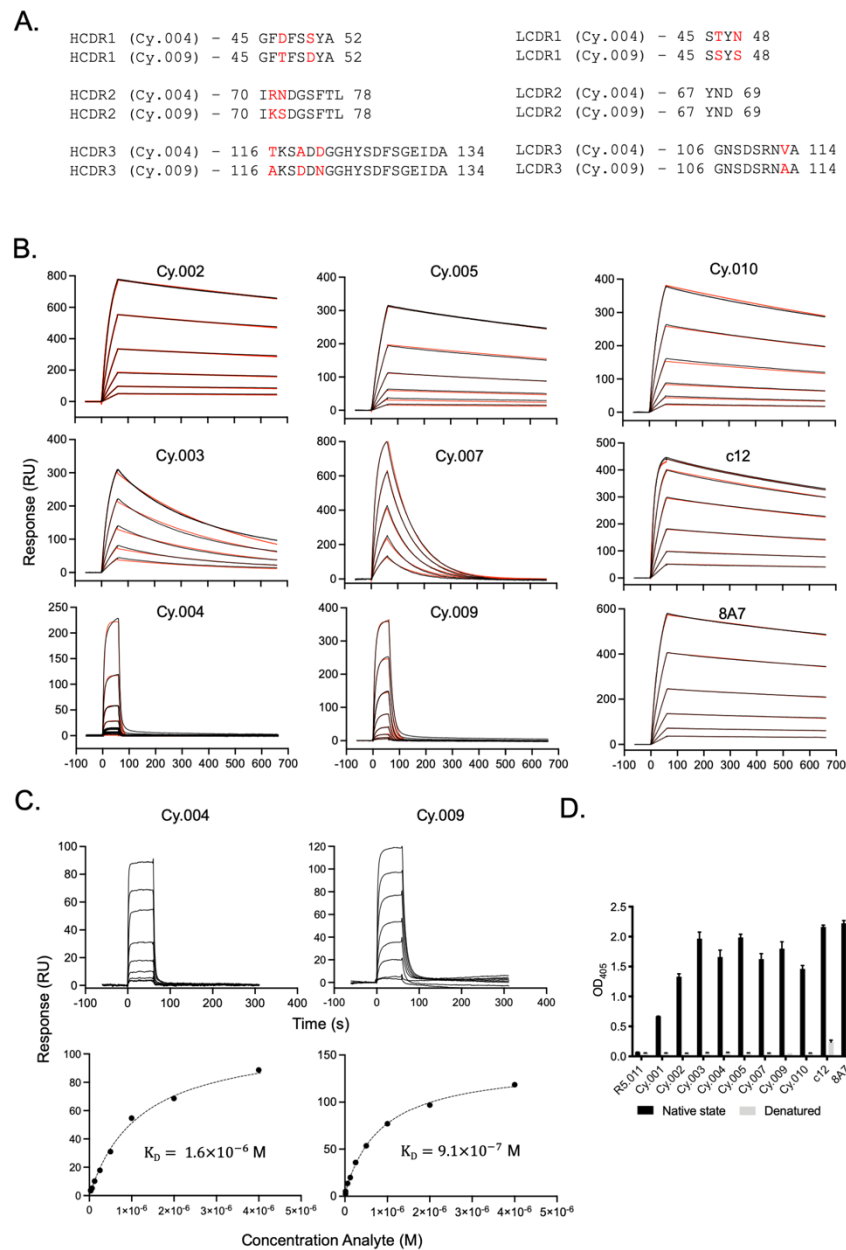


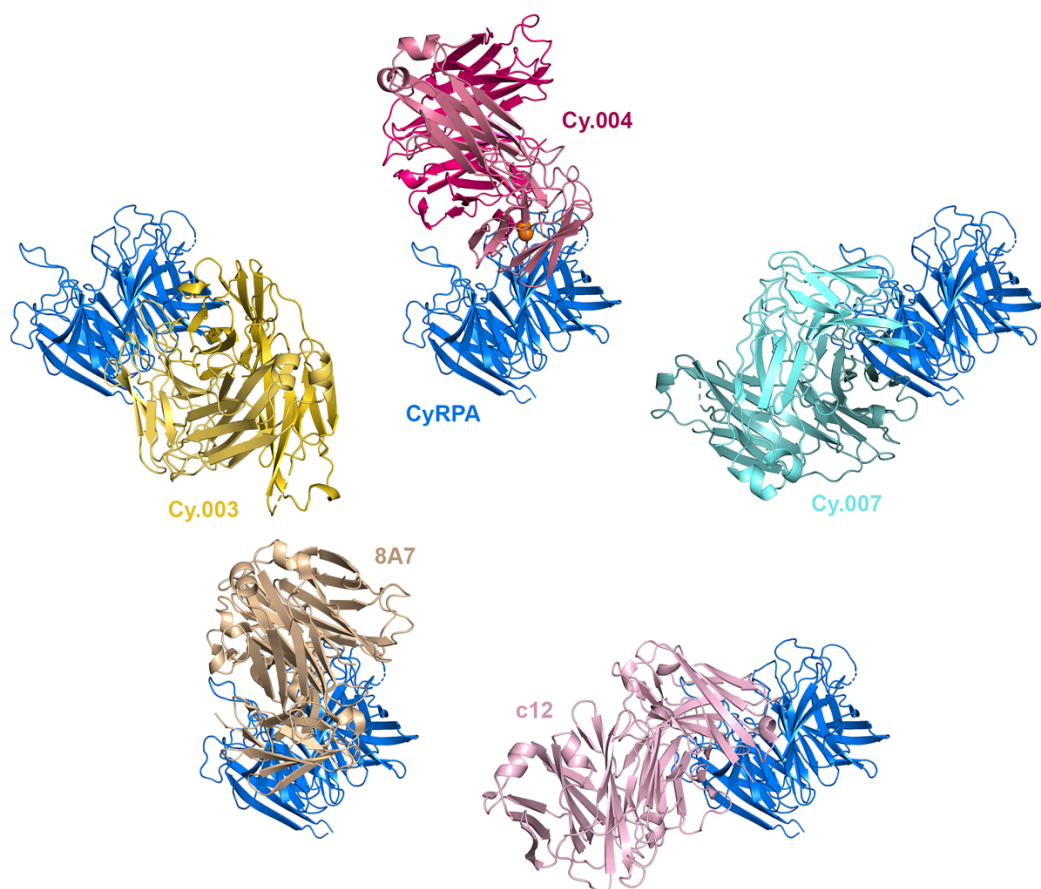
Supplementary Information

Heterotypic interactions drive antibody synergy against a malaria vaccine candidate

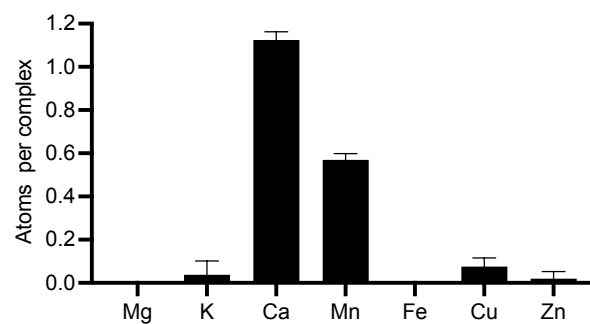
Robert J. Ragotte, David Pulido, Amelia M. Lias, Doris Quinkert, Daniel G.W. Alanine, Abhishek Jamwal, Hannah Davies, Adéla Nacer, Edward D. Lowe, Geoffrey W. Grime, Joseph J. Illingworth, Robert F. Donat, Elspeth F. Garman, Paul W. Bowyer, Matthew K. Higgins*, Simon J. Draper*



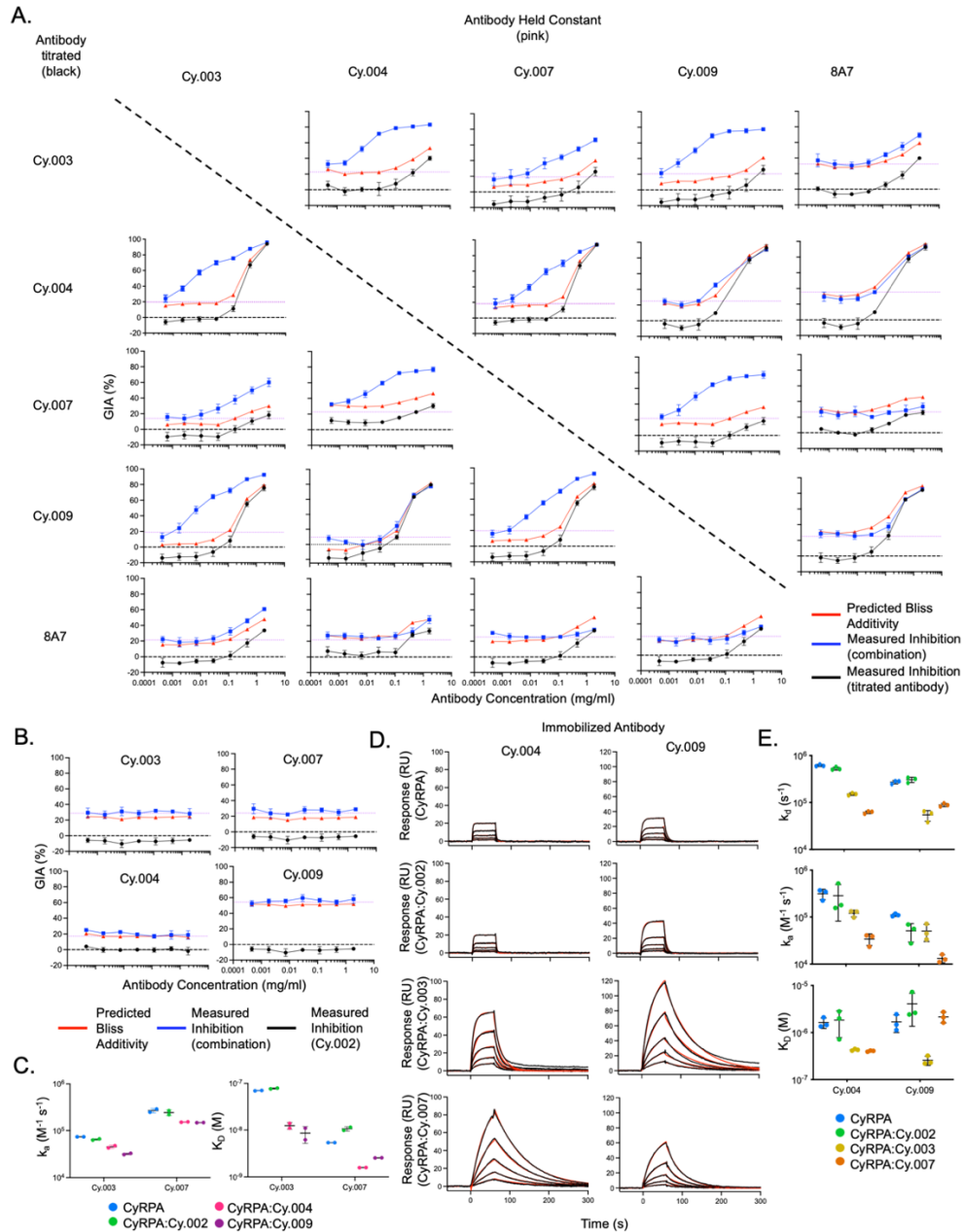
Supplementary Figure 1. (A) Comparison of CDR loops of Cy.004 and Cy.009 with amino acid changes indicated in red. (B) SPR sensorgrams of anti-CyRPA mAb binding to CyRPA across a 6-step 2-fold dilution series starting at either 125 nM for higher affinity mAbs (Cy.002, Cy.003, Cy.005, Cy.010, c12, 8A7) or 500 nM for lower affinity mAbs (Cy.004, Cy.007, Cy.009). (C) Steady state affinity determination of Cy.004 and Cy.009 from a 7-step 2-fold dilution series starting at 4 μ M. (D) ELISA of mAb binding to native state or boiled and reduced CyRPA. Bars indicate the mean and error bars show the standard deviation across three replicates. R5.011 is an anti-RH5 mAb not expected to bind to CyRPA.



Supplementary Figure 2. Structures of CyRPA (blue) bound to growth inhibitory monoclonal antibodies. Cy.003 (yellow), Cy.004 (dark pink), and Cy.007 (light blue) are from this study while c12 (light pink) and 8A7 (gold) are from previous studies ^{22,26}.



Supplementary Figure 3. MicroPIXE data showing the absolute abundance of different metal ions within the Cy.009:CyRPA complex. Bars indicate the mean and error bars show the standard deviation across three replicate measurements.



Supplementary Figure 4. *In vitro* GIA mAb synergy evaluations with one mAb titrated across a 7-step 4-fold dilution curve starting at 2 mg/ml with a second mAb held constant at ~20 % GIA (blue). Red indicates predicted Bliss additivity. Black indicates the inhibition curve of the titrated mAb alone from the same experiment. Pink dashed line indicates measured inhibition of the antibody held constant on its own. Each point is the mean across triplicates with error bars indicating the standard deviation. **(A)** Inhibitory mAb combinations. **(B)** mAbs in combination with Cy.002. **(C)** Summary of k_a and K_D changes of Cy.003 and Cy.007 binding to CyRPA and Fab: CyRPA complexes (representative sensorgrams in Figure 5C) across two replicate experiments with the mean and standard deviation shown by the horizontal line and error bars. **(D)** SPR sensorgrams of Cy.004 and Cy.009 binding to CyRPA compared to Fab: CyRPA complexes, all in the absence of $CaCl_2$. Black lines indicate the measured response while red lines indicate the curve fit. **(E)** Summary of k_d , k_a , and K_D changes of Cy.004 and Cy.009 binding to CyRPA and Fab: CyRPA complexes (representative sensorgrams in panel D) across three replicate experiments with the mean and standard deviation shown by the horizontal line and error bars.

Supplementary Table 1: Antibody binding kinetics summary table

| mAb | Buffer | Ligand | Figure | k_a ($M^{-1}s^{-1}$) | k_d (s^{-1}) | K_D (M) |
|--------|----------------------------------|--------------|--------|--------------------------|----------------------|-----------------------|
| Cy.002 | PBS+P20 | CyRPA | 1 | 3.1×10^5 | 2.9×10^{-4} | 9.4×10^{-10} |
| Cy.003 | PBS+P20 | CyRPA | 1 | 1.2×10^5 | 4.7×10^{-3} | 3.8×10^{-8} |
| Cy.004 | PBS+P20 | CyRPA | 1 | 1.6×10^5 | 4.4×10^{-1} | 2.8×10^{-6} |
| Cy.005 | PBS+P20 | CyRPA | 1 | 1.4×10^5 | 4.1×10^{-4} | 2.8×10^{-9} |
| Cy.007 | PBS+P20 | CyRPA | 1 | 1.0×10^5 | 1.1×10^{-2} | 1.1×10^{-7} |
| Cy.009 | PBS+P20 | CyRPA | 1 | 1.0×10^5 | 1.5×10^{-1} | 1.5×10^{-6} |
| Cy.010 | PBS+P20 | CyRPA | 1 | 2.2×10^5 | 4.7×10^{-4} | 2.1×10^{-9} |
| c12 | PBS+P20 | CyRPA | 1 | 7.4×10^5 | 5.3×10^{-4} | 7.2×10^{-10} |
| 8A7 | PBS+P20 | CyRPA | 1 | 2.5×10^5 | 2.9×10^{-4} | 1.2×10^{-9} |
| Cy.004 | TBS+P20 | CyRPA | 3 | 8.7×10^4 | 2.7×10^{-1} | 3.1×10^{-6} |
| Cy.004 | TBS+P20 (1mM MgCl ₂) | CyRPA | 3 | 6.9×10^5 | 1.7×10^{-1} | 2.4×10^{-7} |
| Cy.004 | TBS+P20 (1mM CaCl ₂) | CyRPA | 3 | 5.4×10^5 | 6.7×10^{-4} | 1.2×10^{-9} |
| Cy.003 | TBS+P20 (1mM CaCl ₂) | CyRPA | 5 | 7.4×10^4 | 5.1×10^{-3} | 7.0×10^{-8} |
| Cy.003 | TBS+P20 (1mM CaCl ₂) | Cy.002:CyRPA | 5 | 6.5×10^4 | 4.8×10^{-3} | 7.7×10^{-8} |
| Cy.003 | TBS+P20 (1mM CaCl ₂) | Cy.004:CyRPA | 5 | 4.8×10^4 | 5.7×10^{-4} | 1.3×10^{-8} |
| Cy.003 | TBS+P20 (1mM CaCl ₂) | Cy.009:CyRPA | 5 | 3.2×10^4 | 2.7×10^{-4} | 8.6×10^{-9} |
| Cy.007 | TBS+P20 (1mM CaCl ₂) | CyRPA | 5 | 2.9×10^5 | 1.6×10^{-3} | 5.4×10^{-9} |
| Cy.007 | TBS+P20 (1mM CaCl ₂) | Cy.002:CyRPA | 5 | 2.4×10^5 | 2.4×10^{-3} | 1.1×10^{-8} |
| Cy.007 | TBS+P20 (1mM CaCl ₂) | Cy.004:CyRPA | 5 | 1.5×10^5 | 2.4×10^{-4} | 1.6×10^{-9} |
| Cy.007 | TBS+P20 (1mM CaCl ₂) | Cy.009:CyRPA | 5 | 1.5×10^5 | 3.8×10^{-4} | 2.6×10^{-9} |
| Cy.004 | PBS+P20 | CyRPA | S4 | 3.1×10^5 | 4.9×10^{-1} | 1.3×10^{-6} |
| Cy.004 | PBS+P20 | Cy.002:CyRPA | S4 | 1.7×10^5 | 3.9×10^{-1} | 1.8×10^{-6} |
| Cy.004 | PBS+P20 | Cy.003:CyRPA | S4 | 1.2×10^5 | 5.9×10^{-2} | 4.1×10^{-7} |
| Cy.004 | PBS+P20 | Cy.007:CyRPA | S4 | 3.4×10^4 | 1.5×10^{-2} | 3.9×10^{-7} |
| Cy.009 | PBS+P20 | CyRPA | S4 | 1.1×10^5 | 1.4×10^{-1} | 8.9×10^{-7} |
| Cy.009 | PBS+P20 | Cy.002:CyRPA | S4 | 5.1×10^4 | 1.7×10^{-1} | 1.5×10^{-6} |
| Cy.009 | PBS+P20 | Cy.003:CyRPA | S4 | 5.0×10^4 | 1.3×10^{-2} | 2.6×10^{-7} |
| Cy.009 | PBS+P20 | Cy.007:CyRPA | S4 | 1.3×10^4 | 2.7×10^{-2} | 2.1×10^{-6} |

Supplementary Table 2: Interacting residues of mAb: CyRPA complexes.

| CyRPA | | | Cy.002 | | | Type of interaction |
|---------|---------|------------|---------|---------|------------|---------------------|
| Chain | Residue | Group | Chain | Residue | Group | |
| A/D | Y185 | Side chain | C/F | S51 | Side chain | Hydrogen bond |
| A/D | K188 | Side chain | B/E | D123 | Side chain | Hydrogen bond |
| A/D | D189 | Side chain | C/F | R74 | Side chain | Hydrogen bond |
| A/D | K220 | Side chain | B/E | T51 | Main chain | Hydrogen bond |
| A/D | K220 | Side chain | B/E | D71 | Side chain | Hydrogen bond |
| A/D | L221 | Main chain | B/E | D50 | Main chain | Hydrogen bond |
| A/D | L221 | Side chain | B/E | V119 | Side chain | Hydrophobic |
| A/D | G222 | Side chain | B/E | V119 | Side chain | Hydrophobic |
| A/D | D245 | Side chain | B/E | R69 | Side chain | Hydrogen bond |
| A/D | D245 | Main chain | C/F | R119 | Side chain | Hydrogen bond |
| A/D | N246 | Side chain | C/F | S115 | Main chain | Hydrogen bond |
| A/D | N246 | Main chain | C/F | D118 | Main chain | Hydrogen bond |
| A/D | N248 | Main chain | C/F | D118 | Side chain | Hydrogen bond |
| CyRPA | | | Cy.003 | | | Type of interaction |
| Chain | Residue | Group | Chain | Residue | Group | |
| A/D/G/J | R135 | Side chain | B/E/H/K | D124 | Main chain | Hydrogen bond |
| A/D/G/J | Y137 | Side chain | C/F/I/L | Y49 | Side chain | Hydrogen bond |
| A/D/G | E143 | Side chain | C/F/I | K84 | Side chain | Hydrogen bond |
| A/D/G/J | N145 | Side chain | B/E/H/K | W125 | Side chain | Hydrogen bond |
| A/D/G/J | N145 | Side chain | C/F/I/L | S48 | Side chain | Hydrogen bond |
| A/D/J | N146 | Main chain | C/F/L | R109 | Side chain | Hydrogen bond |
| A/D/G/J | D203 | Side chain | B/E/H/K | S72 | Side chain | Hydrogen bond |
| A/D/G/J | K204 | Side chain | B/E/H/K | N121 | Main chain | Hydrogen bond |
| A/D/G/J | E206 | Side chain | B/E/H/K | S126 | Side chain | Hydrogen bond |
| G/J | E206 | Side chain | H/K | S126 | Main chain | Hydrogen bond |
| CyRPA | | | Cy.004 | | | Type of interaction |
| Chain | Residue | Group | Chain | Residue | Group | |
| A | E96 | Main chain | C | Y47 | Side chain | Hydrogen bond |
| A/D | D98 | Side chain | B/E | S126 | Main chain | Hydrogen bond |
| A/D | D98 | Main chain | B/E | Y125 | Main chain | Hydrogen bond |
| A/D | D98 | Side chain | C/F | S108 | Side chain | Hydrogen bond |
| A/D | L99 | Main chain | C/F | R111 | Side chain | Hydrogen bond |
| A/D | T100 | Side chain | B/E | G122 | Main chain | Hydrogen bond |
| A/D | T100 | Main chain | B/E | G123 | Main chain | Hydrogen bond |
| A/D | E120 | Side chain | B/E | D120 | Side chain | Metal coordination |
| A/D | E120 | Side chain | B/E | D121 | Side chain | Metal coordination |
| A/D | E122 | Side chain | B/E | D121 | Side chain | Metal coordination |
| A/D | N126 | Side chain | B/E | S50 | Main chain | Hydrogen bond |
| D | F94 | Main chain | F | R111 | Side chain | Hydrogen bond |
| D | T97 | Main chain | F | R111 | Side chain | Hydrogen bond |
| D | D98 | Side chain | E | S126 | Side chain | Hydrogen bond |
| CyRPA | | | Cy.007 | | | Type of interaction |
| Chain | Residue | Group | Chain | Residue | Group | |
| A | K43 | Side chain | B | D122 | Side chain | Hydrogen bond |
| A | E96 | Side chain | C | R108 | Side chain | Hydrogen bond |
| A | K142 | Side chain | B | T126 | Side chain | Hydrogen bond |
| A/D | Y78 | Side chain | B/E | R120 | Side chain | Hydrogen bond |
| A/D | K81 | Side chain | B/E | Y76 | Side chain | Hydrogen bond |
| A/D | T89 | Main chain | B/E | C124 | Main chain | Hydrogen bond |
| A/D | D140 | Main chain | B/E | Y76 | Side chain | Hydrogen bond |
| D | N45 | Side chain | E | S121 | Main chain | Hydrogen bond |
| RH5 | | | R5.015 | | | Type of interaction |
| Chain | Residue | Group | Chain | Residue | Group | |
| A | K378 | Side chain | B | D36 | Side chain | Hydrogen bond |
| A | Q389 | Side chain | B | F107 | Main chain | Hydrogen bond |
| A | Q389 | Side chain | B | F107 | Main chain | Hydrogen bond |
| A | L393 | Side chain | B | W106 | Side chain | Hydrophobic |
| A | N396 | Side chain | C | S31 | Side chain | Hydrogen bond |
| A | N396 | Side chain | C | D50 | Side chain | Hydrogen bond |
| A | K400 | Side chain | C | G28 | Main chain | Hydrogen bond |
| A | K400 | Side chain | C | D50 | Side chain | Hydrogen bond |
| A | N491 | Side chain | B | S110 | Main chain | Hydrogen bond |
| A | F494 | Side chain | B | W106 | Side chain | Hydrophobic |
| A | F494 | Side chain | B | P112 | Side chain | Hydrophobic |
| A | Q502 | Side chain | C | W90 | Main chain | Hydrogen bond |
| A | Q502 | Side chain | C | T92 | Side chain | Hydrogen bond |
| A | N506 | Side chain | C | N25 | Side chain | Hydrogen bond |

Supplementary Table 3: Heterotypic interactions between mAbs binding adjacent epitopes

| Cy.004 | | | Cy.007 | | | |
|--------------|---------|------------|--------------|---------|------------|---------------------|
| Region | Residue | Group | Region | Residue | Group | Type of interaction |
| LCDR3 | D109 | Side chain | LC Framework | S86 | Side chain | Hydrogen bond |
| LCDR3 | D109 | Side chain | LC Framework | S86 | Main chain | Hydrogen bond |
| LCDR3 | S110 | Side chain | LC Framework | K83 | Side chain | Hydrogen bond |
| LCDR3 | N112 | Side chain | LC Framework | G85 | Main chain | Hydrogen bond |
| Cy.003 | | | Cy.007 | | | |
| Region | Residue | Group | Region | Residue | Group | Type of interaction |
| LCDR1 | G45 | Main chain | LCDR3 | N111 | Side chain | Hydrogen bond |
| LC Framework | S87 | Side chain | LCDR3 | N112 | Side chain | Hydrogen bond |
| LC Framework | T90 | Side chain | HC framework | K84 | Side chain | Hydrogen bond |
| Cy.003 | | | Cy.004 | | | |
| Region | Residue | Group | Region | Residue | Group | Type of interaction |
| HC framework | K84 | Side chain | LC Framework | K83 | Main chain | Hydrogen bond |
| LCDR3 | N111 | Side chain | LCDR1 | T46 | Side chain | Hydrogen bond |
| LCDR3 | S112 | Side chain | LC Framework | S84 | Side chain | Hydrogen bond |

Supplementary Table 4: Data collection and refinement statistics

| | R5.015:R5.016:RH5 | Cy.002:CyRPA | Cy.003:CyRPA | Cy.004:CyRPA | Cy.007:CyRPA | Cy.003:Cy.004: Cy.007:CyRPA |
|---------------------------------------|-------------------------------|-------------------------------|--------------------------------|-------------------------------|-------------------------------|--------------------------------|
| Space group | C 2 2 21 | C 1 2 1 | C 1 2 1 | P 1 21 1 | P 21 21 21 | P 43 |
| Cell dimensions a, b, c | 97.74, 163.30, 176.82 | 205.05, 80.69, 117.36 | 354.30, 71.04, 164.79 | 103.06, 80.32, 114.91 | 74.10, 87.00, 342.77 | 164.84, 164.84, 382.30 |
| α, β, γ (°) | 90, 90, 90 | 90, 108.73, 90 | 90, 91.16, 90 | 90, 115.23, 90 | 90, 90, 90 | 90, 90, 90 |
| Wavelength (Å) | 0.9795 | 1.0000 | 0.97624 | 0.97857 | 0.97857 | 0.97950 |
| Resolution (Å) | 48.22 – 2.53 (2.57 – 2.53) | 48.55 – 2.72 (2.81 – 2.72) | 164.76 – 3.14 (3.21 – 3.14) | 47.11 – 2.79 (2.87 – 2.79) | 48.97 – 3.09 (3.22 – 3.09) | 164.84 – 3.27 (3.28 – 3.27) |
| Total Observations | 316074 (16521) | 169805 (15709) | 239064 (15017) | 284862 (13827) | 564609 (62331) | 1115594 (11407) |
| Total Unique | 47342 (2383) | 49035 (4407) | 72415 (4491) | 42022 (2741) | 41692 (4590) | 156679 (1589) |
| R_{pim} (%) | 4.1 (74.8) | 4.7 (48.7) | 13.6 (94.8) | 10.4 (73.7) | 14.4 (99.3) | 4.9 (80.5) |
| R_{merge} (%) | 9.9 (184.3) | 4.9 (52.4) | 13.9 (96.5) | 16.7 (106.3) | 35.7 (248.0) | 12.0 (201.3) |
| R_{meas} (%) | 10.7 (199.0) | 6.8 (71.7) | 19.5 (135.4) | 19.7 (129.9) | 38.5 (267.3) | 12.9 (216.8) |
| $CC_{1/2}$ | 0.999 (0.575) | 0.999 (0.864) | 0.956 (0.425) | 0.992 (0.757) | 0.969 (0.733) | 0.998 (0.586) |
| $I/\sigma(I)$ | 13.1 (1.2) | 13.3 (1.8) | 7.2 (1.3) | 6.8 (0.9) | 5.1(1.0) | 9.4 (0.8) |
| Completeness (%) | 99.6 (99.4) | 99.6 (97.2) | 99.9 (99.9) | 99.9 (87.3) | 99.9 (99.5) | 99.9 (100.0) |
| Multiplicity | 6.7 (6.9) | 3.5 (3.6) | 3.3 (3.3) | 6.8 (5.0) | 13.5 (13.6) | 7.1 (7.2) |
| Wilson B factor (Å ²) | 60 | 65 | 60 | 61 | 109 | 113.8 |
| Refinement | | | | | | |
| Reflections | 47308 | 48960 | 72368 | 42008 | 41616 | 156578 |
| $R_{\text{work}} / R_{\text{free}}$ | 23.6 / 27.6 | 27.0 / 29.8 | 21.9 / 23.9 | 23.9 / 27.7 | 28.7 / 33.2 | 28.5 / 29.8 |
| Average B factor (Å ²) | 63 | 99 | 89 | 90 | 176 | 187 |
| Number of residues | | | | | | |
| Protein | 1172 | 1501 | 3002 | 1494 | 1476 | 6419 |
| Water | 127 | 76 | | | | |
| Ca ²⁺ | | | | 4 | | 8 |
| R.m.s deviations | | | | | | |
| Bond lengths (Å) | 0.009 | 0.009 | 0.009 | 0.009 | 0.008 | 0.007 |
| Bond angles (°) | 1.04 | 1.07 | 1.06 | 1.06 | 0.95 | 0.90 |
| Ramachandran plot | | | | | | |
| Favored (%) | 96.5 | 93.1 | 94.8 | 94.9 | 92.8 | 93.0 |
| Allowed (%) | 3.5 | 6.9 | 5.2 | 5.1 | 7.2 | 7.0 |
| Outliers (%) | 0 | 0 | 0 | 0 | 0.0 | 0 |

Values in parentheses indicate the highest resolution shell.

Supplementary Table 5: Monoclonal antibody sequences

| mAb | Heavy Chain Sequence | Light Chain Sequence |
|--------|--|--|
| Cy.002 | MKCSWVIFFLMAVVSGVNSEVQLQQSGAELVK PGASVKLSCTASGFNIKDTYIHWVKQRPEQGL EWIGRIDPANGNTYSDPKFQDKATIKADTSSN TAYLQLSSLTSEDTAIVYYCARDVLYFDVWGAG TTVTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKP SNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP SVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK TISKAKGQPREPQVYTLPPSRDELTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDSGGSFFLYSKLTVDKSRWQQGNVFCFSVMHE ALHNHYTQKSLSLSPGK | METDTLLLWVLLLWVPGSTGDIVLTQ SPASLAVSLGQRATISCRASESVDSY GNSFMHWYQQKPGQPPKLLISRASNL ESGIPARFSGSGSRTDFTLTINPVEA DDVATYYCQQSNEDRTFGGGTKLEIE RTVAAPSVFIFPPSDEQLKSGTASVV CLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKSTYSLSSLTTLTKAD YEKHKVYACEVTHQGLSSPVTKSFNR GEC |
| Cy.003 | MEWSWVFLFFLSVTTGVHSAVTLDESGGGLQT PGGALSIVCKGSGFFSFSSYTMQWVRQAPGKG LEWVASISSGGGTNYGAAVKGRATISRDNGQS TLRLQLNNLRAEDTGTYICAKHGVNGCDWSYS VGCVDAWGHGTEVIVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQ TYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP CPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGGSFFLYSKLTVDKSRWQQG NVFCFSVMHEALHNHYTQKSLSLSPGK | MSVPTQVLGLLLLWLTDAARCALTQPS SVSANPGETVKITCSGGSSSYGYWYQ QKSPGSAPVTLIYNNQKRPSDIPSRF SGSKSGSTGTLTITGVQAEDEAVYFC GSRDNSGGIFGAGTTLTVLRTVAAPS VFIFPPSDEQLKSGTASVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQ DSKSTYSLSSLTTLTKADYEKHKVY ACEVTHQGLSSPVTKSFNRGEC |
| Cy.004 | MEWSWVFLFFLSVTTGVHSAVTLDESGGGLQT PGGALSIVCKASGFDFSSYAMGWVRQAPGKGL EYVAGIRNDGSFTLYTPAVKGRATISRDNGQS TVRLQLNNLRAEDTATYFCTKSADDGGHYSDF SGEIDAWGHGTEVIVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQ TYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP CPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGGSFFLYSKLTVDKSRWQQG NVFCFSVMHEALHNHYTQKSLSLSPGK | MSVPTQVLGLLLLWLTDAARCALTQPS SVSANPGETVKITCSGSTYNYGWYQQ KSPGSAPVTVIYNDKRPSDIPSRFS GSKSGSTGTLTITGVQAEDEAVYYCG NSDSRNVAFGAGTTLTVLRTVAAPSV FIFPPSDEQLKSGTASVCLLNNFY REAKVQWKVDNALQSGNSQESVTEQD SKSTYSLSSLTTLTKADYEKHKVYA CEVTHQGLSSPVTKSFNRGEC |
| Cy.005 | MNFGSLIFLALILKGVQCEVQLVESGGDLVK PGGSLKLSAASGFTFSNYGLSWVRQTPDKRL EWVAAISSGGSYTYYPDSVKGRFTISRDNANK TLYLQMSLSKADTAMYYCARHTGSHRYAWFT YWQGGLTVTVSAASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVSWNSGALTSGVHT FPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLNGKEYKCKVSNKALP | MAWTPLFFFFVLHCSGSFSQVLVTQS SSASFSLGASAKLTCTLSQHSYTYI EWYQQQPLKPPKYVMELKKDGSHTG DGI PDRFSGSSSGADRYLSISNIQPE DEAIYICGVVDTIKEQFVYVFGGGTK VTVLRTVAAPSVFIFPPSDEQLKSGT ASVCLLNNFYPREAKVQWKVDNALQ SGNSQESVTEQDSKSTYSLSSLTTL SKADYEKHKVYACEVTHQGLSSPVTK SFNRGEC |

| | | |
|--------|--|--|
| | APIEKTISKAKGQPREPQVYTLPPSRDELTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFC SVMHEALHNHYTQKSLSLSPGK | |
| Cy.007 | MEWSWVFLFFLSVTTGVHSAVTLDES GGG LQT PGGTL SLVCKGSGFTTFSSYEMQWVRQAPGKGL EWVADICIGGSYTGYPVAVKGRATISRDDGQS TVRLQLNNLRAEDTGTYTCAKTARSDYCITGL DDIDAWGHGTEVIVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSRDE LTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQKSLSLSPGK | MSVPTQVLGLLLLLWLT DARCALTQPS SVSANPGETVKITCSGGSSDYGWYQQ KSPGSAPVTVIYENNKRPDI PSRFS GSKFGSTHTLTITGVQADDEAVYFCG SRDTNNGAFGAGTTTLTVLRTVAAPSV FIFPPSDEQLKSGTASVVCLLNNFYP REAKVQWKVDNALQSGNSQESVTEQD SKDSTYLSSTLTLSKADYEKHKVYA CEVTHQGLSSPVTKSFNRGEC |
| Cy.009 | MEWSWVFLFFLSVTTGVHSAVTLDES GGG LQT PGGAL SLVCKASGFTTFSDYAMGWVRQAPGKGL EYVAGIKSDGSFTLYGSTVKGRATISRDNQGS IVRLQLNNLRAEDTGTYTCAKSDDNGGHYSDF SGEIDAWGHGTEVIVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQ TYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP CPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVMHEALHNHYTQKSLSLSPGK | MSVPTQVLGLLLLLWLT DARCALTQPS SVSANPGETVKITCSGSSYSYGWYQQ KSPGSAPVTVIYNDKRPDI PSRFS GSKSGSTGTLTITGVQAEDEAVYFCG NSDSRNAAFGAGTTTLTVLRTVAAPSV FIFPPSDEQLKSGTASVVCLLNNFYP REAKVQWKVDNALQSGNSQESVTEQD SKDSTYLSSTLTLSKADYEKHKVYA CEVTHQGLSSPVTKSFNRGEC |
| Cy.010 | MNLGLSFIFLALILKGVQCEVQLVESGGGLVQ PGGSLKLSCAASGFTTFSTYGMWVRQTPDKRL ELVATINSNGGNTYYPDSVKGRFTMSRDNAKN TLYLQMSLKS EDTAMYYCAREGYYYGGYSYA MDYWGGTSVTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTS HTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYI CNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA PELLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA LPAPIEKTISKAKGQPREPQVYTLPPSRDEL TKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPGK | MLHRDMNMLTQLLGLLLLWFAGGKCD IQMTQSPASQSASLGESVTITCLASQ TIGIWLAWYQQKPGKSPQLLIYAASS LADGVPSRFSGSGSGTKFSFKISSLQ AEDFVSYYCQQLYSTPWTFGGGTKLE IKRTVAAPSVFIFPPSDEQLKSGTAS VVCLLNNFYPREAKVQWKVDNALQSG NSQESVTEQDSKDSTYLSSTLTLSK ADYEKHKVYACEVTHQGLSSPVTKSF NRGEC |