2;B1AKP7;G	TARDBP	-0.5188313	0.336924627	1.54E-45
Q4G0J3;D6R9Z6;Q4G0J3-2;H(	LARP7	0.333622	0.338363468	1.43E-39
Q8WWI1-3;E9PMS6;Q8WWI1	LMO7	0.3330173	0.339148037	2.68E-113
O75494;O75494-3;O75494-4;	SRSF10;SRSF12	-0.5158157	0.339969394	2.67E-13
Q9UJV9;H0Y8L8;J3KNN5	DDX41	0.3285542	0.344975552	1.32E-10
Q9Y3I0;E7EQS9	C22orf28;RTCB	-0.3044147	0.345248084	6.45E-104
Q9Y5J9;G3XAN8	TIMM8B	-0.3029842	0.347344116	1.82E-18
Q9NX40;D6RDI5;D6RA54;D6F	OCIAD1	0.3266792	0.347442543	5.88E-21
P62906	RPL10A	0.3614731	0.347610289	2.03E-101
Q9UBD5;Q9UBD5-2;Q9UBD5	ORC3	-0.5054569	0.35056254	1.74E-17
Q16698;B7Z6B8	DECR1	0.323719	0.351360312	2.10E-19
P62861;E9PR30	FAU	0.3588505	0.351386037	8.08E-07
Q15365	PCBP1	-0.5034504	0.352638407	5.12E-22
Q15393;Q15393-3	SF3B3	-0.5030422	0.353061634	1.73E-29
Q53F19;Q53F19-2	C17orf85	-0.5027294	0.353386194	4.72E-22
P08574	CYC1	-0.2982655	0.354315475	1.16E-41
Q9HC35;B5MCW9;B5MBZ0;F	EML4	-0.4995117	0.356735749	3.41E-36
P60510;H3BV22;H3BTA2	PPP4C	-0.4976902	0.358640748	0.00071779
Q9Y2K7;D4QA03;E9PIL6;Q9Y	KDM2A	0.3181076	0.358863386	8.23E-15
Q12906;Q12906-4;Q12906-5;	ILF3	0.3527126	0.360323779	8.73E-73
P61224;P62834;A6NIZ1;F5H8	RAP1B;RAP1A	0.3163395	0.36124826	2.21E-17
P18846;B4DRF9;P16220;Q03(	ATF1;CREB1;CREM	-0.2932644	0.361799635	2.09E-17
P29083	GTF2E1	-0.292635	0.362748548	1.02E-72
Q13263;Q13263-2;M0R0K9	TRIM28	-0.4900723	0.366676969	1.53E-23
P06748;P06748-2;P06748-3	NPM1	0.3477554	0.36764551	0
P55769;B1AHD1	NHP2L1	-0.2885303	0.368974759	3.39E-24
Q9H1E5	TMX4	0.309948	0.369951945	1.46E-12
Q9NS91;F8WE49	RAD18	0.3449841	0.371778902	3.07E-62
Q9UHB7;Q9UHB7-2	AFF4	0.3446865	0.372224387	2.07E-42
O15156;O15156-2	ZBTB7B	-0.4843826	0.372751636	1.94E-08
Q6ZW49;Q6ZW49-4;F8WC23	PAXIP1	0.3064976	0.37470423	3.19E-25
Q99733;F5HFY4;C9JZI7;A8MX	NAP1L4;NAP1L4b	0.3429108	0.37488989	1.87E-121
P13861;Q9BUB1;H7C1L0	PRKAR2A	-0.481617	0.375726844	1.13E-35

Q08211	DHX9	0.3056812	0.375834092	1.36E-24
Q9BRK5;Q9BRK5-4;H0Y3T6;Q	SDF4	-0.4812336	0.376140424	6.44E-32
Q13724;F5H6D0;C9J8D4	MOGS	-0.2834835	0.376720727	8.65E-41
Q9Y2Q9;E5RGC7;E5RK86;E5R	MRPS28	-0.4802361	0.37721787	0.0003874
Q9NXV6	CDKN2AIP	-0.479454	0.378063851	6.05E-16
P43487;C9JJ34;C9JXG8;C9JGV	RANBP1	-0.281805	0.37931893	6.65E-16
P49458;E9PE20;P49458-2	SRP9	-0.2802486	0.381737996	4.91E-33
Q9Y265;Q9Y265-2;H7C4G5;E	RUVBL1	-0.2787018	0.384151595	4.68E-150
Q00325-2;F8VVM2;Q00325;F	SLC25A3	0.3364906	0.38462499	3.59E-20
P46781;B5MCT8;C9JM19	RPS9	0.298727	0.385544118	1.77E-16
P38159;Q96E39;H3BNC1;H3E	RBMX;RBMXL1	0.2976665	0.387038212	4.08E-46
Q14974;B7ZAV6;F5H4R7;J3K1	KPNB1	0.3349133	0.387040283	0
O43681;K7ERW9	ASNA1	-0.4700603	0.388317058	1.07E-07
O95218;O95218-2	ZRANB2	0.3322239	0.391179528	2.47E-196
P80723	BASP1	0.2922058	0.394787486	1.05E-06
P22087;M0R299;M0QXL5;M0	FBL	0.3295898	0.395259586	1.09E-11
O00410;O00410-3;B4E0R6;O0	IPO5	0.28969	0.398388971	1.64E-33
P50991;B7Z9L0;P50991-2	CCT4	0.2890854	0.399257469	9.40E-27
O75400;O75400-2;O75400-3;	PRPF40A	-0.4593906	0.400166281	4.92E-12
O75643	SNRNP200	-0.2681751	0.400823324	1.15E-92
O14980;C9JF49;C9IYM2;F8W	XPO1	0.2873535	0.401751452	0.00014908
Q9NRF9	POLE3	0.2841568	0.406379365	6.05E-11
Q9HCG8;B7WP27;B7WP74	CWC22	0.2834377	0.407424736	1.02E-32
O15355	PPM1G	0.3214588	0.4080156	1.79E-106
P47712;E7EU42	PLA2G4A	-0.4521942	0.408279623	2.88E-23
P62851	RPS25	0.3206387	0.409315751	2.73E-28
P62753;A2A3R7;A2A3R5	RPS6	0.3196239	0.410927716	6.23E-49
P62280;M0QZC5;M0R1H5	RPS11	0.3176613	0.414056272	3.11E-32
O96019;O96019-2;H7C5S0	ACTL6A	0.3174152	0.414449473	4.43E-50
Q6PD62	CTR9	-0.4448795	0.416625877	3.83E-07
P13667	PDIA4	-0.2575932	0.418013265	1.38E-237
P11940;P11940-2;E7EQV3;E7	PABPC1	0.3141422	0.419700941	7.83E-186
P62158;H0Y7A7;F8WBR5;M0	CALM1;CALM2;CALI	0.3138161	0.420226386	2.17E-16
P52272;P52272-2;M0R0Y6;M	HNRNPM	-0.4375553	0.425083023	5.33E-12
P55199	ELL	0.2711163	0.425585336	8.55E-24
P35659;P35659-2;B4DFG0;D6	DEK	-0.2525406	0.42637179	4.63E-186
Q9NV56	MRGBP	-0.4352856	0.427724071	5.69E-09
Q9BRP8;Q9BRP8-2	WIBG	0.2690601	0.428661207	1.80E-10
P17480;P17480-2;E9PKP7	UBTF	0.3072376	0.430906641	1.96E-151
Q9BZK7;O60907;Q9BQ87;C9J	TBL1XR1;TBL1X;TBL	0.2673988	0.43115586	1.67E-14
P39019	RPS19	0.3068314	0.431571344	4.19E-26
Q9H3Q1;B3KUS7	CDC42EP4	-0.4310379	0.432692193	2.87E-168
Q99613;H3BRV0;B5ME19	EIF3C;EIF3CL	0.2660561	0.433178342	1.45E-81
P08865;C9J9K3;A6NE09	RPSA;RPSAP58	0.3056316	0.433537712	3.48E-92
P62826;B5MDF5;F5H018;J3K	RAN	0.3051262	0.434367699	2.79E-17
Q9H814	PHAX	-0.4256477	0.43904444	1.53E-10
P98179	RBM3	0.2617512	0.43969924	6.55E-05
P49770	EIF2B2	-0.42272	0.44251712	4.55E-11
P32119;A6NIW5	PRDX2	-0.4226837	0.442560203	3.86E-15
O75607	NPM3	0.2992916	0.4440148	6.80E-84
P39880;P39880-6;P39880-4;F	CUX1	-0.2399731	0.447580231	8.48E-69
Q14919;E9PQX9;Q14919-2;C	DRAP1	-0.417902	0.448265833	4.13E-17
Q9H4L4;J3KNH7	SENP3	0.2555714	0.449157982	9.78E-07
Q13428;Q13428-3;Q13428-2;	TCOF1	0.2960491	0.449428501	1.51E-243
Q9H2P0	ADNP	-0.2381382	0.450726082	5.05E-188
Q96EY4;D6RA57;H0Y9X1	TMA16	-0.4149628	0.451793595	4.61E-20
P48681	NES	-0.4143543	0.452525828	1.04E-16
P63208;E5RJR5;E5RGM3;E7EI	SKP1	-0.2369156	0.452829157	2.41E-52
Q8N9E0;G3XAI9;Q5BKY9	FAM133A;FAM133B	-0.4140778	0.452858883	5.24E-09
P13639	EEF2	-0.413353	0.453732372	5.75E-34
P62304;A6NHK2	SNRPE	-0.2359886	0.454427375	4.45E-93
Q9UDW1	UQCR10	-0.4125919	0.454650558	9.60E-11
Q9NUP9;G3V1D4	LIN7C	-0.4100437	0.457732594	1.46E-07
P62829;C9JD32;B9ZVP7;J3KT	RPL23	-0.2339287	0.457990327	1.47E-62
Q9Y232;Q9Y232-2;Q9Y232-3;	CDYL	0.249836	0.458038866	1.14E-22
P62244;I3L3P7;I3L246;H3BN9	RPS15A	0.290369	0.459001667	5.14E-38
Q8NEF9	SRFBP1	-0.4085522	0.459542027	4.47E-14
Q12874;E7EUT8	SF3A3	-0.2325878	0.460317942	4.23E-39

Q96EP5;K7EQ02;Q96EP5-2	DAZAP1	0.2478008	0.461213671	1.79E-44
Q96AX1;F5H2X5;H3BMM5	VPS33A	0.2475052	0.461675886	0.00084182
Q12905	ILF2	0.2887573	0.461738695	1.09E-23
Q9BVK6	TMED9	0.2856293	0.467076715	5.53E-78
P21333;Q5HY54;P21333-2	FLNA	0.2827721	0.4719823	8.01E-59
O00505	KPNA3	0.2824554	0.472527651	8.18E-65
Q14157;Q14157-1;Q14157-4;	UBAP2L	0.2821465	0.473060196	5.68E-103
Q86VM9;E7ERS3;Q86VM9-2	ZC3H18	0.2401867	0.473200064	2.97E-20
Q8N556;Q8N556-2	AFAP1	-0.2234402	0.476372723	4.47E-53
Q15024	EXOSC7	0.2376785	0.477185694	0.00050345
Q14331;E9PRR7	FRG1	0.2369328	0.478374308	7.86E-23
Q14318;Q14318-2;J3KQ73;C8	FKBP8	-0.2222805	0.478429712	6.23E-73
P35251;P35251-2	RFC1	0.2349033	0.481616976	1.40E-07
P07437;Q5JP53;F8VYX6;F8VV	TUBB	-0.2202225	0.48209211	0
O15160;O15160-2;E7EQB9	POLR1C	-0.3899612	0.482428224	2.90E-27
Q04637;Q04637-3;Q04637-6;	EIF4G1	-0.3898659	0.482547201	1.13E-18
Q9H1E3	NUCKS1	-0.2191544	0.483998884	4.83E-178
P09132;P09132-2	SRP19	0.2332954	0.484194587	9.05E-21
Q9Y3A6;M0R072;B1AKT3;B1/	TMED5	-0.3874454	0.485572166	9.50E-29
P62273;P62273-2	RPS29	-0.3854198	0.488111565	8.80E-05
Q92791;K7ERA3	LEPREL4	-0.2162933	0.489126403	1.03E-59
Q9BW61	DDA1	0.2299957	0.489507691	3.01E-10
P51648;P51648-2;J3QKK9;K7I	ALDH3A2	-0.3821545	0.492220244	5.18E-24
P22626;P22626-2	HNRNPA2B1	0.2704678	0.493428669	9.30E-114
Q14566	MCM6	-0.2121143	0.496668276	4.57E-182
Q9Y5M8;H7C4H2	SRPRB	-0.2120609	0.496765057	8.91E-72
Q9Y224;G3V4C6	C14orf166	-0.2105179	0.499565682	7.18E-102
Q7Z7H5;Q7Z7H5-3;Q7Z7H5-2	TMED4	0.2666111	0.500256665	2.23E-99
Q9Y3E5;J3KQ48	PTRH2	-0.3756371	0.500475956	5.42E-143
Q9NYF8-3;E9PK91;E9PK09;E9	BCLAF1	0.2205734	0.504850422	5.24E-222
Q06830	PRDX1	0.2637482	0.505357549	6.92E-19
Q7KZ85;Q7KZ85-3	SUPT6H	-0.3702011	0.507417513	6.12E-109
Q13347;Q5TFK1	EIF3I	0.2185497	0.508178447	4.00E-06
Q8IYT4;K7EM02;K7EIJ8;Q8IYT	KATNAL2	-0.3695984	0.508190275	0.002077
Q9BTC0;Q9BTC0-2;Q9BTC0-3	DIDO1	-0.3689537	0.50901752	1.13E-11
Q9H211	CDT1	0.2175293	0.509860928	3.33E-20
Q00839;Q00839-2	HNRNPU	0.2609825	0.510311006	3.71E-164
Q5QJE6;J3KP30	DNTTIP2	0.2605724	0.51104764	4.56E-100
P08579	SNRPB2	-0.2030525	0.513232839	2.19E-65
P54105;E9PMI6;E9PJF4;J3KN	CLNS1A	-0.3649216	0.514207433	1.66E-11
Q13283;F5H4D6	G3BP1	0.2574844	0.516612454	3.44E-148
P62277;J3KMX5	RPS13	-0.1982784	0.522073966	1.04E-15
Q9UNL2;C9JA28;B4E2P2	SSR3	0.2079678	0.525766433	0.0025334
Q9H6Y2;G3V1J0	WDR55	-0.3550091	0.527082179	1.04E-27
Q96B36;Q96B36-2;J3KPM3	AKT1S1	0.2068634	0.527619723	0.00017335
P41091;Q2VIR3;Q2VIR3-2;F8\	EIF2S3;EIF2S3L	0.2066727	0.527940145	2.28E-09
Q9H3P2;B3KSP0;H0Y3X6;C9JI	NELFA;WHSC2	-0.3536434	0.528868762	1.22E-34
Q5C9Z4	NOM1	-0.3535042	0.529051087	2.22E-11
O15446;O15446-2	CD3EAP	0.2500954	0.530054484	8.96E-113
P46100;P46100-2;P46100-5;F	ATRX	0.2053833	0.530108794	6.81E-38
Q07666;Q07666-3;Q07666-2	KHDRBS1	-0.3515911	0.531559412	2.94E-20
Q9BQ15;Q9BQ15-2;C9JT95;C	NABP2	0.2483025	0.533342687	8.83E-66
P14927;P14927-2;B7Z2R2	UQCRB	-0.1918335	0.5341323	7.81E-54
O95373	IPO7	0.2474327	0.534941521	7.08E-195
Q9Y230;B3KQ59;M0R0Y3	RUVBL2	-0.1912613	0.53520964	4.35E-81
P62140;E7ETD8	PPP1CB	0.2471714	0.535422345	9.39E-171
F8W9Q2;Q8N7H5-2;M0QX35	PAF1	0.2018318	0.536105511	2.30E-23
Q6UWP8	SBSN	0.2017288	0.53627993	9.13E-06
Q92945;M0R0I5	KHSRP	-0.3452644	0.539897348	1.49E-18
Q9Y6E0-2;B4DR80;Q9Y6E0;H	STK24	0.1982746	0.54214593	4.23E-56
Q92688;Q92688-2;Q5T6W8	ANP32B	0.2421227	0.544754958	1.33E-118
Q66PJ3;Q66PJ3-2;Q66PJ3-3;F	ARL6IP4	-0.1860294	0.545110643	3.04E-77
P40227;B4DPJ8	CCT6A	0.1958771	0.546236202	1.10E-09
P26599;P26599-2;P26599-3;I	PTBP1	0.241003	0.546835457	1.77E-134
Q01130;J3QL05;J3KP15;B4DN	SRSF2;SFRS2	-0.1842461	0.548506236	5.81E-90
P15408;C9JCN8;P15408-3;P1	FOSL2	-0.3385544	0.548811492	0.00056285
Q13427;C9JN15;Q13427-2;C9	PPIG	-0.3380909	0.549429894	2.26E-40
P09651;P09651-3;F8VXY0;F8\	HNRNPA1;HNRNPA1	0.2373638	0.553625017	2.26E-147

P05388;Q3B7A4;F8VWS0;F8V	RPLP0;RPLP0P6	-0.181551	0.553657495	2.18E-70
O43684;J3QT28;O43684-2;B4	BUB3	0.236496	0.555250197	1.08E-27
O60828;O60828-4;O60828-2;	PQBP1	-0.1803055	0.556046064	2.49E-31
P84098;J3QR09;J3KTE4;J3QL1	RPL19	0.2351532	0.557769346	3.09E-37
P60468	SEC61B	0.2348785	0.55828531	0.0025644
Q13098;Q13098-6;J3QLT0;J3I	GPS1	-0.3310375	0.558882971	1.28E-05
Q8WXI9	GATAD2B	-0.3286285	0.562129537	2.27E-34
Q9NP74;Q9NP74-2;Q9NP74-3	PALMD	-0.1770725	0.562269463	4.77E-36
Q9NX24;D6RC52;D6RCB9;J3C	NHP2	0.2326717	0.562439343	1.42E-121
E9PAV3;F8VZJ2;F8W0W4;H0\	NACA	-0.1762276	0.563901519	9.64E-45
O60573;B9A044;B8ZZJ9;B8ZZ	EIF4E2	0.1843147	0.566174024	2.49E-11
P18754;C9JW69;P18754-2;H7	RCC1	0.1843147	0.566174024	1.31E-36
P19338;H7BY16	NCL	0.2302742	0.566969258	0
O76071	CIAO1	-0.3244419	0.567793411	0.0013845
E5RGW4	NPM1	0.1824055	0.56949959	1.19E-42
Q99729-3;D6R9P3;D6RD18;D	HNRNPAB	-0.1732769	0.569618652	7.10E-23
Q5SSJ5;B0QZK4;Q5SWC8;Q5S	HP1BP3	-0.3224678	0.570473522	0.0001119
Q9NPA8;G3V117;E5RHX8	ENY2	-0.1727943	0.570556274	7.60E-33
P08708;P0CW22;H0YN88;H0\	RPS17;RPS17L	0.2267132	0.573729562	8.41E-48
Q86VP6;Q86VP6-2	CAND1	-0.1699238	0.576148947	5.00E-115
Q13586;E9PQJ4	STIM1	-0.3182354	0.576239799	5.80E-18
Q15165;Q15165-3;J3QT77;Q3	PON2	0.1782379	0.576790907	3.45E-60
Q71UM5;C9JLI6;H0YMV8	RPS27L	0.2249889	0.577016563	4.58E-11
P61313;E7EQV9;E7ENU7	RPL15	0.1779289	0.577333246	1.62E-13
Q92973;Q92973-2;Q92973-3	TNPO1	-0.1691132	0.577732945	7.50E-239
Q86V81;E9PB61	ALYREF	0.2245102	0.577930787	2.82E-113
P35249;H7C1P0	RFC4	0.1768703	0.579193079	9.70E-28
P11021	HSPA5	-0.1681938	0.579531862	5.80E-242
O43447;C9JQD4;A6NM32;H0	PPIH	0.1763935	0.580031759	3.08E-08
Q14966;E7EUZ3;Q14966-5;Q	ZNF638	-0.1675205	0.580850991	4.05E-39
O43670;J3KS31;O43670-3;O4	ZNF207	0.1734238	0.585267831	2.22E-08
Q9UMS4;F5GY56	PRPF19	-0.1651421	0.585522133	2.12E-28
P61201;B4DIH5;P61201-2;H0	COPS2	-0.1647568	0.586280444	1.26E-64
P36954;K7EKS1	POLR2I	0.1720371	0.587720173	6.81E-111
Q9NXS2	QPCTL	0.1706486	0.590180641	4.14E-62
Q9H936;E9PJH7	SLC25A22	0.1705608	0.59033627	6.66E-29
P33993;P33993-3	MCM7	-0.162672	0.59039146	9.70E-251
P12236;I7HJJ0;P12235	SLC25A6;SLC25A4	0.2176247	0.591154338	3.20E-54
Q14839;F5GWX5;Q14839-2	CHD4	-0.3064919	0.592381695	4.72E-66
P62888;E5RI99	RPL30	0.2165756	0.593181156	4.01E-97
Q96RE7	NACC1	-0.1601524	0.595377671	9.47E-98
Q9Y295	DRG1	-0.1594162	0.596838276	9.26E-109
P14316;D6RB34;D6R9N5;D6R	IRF2;IRF1	-0.3025799	0.597804522	3.64E-15
Q6ZRS2;Q6ZRS2-3;Q6ZRS2-2	SRCAP	-0.3009453	0.600077084	0.00034704
Q15233;Q15233-2;C9JYS8	NONO	-0.157444	0.600758891	3.23E-68
P19388	POLR2E	-0.1569958	0.60165156	3.35E-82
O00571;O00571-2;O15523;B4	DDX3X;DDX3Y	0.1637554	0.602464739	7.87E-23
Q9H446;E5RGQ3;Q9H446-2;E	RWDD1	0.1637192	0.602529624	1.28E-05
P07355;P07355-2;H0YMD0;H	ANXA2;ANXA2P2	-0.1560078	0.603621341	3.98E-97
Q16656;Q16656-2;Q96AN2;C	NRF1	0.2111549	0.603704628	4.17E-21
P0DI83	RAB34	0.1624928	0.604727321	3.59E-23
Q9NWS0;M0QYF4;M0QXD5;I	PIH1D1	0.1607113	0.607926007	7.84E-19
P22392;J3KPD9;P22392-2;Q3	NME2;NME1-NME2	-0.2947712	0.608695884	1.76E-39
P62081;B5MCP9	RPS7	0.2077045	0.610446455	6.50E-29
P46013;P46013-2	MKI67	0.1586571	0.611623762	1.51E-06
Q969G3;H7C048;K7EMQ8;C0	SMARCE1	0.1586533	0.611630638	2.76E-18
P25705;P25705-2;K7EQT2;K7	ATP5A1	0.2069435	0.611937945	6.26E-46
P19387	POLR2C	-0.2922707	0.61220215	0.0026766
P62917;G3V1A1;E9PKZ0;E9PI	RPL8	0.204813	0.616121915	2.01E-19
P55084;B5MD38;B4E2W0;F5(	HADHB	-0.1494713	0.61672542	1.76E-134
P61923;F8VWL5;F8VVA7;F8V	COPZ1	-0.2881584	0.6179877	5.00E-07
P78316;E9PFK5;P78316-2	NOP14	0.1548538	0.618496073	1.39E-27
P30101;G5EA52	PDIA3	-0.1481476	0.619394237	9.64E-172
Q9BUJ2;Q9BUJ2-4;B7Z4B8;Q5	HNRNPUL1	0.2029228	0.619844401	8.27E-94
Q12899;A2AE48;A2AE51	TRIM26	0.1536369	0.620702041	5.94E-21
Q14103;Q14103-3;H0YA96;H	HNRNPD	0.2020302	0.621605747	4.42E-45
Q9UN86;Q9UN86-2;D6RAC7;	G3BP2	0.201149	0.62334664	6.45E-111
P56537;B7ZBG9;B7ZBH1	EIF6	0.2009964	0.623648308	3.58E-46

P23497;P23497-4;P23497-2;F	SP100	0.15168	0.624256728	4.28E-35
P26641;B4DTG2;E7EMT2	EEF1G	-0.1453114	0.625129466	2.82E-55
Q6UN15;Q6UN15-4;Q6UN15-	FIP1L1	0.149437	0.628341885	1.23E-32
Q9H4A6	GOLPH3	0.1493359	0.628526265	7.43E-07
Q8NAV1	PRPF38A	0.1985092	0.628574363	2.36E-75
P09661;H0YMA0;H0YLR3	SNRPA1	0.1971779	0.631217992	1.33E-121
P35268;K7EJT5;K7EP65;K7EK	RPL22	0.1953831	0.634789444	1.61E-38
P06493;P06493-2;E5RIU6	CDK1	-0.2750092	0.63664569	6.15E-31
Q9NPE3	NOP10	-0.2749577	0.636719228	5.83E-11
P39656;E7EWT1	DDOST	-0.1394062	0.63714324	3.08E-94
P14406;D6RIE3;D6RGV5;H0U	COX7A2	-0.2739086	0.63821801	4.81E-16
O75179;O75179-5;H0YMS3;C	ANKRD17	-0.2734756	0.63883703	2.56E-10
P62910;D3YTB1;F8W727	RPL32	0.193121	0.639302891	6.73E-93
P30153;B3KQV6;F5H3X9;P30	PPP2R1A;PPP2R1B	-0.2731342	0.639325333	4.88E-30
Q96QC0;F5H5K4	PPP1R10	-0.2730598	0.639431744	1.77E-08
Q13547;F5GXM1	HDAC1	-0.1382732	0.639459282	6.10E-69
Q9UBW8;F5GYF7;F5H248	COPS7A	-0.2717037	0.641372995	9.47E-10
Q9UBV2;Q9UBV2-2	SEL1L	0.1419716	0.642019865	3.41E-17
O43491;E9PHY5;E9PPD9;O43	EPB41L2	-0.1365662	0.642955583	2.16E-85
P32969;E7ESE0;D6RAN4;H0Y	RPL9	0.1907196	0.644108802	1.70E-25
P13010	XRCC5	0.1401768	0.645326732	1.33E-59
Q8IXQ4;Q8IXQ4-2;Q8IXQ4-3	KIAA1704	0.1392765	0.646988088	6.58E-30
Q9NS69	TOMM22	-0.1345081	0.647181208	1.95E-56
Q14676;Q14676-2;E9PGY5;Q	MDC1	0.1890678	0.647423209	1.22E-172
P46777	RPL5	-0.133831	0.648573972	1.19E-125
Q9UFC0	LRWD1	-0.1332798	0.649708709	1.80E-40
P35269;M0R0R9;E7EUG6;M0	GTF2F1	0.1879292	0.649712166	1.53E-220
Q9UJX3;Q9UJX3-2;F8VZ62	ANAPC7	-0.2657032	0.649991863	2.49E-47
P62318;B4DJP7;H3BT13	SNRPD3	0.1866055	0.652377192	2.96E-175
Q96PK6;Q96PK6-3;Q2PYN1;F	RBM14;RBM14-RBM	0.1363029	0.652487964	2.93E-39
Q16181;H0Y3Y4;H0YFF6;B4D	Sep-07	0.1863995	0.652792322	3.51E-23
Q9BYP7;Q9BYP7-2;Q9BYP7-3	WNK3	0.1355515	0.653880938	0.0018478
O14773;O14773-2	TPP1	0.1352196	0.654496493	6.98E-21
Q92896;Q92896-2;H3BQT1;H	GLG1	0.1346493	0.655554807	9.66E-07
O75925;B3KSY9;O75928;H3B	PIAS1;PIAS2	-0.2603531	0.657716254	2.27E-07
P55060;B4DUC5;P55060-3;F8	CSE1L	0.1836929	0.658256625	4.45E-18
Q9UHD8;Q9UHD8-2;Q9UHD8	Sep-09	0.1331539	0.658333065	1.82E-89
Q7Z4V5;Q7Z4V5-2;K7EQZ6;I3	HDGFRP2	0.1830139	0.659630398	1.61E-77
P62701;A6NH36	RPS4X	0.182724	0.660217303	7.66E-125
Q04837;C9K0U8;E7EUY5	SSBP1	-0.257864	0.661322516	4.80E-32
P06730;D6RBW1;P06730-3;P	EIF4E	-0.2577324	0.661513412	1.03E-10
Q13144;E9PC74	EIF2B5	0.1312313	0.66191205	8.54E-94
Q96A33;Q96A33-2	CCDC47	0.1818027	0.662083658	1.89E-147
Q15185;B4DP11;B4DP21	PTGES3	-0.1272526	0.66216878	1.80E-49
O43390;Q2L7G6;O43390-2;E	HNRNPR	0.1305332	0.663213482	7.35E-48
Q86UE4;E5RJU9	MTDH	0.181015	0.663681193	9.39E-66
P23284	PPIB	-0.1262035	0.664347176	1.02E-46
P27348	YWHAQ	-0.2556744	0.664501435	1.02E-118
Q9Y3B4	SF3B14	0.1295147	0.665114115	1.06E-33
Q01105;Q01105-2;Q01105-3;	SET	0.1799946	0.665752914	4.70E-142
P25398	RPS12	0.1799107	0.665923412	2.46E-61
Q9BQG0;Q9BQG0-2;I3L1L3	MYBBP1A	0.1277847	0.668347278	3.16E-12
Q13310;Q13310-2;B1ANR0;Q	PABPC4	0.1270809	0.669664411	1.62E-148
Q96C57;E7ENF1;F5H7W8;F5H	C12orf43	0.1777763	0.670265278	8.97E-64
Q05682;Q05682-3;Q05682-2;	CALD1	0.1265316	0.670693124	9.38E-26
Q14202;Q14202-3;A6NL54;A	ZMYM3	0.1264877	0.670775305	5.17E-22
Q9UNF1;Q5H909;Q9UNF1-2;I	MAGED2	-0.2478352	0.675931631	7.12E-24
P33240;E9PID8;P33240-2;E7E	CSTF2;CSTF2T	-0.2477913	0.675995809	1.81E-11
Q92785;B4DT58;J3KMZ8	DPF2	-0.2470989	0.677009022	3.54E-18
Q8NI22;Q8NI22-2;Q8NI22-3;I	MCFD2	-0.2470512	0.677078825	3.12E-30
O94776	MTA2	0.1741333	0.677701768	3.12E-139
P14314;P14314-2;K7ELL7;K7E	PRKCSH	-0.1196213	0.678079778	4.53E-136
Q9H1C3	GLT8D2	-0.245697	0.679062359	0.00012396
P35606;B4DZI8	COPB2	-0.2449875	0.680102508	2.76E-25
P60228;H0YBR5	EIF3E	-0.2444572	0.680880222	6.87E-06
Q9Y333	LSM2	0.1197796	0.683387656	1.59E-10
Q8IZL8;F8WDZ1;I3L3A8;C9JF	PELP1	-0.2427235	0.683425543	9.95E-05
Q9NQZ2	UTP3	-0.2423363	0.683994464	1.29E-111

P14854	COX6B1	-0.2416744	0.684967368	2.66E-18
P68363;F8VVB9	TUBA1B	-0.1156197	0.686481309	0
Q99848;H7C2Q8	EBNA1BP2	0.1167316	0.689147852	1.88E-58
O00264;B7Z1L3	PGRMC1	-0.1136589	0.690612243	1.79E-50
Q9Y6H1;Q5T1J5	CHCHD2;CHCHD2P9	0.1657963	0.694837667	3.09E-18
Q9H089	LSG1	-0.1112919	0.695611394	8.88E-29
Q96IZ7;Q96IZ7-2;H7C5Q0	RSRC1	-0.2324352	0.698602726	5.15E-43
P38646	HSPA9	-0.1096897	0.699002727	6.50E-221
Q15019;C9J2Q4;B5MCX3;Q15	Sep-02	0.1111736	0.699698064	2.11E-27
Q96ST2;Q96ST2-2;Q96ST2-3	IWS1	0.1629524	0.700719318	6.18E-81
Q8WXX5	DNAJC9	-0.2305813	0.701350732	4.29E-13
P10155;Q5LJA0;P10155-3;P1(	TROVE2	-0.2305012	0.701469562	2.41E-32
P08195;P08195-3;P08195-2;F	SLC3A2	-0.1082458	0.70206412	9.01E-85
O00203;E5RJ68	AP3B1	0.1622543	0.702165867	1.18E-86
Q96JP5;Q96JP5-2	ZFP91	0.1092587	0.703346666	0.00086905
P20290;P20290-2;H0Y9Y1;D6	BTF3	-0.2289009	0.703844847	3.87E-19
P49792;E9PGT0	RANBP2	-0.2285347	0.704388825	8.81E-58
Q13416	ORC2	0.1608658	0.705046361	1.30E-147
P61011;P61011-2;G3V4F7	SRP54	0.1605892	0.705620592	0
Q9BXW9;Q9BXW9-2;Q9BXW9	FANCD2	0.1079617	0.705821722	6.39E-81
P61964	WDR5	0.10746	0.706779824	2.83E-50
Q96MX6;Q8ND98;Q96MX6-2	WDR92;DKFZp434B	-0.2265987	0.707267044	1.47E-21
P09429;Q5T7C4;Q5T7C6	HMGB1	-0.2255936	0.708763104	1.19E-11
P82673;P82673-2	MRPS35	-0.2254143	0.709030072	2.33E-17
H7BZJ3	PDIA3	-0.1049271	0.709119158	1.16E-58
P05141	SLC25A5	-0.1043415	0.71036654	5.21E-49
Q99623;Q99623-2;J3KPX7	PHB2	-0.2244186	0.710513245	2.49E-16
P61513;C9J4Z3;M0R0A1;Q6P	RPL37A	0.1580276	0.710947096	1.40E-23
P14866;P14866-2;M0QXS5;M	HNRNPL	-0.104044	0.711000686	7.28E-125
O94842;B4DPY8	TOX4	-0.2239323	0.711238182	2.93E-22
Q6W2J9;H7C2V9;A6NE70;Q6	BCOR	0.1047726	0.711920652	9.93E-34
P62841;K7EM56;K7ELC2;K7EJ	RPS15	0.157238	0.712591936	2.65E-05
P68371;P04350;A8K854	TUBB4B;TUBB4A;TU	-0.1027985	0.713657326	3.16E-259
Q27J81;Q27J81-2	INF2	0.1027107	0.715873661	6.95E-65
P05387	RPLP2	0.1554184	0.716387301	8.25E-138
O14974;O14974-4;O14974-3;	PPP1R12A	0.1553192	0.716594379	2.48E-239
Q13868;A3KFL1;B4DKK6;A3K	EXOSC2	0.1010418	0.719078962	9.47E-15
P46060;F8W7I9	RANGAP1	0.15341	0.720584671	1.73E-200
Q15554;H3BR06	TERF2	-0.09934616	0.721039142	1.88E-34
P55010;H0YLZ1;H0YN40	EIF5	-0.09774017	0.724482041	1.62E-150
Q16531;F5GY55	DDB1	0.1507511	0.726154261	5.05E-68
Q9UEE9;Q9UEE9-2	CFDP1	-0.2137089	0.726535618	0.0011316
O60341;O60341-2;F6S0T5	KDM1A	-0.09584045	0.72856184	1.61E-106
Q9UBQ5;K7ES31;K7EMQ9;K7	EIF3K	0.09395981	0.732734856	3.01E-33
P52655;J3KNC0	GTF2A1	-0.2085304	0.734326486	1.76E-17
Q96DI7;B4DQJ1	SNRNP40	0.145668	0.736842179	4.39E-46
Q9BXP5;Q9BXP5-5;Q9BXP5-4	SRRT	0.1455536	0.737083403	6.68E-70
P10599;P10599-2	TXN	0.09165764	0.737192563	4.37E-20
P09012;M0R268;M0QZG7;M(	SNRPA	-0.09111404	0.738745377	4.58E-101
P62306;F8W0W6	SNRPF	0.14431	0.739706375	8.07E-77
Q9NYB0	TERF2IP	0.1433029	0.741832722	2.20E-72
Q15459;E9PAW1	SF3A1	-0.08943176	0.742381221	1.76E-221
Q02078;Q14814;Q06413;Q02	MEF2A;MEF2D;MEF	-0.2025204	0.743402844	4.23E-06
O95782;O95782-2;O94973;O	AP2A1;AP2A2	0.08697701	0.746282875	2.19E-13
P68400;E7EU96;P68400-2	CSNK2A1	-0.08728981	0.747018855	3.00E-302
Q9UQ35	SRRM2	0.1406288	0.74748835	1.17E-150
P11279;B4DWL3	LAMP1	-0.1987228	0.749156389	6.55E-07
Q9BT78;D6RFN0;D6RD63;Q9I	COPS4	0.1394329	0.750022076	7.90E-70
P55884;P55884-2	EIF3B	-0.1973572	0.751228906	1.67E-09
Q14160;Q14160-3;Q14160-2	SCRIB	0.1375523	0.754011984	3.49E-97
Q6P1J9	CDC73	-0.08321762	0.755860907	3.02E-42
P38432	COIL	0.08181	0.756358895	1.71E-26
P40939	HADHA	-0.08258629	0.757234637	9.51E-175
O60237;F8W8M3;O60237-4;I	PPP1R12B	-0.1929302	0.757959496	8.51E-09
Q13243;Q13243-3;B4DJK0;B4	SRSF5	-0.08213425	0.758218715	4.90E-66
O43852;O43852-3;O43852-4;	CALU	-0.08208656	0.758322544	1.38E-72
P04406;E7EUT4;E7EUT5	GAPDH	0.1350765	0.759274432	8.58E-122
P19784;H3BSA1;H3BV19	CSNK2A2	-0.08158112	0.759423395	1.06E-203

P00403	MT-CO2	-0.1911392	0.760687725	2.13E-07
P42704	LRPPRC	-0.08002472	0.762816239	8.47E-73
Q5T8P6;Q5T8P6-3;Q5T8P6-2;	RBM26	-0.1890259	0.763910806	7.51E-12
Q9NR30;Q9NR30-2	DDX21	0.1322861	0.765219214	2.46E-41
Q9BTT0;Q5TB20;E9PPH5;Q5T	ANP32E	-0.07776451	0.767751456	2.92E-206
O94992	HEXIM1	-0.1854286	0.769406417	4.43E-07
Q9NZJ4;Q9NZJ4-2	SACS	-0.07531166	0.77311798	0.0067645
Q9NW82;D6RIW8	WDR70	0.1280079	0.774360269	6.27E-61
Q9Y5B9	SUPT16H	0.127285	0.775907967	2.04E-165
O43143	DHX15	0.07170868	0.776175824	3.99E-09
P14678;P63162;P14678-2;B3	SNRPB;SNRPN	-0.07205582	0.780258102	1.04E-127
Q9P0L0;Q9P0L0-2	VAPA	0.0693264	0.780871266	9.25E-12
O75822;B4DUI3;F5H425	EIF3J	-0.0716095	0.781238349	1.48E-35
Q92769;B3KRS5;J3KPW7	HDAC2	0.06877518	0.781958867	5.87E-23
Q15061;C9IZK7	WDR43	-0.07111549	0.782323729	3.79E-35
P04844;P04844-2	RPN2	0.1239796	0.782996165	1.28E-298
Q9BY77;Q9BY77-2;F8WCX5	POLDIP3	0.06766891	0.784142882	2.59E-09
P68366;A8MUB1	TUBA4A	0.06751442	0.784448026	2.45E-237
P32519;P32519-2	ELF1	0.06737328	0.78472683	1.82E-53
P52701;F5H2F9;B4DF41;P527	MSH6	-0.06948471	0.78590974	2.09E-250
Q6UX04;D6REK3;Q6UX04-2	CWC27	0.06654167	0.786370067	4.26E-16
P62995;P62995-3;H7BXF3	TRA2B	-0.06889534	0.787206859	4.08E-24
Q12797;F5H667	ASPH	0.1212387	0.788887404	4.15E-66
P62847;P62847-2;E7ETK0;P6	RPS24	0.1210899	0.789207528	3.48E-16
P43307;C9J3L8;C9J5W0;E9PA	SSR1	0.1208191	0.789790409	2.51E-72
Q7Z5K2;Q7Z5K2-2;Q7Z5K2-3;	WAPAL	0.1206646	0.79012295	7.54E-88
O43172;O43172-2	PRPF4	0.1197777	0.792032721	9.22E-45
O60832;H7C2Q9;H7C0M1;C9	DKC1	-0.1706657	0.792078718	9.42E-14
Q9Y2W1	THRAP3	0.118454	0.794885322	1.64E-243
O43395;E7EVD1	PRPF3	-0.06531525	0.795098691	6.30E-44
O43719	HTATSF1	0.1179848	0.795897136	1.37E-134
P08240;P08240-2	SRPR	0.06170082	0.795954199	7.53E-29
P98175-2;P98175;P98175-3;F	RBM10	-0.06477547	0.796290405	0
P40426;B7Z5Q0;P40426-2;P4	PBX3	-0.1662941	0.798827375	2.44E-11
Q8WX92	NELFB	-0.1660385	0.7992224	5.28E-35
P46783;F6U211	RPS10	-0.06334496	0.79945095	2.84E-62
P62136;P62136-2;A6NNR3;E	PPP1CA	-0.163929	0.80248479	1.28E-151
P08621;P08621-2;P08621-3;F	SNRNP70	0.05830193	0.802702019	1.34E-10
O95365	ZBTB7A	-0.1632156	0.803588767	5.80E-10
P27824;B4DGP8;B4E2T8	CANX	-0.06116486	0.804273927	1.02E-211
Q15029;Q15029-2;K7EJ81	EFTUD2	-0.06023026	0.806343816	2.56E-84
P78527;E7EUY0;P78527-2	PRKDC	0.05605698	0.807167027	1.61E-67
P25490;H0YJV7	YY1	0.112505	0.807738952	3.24E-37
O14617;O14617-5;O14617-4;	AP3D1	-0.1598892	0.808741868	4.48E-35
P01011;G3V3A0;G3V5I3	SERPINA3	-0.15979	0.808895644	0.012304
P27797;K7EJB9	CALR	-0.05867958	0.809781129	2.23E-136
Q16629;Q16629-3;Q16629-2;	SRSF7	0.1114922	0.809932526	6.92E-35
Q9H6T3;Q9H6T3-3;Q9H6T3-2	RPAP3	-0.1585522	0.810815507	3.92E-30
Q9Y2W2;F5H721	WBP11	0.1104546	0.812181353	3.53E-299
O15391	YY2	-0.1566963	0.813695953	2.35E-13
Q96B01;Q96B01-3;Q96B01-2	RAD51AP1	-0.05657005	0.814463112	4.39E-16
P06454;P06454-2;B8ZZQ6	PTMA	-0.05621529	0.815251155	0.00067329
P51610;P51610-3;P51610-2;A	HCFC1	-0.1534405	0.818755384	8.09E-06
Q9NR50;H0Y580;Q9NR50-3;C	EIF2B3	-0.05404854	0.820068173	5.74E-36
P52292	KPNA2	0.1067047	0.820321341	2.64E-185
P25205;J3KQ69;B4DWW4	MCM3	0.04728127	0.824680214	1.32E-70
P42568;B7Z755	MLLT3	0.04674911	0.825745103	0.00010234
P61353;K7EQQ9;K7ELC7	RPL27	-0.05112076	0.826587851	1.30E-14
P35613;P35613-2;P35613-4;F	BSG	-0.0495491	0.830092633	7.13E-132
Q92766;C9JU34;Q92766-3;Q9	RREB1	-0.1458015	0.830655241	6.55E-08
P20645;H0YGT2;H0YF90	M6PR	0.04370499	0.831842828	2.60E-17
Q8WYA6;B4DE16;Q8WYA6-3;	CTNNBL1	-0.04647827	0.83695027	3.78E-263
Q01650	SLC7A5	0.04049683	0.838280092	8.50E-43
P63165;B8ZZN6;B8ZZJ0;B8ZZ	SUMO1	0.03909683	0.841092642	1.60E-05
Q9UKV3;E7EQT4;Q9UKV3-5	ACIN1	0.096838	0.841829999	5.35E-223
Q8IX15;F8WCA3	HOMEZ	0.03853989	0.842212097	4.63E-22
P49790;F6QR24	NUP153	0.03821373	0.842867817	1.78E-34
P0C0S5;Q71UI9;Q71UI9-3;Q7	H2AFZ;H2AFV	0.03821373	0.842867817	1.04E-14

Q9NYL9;H0YKU1;H0YNJ8	TMOD3	-0.1375275	0.843588397	4.24E-67
Q9UGP8	SEC63	-0.04309464	0.844520803	4.01E-267
Q07021;I3L3Q7;I3L3B0	C1QBP	-0.04268074	0.84544785	8.98E-112
P13073;Q86WV2;H3BN72;H3	COX4I1	-0.1351719	0.847278268	1.21E-12
P07910;P07910-4;P07910-2;(	HNRNPC;HNRNPCL1	0.09394836	0.848152345	1.49E-53
O60763;O60763-2;F5H4X1;F5	USO1	-0.04133034	0.848473984	5.03E-111
P10809	HSPD1	-0.04074097	0.849795415	1.58E-112
Q9BRJ6;C9JQV0;H7C0T1;H7C	C7orf50	0.03206444	0.855250523	7.45E-19
H0YNU2;H0YNW9;H0YMH7;C	CTDSPL2	0.03134155	0.856708588	0.00018703
Q9H307;Q9H307-2	PNN	0.08990479	0.857015793	6.53E-66
O00629	KPNA4	0.08955956	0.857773384	1.74E-53
Q9BWJ5	SF3B5	-0.03499413	0.862702006	3.25E-21
Q13185	CBX3	0.08728409	0.86277003	4.85E-77
P42167;G5E972;P42167-2;A2	TMPO	-0.03475189	0.863246858	2.61E-56
P46776;E9PJD9;E9PLL6	RPL27A	-0.03367996	0.865658716	1.50E-23
P09234	SNRPC	-0.03295517	0.86729022	8.19E-84
P55209;F8VUX1;F8VY35;B3KI	NAP1L1	-0.0328064	0.867625177	1.16E-134
P37275;H0YMD3;H0YK86;H0	ZEB1	-0.1219692	0.868019246	2.57E-07
P62316;P62316-2	SNRPD2	-0.03245544	0.868415428	6.59E-109
Q68E01;Q68E01-2;Q68E01-3	INTS3	-0.03174591	0.870013511	1.85E-160
Q7L1Q6;Q7L1Q6-4;Q7L1Q6-3	BZW1	-0.03147507	0.870623672	1.41E-15
Q9NWV8;M0QY17;Q9NWV8-	BABAM1	-0.1186523	0.873244855	4.87E-35
P52434;C9JBJ6;C9JLU1;C9JUA	POLR2H	0.02291298	0.873743915	5.77E-39
P13984	GTF2F2	-0.02958107	0.874892634	7.60E-105
O60684;F5H4G7;F5GYL8;O15	KPNA6;KPNA5	0.08142471	0.87566132	6.49E-97
Q14257;A8MXP8;F8WCY5	RCN2	0.02070808	0.878210326	0.00026448
P20674;H3BNX8;H3BRI0	COX5A	-0.1153507	0.878451922	2.60E-19
P16615;P16615-5;P16615-2;F	ATP2A2	0.07977295	0.879301511	3.06E-136
P52739;D6RJH2;D6R9I2;P527	ZNF131	0.01998901	0.879667778	4.26E-13
P39687;H0YN26	ANP32A	0.07938194	0.880163595	1.83E-143
Q9NYF8;Q9NYF8-2;Q9NYF8-4	BCLAF1	0.07927704	0.88039491	4.04E-235
P61244;P61244-2;Q6V3B1;P6	MAX	-0.1132469	0.881772646	0.0002923
P62269;Q5GGW2;J3JS69	RPS18	0.07734299	0.884661329	1.07E-15
P62891;Q59GN2	RPL39;RPL39P5	0.07692719	0.885579009	0.0016918
Q9BQE9;Q9BQE9-4;Q4VC05;(	BCL7B;BCL7A	-0.1104794	0.886144226	3.66E-05
Q99933;Q99933-4;Q99933-3;	BAG1	0.01579666	0.888173035	2.29E-06
Q9Y2S0	POLR1D	-0.1091595	0.888230316	8.98E-106
P62979;P0CG47;J3QS39;J3QT	RPS27A;UBB;UBC;UI	0.07549095	0.888749964	3.78E-66
P29692;E9PK01;P29692-2;P2	EEF1D	0.07520866	0.889373417	1.27E-98
Q06587;Q06587-2	RING1	-0.02306366	0.889609591	8.88E-110
E9PGZ2;Q32MZ4;Q32MZ4-3;(	LRRFIP1	0.01491928	0.889954689	0.0001358
Q9UNS2;J3QL22;J3QS85;J3KT	COPS3	-0.1065044	0.892428944	1.81E-27
P30508;E7ERM2;P30510;Q29	HLA-C	-0.02166367	0.892776064	1.02E-172
O00422;H7BZW6	SAP18	-0.1059265	0.893343274	0.00099171
P63173;J3KT73;J3QL01	RPL38	-0.02047348	0.895469345	1.46E-28
O95251;O95251-4;E7EUP3;G	KAT7	0.01203728	0.8958109	9.43E-30
P05455;E9PFH8;E7ERC4;E9PC	SSB	0.07208252	0.89628223	3.68E-181
Q9BUF5	TUBB6	-0.1019478	0.899641749	1.32E-43
Q9GZS3;H0YL19;H0YN81	WDR61	0.07016373	0.900526716	7.94E-46
Q07157;Q07157-2;G5E9E7;G	TJP1	-0.1012669	0.90072032	1.10E-12
Q8NCA5;E9PH82;Q8NCA5-2;E	FAM98A	-0.1011734	0.900868374	2.49E-08
Q8NC51;Q8NC51-2	SERBP1	0.06994629	0.901007883	7.19E-155
P18887;F5H8D7	XRCC1	-0.01652145	0.904420893	6.19E-108
Q13435;E9PPJ0;E9PJ04;H0YC	SF3B2	-0.01500893	0.907850127	1.21E-84
Q9Y3U8	RPL36	0.06638336	0.908897326	9.69E-22
Q9ULU4;B7ZM62;H7C4X9;Q9	ZMYND8	0.005449295	0.909218466	3.72E-25
Q96HY6;Q96HY6-2	DDRGK1	-0.09568977	0.909561059	5.34E-106
P30050;P30050-2	RPL12	-0.01410294	0.909905035	7.43E-91
O75496;H7C608;E2QRF9	GMNN	-0.09457588	0.911328167	2.90E-07
Q8NFC6	BOD1L1	0.004323959	0.911511394	4.88E-81
O75821;K7EL20;K7ENA8	EIF3G	0.06482506	0.912350774	9.57E-105
Q9Y678	COPG1	-0.09332275	0.913316686	4.83E-61
P62899;H7C2W9;C9JU56;B7Z	RPL31	-0.01239014	0.913791529	1.35E-72
Q8TAQ2;Q8TAQ2-2;Q8TAQ2-	SMARCC2;SMARCC1	0.003141403	0.913921706	1.19E-64
P11142;E9PKE3;P11142-2;E9I	HSPA8	-0.01221085	0.914198476	3.41E-247
Q9NQC3;Q9NQC3-2;Q9NQC3	RTN4	0.06396294	0.914262088	7.63E-48
E7EWI9;P51991-2;P51991	HNRNPA3	0.06396103	0.914266317	4.75E-28
P62750;H7BY10;K7EJV9;K7ER	RPL23A	0.06363297	0.914993763	1.41E-59

O43707;D6PXK4;F5GXS2;H7C	ACTN4	-0.01152611	0.915752876	7.96E-65
Q15007;Q15007-2	WTAP	-0.09107399	0.916886478	6.28E-110
Q9Y262;B0QY90;Q9Y262-2;J3	EIF3L	0.001293182	0.917690368	1.93E-16
P49755	TMED10	-0.009723663	0.919846065	4.48E-123
Q9H8H0;J3QLQ6;J3QR28;J3Q	NOL11	-0.000377655	0.921098927	1.27E-18
Q9BVI4;F5H303	NOC4L	-0.08795929	0.921833652	9.84E-08
Q9HCY8	S100A14	-0.08720207	0.923036828	1.20E-32
Q9Y2T2	AP3M1	0.05960274	0.92393597	2.63E-46
P24534	EEF1B2	-0.007616043	0.924634969	6.56E-49
P26196	DDX6	-0.08458328	0.927199279	1.23E-15
P42677;Q5T4L4	RPS27	-0.006458282	0.927266789	2.15E-12
O00483	NDUFA4	-0.08410454	0.927960441	2.44E-06
P23246;P23246-2	SFPQ	0.0571804	0.929315307	6.48E-62
Q3B726	TWISTNB	-0.004526138	0.929568094	5.63E-08
O94874;O94874-2;O94874-3	UFL1	-0.004617691	0.929755093	7.42E-23
Q9Y3Y2;Q5T7Y7;Q9Y3Y2-4;Q	CHTOP	-0.08276558	0.930089616	0.005041
P33991;J3KPV4	MCM4	-0.004106522	0.932615231	0
P53618;E9PP73	COPB1	-0.08109093	0.932753305	7.04E-37
Q13330;Q13330-3;Q13330-2;	MTA1	-0.006292343	0.933176296	1.99E-07
P83731;C9JXB8;C9JNW5	RPL24	-0.00352478	0.933938722	5.41E-45
Q8WYP5;Q8WYP5-2;Q8WYP5	AHCTF1	-0.006904602	0.934427412	9.24E-98
Q7Z417	NUFIP2	-0.007385254	0.93540971	3.39E-19
O15042;O15042-2;E7ET15;O1	U2SURP	-0.002750397	0.935700767	2.07E-68
P43246;P43246-2;E9PHA6	MSH2	-0.002447128	0.936390916	5.75E-144
Q9ULC4;Q9ULC4-2;Q9ULC4-3	MCTS1	-0.00888443	0.93847417	1.12E-19
P55795	HNRNPH2	-0.009338379	0.939402267	3.74E-39
Q8N6N3;Q8N6N3-2;Q8N6N3-	C1orf52	-0.07532501	0.941930102	1.73E-55
P47914	RPL29	-0.01091003	0.942616138	1.52E-06
Q86T24	ZBTB33	0.001764297	0.945979574	3.69E-43
Q08945	SSRP1	0.002552032	0.947774016	1.44E-124
Q96D15	RCN3	0.002790451	0.948317181	2.88E-58
Q52LJ0;Q52LJ0-2	FAM98B	-0.06971169	0.950871469	7.00E-21
Q02543;M0R0P7;M0R3D6;M	RPL18A	-0.06857109	0.952689094	8.90E-10
P62875	POLR2L	-0.06810951	0.953424725	1.23E-19
P20020;P20020-5;P20020-2;F	ATP2B1;ATP2B4	-0.01680374	0.954676053	0.00018443
K7ELV2;Q96EE3;Q96EE3-1	SEH1L	-0.01756477	0.95623412	0.0032213
Q15366;Q15366-4;Q15366-5;	PCBP2	-0.0199852	0.961190558	2.60E-14
P17693;Q5RJ85	HLA-G	-0.02008629	0.961397598	9.89E-05
P68104;Q5VTE0;Q05639	EEF1A1;EEF1A1P5;E	0.008897781	0.962238369	4.21E-44
Q86YP4;H7C3H1;F5H7D9;B4E	GATAD2A	-0.02067375	0.962600828	8.96E-34
Q9UBU8;H0YMJ0;H0YLJ3;Q9U	MORF4L1	-0.02085495	0.962971971	4.70E-08
O60216	RAD21	-0.06113052	0.964551825	7.06E-06
Q68CQ4	DIEXF	0.01025391	0.965331264	1.40E-149
Q09028;Q09028-3;Q09028-4;	RBBP4	0.04037666	0.966707406	3.61E-63
P08107;P08107-2;F8VZJ4;E7E	HSPA1A	0.03998947	0.967570176	3.93E-81
P01040;C9J0E4	CSTA	-0.02334595	0.968074994	1.07E-34
Q5SRQ6;P67870;Q5SRQ3	CSNK2B;CSNK2B-LY(	0.03932953	0.969040796	2.23E-141
Q9NY27;Q9NY27-2;Q9NY27-3	PPP4R2	-0.0563755	0.972137181	2.18E-59
Q92572;F5H459	AP3S1	0.03792191	0.972177899	3.02E-77
O60506;O60506-4;O60506-3;	SYNCRIP	0.03667068	0.974966798	3.85E-67
Q99627;H7C3S9;Q99627-2;E9	COPS8	-0.0268898	0.975337086	1.37E-14
O75489;E9PKL8;G3V194;B4D	NDUFS3	-0.05381393	0.976224565	0.00034405
Q03701	CEBPZ	-0.02822495	0.978073636	1.49E-17
Q9UHB9;F5H5Y3;Q9UHB9-2;(	SRP68	0.03491402	0.978882818	1.64E-171
P09874	PARP1	0.01641655	0.979392197	1.48E-116
Q8IYB3;A9Z1X7;Q8IYB3-2;E9F	SRRM1	0.03458786	0.979609956	8.28E-90
Q96DH6;Q96DH6-2;B4DHE8;J	MSI2	-0.02915955	0.979989377	9.19E-32
P12270	TPR	-0.05107307	0.980598724	6.19E-65
P11387	TOP1	-0.02968788	0.981072408	1.76E-50
Q15910;Q15910-2;Q15910-3;	EZH2	-0.0301075	0.981932603	4.15E-06
Q13112	CHAF1B	-0.04926872	0.983478629	3.99E-83
P18621;J3QQT2;J3KRX5;J3QL	RPL17	0.01831245	0.98371946	1.24E-51
Q12888;C9JXV0;A6NNK5;F8V	TP53BP1	0.01889229	0.98504299	4.50E-154
O75475;O75475-2;O75475-3	PSIP1	0.01928711	0.985944233	5.91E-116
P17844;B4DLW8;J3KTA4	DDX5	-0.03232574	0.986480229	6.77E-22
Q01664	TFAP4	0.01989174	0.987324432	2.43E-170
Q9GZT3;H0YJW7;H0YJ40;G3V	SLIRP	0.03067398	0.988336755	1.92E-32
O43818	RRP9	-0.04467392	0.990813226	1.99E-69

P49916;P49916-2;K7EQB6;K7	LIG3	-0.04457474	0.990971559	2.40E-150
Q14694;Q14694-3;Q14694-2	USP10	0.02303505	0.994500244	8.33E-63
Q6UXN9	WDR82	-0.03627014	0.994567626	3.13E-36
Q9UHR5;Q9UHR5-2;J3QQJ0;J	SAP30BP	0.0231781	0.994826828	7.65E-65
Q9Y3D9;J3QLR8	MRPS23	-0.04171562	0.99553595	2.38E-07
Q13011;M0QZW4;M0R248	ECH1	-0.04046059	0.997539587	0.013709
P53999	SUB1	0.02602196	0.998711128	9.40E-82
Q9C005;B4DIS3	DPY30;LOC84661	-0.03948593	0.999095614	2.48E-05
Q12824;Q12824-2;B5MCL5;G	SMARCB1	-0.03891945	1	1.43E-33
P63220;Q8WVC2;Q9BYK1	RPS21	0.02544403	1	3.37E-46

Appendix 4 (Chapter 3)

Identification and quantification of interacting proteins for H2A T101 GlcNAc modified nucleosome versus wild-type nucleosome. Statistically significant interacting partners are denoted with a '+'

Majority Protein Ids	Gene names	log2(Bait/Control)	log10(Intensity)	Significance B value	Statistically Significant Interactor	PEP
P20585	MSH3	5.203152	9.007619775	1.67E-50	+	8.52E-155
Q9ULM3	YEATS2	4.658899	9.146097014	5.30E-41	+	8.90E-163
Q96KM6	ZNF512B	3.355392	9.253677165	2.20E-22	+	8.95E-143
Q5T5X7	BEND3	3.349529	9.670570525	2.59E-22	+	0
Q13472;Q13472-2;B4DK80;B4	TOP3A	2.990828	9.263990933	3.22E-18	+	5.43E-127
Q9UHL9;Q9UHL9-2;E9PFE2;Q	GTF2IRD1	2.81488	8.810628984	2.27E-16	+	7.86E-53
P43246;E9PHA6;P43246-2	MSH2	2.495998	9.119123865	2.73E-13	+	5.35E-103
Q5SW79;Q5SW79-2;Q5SW79	CEP170	2.157217	8.448273355	2.13E-10	+	5.18E-46
Q9H9A7	RMI1	2.139271	8.815677346	2.96E-10	+	1.89E-135
Q6PJG2;F6RU81	ELMSAN1	1.90761	9.574598375	1.63E-08	+	3.04E-184
Q00059;A8MRB2;H7BYN3	TFAM	1.878168	10.12273999	2.63E-08	+	0
Q15853;M0QXT0;Q6YI47;Q15	USF2	1.810692	9.299463715	7.71E-08	+	9.11E-93
Q14676;Q14676-2;E9PGY5;Q	MDC1	1.734467	10.50708641	2.49E-07	+	0
P49959;P49959-2;F8W7U8;B3	MRE11A	1.728312	8.858489074	2.73E-07	+	4.21E-52
Q92878;Q92878-2;Q92878-3	RAD50	1.616215	8.864617862	1.40E-06	+	2.13E-60
P22415;E9PME6;Q7Z5Y1;B1A	USF1;usf1-bd	1.602409	8.758207674	1.70E-06	+	5.41E-121
Q9NZI7;Q9NZI7-4	UBP1	1.58807	9.099438916	2.08E-06	+	8.12E-107
P54727;P54727-2	RAD23B	1.552168	8.819813641	3.41E-06	+	5.06E-97
Q7L0Y3;C9JVB6	TRMT10C	1.550674	9.270189543	3.48E-06	+	3.14E-102
P14868;Q68CR9	DARS;DKFZp781B11	1.542915	9.522561595	3.87E-06	+	7.05E-168
Q6W2J9;Q6W2J9-4;Q6W2J9-	BCOR	1.463539	8.830838781	1.11E-05	+	5.53E-65
Q9Y5B9	SUPT16H	1.368172	10.0839324	3.70E-05	+	0
P29372;A2IDA3;G5E9E2;Q5J9	MPG	1.350128	8.384998193	4.61E-05	+	2.78E-16
Q14807;B7Z265;H3BRB3	KIF22	1.341299	9.47633882	5.13E-05	+	4.78E-273
P11387	TOP1	1.33963	10.82392394	5.24E-05	+	0
Q6SPF0;E9PIW9	SAMD1	1.224108	9.54997137	0.00020018	+	1.01E-138
Q16666;Q16666-2;Q16666-3;	IFI16	1.163898	9.705615717	0.000386823	+	3.57E-184
P35249;C9JZI1;C9J8M3;C9JTT	RFC4	1.093575	10.31492006	0.000806653		0
Q7Z7K6;Q7Z7K6-3;Q7Z7K6-2	CENPV	0.9865608	8.857036834	0.002299314		2.70E-36
P54132;H0YNU5	BLM	0.9744148	9.43806745	0.002575698		7.19E-250
P26641;B4DTG2;E7EMT2	EEF1G	0.9718971	8.653482657	0.002636659		2.15E-40
Q04837;E7EUY5;C9K0U8	SSBP1	0.971714	9.834986253	0.002641144		1.41E-124
Q08945	SSRP1	0.9709053	10.01393212	0.002661035		0
P61964	WDR5	0.9502945	9.234669108	0.003216518		3.54E-27
Q01831;E9PH69	XPC	0.9363556	9.494683221	0.003650028		1.95E-224
Q9NQ55;Q9NQ55-2;C9J3F9;A	PPAN	0.9281845	9.06733128	0.003928218		2.38E-171
Q9ULW0;Q96RR5	TPX2;HCA90	0.9281139	9.34321159	0.003930703		9.17E-144
P40937;P40937-2;F8W9B4	RFC5	0.9035873	10.36174672	0.004885764		0
P35251;P35251-2	RFC1	0.8860779	10.65422469	0.00569107		0
P16070;H0YD13;P16070-18;P	CD44	0.8796597	8.39891174	0.006015031		6.70E-31
Q92769;B3KRS5;J3KPW7	HDAC2	0.8784466	9.424440588	0.006078096		3.35E-84
Q9C005;B4DIS3	DPY30;LOC84661	0.8307762	9.368007805	0.009079642		5.34E-37
H7C0N4	SF1	0.8290997	8.737089227	0.00920593		1.64E-126
Q9H2U1;Q9H2U1-3;Q9H2U1-	DHX36	0.8232994	9.030478281	0.00965502		2.86E-165
P41208	CETN2	0.8177185	8.906991914	0.010105459		7.92E-43
Q9NSU2;Q9NSU2-2;Q9NSU2-	TREX1	0.8154564	9.618790472	0.010293302		5.49E-91
P35250;P35250-2	RFC2	0.784935	10.25355607	0.013149147		0
O75528;O75528-2	TADA3	0.7830696	8.739730529	0.013344485		5.35E-35
Q9H147;F2Z2A4;H7C1M5;H0	DNTTIP1	0.7720375	9.115277591	0.01455303		7.76E-110
P05549;P05549-5;Q5TAV5;Q5	TFAP2A	0.7476006	8.860757123	0.017579001		1.13E-75
Q12800;Q12800-3;Q12800-4;	TFCP2	0.727932	8.888679235	0.020401798		1.48E-75
O60264	SMARCA5	0.7110786	8.848072057	0.023127299		5.26E-100
Q9BQ67;M0QX71	GRWD1	0.7017517	8.827349884	0.024767482		5.03E-71
Q14134;Q14134-2;B7Z8U9;E5	TRIM29	0.6840649	8.393487458	0.028155826		1.48E-27
P35908	KRT2	0.6709728	8.194375567	0.030914587		0
P19388	POLR2E	0.6670685	9.137575634	0.031780975		1.24E-59
Q9UPQ9;Q9UPQ9-1;H0Y720	TNRC6B	0.6643105	8.886349698	0.032405464		2.59E-166
O75955;B4DVY7;B0V109;F8V	FLOT1	0.6460629	8.94144683	0.036807832		8.62E-133
O15160;O15160-2;E7EQB9	POLR1C	0.6309166	9.530775813	0.040839535		1.02E-203
P62841;K7ELC2;K7EQJ5;K7EN	RPS15	0.6225319	9.621290555	0.043228156		1.80E-79
P40938;P40938-2	RFC3	0.6012421	10.29241115	0.049828707		0
P42766;H0Y3A0;F2Z388	RPL35	0.5899181	10.17713232	0.053671039		5.52E-108
Q9P013	CWC15	0.5819836	8.257174405	0.056508225		1.05E-25
P62875	POLR2L	0.575098	8.70923603	0.059070453		6.72E-32
P46013	MKI67	0.5693779	11.76346543	0.061271694		0
Q86TG7	PEG10	0.5462112	9.229988837	0.070892228		1.80E-202
Q92922	SMARCC1	0.5361443	8.705906456	0.075442599		4.69E-114
P13987;E9PNW4;E9PR17;H0Y	CD59	0.5336266	9.724562573	0.076617141		1.49E-60
Q8N9T8;D3YTE0;Q8N9T8-2;H	KRI1	0.53092	8.933082162	0.077896371		5.75E-41
Q68D10;Q68D10-2	SPTY2D1	0.5185642	9.163846876	0.083958921		1.60E-34
P16403	HIST1H1C	0.5108147	10.97582227	0.087952453		2.84E-118
Q9HAN9	NMNAT1	0.5068817	9.057133367	0.090037032		5.38E-65
P0C0S8;Q9BTM1;Q99878;Q9	HIST1H2AG;H2AFJ;H	0.502243	11.25779853	0.092546575		1.61E-167

Q9NVV4-2;Q9NVV4	MTPAP	0.4938374	8.828589012	0.097236961	2.64E-61
P18887;F5H8D7	XRCC1	0.491745	10.65484048	0.098433564	0
P49916;P49916-2;K7ERZ5	LIG3	0.4907417	10.77630157	0.099011479	0
Q8IWC1;Q8IWC1-4;Q8IWC1-2	MAP7D3	0.4831028	8.851117639	0.103501045	1.09E-72
P52434;C9JLU1;C9JBJ6;C9J41	POLR2H	0.4818249	9.602580832	0.104267668	1.11E-78
Q16891;Q16891-2;B9A067;C9	IMMT	0.4755898	8.984585815	0.108072996	4.18E-57
P61158;B4DXW1;F5H3P5	ACTR3	0.4701252	9.021850577	0.111497689	2.55E-68
Q8N556;Q8N556-2	AFAP1	0.4633713	9.261691003	0.11584815	3.53E-39
Q9UKD2	MRTO4	0.4532471	9.373849508	0.122618078	1.16E-42
Q02241;H7BYN4	KIF23	0.4456863	9.60184279	0.127872491	7.81E-216
Q99959;Q99959-2	PKP2	0.4355354	8.786666258	0.135200315	6.37E-116
Q3B726	TWISTNB	0.4226933	9.221753194	0.14493083	3.28E-112
Q6ZNB6;Q6ZNB6-2	NFXL1	0.4153118	8.82087767	0.15076162	1.59E-101
P17275	JUNB	0.412796	8.423884554	0.152789242	2.96E-14
Q7Z739	YTHDF3	0.401186	9.112403893	0.162416041	4.65E-54
Q9Y2D5-4;Q9Y2D5;Q9Y2D5-5	AKAP2	0.4009705	8.96673291	0.162598985	8.28E-145
P46013-2	MKI67	0.3982677	9.331265292	0.164906301	0
P04003	C4BPA	0.3959961	9.144667594	0.166864594	7.83E-117
Q9BRJ6;C9JQV0;H7C0T1;H7C	C7orf50	0.3818321	9.196120893	0.179470672	1.68E-55
O14950;P19105;J3QRS3;P248	MYL12B;MYL12A;M	0.3780212	9.853150436	0.182980299	6.52E-244
P29692;E9PMW7;E9PPR1;E9I	EEF1D	0.3745403	8.819208215	0.18623026	3.04E-51
P13010	XRCC5	0.3691063	11.40348085	0.191388736	0
Q9Y2S0	POLR1D	0.3648777	8.937994051	0.195475059	3.14E-85
Q7Z2E3;Q7Z2E3-7;Q7Z2E3-8;	APTX	0.354866	10.11390994	0.205404155	0
P18077;C9K025;F8WBS5;F8W	RPL35A	0.3545532	9.672458081	0.20572018	9.94E-27
Q14839;F5GWX5;Q14839-2;C	CHD4;CHD5	0.3540897	8.384299639	0.206189085	6.70E-24
Q9H4L4;J3KNH7;J3QL36	SENP3	0.3535614	8.731072784	0.206724545	1.85E-72
P05141	SLC25A5	0.3462181	9.636337422	0.214271611	3.11E-89
O43324;O43324-2;D6RBD7;C	EEF1E1;hCG_20432	0.3398552	8.969061622	0.220970095	1.37E-24
Q9BQB6;Q9BQB6-3;I3L3B4;F8	VKORC1	0.3150311	8.320976677	0.248535591	3.85E-10
A6NHQ2	FBLL1	0.3072548	9.216588111	0.257645528	2.00E-26
P12956;B1AHC9;B1AHC8;F5H	XRCC6	0.3045578	11.55024059	0.260858508	0
O75531	BANF1	0.2982864	8.72084536	0.268436525	4.49E-25
P78316;E9PFK5;P78316-2	NOP14	0.2900066	8.541117248	0.278671044	7.92E-21
O75475;O75475-2;O75475-3	PSIP1	0.2823505	9.758548567	0.288367998	2.77E-127
P11021	HSPA5	0.2816753	9.49843462	0.289233971	7.59E-167
Q9P2I0	CPSF2	0.2735996	9.151431144	0.299727144	2.79E-47
Q96RR1;Q96RR1-3;Q96RR1-2	PEO1	0.2728081	8.639356978	0.300769137	7.76E-68
Q86XK2;Q86XK2-5;Q86XK2-6	FBXO11	0.2692585	8.970388723	0.305471435	3.29E-106
Q8WYP5;Q8WYP5-2;Q8WYP5	AHCTF1	0.2665386	9.948593884	0.309107416	0
Q9UN86	G3BP2	0.2620487	10.44974059	0.315171928	0
Q9BZK7	TBL1XR1	0.260479	8.769015263	0.317310509	2.66E-117
Q6WCQ1;Q6WCQ1-2;Q6WCC	MPRIP	0.2604332	9.999134893	0.317373016	0
P08107;P08107-2;F8VZJ4;E7E	HSPA1A	0.2592964	9.870169721	0.31892786	0
Q9UHB7;Q9UHB7-2	AFF4	0.2577	8.535344764	0.321119829	4.90E-33
Q16576;Q16576-2;E9PC52	RBBP7	0.2513981	9.252828768	0.329868343	8.15E-126
Q5UIP0;Q5UIP0-2	RIF1	0.2457561	9.852296966	0.337830397	0
Q96TA2;Q96TA2-3;Q96TA2-2	YME1L1	0.2405128	8.229835367	0.345339629	1.30E-20
P47756-2;B1AK87;B1AK88;P4	CAPZB	0.2402821	9.611234585	0.345672582	1.75E-183
Q9P1U0	ZNRD1	0.2329597	8.832885564	0.356342366	1.13E-72
Q3MHD2;Q3MHD2-2;K7ELG9	LSM12	0.2324867	8.996511672	0.357038701	1.30E-18
H0Y2S9	MPRIP	0.2252293	8.351061558	0.367829647	0
Q15629;G3XAN4;B4E0K2	TRAM1	0.2239685	9.061791639	0.369724735	2.16E-92
O95478	NSA2	0.2200603	8.951259786	0.375637684	1.74E-21
J3KNL6;O15027;O15027-2;O1	SEC16A	0.21805	9.291834867	0.378701908	1.22E-246
O95816;B4DXE2	BAG2	0.2102928	9.564405646	0.390669193	6.51E-296
Q9H9Y6;F5GZX4;Q9H9Y6-2;F	POLR1B	0.210228	9.749952636	0.390770198	1.14E-250
Q9UBI6	GNG12	0.2050285	9.213331781	0.398919949	1.64E-45
Q9GZS1-2;Q9GZS1;E7EX70	POLR1E	0.2017632	9.711030708	0.404090117	2.53E-90
O15446;O15446-2	CD3EAP	0.1991844	9.979944249	0.4082013	0
P55735;A8MXL6;P55735-2;B4	SEC13	0.1949348	8.639008104	0.415030342	2.57E-107
Q14527;Q14527-2	HLTF	0.1915054	10.46378851	0.420590305	0
Q9Y5S9;Q9Y5S9-2	RBM8A	0.1861095	9.284543523	0.429426421	4.60E-119
Q9BVJ6;F8WD00;E9PEL7;Q9B	UTP14A	0.1778469	9.710117365	0.443163994	3.40E-271
Q9BQ04;E9PLB0;E9PM61	RBM4B	0.1767826	8.855131328	0.444951594	1.81E-103
O94842;B4DPY8	TOX4	0.1746521	8.932636087	0.448542325	2.12E-68
P78527;E7EUY0;P78527-2	PRKDC	0.1735191	11.07518185	0.45045849	0
P62979;P0CG47;J3QS39;J3QT	RPS27A;UBB;UBC;U	0.171257	9.937963993	0.454298205	2.86E-123
P62280;M0QZC5	RPS11	0.1700134	10.61186133	0.456416912	4.29E-156
P60709	ACTB	0.1690083	10.43749689	0.458133476	0
Q13428;Q13428-3;Q13428-4;	TCOF1	0.1683826	9.874985979	0.459203676	2.67E-288
Q14254;J3QLD9;E7EMK3;K7E	FLOT2	0.1645451	9.036189589	0.465798996	1.76E-79
Q96DI7;B4DQJ1	SNRNP40	0.1629162	9.81225808	0.46861423	7.28E-263
Q86V48;Q86V48-2;Q86V48-3	LUZP1	0.1618786	10.28160144	0.470412439	0
Q1ED39	KNOP1	0.1610489	10.14410697	0.471853082	0
Q9UG63;Q75MJ1	ABCF2	0.1579952	9.17388524	0.477176198	1.62E-55
Q86W92-2;Q86W92;Q86W92	PPFIBP1	0.1572647	8.866169148	0.478454478	1.12E-56
Q9NX58	LYAR	0.1486988	10.29258831	0.493582085	0
Q86XZ4	SPATS2	0.1447563	9.162415036	0.50062972	2.41E-76
P62829;J3KT29;C9JD32;B9ZVI	RPL23	0.1436272	10.33237786	0.502657985	2.50E-140

P05187;P10696	ALPP;ALPPL2	0.1425552	9.95335371	0.504587478	3.70E-234
P35580;P35580-2;F8W6L6;P3	MYH10	0.1413879	9.524097401	0.506693067	0
P62750;H7BY10;K7EJV9;K7ER	RPL23A	0.1409054	10.09756964	0.507564862	1.08E-48
Q9BXY0;H0YBV6	MAK16	0.1393261	8.380844126	0.510423507	4.49E-19
Q14126	DSG2	0.1379795	9.337439293	0.512867584	3.13E-248
O95985;O95985-3;O95985-2;	TOP3B	0.1367416	8.775610448	0.515119701	9.98E-63
Q9NRR4;Q9NRR4-2;Q9NRR4-	DROSHA	0.1353149	9.258613341	0.517721719	4.73E-151
Q06787-6;Q06787-5;Q06787;	FMR1	0.1348038	10.1831844	0.518655644	0
P19447;G3V1S1	ERCC3	0.1333656	9.083395108	0.521287844	1.18E-115
Q9NZ01;B3KSQ1	TECR	0.123127	9.36363078	0.540224128	7.29E-43
O60306	AQR	0.1230278	8.707621267	0.540409233	9.01E-25
Q5BKZ1;Q5BKZ1-3	ZNF326	0.1208134	9.316578352	0.54455031	1.42E-134
O95831;O95831-3;Q1L6K4;O	AIFM1	0.1194439	8.974649834	0.547119153	4.60E-35
Q9P2E9;Q9P2E9-2;Q9P2E9-3;	RRBP1	0.1181469	10.02411607	0.549557558	0
P05114;A6NL93;A6NEL0	HMGN1	0.1142998	9.629277048	0.556821658	9.4004E-191
Q86VM9;E7ERS3;Q86VM9-2	ZC3H18	0.1138611	9.194708552	0.557652951	3.72E-149
O75128;O75128-2;O75128-3;	COBL	0.1137981	9.388243337	0.557772273	8.67E-157
Q13428-6;J3KQ96;Q13428-7;	TCOF1	0.1127548	8.389343311	0.559751934	1.28E-291
P55795	HNRNPH2	0.1126308	9.093491727	0.559987403	2.77E-186
P68133;P68032;Q5T8M8;A6N	ACTA1;ACTC1;ACTG	0.106514	10.76376482	0.571664341	0
Q9BVP2;Q9BVP2-2	GNL3	0.1063538	9.552412674	0.571971741	3.16E-192
Q9Y3F4;B4DNJ6;B0AZV0	STRAP	0.1053314	8.869958847	0.573935094	4.95E-60
P27635;F8W7C6	RPL10	0.1041431	10.38008455	0.57622113	2.90E-279
P48651;B4DE85;Q9BUQ5	PTDSS1	0.1008911	8.911136293	0.582499327	4.51E-116
P78346;Q5VU11;P78346-2;Q	RPP30	0.0987339	8.410810964	0.586681463	2.44E-26
C9JB33;C9J9U2;C9J1F6;C9JI9	PRRC2A	0.09652138	8.497095589	0.590985231	5.77E-273
E7EUE1;P28288;F5GYC1;P28	ABCD3	0.09364891	9.70865031	0.596594268	7.33E-200
O95602;B9ZVN9	POLR1A	0.09275055	10.01795107	0.598353451	0
Q8WWI1-3;Q8WWI1;E9PMS	LMO7	0.0922699	10.52277016	0.599295636	0
O43823	AKAP8	0.09213066	9.434521001	0.599568696	1.75E-129
Q9H0H5;H0YIK5;F8VRD2	RACGAP1	0.09019852	9.564583221	0.603363671	2.16E-128
Q16643;Q16643-2;A8MV58;D	DBN1	0.08807945	10.04178732	0.607538153	0
Q9UHB6;Q9UHB6-4;F8VQE1;	LIMA1	0.08806992	10.38426379	0.607556969	0
P31943;G8JLB6;E9PCY7;D6RII	HNRNPH1	0.08580589	10.2824635	0.612031259	0
Q14966;Q14966-3;Q14966-4	ZNF638	0.08462906	10.25775055	0.614362729	0
P32780;B3KXE0;E9PM51	GTF2H1	0.08390045	8.71452255	0.615808157	2.38E-61
Q14146	URB2	0.08298492	9.399639115	0.617626517	2.05E-155
Q5T5U3;E7ESW5;Q5T5U3-3;F	ARHGAP21	0.08247757	9.205041879	0.618635202	2.80E-148
Q99590;Q99590-2;F8VXG7;F8	SCAF11	0.08238792	9.708242386	0.618813503	3.30E-241
O75607	NPM3	0.0814724	9.705966289	0.620635734	1.90E-124
P09874	PARP1	0.07997513	11.99531045	0.62362086	0
Q14331;E9PRR7	FRG1	0.07813644	8.686966779	0.627295142	2.06E-23
Q96BK5	PINX1	0.07559204	8.468096135	0.632394945	1.94E-25
Q9UHI6	DDX20	0.07508087	9.585562241	0.633421615	4.04E-234
Q13823	GNL2	0.06962204	9.189602593	0.644429258	3.00E-63
Q9UNL2;C9JA28;B4E2P2	SSR3	0.06877327	8.961786412	0.646147895	2.70E-13
Q09666	AHNAK	0.06796455	9.36599312	0.647787186	3.46E-171
P61619;B4DR61;P61619-3	SEC61A1	0.06776619	9.200959878	0.648189538	4.36E-112
P68363	TUBA1B	0.06492424	9.468096135	0.653965233	8.26E-158
P22087;M0QXL5;M0R299;M0	FBL	0.06166458	10.75059324	0.660615428	0
P53803	POLR2K	0.06099701	8.265242469	0.66198071	0.0030666
P49454	CENPF	0.05834579	10.82079894	0.667413893	0
Q15717;B4DVB8;M0QZR9	ELAVL1	0.05807877	9.847831678	0.667962094	9.35E-131
P51114;B4DXZ6;P51114-3	FXR1	0.05799103	10.55450127	0.668142256	0
P55769;B1AHD1	NHP2L1	0.05763626	10.19426452	0.668870931	9.03E-99
Q14684;Q14684-2	RRP1B	0.05705261	10.45680618	0.670070398	0
P49790;F6QR24	NUP153	0.05698395	9.587531375	0.670211567	4.05E-181
P11142;E9PKE3;P11142-2;E9I	HSPA8	0.0567131	10.58113011	0.670768515	0
P60660;P60660-2;F8W1R7;G	MYL6	0.05565834	10.06194229	0.672939194	6.20E-111
Q7LGA3;Q7LGA3-3;Q7LGA3-2	HS2ST1	0.05290604	9.083215862	0.678616181	7.19E-37
Q14157-1;Q14157;Q14157-4;	UBAP2L	0.04972076	10.56428722	0.685209041	0
Q9H2Y7;E9PE29;H3BS99	ZNF106	0.04731369	9.494766629	0.690207176	0
P52292	KPNA2	0.04666328	9.717628902	0.691560036	1.93E-144
Q93077;Q7L7L0;P04908	HIST1H2AC;HIST3H2	0.04554367	10.09981871	0.693891163	2.45E-166
P49750;P49750-4;P49750-3;H	YLPM1	0.04442406	10.1072439	0.696225191	0
Q9NX24;D6RC52;D6RCB9;J3C	NHP2	0.04339981	10.12270725	0.698362933	3.87E-291
Q8IVT2	MISP	0.04174423	9.780432533	0.701823409	0
Q96PK6	RBM14	0.04145432	10.47242	0.702430031	0
Q15149;Q15149-4;Q15149-2;	PLEC	0.04141617	10.90334506	0.702509863	0
P47755;F8W9N7;C9JUG7;B4D	CAPZA2	0.03849792	8.996568582	0.708626735	1.39E-87
Q9Y3T9	NOC2L	0.03768539	9.233173855	0.710333233	2.77E-30
Q76FK4;Q76FK4-4;Q76FK4-2;	NOL8	0.03704453	9.617912031	0.71168023	0
O60832;O60832-2;C9IYT0;H7	DKC1	0.03619766	10.60167982	0.713461571	0
O00567	NOP56	0.03519249	10.30687517	0.715577939	0
Q9C0J8	WDR33	0.03181076	8.647275361	0.722714069	1.27E-53
P20700;E9PBF6	LMNB1	0.02917671	9.185881978	0.728289237	2.21E-214
Q9HAV0	GNB4	0.02828598	8.759176625	0.730177815	8.69E-126
P52907	CAPZA1	0.02633476	9.755577605	0.7343206	4.83E-168
P68104;Q5VTE0	EEF1A1;EEF1A1P5	0.02523232	9.274688842	0.736664726	9.52E-53
Q9UPN4;Q9UPN4-2;Q9UPN4	AZI1	0.02323914	8.511522413	0.740909022	4.56E-19

O75691	UTP20	0.02298355	9.958625989	0.74145384	0
Q9UKM9;Q9UKM9-2;Q5QPL9	RALY	0.02144814	8.676647892	0.744729537	2.21E-24
P14678;P63162;P14678-2;B3	SNRPB;SNRPN	0.0210762	9.741805307	0.745523727	1.56E-87
P05783;F8VZY9	KRT18	0.02093124	11.41193942	0.74583333	0
Q9H0A0;E7ESU4	NAT10	0.01998138	10.91248776	0.747863062	0
O14925;Q5SRD1;E7EP42;C9J9	TIMM23;TIMM23B	0.01935768	8.086822357	0.74919679	1.35E-20
A0AV96;A0AV96-2;D6R9D6;B	RBM47	0.01812935	8.898818391	0.751825651	3.89E-85
P51116	FXR2	0.01537514	10.35378163	0.757730611	0
P35579;P35579-2	MYH9	0.0148201	11.08217478	0.758922326	0
P46778;M0R181;G3V1B3	RPL21	0.01477432	10.51880337	0.759020637	1.01E-83
P08670;B0YJC4	VIM	0.01421356	10.98803695	0.760225267	0
O95782;O95782-2	AP2A1	0.01382065	9.418152081	0.761069674	1.70E-150
P14923	JUP	0.01375961	9.715610631	0.76120087	3.05E-196
Q9Y608;Q9Y608-2;Q9Y608-4;	LRRFIP2	0.01296806	9.012837225	0.762902933	9.82E-74
O94906;O94906-2	PRPF6	0.01277924	9.608857511	0.763309138	1.41E-262
Q7Z2W4;C9J6P4;Q7Z2W4-2;C	ZC3HAV1	0.01262665	9.568975721	0.763637431	0
P57678;I3L2C7	GEMIN4	0.01233673	9.514321914	0.764261306	1.29E-177
Q9ULL5-3;Q9ULL5;Q9ULL5-2	PRR12	0.01231003	8.920519857	0.764318776	2.48E-60
P62910;D3YTB1;F8W727	RPL32	0.01116943	10.57577652	0.766774767	3.53E-72
Q9Y4W2;Q9Y4W2-3;Q9Y4W2	LAS1L	0.0110836	8.722378864	0.766959677	9.77E-111
P62241;Q5JR95	RPS8	0.0104332	10.81614183	0.768361319	0
P62269	RPS18	0.009700775	10.06333336	0.769940614	1.27E-251
P63096;P63096-2	GNAI1	0.009231567	8.3143729	0.770952852	1.35E-115
O00159;O00159-3;O00159-2;	MYO1C	0.007902145	10.34177075	0.773822974	0
P62888;E5RI99	RPL30	0.007274628	10.69488586	0.775178815	2.79E-231
Q99848;H7C2Q8	EBNA1BP2	0.005825043	10.02690081	0.778313464	1.89E-133
Q9BYW2;H7C3H4;Q9BYW2-2	SETD2	0.00569725	8.642038921	0.778589982	1.90E-19
Q9NYF8;Q9NYF8-2;Q9NYF8-4	BCLAF1	0.005689621	10.09443619	0.778606491	1.91E-287
P51991	HNRNPA3	0.004970551	10.0489465	0.780162952	0
Q9NUW8;Q86TV8;G3V2F4;E7	TDP1	0.00450325	9.097396151	0.781174918	1.96E-160
Q92804;Q92804-2;K7EPT6	TAF15	0.000331879	10.07972378	0.790224496	4.80E-264
Q9BQG0;Q9BQG0-2;I3L1L3	MYBBP1A	-0.000461578	10.40937511	0.791949109	0
Q5T3I0;Q5T3I0-3;E9PAV9;F8\	GPATCH4	-0.00091362	10.12823767	0.792932096	0
O60814;Q99877;Q93079;P58	HIST1H2BK;HIST1H2	-0.00188446	11.41370201	0.795044349	3.22E-232
Q08J23;Q08J23-2;G3V1R4	NSUN2	-0.003662109	8.79698346	0.798915858	2.00E-57
Q9NW13;Q9NW13-2	RBM28	-0.004320145	9.401951676	0.800350241	1.14E-121
Q15365	PCBP1	-0.004419327	9.473997604	0.800566496	2.18E-189
O76094;O76094-2	SRP72	-0.004842758	9.530545459	0.801489912	1.49E-216
P62136;P62136-2;A6NNR3;E9	PPP1CA	-0.00730896	9.692344503	0.806873659	0
Q69YQ0;F5H1H6;F8WAN1;C9	SPECC1L	-0.008256912	9.712826413	0.808945501	0
P67809;H0Y449	YBX1	-0.008335114	10.31468865	0.809116478	0
Q63ZY4	ATXN2L	-0.008653641	10.06829721	0.809812989	1.13E-258
P26373;P26373-2;J3QSB4	RPL13	-0.009284973	10.71999383	0.811193944	4.76E-167
Q15390;E5RJS5;H0YBZ4;E7EP	MTFR1	-0.01117134	8.790080991	0.815323605	1.95E-29
Q14677-3;Q14677;Q14677-2	CLINT1	-0.01265526	8.905223638	0.818575832	6.01E-51
P09651;P09651-3;F8VXY0;F8\	HNRNPA1;HNRNPA1	-0.01422119	10.61936468	0.822011196	1.06E-246
O00425	IGF2BP3	-0.0165062	9.798705878	0.827030178	1.11E-231
P84098;J3QR09;J3KTE4;J3QL1	RPL19	-0.01677704	10.14185722	0.827625555	6.39E-81
P46087-4;P46087;P46087-2;F	NOP2	-0.0177269	10.37906972	0.829714349	0
Q9NVI7-2;Q9NVI7;H0Y2W2;C	ATAD3A	-0.01906395	10.15902549	0.832656637	2.52E-300
Q8NCA5;Q8NCA5-2;E9PH82;E	FAM98A	-0.02179909	9.668935427	0.83868279	1.03E-278
Q13435;E9PPJ0	SF3B2	-0.02276993	9.958128893	0.840824076	1.59E-245
P78406;E9PQ57;E9PPG9	RAE1	-0.02628326	9.241098009	0.848582828	1.72E-85
P68431;Q71DI3;P84243;Q16(	HIST1H3A;HIST2H3A	-0.02737045	11.53540806	0.850986756	1.39E-147
Q5M775;Q5M775-4;Q5M775	SPECC1	-0.02793312	9.464370301	0.85223144	0
O43795;O43795-2;E9PDF6	MYO1B	-0.03231812	9.554525501	0.861943915	2.84E-204
Q9Y224;G3V4C6	C14orf166	-0.03235817	9.776512319	0.862032732	6.98E-218
P06746;E7EW18;H0YBJ0;B7Z	POLB	-0.033041	9.695962986	0.863547105	7.57E-259
Q5JTH9;Q5JTH9-2;Q5JTH9-3;I	RRP12	-0.03389549	9.884359152	0.865442894	0
Q9BYJ9;F8W840	YTHDF1	-0.03462982	8.798070278	0.867072706	4.53E-76
Q15293;B7Z1M1	RCN1	-0.0367794	8.222326211	0.871846835	1.77E-38
Q9BY89	KIAA1671	-0.03746223	9.351061558	0.873364359	7.63E-189
P08174;P08174-2;H3BLV0;Q1	CD55	-0.03770447	9.584930228	0.873902811	1.00E-166
Q8WTT2;A6NJZ9;F5H677	NOC3L	-0.03775024	9.257366539	0.874004572	5.84E-65
Q9Y520;Q9Y520-4;E7EPN9;Q	PRRC2C	-0.0378952	10.17776729	0.87432683	0
Q14247;Q14247-3;Q14247-2	CTTN	-0.03975677	10.05311687	0.878467131	7.50E-197
P52272;P52272-2	HNRNPM	-0.04072571	11.06397101	0.880623447	0
Q13813;Q13813-3;Q13813-2;	SPTAN1	-0.04117775	10.17382704	0.881629749	0
P62906	RPL10A	-0.041996	10.65220765	0.883451768	7.32E-137
Q7Z417	NUFIP2	-0.04325294	10.10809124	0.886251825	0
H7BY36	EWSR1	-0.04328537	8.924077603	0.886324076	4.86E-149
Q15058	KIF14	-0.04502106	9.420665232	0.890192996	0
Q9BYG3;C9J808;E9PFS2;C9J6	MKI67IP	-0.0458374	9.625003601	0.892013575	8.32E-221
Q8N684;Q8N684-2;Q8N684-3	CPSF7	-0.04589081	9.416640507	0.892132698	4.58E-127
Q15427	SF3B4	-0.04614067	8.72376753	0.892690057	2.93E-56
P30050;P30050-2	RPL12	-0.04658508	10.65192703	0.89368152	1.08E-196
Q5VT52;Q5VT52-3;Q5VT52-2	RPRD2	-0.04759026	9.230882999	0.895924626	9.60E-178
Q9UQR1	ZNF148	-0.04787445	8.615855401	0.896558976	4.39E-33
Q9NVP1	DDX18	-0.0492115	9.746540792	0.899544284	2.67E-135
P36578;H3BM89	RPL4	-0.05010986	11.01665734	0.901550905	0

P08621;P08621-2;P08621-3	SNRNP70	-0.05016518	9.603955885	0.901674475	2.84E-96
P49458;E9PE20;P49458-2	SRP9	-0.05049515	9.446785619	0.902411688	1.63E-25
Q9P0L0;Q9P0L0-2	VAPA	-0.05179214	9.248880166	0.90531021	4.20E-35
Q9BUJ2;Q9BUJ2-4;B7Z4B8;Q	HNRNPUL1	-0.05268478	10.22354786	0.90730581	0
P52597	HNRNPF	-0.05280113	9.9933304	0.907565964	2.03E-133
O60318	MCM3AP	-0.05370712	8.141919874	0.909592088	1.88E-13
Q96KR1	ZFR	-0.05573463	9.861582199	0.914128452	0
Q13045;J3QLG3;Q13045-2	FLII	-0.0561657	9.062581984	0.915093276	8.07E-150
P14373;P14373-2	TRIM27	-0.05706978	9.34084055	0.917117248	1.14E-190
Q14690	PDCD11	-0.05773544	10.410929	0.918607816	0
O75477;B0QZ43	ERLIN1	-0.05860901	8.775566762	0.920564353	8.01E-50
Q5T6F2;F5H2U4;E7EWG4;A6	UBAP2	-0.05866623	9.163578765	0.920692528	6.04E-126
P62917;E9PKZ0;E9PKU4;G3V	RPL8	-0.06013107	10.76945856	0.923974484	0
Q14103;Q14103-3;H0YA96;H	HNRNPD	-0.06043625	9.65750522	0.92465839	6.05E-125
P50402;Q5HY57	EMD	-0.0606823	9.161906792	0.925209829	4.90E-86
P07910-4;P07910-2;G3V4W0	HNRNPC;HNRNPCL1	-0.06105804	9.87409896	0.926052019	1.95E-85
Q96EY1;Q96EY1-2;E7ES32	DNAJA3	-0.06270981	9.586013116	0.929755206	1.61E-141
P62316;P62316-2	SNRPD2	-0.0632	9.854779559	0.930854485	6.56E-67
Q9P275;Q9P275-2;E9PEW0	USP36	-0.06350708	10.02836788	0.931543206	0
P61353;K7ELC7;K7EQQ9	RPL27	-0.06390762	10.69105496	0.932441614	1.93E-164
Q86V81	ALYREF	-0.06393623	10.49099729	0.932505789	0
Q8NFJ5	GPRC5A	-0.06670952	8.9139833	0.938728538	1.88E-47
Q8IWR0;I3L2K5	ZC3H7A	-0.07073784	8.861659842	0.947773925	8.61E-93
P53007	SLC25A1	-0.07081985	8.329865486	0.947958161	1.00E-16
Q02543;M0R1A7;M0R3D6;M	RPL18A	-0.07212257	10.39346991	0.950884891	5.57E-218
Q16594;Q9HBM6;D6RHW1;D	TAF9;TAF9B	-0.07247353	7.979621206	0.951673466	9.42E-05
Q9UII2	ATPIF1	-0.07579613	9.511883361	0.959141452	0.00015845
Q8IWX8;J3QK89	CHERP	-0.07659531	9.311817412	0.960938273	1.15E-110
Q9Y2X3	NOP58	-0.07680702	10.34645078	0.961414314	0
Q9Y5A9;Q9Y5A9-2	YTHDF2	-0.07715225	9.558144341	0.96219059	7.68E-114
O15226;G3V1N1	NKRF	-0.07773209	9.890678054	0.963494472	6.57E-304
Q5JSZ5;Q5JSZ5-5	PRRC2B	-0.07791901	8.708284896	0.963914823	2.74E-103
P63261;I3L3I4;I3L3I0;I3L1U9;	ACTG1	-0.07878494	11.9811025	0.965862294	0
P38646	HSPA9	-0.07881927	8.709736238	0.965939511	3.14E-72
P98175-3;P98175-4	RBM10	-0.07969284	9.74872281	0.967904354	1.84E-301
Q6NZI2;Q6NZI2-2	PTRF	-0.08065796	9.092018471	0.970075345	2.20E-88
Q01082;Q01082-2	SPTBN1	-0.08122635	9.84538334	0.971354018	0
P62873;F6UT28;B1AKQ8	GNB1	-0.08517838	9.390917452	0.980246513	2.49E-216
Q00610;Q00610-2	CLTC	-0.08565712	9.69599797	0.981323929	0
Q14498;Q14498-2;Q14498-3;	RBM39	-0.0873661	9.86193447	0.98517027	0
Q13148;Q13148-2;K7EJM5;K	TARDBP	-0.08778572	8.880030013	0.98611474	3.29E-72
Q12965	MYO1E	-0.08973312	9.750384954	0.990498174	1.42E-227
Q15646;Q15646-2	OASL	-0.09014893	8.08300067	0.99143415	6.07E-12
O14974;O14974-4;O14974-2;	PPP1R12A	-0.09098434	10.25331377	0.993314722	0
P43307;P43307-2;F5H5Y2;C9	SSR1	-0.09241867	8.554949256	0.996543549	2.77E-13
Q6PKG0;Q6PKG0-3;E5RH50	LARP1	-0.09308052	9.91755277	0.998033468	0
Q16637;Q16637-4;Q16637-2;	SMN1	-0.09395409	9.442432731	1	5.33E-138
P62263;E5RH77	RPS14	-0.09495354	10.49462761	0.997833647	1.81E-219
Q13310-3;Q13310;Q13310-2;	PABPC4	-0.09654236	10.28101063	0.994389846	0
O75369;O75369-2;O75369-9;	FLNB	-0.0998745	8.724013575	0.987167789	1.54E-90
P46779;C9JB50;G5E9L2;H0YN	RPL28	-0.1008587	9.699907069	0.985034832	2.22E-48
Q16629;Q16629-3;Q16629-2;	SRSF7	-0.1020432	9.988585709	0.982467985	5.24E-72
P51571;H7C1C6;A6NLM8	SSR4	-0.1032219	8.899262234	0.979913719	4.27E-58
P39023;G5E9G0;B5MCW2;H7	RPL3	-0.1046867	10.79976774	0.976739776	0
P07814	EPRS	-0.1047764	9.999748036	0.976545549	0
P62140;E7ETD8	PPP1CB	-0.1060772	10.48084022	0.973727349	0
O43143	DHX15	-0.107317	9.887228962	0.971041687	8.57E-194
Q9NR30;Q9NR30-2	DDX21	-0.1073761	10.76767522	0.970913609	0
P35637;P35637-2;H3BPE7	FUS	-0.1085663	11.02139606	0.968335698	0
P24928	POLR2A	-0.110445	8.933244258	0.964267082	7.85E-125
Q14444;Q14444-2;G3V153;E	CAPRIN1	-0.1104679	10.48706764	0.964217521	0
Q9H583;Q5T3Q7	HEATR1	-0.1106434	9.112034951	0.963837555	6.72E-171
P29558;P29558-2;B4DN88;E7	RBMS1	-0.112093	8.794418331	0.960699028	4.32E-30
Q7L2E3-2;Q7L2E3-3;H7BXY3	DHX30	-0.1159191	9.54409286	0.952418021	6.53E-192
Q9Y4A5;H0Y4W2;Q9Y4A5-2;F	TRRAP	-0.1162643	8.864154956	0.951671071	2.12E-88
Q92841;H3BLZ8;Q92841-3;Q	DDX17	-0.1170387	11.2592354	0.949995747	0
Q07157;Q07157-2;G5E9E7;G	TJP1	-0.1173077	8.925879089	0.949413974	2.30E-62
O43390;Q2L7G6;E7ETM7	HNRNPR	-0.1182899	10.2656667	0.947289289	4.66E-232
Q15070;C9JC63;Q15070-3;E7	OXA1L	-0.118494	8.178257321	0.946847896	5.69E-07
O75165	DNAJC13	-0.1187572	9.421751957	0.946278648	7.12E-215
P38159;H3BT71;P38159-2;H0	RBMX;RBMXL1	-0.1201973	10.1472743	0.943164772	2.26E-175
O15234	CASC3	-0.1204109	8.705607163	0.942702919	4.35E-30
Q00325-2;F8VVM2;Q00325	SLC25A3	-0.1208115	9.417089545	0.941836997	8.59E-69
Q92576-2;Q92576;E7EVH3;E	PHF3	-0.1208839	9.969094266	0.941680313	0
P61254;Q9UNX3;J3QRI7;J3Q	RPL26;RPL26L1;KRB	-0.1210575	10.17049641	0.941305107	2.47E-53
Q92522	H1FX	-0.1218414	9.051731196	0.939610657	1.70E-48
P62158;H0Y7A7;E7ETZ0;E7EN	CALM1;CALM2;CALI	-0.1219845	10.15293014	0.93930148	1.50E-170
P11940;E7EQV3;P11940-2;E7	PABPC1;PABPC3	-0.1223145	10.93402855	0.938588347	0
Q9UKV8;Q9UKV8-2	AGO2	-0.1223488	8.952952188	0.938514151	7.56E-103
P43243;A8MXP9;D6REM6;D6	MATR3	-0.1235619	10.61836193	0.935892906	0

P17844;J3KTA4;B4DLW8	DDX5	-0.1245079	11.08539762	0.933849146	0
P83111;P83111-2	LACTB	-0.1261482	10.12775252	0.93030657	2.31E-302
P80723	BASP1	-0.1265621	9.623042434	0.929412903	1.58E-112
Q86UE4	MTDH	-0.127079	10.38401273	0.928296973	0
P11388;P11388-2;P11388-3;F	TOP2A	-0.1277542	10.52757835	0.926839478	0
P12236;I7HJJ0	SLC25A6	-0.1277962	9.967046938	0.926748907	9.72E-135
O43395;E7EVD1	PRPF3	-0.1299896	9.444497601	0.922015875	9.49E-126
P02545;Q6UYC3;P02545-3;D(	LMNA	-0.1300964	9.547417773	0.921785466	1.47E-132
P23246;P23246-2	SFPQ	-0.1303444	10.95565889	0.921250613	0
Q9H7E2;Q9H7E2-3;Q9H7E2-2	TDRD3	-0.1310081	9.279210513	0.91981903	1.55E-92
P05388;Q3B7A4;F8VWS0;F8V	RPLP0;RPLP0P6	-0.1311874	10.59099779	0.919432382	2.95E-230
Q9NPE3	NOP10	-0.1312962	9.912859475	0.919197935	3.31E-82
Q969Q0;P83881;J3KQN4;H7E	RPL36AL;RPL36A	-0.1326256	9.799567977	0.916331671	2.41E-36
Q00839;Q00839-2	HNRNPU	-0.1330833	10.20297846	0.915344972	0
P62424;Q5T8U2	RPL7A	-0.1331329	11.0227994	0.915238088	0
Q15637-6;Q15637-2;Q15637-	SF1	-0.1362057	9.535167485	0.90861842	2.65E-87
Q9UMS4;F5GY56	PRPF19	-0.1372128	10.5804916	0.906450202	0
P20042	EIF2S2	-0.1375465	9.371215682	0.905731723	4.92E-167
P40429;M0QYS1	RPL13A	-0.1375561	10.09527399	0.905711196	4.38E-59
Q96SB4;B4DS61;H3BLV9;Q96	SRPK1	-0.1389236	8.789855584	0.902768303	6.75E-37
P62753;A2A3R5	RPS6	-0.1431999	11.30541586	0.893574918	8.55E-223
P04899;B4E2X5;P04899-3;P0	GNAI2	-0.1438751	8.740654753	0.892124605	9.64E-155
Q86XI2;Q86XI2-2;E7EUH9;H0	NCAPG2	-0.148901	8.349549484	0.881340853	2.47E-38
P31689;B7Z5C0	DNAJA1	-0.1498299	9.22940024	0.879350148	1.34E-143
Q9Y2R4;A8MTP9	DDX52	-0.1520767	9.590451708	0.874538026	0
P62314;J3QLI9	SNRPD1	-0.1521378	10.1654224	0.87440737	5.57E-97
P05387	RPLP2	-0.152256	10.6949823	0.874154234	0
Q96HS1;Q96HS1-2;F5GXG4	PGAM5	-0.154253	9.461753566	0.869881467	1.22E-76
P42167;G5E972;P42167-2;A2	TMPO	-0.1545696	9.750662646	0.869204373	9.63E-192
Q8NI36;D6R922	WDR36	-0.1546822	9.924046566	0.868963742	0
Q5VUA4;Q5VUA4-2	ZNF318	-0.1569672	8.778766066	0.864080366	2.26E-49
Q9Y230;B3KQ59;M0R0Y3	RUVBL2	-0.1586189	9.57634135	0.860553532	1.65E-111
P62277;J3KMX5	RPS13	-0.1587048	10.43504764	0.860370343	2.98E-100
Q12874;E7EUT8	SF3A3	-0.1591492	7.872424345	0.859421948	1.67E-06
P56537;B7ZBG9	EIF6	-0.1592026	9.663719766	0.859307991	2.12E-221
P63167	DYNLL1	-0.1595306	9.672734972	0.858608036	3.09E-121
Q13151	HNRNPA0	-0.1597996	9.55855258	0.858034319	2.71E-207
P06748;P06748-2;P06748-3	NPM1	-0.1633301	11.56188813	0.850509817	0
Q96C57;E7ENF1;F5H7W8;H0\	C12orf43	-0.1639557	9.83683661	0.849177863	0
O00571;O00571-2;O15523;B4	DDX3X;DDX3Y	-0.1651325	10.45679101	0.846673495	0
Q13283;F5H4D6	G3BP1	-0.1651535	10.55692936	0.846628861	0
Q96CW1;Q96CW1-2;E9PFW3	AP2M1	-0.165741	9.278273326	0.845379298	4.88E-115
Q9NVN8	GNL3L	-0.1659203	9.119750624	0.844998015	1.08E-68
Q10570	CPSF1	-0.1661358	9.341810289	0.844539712	1.46E-211
P10412;P16402	HIST1H1E;HIST1H1C	-0.1662216	11.39445168	0.844357217	5.63E-129
P62244;I3L3P7;I3L246;H3BN9	RPS15A	-0.1676903	9.974856965	0.841235824	2.01E-64
Q13155;A8MU58;F8W950	AIMP2	-0.1678982	9.118000033	0.840794164	4.98E-56
P39880;P39880-2;P39880-3;F	CUX1	-0.1696739	9.260142969	0.837023883	2.09E-186
O95425;O95425-2;F5H2Q5	SVIL	-0.1704979	8.918109006	0.835275672	1.96E-129
H9KV59;O43663;O43663-2;F8	PRC1	-0.1705513	9.437623743	0.83516239	2.15E-180
P54136;P54136-2;F5H3T8	RARS	-0.1750546	9.539590421	0.825622824	4.24E-252
Q15269	PWP2	-0.1773033	9.717379212	0.820868629	7.23E-251
Q01130;J3QL05;J3KP15;B4DN	SRSF2;SFRS2;SRSF8	-0.1785679	8.002727473	0.818198027	2.63E-20
Q9P0K7;Q9P0K7-4;Q9P0K7-3	RAI14	-0.1788177	9.947316064	0.8176706	0
Q03701	CEBPZ	-0.1817532	10.12949654	0.811480579	0
Q8IY81	FTSJ3	-0.1825047	9.681865087	0.809897746	0
Q08211	DHX9	-0.1826	10.35435818	0.809696934	0
O75643	SNRNP200	-0.1829681	10.33150828	0.808921919	0
Q07065	CKAP4	-0.1862831	9.481600265	0.801951292	7.42E-186
Q8WUU5	GATAD1	-0.1901531	7.955495329	0.793833481	1.18E-27
P38432	COIL	-0.190937	9.558684576	0.7921918	2.21E-164
Q9Y3I0	C22orf28	-0.1917553	9.930490565	0.790479203	3.27E-221
P47914	RPL29	-0.1920128	10.21921766	0.789940483	1.04E-18
Q8IWS0;E9PC97;B4E0G4;Q5J	PHF6	-0.1928825	9.224584854	0.788121549	9.70E-38
O94905;E5RHW4	ERLIN2	-0.1930161	8.81474688	0.787842429	9.23E-70
Q07020;F8VWC5;H0YHA7;J3C	RPL18	-0.1940632	10.57860483	0.785654275	7.74E-172
Q16795	NDUFA9	-0.1944122	8.394924244	0.784925266	7.79E-30
Q9Y3U8;J3QSB5	RPL36	-0.1946812	10.19884945	0.784363699	3.58E-61
Q9BV38;K7EIR0;K7EML4	WDR18	-0.1955509	8.592287816	0.782548337	7.53E-37
Q12797;F5H667	ASPH	-0.1964493	9.875385416	0.780674502	4.80E-241
P25398	RPS12	-0.198904	10.0280423	0.775560799	7.53E-188
P83731;C9JXB8;C9JNW5	RPL24	-0.1990433	10.28076043	0.775271033	3.73E-31
P15328	FOLR1	-0.1990948	9.216878142	0.775163868	1.94E-114
Q15393	SF3B3	-0.1997929	9.698300675	0.773711601	0
O43159;E9PPY3	RRP8	-0.2005444	8.863822309	0.772149118	3.20E-47
Q01844;Q01844-6;B0QYK0;Q	EWSR1	-0.2007256	10.58775585	0.771772515	5.40E-286
Q7Z460;Q7Z460-3;B7ZLX3;F5	CLASP1;CLASP2	-0.2029037	8.189630658	0.767249582	2.45E-20
P56182	RRP1	-0.2037067	9.203223325	0.765584185	1.31E-237
P61978;P61978-2;Q5T6W5;P(	HNRNPK	-0.2044487	9.915874503	0.764046336	1.16E-299
Q9NPA8;G3V117;E5RHX8	ENY2	-0.205925	8.462682442	0.760989225	7.82E-07

O43707;D6PXK4	ACTN4	-0.206934	9.622804428	0.758901945	1.24E-204
Q9P2N5	RBM27	-0.2087097	9.079362164	0.755232762	4.95E-120
Q15061	WDR43	-0.2087574	8.343743295	0.755134309	1.09E-23
Q9BWF3;E9PB51;Q9BWF3-4;	RBM4	-0.2096901	9.357382103	0.753209383	1.27E-102
P21333;Q5HY54;P21333-2	FLNA	-0.2099648	9.564831704	0.752642826	0
Q9NZI8;Q9NZI8-2	IGF2BP1	-0.2123318	9.829213688	0.74776575	2.26E-155
P07437;Q5JP53;F8VYX6;F8VV	TUBB;TUBB2B;TUBB	-0.2130795	9.221648928	0.746227293	4.77E-55
P61247;D6RAT0;D6RG13;D6R	RPS3A	-0.2133675	10.6490134	0.745634942	4.37E-261
Q9NY12;Q9NY12-2	GAR1	-0.2142563	10.26173855	0.743807842	1.21E-102
Q86SQ0;Q86SQ0-2;Q86SQ0-3	PHLDB2	-0.2155533	8.769598848	0.741144277	1.37E-65
O60506;O60506-2;O60506-3;	SYNCRIP	-0.217701	9.795316807	0.736740552	9.60E-296
Q9H8M2;Q9H8M2-6;Q9H8M	BRD9	-0.2179317	8.108023509	0.736267839	1.85E-09
G5E9M5;Q12906;Q12906-4;C	ILF3	-0.2186832	10.38059108	0.734729283	0
Q9BY77-2	POLDIP3	-0.2196445	10.31130875	0.732762734	0
Q92900;Q92900-2	UPF1	-0.2199078	10.23661283	0.732224579	0
Q9Y446	PKP3	-0.2206745	9.537995295	0.730657661	2.98E-167
P46940;H0YLE8	IQGAP1	-0.2224655	9.461738568	0.727002009	6.85E-270
P08754	GNAI3	-0.2247791	9.626093889	0.722288833	3.72E-217
Q9Y3A4	RRP7A	-0.2285099	9.769694806	0.714710911	2.31E-216
Q9UKV3;E7EQT4;Q9UKV3-5;C	ACIN1	-0.2286644	9.158422807	0.714397701	3.13E-79
Q96IZ0;H0YI16	PAWR	-0.2361259	8.807149268	0.699328971	6.34E-105
O76021;J3QSV6;I3L3U9;I3L3C	RSL1D1	-0.2382507	10.14176323	0.695059194	0
Q9NZB2;Q9NZB2-4;Q9NZB2-(	FAM120A	-0.2399387	9.640103625	0.691674008	0
P18583;P18583-3;P18583-5;F	SON	-0.2414989	8.641959693	0.688550571	7.03E-26
Q8IZH2;Q8IZH2-2;H7C5E4	XRN1	-0.2416077	8.462383022	0.68833312	5.55E-55
P17096;P17096-3;H7BYM6	HMGA1	-0.2421494	9.843998505	0.687250065	1.37E-35
Q9BUQ8	DDX23	-0.242321	10.02918079	0.686906977	4.22E-235
Q8N3X1;Q8N3X1-2	FNBP4	-0.2453098	9.223651667	0.680943826	2.65E-103
Q9HCE1;Q5JR04;Q9HCE1-2	MOV10	-0.2533684	9.723726509	0.664965718	1.60E-302
P27105;B4E2V5	STOM	-0.2569504	9.457579147	0.657911529	5.05E-73
Q9UM00;J3QQY2;Q9UM00-2	TMCO1	-0.2604408	8.665937285	0.651066812	4.77E-22
P46782;M0R0F0;M0R0R2;M0	RPS5	-0.261528	9.457018503	0.648940811	2.05E-54
Q9H0D6;Q9H0D6-2;B4DZC3	XRN2	-0.2616501	9.494015375	0.64870228	4.39E-165
Q9Y4P3;E9PF19	TBL2	-0.2620621	9.646423333	0.647897505	4.00E-186
P15880;H0YEN5;E9PQD7;E9P	RPS2	-0.2622452	10.24657243	0.647539959	6.67E-75
P50914;E7EPB3	RPL14	-0.2625885	10.45824492	0.646869779	3.58E-59
O00712;Q5VW26;O00712-4;C	NFIB	-0.2647915	8.414087152	0.642576292	1.28E-63
Q9UNX4	WDR3	-0.2648697	10.01405828	0.642424101	0
Q9NYL9;H0YNJ8;H0YKU1	TMOD3	-0.26791	9.715610631	0.636518888	0
P55265;P55265-5;P55265-4;E	ADAR	-0.2689819	9.799843488	0.634442344	0
Q9UKS6;E9PIY1	PACSIN3	-0.2691631	8.609103283	0.63409161	6.92E-114
Q99459	CDC5L	-0.2696304	10.01481445	0.633187465	0
P63173;J3KT73;J3QL01	RPL38	-0.2699471	9.741356481	0.632575172	2.78E-31
Q01085;Q01085-2;Q49AS9;C	TIAL1;TIA1	-0.2700272	8.659041028	0.632420295	1.51E-50
P48634	PRRC2A	-0.2706718	9.79400678	0.631174486	2.59E-275
Q96S97;C9JJV6;C9JZL8;C9J5N	MYADM	-0.2737846	8.204255678	0.625174006	7.49E-09
Q6UN15;Q6UN15-3;Q6UN15-	FIP1L1	-0.2741356	9.457594289	0.624499027	4.35E-71
P14866;M0QXS5;P14866-2	HNRNPL	-0.2743053	10.39569325	0.624172656	0
P46776;E9PLL6;E9PJD9	RPL27A	-0.2774639	10.42109366	0.618113452	1.40E-113
Q9NPF5;Q5TG39;Q5TG40	DMAP1	-0.2792435	8.929628358	0.614711031	4.67E-86
P35268;K7ERI7;K7ELC4;K7EM	RPL22	-0.2808723	10.32699091	0.611603951	1.27E-171
O43660;A8MW61;O43660-2	PLRG1	-0.2860928	9.77889615	0.601693226	1.01E-124
P36873;F8VYE8;P36873-2;F8\	PPP1CC	-0.2905483	9.718335579	0.593292287	0
Q9H6R4;Q9H6R4-4;Q9H6R4-;	NOL6	-0.2905998	10.18052728	0.593195502	0
O14979-3;O14979-2;O14979	HNRPDL	-0.2925587	9.854269596	0.589519465	7.20E-138
P62249;M0R210;M0R3H0;M0	RPS16	-0.296524	10.14646913	0.582110243	5.72E-47
Q02880-2;Q02880;E9PCY5	TOP2B	-0.3002853	9.863739107	0.575122813	0
Q92499	DDX1	-0.3010941	10.09194819	0.57362564	0
Q9NY61;K7ERC2	AATF	-0.3018532	9.290479813	0.572221958	5.40E-109
Q15366-4;Q15366-6;Q15366-	PCBP2	-0.3024826	9.469983926	0.57105934	3.56E-100
P62861;E9PR30	FAU	-0.3084946	9.803354676	0.56001162	1.05E-12
P46777	RPL5	-0.3087769	10.54484907	0.55949544	8.72E-173
Q8TED0;B4DXK8;H0Y8P4;B4D	UTP15	-0.3096733	8.581403462	0.55785775	3.94E-17
Q9Y265;Q9Y265-2;E7ETR0;H7	RUVBL1	-0.3103714	9.753184581	0.55658406	2.67E-220
Q14980;Q14980-2;Q14980-4;	NUMA1	-0.3109093	10.1153442	0.55560366	0
P62995;P62995-3;H7BXF3	TRA2B	-0.3129272	9.229809783	0.551932956	1.21E-79
Q86W42;Q86W42-3;Q86W42	THOC6	-0.3138561	9.150725747	0.550247334	2.57E-70
Q12788;J3KNP2	TBL3	-0.3160057	10.04206335	0.54635627	0
P84090;G3V279	ERH	-0.3160439	10.50147007	0.546287342	5.58E-102
O60684;F5H4G7;F5GYL8;P52	KPNA6;KPNA1	-0.3180962	8.323520228	0.542585358	3.03E-14
Q9Y2W1	THRAP3	-0.3187428	10.22983537	0.541421623	4.31E-191
Q02878;F8W181	RPL6	-0.3188858	10.66466078	0.541164328	6.24E-149
P46781;B5MCT8;C9JM19	RPS9	-0.3222847	10.0364692	0.53506902	1.61E-71
Q9NQG5	RPRD1B	-0.323925	8.792524759	0.532139834	1.13E-47
P62081;B5MCP9	RPS7	-0.3261452	10.48200126	0.528188193	1.93E-249
O75494;O75494-3;O75494-4;	SRSF10	-0.326746	8.941203243	0.527121382	3.09E-45
P06241;P06241-2;P06241-3;C	FYN	-0.3291779	8.500853711	0.522814596	3.73E-35
P62847;P62847-2;E7ETK0;P6	RPS24	-0.3353119	10.1121356	0.512032209	8.61E-20
Q6P2Q9	PRPF8	-0.3365288	10.46196349	0.509907039	0
O15042;O15042-2;E7ET15;O1	U2SURP	-0.3458862	9.684665864	0.493720685	2.98E-154

Q12905	ILF2	-0.3459377	10.01275289	0.493632371	0
Q13247;Q13247-3	SRSF6	-0.350729	9.608707843	0.485453044	4.62E-44
Q01081;Q01081-2;Q8WU68;I	U2AF1;U2AF1L4	-0.3536186	9.089869802	0.480555744	2.58E-18
P49207	RPL34	-0.3541985	9.693023068	0.479576304	2.91E-08
P62318;B4DJP7;H3BT13	SNRPD3	-0.3577328	9.947908931	0.473629849	1.24E-166
Q13769;F8WCP5	THOC5	-0.3580837	9.259880447	0.473041597	5.16E-90
P62899;C9JU56;B7Z4E3;P628	RPL31	-0.3596344	9.9562597	0.470447235	2.10E-30
O75533	SF3B1	-0.3603973	9.810232518	0.469173685	0
Q15046;Q15046-2	KARS	-0.3615017	9.225541877	0.467333604	1.06E-113
P19338;H7BY16	NCL	-0.362339	10.9382795	0.465941119	0
Q86VV8;J3KTD2;Q86VV8-2;Q	RTTN	-0.3630657	8.062431553	0.464734478	0.0036531
P39019;M0R2L9;M0QXK4;M(	RPS19	-0.3635769	10.06460772	0.463886754	1.60E-86
Q96T58	SPEN	-0.3645401	9.339133306	0.462291706	3.76E-161
P26599;P26599-2;P26599-3;I	PTBP1	-0.3659821	10.37623011	0.459909603	0
Q15233;Q15233-2;H7C367;C	NONO	-0.3663101	10.67607144	0.459368604	0
P61160;P61160-2;F5H6T1	ACTR2	-0.3689003	8.887290894	0.455109766	1.62E-49
Q86UP2;Q86UP2-2;Q86UP2-3	KTN1	-0.3709278	9.938309532	0.451791653	0
O60287	URB1	-0.3745041	10.03177191	0.445972391	0
P22626;P22626-2	HNRNPA2B1	-0.376236	10.64163273	0.44316973	0
Q7Z6E9;Q7Z6E9-2;Q7Z6E9-4;	RBBP6	-0.3769131	9.515290862	0.44207672	1.16E-251
Q9UHB9;F5H5Y3;G3V1U4;Q9	SRP68	-0.3801117	9.127202018	0.436934305	2.72E-175
P41252;J3KR24	IARS	-0.3823681	9.730669248	0.433327518	0
Q96J01;Q6NZ53	THOC3	-0.3836021	8.598779567	0.431362224	1.50E-32
Q9NR56;C9JP00;Q9NR56-3;Q	MBNL1;MBNL2;MBl	-0.388628	8.488578917	0.423411851	2.87E-16
Q9NXF1;Q9NXF1-2;B7Z9D5	TEX10	-0.3903885	8.687430855	0.420647368	1.14E-46
P26196	DDX6	-0.3943176	9.914385474	0.414515808	5.10E-219
Q9BY77;F8WCX5	POLDIP3	-0.3978653	9.030559245	0.409025216	0
P18621;J3QQT2;J3KRX5;J3QL	RPL17	-0.3980598	10.51390979	0.408725377	3.83E-84
P16401	HIST1H1B	-0.400898	10.90669052	0.404366139	1.69E-151
P61513;C9J4Z3;M0R0A1;Q6P	RPL37A	-0.4010773	9.764818503	0.404091694	2.07E-31
Q15029;Q15029-2;K7EJ81	EFTUD2	-0.4027615	10.12201917	0.401519112	0
P04844;P04844-2;Q5JYR4;Q5	RPN2	-0.4056625	8.985529758	0.397110862	1.19E-131
P37108;H0YLA2	SRP14	-0.4071884	9.475961589	0.394804018	1.70E-80
Q9UQ80;F8VTY8	PA2G4	-0.4073296	9.178833117	0.394591046	9.77E-45
P26368;K7ENG2;P26368-2	U2AF2	-0.4084625	9.462891914	0.392884026	6.31E-86
Q9H6R0;I3L1L6;Q9H6R0-2	DHX33	-0.4100189	9.771116924	0.39054634	3.36E-202
Q04637;Q04637-3;Q04637-5;	EIF4G1	-0.4127369	9.205123129	0.386484304	3.36E-196
Q12904;Q12904-2	AIMP1	-0.4129982	9.321494867	0.386095142	9.92E-132
Q96I25;Q5W011;Q5W010	RBM17	-0.4145927	9.032497883	0.383725589	2.88E-99
Q92614;Q92614-4;Q92614-3;	MYO18A	-0.4156857	9.074962643	0.382106635	2.47E-190
Q71RC2;Q71RC2-5;Q71RC2-4	LARP4	-0.4213448	9.631697372	0.373790859	2.25E-302
Q8IWA0	WDR75	-0.4265575	8.604193642	0.366230838	5.55E-75
Q9H0S4	DDX47	-0.4316521	10.02345824	0.358935189	1.16E-234
P62306	SNRPF	-0.439043	9.451893845	0.348514583	2.63E-21
P78549;H3BRL9;H3BPD5	NTHL1	-0.4414482	9.409172019	0.345165396	5.00E-192
Q13895;H7BY94	BYSL	-0.4414787	8.481614592	0.345123033	8.88E-36
P62913;P62913-2;Q5VVC8;Q!	RPL11	-0.4434185	10.27962132	0.342437117	1.23E-109
P08708;P0CW22;H0YN88;H0\	RPS17;RPS17L	-0.4458961	10.33767885	0.339025929	2.84E-239
P32969;D6RAN4;H0Y9V9;E7E	RPL9	-0.4472923	10.22047421	0.337113328	4.54E-253
Q96AG4	LRRC59	-0.4541245	10.36246362	0.327854383	0
P62879;C9JXA5;C9JIS1;E7EP3	GNB2	-0.4603138	9.843905196	0.319610365	1.77E-186
P38919	EIF4A3	-0.4613094	9.514720374	0.318296983	3.73E-144
P08865;C9J9K3;A6NE09	RPSA;RPSAP58	-0.462059	8.862238747	0.317310509	7.21E-115
O43290	SART1	-0.4641495	9.669233175	0.314570027	0
Q8WWK9;E9PD90	CKAP2	-0.4657326	8.487675606	0.312505047	8.05E-38
O95619;F8W0J4;F8W1B9;F8\	YEATS4	-0.4659081	8.581016157	0.312276709	1.03E-14
Q8TDN6	BRIX1	-0.4701252	10.30655369	0.306822217	1.57E-231
Q96EP5;K7EQ02;Q96EP5-2	DAZAP1	-0.4734993	9.027104866	0.302503848	2.90E-39
P05386	RPLP1	-0.4755974	10.55623011	0.299839082	2.49E-135
Q6P5R6;C9JYQ9;H0Y8C2	RPL22L1	-0.477478	9.138334282	0.297463828	3.54E-68
Q9Y221;Q9Y221-2;J3QLW7	NIP7	-0.4786301	9.604744304	0.296015033	1.21E-101
Q71UM5;H0YMV8;C9JLI6	RPS27L	-0.4824524	9.439537948	0.29124198	1.16E-49
P62701;A6NH36	RPS4X	-0.4877357	10.61789109	0.284730134	0
P62266;D6RD47	RPS23	-0.4894485	9.914697431	0.282640379	1.16E-28
Q16698;B7Z6B8;E5RJG7;E5RI	DECR1	-0.4902115	9.853588712	0.281712886	1.29E-119
P23396;E9PPU1;J3KN86;E9PL	RPS3	-0.4902229	10.24427712	0.281698989	5.36E-229
Q9Y5M8;H7C4H2	SRPRB	-0.5089417	8.537730968	0.259589409	6.70E-33
P19387	POLR2C	-0.5091534	8.312388949	0.259346414	1.82E-24
P62851	RPS25	-0.5105152	9.83831376	0.257787128	2.45E-29
Q9Y5J1	UTP18	-0.5144024	9.561959579	0.253372206	3.48E-174
O96019;O96019-2;H7C5S0	ACTL6A	-0.5207176	9.25459641	0.246312366	9.39E-162
Q29RF7	PDS5A	-0.5223732	8.634517574	0.244484613	1.02E-104
P53680;M0R0N4;M0QYZ2;P5	AP2S1	-0.524929	8.304878118	0.2416817	1.69E-06
Q9HC52	CBX8	-0.5255508	9.442918545	0.241003231	3.66E-93
Q9UNQ0;Q9UNQ0-2	ABCG2	-0.528019	8.527346293	0.238323399	4.34E-65
P62857	RPS28	-0.5321579	9.399050382	0.233876747	1.11E-63
Q13123;E7EQZ7	IK	-0.5379963	8.970718704	0.227704747	8.98E-65
Q9Y3B4	SF3B14	-0.5446053	9.017116849	0.220859264	1.94E-40
P60842;J3KT12;P60842-2;J3K	EIF4A1;EIF4A2	-0.5469437	8.3545118	0.218472868	1.84E-41
P18124;A8MUD9	RPL7	-0.5494118	10.62406541	0.215974267	7.80E-185

O00566;C9JX83	MPHOSPH10	-0.5579529	8.894304984	0.207486579		6.81E-32
O95639;O95639-3;O95639-2;	CPSF4	-0.5602951	8.663239065	0.205201859		6.32E-46
Q9NUL3;Q9NUL3-8;Q9NUL3-	STAU2	-0.5606956	8.969690754	0.204812988		5.97E-74
P47897;B4DWJ2	QARS	-0.5652561	9.247261127	0.200423145		1.41E-118
O15381;O15381-5;H0Y8B6;O	NVL	-0.5668411	9.310374642	0.19891364		7.89E-105
Q8TDD1-2;Q8TDD1	DDX54	-0.5680752	9.518606053	0.197744136		1.86E-120
Q9Y3Y2;Q9Y3Y2-4;Q9Y3Y2-3;	CHTOP	-0.585537	8.926141719	0.181731666		1.84E-26
Q9UKJ3-2;Q9UKJ3	GPATCH8	-0.5859604	8.335197045	0.181355694		6.77E-81
Q8NI27	THOC2	-0.5951595	9.47693302	0.17332952		2.41E-265
P62308;Q49AN9;F5H013;A8M	SNRPG	-0.5977936	8.795240265	0.171080967		0.00091538
P42677;Q5T4L4	RPS27	-0.6008339	10.23042337	0.168512846		2.42E-58
P63220;Q9BYK2;Q8WVC2;Q9	RPS21	-0.6066952	8.152563514	0.163643711		5.89E-19
Q53GS9;B9A018;B8ZZD1;G5E	USP39	-0.6109009	9.65065715	0.160215764		3.79E-169
P84103;B4E241	SRSF3;SFRS3	-0.6168346	9.927164974	0.155472055		8.13E-63
P62805	HIST1H4A	-0.6179047	12.06572906	0.154628097		0
Q9P035;B4DRF4;H3BS72;H3B	PTPLAD1	-0.6381073	8.896702545	0.139339361		2.27E-45
Q7RTV0	PHF5A	-0.6436462	9.365057221	0.135357935		2.25E-85
P62273;P62273-2	RPS29	-0.6496696	9.048635988	0.131128643		1.18E-10
O95400	CD2BP2	-0.65942	9.107006346	0.124500592		5.22E-68
Q8N8A6	DDX51	-0.6594467	9.008003672	0.124482806		6.28E-82
P46783;F6U211;Q9NQ39	RPS10;RPS10P5	-0.6643448	9.866984015	0.121253693		6.37E-78
Q99729-3;D6R9P3;D6RD18;D	HNRNPAB	-0.6670761	8.956557392	0.119481704		3.38E-27
P61313;E7EQV9;E7ENU7;E7E	RPL15	-0.6673355	10.23904909	0.119314475		3.55E-91
Q8NC51;Q8NC51-3;Q8NC51-;	SERBP1	-0.6684284	9.13871311	0.118611913		7.31E-84
P63010;P63010-2;Q7Z451;K7	AP2B1	-0.6687508	9.485366466	0.118405321		2.79E-163
Q92979	EMG1	-0.6722107	9.103324707	0.116205548		8.11E-39
P98175-2;P98175	RBM10	-0.6900864	8.783346067	0.105347712		1.96E-283
Q15287;H3BV80;H3BMM9;H	RNPS1	-0.6902237	9.203386492	0.105267526		1.45E-80
P52948;P52948-2;P52948-4;F	NUP98	-0.6968765	8.773552419	0.101440654		1.42E-92
Q00577	PURA	-0.7140636	8.788684408	0.092065792		5.92E-76
Q96FV9	THOC1	-0.7201958	9.162175937	0.088894455		7.79E-120
Q96DH6;Q96DH6-2;B4DHE8;I	MSI2	-0.7328339	8.922896651	0.082636083		4.13E-45
O43251-6;O43251-8;O43251;	RBFOX2;RBM9	-0.7335892	8.393943539	0.082273663		3.14E-13
Q14978-2;Q14978	NOLC1	-0.7388191	11.06498182	0.0797994		0
Q15397	KIAA0020	-0.7415066	8.541554284	0.078551701		4.87E-31
P41091;Q2VIR3;Q2VIR3-2;F8	EIF2S3;EIF2S3L	-0.7439327	9.922658	0.077438997		1.06E-170
Q9BQ39	DDX50	-0.7636795	8.9933304	0.06885236		4.99E-142
O43293;O43293-2	DAPK3	-0.7854919	9.087000121	0.060293204		3.98E-85
Q92797;Q92797-2;M0R3C7	SYMPK	-0.7928715	8.57953209	0.057605153		7.42E-39
P60866;P60866-2;E5RJX2	RPS20	-0.8076496	10.0695571	0.052521162		1.79E-40
Q8IUE6	HIST2H2AB	-0.8097305	11.36144451	0.051836357		2.61E-205
Q7KZF4	SND1	-0.8131237	9.337738717	0.050735733		6.13E-135
Q8IX01;Q8IX01-4;M0R2Z9;Q8	SUGP2	-0.8142853	9.06092437	0.050363486		4.08E-85
P40939	HADHA	-0.8233585	8.501702692	0.047533848		1.56E-22
Q9UKF6;G5E9W3	CPSF3	-0.8560791	9.222508376	0.038414755		3.92E-116
O75934	BCAS2	-0.8579731	9.533276238	0.037935883		1.19E-243
P42695;E9PKK4;G3V1A9	NCAPD3	-0.8629417	8.151859956	0.036703697		4.07E-30
O75400;O75400-2;O75400-3	PRPF40A	-0.8715191	8.714631481	0.034656776		5.37E-33
Q07666;Q07666-3;Q07666-2	KHDRBS1	-0.8747406	9.88912795	0.033913582		1.22E-127
Q5SY16	NOL9	-0.8849945	8.94182437	0.031638077		2.61E-49
P62854;Q5JNZ5;F8VZW7	RPS26;RPS26P11	-0.8953152	10.09219412	0.029481244		4.33E-24
P62891;Q59GN2	RPL39;RPL39P5	-0.9158974	9.651985105	0.025555219		1.30E-06
Q15050	RRS1	-0.9335155	9.145382892	0.022562257		4.80E-147
P09234	SNRPC	-0.9624233	9.171667959	0.018309543		7.46E-112
P08240;P08240-2	SRPR	-0.9698486	8.267242149	0.017337565		5.16E-58
Q9BTC0;Q9BTC0-1	DIDO1	-0.9897251	9.483044982	0.014955018		2.75E-120
P05198;H0YJS4;G3V4T5	EIF2S1	-1.004147	9.386641626	0.013411763		1.98E-84
P09429;Q5T7C4;Q5T7C6	HMGB1	-1.004883	9.194431083	0.013336898		1.73E-46
O15144	ARPC2	-1.014904	8.680580245	0.012353999		1.76E-55
Q96QC0;F5H5K4	PPP1R10	-1.022547	8.910143961	0.011648076		1.67E-25
Q14011;K7ELV6;K7ENX8;K7EJ	CIRBP	-1.042559	9.032940938	0.009966337		7.23E-51
P21796	VDAC1	-1.058601	8.707544629	0.008778112		1.43E-18
Q8IZL8;I3L3A8;C9JFV4;Q8IZL8	PELP1	-1.086298	8.635232346	0.007021602		3.34E-91
H3BQM0;B4DV38;Q8NDF8-3;	PAPD5	-1.09243	8.796109264	0.006678249		3.13E-61
Q9UNQ2;D6RCL3	DIMT1	-1.110624	8.528067841	0.00574655		2.87E-18
Q9H307;Q9H307-2	PNN	-1.123569	9.629705145	0.00515683		1.23E-99
P62304;A6NHK2	SNRPE	-1.126583	9.479431337	0.005027644		2.51E-102
Q6ZRS2;Q6ZRS2-3;Q6ZRS2-2	SRCAP	-1.135761	8.770329071	0.004652026		1.12E-89
Q96C19;H0Y4Y4	EFHD2	-1.15164	9.188112537	0.004061734		1.69E-86
P26038	MSN	-1.162971	8.470601574	0.003682981		1.83E-19
P42285;F5H7E2	SKIV2L2	-1.168327	9.237065953	0.003515391		8.81E-103
Q6UXN9	WDR82	-1.189903	8.729334909	0.002908242		9.53E-99
Q9ULV3;Q9ULV3-5;H0Y5D5;C	CIZ1	-1.226894	8.808852148	0.002085597		2.99E-74
Q86U38;A8MY76	NOP9	-1.258022	8.419228564	0.001565136		1.15E-34
Q8NE71;Q8NE71-2;H0YGW7	ABCF1	-1.291079	9.526597709	0.001145443		7.49E-282
P17480	UBTF	-1.384718	10.54815593	0.000454023	+	0
Q9NRW3	APOBEC3C	-1.428617	9.00134423	0.000288103	+	7.67E-59
Q9H7B2;Q5VXM9;Q5VXN0	RPF2	-1.466946	8.997565483	0.000191562	+	2.16E-31
P15924;P15924-2	DSP	-1.473267	8.991651299	0.000178917	+	1.01E-121
P35659;P35659-2;B4DFG0;D6	DEK	-1.731609	9.239624765	8.63E-06	+	3.33E-60

Q14978-3	NOLC1	-1.732128	9.69348072	8.58E-06	+	0
Q5SSJ5;B0QZK4;Q5SSJ5-2;Q5	HP1BP3	-1.816868	9.346392098	2.86E-06	+	1.38E-82
P98179	RBM3	-1.844303	9.77566141	1.98E-06	+	1.14E-51
P53999	SUB1	-2.018219	9.398582289	1.72E-07	+	1.39E-43
P07355;P07355-2;H0YN42;A6	ANXA2;ANXA2P2	-2.436432	9.253895057	1.97E-10	+	3.77E-103
Q86Y91-2;H9KV46;Q86Y91-3;	KIF18B	-3.287724	8.700331552	4.09E-18	+	2.35E-44
Q9BYP7;Q9BYP7-2;Q9BYP7-3	WNK3	-7.711468	11.1104887	3.93E-95	+	0.0015059

Appendix 5 (Chapter 4)

Identification and quantification of interacting proteins for H2B S36 GlcNAc modified nucleosome versus wild-type nucleosome. Statistically significant interacting partners are denoted with a '+'

Majority Protein Ids	Gene names	log2(Bait/Control)	log10(Intensity)	Significance B value	Statistically Significant Interactor	PEP
Q9BYP7;Q9BYP7-2;Q9BYP7-3	WNK3	9.26315	9.32842	1.46E-158	+	0.0042837
Q02880;Q02880-2;E9PCY5	TOP2B	2.44198	7.81972	2.93E-12	+	1.53E-94
Q14679;H7C2S3;H7C421;H7B	TTLL4	2.03976	7.94652	6.22E-09	+	0.0022379
Q6P5R6;C9JYQ9;H0Y8C2	RPL22L1	2.03391	7.42625	6.89E-09	+	2.19E-49
Q14671;Q14671-2;E9PR38;E7	PUM1	1.82865	7.01628	2.03E-07	+	6.37E-82
P55735;A8MXL6;P55735-2;B4	SEC13	1.74612	7.37129	7.19E-07	+	2.11E-10
Q14247;Q14247-3;Q14247-2;	CTTN	1.69458	7.62851	1.54E-06	+	4.71E-10
O75607	NPM3	1.49509	7.57684	2.38E-05	+	5.36E-25
Q99848;H7C2Q8	EBNA1BP2	1.49073	7.60547	2.52E-05	+	3.56E-07
Q9UBU8;Q15014;H0YM21;Q5	MORF4L1;MORF4L2	1.45827	6.93124	3.81E-05	+	0.00011084
Q08945;E9PPZ7;E9PMD4	SSRP1	1.32587	7.16814	0.000189011	+	3.44E-19
P35573;P35573-2;P35573-3	AGL	1.27242	7.90214	0.000346567	+	0.0039035
P54289;P54289-3;H0Y715;P5	CACNA2D1	1.26178	7.15954	0.000389963	+	0.0011309
Q99590;Q99590-2;F8VXG7	SCAF11	1.22328	7.42857	0.0005931	+	1.47E-09
P56537;B7ZBG9;B7ZBH1	EIF6	1.17061	7.31559	0.0010326	+	6.54E-35
Q8NC51;Q8NC51-3;Q8NC51-4	SERBP1	1.09633	7.95501	0.00217414		2.45E-19
Q9H2U1;Q9H2U1-2;F5GZS0;E	DHX36	1.09042	7.65706	0.00230249		2.45E-117
Q6SPF0;E9PIW9	SAMD1	1.0748	7.25329	0.00267584		2.48E-13
Q5VT52;Q5VT52-3;B4E2Q6;Q	RPRD2	1.06396	7.32385	0.00296686		1.53E-46
Q9BY44;B4DQ14;F8WAE5;B4	EIF2A	1.02005	7.08045	0.00446352		5.73E-12
Q9BQG0;Q9BQG0-2;I3L1L3	MYBBP1A	1.01668	7.70455	0.00460305		2.67E-39
Q7L2E3;Q7L2E3-2;Q7L2E3-3;I	DHX30	0.947351	7.77581	0.00849225		2.38E-68
H7C4H8	SLBP	0.942533	7.70789	0.0088492		0.0045004
Q5T6F2;F5H2U4;A6NCA8;Q5J	UBAP2	0.926317	7.8036	0.0101511		3.48E-97
Q6UXN9	WDR82	0.921844	6.88991	0.010539		1.15E-14
P07437;Q5ST81;Q5JP53;F8VY	TUBB;TUBB4B;TUBB	0.917795	7.47516	0.0109015		5.72E-85
Q13595;Q13595-2;B4DQI6;B4	TRA2A	0.900612	7.16498	0.0125659		3.52E-15
O96019;O96019-2	ACTL6A	0.888437	8.22227	0.0138777		1.95E-81
P98179	RBM3	0.873795	7.73523	0.0156144		2.53E-112
Q9NZI7;Q9NZI7-4	UBP1	0.857336	6.89381	0.0177922		4.67E-13
Q9NPE3	NOP10	0.843405	7.09461	0.0198391		3.09E-13
P38432	COIL	0.831491	7.1474	0.0217497		7.58E-11
Q15651;P05204;Q15651-2	HMGN3;HMGN2	0.795752	7.33329	0.0284726		3.22E-05
P11388;P11388-2;P11388-3;F	TOP2A	0.746344	8.29994	0.0406637		2.93E-118
P58317;K7EQI1;K7EPQ9	ZNF121	0.741423	6.54219	0.0420906		1.77E-06
Q9BRJ6;C9JQV0;H7C0T1;H7C	C7orf50	0.729973	7.32298	0.0455752		8.57E-10
P42285;D6REC7;F5H7E2	SKIV2L2	0.721502	6.56036	0.0483069		1.72E-16
Q13769	THOC5	0.715172	7.17571	0.0504372		3.73E-14
P62081;B5MCP9	RPS7	0.708904	8.77791	0.0526232		3.32E-170
Q9H2Y7;H3BS99;E9PE29	ZNF106	0.707739	6.90305	0.0530383		4.66E-05
Q9UII2	ATPIF1	0.704435	8.05576	0.0542299		1.56E-05
F8W726;Q5VU77	UBAP2L	0.703228	7.2921	0.0546709		0
O00567	NOP56	0.687588	7.7409	0.0606591		4.96E-21
Q6UN15;Q6UN15-3;Q6UN15-	FIP1L1	0.668102	7.87916	0.0688699		1.47E-90
Q9UQ80;F8VTY8;F8VR77;F8V	PA2G4	0.650398	7.05273	0.0771017		3.13E-14
A0AV96;D6RBS9;D6R9D6;A0A	RBM47	0.638027	7.4135	0.0833166		8.25E-47
Q5T3I0;Q5T3I0-3;E9PAV9;F8\	GPATCH4	0.635086	7.84421	0.0848524		2.05E-130
P52434;C9JBJ6;C9JLU1;C9JCU	POLR2H	0.624895	7.02629	0.0903516		0.00087804
Q15717;B4DVB8;M0QZR9	ELAVL1	0.611444	8.63878	0.098045		4.32E-127
P62851	RPS25	0.608627	8.44295	0.0997207		5.34E-19
Q96C19;H0Y4Y4	EFHD2	0.608227	7.12031	0.0999609		1.97E-12
Q6IBS0;D6RG15	TWF2	0.578995	8.7791	0.118764		0.00047787
P08621;P08621-2;P08621-3	SNRNP70	0.560966	7.3499	0.131677		2.26E-10
Q9H0H5;F8VRD2;F8W1E5	RACGAP1	0.549255	7.2788	0.140631		1.90E-68
O14950;P19105;J3QRS3	MYL12B;MYL12A	0.5478	7.83735	0.141776		6.50E-122
Q9P1U0	ZNRD1	0.547691	7.36491	0.141861		8.84E-16
O43660;O43660-2;A8MW61	PLRG1	0.540051	7.68581	0.147992		2.48E-125
P18124;A8MUD9	RPL7	0.529812	8.61047	0.156522		1.36E-54
Q9H6R4;G8JLK7;Q9H6R4-4;Q	NOL6	0.518517	7.01565	0.166358		2.16E-09
Q9P2E9;Q9P2E9-3;Q9P2E9-2;	RRBP1	0.517353	7.04984	0.167398		2.63E-230
P17480;P17480-2;E9PKP7	UBTF	0.499317	8.13085	0.184134		1.52E-30
O75531	BANF1	0.498514	6.57734	0.184907		0.00018514
Q9Y224;G3V4C6	C14orf166	0.493183	8.41073	0.1901		5.41E-206
Q14677;Q14677-2;Q14677-3	CLINT1	0.485075	7.40572	0.198202		1.53E-18
Q00839;Q00839-2	HNRNPU	0.481356	7.92605	0.202002		9.22E-107
Q14103;Q14103-3;H0YA96;H	HNRNPD	0.47921	8.43996	0.204219		1.67E-76
P26599;P26599-2;P26599-3;A	PTBP1	0.477663	9.4191	0.205827		0
P52298;C9JQX9;B3KSB0;P522	NCBP2	0.46361	6.83691	0.220866		1.62E-06
Q96PK6	RBM14	0.459089	8.98652	0.225866		1.70E-95
Q8NCA5;Q8NCA5-2;E9PH82	FAM98A	0.457817	8.28623	0.227288		7.03E-82
Q9NY12;Q9NY12-2	GAR1	0.449207	7.52179	0.237078		1.18E-14
P33778;Q16778;Q99877;Q93	HIST1H2BB;HIST2H2	0.446098	10.3592	0.240686		4.21E-38
Q92900;Q92900-2	UPF1	0.44404	9.03543	0.243095		0

Q9HAV0	GNB4	0.440758	6.57259	0.246973	2.62E-87
P55081	MFAP1	0.439354	6.65764	0.248644	6.78E-08
J3KNL6;O15027;O15027-2;O1	SEC16A	0.430716	7.66006	0.259104	1.71E-24
Q8NE71;Q8NE71-2;H0YGW7;	ABCF1	0.428398	7.64945	0.261961	2.35E-49
Q9H7E2;Q9H7E2-2;Q9H7E2-3	TDRD3	0.427732	7.47787	0.262785	4.84E-18
Q9P0K7;Q9P0K7-4;Q9P0K7-3	RAI14	0.420071	8.22316	0.272407	6.47E-300
P30050;P30050-2	RPL12	0.418739	8.834	0.274103	1.15E-89
P14373;P14373-2;B0V297	TRIM27	0.403822	7.58153	0.2936	3.07E-62
P46776;E9PJD9;E9PLL6	RPL27A	0.392719	8.68173	0.308702	5.15E-18
Q9Y3U8;J3QSB5	RPL36	0.387697	8.11076	0.315699	1.62E-26
Q92576;Q92576-2;E7EVH3	PHF3	0.386551	8.56647	0.317311	3.25E-179
Q6PJG2;F6RU81;H7C1L3	ELMSAN1	0.385214	7.46064	0.319197	6.95E-17
Q9NZ01;M0R3C3;Q9NZ01-2;I	TECR	0.383318	7.29283	0.321885	3.10E-06
P05187;P10696	ALPP;ALPPL2	0.373743	8.08728	0.335682	2.03E-234
Q5BKZ1	ZNF326	0.372828	7.27091	0.337021	4.93E-08
Q96I24	FUBP3	0.37266	7.98464	0.337267	7.38E-28
P46782;M0R0F0;M0R0R2;M0	RPS5	0.370583	8.29314	0.340319	1.03E-93
P84103;B4E241	SRSF3;SFRS3	0.366156	8.09096	0.346883	3.27E-31
Q2TAY7;B4E3L0	SMU1	0.357265	6.96509	0.360305	1.11E-05
Q16643;Q16643-2;A8MV58;I	DBN1	0.350698	8.20585	0.370426	2.11E-178
P08670;B0YJC4;B0YJC5	VIM	0.336283	9.85089	0.393256	0
Q14683	SMC1A	0.334784	6.86674	0.395678	9.61E-08
P84090;G3V279	ERH	0.333447	8.4838	0.397846	2.71E-150
Q13148;Q13148-2;B1AKP7;G	TARDBP	0.332197	7.45261	0.399878	3.28E-19
P11387	TOP1	0.332134	8.97284	0.399981	0
O43823	AKAP8	0.329065	7.91132	0.405	1.71E-43
Q9H307;Q9H307-2	PNN	0.328657	7.07711	0.40567	7.42E-06
Q9NVI7-2;Q9NVI7;Q9NVI7-3;	ATAD3A;ATAD3B	0.328239	8.21595	0.406357	6.12E-21
O95782;O95782-2	AP2A1	0.327909	7.70064	0.406899	6.12E-55
P16070;H0YD13;H0Y2P0;P16	CD44	0.327345	7.11032	0.407829	2.55E-13
Q13310;Q13310-2;B1ANR0;Q	PABPC4	0.327158	8.89453	0.408138	0
Q14978;Q14978-3;Q14978-2	NOLC1	0.322495	8.70641	0.415871	5.70E-19
P41208	CETN2	0.322418	6.86465	0.415998	1.12E-49
Q10570	CPSF1	0.321112	7.67997	0.418181	3.21E-83
P38159;H0Y6E7;H3BT71;P38	RBMX;RBMXL1	0.317596	8.14684	0.424086	1.22E-49
Q9Y5S9;Q9Y5S9-2	RBM8A	0.316153	7.16316	0.426525	2.00E-06
Q7Z417	NUFIP2	0.315695	8.51679	0.427301	1.02E-157
P62913;P62913-2;Q5VVC9;Q	RPL11	0.31493	8.71633	0.428598	2.83E-23
Q9C0J8;Q9C0J8-2;C9J8B4;Q9	WDR33	0.307783	7.22183	0.440827	8.49E-16
P68104;Q5VTE0;A6PW80;Q5	EEF1A1;EEF1A1P5	0.30551	7.19656	0.444759	1.69E-05
Q9UKV8;Q9UKV8-2	AGO2	0.303135	7.60811	0.448887	6.16E-77
Q8IWR0;I3L2K5	ZC3H7A	0.30065	7.22474	0.45323	1.61E-06
Q8IWX8;J3QK89	CHERP	0.298851	7.79047	0.456389	1.91E-27
P46781;B5MCT8;C9JM19	RPS9	0.298586	8.42778	0.456855	3.16E-30
Q12906;Q12906-4;Q12906-5;	ILF3	0.292557	8.38272	0.467538	3.60E-43
O15160;O15160-2;E7EQB9	POLR1C	0.288078	8.0849	0.475561	2.65E-192
Q13247;Q13247-3	SRSF6	0.287949	7.9195	0.475795	1.07E-19
P14868;Q68CR9;H7BZ35	DARS;DKFZp781B11	0.286196	6.74309	0.478957	8.85E-05
P61353;K7EQQ9;K7ELC7	RPL27	0.283922	8.3082	0.483075	5.17E-13
O60284;E5RHS3	ST18	0.281277	7.35463	0.487891	0.0039526
Q9UMS4;F5GY56	PRPF19	0.28055	8.50282	0.489218	2.97E-59
Q6P2Q9	PRPF8	0.27898	8.62226	0.492092	0
P60660;P60660-2;F8W1R7;G	MYL6	0.278172	8.35959	0.493576	2.44E-54
P52907	CAPZA1	0.27574	8.19374	0.498053	1.06E-34
Q09666	AHNAK	0.274948	7.62003	0.499515	3.78E-15
P39019;M0R2L9;M0QXK4;M0	RPS19	0.274448	9.02473	0.500439	6.79E-45
P57678;I3L2C7	GEMIN4	0.274145	7.4255	0.501001	1.02E-21
O14974;O14974-5;O14974-4;	PPP1R12A	0.271795	8.52677	0.505361	3.16E-64
Q9Y446	PKP3	0.269497	8.03294	0.509645	3.71E-48
P39880;P39880-2;P39880-3;F	CUX1	0.265533	6.75917	0.517077	2.75E-19
Q9H0A0;E7ESU4	NAT10	0.259386	8.30835	0.528715	1.69E-283
P04792;C9J3N8;F8WE04	HSPB1	0.258043	7.02653	0.531274	2.21E-12
Q8TDD1;Q8TDD1-2	DDX54	0.257032	6.46574	0.533205	0.00057422
P62158;H0Y7A7;E7ETZ0;E7EN	CALM1;CALM2	0.252914	8.61317	0.541108	7.90E-74
P17844;J3KTA4;B4DLW8	DDX5	0.249571	9.44767	0.547568	0
Q01081;Q01081-2;Q8WU68;I	U2AF1;U2AF1L4	0.249247	6.96696	0.548196	1.35E-09
Q9H9Y6;Q9H9Y6-2;F5GZX4;F	POLR1B	0.248549	7.84858	0.549551	3.56E-209
Q9Y520;Q9Y520-3;Q9Y520-4;	PRRC2C	0.244476	8.46342	0.557483	2.71E-172
Q9BUQ8	DDX23	0.24234	8.30261	0.561666	7.47E-37
P21333;Q5HY54;P21333-2	FLNA	0.24041	7.45682	0.565459	2.24E-15
Q13748;P68363;Q9BQE3;Q71	TUBA3C;TUBA1B;TU	0.237593	7.0976	0.571017	1.04E-06
O60832;O60832-2;C9IYT0;H7	DKC1	0.235037	8.28809	0.576082	7.78E-32
Q9P275;Q9P275-2;E9PEW0	USP36	0.23271	7.5701	0.580711	2.01E-39
Q96HS1;Q96HS1-2	PGAM5	0.232628	7.96319	0.580875	1.03E-18
P26196	DDX6	0.230679	8.52609	0.584767	1.26E-191
Q9BYG3;H7BZL0;C9J808	MKI67IP	0.230671	6.42553	0.584782	6.26E-08
Q14157;Q14157-5;Q14157-3	UBAP2L	0.224239	9.27284	0.597709	0
Q2NL82	TSR1	0.222908	7.01418	0.600401	3.72E-12
Q9Y5B9	SUPT16H	0.217094	7.40524	0.61222	4.69E-26
P62244;I3L3P7;I3L246;H3BN9	RPS15A	0.216745	8.56323	0.612933	7.75E-36

H7BY36	EWSR1	0.212492	7.13287	0.621649	2.91E-65
P25398	RPS12	0.212383	8.9768	0.621872	3.69E-70
P31943;E9PCY7;G8JLB6;D6RI	HNRNPH1	0.211935	8.7914	0.622794	5.53E-234
Q8TAQ2;Q8TAQ2-2;Q8TAQ2-	SMARCC2	0.210522	7.0769	0.625705	4.00E-43
P35579;P35579-2	MYH9	0.208656	9.10988	0.629555	0
Q9NYF8;Q9NYF8-2;Q9NYF8-4	BCLAF1	0.2076	7.50672	0.63174	1.20E-21
O95816;B4DXE2	BAG2	0.205332	7.71104	0.636442	1.37E-155
P46087;P46087-2;P46087-4;F	NOP2	0.204666	7.65784	0.637825	1.36E-33
Q9Y4P3;E9PF19	TBL2	0.203535	7.14092	0.640177	5.32E-13
P04003	C4BPA	0.199205	8.22991	0.649215	3.02E-75
P16401	HIST1H1B	0.197968	8.75465	0.651809	1.46E-36
P62269	RPS18	0.197962	9.12392	0.651821	2.25E-71
Q9NYL9;H0YNJ8	TMOD3	0.196127	7.87604	0.655673	8.31E-159
Q9GZS1-2;Q9GZS1;E7EX70	POLR1E	0.19298	7.97276	0.662302	3.63E-21
P43243;A8MXP9;D6REM6;D6	MATR3	0.191755	8.75029	0.664888	3.84E-159
P05388;F8VU65;Q3B7A4;F8V	RPLP0;RPLP0P6	0.190247	8.82235	0.66808	1.58E-43
P38646	HSPA9	0.188446	7.86504	0.671898	7.75E-72
P28288;P28288-2;F5GYC1;E7	ABCD3	0.187405	7.73979	0.67411	4.27E-74
O76021;J3QSV6;B4DJ58;I3L3	RSL1D1	0.187134	7.63096	0.674686	7.21E-101
Q14134;Q14134-2	TRIM29	0.177561	7.11701	0.695154	3.79E-50
P62857	RPS28	0.176243	7.91693	0.69799	9.81E-17
P11142;E9PKE3;P11142-2;E9	HSPA8	0.172556	9.10626	0.705946	7.14E-243
Q6WCQ1;Q6WCQ1-3;Q6WCC	MPRIP	0.172419	8.39658	0.706243	9.51E-210
P33240;E9PID8;P33240-2;E7E	CSTF2	0.169283	6.83636	0.713035	1.18E-05
Q7Z739	YTHDF3	0.167154	8.01874	0.717659	2.55E-46
Q8WXF1;Q8WXF1-2	PSPC1	0.163271	8.62135	0.726122	3.49E-99
P67809;H0Y449	YBX1	0.160101	9.06266	0.733055	0
P98175-2;P98175;P98175-3;F	RBM10	0.155653	8.42218	0.74282	8.33E-82
P62316;K7ERG4;P62316-2	SNRPD2	0.150946	8.0881	0.753199	5.05E-18
E7EWI9;P51991-2;P51991	HNRNPA3	0.148417	8.87322	0.758794	1.74E-109
Q86V48;Q86V48-2;Q86V48-3	LUZP1	0.146395	8.5984	0.763276	0
P41091;Q2VIR3;Q2VIR3-2;F8\	EIF2S3;EIF2S3L	0.141693	8.16826	0.773729	8.67E-38
Q92841;H3BLZ8;Q92841-3;Q	DDX17	0.1367	9.63477	0.784876	0
P19447;G3V1S1	ERCC3	0.135344	7.1173	0.787911	3.00E-11
P52597	HNRNPF	0.134619	8.27333	0.789534	1.11E-80
Q12905	ILF2	0.133234	8.07777	0.792638	1.07E-41
Q9UN86;Q9UN86-2	G3BP2	0.133038	9.33193	0.793079	6.51E-185
P15328	FOLR1	0.132984	7.89459	0.793199	4.96E-52
P62979;P0CG47;J3QS39;J3QT	RPS27A;UBB;UBC;U	0.130869	8.3529	0.797948	8.21E-136
P08107;P08107-2;F8VZJ4;E7E	HSPA1A	0.130322	8.37643	0.799178	2.29E-69
P23246;P23246-2	SFPQ	0.130226	10.5742	0.799392	0
Q15366;Q15366-4;Q15366-5;	PCBP2	0.129383	7.98331	0.801288	2.83E-70
Q9UHB6;Q9UHB6-4;F8VQE1;I	LIMA1	0.126556	8.75651	0.807653	1.10E-194
Q8WWI1-3;E9PMS6;Q8WWI1	LMO7	0.126476	8.55728	0.807833	0
Q96KR1	ZFR	0.124645	8.02247	0.811963	5.39E-293
Q15427	SF3B4	0.123835	7.65685	0.813793	1.40E-31
O60506;O60506-2;O60506-3;	SYNCRIP	0.123219	8.69943	0.815185	0
P62888;E5RI99	RPL30	0.121977	8.89713	0.817991	2.90E-165
Q9BRP8;Q9BRP8-2	WIBG	0.121363	6.89795	0.81938	3.19E-09
Q14011;K7ELV6;K7ENX8;K7EJ	CIRBP	0.121223	7.72003	0.819695	2.90E-143
Q96K37	SLC35E1	0.119009	6.71252	0.824708	5.02E-60
Q9NZB2;Q9NZB2-6;Q9NZB2-4	FAM120A	0.116892	8.41797	0.829508	1.55E-132
P49750-4;P49750;F8VU51;P4	YLPM1	0.116888	8.25725	0.829517	5.39E-63
P05198;H0YJS4;G3V4T5	EIF2S1	0.116669	7.91263	0.830014	2.50E-81
P49790;F6QR24	NUP153	0.115482	7.65413	0.832707	5.51E-80
Q9BUJ2;Q9BUJ2-4;B7Z4B8;Q	HNRNPUL1	0.113409	8.69209	0.837417	1.13E-232
P35637;P35637-2;H3BPE7	FUS	0.112421	9.40259	0.839664	7.42E-117
P60709	ACTB	0.111446	10.4089	0.841882	0
P38919	EIF4A3	0.111143	7.67116	0.842572	1.47E-15
Q14966;Q14966-3;Q14966-4;	ZNF638	0.110336	8.34298	0.844409	1.54E-184
P08708;P0CW22;H0YN88;H0\	RPS17;RPS17L	0.108885	8.43404	0.847716	5.97E-128
Q9Y2S0	POLR1D	0.106667	7.30916	0.852775	1.21E-173
Q16629;Q16629-3;Q16629-2;	SRSF7	0.104292	7.39749	0.858198	6.69E-19
Q01844;Q01844-6;B0QYK0;Q	EWSR1	0.101166	9.26682	0.865347	6.96E-187
P26373;J3QSB4;P26373-2	RPL13	0.0997734	8.82596	0.868534	2.33E-53
P62753;A2A3R7;A2A3R5	RPS6	0.098217	8.85457	0.8721	2.62E-148
O75533	SF3B1	0.0952988	8.10554	0.878793	1.02E-43
Q9Y5A9;Q9Y5A9-2	YTHDF2	0.0943871	8.4207	0.880885	7.26E-89
Q9Y2W1	THRAP3	0.0914669	7.83734	0.887594	5.42E-45
P83111;P83111-2	LACTB	0.0908318	8.07628	0.889054	9.65E-24
O75643	SNRNP200	0.0888824	8.65719	0.893537	0
Q86TG7;Q86TG7-2	PEG10	0.0881081	7.90422	0.89532	7.57E-177
O00425	IGF2BP3	0.0874996	8.65854	0.89672	0
O00571;O00571-2;O15523;B4	DDX3X;DDX3Y	0.0873547	8.81301	0.897054	3.79E-205
Q96T60;M0R3C8;M0QYH2	PNKP	0.086853	7.58795	0.898209	5.01E-15
Q13283;F5H4D6	G3BP1	0.0861912	9.52558	0.899733	3.00E-292
Q96DH6;Q96DH6-2;B4DHE8;J	MSI2	0.0856094	8.04246	0.901073	8.14E-183
P14678;P63162;P14678-2;B3	SNRPB;SNRPN	0.0811138	7.7579	0.911439	4.75E-12
P62314;J3QLR7;J3QLI9	SNRPD1	0.0806389	7.80602	0.912535	1.49E-09
Q14684;Q14684-2	RRP1B	0.0791645	7.41616	0.915938	1.25E-47

P13987;E9PNW4;E9PR17	CD59	0.0782337	8.02861	0.918087	2.96E-30
P62847;P62847-2;E7ETK0;P6	RPS24	0.077734	8.30822	0.919242	1.08E-21
Q07955;Q07955-3;J3KTL2;Q0	SRSF1	0.0747356	7.75113	0.92617	1.87E-17
Q8NI36;D6R922	WDR36	0.0746479	7.98994	0.926373	5.47E-54
Q9NZI8;Q9NZI8-2	IGF2BP1	0.0728073	8.46976	0.930629	0
Q3B726	TWISTNB	0.0708942	7.80171	0.935055	6.37E-19
P62750;H7BY10;K7EJV9;K7ER	RPL23A	0.0656223	8.85226	0.947262	2.54E-27
P62263;E5RH77	RPS14	0.0647373	8.8353	0.949312	2.39E-28
Q15149;Q15149-4;Q15149-2;	PLEC	0.0635757	9.25103	0.952004	0
O95602;B9ZVN9	POLR1A	0.0608711	8.5204	0.958273	1.32E-242
Q86W92;Q86W92-2;Q86W92	PPFIBP1	0.0605412	7.36312	0.959038	1.98E-23
Q02878;F8W181	RPL6	0.05966	8.94892	0.961082	1.44E-215
P78406;E9PQ57;E9PPG9	RAE1	0.0588818	7.41462	0.962886	2.73E-21
P51114;B4DXZ6;P51114-3	FXR1	0.0588398	8.97501	0.962984	0
Q9UHB9;Q9UHB9-3;F5H5Y3;(	SRP68	0.058382	6.72453	0.964045	9.11E-05
Q14444;Q14444-2;G3V153;E	CAPRIN1	0.0578671	9.41785	0.96524	8.62E-298
Q00610;Q00610-2	CLTC	0.0577717	7.99349	0.965461	2.27E-45
P55265;P55265-5;P55265-3;H	ADAR	0.0563545	7.31088	0.968748	1.95E-46
P62318;B4DJP7;H3BT13	SNRPD3	0.0552979	8.31101	0.9712	6.67E-57
Q8IUE6	HIST2H2AB	0.0534515	10.1817	0.975484	2.38E-97
O43290	SART1	0.0531368	8.06789	0.976214	1.41E-248
Q9Y3I0	C22orf28	0.0517521	8.5198	0.979428	7.86E-240
O43390;O43390-2;Q2L7G6	HNRNPR	0.051281	8.25302	0.980522	1.77E-143
Q9Y2X3	NOP58	0.0500889	7.73264	0.983289	2.39E-18
O15226;G3V1N1	NKRF	0.0498276	7.64681	0.983895	1.63E-28
P62306	SNRPF	0.0493183	8.14239	0.985077	2.12E-56
P35268;K7EJT5;K7EP65;K7EK	RPL22	0.0465736	8.85706	0.991449	6.43E-46
Q13428-3;Q13428-8;Q13428;	TCOF1	0.044857	8.48146	0.995434	2.23E-88
Q13435;E9PPJ0;E9PJ04;H0YC	SF3B2	0.0428905	8.26243	1	9.43E-76
Q5SW79;Q5SW79-2;Q5SW79	CEP170	0.0424271	6.61286	0.999057	2.20E-05
Q13813;Q13813-3;Q13813-2;	SPTAN1	0.0384922	7.3786	0.99105	1.27E-18
P62917;E9PKZ0;E9PIZ3;E9PKI	RPL8	0.0381374	8.84033	0.990328	1.52E-58
Q9UBB4;Q9UBB4-2;B1AHE4	ATXN10	0.0377884	7.13325	0.989618	1.23E-20
Q8IWS0;Q8IWS0-2;Q5JRC6;E	PHF6	0.0366955	7.22089	0.987394	8.55E-08
Q14498;G3XAC6;Q14498-2;Q	RBM39	0.0366898	8.06277	0.987382	2.88E-65
Q9BYW2;H7BZ93;C9JG86;H7I	SETD2	0.0337868	7.10904	0.981476	3.37E-16
Q9NR30;Q9NR30-2	DDX21	0.0329933	8.79956	0.979862	3.37E-235
Q08211	DHX9	0.0329418	8.59696	0.979757	9.12E-251
P51116	FXR2	0.0327129	8.80388	0.979292	5.61E-216
P02545;Q6UYC3;P02545-3;P0	LMNA	0.0322971	7.71745	0.978446	4.35E-81
O15446;O15446-2	CD3EAP	0.0283947	8.00792	0.970509	2.05E-97
P62424;Q5T8U2;Q5T8U3	RPL7A	0.0237579	9.04665	0.961082	1.98E-229
Q9NUL3;G5EA18;Q9NUL3-4;E	STAU2	0.0230579	7.61656	0.959659	3.73E-25
P07910;P07910-2;G3V4W0;B	HNRNPC;HNRNPCL1	0.0221863	8.35033	0.957888	2.13E-68
Q15393;Q15393-3	SF3B3	0.0193748	8.41032	0.952176	2.94E-119
Q92499	DDX1	0.0164909	8.48253	0.946319	4.59E-147
P62906	RPL10A	0.0142212	8.8187	0.941712	5.08E-74
Q3MHD2;Q3MHD2-2;K7ELG9	LSM12	0.0140686	7.95933	0.941402	7.93E-11
Q99567;J3KMX1	NUP88	0.0105972	7.42721	0.93436	8.58E-17
Q9NRR4;Q9NRR4-3;Q9NRR4-	DROSHA	0.00731277	7.52605	0.927701	1.47E-25
O95831;O95831-3;Q1L6K4;O	AIFM1	0.00605392	7.15134	0.92515	1.21E-11
P17066;P48741	HSPA6;HSPA7	0.00538445	7.51168	0.923794	1.80E-22
Q9Y608;Q9Y608-2;Q9Y608-4;	LRRFIP2	0.00268745	7.1271	0.918333	4.22E-11
Q92804;K7EPT6;Q92804-2	TAF15	-0.00159454	7.69227	0.90967	3.98E-72
Q16576;Q16576-2;E9PC52;Q	RBBP7	-0.00201797	6.67846	0.908814	5.65E-16
P35250;P35250-2;H7C5P4	RFC2	-0.00330925	8.71803	0.906204	6.39E-233
P08754	GNAI3	-0.00388527	7.87749	0.90504	3.42E-28
Q5T5X7	BEND3	-0.00857735	7.81952	0.895567	9.20E-147
Q7LGA3;Q7LGA3-3;Q7LGA3-2	HS2ST1	-0.0106812	6.66285	0.891324	7.06E-20
P62280;M0QZC5;M0R1H5	RPS11	-0.0112514	8.83346	0.890174	1.44E-163
P11940;P11940-2;E7EQV3;E7	PABPC1;PABPC3	-0.0132103	9.5809	0.886227	0
P62701	RPS4X	-0.0168343	9.11538	0.878933	3.23E-149
Q6ZRS2;Q6ZRS2-3;Q6ZRS2-2	SRCAP	-0.0174389	7.47573	0.877717	1.28E-48
Q9NW13;C9JE21;C9JAA9;Q9N	RBM28	-0.0188522	6.44829	0.874875	5.71E-21
P46013	MKI67	-0.019268	9.67486	0.87404	0
Q06787-6;Q06787-5;Q06787;	FMR1	-0.022274	8.35251	0.868003	1.45E-178
Q15269	PWP2	-0.0224648	7.90952	0.86762	2.94E-67
Q96EY1;Q96EY1-2	DNAJA3	-0.0232563	7.47409	0.866032	3.88E-06
P61254;J3QRI7;J3QQQ9;J3QC	RPL26;KRBA2;RPL26	-0.0237522	8.76784	0.865037	2.48E-35
P61978;P61978-2;Q5T6W5;P	HNRNPK	-0.0239277	8.63923	0.864685	1.15E-189
Q7Z2W4;Q7Z2W4-2;C9J6P4;(	ZC3HAV1	-0.024086	8.09729	0.864368	4.47E-209
O75955;B0V114;B0V113;B0V	FLOT1	-0.0242939	6.75511	0.863951	0.0020337
P47914	RPL29	-0.0244598	8.5756	0.863618	8.37E-13
Q15365	PCBP1	-0.0247898	7.53014	0.862957	1.74E-45
P62241;Q5JR95	RPS8	-0.0306339	9.14607	0.851256	1.48E-222
P47756-2;P47756;B1AK87;B1	CAPZB	-0.034874	7.49035	0.842786	8.50E-88
P09429;Q5T7C4;Q5T7C6	HMGB1	-0.0362091	7.99977	0.840123	3.61E-12
O95400	CD2BP2	-0.0391445	7.71771	0.834275	1.46E-46
Q02241;Q02241-2;H7BYN4;B	KIF23	-0.0393162	7.8322	0.833933	4.66E-57
P37108;H0YLA2	SRP14	-0.0421677	8.28106	0.828261	1.25E-35

P39023;G5E9G0;H7C422;B5M	RPL3	-0.0443802	8.94058	0.823866	6.18E-131
Q00325-2;F8VVM2;Q00325;F	SLC25A3	-0.0455151	7.98506	0.821614	8.82E-34
P36873;F8VYE8;P36873-2;F8\	PPP1CC;PPP1CA	-0.0486298	7.10673	0.815441	0
P13861;H7C1L0;Q9BUB1	PRKAR2A	-0.0516624	6.70168	0.809441	0.00034725
P11021	HSPA5	-0.0520554	7.9673	0.808664	4.93E-106
Q16698;B7Z6B8;E5RJD2;E5RJ	DECR1	-0.0528011	8.12665	0.807191	3.52E-52
P49207	RPL34	-0.0534782	8.38052	0.805853	0.0016239
P14866;M0QXS5;P14866-2	HNRNPL	-0.0536461	8.88213	0.805522	5.63E-169
Q8WWM7;Q8WWM7-6;Q8W	ATXN2L	-0.054533	8.66261	0.803772	7.17E-105
Q99459	CDC5L	-0.0569515	7.821	0.799003	7.10E-89
Q96DI7;B4DQJ1	SNRNP40	-0.0584164	8.28666	0.796119	6.46E-57
Q9Y4K1	AIM1	-0.0614166	7.16684	0.79022	4.52E-14
P37198;M0QXN5	NUP62	-0.0629845	7.81187	0.787142	0.00050582
Q02543;M0R117;B4DM74;M	RPL18A	-0.0648327	8.55134	0.783518	9.11E-57
Q99700;H0YH87;Q99700-2;F	ATXN2	-0.0650444	8.14482	0.783103	1.33E-57
Q9BY77;F8WCX5	POLDIP3	-0.0656166	8.60132	0.781982	1.60E-90
P61247;D6RG13;D6RAT0;D6R	RPS3A	-0.0681	9.03109	0.777123	2.29E-89
P63167;Q96FJ2;F8VXI7;F8VXI	DYNLL1;DYNLL2	-0.0685921	8.06741	0.776161	2.43E-133
P20042	EIF2S2	-0.0719318	7.87288	0.769642	1.41E-56
P62273;P62273-2	RPS29	-0.074564	7.71461	0.764516	1.13E-30
O94906;O94906-2	PRPF6	-0.0752735	8.19626	0.763136	2.63E-57
Q15287;H3BR57;H3BPG5;H3I	RNPS1	-0.075592	6.99845	0.762516	4.36E-11
P80723;P80723-2	BASP1	-0.076685	8.24222	0.760393	1.46E-23
Q12965	MYO1E	-0.077116	7.90706	0.759555	0
P62249;M0R210;M0R3H0;M0	RPS16	-0.0784721	8.69879	0.756924	4.91E-30
P14923	JUP	-0.0846157	8.01849	0.745036	2.08E-54
P05783;F8VZY9	KRT18	-0.0854683	10.3722	0.743391	0
P19338;H7BY16	NCL	-0.0870094	8.71263	0.74042	5.46E-178
P42677;Q5T4L4	RPS27	-0.0898743	8.76969	0.734909	8.85E-32
P16989-2;P16989;P16989-3	YBX3	-0.0905533	7.89411	0.733604	1.98E-183
P84098;J3QR09;J3KTE4	RPL19	-0.0909443	8.81147	0.732854	6.65E-112
P35659;P35659-2;B4DFG0;D6	DEK	-0.0911655	7.72309	0.732429	3.56E-28
Q96EP5;K7EQ02;Q96EP5-2;K	DAZAP1	-0.0947132	8.59969	0.72563	4.05E-126
P15880;H0YEN5;E9PQD7;I3L4	RPS2	-0.0955143	8.49241	0.724098	6.39E-98
Q99729-3;D6R9P3;D6RD18;D	HNRNPAB	-0.0978088	7.72639	0.719715	4.18E-24
Q9Y3B4	SF3B14	-0.0980816	7.4959	0.719195	4.11E-32
P35251;P35251-2	RFC1	-0.100058	9.02321	0.715429	0
Q9NXV6	CDKN2AIP	-0.100857	6.65762	0.713908	2.14E-08
O00159;O00159-3;O00159-2;	MYO1C	-0.107294	8.6493	0.701697	0
Q9ULL5-3;Q9ULL5-2;Q9ULL5	PRR12	-0.110184	7.29831	0.69624	4.09E-18
P40429;M0QYS1	RPL13A	-0.113897	8.51841	0.689251	2.85E-25
P55795	HNRNPH2	-0.115559	7.60989	0.686133	5.42E-192
Q15233;Q15233-2;H7C367;C	NONO	-0.117054	10.4949	0.683331	0
Q14690	PDCD11	-0.119095	7.32002	0.679513	1.10E-59
Q86V81;E9PB61	ALYREF	-0.1194	8.70327	0.678943	1.10E-106
P42167;P42167-2;G5E972;P4	TMPO	-0.119558	6.81516	0.678648	1.70E-07
Q14527;Q14527-2	HLTF	-0.120897	9.0333	0.676149	0
P08174;P08174-2;H3BLV0;Q1	CD55	-0.120947	7.98558	0.676056	1.08E-16
Q9NX24;D6RC52;D6RCB9;J3C	NHP2	-0.124115	7.64635	0.670158	5.75E-55
Q8TDN6	BRIX1	-0.124802	8.19229	0.668883	4.38E-16
Q15029;Q15029-2;K7EJ81	EFTUD2	-0.126226	8.44889	0.666239	1.66E-245
Q16637;Q16637-4;Q16637-2;	SMN1	-0.12759	7.68054	0.663712	2.70E-31
P35580;P35580-2;F8W6L6;P3	MYH10	-0.128181	7.15857	0.662618	2.61E-84
Q6W2J9;H7BZ37;H7C2V9;A6I	BCOR	-0.131544	6.90096	0.656408	8.36E-17
P46777	RPL5	-0.133177	8.81889	0.653401	2.92E-85
P27635;F8W7C6;B8A6G2;A6(	RPL10	-0.137604	8.86415	0.645278	1.35E-62
H9KV59;O43663;O43663-2;F	PRC1	-0.142401	7.81715	0.636522	2.52E-120
Q6PKG0;Q6PKG0-3;E5RH50	LARP1	-0.142403	8.45678	0.636519	6.35E-186
P05141	SLC25A5	-0.147854	7.47347	0.626631	2.33E-18
P36578;H3BM89	RPL4	-0.148781	9.1209	0.624956	5.08E-174
Q9BYJ9;F8W840	YTHDF1	-0.150942	7.56571	0.621059	2.70E-50
Q6FI13;P0C0S8;Q9BTM1;Q16	HIST2H2AA3;HIST1H	-0.151098	8.37544	0.620777	1.93E-25
P60866;P60866-2;E5RJX2;G3)	RPS20	-0.153728	8.54432	0.61605	5.35E-30
P06748;P06748-2;P06748-3	NPM1	-0.155865	9.81902	0.612221	0
Q01780;K7EJ37;B4DKG8;Q01	EXOSC10	-0.159271	6.46581	0.606139	0.0041581
O75475;O75475-2;O75475-3	PSIP1	-0.159899	7.27869	0.605021	4.21E-27
Q9Y230;B3KQ59;M0R0Y3	RUVBL2	-0.162188	8.20989	0.600953	5.63E-53
P26368;K7ENG2;P26368-2	U2AF2	-0.163031	7.86143	0.599457	2.42E-09
P49454	CENPF	-0.167242	8.90196	0.592013	0
P13010	XRCC5	-0.167309	10.2933	0.591895	0
Q86XZ4;F8VS10	SPATS2	-0.170856	7.21748	0.585657	4.37E-13
Q69YQ0;F8WAN1;F5H1H6;C9	SPECC1L	-0.173248	6.89655	0.581469	9.10E-19
P09874	PARP1	-0.17342	10.6807	0.581169	0
Q00059;A8MRB2;H7BYN3	TFAM	-0.175461	8.11777	0.577607	3.58E-41
P22415;E9PME6;B1AQP1;Q7	USF1;usf1-bd	-0.175701	7.34315	0.577189	1.13E-28
Q9NX58	LYAR	-0.178881	8.61987	0.571662	2.16E-168
Q71RC2;Q71RC2-5;Q71RC2-3	LARP4	-0.183674	8.35889	0.563379	5.16E-129
Q9NYB0	TERF2IP	-0.185839	7.06092	0.559657	2.96E-15
Q15637-2;Q15637-4;Q15637	SF1	-0.185936	8.31806	0.55949	1.67E-41
P50914;E7EPB3	RPL14	-0.186756	8.70413	0.558083	1.73E-100

O15042;O15042-2;E7ET15;O1	U2SURP	-0.187304	7.77662	0.557145	4.27E-37
Q9H147;F2Z2A4;H0Y501;H7C	DNTTIP1	-0.194832	7.25602	0.544324	7.12E-42
Q7RTV0	PHF5A	-0.196917	7.71233	0.5408	2.08E-35
P18887;F5H8D7	XRCC1	-0.201687	8.7582	0.532779	5.39E-158
Q07666;Q07666-3;Q07666-2	KHDRBS1	-0.208923	9.26005	0.520727	0
Q14980;Q14980-2;Q14980-4;	NUMA1	-0.20937	8.42599	0.519988	0
Q9HCE1;Q9HCE1-2;Q5JR04	MOV10	-0.209383	8.41419	0.519966	2.50E-246
P62140;E7ETD8;C9J9S3;C9JP4	PPP1CB;PPP1CA	-0.211248	8.52385	0.516884	0
P40937;P40937-2;F8W9B4	RFC5	-0.211298	8.77981	0.516803	8.85E-285
P23396;J3KN86;E9PPU1;E9PL	RPS3	-0.213974	8.90348	0.512399	6.43E-141
Q16666;Q16666-3;Q16666-2;	IFI16	-0.214148	8.93001	0.512114	9.89E-172
P52272;P52272-2	HNRNPM	-0.214657	9.42501	0.511278	0
Q6ZNL6;Q6ZNL6-2;B7ZM68	FGD5	-0.215496	6.97434	0.509903	5.41E-12
Q6I9Y2	THOC7	-0.221521	7.10626	0.500085	1.46E-17
P62861;E9PR30	FAU	-0.222246	7.99869	0.498911	2.63E-09
P62829;C9JD32;J3KT29;J3KTJ	RPL23	-0.224804	8.23707	0.494779	1.69E-16
Q96C57;E7ENF1;G5EA44;F5H	C12orf43	-0.225243	7.55963	0.494072	1.73E-20
P16403	HIST1H1C	-0.239105	9.41809	0.472017	7.19E-40
P46779;C9JB50;G5E9L2;H0YL	RPL28	-0.24358	8.34637	0.465015	3.78E-09
P55769;B1AHD1	NHP2L1	-0.248896	7.48126	0.456773	2.80E-20
Q96AG4	LRRC59	-0.253733	8.42946	0.449345	3.87E-26
P46778;G3V1B3;M0R181	RPL21	-0.253778	8.48184	0.449275	2.53E-42
Q8N684;Q8N684-2;Q8N684-3	CPSF7	-0.259247	7.48382	0.440961	5.91E-88
P62910;D3YTB1;F8W727	RPL32	-0.259459	8.68332	0.440641	7.93E-90
Q07020;G3V203;J3QQ67;F8V	RPL18	-0.259989	8.75254	0.43984	4.24E-93
P49458;E9PE20;P49458-2	SRP9	-0.266308	7.43764	0.430358	3.20E-11
P78527;E7EUY0;P78527-2	PRKDC	-0.268276	9.78623	0.427429	0
P62805	HIST1H4A	-0.269131	10.8971	0.426161	0
Q13547;F5GXM1	HDAC1	-0.274279	7.04759	0.418568	4.05E-07
Q04637;Q04637-3;Q04637-6;	EIF4G1	-0.275742	7.88588	0.416425	1.22E-51
P09651;P09651-3;F8VXY0;F8\	HNRNPA1;HNRNPA1	-0.275789	9.21283	0.416355	1.88E-192
P12956;B1AHC8;B1AHC9;F5H	XRCC6	-0.276306	10.3476	0.4156	0
Q7Z2E3;Q7Z2E3-7;Q7Z2E3-9;	APTX	-0.277491	8.56965	0.413871	3.65E-46
P49916;P49916-2	LIG3	-0.282139	9.31283	0.40713	0
P32969;D6RAN4;H0Y9R4;E7E	RPL9	-0.287498	8.15564	0.399439	4.52E-104
P62899;H7C2W9;C9JU56;B7Z	RPL31	-0.291798	8.14063	0.393333	4.36E-60
Q86UE4;E5RJU9	MTDH	-0.304701	8.067	0.37535	4.15E-116
Q14694;Q14694-3;Q14694-2	USP10	-0.315351	7.99066	0.360896	1.64E-11
P61244;P61244-2;G3V570;G3	MAX	-0.317636	7.30965	0.357841	3.68E-08
P83731;C9JXB8;C9JNW5	RPL24	-0.320759	8.40893	0.353693	2.59E-36
P61313;E7EQV9;E7ENU7;E7E	RPL15	-0.321733	8.4727	0.352404	5.25E-37
Q9NVP1	DDX18	-0.322729	6.76979	0.351091	0.0029815
Q01130;J3QL05;J3KP15;B4DN	SRSF2;SFRS2	-0.323078	6.59199	0.350631	0.00063184
P42766;H0Y3A0;F2Z388	RPL35	-0.332802	8.42671	0.337979	2.81E-12
P18621;J3QQT2;J3KRX5;J3QL	RPL17	-0.334827	8.85552	0.335381	7.07E-147
P48634;P48634-2;P48634-4;C	PRRC2A	-0.344307	7.76991	0.323394	1.86E-28
Q12788;J3KNP2	TBL3	-0.349205	8.00264	0.317311	2.91E-73
P22626;P22626-2	HNRNPA2B1	-0.349556	9.20623	0.316878	0
O15347;E9PES6;E7ES08;E7EC	HMGB3	-0.354115	7.21498	0.311289	9.03E-05
Q92522	H1FX	-0.354778	7.49577	0.310481	1.00E-24
P40938;P40938-2	RFC3	-0.36355	8.36031	0.299929	2.69E-166
O14979;O14979-3;O14979-2	HNRPDL	-0.372303	8.43045	0.289641	8.86E-162
Q8N3X1;Q8N3X1-2	FNBP4	-0.373825	7.86404	0.287877	1.68E-59
Q9NSU2;Q9NSU2-2;Q9NSU2-	TREX1	-0.38209	8.35608	0.278423	4.83E-76
P56182	RRP1	-0.392485	6.98163	0.266835	1.47E-10
Q9BTD8;K7EQ03;Q9BTD8-4;C	RBM42	-0.39942	6.27736	0.259291	1.91E-11
O43143	DHX15	-0.409718	7.89159	0.248364	1.49E-122
P35249;C9JZI1;C9J8M3;C9JTT	RFC4	-0.413052	8.60759	0.244897	3.31E-48
Q9NRW3	APOBEC3C	-0.423693	6.51171	0.234057	3.35E-10
P62277;J3KMX5	RPS13	-0.423782	8.40863	0.233967	2.57E-27
P35908	KRT2	-0.425655	8.83463	0.232095	0
Q9Y265;E7ETR0;Q9Y265-2	RUVBL1	-0.427826	7.89642	0.22994	2.17E-111
Q9H6R0;I3L1L6	DHX33	-0.429804	7.32807	0.227988	3.94E-22
P31689;B7Z5C0	DNAJA1	-0.433968	6.8129	0.223917	7.29E-05
P63173;J3KT73;J3QL01	RPL38	-0.435621	8.21115	0.222315	3.36E-09
P12236;I7HJJ0;P12235	SLC25A6;SLC25A4	-0.437935	8.08583	0.220087	7.05E-26
Q9ULV3;Q9ULV3-5;Q5SYW2;I	CIZ1	-0.456097	7.61728	0.203154	1.89E-21
P68431;P84243;Q71DI3;K7EK	HIST1H3A;H3F3A;HI	-0.457737	10.1701	0.201673	9.34E-45
Q53GS9;B9A018;Q53GS9-2;B	USP39	-0.461231	8.20134	0.198544	1.07E-51
P06746;H0YBJ0;E7EW18;B7Z	POLB	-0.473658	8.00758	0.187703	1.54E-26
Q14676;Q14676-2;E9PGY5;Q	MDC1	-0.47443	8.89149	0.187044	6.23E-165
Q96J01;Q6NZ53;D6RGZ2	THOC3	-0.480488	7.08522	0.181934	4.36E-06
P19387;H3BRR2	POLR2C	-0.484644	6.99022	0.178489	6.98E-05
P05386	RPLP1	-0.485329	8.54463	0.177926	6.05E-21
Q9UKF6;G5E9W3	CPSF3	-0.499716	7.47757	0.166401	4.68E-19
P0C0S5;Q71UI9;Q71UI9-3;Q7	H2AFZ;H2AFV	-0.503906	7.32391	0.163152	1.75E-11
P62854	RPS26	-0.517189	8.41812	0.153169	2.69E-21
P62879;C9JXA5;C9JZN1;C9JIS	GNB2	-0.5278	8.33824	0.145534	1.24E-86
P05423	POLR3D	-0.533064	6.53142	0.141856	1.19E-05
Q12926;Q12926-2;B1AM49;P	ELAVL2;ELAVL4	-0.536987	7.05561	0.139162	4.02E-13

Q15853;M0QXT0;Q6YI47;Q1!	USF2	-0.54118	7.71254	0.136326		6.22E-66
Q96I25;Q5W011;Q5W010;Q!	RBM17	-0.549324	7.87346	0.130946		3.47E-48
O00712;Q5VW26;O00712-4;(	NFIB	-0.555546	6.93585	0.126947		0.0010059
Q12800;Q12800-2;Q12800-3;	TFCP2	-0.559534	7.53864	0.124435		3.15E-146
O60318	MCM3AP	-0.570406	6.89209	0.117782		8.99E-08
P19388	POLR2E	-0.574791	7.65594	0.115179		3.35E-14
P62266;D6RD47	RPS23	-0.611412	8.68852	0.0951704		2.32E-15
Q9ULW0;Q96RR5	TPX2;HCA90	-0.64431	7.43209	0.0796646		1.73E-26
Q86VM9;E7ERS3;H3BRH3;Q8	ZC3H18	-0.651989	7.29356	0.0763581		7.38E-10
Q8IYH5;Q8IYH5-2;Q8IYH5-4	ZZZ3	-0.652811	7.14242	0.0760108		2.30E-10
Q14191	WRN	-0.654345	7.00741	0.0753665		6.14E-27
P47755;F8W9N7;C9JUG7;B4I	CAPZA2	-0.658733	6.91462	0.0735471		9.98E-09
P68133;P68032;P63267;P627	ACTA1;ACTC1;ACTG	-0.65889	9.46461	0.0734829		2.10E-163
Q92922	SMARCC1	-0.667311	7.16095	0.070095		3.30E-45
Q92979	EMG1	-0.669971	7.33359	0.0690515		3.40E-11
Q9UHI6;E9PJ60	DDX20	-0.675039	7.37674	0.0670994		9.59E-13
P05387;H0YDD8	RPLP2	-0.687382	8.95944	0.0625347		1.03E-166
P62995;P62995-3;H7BXF3	TRA2B	-0.697872	7.29041	0.0588596		1.17E-18
P63261;I3L3I4;I3L3I0;I3L1U9;	ACTG1	-0.703913	8.4365	0.0568261		0
Q9P2I0;H0YJF4	CPSF2	-0.708792	7.38443	0.0552266		9.76E-10
Q9BZK7	TBL1XR1	-0.734209	7.359	0.0474889		9.24E-24
Q07065	CKAP4	-0.740551	6.95441	0.0457071		3.44E-29
P31942;P31942-2;P31942-3;F	HNRNPH3	-0.74967	6.89672	0.043244		1.95E-52
P46783;F6U211	RPS10	-0.788298	8.56236	0.0340177		1.18E-22
O95758;O95758-2;O95758-1;	PTBP3	-0.803415	7.2481	0.0308954		2.15E-10
P05114;A6NL93;A6NEL0	HMGN1	-0.803471	7.23779	0.0308844		0.00092199
P61513;C9J4Z3;M0R0A1;Q6P	RPL37A	-0.812607	8.17699	0.0291199		7.87E-39
Q9Y3A4	RRP7A	-0.823929	7.25935	0.0270542		6.45E-06
Q9H7E9;Q9H7E9-2	C8orf33	-0.8312	6.61035	0.0257954		3.09E-08
Q9BWJ5	SF3B5	-0.886873	7.69847	0.0177272		2.21E-16
P50750;P50750-2	CDK9	-0.887175	6.59968	0.0176903		6.24E-08
P57088;H0Y8N0;D6RAA6	TMEM33	-0.897221	6.76561	0.0165003		0.00071083
Q7Z7G8;Q7Z7G8-4;Q7Z7G8-3	VPS13B	-0.927578	7.7752	0.0133206		0.0020825
Q9UNX4	WDR3	-0.967518	7.67711	0.0099678		5.38E-60
Q04837;E7EUY5;C9K0U8	SSBP1	-1.01152	8.49596	0.00716303		1.68E-256
Q5UIP0;Q5UIP0-2	RIF1	-1.01324	7.96968	0.00706943		2.90E-115
Q13151	HNRNPA0	-1.02173	8.08881	0.00662351		9.03E-223
Q14331;E9PRR7	FRG1	-1.13004	6.93511	0.00277675		7.04E-10
O43795;O43795-2;E9PDF6	MYO1B	-1.1668	7.69446	0.00203424		4.57E-128
P78549;H3BPD5;H3BRL9	NTHL1	-1.23056	7.98065	0.00116302	+	1.13E-113
Q01085;P31483;C9JTN7;P314	TIAL1;TIA1	-1.80942	7.46678	2.31E-06	+	3.72E-12
Q14126	DSG2	-1.99006	7.33226	2.16E-07	+	1.02E-88
P07814	EPRS	-2.01804	7.17254	1.47E-07	+	7.75E-15
P43246;E9PHA6;P43246-2	MSH2	-2.37116	7.99025	7.42E-10	+	2.26E-127
Q9BQ67;M0QX71	GRWD1	-2.52108	7.24077	6.19E-11	+	3.11E-28
Q12797;F5H667	ASPH	-2.54909	7.27159	3.83E-11	+	4.57E-23
P35658;P35658-2;P35658-4;F	NUP214	-2.90807	7.17739	5.23E-14	+	5.27E-143
P45880;B4DKM5;P45880-2;P	VDAC2	-3.47411	7.8909	2.97E-19	+	0.00070491
P20585	MSH3	-3.63078	7.98234	7.30E-21	+	1.88E-109
Q13472;B4DK80;Q13472-2;B	TOP3A	-5.633	7.55175	1.72E-47	+	2.94E-91

Appendix 6 (Chapter 4)

Identification and quantification of interacting proteins for H2B S36 thiophosphate modified nucleosome versus wild-type nucleosome. Statistically significant interacting partners are denoted with a '+'

Majority Protein Ids	Gene names	log2(Bait/Control)	log10(Intensity)	Significance B value	Statistically Significant Interactor	PEP
Q02880;Q02880-2;E9PCY5	TOP2B	5.18737	8.08789	7.92E-30	+	1.47E-211
Q13595;Q13595-2;B4DQI6;B4	TRA2A	2.23397	7.61254	1.15E-06	+	4.81E-13
Q6P5R6;C9JYQ9;H0Y8C2	RPL22L1	1.95404	7.51525	2.15E-05	+	3.24E-44
P36873;F8VYE8;P36873-2;F8\	PPP1CC	1.91654	7.92722	3.09E-05	+	0
Q7Z7G8;Q7Z7G8-4;Q7Z7G8-3	VPS13B	1.75606	8.40691	0.00013644	+	0.0012561
Q86UP2;Q86UP2-2;Q86UP2-3	KTN1	1.65446	7.40606	0.00032869	+	7.98E-18
P05549;P05549-5;Q5TAV5;Q5	TFAP2A;TFAP2E	1.558	6.75248	0.00072511	+	3.01E-31
Q5VT52;Q5VT52-3;Q5VT52-2	RPRD2	1.51322	7.5799	0.00103205	+	1.47E-71
Q13045;Q13045-2;J3QLG3	FLII	1.4689	7.66119	0.00145064		3.89E-202
P41252;Q5TCD1	IARS	1.44629	6.94726	0.00171984		5.70E-05
Q9BYP7;Q9BYP7-2;Q9BYP7-3	WNK3	1.44012	7.56265	0.001801		0.0060563
Q99848;H7C2Q8	EBNA1BP2	1.32538	7.67925	0.00411193		1.30E-08
Q09161	NCBP1	1.28323	7.34579	0.00548726		4.19E-15
Q9Y2W1	THRAP3	1.22754	7.7876	0.00793727		1.47E-17
H7C4H8	SLBP	1.22346	7.88537	0.00815033		0.0039238
P62857	RPS28	1.22327	8.43785	0.00816032		8.07E-26
P07437;Q5ST81;Q5JP53;F8VY	TUBB;TUBB4B;TUBB	1.21695	7.6229	0.00850075		6.77E-85
O75607	NPM3	1.20834	7.62047	0.00898544		3.73E-21
P19388	POLR2E	1.19393	7.9619	0.00985198		1.37E-24
Q9UBB4;Q9UBB4-2;B1AHE4	ATXN10	1.16473	7.2975	0.0118389		8.74E-18
Q9UG63;Q75MJ1	ABCF2	1.15368	7.65877	0.0126789		2.18E-37
P55735;A8MXL6;P55735-2;B4	SEC13	1.15191	7.66905	0.0128181		3.00E-63
P68104;Q5VTE0	EEF1A1;EEF1A1P5	1.14931	7.70683	0.0130259		6.85E-16
P98179	RBM3	1.13571	7.72303	0.0141586		7.80E-30
P11388;P11388-2;P11388-3;F	TOP2A	1.06323	8.63337	0.0217801		1.95E-243
P14923	JUP	1.04944	8.21099	0.0235794		1.37E-61
Q96C19;H0Y4Y4	EFHD2	1.04697	7.54759	0.0239151		1.85E-06
Q01081;Q01081-2;Q01081-4	U2AF1	1.04339	7.47854	0.0244082		1.96E-15
Q9P1U0	ZNRD1	1.02677	7.70215	0.0268183		2.19E-14
Q9NZI7;Q9NZI7-4	UBP1	1.02446	7.26024	0.0271676		3.56E-77
Q96FV9;Q96FV9-2	THOC1	1.02169	7.42131	0.0275931		8.19E-11
Q9UHL9;Q9UHL9-2;E9PFE2;Q	GTF2IRD1	1.00454	7.39131	0.0303587		4.34E-10
Q9BY44;B4DQ14;F8WAE5;B4	EIF2A	0.989067	7.14786	0.0330541		1.32E-11
O15182;H0YBL5;E5RH67;E5RI	CETN3	0.980799	7.07449	0.0345767		2.01E-12
Q13813;Q13813-3;Q13813-2;	SPTAN1	0.968058	7.67919	0.0370401		1.61E-62
Q86SQ0;E9PFQ4;Q86SQ0-2;C	PHLDB2	0.933657	7.55898	0.044449		9.44E-13
Q92769;B3KRS5;J3KPW7;Q5T	HDAC2;HDAC1	0.920656	7.43631	0.0475573		4.99E-19
Q09028;Q09028-3;H0YF10;Q	RBBP4	0.91641	7.73904	0.0486112		5.29E-20
Q92522	H1FX	0.840366	7.8068	0.071057		5.03E-23
Q14247;Q14247-3;Q14247-2;	CTTN	0.829243	7.66854	0.074961		3.83E-07
Q8IY81	FTSJ3	0.819248	7.15588	0.0786164		2.43E-10
P22087;M0R0P1;M0QXL5;M	FBL	0.813818	8.01561	0.0806626		7.99E-10
Q9NPE3	NOP10	0.81255	7.19565	0.0811467		2.74E-09
Q9NYL9;H0YNJ8;H0YKU1	TMOD3	0.8071	7.92614	0.0832534		1.21E-54
Q6UXN9	WDR82	0.804993	6.97248	0.0840801		2.20E-07
O76021;J3QSV6;B4DJ58;I3L3I	RSL1D1	0.792276	7.89775	0.0892094		4.04E-42
Q9BZF9;F5H2B9;H0YNH8;G3>	UACA	0.780195	7.44039	0.0943131		1.51E-06
Q9H147;F2Z2A4;H0Y501;H7C	DNTTIP1	0.771343	7.61567	0.0981993		6.40E-52
O15446;O15446-2	CD3EAP	0.757326	8.2355	0.104613		3.40E-137
P41208	CETN2	0.746214	7.0904	0.109931		7.88E-70
Q9P0K7;Q9P0K7-4;Q9P0K7-3	RAI14	0.744946	8.39602	0.110552		1.23E-295
Q12797;F5H667	ASPH	0.720211	7.53451	0.12321		1.07E-33
P62861;E9PR30	FAU	0.694452	8.18415	0.137566		4.48E-07
P63010;P63010-2;Q7Z451;K7	AP2B1	0.690228	7.85661	0.140039		3.34E-38
Q9NW13;Q9NW13-2;H7C5G8	RBM28	0.67861	6.89358	0.147017		4.94E-19
P31942;P31942-2;P31942-3;F	HNRNPH3	0.660498	7.13258	0.15842		9.47E-45
Q96T60;M0R3C8;M0QYH2	PNKP	0.65687	7.85282	0.160783		1.36E-18
Q9UQ80;F8VTY8	PA2G4	0.637501	7.78424	0.173849		5.89E-18
P83111	LACTB	0.632011	8.38216	0.177693		1.54E-66
P52292	KPNA2	0.60704	7.42002	0.195978		2.77E-16
Q8WYQ5;Q8WYQ5-3	DGCR8	0.604275	7.36105	0.198085		2.90E-16
F8WBL2;Q13895	BYSL	0.603827	6.72679	0.198428		0.0014384
Q9Y5B9	SUPT16H	0.597828	7.77822	0.203061		5.63E-17
Q9H0D6;Q9H0D6-2;B4DZC3	XRN2	0.593164	7.33177	0.206716		1.64E-35
P30050;P30050-2	RPL12	0.589212	8.90981	0.209851		1.59E-149
P16070;H0YD13;H0Y2P0;P16(	CD44	0.586559	7.21189	0.211975		1.73E-12
O15042;O15042-2;E7ET15;O1	U2SURP	0.586475	7.95977	0.212043		3.09E-35

Q7Z417	NUFIP2	0.584913	8.60915	0.213301	5.42E-209
P62851	RPS25	0.584084	8.5719	0.213971	5.20E-11
Q9NY12;Q9NY12-2	GAR1	0.583529	8.13405	0.214421	3.85E-13
P47756-2;P47756;B1AK85;B1	CAPZB	0.583038	7.68577	0.214818	1.05E-40
Q09666	AHNAK	0.581373	7.58888	0.216172	2.59E-16
Q14498;Q14498-3;Q14498-2;	RBM39	0.578022	8.23639	0.218915	1.13E-65
Q9GZN1;F8W057;F8VP72;F8\	ACTR6	0.574018	7.15933	0.222225	1.11E-22
Q9BYG3;H7BZL0;C9J808	MKI67IP	0.555769	6.58988	0.237768	3.00E-15
H7BY36	EWSR1	0.548738	7.40352	0.243955	2.71E-69
P78549;H3BPD5;H3BRL9	NTHL1	0.546757	8.10085	0.24572	2.55E-218
O14950;P19105;J3QRS3;P248	MYL12B;MYL12A;M	0.544773	7.97509	0.247495	5.91E-106
Q08945;E9PPZ7;E9PMD4	SSRP1	0.529287	6.95243	0.261661	2.87E-19
Q8IWA0	WDR75	0.510056	6.97309	0.280022	1.75E-08
P05386	RPLP1	0.502609	8.72858	0.28736	2.02E-25
Q13148;Q13148-2;B1AKP7;G	TARDBP	0.501566	7.59449	0.288399	7.83E-34
Q9UBI6	GNG12	0.500418	7.12853	0.289545	0.0028912
P08670;B0YJC4;B0YJC5	VIM	0.498863	9.97357	0.291101	0
P52434;C9JBJ6;C9JLU1;C9JUA	POLR2H	0.497505	7.57215	0.292465	1.49E-14
Q6SPF0;E9PIW9	SAMD1	0.486095	7.32185	0.304095	1.45E-16
P55795	HNRNPH2	0.485889	7.70252	0.304308	2.24E-200
Q14978;Q14978-3;Q14978-2	NOLC1	0.482082	8.75324	0.308258	3.88E-48
O15160;O15160-2;E7EQB9	POLR1C	0.47369	8.33959	0.317084	5.20E-202
Q99729-3;D6R9P3;D6RD18;D	HNRNPAB	0.473476	7.95458	0.317311	1.17E-25
Q9H6S0;D6RA70	YTHDC2	0.472967	7.0242	0.317852	1.42E-09
P26196	DDX6	0.470352	8.56031	0.32064	1.22E-169
Q96J01;D6RGZ2;D6REC9;Q6N	THOC3	0.465874	7.22699	0.325452	5.96E-06
Q9H6R0	DHX33	0.463491	7.29839	0.32803	1.17E-15
Q9NYF8;Q9NYF8-3;E9PK09;E9	BCLAF1	0.457418	7.50102	0.334664	1.57E-15
P55265;P55265-5;P55265-3;H	ADAR	0.456984	7.53538	0.335142	6.17E-57
P55769;B1AHD1	NHP2L1	0.456285	7.53537	0.335911	5.64E-09
Q16576;Q16576-2;E9PC52;Q9	RBBP7	0.454992	7.14273	0.337338	8.78E-24
Q9Y224;G3V4C6	C14orf166	0.454523	8.60931	0.337857	1.64E-187
Q5T8P6;Q9P2N5;Q5T8P6-3;Q	RBM26;RBM27	0.450462	7.09489	0.342368	0.00014513
Q8IWR0;I3L2K5	ZC3H7A	0.443865	7.51783	0.349778	1.44E-08
Q96DH6;Q96DH6-2;B4DHE8;J	MSI2	0.432186	8.20379	0.363144	5.74E-136
P15328	FOLR1	0.430996	7.92007	0.364523	3.51E-59
O95602;B9ZVN9	POLR1A	0.426336	8.66549	0.369957	1.12E-302
Q96HS1;Q96HS1-2	PGAM5	0.425898	8.11564	0.370471	2.25E-12
Q9Y446;E9PKC4	PKP3	0.422667	8.08019	0.374271	5.44E-86
P26599;P26599-2;P26599-3	PTBP1	0.421326	9.53056	0.375855	0
Q9BQG0;Q9BQG0-2;I3L1L3	MYBBP1A	0.415642	7.92259	0.382616	2.08E-58
P18124;A8MUD9	RPL7	0.414572	8.59569	0.383897	2.67E-79
Q14677;Q14677-2;Q14677-3	CLINT1	0.397835	7.53455	0.404275	7.66E-14
F8W726;Q5VU77	UBAP2L	0.393911	6.96992	0.409144	0
Q15646	OASL	0.38822	6.85566	0.416269	6.38E-17
P35268;K7EJT5;K7EP65;K7EK9	RPL22	0.384869	8.9768	0.420498	1.84E-26
Q8NE71;Q8NE71-2;H0YGW7;	ABCF1	0.383512	7.87185	0.422217	1.17E-78
Q14103;Q14103-3;H0YA96;H	HNRNPD	0.360994	8.34492	0.45135	1.38E-59
P21333;Q5HY54;P21333-2	FLNA	0.353785	7.58754	0.460913	1.28E-42
Q07955;Q07955-3;J3KTL2;Q0	SRSF1	0.349379	7.40145	0.466812	5.35E-12
Q69YQ0;F8WAN1;F5H1H6;C9	SPECC1L	0.346689	7.139	0.470433	9.03E-19
Q16643;Q16643-2;A8MV58;D	DBN1	0.340839	8.49318	0.478363	4.70E-133
Q03701	CEBPZ	0.340555	7.39162	0.47875	8.28E-14
O43707;H7C144;F5GXS2;D6P	ACTN4	0.336807	7.27407	0.483871	6.53E-44
P05423	POLR3D	0.336063	7.36909	0.484891	1.19E-32
Q8NCA5;Q8NCA5-2;E9PH82	FAM98A	0.335436	8.44509	0.485753	1.59E-103
J3KNL6;O15027;O15027-2;O1	SEC16A	0.332565	7.91264	0.489703	1.28E-43
Q13748;P68363;Q9BQE3;Q71	TUBA3C;TUBA1B;TU	0.32967	7.3687	0.493705	9.30E-24
O75494;O75494-3;O75494-4;	SRSF10	0.328516	7.48889	0.495305	0.00013088
P19447;G3V1S1	ERCC3	0.324545	7.28062	0.500832	5.55E-43
P04792;C9J3N8;F8WE04	HSPB1	0.315392	7.10605	0.513695	8.17E-07
Q12906;G5E9M5;Q12906-4;C	ILF3	0.313969	8.5189	0.51571	9.29E-80
P04003	C4BPA	0.308872	8.37976	0.522961	5.56E-106
Q15717;B4DVB8;M0QZR9	ELAVL1	0.305983	8.83497	0.527095	4.37E-67
Q9Y5S9;Q9Y5S9-2	RBM8A	0.30397	7.2867	0.529983	2.72E-11
Q13283;F5H4D6	G3BP1	0.301291	9.59418	0.533843	0
P14678;P63162;P14678-2;B3	SNRPB;SNRPN	0.301113	7.81824	0.534099	2.88E-10
P14868;H7BZ35;Q68CR9	DARS;DKFZp781B11	0.300175	6.60973	0.535454	0.0030022
P17480;P17480-2;E9PKP7	UBTF	0.296289	8.39026	0.541083	1.69E-68
O43390;O43390-2;Q2L7G6;E	HNRNPR	0.29307	8.52907	0.54577	3.56E-178
Q14157-1;Q14157;Q14157-4;	UBAP2L	0.288931	9.36472	0.551824	0
Q9UN86;Q9UN86-2	G3BP2	0.288774	9.58834	0.552054	1.80E-121
Q3B726	TWISTNB	0.283628	7.94215	0.559629	1.42E-34
Q9H0H5;F8VRD2;F8W1E5	RACGAP1	0.269938	7.43311	0.580025	3.62E-63

P51114;B4DXZ6;P51114-3	FXR1	0.269604	9.02494	0.580526	0
Q8IVT2	MISP	0.266846	7.41564	0.584678	1.88E-07
P40937;P40937-2;F8W9B4;F5	RFC5	0.266169	8.94265	0.5857	1.46E-218
P52907	CAPZA1	0.263186	8.06435	0.59021	1.30E-28
Q9H307;Q9H307-2	PNN	0.262121	7.2824	0.591823	2.46E-06
P38646	HSPA9	0.261549	7.98595	0.592691	7.23E-109
Q86W42;Q86W42-3;Q86W42	THOC6	0.261229	7.33122	0.593177	5.32E-06
P20042	EIF2S2	0.259392	8.03185	0.595968	5.84E-41
P08754	GNAI3	0.2577	8.00217	0.598545	3.23E-35
Q92900;Q92900-2	UPF1	0.256973	9.13088	0.599653	4.37E-299
Q86V81;E9PB61	ALYREF	0.254555	8.87829	0.603348	1.10E-81
Q7Z739	YTHDF3	0.253386	7.98888	0.605137	2.84E-44
O94842;O15405;O15405-2;B4	TOX4;TOX3;TOX;TO	0.251823	6.86935	0.607533	5.44E-21
Q14684;Q14684-2	RRP1B	0.251791	7.68215	0.607582	3.11E-51
Q02978;F5GY65;I3L1P8	SLC25A11	0.249615	7.15634	0.610926	9.59E-05
Q6WCQ1;Q6WCQ1-2;Q6WCC	MPRIP	0.243547	8.46225	0.620291	1.58E-199
Q9UKV8;Q9UKV8-2	AGO2	0.239109	7.81255	0.627181	1.50E-76
P16401	HIST1H1B	0.235176	8.80014	0.633314	1.46E-31
P08107;F8VZJ4;P08107-2;E7E	HSPA1A	0.232975	8.3557	0.636757	2.03E-73
Q02241;Q02241-2;H7BYN4;B	KIF23	0.232969	8.11434	0.636766	7.59E-78
P13987;E9PNW4;E9PR17	CD59	0.226767	8.06277	0.646512	2.78E-35
P63261;I3L3I4;I3L3I0;I3L1U9;	ACTG1	0.223816	10.6229	0.651169	0
Q92499	DDX1	0.223423	8.69551	0.651791	1.17E-247
P62906	RPL10A	0.222303	8.84783	0.653562	1.17E-68
Q9NZB2;Q9NZB2-6;Q9NZB2-4	FAM120A	0.219309	8.52055	0.65831	5.95E-150
P35579;P35579-2	MYH9	0.217146	9.2583	0.661748	0
P62241;Q5JR95	RPS8	0.21339	9.23855	0.667734	8.79E-220
P05187;P10696	ALPP;ALPPL2	0.212336	8.33872	0.669419	2.70E-167
Q99459	CDC5L	0.205034	8.01874	0.681129	1.35E-85
Q9Y4K1	AIM1	0.200703	7.26048	0.688112	2.44E-19
O95758;O95758-2;O95758-1;	PTBP3	0.199434	7.57456	0.690162	2.39E-19
P61247;D6RG13;D6RAT0;D6R	RPS3A	0.198507	9.15957	0.691662	1.16E-89
P08621;P08621-2	SNRNP70	0.197203	7.40224	0.693775	5.61E-21
P62158;H0Y7A7;E7ETZ0;E7EM	CALM1;CALM2	0.193785	8.51463	0.699321	3.04E-56
P14866;M0QXS5;P14866-2	HNRNPL	0.193514	9.1012	0.699761	1.91E-168
Q6PJG2;F6RU81;H7C1L3	ELMSAN1	0.190437	7.61293	0.704768	7.08E-17
Q96K37	SLC35E1	0.190235	6.81931	0.705098	3.91E-36
P67809;H0Y449	YBX1	0.189598	9.2065	0.706137	0
P09429;Q5T7C4;Q5T7C6	HMGB1	0.185848	8.1183	0.712261	6.94E-13
O75533	SF3B1	0.185791	8.19532	0.712355	1.07E-45
P56537;B7ZBG9;F8WD20;B7Z	EIF6	0.183947	7.18472	0.715374	7.69E-30
Q04637;Q04637-3;Q04637-5;	EIF4G1	0.181761	8.07802	0.718958	5.99E-81
Q9C0J8;Q9C0J8-2;C9J8B4;Q9	WDR33	0.181162	6.88152	0.719941	0.0004196
Q8IWX8;J3QK89	CHERP	0.18066	7.80899	0.720765	9.90E-58
Q9P275;Q9P275-2;E9PEW0	USP36	0.177036	7.61475	0.726726	1.34E-44
Q9ULW0;Q96RR5	TPX2;HCA90	0.172918	7.52071	0.73352	4.54E-36
Q86XZ4;F8VS10	SPATS2	0.172396	7.47433	0.734383	1.81E-23
P78406;E9PPG9;E9PQ57	RAE1	0.171295	7.44334	0.736203	4.85E-23
Q13547;F5GXM1	HDAC1	0.17116	7.8173	0.736427	5.32E-22
Q2TAY7;B4E3L0	SMU1	0.169752	7.02403	0.738757	0.00098651
P14384;F8VVI6;F8W111	CPM	0.169142	6.74789	0.739768	0.000941
Q15366;Q15366-4;Q15366-5;	PCBP2	0.166842	8.06089	0.743583	1.02E-61
Q6PKG0;Q6PKG0-3;E5RH50	LARP1	0.164875	8.69602	0.746849	9.92E-245
P17844;J3KTA4;B4DLW8	DDX5	0.163033	9.49157	0.749913	0
O95782;O95782-2	AP2A1	0.162855	7.65642	0.750208	3.44E-45
Q96I24	FUBP3	0.162519	8.00975	0.750767	2.33E-56
Q9Y265;E7ETR0;Q9Y265-2	RUVBL1	0.162001	8.4936	0.751631	4.94E-122
Q13428-3;Q13428-8;Q13428;	TCOF1	0.160299	8.63923	0.754466	3.76E-172
P07910;P07910-2;G3V576;G3	HNRNPC;HNRNPCL1	0.159176	8.50928	0.75634	1.02E-45
P46782;M0R0F0;M0R0R2;M0	RPS5	0.158478	8.40031	0.757505	1.85E-84
Q9H7E9;Q9H7E9-2	C8orf33	0.157621	6.85579	0.758935	3.58E-19
P62263;E5RH77	RPS14	0.147589	8.99277	0.775749	1.27E-27
Q15393;Q15393-3	SF3B3	0.146458	8.56005	0.777651	2.08E-205
F5GWP8	JUP	0.14567	7.47934	0.778977	2.20E-90
Q92841;H3BLZ8;Q92841-3;Q	DDX17	0.145008	9.73607	0.780091	0
Q12800;Q12800-4;Q12800-2;	TFCP2	0.143732	7.82719	0.782241	2.44E-197
P54098	POLG	0.142962	6.89378	0.78354	1.45E-28
Q9H0A0;E7ESU4	NAT10	0.14208	8.37101	0.785026	0
P37108;H0YLA2	SRP14	0.13891	8.24306	0.790378	4.11E-45
P35251;P35251-2	RFC1	0.137239	9.19276	0.793204	0
Q92576;Q92576-2;E7EVH3	PHF3	0.136662	8.60467	0.794182	1.20E-245
P31689;B7Z5C0	DNAJA1	0.135479	6.99883	0.796184	5.53E-05
Q86TG7;Q86TG7-2	PEG10	0.134943	7.97143	0.797091	4.89E-102
P61978;P61978-2;Q5T6W5;P	HNRNPK	0.134754	8.79886	0.797411	1.02E-193

P51991;E7EWI9;P51991-2	HNRNPA3	0.133738	8.93432	0.799134	5.97E-133
P62847;P62847-2;E7ETK0;P6	RPS24	0.133318	8.62596	0.799845	9.12E-18
Q5T6F2;F5H2U4;A6NCA8;Q5J	UBAP2	0.131645	8.10867	0.802683	1.49E-39
O43795;O43795-2;E9PDF6	MYO1B	0.129423	7.99288	0.806456	3.44E-115
P61244;P61244-2;G3V5L1;G3	MAX	0.129166	7.38968	0.806894	9.21E-95
Q9BUQ8	DDX23	0.128717	8.3407	0.807655	3.36E-38
O14979;O14979-3;O14979-2	HNRPDL	0.12673	8.641	0.811035	2.72E-127
Q9BSA4;B4DKD1	TTYH2	0.123259	7.274	0.816948	0.0013052
O00159;O00159-3;O00159-2;	MYO1C	0.122526	8.85155	0.818196	0
Q9Y383;Q9Y383-3;Q9Y383-2;	LUC7L2;C7orf55	0.121271	6.73244	0.820337	0.0019175
Q8NI27	THOC2	0.11689	7.57621	0.827821	3.49E-71
P12236;I7HJJ0;P12235	SLC25A6;SLC25A4	0.115593	8.24905	0.830039	3.03E-42
O60832;O60832-2;H7C0M1;C	DKC1	0.115513	8.36808	0.830176	9.53E-58
Q01780;K7EJ37;B4DKG8;Q01	EXOSC10	0.114403	6.60465	0.832076	1.05E-09
Q9NXV6;J3KNE1;D6RGD2	CDKN2AIP	0.110966	6.95973	0.837965	1.07E-05
Q9BUJ2;Q9BUJ2-4;B7Z4B8;Q9	HNRNPUL1	0.107082	8.74572	0.84463	8.39E-218
Q14807;B7Z265;H3BRB3	KIF22	0.106785	7.44507	0.845141	6.78E-22
P11387	TOP1	0.0994015	9.12369	0.857843	0
P61313;E7EQV9;E7ENU7;E7E	RPL15	0.0987053	8.4648	0.859043	3.72E-29
Q96EY1;Q96EY1-2	DNAJA3	0.0976448	7.66825	0.860871	1.85E-24
Q16637;Q16637-4;Q16637-2;	SMN1	0.0906887	7.65701	0.872881	4.22E-43
Q07666;Q07666-3;Q07666-2	KHDRBS1	0.0900536	9.36556	0.873979	6.34E-214
P61964	WDR5	0.0890045	7.43859	0.875793	6.37E-29
Q9UHB6;Q9UHB6-4;F8VQE1;I	LIMA1	0.0887718	8.98227	0.876195	2.79E-166
Q9Y3B4	SF3B14	0.0881367	7.60909	0.877294	1.47E-19
P31943;E9PCY7;G8JLB6;D6RI	HNRNPH1	0.0854912	8.94622	0.881873	2.00E-183
Q9H7E2;Q9H7E2-2;Q9H7E2-3	TDRD3	0.085207	7.66483	0.882365	1.43E-20
P46776;E9PJD9;E9PLL6	RPL27A	0.0800114	8.74422	0.891371	1.07E-18
P62979;P0CG47;J3QS39;J3QT	RPS27A;UBB;UBC;UI	0.0763111	8.39627	0.897793	1.40E-152
Q14134;Q14134-2	TRIM29	0.0739689	7.51866	0.901862	1.00E-43
Q96KR1	ZFR	0.0733471	8.13991	0.902942	5.74E-129
P33778;Q16778;Q99877;Q93	HIST1H2BB;HIST2H2	0.073204	10.5637	0.903191	1.19E-46
Q01844;Q01844-6;B0QYK0;Q	EWSR1	0.0726814	9.32506	0.904099	1.71E-103
Q14966;Q14966-3;Q14966-4;	ZNF638	0.0711384	8.58015	0.906782	1.07E-225
O60506;O60506-2;O60506-3;	SYNCRIP	0.0630322	8.87477	0.920892	0
P49790;F6QR24	NUP153	0.0606823	7.60869	0.924987	5.15E-121
Q00610;Q00610-2	CLTC	0.0598106	8.0859	0.926507	7.91E-67
P42167;P42167-2;G5E972;P4	TMPO	0.053524	7.60267	0.937474	2.91E-33
Q8WWI1-3;E9PMS6;Q8WWI1	LMO7	0.0528946	8.61561	0.938573	8.51E-225
Q96PK6	RBM14	0.0523891	8.956	0.939455	2.84E-71
O95831;O95831-3;Q1L6K4;O	AIFM1	0.0523281	7.28165	0.939562	2.13E-11
P35250;P35250-2	RFC2	0.0473232	8.79191	0.948303	5.80E-224
Q9H9Y6;F5GZX4;Q9H9Y6-2;F	POLR1B	0.0472069	8.29979	0.948506	2.48E-263
O00425	IGF2BP3	0.04636	8.81977	0.949986	3.19E-276
P15880;H0YEN5;E9PQD7;I3L4	RPS2	0.0463524	8.61099	0.949999	3.21E-62
P62995;P62995-3	TRA2B	0.0453129	7.3965	0.951816	7.72E-16
Q7Z2W4;Q7Z2W4-2;C9J6P4;C	ZC3HAV1	0.0442772	8.02934	0.953626	6.92E-162
O95816;B4DXE2	BAG2	0.0432034	7.77748	0.955503	1.24E-152
P68133;P68032;P63267;P627	ACTA1;ACTC1;ACTG	0.0422935	9.64058	0.957094	1.23E-136
P36578;H3BM89	RPL4	0.0410957	9.17272	0.959188	3.75E-211
Q9HAV0	GNB4	0.0396652	6.5895	0.96169	8.48E-48
Q9Y3A4;Q9NSQ0	RRP7A;RRP7B	0.0343552	7.62563	0.970979	4.24E-08
P11142;E9PKE3;P11142-2;E9I	HSPA8	0.0343246	9.17667	0.971032	2.01E-263
P62879;C9JXA5;C9JZN1;C9JIS	GNB2	0.0341511	8.31423	0.971336	2.55E-109
P48634	PRRC2A	0.0330524	7.95506	0.973258	6.57E-34
Q9UII2	ATPIF1	0.0319214	7.78352	0.975238	0.00064699
Q14257;A8MXP8;F8WCY5	RCN2	0.0317211	6.66298	0.975588	2.01E-09
P35659;P35659-2;B4DFG0;D6	DEK	0.0294399	7.86558	0.979581	1.47E-30
Q9NX24;D6RC52;D6RCB9;J3C	NHP2	0.0286865	7.92975	0.980899	9.24E-70
P98175-2;P98175;P98175-3;F	RBM10	0.0271454	8.5618	0.983597	1.02E-72
Q15149;Q15149-4;Q15149-2;	PLEC	0.0248489	9.41964	0.987617	0
P61353;K7EQQ9;K7ELC7	RPL27	0.0243206	8.36611	0.988542	9.04E-15
O14974;O14974-5;O14974-4;	PPP1R12A	0.0227375	8.54214	0.991314	6.27E-84
Q8TAQ2;Q8TAQ2-2;Q8TAQ2-	SMARCC2	0.0224972	7.22742	0.991735	1.75E-36
P25398	RPS12	0.0219193	9.03419	0.992747	9.97E-62
O00571;O00571-2;O15523;B4	DDX3X;DDX3Y	0.0215569	8.99002	0.993381	2.52E-195
Q08211	DHX9	0.0177765	8.79435	1	0
Q9BY77;Q9BY77-2;F8WCX5	POLDIP3	0.0145607	8.69983	0.993455	1.23E-92
Q12965	MYO1E	0.0096302	8.03711	0.983421	7.65E-154
P39019;M0R2L9;M0QXK4;M0	RPS19	0.00840187	9.05763	0.980922	1.85E-46
Q8IUE6	HIST2H2AB	0.00397873	10.2282	0.971924	6.22E-65
Q99567;J3KMX1	NUP88	0.00141716	7.52696	0.966714	9.11E-16
Q6P2Q9	PRPF8	-0.000188828	8.68048	0.963449	0
Q96EP5;Q96EP5-2;K7EQ02;K7	DAZAP1	-0.00198364	8.86968	0.9598	2.80E-149

P43243;A8MXP9;D6REM6;D6	MATR3	-0.00494194	8.81702	0.953788	6.68E-144
Q9Y2X3	NOP58	-0.00496674	7.79644	0.953738	1.24E-39
Q00839;Q00839-2	HNRNPU	-0.00717926	7.91896	0.949243	1.43E-95
Q9GZS1-2;Q9GZS1;E7EX70	POLR1E	-0.00896454	8.0003	0.945617	6.57E-21
Q9NUL3;Q9NUL3-4;E5RJN7;E	STAU2	-0.01087	7.70738	0.941749	2.35E-25
P27635;F8W7C6;B8A6G2;A6(	RPL10	-0.0114632	8.96633	0.940545	3.53E-74
P62314;J3QLR7;J3QLI9	SNRPD1	-0.0123901	7.89173	0.938664	1.34E-07
Q07020;F8VWC5;G3V203;H0'	RPL18	-0.012928	8.77498	0.937572	2.69E-97
Q99700;H0YH87;Q99700-2;F{	ATXN2	-0.0140953	8.30959	0.935204	6.01E-87
Q86V48;Q86V48-2;Q86V48-3	LUZP1	-0.0163822	8.64694	0.930566	0
Q8NC51;Q8NC51-3;Q8NC51-4	SERBP1	-0.0167923	7.98102	0.929735	2.40E-14
P08174;P08174-2;H3BLV0;Q1	CD55	-0.0171089	7.91257	0.929093	5.11E-36
P53999	SUB1	-0.0174828	6.92149	0.928335	4.76E-11
Q9Y3I0	C22orf28	-0.0175114	8.63646	0.928277	2.59E-216
Q9NX58	LYAR	-0.02244	8.83133	0.918293	2.51E-229
O43660;O43660-2;A8MW61	PLRG1	-0.0243587	7.64375	0.914409	8.16E-171
Q9NR56;Q9NR56-3;Q9NR56-4	MBNL1;MBNL2;MBI	-0.0244656	7.59532	0.914193	0.00044332
P22626;P22626-2	HNRNPA2B1	-0.0247707	9.29868	0.913575	0
Q9NRR4;Q9NRR4-3;Q9NRR4-	DROSHA	-0.026268	7.58069	0.910547	3.22E-21
O60841	EIF5B	-0.027113	6.83756	0.908838	0.0051343
P51116	FXR2	-0.029108	8.98445	0.904805	5.28E-242
P80723;P80723-2	BASP1	-0.0299873	8.24155	0.903029	9.84E-16
Q9Y520;Q9Y520-4;E7EPN9;Q!	PRRC2C	-0.0314198	8.55391	0.900136	7.66E-169
P52597	HNRNPF	-0.0316582	8.41762	0.899654	6.89E-122
Q9UKF6;G5E9W3	CPSF3	-0.0319309	7.61271	0.899103	1.38E-50
Q5T5X7	BEND3	-0.0346699	8.04696	0.893576	5.95E-154
P52272;P52272-2	HNRNPM	-0.0347843	9.61379	0.893345	0
P39880;P39880-4;P39880-2;F	CUX1	-0.0410347	7.1695	0.880752	1.52E-30
Q8N556;Q8N556-2	AFAP1	-0.0424614	7.21	0.877882	0.0023602
P52429;I3L112	DGKE	-0.0470276	7.091	0.868706	0.004068
Q9UHI6;E9PJ60	DDX20	-0.049305	7.7294	0.864136	2.35E-87
P49750-4;P49750;F8VU51;P4	YLPM1	-0.0496616	8.202	0.86342	3.10E-93
Q9Y5A9;Q9Y5A9-2	YTHDF2	-0.0504093	8.41981	0.861921	5.70E-70
Q16666;Q16666-3;Q16666-2;	IFI16	-0.0505867	9.03755	0.861566	6.76E-248
Q13310;Q13310-2;B1ANR0;Q	PABPC4	-0.052	8.99123	0.858734	0
P62140;E7ETD8;C9J9S3;C9JP4	PPP1CB	-0.0549831	8.76666	0.852762	0
P46013;P46013-2	MKI67	-0.0560703	9.78943	0.850587	0
O43182;O43182-3;O43182-2	ARHGAP6	-0.0597801	8.12097	0.843176	5.02E-05
P05198;H0YJS4;G3V4T5	EIF2S1	-0.0598946	8.03379	0.842948	2.35E-52
P23396;J3KN86;E9PPU1;E9PL	RPS3	-0.0601349	8.75199	0.842469	5.24E-129
P11940;P11940-2;E7EQV3;E7	PABPC1;PABPC3	-0.064003	9.7058	0.834758	0
Q5BKZ1;Q5BKZ1-2	ZNF326	-0.0668087	7.52157	0.829174	5.77E-14
Q6I9Y2	THOC7	-0.0673313	7.01937	0.828135	7.97E-08
Q9NR30;Q9NR30-2	DDX21	-0.0701618	8.88192	0.822513	2.91E-265
Q5T5U3	ARHGAP21	-0.0707264	7.11631	0.821393	3.12E-32
P28288;P28288-2;F5GYC1;E7	ABCD3	-0.0734615	7.93608	0.815971	7.11E-81
Q00325-2;F8VVM2;Q00325;F	SLC25A3	-0.07617	8.10411	0.81061	3.04E-79
O43823	AKAP8	-0.0766983	7.94421	0.809565	3.68E-48
Q14527;Q14527-2	HLTF	-0.0784874	9.22742	0.80603	0
Q99590;Q99590-2;F8VXG7	SCAF11	-0.0795155	7.53753	0.804	4.89E-23
P18887;F5H8D7	XRCC1	-0.0838108	8.92749	0.795535	5.15E-128
P62888;E5RI99	RPL30	-0.0854816	8.96655	0.792249	2.79E-151
Q8WXF1;Q8WXF1-2	PSPC1	-0.0865097	8.70395	0.790228	5.43E-109
P49916;P49916-2	LIG3	-0.0888309	9.41355	0.785672	0
P35580;P35580-2;F8W6L6;P3	MYH10	-0.0900707	7.26586	0.783241	1.42E-81
Q13435;E9PPJ0;E9PJ04;H0YC	SF3B2	-0.0902824	8.39564	0.782826	1.06E-115
Q8NI36;D6R922	WDR36	-0.090992	8.29385	0.781437	1.63E-160
Q96DI7;B4DQJ1	SNRNP40	-0.0925789	8.45806	0.77833	1.01E-86
Q9NZI8;Q9NZI8-2	IGF2BP1	-0.0968666	8.64565	0.769956	5.73E-278
Q9NVI7-2;Q9NVI7;Q9NVI7-3;	ATAD3A;ATAD3B	-0.0984116	8.11317	0.766945	5.01E-65
Q06787;Q06787-6;Q06787-4;	FMR1	-0.10107	8.56502	0.761771	3.93E-169
Q9HCE1;Q9HCE1-2;Q5JR04	MOV10	-0.103352	8.36218	0.757341	1.40E-164
Q8NEY1;Q8NEY1-2;Q8NEY1-6	NAV1	-0.104286	6.88602	0.755528	2.36E-13
O94906;O94906-2	PRPF6	-0.105392	8.31245	0.753384	7.49E-145
Q8IYH5;Q8IYH5-2;Q8IYH5-4	ZZZ3	-0.10865	7.28124	0.747081	1.65E-10
Q9NZ01;B3KSQ1;M0R3C3;Q9	TECR	-0.112892	7.64273	0.7389	2.57E-09
Q9ULL5-3;Q9ULL5-2;Q9ULL5	PRR12	-0.118025	7.31576	0.72904	9.77E-35
P49458;E9PE20;P49458-2	SRP9	-0.121145	7.76752	0.723067	6.78E-14
O75934	BCAS2	-0.122932	7.14628	0.719654	4.18E-28
O00567	NOP56	-0.123077	7.87124	0.719377	1.13E-29
O15226;G3V1N1	NKRF	-0.123505	7.86337	0.718562	5.35E-29
P60660;P60660-2;F8W1R7;G:	MYL6	-0.127127	8.49678	0.711665	1.52E-49
Q15853;M0QXT0;Q6YI47;Q1!	USF2	-0.1276	7.78585	0.710767	5.29E-48
P23246;P23246-2	SFPQ	-0.127895	10.6556	0.710205	0

O15143;F8WCG3	ARPC1B	-0.129658	6.67587	0.70686	2.90E-05
P84090;G3V279	ERH	-0.131386	8.43014	0.703586	4.64E-108
P62244;I3L3P7;I3L246;H3BN9	RPS15A	-0.131565	8.58531	0.703246	1.23E-36
Q8IY67-2;E9PAU2;K7EQG2	RAVER1	-0.133587	7.37378	0.699423	4.98E-08
P46781;B5MCT8;C9JM19	RPS9	-0.133604	8.43646	0.699391	7.25E-27
Q9H2U1;Q9H2U1-2;F5GZS0;E	DHX36	-0.133675	7.93449	0.699258	2.35E-106
Q6ZNL6;Q6ZNL6-2;B7ZM68	FGD5	-0.134172	7.07379	0.698318	3.87E-16
P07814	EPRS	-0.136959	7.33648	0.693064	1.33E-17
P62899;H7C2W9;C9JU56;B7Z	RPL31	-0.141138	8.27878	0.685212	3.13E-26
O95400	CD2BP2	-0.142874	7.71685	0.681961	1.41E-48
P38159;H0Y6E7;H3BT71;P381	RBMX;RBMXL1	-0.149929	8.31125	0.668808	1.22E-75
Q71RC2;Q71RC2-5;Q71RC2-3	LARP4	-0.155767	8.39303	0.657999	3.64E-178
P46778;G3V1B3;M0R181	RPL21	-0.158396	8.54324	0.653156	9.95E-21
P30876;C9J4M6;C9J2Y9	POLR2B	-0.158773	7.38977	0.652462	4.21E-06
P14373;P14373-2;B0V297	TRIM27	-0.15967	7.75213	0.650814	7.00E-106
P35637;P35637-2;H3BPE7	FUS	-0.160055	9.53508	0.650106	9.52E-136
Q7Z2E3;Q7Z2E3-7;Q7Z2E3-8;	APTX	-0.163284	8.53444	0.644188	7.59E-39
O43143	DHX15	-0.165651	8.32278	0.639864	6.08E-197
O75643	SNRNP200	-0.170158	8.71565	0.631664	0
H9KV59;O43663;O43663-2;F8	PRC1	-0.170696	8.12723	0.630689	5.31E-155
P38919	EIF4A3	-0.173513	7.71461	0.62559	4.50E-18
Q8WWM7	ATXN2L	-0.175591	8.75693	0.621842	1.25E-131
P17066;P48741	HSPA6;HSPA7	-0.177998	7.56624	0.61751	1.52E-21
P05114;A6NL93;A6NEL0	HMGN1	-0.179705	7.47621	0.614447	1.85E-05
Q12926;Q12926-2;B1AM49;P	ELAVL2;ELAVL4	-0.1821	7.5155	0.610158	2.12E-26
P40938;P40938-2	RFC3	-0.182144	8.72678	0.61008	1.42E-131
Q7LGA3;Q7LGA3-3;Q7LGA3-2	HS2ST1	-0.184088	6.76929	0.606611	9.69E-07
P62269	RPS18	-0.186428	9.14603	0.602446	8.29E-60
Q15233;Q15233-2;H7C367;C9	NONO	-0.187374	10.6594	0.600766	0
P78527;E7EUY0;P78527-2	PRKDC	-0.197643	9.93602	0.582666	0
Q14011;K7ELV6;K7ENX8;K7EJ	CIRBP	-0.201942	7.77597	0.575165	3.63E-58
Q15434;F6W1U9;F8W1T6	RBMS2	-0.202425	6.67246	0.574326	2.61E-08
P60709	ACTB	-0.203537	8.86212	0.572395	0
A0AV96;D6RBS9;D6R9D6;A0A	RBM47	-0.205568	7.45477	0.568875	2.27E-64
P16403	HIST1H1C	-0.209435	9.4706	0.562204	3.80E-34
Q10570	CPSF1	-0.211239	7.78381	0.559103	1.04E-67
Q5UIP0;Q5UIP0-2	RIF1	-0.211929	8.31871	0.557919	3.22E-146
Q9H2Y7;H3BNX5;H3BS99;E9F	ZNF106	-0.217688	6.98062	0.548091	2.80E-13
Q5T3I0;Q5T3I0-3;E9PAV9;F8\	GPATCH4	-0.220312	7.91937	0.54364	8.39E-135
Q3MHD2;Q3MHD2-2;K7ELG9	LSM12	-0.220806	8.02469	0.542804	2.64E-18
Q9Y3U8;J3QSB5	RPL36	-0.221552	8.17918	0.541543	1.69E-24
Q9BYW2;H7BZ93;Q9BYW2-3;	SETD2	-0.227007	7.09944	0.532368	3.59E-18
P08708;P0CW22;H0YN88;H0\	RPS17;RPS17L	-0.229837	8.37094	0.527638	4.65E-82
P11021	HSPA5	-0.231192	8.14659	0.525383	5.30E-131
P41091;Q2VIR3;Q2VIR3-2;F8\	EIF2S3;EIF2S3L	-0.234524	8.18814	0.519855	4.10E-50
Q9NW08;F8VRE2;Q9NW08-2	POLR3B	-0.234537	6.42095	0.519833	0.0058718
P0C0S5;Q71UI9;Q71UI9-3;Q7	H2AFZ;H2AFV	-0.237638	7.41557	0.514714	3.28E-15
P09874	PARP1	-0.238449	10.6977	0.513381	0
Q13151	HNRNPA0	-0.242064	8.32883	0.507457	0
Q14444;Q14444-2;G3V153;E9	CAPRIN1	-0.242558	9.43962	0.506651	6.23E-184
P62318;B4DJP7;H3BT13	SNRPD3	-0.244122	8.36847	0.504101	1.42E-52
P35658;P35658-2;P35658-4;F	NUP214	-0.245638	7.58451	0.501635	2.72E-168
Q15287;H3BR57;H3BPG5;H3E	RNPS1	-0.245882	7.05415	0.501239	6.75E-12
Q969G3;H7C048;K7EMQ8;C0	SMARCE1	-0.246321	6.82223	0.500527	8.86E-10
Q16629;Q16629-3;Q16629-2;	SRSF7	-0.247997	7.43334	0.497811	3.31E-24
Q00059;A8MRB2;H7BYN3	TFAM	-0.248177	8.25171	0.497521	6.96E-40
P62805	HIST1H4A	-0.251419	10.9021	0.492293	0
P62753;A2A3R7;A2A3R5	RPS6	-0.25181	8.90149	0.491665	2.34E-87
P62424;Q5T8U2;Q5T8U3	RPL7A	-0.254028	9.13341	0.488108	7.71E-172
P62910;D3YTB1;F8W727	RPL32	-0.254068	8.76689	0.488043	2.21E-67
P16989;P16989-2;P16989-3	YBX3	-0.256075	8.18304	0.484838	6.37E-154
P43246;E9PHA6;P43246-2	MSH2	-0.259686	8.09902	0.479099	2.97E-132
P62280;M0QZC5	RPS11	-0.261028	8.85401	0.476974	3.36E-55
P62750;H7BY10;K7EJV9;K7ER	RPL23A	-0.261452	8.88395	0.476305	7.31E-24
P19338;H7BY16	NCL	-0.26334	8.77276	0.473328	0
Q9BZK7	TBL1XR1	-0.266621	7.51685	0.468181	7.19E-15
Q8N684;Q8N684-2;Q8N684-3	CPSF7	-0.269691	7.7894	0.46339	6.47E-51
Q9Y2S0	POLR1D	-0.273426	7.73902	0.457602	8.28E-100
O43290	SART1	-0.27869	8.11817	0.449511	3.23E-220
P12956;B1AHC8;B1AHC9;F5H	XRCC6	-0.280518	10.4348	0.446722	0
Q07065	CKAP4	-0.280994	7.09153	0.445996	4.56E-25
P84098;J3QR09;J3KTE4	RPL19	-0.281584	8.64946	0.445099	1.05E-92
P62306	SNRPF	-0.285477	7.97341	0.439202	2.01E-19
Q6UN15;Q6UN15-3;Q6UN15-	FIP1L1	-0.28616	8.08314	0.438173	9.94E-96

Q9BQ04;E9PLB0;E9PM61	RBM4B	-0.292826	6.86713	0.428194	1.82E-23
P18621;J3QQT2;J3KRX5;J3QL	RPL17	-0.303349	9.02362	0.412713	2.97E-84
P09651;P09651-3;F8VXY0;F8	HNRNPA1;HNRNPA1	-0.30476	9.25643	0.410662	1.42E-273
P05783;F8VZY9	KRT18	-0.307064	10.4527	0.407327	0
Q7L2E3;Q7L2E3-2;Q7L2E3-3;I	DHX30	-0.309975	8.15112	0.403138	2.58E-77
Q9UHB9;Q9UHB9-3;F5H5Y3;(	SRP68	-0.311596	6.92922	0.400815	4.14E-08
Q9Y4P3;E9PF19	TBL2	-0.31246	7.53909	0.399581	1.33E-16
P40429;M0QYS1	RPL13A	-0.315079	8.6242	0.395854	3.41E-25
Q14683;H0Y7K8	SMC1A	-0.320566	6.9242	0.388112	8.28E-18
P35249;C9JZI1;C9J8M3;C9JTT	RFC4	-0.321735	8.7589	0.386474	2.28E-95
Q9BYJ9;F8W840	YTHDF1	-0.322491	7.61627	0.385418	1.03E-42
P61254;J3QRI7;J3QQQ9;J3QC	RPL26;KRBA2;RPL26	-0.322544	8.88285	0.385344	2.31E-34
Q9BTD8;K7EQ03;Q9BTD8-4;C	RBM42	-0.328363	6.36961	0.377271	1.90E-22
Q9UMS4;F5GY56	PRPF19	-0.332071	8.40615	0.372181	1.47E-62
P49454	CENPF	-0.333689	8.98438	0.369975	0
Q02543;M0R117;B4DM74;M	RPL18A	-0.334042	8.58457	0.369495	2.92E-46
P46087;P46087-2;P46087-4;F	NOP2	-0.335291	8.10981	0.367797	1.24E-52
P62829;C9JD32;B9ZVP7;J3KT	RPL23	-0.336613	8.34173	0.366007	2.81E-32
Q9P2I0	CPSF2	-0.337709	7.53596	0.364525	1.51E-13
P62701	RPS4X	-0.341076	9.22045	0.360001	1.82E-184
P06748;P06748-2;P06748-3	NPM1	-0.341431	9.94612	0.359526	0
Q9ULV3;Q9ULV3-5;H0Y5D5;C	CIZ1	-0.341545	7.71815	0.359373	2.08E-93
P49207	RPL34	-0.343452	8.4216	0.356828	1.98E-05
P46777	RPL5	-0.347391	8.82265	0.351609	2.73E-87
P02545;Q6UYC3;P02545-3;P(	LMNA	-0.35103	7.5923	0.34683	1.75E-30
Q14980;Q14980-2;Q14980-4;	NUMA1	-0.351582	8.53458	0.34611	0
Q15390;E5RIB6;E5RJS5	MTFR1	-0.35474	6.8856	0.342001	0.004093
Q15029;Q15029-2;K7EJ81	EFTUD2	-0.357559	8.64139	0.338361	1.59E-143
P84103;B4E241	SRSF3;SFRS3	-0.359062	7.91208	0.33643	5.70E-38
P63173;J3KT73;J3QL01	RPL38	-0.360374	8.08817	0.33475	9.42E-08
P42677;Q5T4L4	RPS27	-0.364883	8.83303	0.329019	3.93E-24
P05387;H0YDD8	RPLP2	-0.366629	9.14464	0.326818	1.14E-138
P05388;Q3B7A4;F8VWS0;F8V	RPLP0;RPLP0P6	-0.367691	8.8569	0.325483	2.55E-114
P60866;P60866-2;E5RJX2	RPS20	-0.368708	8.47643	0.324208	4.48E-25
P62917;E9PKZ0;E9PIZ3;E9PKI	RPL8	-0.369074	8.86858	0.32375	6.05E-55
Q12788;J3KNP2	TBL3	-0.370089	8.1329	0.322482	1.12E-84
Q9Y230;B3KQ59;M0R0Y3	RUVBL2	-0.373737	8.26869	0.317951	5.20E-82
P07305;P07305-2	H1F0	-0.374256	6.77796	0.317311	0.0015397
P62249;M0R210;M0R3H0;M(	RPS16	-0.380068	8.74302	0.310189	1.54E-28
Q5SW79;Q5SW79-2;Q5SW79	CEP170	-0.380852	6.62415	0.309237	1.88E-05
P47914	RPL29	-0.380922	8.59299	0.309151	1.27E-13
Q15269	PWP2	-0.381111	7.90841	0.308922	4.08E-72
Q9UBU8;Q15014;H0YM21;Q5	MORF4L1;MORF4L2	-0.381371	6.64983	0.308608	0.0001027
O60264	SMARCA5	-0.383501	6.66855	0.306033	5.70E-05
P26373;J3QSB4;P26373-2;H3	RPL13	-0.384211	8.88665	0.305178	2.82E-29
P42766;H0Y3A0;F2Z388	RPL35	-0.385727	8.45883	0.303358	1.67E-14
Q02878;F8W181	RPL6	-0.386726	9.03663	0.302162	4.94E-86
P13010	XRCC5	-0.387352	10.2723	0.301414	0
P22415;E9PME6;B1AQP1;Q7	USF1;usf1-bd	-0.388359	7.38489	0.300214	2.70E-20
P15924;P15924-2	DSP	-0.401293	6.93925	0.285085	0.00028265
P50914;E7EPB3	RPL14	-0.4084	8.6612	0.276996	1.09E-95
P63167;Q96FJ2;F8VXI7;F8VXI	DYNLL1;DYNLL2	-0.415585	8.12555	0.268977	1.81E-79
Q01085;P31483;C9JTN7;P314	TIAL1;TIA1	-0.417271	7.65565	0.267119	4.32E-19
Q9Y608;Q9Y608-2;C9JSU1;Q5	LRRFIP2	-0.420097	7.29241	0.264023	2.04E-13
P57088;H0Y8N0;D6RAA6	TMEM33	-0.421375	6.90995	0.262632	0.0031404
P63220;Q9BYK2;Q8WVC2;Q9	RPS21	-0.423613	6.48845	0.260208	0.0033381
P62277;J3KMX5	RPS13	-0.428606	8.45466	0.254855	1.23E-32
Q8TDN6	BRIX1	-0.43573	8.35317	0.247351	1.94E-62
Q9NSU2;Q9NSU2-2;Q9NSU2-	TREX1	-0.435833	8.4607	0.247243	2.28E-88
Q9UNX4	WDR3	-0.437351	7.90498	0.245665	4.74E-61
P32969;D6RAN4;E7ESE0;H0Y	RPL9	-0.438656	8.23114	0.244314	3.52E-122
Q14676;Q14676-2;E9PGY5;Q	MDC1	-0.43961	9.02747	0.24333	2.14E-240
Q96I25;Q5W011;Q5W010;H0	RBM17	-0.445431	7.82168	0.237383	2.10E-47
Q13247;Q13247-3	SRSF6	-0.457176	7.68813	0.225699	2.96E-08
Q9BRP8;Q9BRP8-2	WIBG	-0.477728	7.00139	0.206253	5.47E-15
P46779;C9JB50;G5E9L2;H0YL	RPL28	-0.477734	8.29826	0.206248	7.94E-10
P39023;G5E9G0;H7C422;B5M	RPL3	-0.479593	9.04179	0.20455	2.38E-121
P83731;C9JXB8;C9JNW5	RPL24	-0.49231	8.49837	0.193213	3.39E-29
Q6W2J9;H7BZ37;H7C2V9;A6I	BCOR	-0.494879	6.92182	0.19098	2.47E-07
O75475;O75475-2;O75475-3	PSIP1	-0.49637	7.53925	0.189692	9.16E-31
Q6P1K8;Q13888;J3KQC7;F5G	GTF2H2C;GTF2H2	-0.506372	6.70563	0.181222	4.35E-08
P62873;B3KVK2;F6X3N5;F6U	GNB1	-0.507189	7.81397	0.180543	6.40E-23
Q8N3X1;Q8N3X1-2	FNBP4	-0.511894	7.9565	0.176667	6.88E-60
Q9BWJ5	SF3B5	-0.51442	7.62623	0.174613	9.55E-12

Q9NYB0	TERF2IP	-0.518627	7.01068	0.17123		6.47E-09
Q7RTV0	PHF5A	-0.526907	7.80735	0.164716		3.73E-35
P62273;P62273-2	RPS29	-0.527895	7.88178	0.163952		2.08E-24
P62913;P62913-2;Q5VVC9;Q	RPL11	-0.544024	8.91611	0.151845		5.66E-66
P62081;B5MCP9	RPS7	-0.573246	8.63082	0.131661		3.83E-182
Q86UE4;E5RJU9;H0YB56	MTDH	-0.590635	8.03306	0.120676		1.45E-78
Q53GS9;Q53GS9-2;B9A018;B	USP39	-0.592915	8.21293	0.119291		2.18E-51
Q92804;K7EPT6;Q92804-2	TAF15	-0.595976	8.01824	0.117451		4.92E-71
Q9ULM3	YEATS2	-0.598461	7.1702	0.115973		4.20E-27
Q9Y3Y2;Q9Y3Y2-4;Q9Y3Y2-3	CHTOP	-0.601954	6.67625	0.113921		3.64E-28
Q6FI13;P0C0S8;Q9BTM1;Q16	HIST2H2AA3;HIST1H	-0.607811	8.28513	0.110544		5.13E-14
Q14690	PDCD11	-0.637209	7.42326	0.0947726		6.67E-57
Q96C57;E7ENF1;G5EA44;F5H	C12orf43	-0.639296	7.58899	0.0937255		4.14E-30
Q86VM9;E7ERS3;Q86VM9-2	ZC3H18	-0.650585	7.46433	0.0882201		5.40E-24
Q15427	SF3B4	-0.667976	7.61283	0.0802523		3.58E-44
Q96C92;H7C331;Q96C92-4;Q	SDCCAG3	-0.66864	6.77625	0.0799602		7.30E-10
P68431;P84243;Q71DI3;K7EK	HIST1H3A;H3F3A;HI	-0.669418	10.2035	0.0796188		7.28E-30
P62854;Q5JNZ5;F8VZW7	RPS26;RPS26P11	-0.678932	8.55261	0.0755402		4.96E-25
P38432	COIL	-0.695581	6.97254	0.068814		2.42E-14
Q16698;B7Z6B8;E5RJG7;E5RF	DECR1	-0.71262	8.25686	0.0624481		1.57E-86
Q15637-2;Q15637-4;Q15637-	SF1	-0.719412	8.20914	0.06005		1.57E-26
Q969Q0;P83881;H7BZ11;H0Y	RPL36AL;RPL36A	-0.750307	7.83537	0.0500854		1.47E-06
Q13889;F5H6X0;F5GXG6;F5G	GTF2H3	-0.809944	6.68928	0.0347417		6.25E-22
Q96AG4	LRRC59	-0.843418	8.52751	0.0280389		7.02E-35
P35908	KRT2	-0.853456	8.9069	0.0262598		0
Q15365	PCBP1	-0.87977	7.22873	0.0220521		1.17E-54
P62891;Q59GN2	RPL39;RPL39P5	-0.88014	8.06926	0.0219974		0.0012659
P61513;C9J4Z3;M0R0A1;Q6P	RPL37A	-0.883423	8.2577	0.0215171		9.20E-48
P05141	SLC25A5	-0.894421	7.47844	0.0199738		3.06E-25
Q92922;F8WE13	SMARCC1	-0.899494	7.19629	0.019295		2.44E-37
Q14126	DSG2	-0.918421	7.51012	0.0169376		5.15E-78
O96019;O96019-2	ACTL6A	-0.944464	7.98791	0.0141085		2.40E-96
O60318	MCM3AP	-0.948439	6.90565	0.0137155		2.01E-17
Q14191	WRN	-0.98377	7.0834	0.0106263		2.31E-32
P52701;P52701-2;F5H2F9;B4	MSH6	-0.996475	7.16744	0.00967702		1.78E-24
Q04837;E7EUY5;C9K0U8	SSBP1	-1.0343	8.50214	0.00728255		4.10E-128
P06746;H0YBJ0;B7Z1W5;E7E	POLB	-1.04766	7.75629	0.00657312		1.57E-19
P54132;H0YNU5	BLM	-1.06284	7.613	0.00584336		1.33E-69
P62304;A6NHK2	SNRPE	-1.13158	6.8766	0.00337021		5.29E-37
P46783;F6U211;Q9NQ39	RPS10;RPS10P5	-1.18276	8.67422	0.00219622		1.33E-24
P19387;H3BRR2	POLR2C	-1.20741	7.07059	0.00177671		1.49E-10
P62316;P62316-2	SNRPD2	-1.22143	7.87949	0.00157246		1.85E-19
Q6ZRS2;Q6ZRS2-3;Q6ZRS2-2	SRCAP	-1.23085	7.45176	0.00144746		6.01E-31
O75477;O94905;O94905-2;O	ERLIN1;ERLIN2	-1.23819	7.13615	0.00135665		1.78E-10
Q9BQ67;M0QX71	GRWD1	-1.4091	7.38066	0.00027298	+	2.36E-09
O15145;F8VR50;C9JZD1	ARPC3	-1.45367	6.40427	0.000174474	+	2.18E-05
P26368;K7ENG2;P26368-2	U2AF2	-1.47399	8.17476	0.000141682	+	3.33E-28
Q13472;B4DK80;Q13472-2;B4	TOP3A	-1.50957	7.7343	9.78E-05	+	9.56E-88
Q14331;E9PRR7	FRG1	-1.65581	6.93083	1.96E-05	+	5.63E-08
Q96CW1;Q96CW1-2;E9PFW3	AP2M1	-1.93282	7.08632	6.50E-07	+	5.23E-05
Q12905	ILF2	-2.03527	7.9348	1.63E-07	+	2.01E-41
P29372;G5E9E2;Q5J9I4;P293	MPG	-2.70047	6.82334	4.10E-12	+	4.64E-08
P20585	MSH3	-4.27251	7.96593	7.12E-28	+	8.03E-114

Appendix 7 (Chapter 4)

Identification and quantification of interacting proteins for H2B S36 GlcNAc modified nucleosome versus H2B S36 thiophosphate modified nucleosome. Statistically significant interacting partners are denoted with a '+'

Majority Protein Ids	Gene names	log2(Bait/Control)	log10(Intensity)	Significance B value	Statistically Significant Interactor	PEP
Q9BYP7;Q9BYP7-2;Q9BYP7-3	WNK3	7.8174	9.33171	2.59E-164	+	0.0040162
Q9UBU8;Q15014;H0YM21;Q5	MORF4L1;MORF4L2	1.83396	6.96915	4.34E-10	+	0.00014546
P38432	COIL	1.52148	7.18224	2.74E-07	+	5.94E-10
Q9H0D6;Q9H0D6-2;B4DZC3	XRN2	1.38463	7.32418	3.19E-06	+	9.30E-20
Q86W92;Q86W92-2;F5GZP6;	PPFIBP1	1.31755	7.13066	9.78E-06	+	3.38E-19
Q12905	ILF2	1.31144	8.01515	1.08E-05	+	3.66E-45
P62891;Q59GN2	RPL39;RPL39P5	1.27351	8.12564	1.98E-05	+	0.0014404
Q07955;Q07955-3;J3KTL2;Q0	SRSF1	1.25842	7.78001	2.51E-05	+	1.82E-14
Q15365	PCBP1	1.07284	7.46601	0.00037081	+	6.68E-29
P62316;P62316-2	SNRPD2	1.0699	7.97226	0.000385693	+	2.29E-21
P06746;H0YBJ0;E7EW18;B7Z	POLB	0.940134	7.90793	0.00198422		1.48E-24
Q9H2Y7;H3BNX5;H3BS99;E9F	ZNF106	0.919754	7.09681	0.00252112		9.86E-14
O43290	SART1	0.895887	8.16256	0.003317		6.31E-191
P84090;G3V279	ERH	0.893387	8.57172	0.00341243		4.69E-107
P35573;P35573-2;P35573-3	AGL	0.892569	8.02739	0.0034442		0.003195
O15234;J3KSY7	CASC3	0.889362	7.58173	0.00357129		1.90E-07
O15347;E9PES6;E7ES08;E7EC	HMGB3	0.859945	7.09279	0.00495237		3.80E-05
O75531	BANF1	0.851061	6.64006	0.00545568		0.00010969
Q15427	SF3B4	0.786194	7.68633	0.0107623		7.01E-40
Q6PIY7;D6RAF2;Q6PIY7-2	PAPD4	0.762207	6.60496	0.0136697		4.12E-08
P08708;P0CW22;H0YN88;H0	RPS17;RPS17L	0.727337	8.46985	0.0191295		3.58E-115
P62081;B5MCP9	RPS7	0.724001	8.85866	0.0197404		1.85E-114
Q7L2E3;Q7L2E3-2;Q7L2E3-3;I	DHX30	0.692871	8.22632	0.026311		1.16E-74
Q9UII2	ATPIF1	0.666864	8.12208	0.0331732		3.71E-05
P46779;C9JB50;G5E9L2;H0YL	RPL28	0.663984	8.43688	0.03402		3.06E-09
P84103;B4E241	SRSF3;SFRS3	0.654144	8.14255	0.0370536		5.48E-44
Q96DH6;Q96DH6-2;B4DHE8;J	MSI2	0.647203	8.17863	0.0393294		9.35E-41
Q9BRP8;Q9BRP8-2	WIBG	0.626732	6.96903	0.0467441		4.25E-08
Q8NI27	THOC2	0.609819	7.62548	0.0537263		1.42E-61
P49458;E9PE20;P49458-2	SRP9	0.588287	7.68252	0.0638552		1.08E-14
Q6FI13;P0C0S8;Q9BTM1;Q16	HIST2H2AA3;HIST1H	0.581387	8.3272	0.0674174		2.85E-21
Q8IWX8;J3QK89	CHERP	0.569551	7.93309	0.0739065		1.28E-54
Q10570	CPSF1	0.566109	7.80144	0.0758873		4.57E-74
Q14011;K7ELV6;K7ENX8;K7EJ	CIRBP	0.564539	7.75925	0.0768047		7.65E-145
Q9H0H5;F8VRD2;F8W1E5	RACGAP1	0.553802	7.54736	0.0833243		1.48E-33
Q14978;Q14978-3;Q14978-2	NOLC1	0.52594	8.93471	0.10235		2.94E-46
Q9NYL9;H0YNJ8	TMOD3	0.522717	8.08792	0.104758		2.68E-145
P26373;J3QSB4;P26373-2;H3	RPL13	0.52269	8.95489	0.104778		2.78E-44
Q14331;E9PRR7	FRG1	0.520161	6.80615	0.106699		2.47E-07
P56182	RRP1	0.511522	7.0054	0.113471		5.65E-12
Q9Y4P3;E9PF19	TBL2	0.510302	7.5736	0.114455		4.50E-17
Q9UKM9;Q9UKM9-2;Q5QPM	RALY	0.51004	6.87703	0.114667		0.0010559
P62273;P62273-2	RPS29	0.507662	7.94597	0.116605		2.22E-11
O00567	NOP56	0.494804	7.90293	0.127536		3.29E-13
P62424;Q5T8U2;Q5T8U3	RPL7A	0.492537	9.17371	0.129544		4.54E-170
Q9NZ01;M0R3C3;B3KSQ1	TECR	0.490694	7.63447	0.131193		4.81E-08
P68431;P84243;Q71DI3;K7EK	HIST1H3A;H3F3A;HI	0.489513	10.3701	0.132259		6.45E-34
P46783;F6U211	RPS10	0.487106	8.47095	0.134452		5.27E-23
Q9UMS4;F5GY56	PRPF19	0.483858	8.50219	0.137456		1.86E-47
Q96C57;E7ENF1;G5EA44;F5H	C12orf43	0.482666	7.6186	0.138571		8.60E-14
P41091;Q2VIR3;H7BZU1;Q2V	EIF2S3;EIF2S3L	0.48173	8.17164	0.139452		7.05E-20
P22087;M0R0P1;M0QXL5;MC	FBL	0.46843	8.11271	0.152434		1.62E-11
Q14191	WRN	0.460213	6.91023	0.160903		1.45E-23
Q01831;E9PH69	XPC	0.454208	7.07192	0.167313		1.37E-09
P33778;Q16778;Q99877;Q93	HIST1H2BB;HIST2H2	0.448997	10.5752	0.173029		3.93E-41
P39019;M0R2L9;M0QXK4;MC	RPS19	0.446272	9.12388	0.176077		3.00E-48
O95782;O95782-2	AP2A1	0.441666	7.81976	0.181318		3.73E-51
Q86UE4;E5RJU9	MTDH	0.434378	8.07092	0.189846		5.78E-68
Q16637;Q16637-4;Q16637-2;	SMN1	0.433699	7.81174	0.190655		4.77E-24
Q14690	PDCD11	0.424913	7.30822	0.201356		1.45E-12
Q9Y3U8;J3QSB5	RPL36	0.419504	8.25249	0.208159		8.07E-18
Q5SW79;Q5SW79-2;Q5SW79	CEP170	0.417624	6.68442	0.210563		6.77E-05
Q9Y608;Q9Y608-2;Q9Y608-4;	LRRFIP2	0.41717	7.20855	0.211146		3.07E-16
Q7RTV0	PHF5A	0.417164	7.77324	0.211154		1.47E-31
P46087;P46087-2;P46087-4;F	NOP2	0.410536	8.10092	0.219803		1.25E-40
O15226;G3V1N1	NKRF	0.408751	7.81977	0.222176		1.93E-29
Q9GZS1-2;Q9GZS1;E7EX70	POLR1E	0.408596	8.04731	0.222382		1.99E-20

O43143	DHX15	0.402119	8.34001	0.23115	7.39E-106
Q96QC0;F5H5K4	PPP1R10	0.397572	6.82485	0.23745	9.34E-08
Q00839;Q00839-2	HNRNPU	0.396141	7.96075	0.239457	2.19E-51
Q9HAV0	GNB4	0.395451	6.69439	0.24043	5.13E-74
Q9Y3F4;B4DNJ6;B0AZV0	STRAP	0.395426	6.98286	0.240465	4.44E-15
Q9P275;Q9P275-2;E9PEW0	USP36	0.384161	7.5923	0.256733	6.13E-39
Q9Y224;G3V4C6	C14orf166	0.377842	8.67744	0.266187	4.71E-83
O95985;H0Y6W0;O95985-3;C	TOP3B	0.375895	7.28314	0.269148	2.84E-11
O60318	MCM3AP	0.372431	6.81408	0.27447	1.30E-12
P14678;P63162;P14678-2;B3	SNRPB;SNRPN	0.371006	7.79047	0.27668	1.22E-11
Q9BRJ6;C9JQV0;H7C0T1;H7C	C7orf50	0.364447	7.27114	0.287011	5.20E-10
Q9UHB9;Q9UHB9-3;F5H5Y3;(	SRP68	0.364273	6.97012	0.287288	1.13E-07
P62917;E9PKZ0;E9PIZ3;E9PKI	RPL8	0.361454	8.89952	0.29181	4.36E-52
Q6W2J9;H7BZ37;H7C2V9;A6I	BCOR	0.357677	6.95887	0.297942	1.30E-11
M0QZM1	HNRNPM	0.354155	7.78574	0.30374	2.13E-120
Q15637-2;Q15637-4;Q15637	SF1	0.35359	8.43656	0.304676	1.71E-37
P47914	RPL29	0.350807	8.64146	0.309317	3.54E-13
P62269	RPS18	0.350506	9.24438	0.309823	2.94E-63
P62306;F8W0W6	SNRPF	0.346344	8.08799	0.316859	8.97E-39
A0AV96;D6RBS9;D6R9D6;A0A	RBM47	0.346079	7.46	0.317311	5.61E-15
P10412;P16402	HIST1H1E;HIST1H1D	0.345766	7.78246	0.317844	6.16E-43
P83731;C9JXB8;C9JNW5	RPL24	0.34481	8.52599	0.319478	5.50E-22
Q9Y2S0	POLR1D	0.343363	7.71708	0.321963	2.30E-163
O75643	SNRNP200	0.341297	8.76701	0.325531	0
Q02878;F8W181	RPL6	0.340181	9.06254	0.327468	2.72E-177
Q92576;Q92576-2;E7EVH3	PHF3	0.337505	8.69272	0.332147	4.71E-263
Q8WW12;Q8WW12-2	PCNP	0.335337	7.14644	0.335969	5.49E-05
P63167;Q96FJ2;F8VXI7;F8VXI	DYNLL1;DYNLL2	0.331558	8.20175	0.342697	3.46E-115
P61244;P61244-2;G3V5L1;G3	MAX	0.328859	7.53135	0.347554	3.53E-95
P62318;B4DJP7;H3BT13	SNRPD3	0.327682	8.40276	0.349686	1.66E-49
Q9BWJ5	SF3B5	0.327618	7.67721	0.349804	1.66E-14
Q9NYB0	TERF2IP	0.327141	7.10775	0.35067	3.68E-18
P62913;P62913-2;Q5VVC9;Q5	RPL11	0.326815	8.98135	0.351264	1.01E-61
Q8N3X1;Q8N3X1-2	FNBP4	0.322533	7.93224	0.359113	1.26E-62
P39023;H7C422;G5E9G0;B5M	RPL3	0.32185	9.07525	0.360374	1.19E-111
P62249;M0R210;M0R3H0;M(	RPS16	0.320477	8.80064	0.36292	1.02E-30
P62750;H7BY10;K7EJV9;K7ER	RPL23A	0.31916	8.97422	0.365371	1.20E-24
P46781;B5MCT8;C9JM19	RPS9	0.316595	8.5095	0.370177	1.26E-27
Q16629;Q16629-3;Q16629-2;	SRSF7	0.315521	7.58003	0.3722	3.06E-12
O60832;O60832-2;C9IYT0;H7	DKC1	0.314548	8.32019	0.374039	8.39E-35
Q14683	SMC1A	0.311964	6.95755	0.378952	4.56E-12
P46776;E9PJD9;E9PLL6	RPL27A	0.311939	8.836	0.378999	5.71E-21
P07814	EPRS	0.311651	7.1067	0.379549	2.54E-10
Q9Y3I0	C22orf28	0.308723	8.70296	0.385168	2.51E-243
P43246;E9PHA6;P43246-2	MSH2	0.305681	7.75544	0.391059	1.93E-44
Q8TDN6	BRIX1	0.305285	8.41305	0.391832	3.14E-52
F8W726;Q5VU77	UBAP2L	0.303661	7.37088	0.395001	0
P39880;P39880-4;P39880-2;F	CUX1	0.300907	7.20629	0.400415	2.72E-08
P55735;A8MXL6;P55735-2;B4	SEC13	0.298761	7.77802	0.404663	1.86E-46
Q13310;Q13310-2;B1ANR0;Q	PABPC4	0.298489	9.02567	0.405205	0
P63096;P04899;P63096-2;P0	GNAI1;GNAI2;GNAT	0.288626	6.96871	0.425092	4.31E-12
Q71RC2;Q71RC2-5;Q71RC2-3	LARP4	0.286594	8.46768	0.429257	2.09E-169
P49207	RPL34	0.284452	8.46667	0.433675	0.00011348
Q9GZT3;H0YJW7;H0YJ40;G3V	SLIRP	0.284393	6.72261	0.433797	2.67E-12
O75607	NPM3	0.281115	7.75891	0.440612	4.89E-14
P50914;E7EPB3	RPL14	0.279715	8.69854	0.44354	1.77E-56
O14974;O14974-5;O14974-4;	PPP1R12A	0.279305	8.65138	0.4444	5.62E-90
Q8IWS0;Q8IWS0-2;Q5JRC6;E	PHF6	0.275072	7.32683	0.45333	2.58E-20
P08590;P05976;P05976-2	MYL3;MYL1	0.273014	7.44264	0.457708	0.00013355
Q14444;Q14444-2;G3V153;E	CAPRIN1	0.269609	9.51095	0.465003	4.58E-230
P46777	RPL5	0.269522	8.85916	0.465192	4.84E-91
Q9NR56;Q9NR56-3;Q9NR56-	MBNL1;MBNL2;MBI	0.266994	7.66502	0.47065	8.40E-05
P16401	HIST1H1B	0.26297	8.90932	0.479414	1.56E-32
O43390;O43390-2;Q2L7G6;E	HNRNPR	0.262697	8.49726	0.480011	4.04E-83
Q96AG4	LRRC59	0.26148	8.22123	0.48268	1.12E-26
Q96I24	FUBP3	0.260267	8.12248	0.485349	4.74E-28
P02545;Q6UYC3;P02545-3;P(	LMNA	0.259171	7.77487	0.487769	1.11E-74
P62854;Q5JNZ5;F8VZW7	RPS26;RPS26P11	0.256832	8.54054	0.49295	5.56E-22
P37108;H0YLA2	SRP14	0.255487	8.48282	0.495942	1.27E-41
P51531;P51531-2;P51532;P5	SMARCA2;SMARCA4	0.252062	7.0141	0.50361	9.53E-05
Q86TG7;Q86TG7-2	PEG10	0.245764	8.06074	0.517868	1.28E-80
Q5T6F2;F5H2U4;A6NCA8;Q5J	UBAP2	0.242996	8.19676	0.524198	1.22E-92
Q9ULL5-3;Q9ULL5-2;Q9ULL5	PRR12	0.240137	7.35951	0.53078	2.23E-24
P62753;A2A3R7;A2A3R5	RPS6	0.24008	8.96316	0.530912	3.75E-100

P61254;J3QRI7;J3QQQ9;J3QC	RPL26;KRBA2;RPL26	0.238678	8.85549	0.534155	8.35E-29
P08174;P08174-2;H3BLV0;Q1	CD55	0.237133	7.98481	0.53774	2.06E-20
P98175-2;P98175;P98175-3;F	RBM10	0.236912	8.58755	0.538255	3.45E-70
P22626;P22626-2	HNRNPA2B1	0.236132	9.35174	0.54007	1.34E-232
P52907	CAPZA1	0.234966	8.27263	0.542789	4.34E-36
O94906;O94906-2	PRPF6	0.230116	8.34934	0.554175	1.12E-126
Q96PK6	RBM14	0.229248	9.10315	0.556225	5.65E-82
Q3MHD2;Q3MHD2-2;K7ELG9	LSM12	0.229221	8.071	0.556288	2.75E-16
P05783;F8VZY9	KRT18	0.228745	10.5274	0.557415	0
P84098;J3QR09;J3KTE4	RPL19	0.228613	8.74378	0.557727	8.09E-94
P14384;F8VVI6;F8W111	CPM	0.226452	6.84188	0.562853	0.0017891
P42766;H0Y3A0;F2Z388	RPL35	0.223351	8.39948	0.570249	2.62E-15
P19338;H7BY16	NCL	0.222429	8.78777	0.572455	0
P08621;P08621-2;P08621-3	SNRNP70	0.218599	7.56627	0.581669	1.22E-15
Q9NZI8;Q9NZI8-2	IGF2BP1	0.215157	8.76361	0.590011	2.51E-269
Q92900;Q92900-2	UPF1	0.214521	9.2401	0.591555	0
Q92841;H3BLZ8;Q92841-3;Q	DDX17	0.214163	9.78408	0.592428	0
Q9UN86;Q9UN86-2	G3BP2	0.210876	9.66231	0.600457	4.32E-140
P62805	HIST1H4A	0.210625	10.9946	0.601074	4.95E-290
Q8N684;Q8N684-2;Q8N684-3	CPSF7	0.210239	7.81836	0.602019	4.20E-89
P22415;E9PME6;Q7Z5Y1;B1A	USF1;usf1-bd	0.206938	7.36918	0.610143	3.00E-09
P49454	CENPF	0.2054	8.98921	0.613942	0
P62851	RPS25	0.202488	8.72677	0.621168	2.26E-09
Q16698;B7Z6B8;E5RJG7;E5RF	DECR1	0.201576	8.18808	0.623438	1.72E-62
Q9H6R0	DHX33	0.198421	7.40092	0.631319	4.36E-22
Q15029;Q15029-2;K7EJ81	EFTUD2	0.196796	8.68549	0.635396	2.60E-247
Q86V48;Q86V48-2;Q86V48-3	LUZP1	0.19611	8.75264	0.637121	0
P13010	XRCC5	0.18898	10.3363	0.655154	0
Q13148;Q13148-2;B1AKP7;G	TARDBP	0.188765	7.62535	0.655703	1.04E-22
Q9Y230;B3KQ59;M0R0Y3	RUVBL2	0.188507	8.18367	0.656358	1.30E-55
P23246;P23246-2	SFPQ	0.188145	10.7181	0.657281	0
P62701	RPS4X	0.187233	9.23862	0.659605	3.03E-146
Q96CW1;Q96CW1-2;E9PFW3	AP2M1	0.185255	7.225	0.664658	8.76E-06
P62888;E5RI99	RPL30	0.184645	9.00749	0.66622	2.74E-148
Q8WXF1;Q8WXF1-2	PSPC1	0.184166	8.79364	0.667447	2.76E-99
P51116	FXR2	0.183414	8.95953	0.669374	4.21E-176
P04843;F8WF32	RPN1	0.182894	6.99567	0.67071	0.00041962
P36578;H3BM89	RPL4	0.182627	9.26129	0.671396	1.65E-157
Q2TAY7;B4E3L0	SMU1	0.181864	7.11203	0.673357	2.19E-05
P17066;P48741	HSPA6;HSPA7	0.177755	7.61688	0.683954	1.41E-22
P35637;P35637-2;H3BPE7	FUS	0.174984	9.69141	0.691138	8.11E-117
Q9NUL3;Q9NUL3-4;E5RJN7;E	STAU2	0.1745	7.75507	0.692397	1.54E-21
P62277;J3KMX5	RPS13	0.174107	8.47767	0.693418	4.43E-30
P61978;P61978-2;Q5T6W5;P	HNRNPK	0.173946	8.83408	0.693835	2.79E-69
Q12788;J3KNP2	TBL3	0.171841	8.08529	0.69932	6.18E-45
P42677;Q5T4L4	RPS27	0.171652	8.87156	0.699813	6.23E-21
Q14247;Q14247-3;Q14247-2;	CTTN	0.170561	7.82574	0.702661	3.12E-12
O95816;B4DXE2	BAG2	0.169693	7.84724	0.70493	3.91E-41
P05141	SLC25A5	0.169136	8.24895	0.706388	1.10E-22
Q96DI7;B4DQJ1	SNRNP40	0.168037	8.46087	0.709266	1.48E-58
Q6UN15;Q6UN15-3;Q6UN15-	FIP1L1	0.167866	8.17641	0.709716	6.81E-89
Q7LGA3;Q7LGA3-3;Q7LGA3-2	HS2ST1	0.167759	6.81285	0.709997	5.57E-21
Q8IUE6	HIST2H2AB	0.165936	10.2804	0.714785	2.70E-74
O60563;A9XU13	CCNT1;CYCT1b	0.165625	7.18792	0.715602	0.0012565
Q15287;H3BR57;H3BPG5;H3E	RNPS1	0.164656	7.0952	0.718152	6.81E-11
Q99848;H7C2Q8	EBNA1BP2	0.159679	7.8267	0.731297	9.81E-05
Q14677;Q14677-2;Q14677-3	CLINT1	0.155966	7.68265	0.741159	1.24E-27
Q6SPF0;E9PIW9	SAMD1	0.153854	7.43664	0.746785	4.18E-13
Q9UKV8;Q9UKV8-2	AGO2	0.149708	7.8945	0.757873	7.33E-80
P38919	EIF4A3	0.147987	7.77962	0.762489	2.48E-19
Q13247;Q13247-3;Q08170	SRSF6;SRSF4	0.146797	7.97346	0.765686	3.85E-18
O43823	AKAP8	0.14558	8.01275	0.76896	1.24E-45
Q9BY44;B4DQ14;F8WAE5;B4	EIF2A	0.145559	7.32683	0.769017	2.25E-12
Q9Y5A9;Q9Y5A9-2	YTHDF2	0.145	8.54539	0.770521	3.49E-87
P18124;A8MUD9	RPL7	0.144066	8.67651	0.77304	4.40E-87
P62280;M0QZC5;M0R1H5	RPS11	0.141529	8.96074	0.779888	3.38E-142
P21333;Q5HY54;P21333-2	FLNA	0.140337	7.6709	0.783112	3.04E-36
P08651;P08651-4;P08651-5;F	NFIC	0.13891	7.10479	0.786976	0.0018733
P16989-2;P16989;P16989-3	YBX3	0.138079	8.15652	0.78923	1.92E-116
P17844;J3KTA4;B4DLW8	DDX5	0.137999	9.58705	0.789447	0
Q99700;H0YH87;Q99700-2;F	ATXN2	0.136915	8.40737	0.792387	6.99E-78
P23396;J3KN86;E9PPU1;E9PL	RPS3	0.135412	8.92939	0.79647	1.58E-84
Q9BWF3;Q9BWF3-3;D6R9K7;	RBM4	0.134285	6.75902	0.799536	1.79E-42
Q9UBI6	GNG12	0.132536	7.23977	0.8043	0.0029565

Q9Y4K1	AIM1	0.130886	7.29217	0.8088	1.11E-12
Q8NC51;Q8NC51-3;Q8NC51-4	SERBP1	0.12957	8.12597	0.812394	6.96E-17
P32969;D6RAN4;E7ESE0;H0Y9	RPL9	0.12859	8.2335	0.815074	3.27E-51
P78406;E9PQ57;E9PPG9	RAE1	0.126339	7.54965	0.821235	2.24E-33
P63010;K7EJT8;P63010-2;Q7	AP2B1	0.126204	7.9067	0.821606	3.07E-28
P40429;M0QYS1	RPL13A	0.12619	8.70666	0.821642	2.90E-26
Q9H307;Q9H307-2	PNN	0.125776	7.30705	0.822777	7.95E-05
Q5T3I0;Q5T3I0-3;E9PAV9;F8\	GPATCH4	0.125551	8.01674	0.823394	2.46E-116
Q06787-6;Q06787-5;Q06787;	FMR1	0.125504	8.64556	0.823524	7.70E-154
Q01844;Q01844-6;B0QYK0;Q	EWSR1	0.125307	9.38391	0.824063	2.51E-162
P43243;A8MXP9;D6REM6;H0	MATR3	0.124615	8.91633	0.825962	1.25E-165
P62263;E5RH77	RPS14	0.124197	9.00557	0.827108	3.57E-31
Q13435;E9PPJ0;E9PJ04;H0YC	SF3B2	0.121965	8.43705	0.833238	5.95E-116
Q7Z417	NUFIP2	0.121881	8.7263	0.833468	1.99E-179
P52434;C9JBJ6;C9JLU1;C9JUA	POLR2H	0.121723	7.61243	0.833904	2.22E-10
Q04837;E7EUY5;C9K0U8	SSBP1	0.121443	8.31551	0.834675	6.74E-174
Q9C0J8;Q9C0J8-2;C9J8B4;Q9	WDR33	0.120985	7.2529	0.835934	7.80E-12
Q96EP5;Q96EP5-2;K7EQ02;K	DAZAP1	0.120031	8.8472	0.838558	1.10E-119
Q96KR1	ZFR	0.117561	8.1623	0.845364	2.12E-234
Q9Y2W1	THRAP3	0.115396	8.05308	0.851338	9.41E-47
Q9Y446	PKP3	0.11338	8.13434	0.856909	1.20E-83
Q6UXN9	WDR82	0.111233	7.10435	0.862852	6.66E-12
Q9NRR4;Q9NRR4-3;Q9NRR4-	DROSHA	0.106119	7.56588	0.877033	2.24E-22
P49750;P49750-4;F8VU51;P4	YLPM1	0.10535	8.31767	0.879168	2.37E-98
H7C0N4	SF1	0.1042	7.44804	0.882364	5.12E-26
Q5T5X7	BEND3	0.102221	8.10578	0.887871	1.01E-142
Q14103;Q14103-3;H0YA96;H	HNRNPD	0.101545	8.50529	0.88975	3.10E-47
Q00059;A8MRB2;H7BYN3	TFAM	0.100288	8.28838	0.89325	6.25E-42
P49790;F6QR24	NUP153	0.0973206	7.72183	0.901522	8.63E-118
Q8NI36;D6R922	WDR36	0.0963936	8.32478	0.904108	3.41E-135
P38159;H0Y6E7;H3BT71;P381	RBMX;RBMXL1	0.0956497	8.33417	0.906184	4.61E-71
Q7Z2E3;Q7Z2E3-7;Q7Z2E3-9;	APTX	0.094677	8.55648	0.9089	5.21E-36
O95400	CD2BP2	0.0942364	7.78068	0.91013	2.27E-25
P60660;P60660-2;F8W1R7;G	MYL6	0.093174	8.62487	0.913098	1.02E-58
P08107;P08107-2;F8VZJ4;E7E	HSPA1A	0.0925484	8.59164	0.914846	1.79E-58
O14950;P19105;J3QRS3;P248	MYL12B;MYL12A;M	0.0907841	8.04505	0.919778	8.03E-117
Q92804;K7EPT6;Q92804-2	TAF15	0.0893135	7.99783	0.923891	1.02E-65
P63173;J3KT73;J3QL01	RPL38	0.0886192	8.07875	0.925834	2.20E-06
Q9H0A0;E7ESU4	NAT10	0.0867748	8.40606	0.930997	0
P30050;P30050-2	RPL12	0.0827332	9.02428	0.94232	2.72E-170
P31943;E9PCY7;G8JLB6;D6RI	HNRNPH1	0.0790901	9.00587	0.952537	1.17E-156
O43663;F8W9B5;H9KV59;O4	PRC1	0.0781555	8.08332	0.955159	3.59E-68
P38646	HSPA9	0.077919	8.06401	0.955823	6.10E-106
O60506;O60506-2;O60506-3;	SYNCRIP	0.0751419	8.91694	0.963618	0
Q5SSJ5;B0QZK4;Q5SWC8;Q5S	HP1BP3	0.0743275	6.68748	0.965905	0.0047088
Q6P5R6;C9JYQ9;H0Y8C2	RPL22L1	0.0742264	7.67835	0.966189	8.39E-49
P05187;P10696	ALPP;ALPPL2	0.0736561	8.38178	0.967791	1.55E-201
Q16643;Q16643-2;A8MV58;D	DBN1	0.0733967	8.5612	0.968519	3.51E-186
Q13769	THOC5	0.0729847	7.25633	0.969676	1.79E-12
Q9P035;B4DRF4;H3BS72	PTPLAD1	0.0726604	6.75166	0.970587	1.99E-16
P62906	RPL10A	0.0700665	8.91134	0.977874	1.19E-75
Q9BZK7	TBL1XR1	0.0685196	7.43731	0.98222	3.39E-19
P07910;P07910-2;G3V4W0;B	HNRNPC	0.0685062	8.5567	0.982257	1.07E-52
Q8WWM7	ATXN2L	0.0684109	8.85269	0.982525	1.24E-134
Q9UHB6;Q9UHB6-4;F8VQE1;I	LIMA1	0.0683002	9.01833	0.982836	9.14E-181
P26599;P26599-2;P26599-3;A	PTBP1	0.0680943	9.63115	0.983415	0
Q14684;Q14684-2	RRP1B	0.0658417	7.65066	0.989745	1.33E-47
Q14980;Q14980-2;Q14980-4;	NUMA1	0.0622959	8.45478	0.999711	0
Q8WWI1-3;E9PMS6;Q8WWI1	LMO7	0.0621929	8.68707	1	5.21E-283
Q15149;Q15149-4;Q15149-2;	PLEC	0.0621109	9.44939	0.999846	0
P12956;B1AHC8;B1AHC9;F5H	XRCC6	0.0608063	10.4565	0.997394	0
Q99590;Q99590-2;F8VXG7	SCAF11	0.0594807	7.72106	0.994902	3.30E-22
Q12906;G5E9M5;Q12906-4;C	ILF3	0.0594673	8.65105	0.994877	2.06E-85
Q9Y2X3	NOP58	0.0578747	7.91454	0.991883	1.82E-43
Q07065	CKAP4	0.0561848	7.23358	0.988707	6.81E-25
P52272;P52272-2	HNRNPM	0.0553627	9.66049	0.987162	1.01E-296
Q9Y520;Q9Y520-4;E7EPN9;Q	PRRC2C	0.0542965	8.58763	0.985158	1.60E-157
Q9UNX4	WDR3	0.052269	7.9059	0.981348	7.35E-45
P52597	HNRNPF	0.0518169	8.50058	0.980498	7.03E-109
P62979	RPS27A	0.0489655	8.49365	0.97514	4.03E-87
Q92922	SMARCC1	0.0488758	7.15585	0.974972	2.36E-20
Q02543;M0R117;B4DM74;M	RPL18A	0.0487595	8.62218	0.974753	5.90E-47
P25398	RPS12	0.047781	9.16107	0.972915	2.69E-66
P09874	PARP1	0.0466347	10.755	0.970762	0

Q6P2Q9	PRPF8	0.0464897	8.78405	0.97049	9.26E-263
Q15233;Q15233-2;H7C367;C9	NONO	0.0431519	10.6722	0.964221	0
P05198;H0YJS4;G3V4T5	EIF2S1	0.0426369	7.95812	0.963254	2.90E-35
Q6WCQ1;Q6WCQ1-2;Q6WCC	MPRIP	0.0415668	8.54296	0.961245	2.21E-161
Q00325-2;F8VVM2;Q00325;F	SLC25A3	0.0411701	8.14255	0.9605	4.25E-48
P28288;P28288-2;F5GYC1;E7	ABCD3	0.0405331	7.92822	0.959304	3.24E-57
Q9NX58	LYAR	0.0354023	8.8631	0.949675	9.57E-240
Q14527;Q14527-2	HLTF	0.0345421	9.23358	0.948062	0
P57678;I3L2C7;I3L399	GEMIN4	0.0302677	7.61402	0.940047	6.47E-13
O75533	SF3B1	0.0256634	8.28178	0.93142	5.10E-43
Q9NPE3	NOP10	0.0252628	7.31698	0.93067	7.53E-13
P62244;I3L3P7;I3L246;H3BN9	RPS15A	0.0186806	8.67492	0.918353	3.04E-37
Q7Z2W4;Q7Z2W4-2;C9J6P4;C	ZC3HAV1	0.0178967	8.16382	0.916888	6.58E-143
P61353;K7EQQ9;K7ELC7	RPL27	0.0151291	8.41943	0.911716	2.05E-13
Q15853;M0QXT0;Q6YI47;Q15	USF2	0.014782	7.793	0.911067	5.29E-38
Q9Y5S9;Q9Y5S9-2	RBM8A	0.00665092	7.39903	0.895895	1.02E-06
P11021	HSPA5	0.00396538	8.15177	0.890893	7.67E-138
Q9ULV3;Q9ULV3-5;Q5SYW2;I	CIZ1	0.0039196	7.7831	0.890807	1.04E-88
Q99567;J3KMX1	NUP88	-0.00165558	7.64162	0.880436	2.41E-19
P11940;P11940-2;E7EQV3;E7	PABPC1;PABPC3	-0.00519943	9.74765	0.873853	0
P56537;B7ZBG9;B7ZBH1	EIF6	-0.00571442	7.47292	0.872898	1.44E-34
Q86VM9;E7ERS3;Q86VM9-2	ZC3H18	-0.00703049	7.43008	0.870456	1.26E-13
O00425	IGF2BP3	-0.00764275	8.73389	0.86932	8.49E-152
P08670;B0YJC4;B0YJC5	VIM	-0.00876236	10.0489	0.867245	0
P62158;H0Y7A7;E7ETZ0;E7EM	CALM1;CALM2;CALI	-0.00945473	8.59279	0.865961	2.65E-69
Q15366;Q15366-4;Q15366-5;	PCBP2;PCBP3	-0.0100327	8.21574	0.864891	3.33E-38
P61513;C9J4Z3;M0R0A1;Q6P	RPL37A	-0.0104485	8.23596	0.86412	1.81E-48
P06748;P06748-2;P06748-3	NPM1	-0.0134144	9.98672	0.85863	0
Q09666	AHNAK	-0.0138664	7.74844	0.857793	2.90E-17
Q8NCA5;Q8NCA5-2;E9PH82	FAM98A	-0.0144463	8.50705	0.856721	3.43E-96
O00571;O00571-2;O15523;B4	DDX3X;DDX3Y	-0.0177288	9.06153	0.850655	6.30E-202
P14868;Q68CR9;H7BZ35	DARS;DKFZp781B11	-0.0195847	6.85275	0.847229	8.51E-05
P62910;D3YTB1;F8W727	RPL32	-0.0222416	8.76834	0.84233	1.26E-59
P60866;P60866-2;E5RJX2	RPS20	-0.0243778	8.63012	0.838395	3.87E-25
Q8TAQ2;Q8TAQ2-2;Q8TAQ2-	SMARCC2	-0.0305061	7.22199	0.82713	1.56E-34
Q9NSU2;Q9NSU2-2;Q9NSU2-	TREX1	-0.0317059	8.46739	0.824928	2.96E-41
P11142;E9PKE3;P11142-2;E9I	HSPA8	-0.0321732	9.23882	0.824071	3.83E-233
P35580;P35580-2;F8W6L6;P3	MYH10	-0.0327816	7.25909	0.822956	1.36E-45
Q9NUW8;H0YJ44;Q86TV8;G3	TDP1	-0.0335865	7.27353	0.82148	5.58E-07
Q9P0K7;Q9P0K7-4;Q9P0K7-3;	RAI14	-0.0351639	8.52736	0.818591	3.45E-253
Q9NVI7-2;Q9NVI7;Q9NVI7-3;	ATAD3A;ATAD3B	-0.0381145	8.2675	0.813193	1.89E-62
P48634	PRRC2A	-0.0387516	8.29203	0.812029	1.45E-29
P51114;B4DXZ6;P51114-3;P5	FXR1	-0.042942	9.16524	0.804381	4.43E-231
Q9H7E2;Q9H7E2-2;Q9H7E2-3	TDRD3	-0.0434303	7.69075	0.803491	1.37E-30
Q14676;Q14676-2;E9PGY5;F8	MDC1	-0.0492439	9.02987	0.792915	1.29E-186
O95831;O95831-3;Q1L6K4;O9	AIFM1	-0.0519333	7.33254	0.788035	1.84E-15
P46782;M0R0F0;M0R0R2;M0	RPS5	-0.052454	8.43557	0.787091	1.79E-70
Q08211	DHX9	-0.0538826	8.74536	0.784503	0
Q9BUQ8	DDX23	-0.054409	8.51602	0.78355	1.10E-37
Q9BY77;F8WCX5	POLDIP3	-0.0547428	8.73361	0.782946	6.13E-91
Q07020;G3V203;J3QQ67;F8V	RPL18	-0.0549259	8.90166	0.782614	1.23E-102
Q13428-3;Q13428-8;Q13428;	TCOF1	-0.05546	8.68511	0.781648	1.34E-153
P19447;G3V1S1	ERCC3	-0.0574131	7.33516	0.778118	4.96E-40
Q9NR30;Q9NR30-2	DDX21	-0.061367	8.93759	0.770984	1.34E-250
P04792;C9J3N8;F8WE04	HSPB1	-0.0629978	7.18264	0.768048	1.25E-11
P46013	MKI67	-0.0646324	9.84085	0.765108	0
P78527;E7EUY0;P78527-2	PRKDC	-0.0648079	9.92154	0.764792	0
Q7Z739	YTHDF3	-0.0670528	8.03858	0.76076	8.20E-48
Q6PJG2;F6RU81;H7C1L3	ELMSAN1	-0.0683537	7.61157	0.758427	1.06E-12
Q12965	MYO1E	-0.0686798	8.08361	0.757842	4.07E-253
Q9UKF6;G5E9W3	CPSF3	-0.0695648	7.60694	0.756256	1.07E-28
P11387	TOP1	-0.0704994	9.17551	0.754583	0
Q14966;Q14966-3;Q14966-4;	ZNF638	-0.0722389	8.57959	0.751471	2.29E-135
P20042	EIF2S2	-0.0740585	8.01427	0.74822	1.03E-62
Q96K37	SLC35E1	-0.0768394	6.8761	0.743261	2.24E-59
P04003	C4BPA	-0.0769367	8.41631	0.743087	4.73E-76
Q15393;Q15393-3	SF3B3	-0.0773392	8.6151	0.742371	1.01E-172
O15160;O15160-2;E7EQB9	POLR1C	-0.0803356	8.41358	0.737041	7.95E-99
O43660;O43660-2;A8MW61;	PLRG1	-0.0808239	7.71278	0.736173	4.19E-151
P67809;H0Y449	YBX1	-0.0809517	9.24721	0.735946	0
P61313;E7EQV9;E7ENU7;E7E	RPL15	-0.081337	8.48712	0.735262	2.11E-27
O43684;J3QSX4;J3QT28;O43	BUB3	-0.0817242	6.80154	0.734575	9.02E-13
Q6ZNL6;Q6ZNL6-2;B7ZM68	FGD5	-0.0869541	7.09552	0.725313	1.19E-11
Q3B726	TWISTNB	-0.0888691	7.87126	0.721932	1.85E-28

P17480;P17480-2;E9PKP7	UBTF	-0.0894222	8.44323	0.720956	7.90E-58
P62873;F6X3N5;F6UT28;B1AI	GNB1	-0.0917931	7.98353	0.716779	4.08E-56
Q13748;P68363;Q9BQE3;Q71	TUBA3C;TUBA1B;TU	-0.0920715	7.33941	0.716289	5.82E-15
P80723;P80723-2	BASP1	-0.0965748	8.35744	0.708381	2.91E-27
P83111	LACTB	-0.096735	8.4675	0.7081	2.32E-39
Q9NZB2;Q9NZB2-6;Q9NZB2-4	FAM120A	-0.0976582	8.63703	0.706483	2.16E-160
Q13283;F5H4D6	G3BP1	-0.102713	9.71117	0.697652	0
B7Z528	OXCT1	-0.103268	6.87098	0.696685	0.0027403
P62241;Q5JR95	RPS8	-0.105549	9.27207	0.692715	1.43E-166
Q14157;Q14157-5;Q14157-1;	UBAP2L	-0.109388	9.45944	0.686052	0
P13987;E9PNW4;E9PR17	CD59	-0.112392	8.14355	0.680856	5.72E-21
B0LM41	RBM14	-0.113853	6.99549	0.678334	2.45E-82
P16403	HIST1H1C	-0.114077	9.56764	0.677949	8.54E-40
Q9NX24;D6RC52;D6RCB9;J3C	NHP2	-0.114712	7.94793	0.676854	4.78E-49
P35579;P35579-2	MYH9	-0.114908	9.31262	0.676516	0
Q13151	HNRNPA0	-0.125877	8.32672	0.657719	5.55E-291
Q02880;Q02880-2;E9PCY5	TOP2B	-0.126076	8.26014	0.657381	4.29E-219
J3KNL6;O15027;O15027-2;O1	SEC16A	-0.12641	7.85772	0.656813	2.05E-43
P18887;F5H8D7	XRCC1	-0.127014	8.92784	0.655784	2.33E-133
P26196	DDX6	-0.12801	8.71999	0.65409	4.30E-210
Q92769;B3KRS5;J3KPW7;Q5T	HDAC2;HDAC1	-0.129194	7.75967	0.652077	7.30E-41
O00712;Q5VW26;O00712-4;(	NFIB	-0.136538	7.01511	0.639658	0.00044761
Q8IWR0;I3L2K5	ZC3H7A	-0.148787	7.59814	0.619165	4.93E-11
Q15269	PWP2	-0.149578	8.00664	0.61785	1.46E-40
P46778	RPL21	-0.150417	8.5814	0.616458	5.77E-32
Q9BUJ2;Q9BUJ2-4;B7Z4B8;Q!	HNRNPUL1	-0.151363	8.82712	0.61489	3.85E-228
Q6ZRS2;Q6ZRS2-3;Q6ZRS2-2	SRCAP	-0.152876	7.31938	0.612388	5.42E-36
P08754	GNAI3	-0.155573	8.0103	0.607936	1.62E-32
P62899;H7C2W9;C9JU56;B7Z	RPL31	-0.15625	8.29677	0.606821	9.70E-65
Q6I9Y2	THOC7	-0.159821	6.98002	0.600954	2.85E-14
P15328	FOLR1	-0.162378	7.96019	0.596768	5.54E-36
P30876;C9J4M6;C9J2Y9	POLR2B	-0.162685	7.4452	0.596266	5.68E-06
Q53GS9;B9A018;Q53GS9-2;B	USP39	-0.164299	8.1401	0.593633	3.46E-53
P61247;D6RG13;D6RAT0;D6R	RPS3A	-0.170574	9.22162	0.583443	2.54E-95
Q9NZI7;Q9NZI7-4	UBP1	-0.172735	7.25964	0.579953	4.39E-84
P05388;Q3B7A4;F8VWS0;F8V	RPLP0;RPLP0P6	-0.173521	8.95461	0.578686	1.82E-116
Q15717;B4DVB8;M0QZR9	ELAVL1	-0.175222	8.86477	0.575948	7.41E-96
P27635;F8W7C6	RPL10	-0.176561	9.1247	0.573798	1.66E-67
P62861;E9PR30	FAU	-0.177057	8.256	0.573002	3.22E-09
Q9BYW2;H7BZ93;Q9BYW2-3;	SETD2	-0.177362	7.11544	0.572513	5.98E-12
Q9ULW0;Q96RR5	TPX2;HCA90	-0.177364	7.29829	0.57251	1.27E-07
P49916;P49916-2	LIG3	-0.178734	9.4098	0.570317	0
Q8N556;Q8N556-2	AFAP1	-0.178814	7.62006	0.570188	1.04E-05
P55769;B1AHD1	NHP2L1	-0.181055	7.61067	0.566608	5.03E-15
P98179	RBM3	-0.183367	7.88277	0.562927	5.39E-93
Q9Y3B4	SF3B14	-0.191835	7.66322	0.549539	5.54E-28
Q8WYQ5;Q8WYQ5-3	DGCR8	-0.195053	7.37229	0.544494	2.03E-17
Q99459	CDC5L	-0.198042	8.05146	0.539829	6.69E-79
Q16666;Q16666-3;Q16666-2;	IFI16	-0.202715	8.97765	0.532574	9.38E-215
Q96HS1;Q96HS1-2	PGAM5	-0.2075	8.21354	0.525197	2.23E-16
Q9H2U1;Q9H2U1-3;Q9H2U1-	DHX36	-0.207857	8.05227	0.524649	2.25E-65
Q9NXV6;J3KNE1;D6RGD2	CDKN2AIP	-0.217472	6.98169	0.509994	2.06E-10
P47756-2;P47756;B1AK87;B1	CAPZB	-0.220743	7.78743	0.505058	4.63E-73
P09429;Q5T7C4;Q5T7C6	HMGB1	-0.22769	8.14023	0.494659	3.65E-09
Q92499	DDX1	-0.230127	8.67259	0.491037	9.70E-201
P62140;E7ETD8	PPP1CB	-0.243975	7.88633	0.470736	1.36E-282
Q9HCE1;Q9HCE1-2;Q5JR04	MOV10	-0.244495	8.5203	0.469981	9.81E-210
P18621;J3QQT2;J3KRX5;J3QL	RPL17	-0.245401	8.91403	0.468671	2.88E-120
Q9UBB4;B1AHE4;Q9UBB4-2	ATXN10	-0.246483	7.32942	0.467109	1.12E-17
P63261;I3L3I4;I3L3I0;I3L1U9;	ACTG1	-0.247959	10.6568	0.464981	0
P55795	HNRNPH2	-0.254293	7.78873	0.455914	4.67E-170
O00159;O00159-3;O00159-2;	MYO1C	-0.254814	8.88414	0.455173	1.95E-161
Q9NYF8;Q9NYF8-2;Q9NYF8-4	BCLAF1	-0.255535	7.65224	0.454148	1.03E-17
P62314;J3QLR7;J3QLI9	SNRPD1	-0.262848	7.93169	0.443828	5.59E-10
P16070;H0YD13;H0Y2P0;P16(	CD44	-0.264906	7.13168	0.440948	2.67E-14
Q14498;Q14498-2;G3XAC6;Q	RBM39	-0.270658	8.25943	0.432955	1.53E-41
P0C0S5;Q71UI9;Q71UI9-3;Q7	H2AFZ;H2AFV	-0.271925	7.28753	0.431206	2.62E-15
Q9P2E9;Q9P2E9-3;Q9P2E9-2;	RRBP1	-0.272984	7.42305	0.429748	1.38E-104
P62847;P62847-2;E7ETK0;P6;	RPS24	-0.275093	8.63363	0.426851	1.73E-19
Q12800;Q12800-4;Q12800-2;	TFCP2	-0.275198	7.8566	0.426707	6.33E-120
Q9BYJ9;F8W840	YTHDF1	-0.276304	7.57104	0.425192	4.26E-44
Q9HC52	CBX8	-0.277943	7.25537	0.422955	1.18E-45
Q01780;K7EJ37;B4DKG8;Q01	EXOSC10	-0.27932	6.63035	0.421079	2.70E-08
Q07666;Q07666-3;Q07666-2	KHDRBS1	-0.288322	9.41642	0.408941	0

P35251;P35251-2	RFC1	-0.293398	9.17765	0.40219	0
P29558;E7ETU5;P29558-2;B4	RBMS1	-0.298227	7.07933	0.395829	1.85E-07
P26368;K7ENG2;P26368-2	U2AF2	-0.301346	8.03922	0.391754	1.35E-17
P07437;P68371;Q9BVA1;Q13	TUBB;TUBB4B;TUBB	-0.303621	7.6997	0.388797	3.25E-50
Q14671;Q14671-2;E9PR38;E7	PUM1	-0.304758	7.39988	0.387325	2.14E-83
O75955;B0V114;B0V113;B0V	FLOT1	-0.30912	6.94345	0.381707	0.0017357
P0CG12	CHTF8	-0.310194	6.93514	0.380332	2.67E-06
P14373;P14373-2;B0V297	TRIM27	-0.311323	7.84184	0.378889	4.96E-112
Q6PKG0;Q6PKG0-3;E5RH50	LARP1	-0.3127	8.69691	0.377134	3.82E-209
Q53F19;Q53F19-2	C17orf85	-0.315987	6.8912	0.372966	6.26E-05
E7EWI9;P51991-2;P51991	HNRNPA3	-0.319412	9.04116	0.368652	8.31E-81
Q92522	H1FX	-0.32218	7.91399	0.365189	1.61E-29
P19388	POLR2E	-0.326668	8.01448	0.359617	7.03E-25
Q9BYG3;H7BZL0;C9J808	MKI67IP	-0.330755	6.64975	0.354589	1.90E-08
Q14134;Q14134-2	TRIM29	-0.331141	7.51048	0.354118	2.74E-33
Q9Y4B5	SOGA2	-0.331974	6.77408	0.353099	0.00091911
O95602;B9ZVN9	POLR1A	-0.341448	8.74017	0.341648	2.19E-274
O43395;E7EVD1;B4DSY9	PRPF3	-0.343044	7.24711	0.339742	1.08E-07
Q08945;E9PPZ7;E9PMD4	SSRP1	-0.351658	7.23467	0.329577	4.11E-32
Q8IYH5;Q8IYH5-2;Q8IYH5-4	ZZZ3	-0.35498	7.31088	0.325708	6.95E-11
Q86V81;E9PB61	ALYREF	-0.360435	8.94832	0.319422	2.61E-94
Q12926;Q12926-2;B1AM49;B	ELAVL2	-0.360525	7.51843	0.31932	6.08E-24
P35659;P35659-2;B4DFG0;D6	DEK	-0.362284	7.90283	0.317311	1.09E-18
P40938;P40938-2	RFC3	-0.362885	8.72013	0.316626	5.84E-133
Q04637;Q04637-3;Q04637-5;	EIF4G1	-0.364193	8.16917	0.315139	1.92E-80
P35268;K7EJT5;K7EP65;K7EK	RPL22	-0.370163	9.03619	0.308411	5.04E-55
O75475-2;O75475-3;O75475	PSIP1	-0.370188	7.45492	0.308383	3.56E-29
Q9P2I0	CPSF2	-0.37672	7.51037	0.301131	3.92E-15
Q99729-3;D6R9P3;D6RD18;D	HNRNPAB	-0.377621	8.00604	0.300141	7.15E-29
Q96C19;H0Y4Y4	EFHD2	-0.378107	7.57888	0.299607	2.07E-14
Q9Y5B9	SUPT16H	-0.38633	7.77098	0.290672	1.37E-23
O15446;O15446-2	CD3EAP	-0.390999	8.33742	0.285679	7.25E-143
Q96I25;Q5W011;Q5W010;H0	RBM17	-0.397406	7.9602	0.278923	3.40E-48
Q9BQG0;Q9BQG0-2;I3L1L3	MYBBP1A	-0.404476	8.02251	0.271594	7.99E-36
Q02241;Q02241-2;B4E1K0;H7	KIF23	-0.404785	8.08174	0.271277	2.49E-69
P15880;H0YEN5;E9PQD7	RPS2	-0.406464	8.64897	0.269558	4.43E-58
P55265;P55265-5;P55265-3;I	ADAR	-0.412613	7.56929	0.263325	5.23E-32
Q96EY1;Q96EY1-2	DNAJA3	-0.427204	7.55058	0.248934	2.27E-10
Q9UPQ9-1;H0Y720;Q9UPQ9;I	TNRC6B	-0.435982	6.8849	0.240547	2.83E-10
Q5M775;Q5M775-5;Q5M775	SPECC1	-0.440422	7.17629	0.236381	7.96E-21
P09651;P09651-3;F8VXY0;F8	HNRNPA1;HNRNPA1	-0.440655	9.36006	0.236164	4.15E-228
P35250;P35250-2;H7C5P4	RFC2	-0.448225	8.76967	0.229184	9.50E-152
Q09028;Q09028-3;H0YF10;Q	RBBP4	-0.455431	7.81423	0.222677	1.11E-21
P68104;Q5VTE0	EEF1A1;EEF1A1P5	-0.456152	7.69588	0.222033	4.38E-15
P14866;M0QXS5;P14866-2	HNRNPL	-0.460104	9.11291	0.218529	3.25E-151
Q9BZE4;B4DY13;B7Z7A3;Q5T	GTPBP4	-0.465698	7.05223	0.213636	0.00013378
P52948;P52948-2;P52948-4;F	NUP98	-0.478352	7.37745	0.202863	1.48E-13
P57088;H0Y8N0;D6RAA6	TMEM33	-0.481468	6.8535	0.200271	0.0010199
P05386	RPLP1	-0.481787	8.76687	0.200007	9.74E-21
Q9P1U0	ZNRD1	-0.484739	7.76439	0.197577	1.86E-15
Q9Y3A4;Q9NSQ0	RRP7A;RRP7B	-0.495743	7.55315	0.188709	1.22E-06
Q00610;Q00610-2	CLTC	-0.498909	8.16289	0.186212	3.82E-52
Q14126	DSG2	-0.51092	7.21656	0.176964	1.24E-84
P60709	ACTB	-0.519735	8.85371	0.170396	0
O43795;O43795-2;E9PDF6	MYO1B	-0.523024	7.96267	0.167994	9.67E-139
Q69YQ0;C9JLY8;C9J8U1;F8W	SPECC1L	-0.5256	7.05645	0.166129	3.87E-18
P11388;P11388-2;P11388-3;F	TOP2A	-0.529716	8.73766	0.163183	3.61E-262
O14979;O14979-3;O14979-2	HNRPDL	-0.536139	8.66253	0.158665	1.46E-79
Q8NE71;Q8NE71-2;H0YGW7;	ABCF1	-0.552801	7.96141	0.147385	6.92E-57
P78549;H3BPD5;H3BRL9	NTHL1	-0.554813	8.02313	0.146066	2.86E-158
P05114;A6NL93;A6NEL0	HMGN1	-0.565031	7.38571	0.139504	2.32E-05
P62879;C9JZN1;C9JIS1;C9JXA	GNB2	-0.567591	8.36728	0.137896	1.06E-104
P35249;C9JZI1;C9J8M3;C9JTT	RFC4	-0.567688	8.6204	0.137835	4.58E-65
P31689;B7Z5C0	DNAJA1	-0.575098	6.99569	0.133263	0.0014722
H7BY36	EWSR1	-0.586666	7.51014	0.126361	1.02E-66
Q96T60;M0R3C8;M0QYH2	PNKP	-0.599939	7.72843	0.118788	6.59E-18
P31942;P31942-2;P31942-3;F	HNRNPH3	-0.601896	7.18817	0.117703	2.14E-41
Q01085;P31483;C9JTN7;P314	TIAL1;TIA1	-0.609638	7.68207	0.113483	6.65E-22
Q86XZ4;F8VS10	SPATS2	-0.641024	7.4927	0.0975868	3.74E-19
Q562R1	ACTBL2	-0.64603	9.86282	0.095224	2.28E-40
O76021;J3QSV6;B4DJ58;I3L3	RSL1D1	-0.669418	7.97792	0.0847872	1.84E-88
Q13813;Q13813-3;Q13813-2;	SPTAN1	-0.671131	7.74297	0.0840607	1.05E-67
P40937;P40937-2;F8W9B4	RFC5	-0.69076	8.94028	0.07609	1.21E-159
Q8WYP5;Q8WYP5-2;Q8WYP5	AHCTF1	-0.694029	7.29946	0.0748244	2.82E-12

Q96J01;Q6NZ53	THOC3	-0.696838	7.31074	0.0737505		1.79E-08
Q9NW13;Q9NW13-2;H7C5G8	RBM28	-0.703159	6.91368	0.0713805		1.06E-07
P68133;P68032;P63267;P627	ACTA1;ACTC1;ACTG	-0.706818	9.62143	0.0700376		2.37E-125
P12236;I7HJJ0;P12235	SLC25A6;SLC25A4	-0.714664	7.43629	0.067227		2.04E-18
P62829;C9JD32;J3KT29;B9ZVI	RPL23	-0.721087	8.39834	0.0649964		3.95E-18
P05387;H0YDD8	RPLP2	-0.737457	9.12011	0.0595853		7.04E-113
Q13547;F5GXM1	HDAC1	-0.737635	7.28767	0.0595288		2.64E-22
P36873;F8VYE8;P36873-2;F8\	PPP1CC	-0.741373	8.76973	0.0583479		0
O15042;O15042-2;E7ET15;E7	U2SURP	-0.745697	7.95298	0.0570064		4.96E-32
P62995;P62995-3;H7BXF3	TRA2B	-0.748755	7.33222	0.0560735		6.51E-11
Q9H9Y6;F5GZX4;Q9H9Y6-2;F8	POLR1B	-0.808977	8.2858	0.0401367		0
P05423	POLR3D	-0.874744	7.36622	0.0272947		3.83E-38
Q16576;Q16576-2;E9PC52	RBBP7	-0.884354	7.402	0.0257531		1.63E-18
P48651;B4DE85;Q9BUQ5	PTDSS1	-0.895245	7.09072	0.0240975		9.99E-05
P14923	JUP	-0.896725	8.32942	0.0238797		1.69E-43
Q9H147;F2Z2A4;H0Y501;H7C	DNTTIP1	-0.971867	7.61113	0.0148473		8.87E-15
P41208	CETN2	-0.972036	7.08189	0.0148309		7.07E-28
Q86SQ0;E9PFQ4;Q86SQ0-2;C	PHLDB2	-0.982718	7.51929	0.0138302		1.09E-08
Q9H7E9;Q9H7E9-2	C8orf33	-0.994509	6.81773	0.0127951		5.80E-05
O96019;O96019-2	ACTL6A	-1.02626	8.21746	0.0103408		9.37E-61
P62266;D6RD47	RPS23	-1.04869	8.48353	0.00886866		1.36E-06
P62857	RPS28	-1.05265	8.46494	0.00862946		1.32E-21
O95758;O95758-2;O95758-1;	PTBP3	-1.09749	7.49541	0.0062947		4.69E-14
Q9BQ67;M0QX71	GRWD1	-1.11764	7.11826	0.00544443		3.44E-24
P61964	WDR5	-1.23595	7.44069	0.00222659		4.12E-32
Q5BKZ1	ZNF326	-1.24042	7.68195	0.0021496		1.23E-16
Q13595;Q13595-2;B4DQI6;B4	TRA2A	-1.33897	7.6736	0.000963717	+	2.01E-07
Q5UIP0;Q5UIP0-2	RIF1	-1.43764	8.21429	0.000410315	+	9.03E-110
Q12797;F5H667	ASPH	-1.45142	7.38792	0.000362696	+	3.69E-16
Q9Y265;E7ETR0;Q9Y265-2	RUVBL1	-1.46051	8.47016	0.000334197	+	2.20E-122
Q9UG63;Q75MJ1	ABCF2	-1.47673	7.64296	0.000288457	+	4.07E-31
Q86UP2;Q86UP2-2;Q86UP2-3	KTN1	-1.62863	7.41275	6.80E-05	+	1.92E-82
Q9UQ80;F8VTY8;F8VR77;F8V	PA2G4	-2.04324	7.82237	7.05E-07	+	2.87E-21
P42167;P42167-2;G5E972;P4	TMPO	-2.07827	7.58103	4.59E-07	+	2.33E-32
Q7Z7G8;Q7Z7G8-4;Q7Z7G8-3	VPS13B	-2.68929	8.38824	9.05E-11	+	0.0032301

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