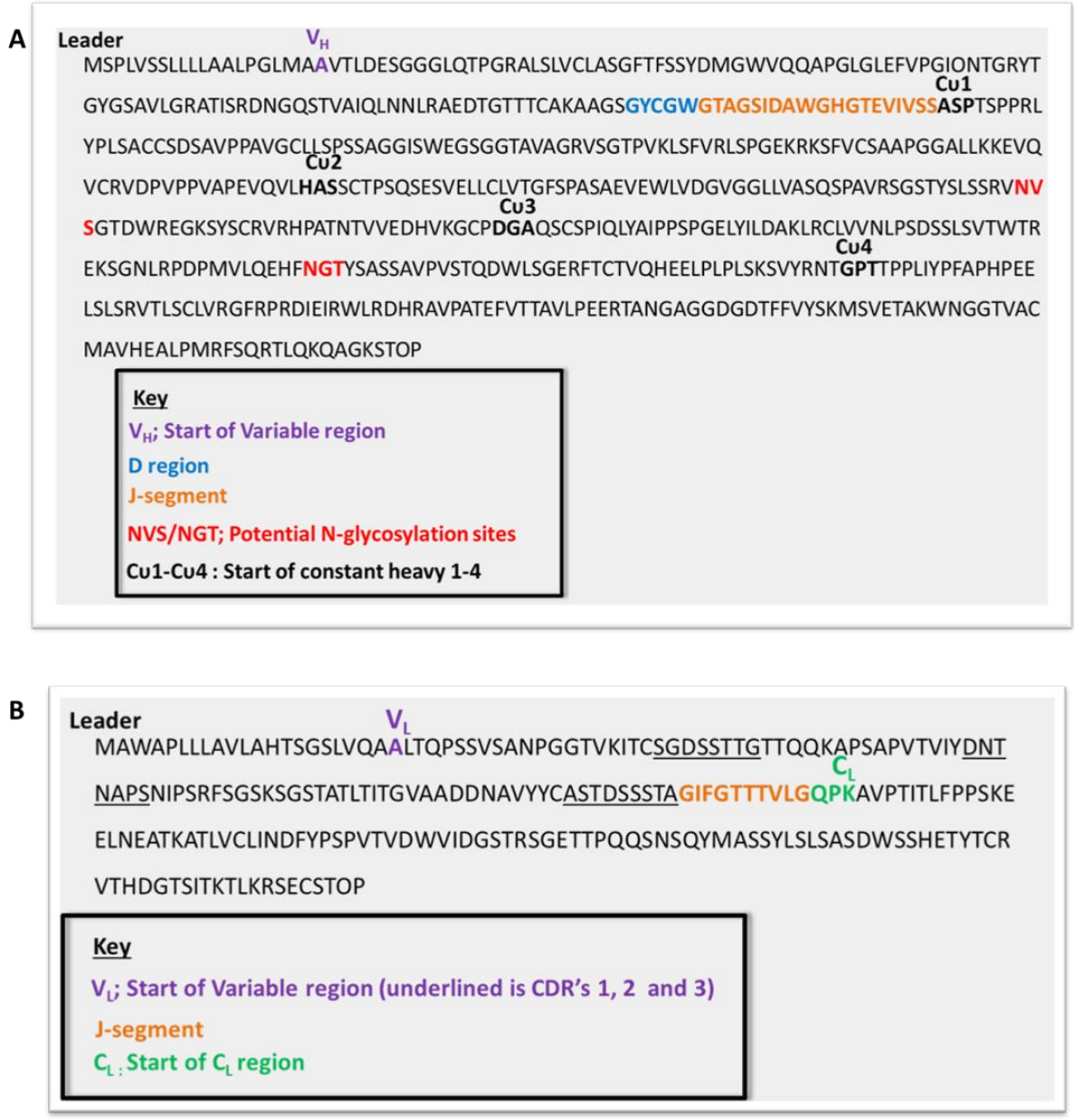



Fig 1. Full IgY Sequence: (A) The complete amino acid sequence of IgY upsilon heavy chain including leader sequence and rearranged VDJ sequences and (B) The amino acid sequence chicken λ light chain. Numbering for chicken IgY heavy chain is based on the deduced amino acid sequences from cDNA, starting from the first alanine in the VH region [42,43] Numbering for chicken light chain immunoglobulin is derived from the nucleotide sequence from recombinant cDNA plasmids constructed from chicken spleen poly(A)-containing RNA [43].

**Supplementary Information: Generation of IgY model:**

| | |
|---|---|
| Avian IgY | AVTLDESGGGLQTPGRALSLVCLASGFTFSSYDMGWVQQAPGLGLEFVPGIONTGR |
| | YTGYGSAVLGRATISRDNGQSTVAIQLNNLRAEDTGTTTCAKAAGSGYCGWGTAGS |
| | IDAWGHGTEVIVSSASPTSPPRLYPLSACCSDSAVPPAVGCLLSPSSAGGISWEGS |
| | GGTAVAGRVSGTPVKLSFVRLSPGEKRKSFVCSAAPGGALLKKEVQVCRVDPVPPV |
| hIgE | DF |
| | APEVQVLHASSCT--PSQSESVELLCLVTGFSPASAEVEWLVDGVGGLLVASQSPA |
| | TPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTAST |
| | VRSGSTYSLSSRVNVSGTDWREGKSYSCRVRHPATNTVVEDHVKGCPDGAQSCS*PI* |
| | TQEGELASTQSELTLSQKHWLSDRTYTCQVTYQGH--TFEDSTKKCADS--NPRGV |
| | *QLYAIPPSPGELYISLDAKLRCLVVNL-PSDSSLSVTWTREKSGNLRPDPMVLQEH* |
| | SAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQ |
| | *FNGTYSASSAVPVSTQDWLSGERFTCTVQHEELPLPLSKSVYRNTGPTTPPLIYPF* |
| | RNGTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAF |
| | *APHPEELSLSRVTLSCLVRGFRPRDIEIRWLRDHRAVPATEFVTTAVLPEERTANG* |
| | ATPEWPGSRDKRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTK----G |
| | *DGDTFFVYSKMSVETAKW-NGGTVACMAVHEAL-PMRFSQRTLQKQAGK* |
| | SG--FFVFSRLEVTRAEWEQKDEFICRAVHEAASPSQTVQRAVSVNPG |

Avian IgY Sequence (Supplementary Figure 1): The section in italics corresponds to the sequence from the crystal structure 2w59.pdb- The crystal structure of avian IgY-Fc-3-4 Fragment.

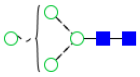
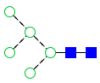
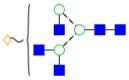
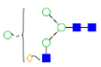
hIgE – Sequence from the crystal structure 1o0v.pdb - The crystal structure of human IgE Fc.

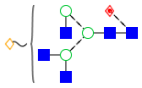
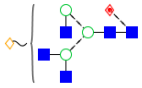
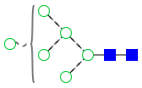
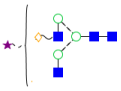
The sequence alignment for the region PVAPEVQV … PDGAQSCS of IgY to hIgE was based on the Clustal alignment of the two sequences.

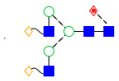
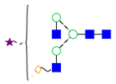
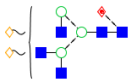
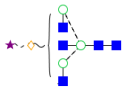
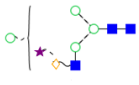
The sequence alignment for the region PIQLYAIP … RTLQKQAG of IgY to hIgE was performed by alignment of the three-dimensional structures (2w59 and 1o0v) in pymol.

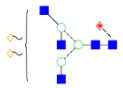
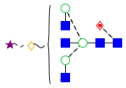
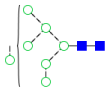
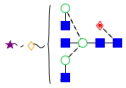
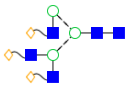
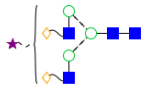
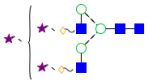
The homology model was generated using: (i) a hIgG Fab domain crystal structure (for the IgY light chain and the IgY heavy chain sequence AVTLDESG … LKKEVQVC) which was linked to; (ii) a random coil sequence RVDPVP (for the IgY heavy chain linker region between domains Cu1 and Cu2) which was linked to; (iii) the hIgE Fc crystal structure (for the IgY heavy chain sequence PVAPEVQV … RTLQKQAG).

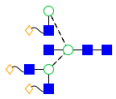
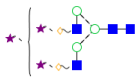
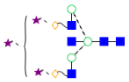
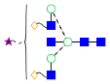
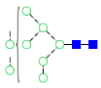
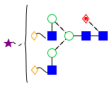
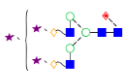
**Table 2: Summary of *N*-glycans identified from IgY purified form avian serum**

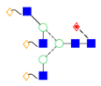
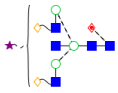
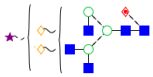
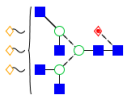
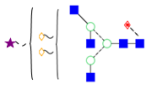
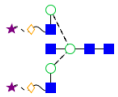
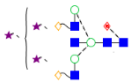
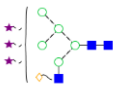
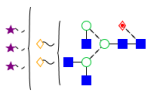
| Peak | Structure | | Peak area (%) | GU | Experimental mass (m/z) | Theoretical mass (m/z) | Ion Specie |
|---|---|---|---|---|---|---|---|
| 5 | M4 |  | 0.02 | 5.34 | --- | 1191.4421 | $[M-H]^-$ |
| 9 | M5 |  | 2.17 | 6.14 | 1353.514<br>676.2448 | 1353.4949<br>676.2438 | $[M-H]^-$<br>$[M-2H]^{-2}$ |
| | FA2B |  | | | 891.8257 | 891.8390 | $[M-2H]^{-2}$ |
| | FA3 |  | | | | | |
| | A2[6]G1 |  | | | 798.2899 | 798.2968 | $[M-2H]^{-2}$ |
| 10 | A2[3]G1 |  | 0.22 | 6.51 | 798.2899 | 798.2968 | $[M-2H]^{-2}$ |
| | A3G1 |  | | | 899.8270 | 899.8365 | $[M-2H]^{-2}$ |
| | A2BG1 |  | | | | | |
| 11 | M5A1 |  | 0.17 | 6.61 | 777.7769 | 777.7835 | $[M-2H]^{-2}$ |
| | M4A1G1 |  | | | | | |

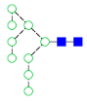
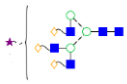
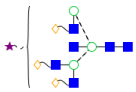
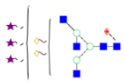
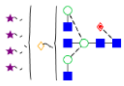
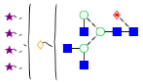
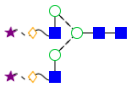
| Peak | Structure | | Peak area (%) | GU | Experimental mass (m/z) | Theoretical mass (m/z) | Ion Specie |
|---|---|---|---|---|---|---|---|
| 12 | FA3G1 |  | 2.26 | 6.90 | 972.8573 | 972.8654 | $[M-2H]^{-2}$ |
| | FA2BG1 |  | | | | | |
| 13 | FA3G1 |  | 1.22 | 7.04 | 972.8509 | 972.8654 | $[M-2H]^{-2}$ |
| | FA2BG1 |  | | | | | |
| 14 | M6 |  | 0.44 | 7.14 | 757.2596 | 757.2702 | $[M-2H]^{-2}$ |
| | A2G2 |  | | | 879.3184 | 879.3232 | $[M-2H]^{-2}$ |
| 15 | A2BG2 |  | 0.92 | 7.32 | 980.8661 | 980.8629 | $[M-2H]^{-2}$ |
| | A2[6]G1S1* |  | | | 943.8293 | 943.8445 | $[M-2H]^{-2}$ |

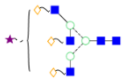
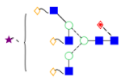
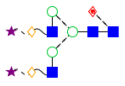
| Peak | Structure | | Peak area (%) | GU | Experimental mass (m/z) | Theoretical mass (m/z) | Ion Specie |
|---|---|---|---|---|---|---|---|
| 16 | FA2G2 |  | 0.59 | 7.52 | 952.3262 | 952.3521 | $[M-2H]^{-2}$ |
| | M5A1G1 |  | | | 858.7934 | 858.8099 | $[M-2H]^{-2}$ |
| | A2[3]G1S1* |  | | | 943.8293 | 943.8445 | $[M-2H]^{-2}$ |
| 17 | FA2BG2 |  | 5.14 | 7.69 | 1053.8828 | 1053.8918 | $[M-2H]^{-2}$ |
| | FA3G2 |  | | | | | |
| | A3G1S1* |  | | | --- | 1045.3842 | $[M-2H]^{-2}$ |
| | A2BG1S1* |  | | | --- | 1045.3842 | $[M-2H]^{-2}$ |
| | M4A1G1S1* |  | | | 923.3214 | 923.3312 | $[M-2H]^{-2}$ |

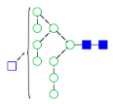
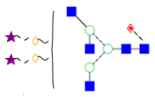
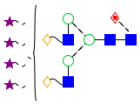
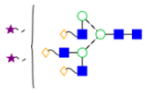
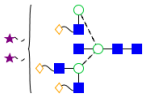
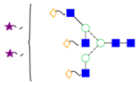
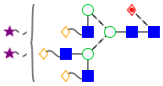
| Peak | Structure | | Peak area (%) | GU | Experimental mass (m/z) | Theoretical mass (m/z) | Ion Specie |
|---|---|---|---|---|---|---|---|
| 18 | FA3'G2 |  | 1.60 | 7.93 | 1053.8828 | 1053.8918 | $[M-2H]^{-2}$ |
| | FA2BG1S1* |  | | | 1118.4037 | 1118.4131 | $[M-2H]^{-2}$ |
| | FA3G1S1* |  | | | | | |
| 19 | M7 |  | 0.51 | 8.02 | 838.2908 | 838.2966 | $[M-2H]^{-2}$ |
| | FA2BG1S1* |  | | | 1118.4243 | 1118.4131 | $[M-2H]^{-2}$ |
| | FA3G1S1* |  | | | | | |
| 20 | A3G3 |  | 16.38 | 8.36 | --- | 1061.8893 | $[M-2H]^{-2}$ |
| | A2G2S1* |  | | | 1024.8506 | 1024.8709 | $[M-2H]^{-2}$ |
| | A2G2S3* |  | | | --- | 1315.9663 | $[M-2H]^{-2}$ |

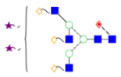
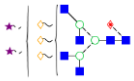
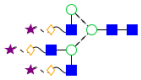
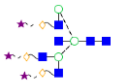
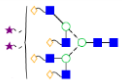
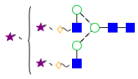
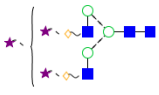
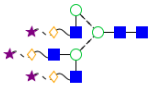
| Peak | Structure | | Peak area (%) | GU | Experimental mass (m/z) | Theoretical mass (m/z) | Ion Specie |
|---|---|---|---|---|---|---|---|
| 21 | A3BG3 |  | 0.65 | 8.51 | --- | 1163.4290 | $[M-2H]^{-2}$ |
| | A2G2S3* |  | | | --- | 1315.9663 | $[M-2H]^{-2}$ |
| | A2BG2S3* |  | | | --- | 1417.5060 | $[M-2H]^{-2}$ |
| 22 | FA3G3 |  | 2.12 | 8.64 | 1134.9095 | 1134.9182 | $[M-2H]^{-2}$ |
| | A2BG2S1* |  | | | 1126.4175 | 1126.4106 | $[M-2H]^{-2}$ |
| | A3’G3 |  | | | --- | 1061.8893 | $[M-2H]^{-2}$ |
| 23 | M8 |  | 4.00 | 8.78 | 919.3203 | 919.3230 | $[M-2H]^{-2}$ |
| | FA2G2S1* |  | | | 1097.8785 | 1097.8998 | $[M-2H]^{-2}$ |
| | M5A1G1S1* |  | | | 1004.3476 | 1004.3576 | $[M-2H]^{-2}$ |
| | FA2G2S3* |  | | | --- | 1388.9953 | $[M-2H]^{-2}$ |

| Peak | Structure | | Peak area (%) | GU | Experimental mass (m/z) | Theoretical mass (m/z) | Ion Specie |
|---|---|---|---|---|---|---|---|
| 24 | FA3’G3 |  | 8.68 | 9.00 | 1134.9095 | 1134.9182 | $[M-2H]^{-2}$ |
| | FA2BG2S1* |  | | | 1199.4524 | 1199.4395 | $[M-2H]^{-2}$ |
| | FA3G2S1* |  | | | | | |
| 25 | FA4G3 |  | 3.93 | 9.23 | --- | 1236.4579 | $[M-2H]^{-2}$ |
| | FA3’G2S1* |  | | | 1199.4240 | 1199.4395 | $[M-2H]^{-2}$ |
| | A2G2S2* |  | | | 1170.4113 | 1170.4186 | $[M-2H]^{-2}$ |
| | FA2BG2S3* |  | | | --- | 1490.5349<br>993.3542 | $[M-2H]^{-2}$<br>$[M-3H]^{-3}$ |
| | M5A1G1S3* |  | | | --- | 1295.4530<br>863.2996 | $[M-2H]^{-2}$<br>$[M-3H]^{-3}$ |
| | FA3G2S3* |  | | | --- | 1490.5349<br>993.3542 | $[M-2H]^{-2}$<br>$[M-3H]^{-3}$ |

| Peak | Structure | | Peak area (%) | GU | Experimental mass (m/z) | Theoretical mass (m/z) | Ion Specie |
|---|---|---|---|---|---|---|---|
| 26 | M9 |  | 5.11 | 9.51 | 1000.3368 | 1000.3495 | $[M-2H]^{-2}$ |
| | A3G3S1* |  | | | 1207.4227 | 1207.4370 | $[M-2H]^{-2}$ |
| 27 | A3BG3S1* |  | 24.92 | 9.65 | --- | 1308.9767 | $[M-2H]^{-2}$ |
| | FA3'G2S3* |  | | | --- | 1490.5349<br>993.3542 | $[M-2H]^{-2}$<br>$[M-3H]^{-3}$ |
| | FA2BG1S4* |  | | | --- | 1555.0562<br>1036.3684 | $[M-2H]^{-2}$<br>$[M-3H]^{-3}$ |
| | FA3G1S4* |  | | | --- | 1555.0562<br>1036.3684 | $[M-2H]^{-2}$<br>$[M-3H]^{-3}$ |
| | A2G2S2* |  | | | 1170.4043 | 1170.4186 | $[M-2H]^{-2}$ |

| Peak | Structure | | Peak area (%) | GU | Experimental mass (m/z) | Theoretical mass (m/z) | Ion Specie |
|---|---|---|---|---|---|---|---|
| 28 | FA3G3S1* |  | 0.67 | 9.82 | --- | 1280.4659 | $[M-2H]^{-2}$ |
| | A4G4 |  | | | 1244.4453 | 1244.4554 | $[M-2H]^{-2}$ |
| | A3'G3S1* |  | | | 1207.4299 | 1207.4370 | $[M-2H]^{-2}$ |
| | A2BG2S2* |  | | | --- | 1271.9583 | $[M-2H]^{-2}$ |
| | A4G4S4* |  | | | --- | 1826.6462<br>1217.4284 | $[M-2H]^{-2}$<br>$[M-3H]^{-3}$ |
| 29 | FA3'G3S1* |  | 0.24 | 9.90 | --- | 1280.4659 | $[M-2H]^{-2}$ |
| | FA2G2S2* |  | | | 1243.4315 | 1243.4476 | $[M-2H]^{-2}$ |
| 30 | FA4G4 |  | 1.19 | 10.06 | --- | 1317.4843 | $[M-2H]^{-2}$ |
| | FA2BG2S2* |  | | | 1344.9840 | 1344.9872 | $[M-2H]^{-2}$ |

| Peak | Structure | | Peak area (%) | GU | Experimental mass (m/z) | Theoretical mass (m/z) | Ion Specie |
|---|---|---|---|---|---|---|---|
| 31 | M9Glc |  | 10.11 | 10.24 | 1081.3684 | 1081.3759 | $[M-2H]^{-2}$ |
| | FA3'G2S2* |  | | | 1344.9840 | 1344.9872 | $[M-2H]^{-2}$ |
| | FA2G2S4* |  | | | --- | 1534.5430<br>1022.6929 | $[M-2H]^{-2}$<br>$[M-3H]^{-3}$ |
| | A3G3S2* |  | | | 1352.9702 | 1352.9847 | $[M-2H]^{-2}$ |
| 32 | A3BG3S2* |  | 0.97 | 10.67 | --- | 1454.5244 | $[M-2H]^{-2}$ |
| 33 | A3'G3S2* |  | 1.11 | 10.80 | 1352.9626 | 1352.9847 | $[M-2H]^{-2}$ |
| 34 | FA3G3S2* |  | 0.65 | 11.17 | --- | 1426.0137 | $[M-2H]^{-2}$ |
| | A3G3S3* |  | | | 1498.5284<br>998.6880 | 1498.5324<br>998.6858 | $[M-2H]^{-2}$<br>$[M-3H]^{-3}$ |

| Peak | Structure | | Peak area (%) | GU | Experimental mass (m/z) | Theoretical mass (m/z) | Ion Specie |
|---|---|---|---|---|---|---|---|
| 35 | FA3'G3S2* |  | 0.06 | 11.33 | --- | 1426.0137 | $[M-2H]^{-2}$ |
| | FA4G3S2* |  | | | --- | 1527.5533 | $[M-2H]^{-2}$ |
| | A3G3S3* |  | | | 1498.5126<br>998.6880 | 1498.5324<br>998.6858 | $[M-2H]^{-2}$<br>$[M-3H]^{-3}$ |
| | A3BG3S3* |  | | | --- | 1673.1010<br>1115.0649 | $[M-2H]^{-2}$<br>$[M-3H]^{-3}$ |
| 36 | A3G3S3* |  | 0.10 | 11.46 | 1498.5284<br>998.6880 | 1498.5324<br>998.6858 | $[M-2H]^{-2}$<br>$[M-3H]^{-3}$ |
| | A4G4S2* |  | | | 1535.5466 | 1535.5508 | $[M-2H]^{-2}$ |
| | A2G2S3* |  | | | --- | 1315.9663<br>876.9757 | $[M-2H]^{-2}$<br>$[M-3H]^{-3}$ |
| 37 | A2G2S3* |  | 2.81 | 11.59 | --- | 1315.9663<br>876.9757 | $[M-2H]^{-2}$<br>$[M-3H]^{-3}$ |
| | A3G3S3* |  | | | 1498.5284<br>998.6880 | 1498.5324<br>998.6858 | $[M-2H]^{-2}$<br>$[M-3H]^{-3}$ |

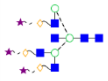
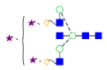
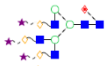
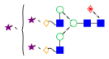
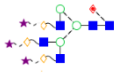
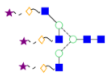
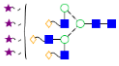
| Peak | Structure | | Peak area (%) | GU | Experimental mass (m/z) | Theoretical mass (m/z) | Ion Specie |
|---|---|---|---|---|---|---|---|
| 38 | A3'G3S3* |  | 0.13 | 11.92 | --- | 1498.5324<br>998.6858 | $[M-2H]^{-2}$<br>$[M-3H]^{-3}$ |
| | A3BG3S3* |  | | | --- | 1600.0721<br>1066.3790 | $[M-2H]^{-2}$<br>$[M-3H]^{-3}$ |
| | A2BG2S3* |  | | | --- | 1417.5060<br>944.6682 | $[M-2H]^{-2}$<br>$[M-3H]^{-3}$ |
| | FA3G3S3* |  | | | --- | 1571.5614<br>1047.3718 | $[M-2H]^{-2}$<br>$[M-3H]^{-3}$ |
| 39 | FA2G2S3* |  | 0.52 | 12.09 | --- | 1388.9953<br>925.6611 | $[M-2H]^{-2}$<br>$[M-3H]^{-3}$ |
| | FA3G3S3* |  | | | --- | 1571.5614<br>1047.3718 | $[M-2H]^{-2}$<br>$[M-3H]^{-3}$ |
| 40 | M5A1G1S3* |  | 0.10 | 12.66 | --- | 1295.4530<br>863.2996 | $[M-2H]^{-2}$<br>$[M-3H]^{-3}$ |
| | A3'G3S3* |  | | | 1498.5284<br>998.6880 | 1498.5324<br>998.6858 | $[M-2H]^{-2}$<br>$[M-3H]^{-3}$ |
| | A4G4S3* |  | | | --- | 1681.0985<br>1120.3966 | $[M-2H]^{-2}$<br>$[M-3H]^{-3}$ |
| | FA2BG2S3* |  | | | --- | 1490.5349<br>993.3542 | $[M-2H]^{-2}$<br>$[M-3H]^{-3}$ |
| | A3G3S4* |  | | | --- | 1644.0801<br>1095.7177 | $[M-2H]^{-2}$<br>$[M-3H]^{-3}$ |

Table of *N*-glycans released from IgY purified from serum. The HILIC-chromatogram was separated into 40 peaks and structural assignment carried made using established methods (Royle et al., 2008) and the software tool GlycoBase (https://glycobase.nibrt.ie). *Sialic acid linkages; WAX fractions were separated out into 5 fractions; S1: Monosialylated, S2: Disialylated, S3: Trisialylated, S3J: Trisialylated and S4: Tetrasialylated. All monosialylated glycans are linked by α2-3 and α2-6; Disialylated glycans have all combinations of α2-3 and α2-6 linkages [i.e. (3, 3), (3, 6) and (6, 6)]; Trisialylated glycans have all combinations of α2-3 and α2-6 linkages except (6, 6, 6) [i.e. (3, 3, 3), (3, 3, 6) and (3, 6, 6)]; and Tetrasialylated glycans have all combinations of α2-3 and α2-6 linkages [i.e. (3,3,3,3), (3,3,3,6) , (3,3,6,6) and (6,6,6,6)]. Structure abbreviations: all *N*-glycans have two core GlcNAcs; F at the start of the abbreviation indicates a core-fucose α1,6-linked to the inner GlcNAc; Mx, number (x) of mannose on core GlcNAcs; Ax, number of antenna (GlcNAc) on trimannosyl core; A2, biantennary with both GlcNAcs as β1,2-linked; A3, triantennary with a GlcNAc linked β1,2 to both mannose and the third GlcNAc linked β1,4 to the α1,3 linked mannose; A3' , isomer with the third GlcNAc linked β1-6 to the α1-6 linked mannose; A4, GlcNAcs linked as A3 with additional GlcNAc β1,6 linked to α1,6 mannose; B, bisecting GlcNAc linked β1,4 to β1,3 mannose; Gx, number (x) of β1,4 linked galactose on antenna; F(x), number (x) of fucose linked α1,3 to antenna GlcNAc; Sx, number (x) of sialic acids linked mostly to galactose (Structures with more sialic acids then galactoses may have some sialic acids linked to GlcNAc or another sialic acid in form of polysialic acid.).

| Peak | Unfractionated | | S0 | | | | | S1 | | | | S2 | | | | S3 | | | | S3J | | | | S4 | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | % Area | GU | % Area | GU | All sialic acids [3] and [6] | | | % Area | GU | All sialic acids [3] and [6] | | % Area | GU | All sialic acids [3] and [6] | | % Area | GU | All sialic acids [3] and [6] | | % Area | GU | All sialic acids [3] and [6] | | % Area | GU | All sialic acids [3] and [6] | |
| **1** | 0.00 | **4.57** | 0.03 | **4.66** | | | | | | | | | | | | | | | | | | | | | | | |
| **2** | 0.01 | **4.80** | 0.11 | **4.79** | | | | | | | | | | | | | | | | | | | | | | | |
| **3** | 0.00 | **5.06** | 0.01 | **5.02** | | | | | | | | | | | | | | | | | | | | | | | |
| **4** | 0.05 | **5.16** | 0.16 | **5.12** | | | | | | | | | | | | | | | | | | | | | | | |
| **5** | 0.02 | **5.34** | 0.05 | **5.30** | M4 | | | | | | | | | | | | | | | | | | | | | | |
| **6** | 0.02 | **5.62** | 0.01 | **5.43** | | | | | | | | | | | | | | | | | | | | | | | |
| | | | 0.07 | **5.57** | | | | | | | | | | | | | | | | | | | | | | | |
| **7** | 0.06 | **5.74** | 0.22 | **5.70** | | | | | | | | | | | | | | | | | | | | | | | |
| | | | 0.01 | **5.83** | | | | | | | | | | | | | | | | | | | | | | | |
| **8** | 0.01 | **5.90** | 0.00 | **5.90** | | | | | | | | | | | | | | | | | | | | | | | |
| **9** | 2.17 | **6.14** | 7.51 | **6.10** | M5 A2[6]G1 | FA2B | FA3 | | | | | | | | | | | | | | | | | | | | |
| | | | 0.83 | **6.48** | A2[3]G1 | | | | | | | | | | | | | | | | | | | | | | |
| **10** | 0.22 | **6.51** | 0.62 | **6.58** | A3G1 | A2BG1 | | | | | | | | | | | | | | | | | | | | | |
| **11** | 0.17 | **6.61** | 0.03 | **6.74** | M5A1 | M4A1G1 | | | | | | | | | | | | | | | | | | | | | |
| **12** | 2.26 | **6.90** | 7.67 | **6.87** | FA2BG1 | FA3G1 | | | | | | | | | | | | | | | | | | | | | |
| **13** | 1.22 | **7.04** | 4.30 | **7.01** | FA2BG1 | FA3G1 | | | | | | | | | | | | | | | | | | | | | |
| **14** | 0.44 | **7.14** | 1.16 | **7.09** | M6 | A2G2 | | 0.23 | **7.13** | | | | | | | | | | | | | | | | | | |
| **15** | 0.92 | **7.32** | 3.08 | **7.29** | A2BG2 | | | 0.05 | **7.25** | | | | | | | | | | | | | | | | | | |
| | | | | | | | | 0.12 | **7.40** | A2[6]G1S1 | | | | | | | | | | | | | | | | | |
| **16** | 0.59 | **7.52** | 1.83 | **7.49** | FA2G2 | M5A1G1 | | 0.18 | **7.45** | A2[3]G1S1 | | | | | | | | | | | | | | | | | |
| **17** | 5.14 | **7.69** | 16.23 | **7.66** | FA2BG2 | FA3G2 | | 1.10 | **7.57** | A3G1S1 | A2BG1S1 | | | | | | | | | | | | | | | | |
| | | | | | | | | 0.06 | **7.77** | M4A1G1S1 | | | | | | | | | | | | | | | | | |
| **18** | 1.60 | **7.93** | 2.57 | **7.91** | FA3'G2 | | | 2.67 | **7.89** | FA2BG1S1 | FA3G1S1 | | | | | | | | | | | | | | | | |
| **19** | 0.51 | **8.02** | | | M7 | | | 1.11 | **7.98** | FA2BG1S1 | FA3G1S1 | | | | | | | | | | | | | | | | |
| | | | | | M7 | | | 0.42 | **8.12** | | | | | | | | | | | | | | | | | | |
| **20** | 16.38 | **8.36** | 0.63 | **8.28** | A3G3 | | | 49.59 | **8.32** | A2G2S1 | | | | | | | | | | 2.62 | **8.35** | A2G2S[3,3,3]3 | | | | | |
| **21** | 0.65 | **8.51** | | | A3BG3 | | | 0.95 | **8.45** | | | | | | | | | | | 27.27 | **8.48** | A2G2S3 | A2BG2S3 | | | | |
| **22** | 2.12 | **8.64** | 3.46 | **8.63** | FA3G3 A3'G3 | | | 3.53 | **8.58** | A2BG2S1 | | 0.15 | **8.56** | | | | | | | | | | | | | | |
| **23** | 4.00 | **8.78** | 3.45 | **8.75** | M8 | | | 8.60 | **8.73** | FA2G2S1 | M5A1G1S1 | 0.21 | **8.72** | | | | | | | 11.35 | **8.88** | FA2G2S3 | | | | | |
| **24** | 8.68 | **9.00** | 0.33 | **9.10** | FA3'G3 | | | 25.12 | **8.96** | FA2BG2S1 | FA3G2S1 | | | | | | | | | | | | | | | | |
| **25** | 3.93 | **9.23** | 0.75 | **9.30** | FA4G3 | | | 1.03 | **9.18** | FA3'G2S1 | | 9.92 | **9.16** | A2G2S[3,3]2 | | | | | | 3.78 | **9.12** | FA2BG2S3 | M5A1G1S3 | | | | |
| **26** | 5.11 | **9.51** | 17.73 | **9.48** | M9 | | | 1.22 | **9.46** | A3G3S1 | | 0.17 | **9.38** | | | | | | | | | FA3G2S3 | | 3.58 | **9.41** | | |
| **27** | 24.92 | **9.65** | | | | | | 0.94 | **9.58** | A3BG3S1 | | 74.91 | **9.58** | A2G2S2 | | | | | | 2.49 | **9.58** | FA3'G2S3 | | 7.18 | **9.57** | FA2BG1S4 | FA3G1S4 |
| **28** | 0.67 | **9.82** | 0.11 | **9.77** | A4G4 | | | 1.42 | **9.70** | A3'G3S1 | FA3G3S1 | 1.89 | **9.75** | A2BG2S2 | | | | | | | | | | 46.99 | **9.82** | A2G2S4 | |
| **29** | 0.24 | **9.90** | | | | | | 0.54 | **9.93** | FA3'G3S1 | | 2.89 | **9.99** | FA2G2S2 | | | | | | | | | | | | | |
| **30** | 1.19 | **10.06** | 0.08 | **9.99** | FA4G4 | | | 0.21 | **10.07** | | | 3.71 | **10.13** | FA2BG2S2 | FA3G2S2 | | | | | | | | | | | | |
| **31** | 10.11 | **10.24** | 26.35 | **10.23** | M9Glc | | | 0.08 | **10.20** | | | 2.00 | **10.26** | FA3'G2S2 | | | | | | | | | | 34.84 | **10.23** | FA2G2S4 | |
| | | | 0.45 | **10.39** | | | | 0.49 | **10.43** | | | 0.46 | **10.37** | A3G3S2 | | | | | | | | | | | | | |
| **32** | 0.97 | **10.67** | | | | | | | | | | 0.13 | **10.53** | A3BG3S2 | | | | | | | | | | | | | |
| **33** | 1.11 | **10.80** | 0.15 | **10.86** | | | | 0.26 | **10.82** | | | 2.84 | **10.71** | A3'G3S2 | | | | | | | | | | | | | |
| **34** | 0.65 | **11.17** | | | | | | 0.08 | **11.06** | | | | | FA3G3S2 | | 12.08 | **11.05** | A3G3S3 | | | | | | | | | |
| **35** | 0.06 | **11.33** | | | | | | 0.01 | **11.25** | | | 0.23 | **11.07** | FA3'G3S2 | FA4G3S2 | 83.29 | **11.46** | A3G3S3 | A3BG3S3 | | | | | | | | |
| **36** | 0.04 | **11.46** | | | | | | | | | | 0.48 | **11.51** | A4G4S2 | | | | | | 4.71 | **11.48** | A3G3S3 | A2G2S3 | | | | |
| **37** | 2.81 | **11.59** | | | | | | | | | | | | | | | | | | 9.61 | **11.80** | A3G3S3 | A2G2S3 | | | | |
| **38** | 0.13 | **11.92** | | | | | | | | | | | | | | 4.63 | **11.95** | A3'G3S3 | | 2.72 | **11.99** | A3BG3S3 | A2BG2S3 | | | | |
| **39** | 0.52 | **12.09** | | | | | | | | | | | | | | | | FA3G3S3 | | 16.02 | **12.12** | FA3G3S3 | FA2G2S3 | | | | |
| **40** | 0.10 | **12.66** | | | | | | | | | | | | | | | | | | 2.74 | **12.44** | A3'G3S3 | M5A1G1S3 | | | | |
| | | | | | | | | | | | | | | | | | | | | 14.68 | **12.61** | A4G4S3 | FA2BG2S3 | 7.41 | **12.56** | A3G3S4 | |
| | 0.06 | **12.76** | | | | | | | | | | | | | | | | | | 2.01 | **12.80** | | | | | | |
| | 0.06 | **13.00** | | | | | | | | | | | | | | | | | | | | | | | | | |
| | 0.03 | **13.26** | | | | | | | | | | | | | | | | | | | | | | | | | |
| | 0.04 | **13.40** | | | | | | | | | | | | | | | | | | | | | | | | | |
| | 0.00 | **13.61** | | | | | | | | | | | | | | | | | | | | | | | | | |