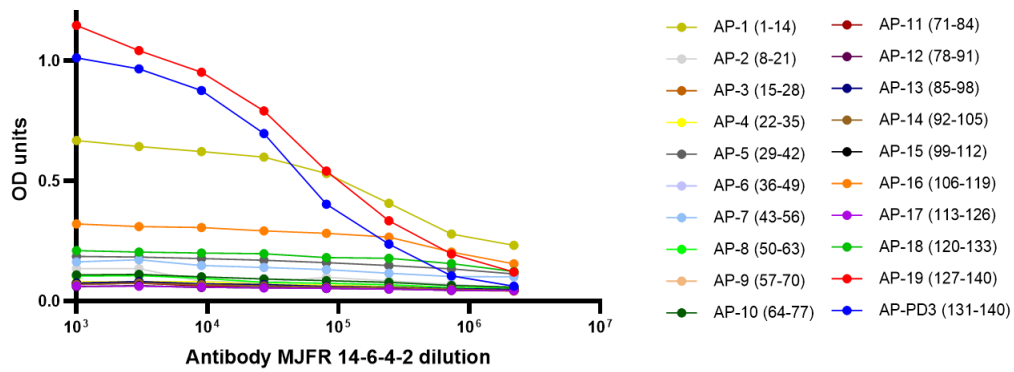
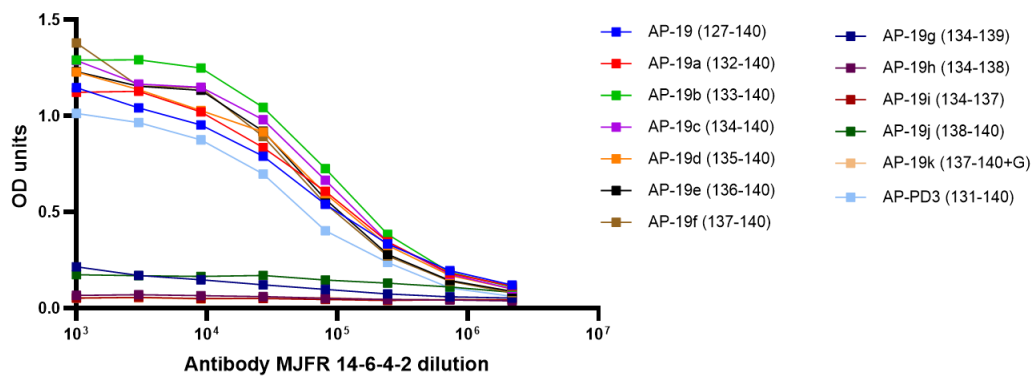


Supplementary information

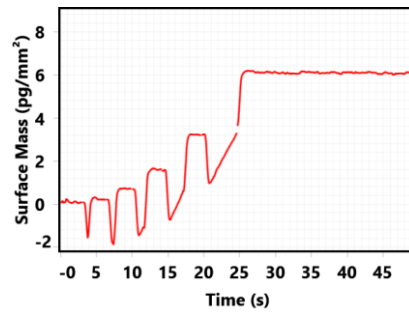
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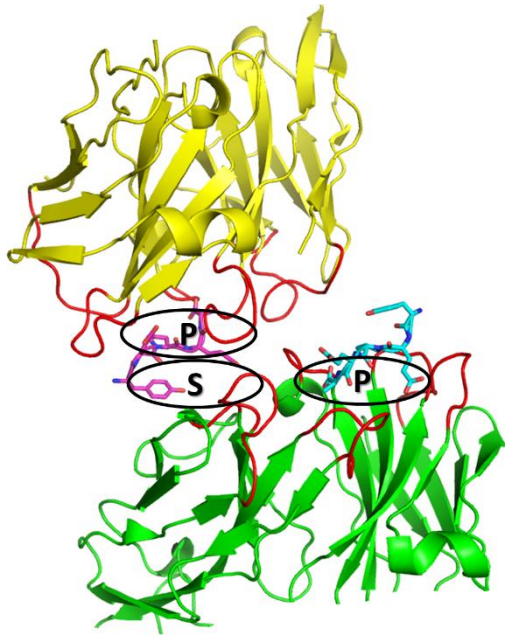
B



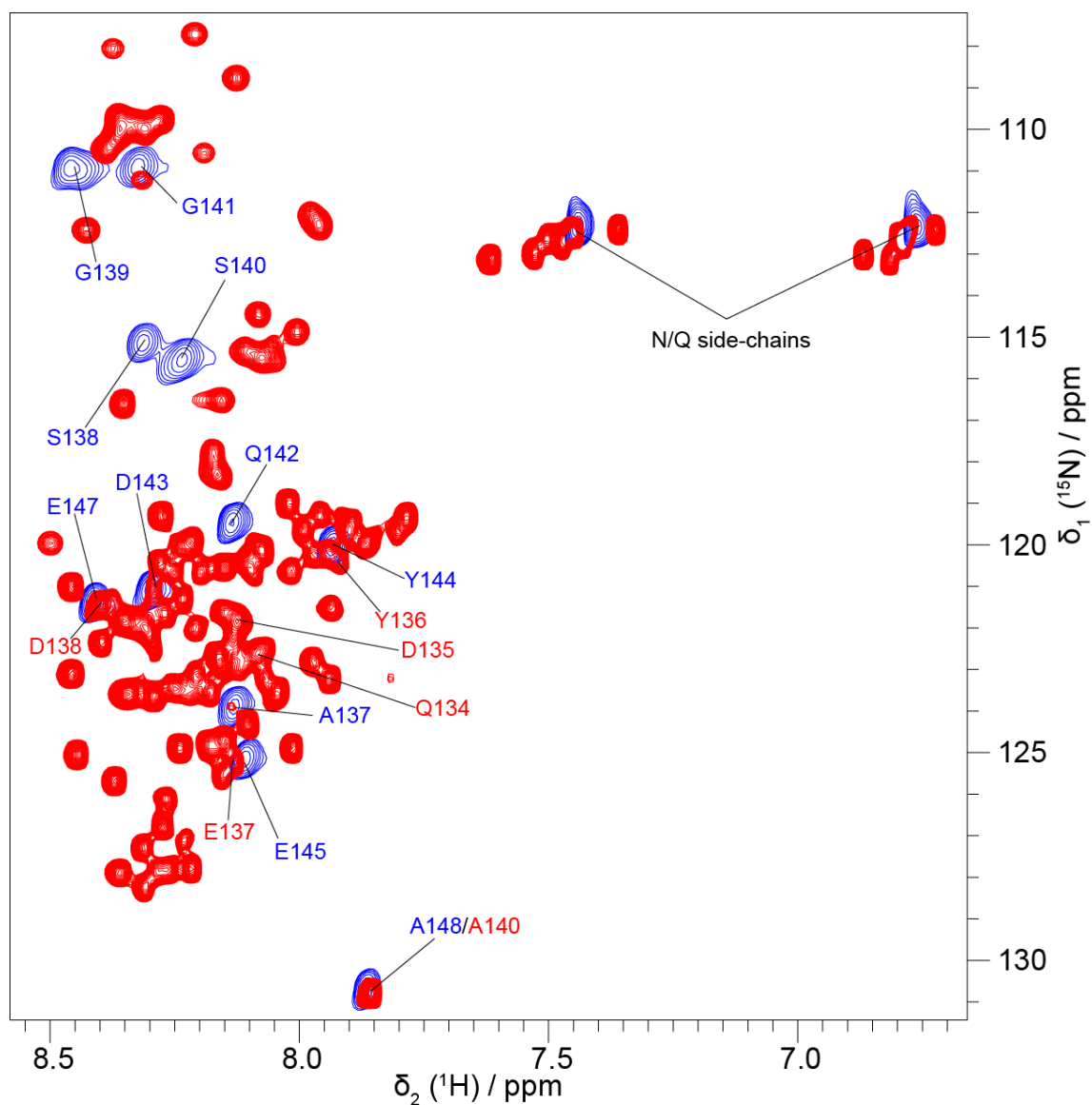
Supplementary Figure 1. Mapping of epitope by ELISA (full data). (A) initial and (B) fine mapping of epitope.



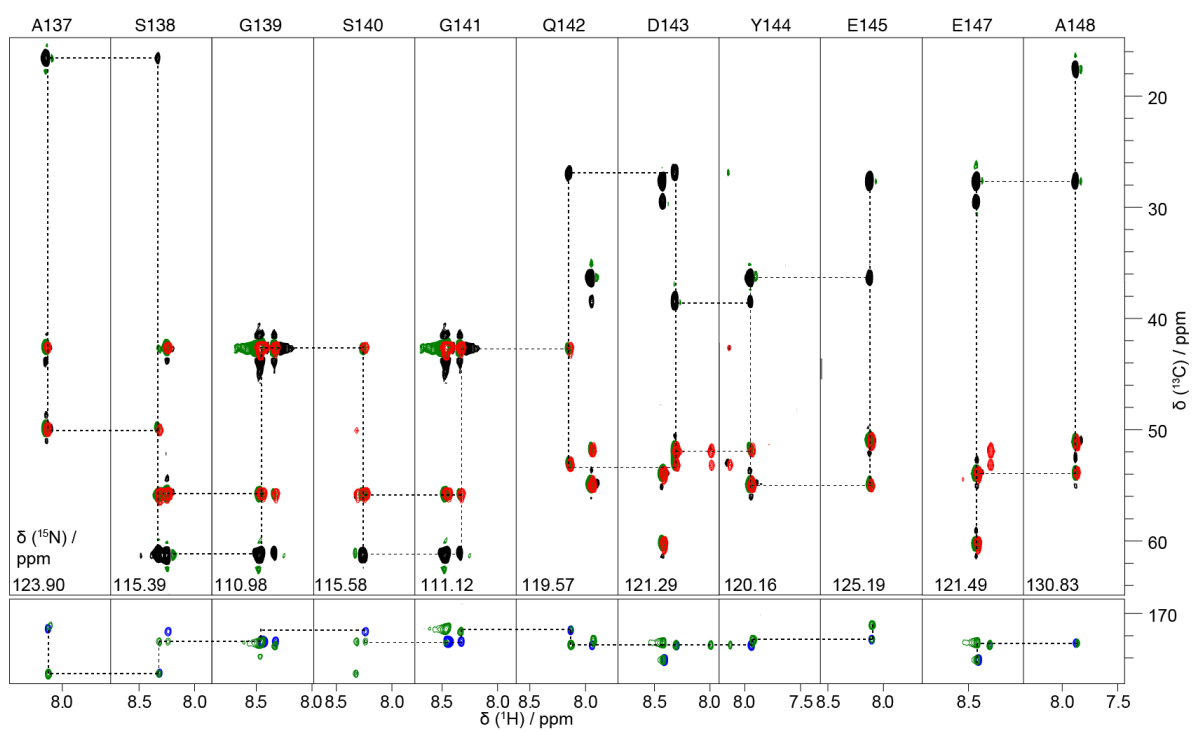
Supplementary Figure 2. Grating-coupled interferometry (GCI) sensorgrams obtained using the WaveRAPID experiment for the control AP205 VLP binding to immobilised MJFR14-6-4-2 antibody.



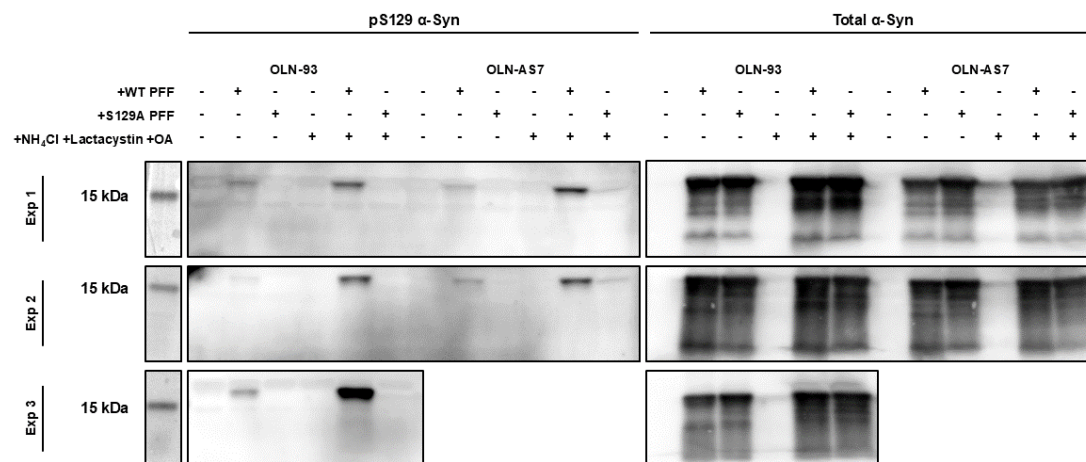
Supplementary Figure 3. Packaging of Fab-peptide complex in a crystal lattice. The crystal contacts among asymmetric units in $P2_12_12_1$ space group are such that each peptide is making interactions with two Fab fragments, variable domains of which are shown in yellow and green. The first or “primary” site, encircled as “P” is due to interactions of the peptide with a number of CDR loops (red). The second or “secondary” site, encircled as “S” is due to interactions of the same peptide with another Fab monomer in the crystal lattice.



Supplementary Figure 4. The overlay of 2D ^1H - ^{15}N HSQC spectra: blue - MJFR14-6-4-2 epitope, red - full length α -syn. The resonance assignments only for the MJFR14-6-4-2 epitope corresponding region in α -syn are shown. The largest NH chemical shift deviation is for Q142 (epitope)/Q134 (α -syn) amino acid since its closest to the Gly-Ser linker.

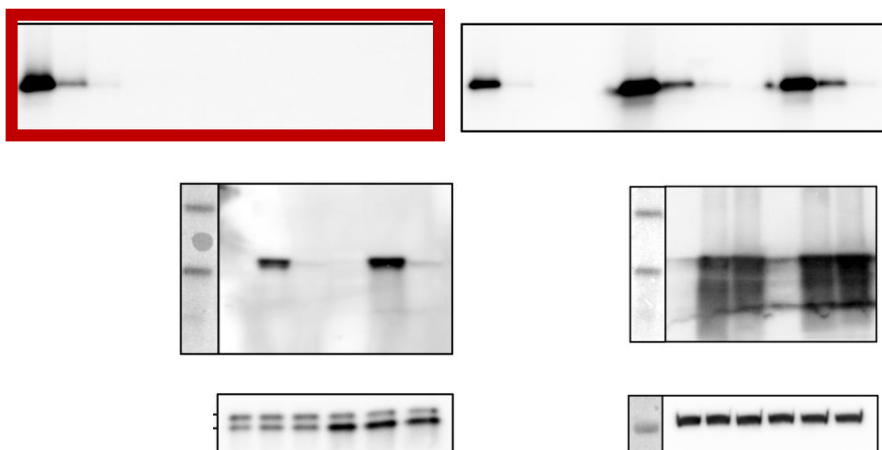


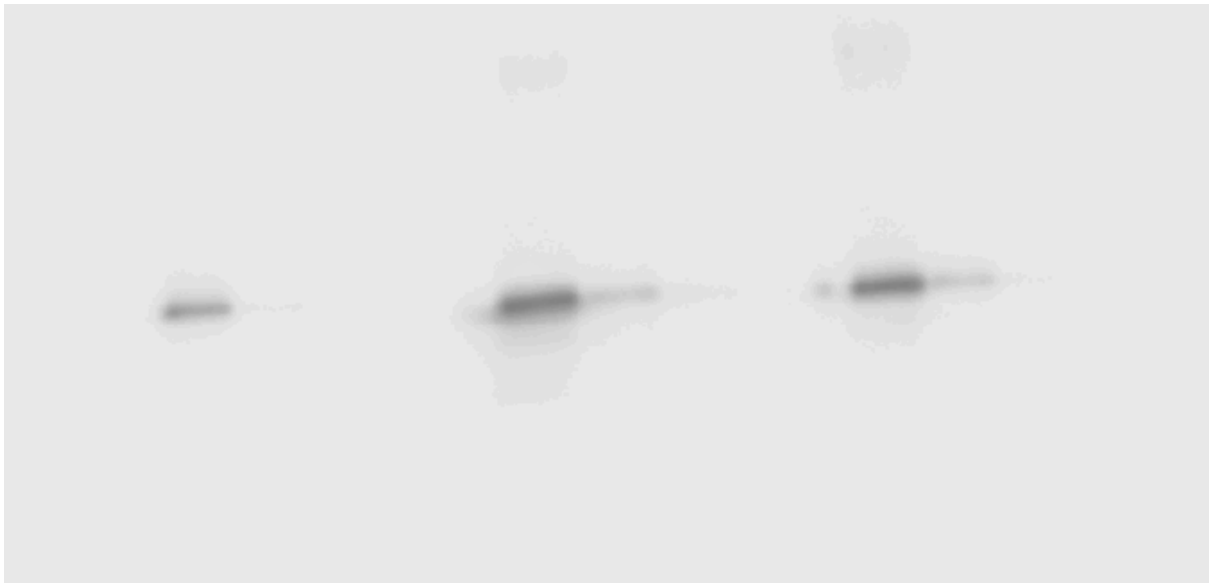
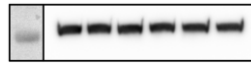
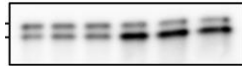
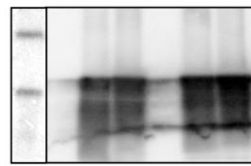
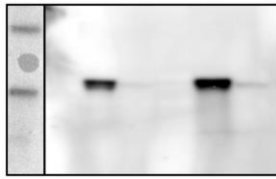
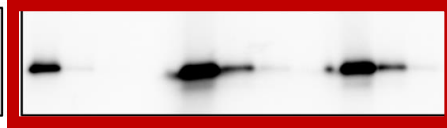
Supplementary Figure 5. The 2D projections of 3D assignment spectra for sequence assignments of the MJFR14-6-4-2 epitope. The backbone walk for $\text{C}\alpha_{i-1}$ - $\text{C}\alpha_i$, $\text{C}\beta_{i-1}$ - $\text{C}\beta_i$ and CO_{i-1} - CO_i pairs for adjacent amino acids are connected with striped lines.

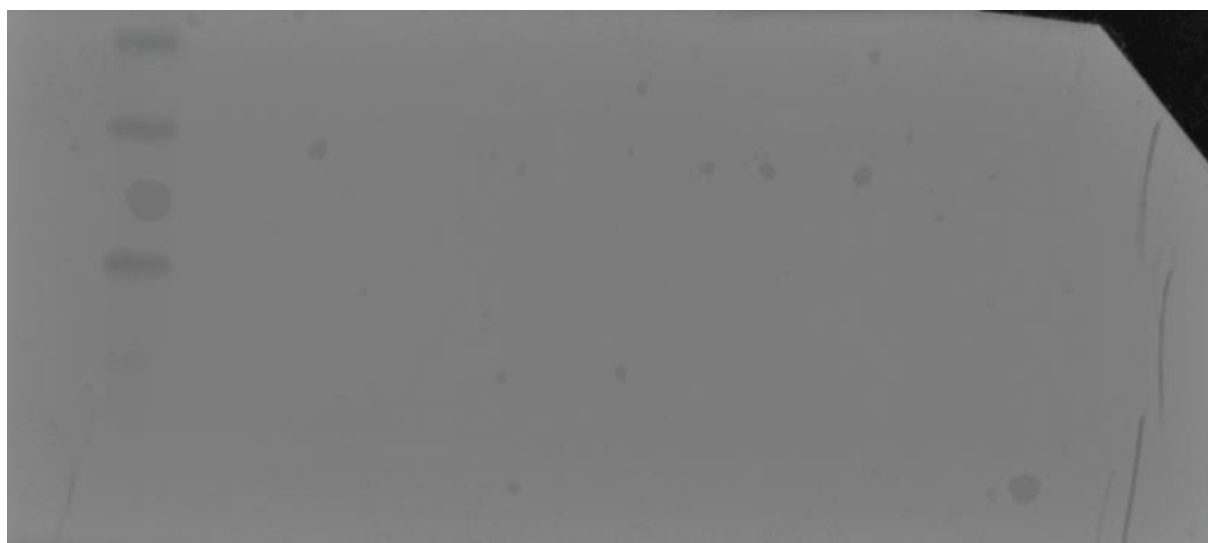
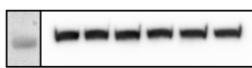
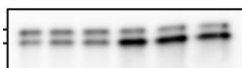
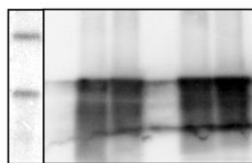
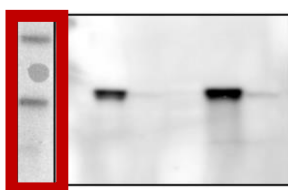
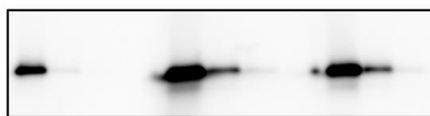


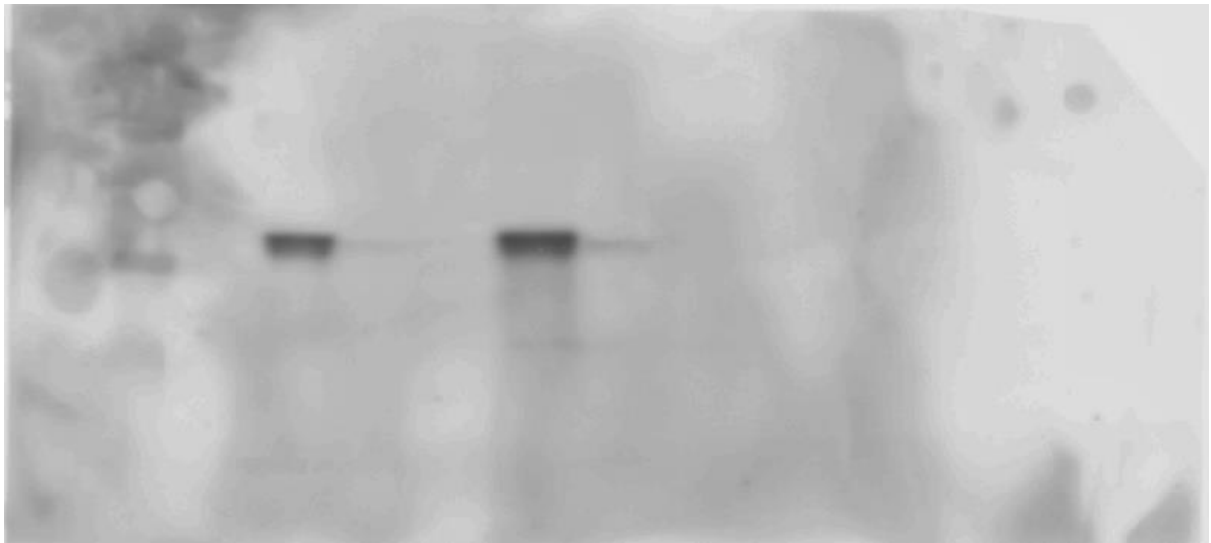
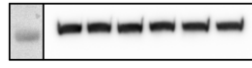
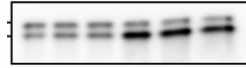
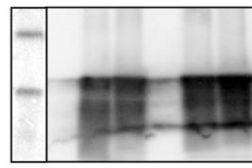
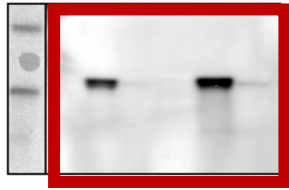
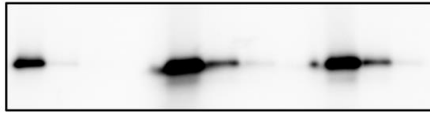
Supplementary Figure 6. Western Blots of insoluble phosphorylated and total α -syn in OLN-93 and OLN-AS7 cells treated with WT PFFs or S129A PFFs and 20mM ammonium chloride, 10 μ M lactacystin and 10nM okadaic acid. Uncropped Western blots are shown in Supplementary Figure 8.

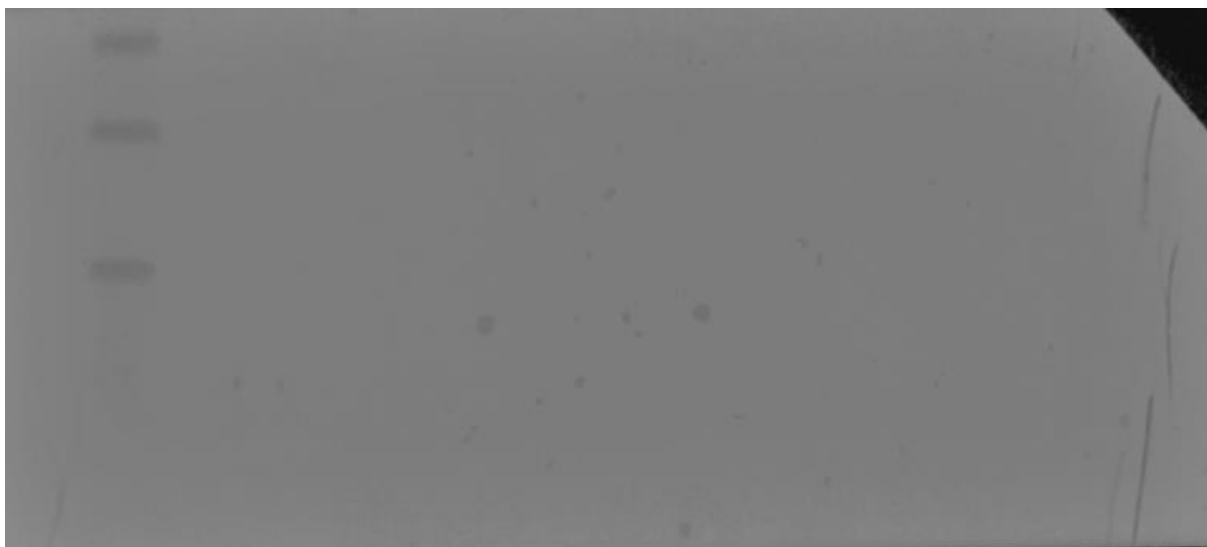
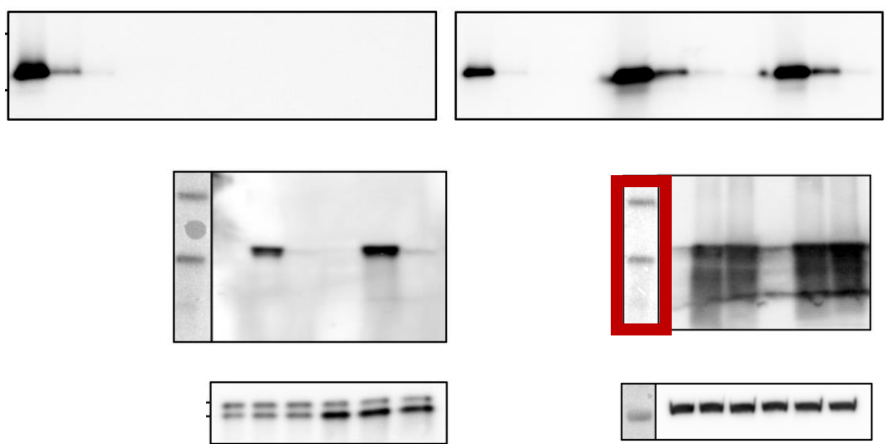
Supplementary Figure 7. Uncropped Western Blot images from Figure 9. Uncropped blots are shown individually, marked red in overview image of Figure 9.

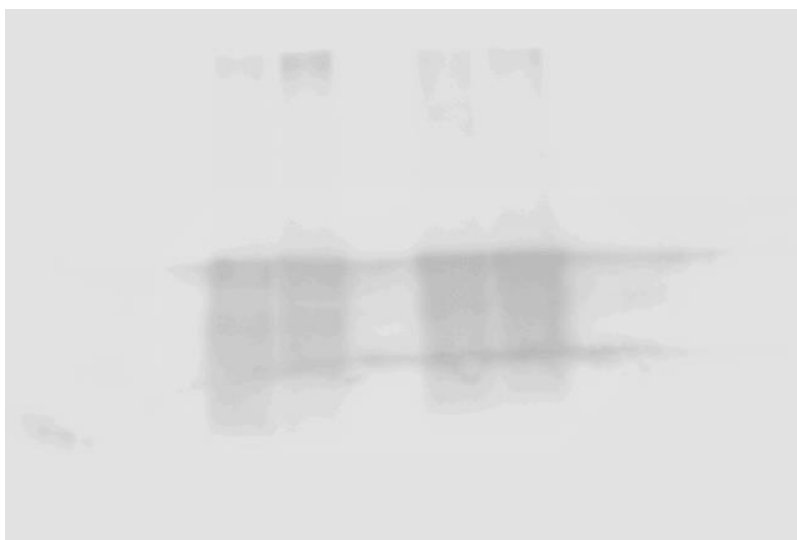
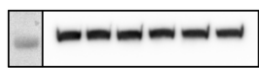
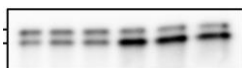
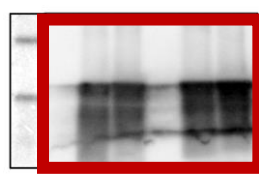
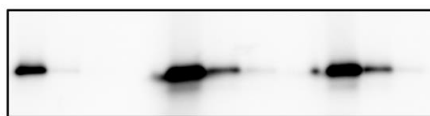


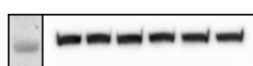
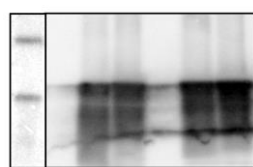
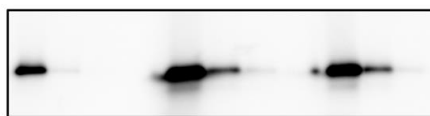


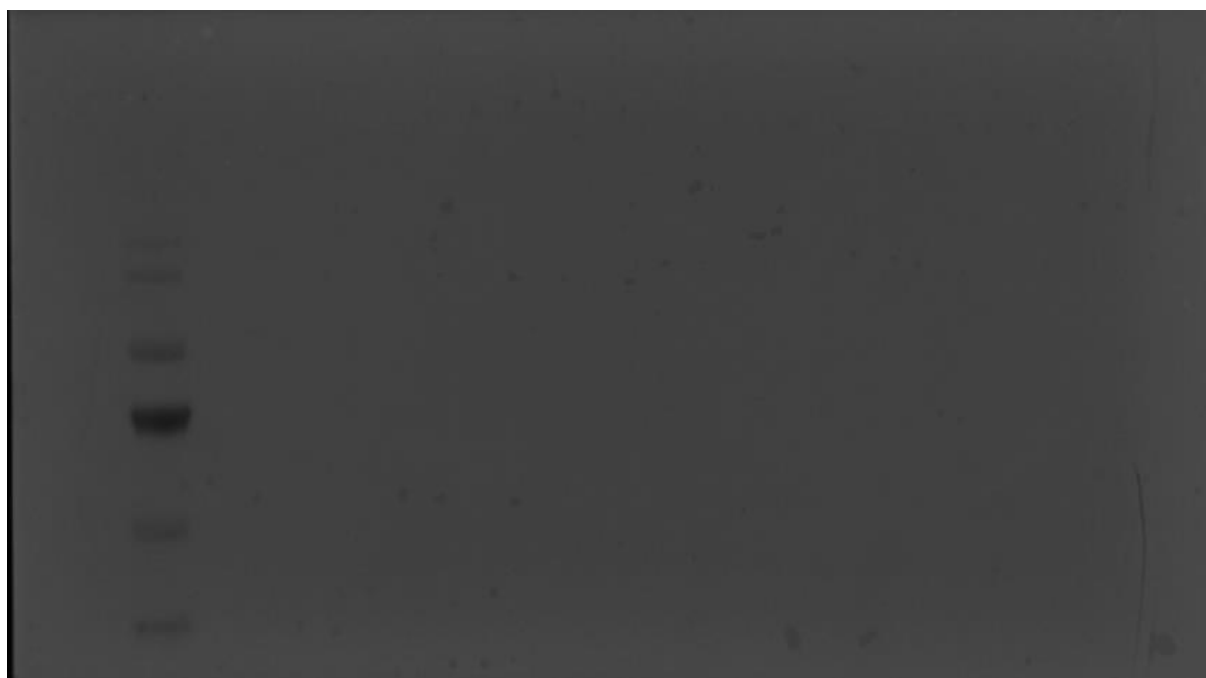
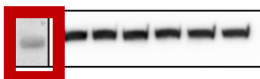
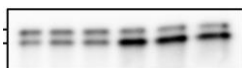
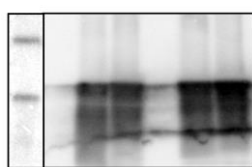
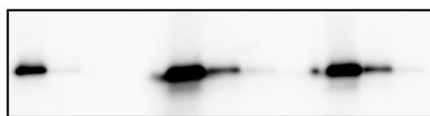


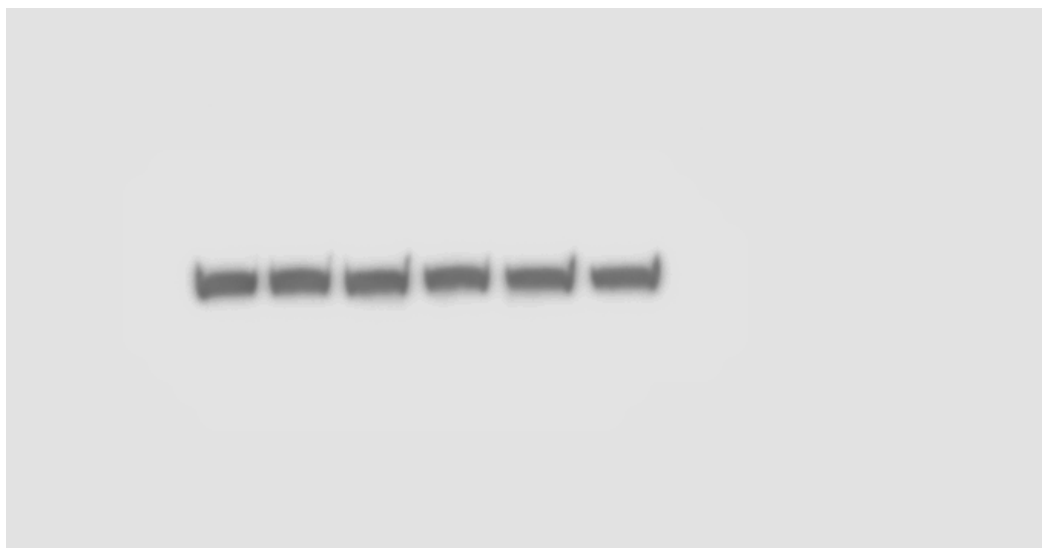
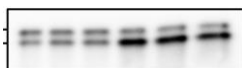
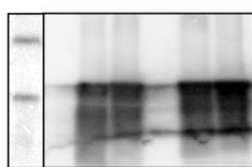
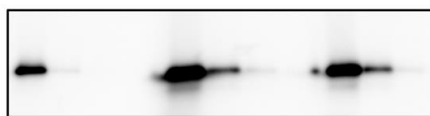




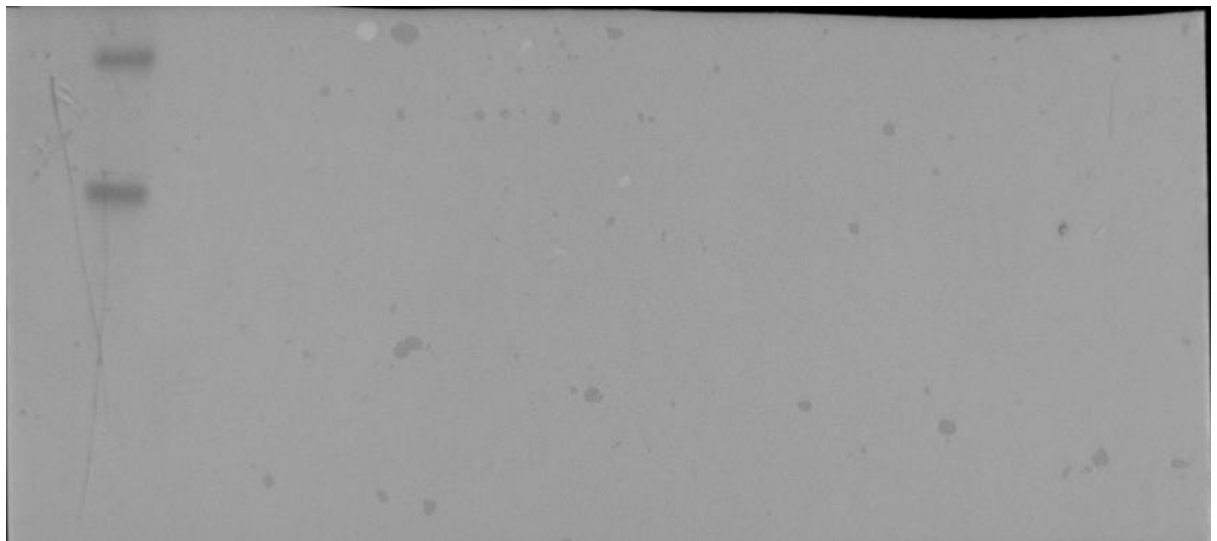
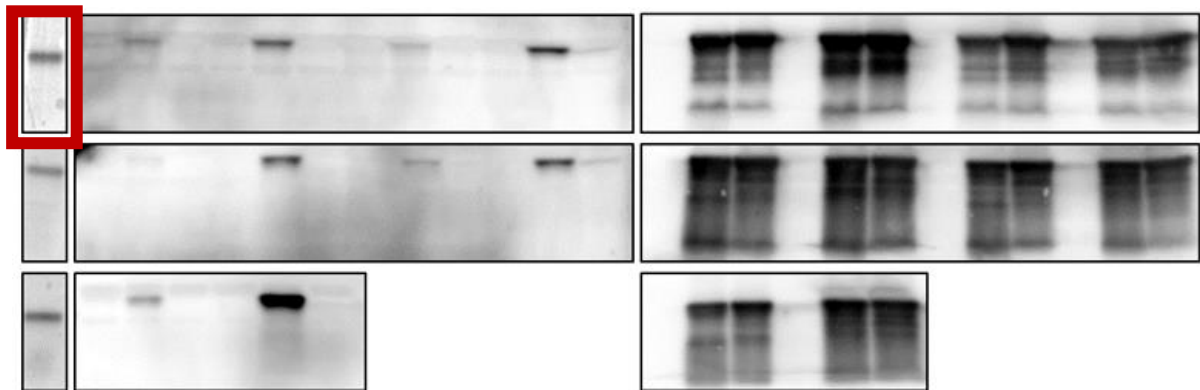


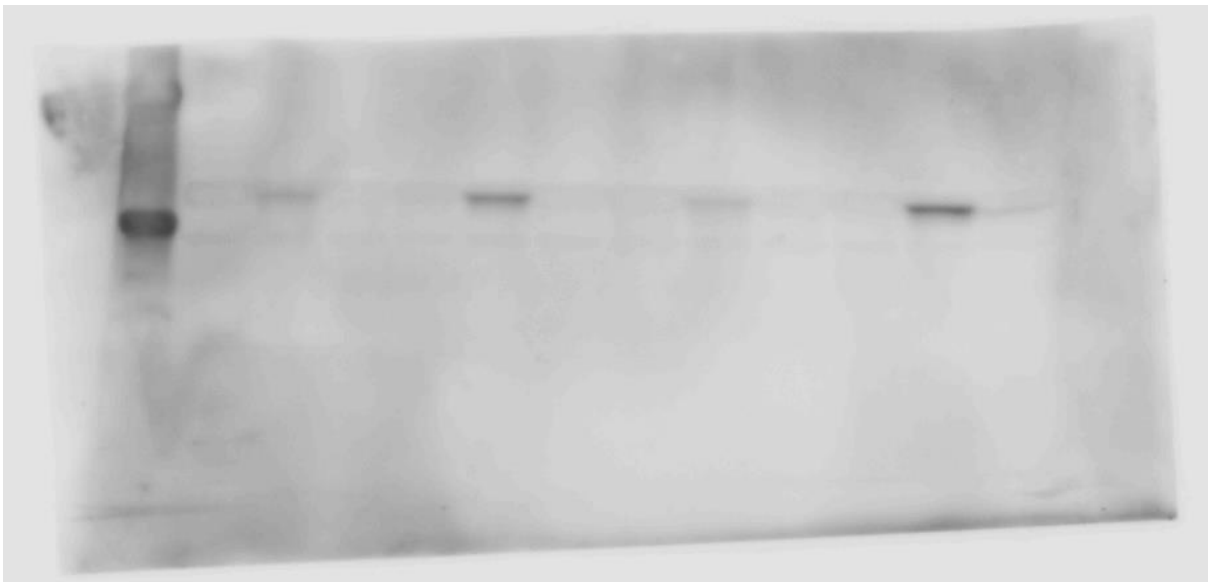
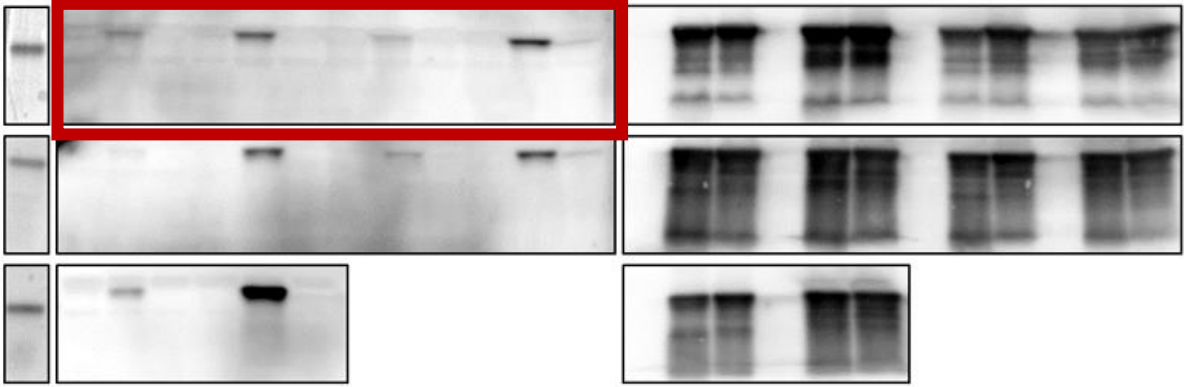


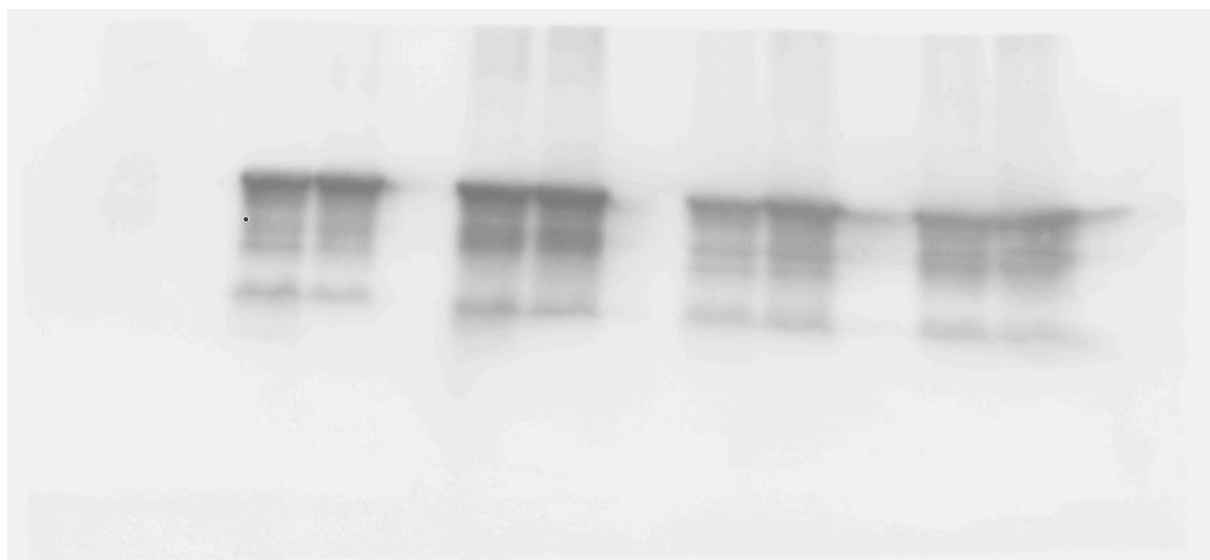
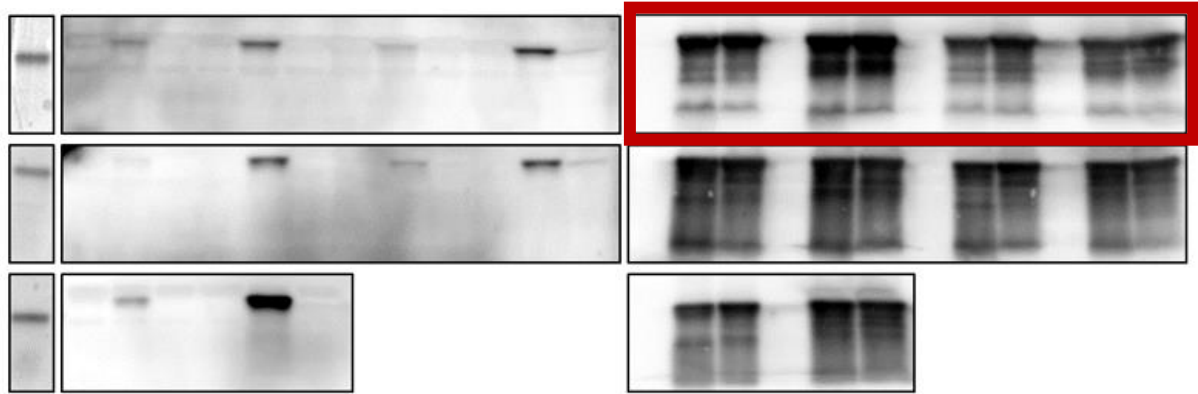


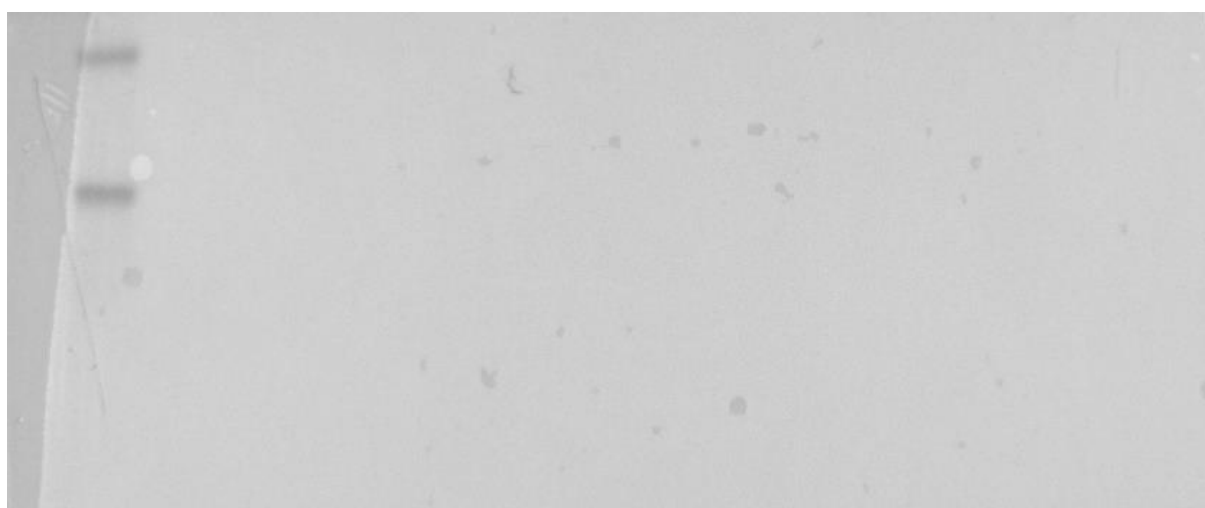
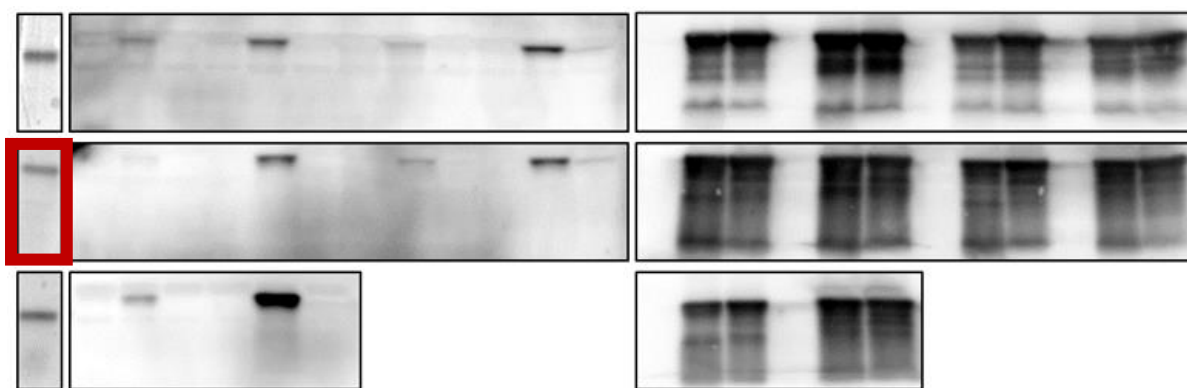


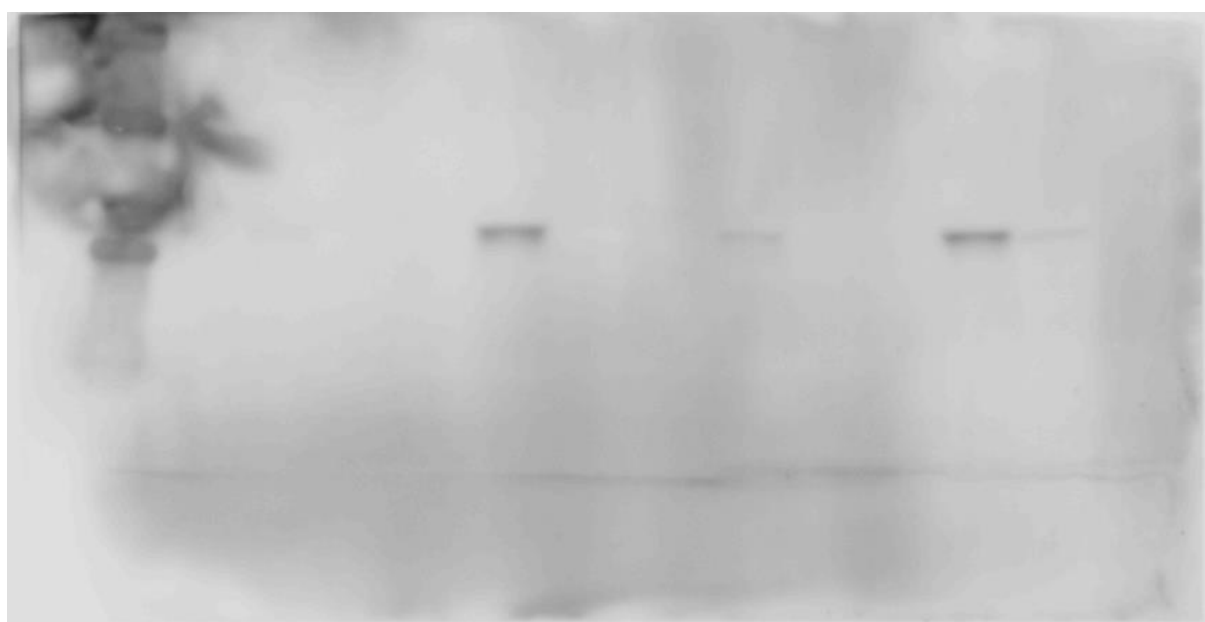
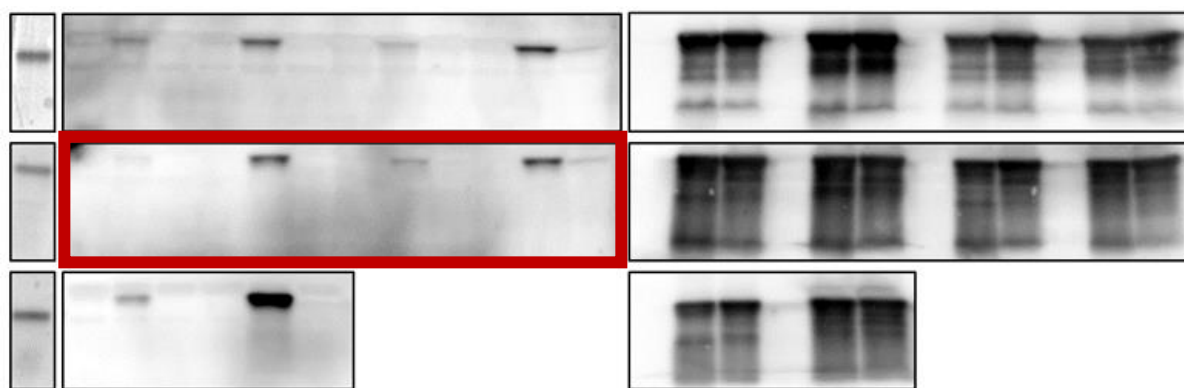
Supplementary Figure 8. Uncropped Western Blot images from Supplementary Figure 6. Uncropped blots are shown individually, marked red in overview image of Supplementary Figure 6.

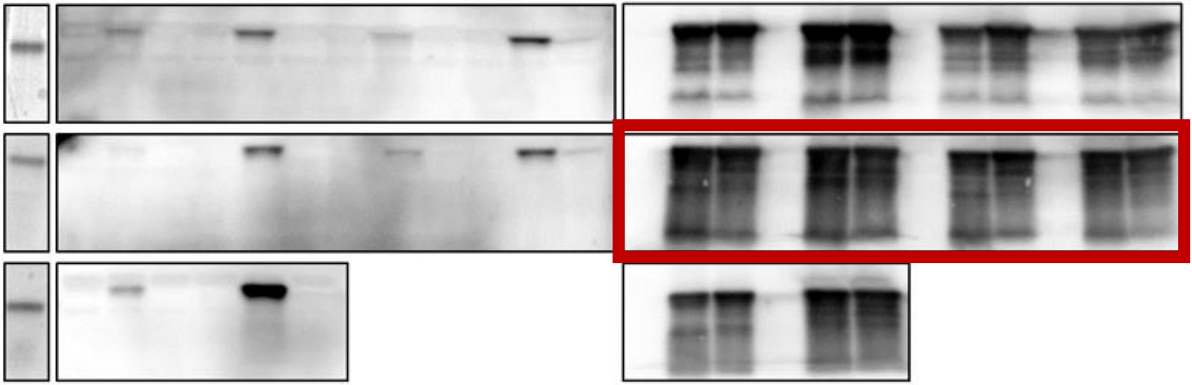


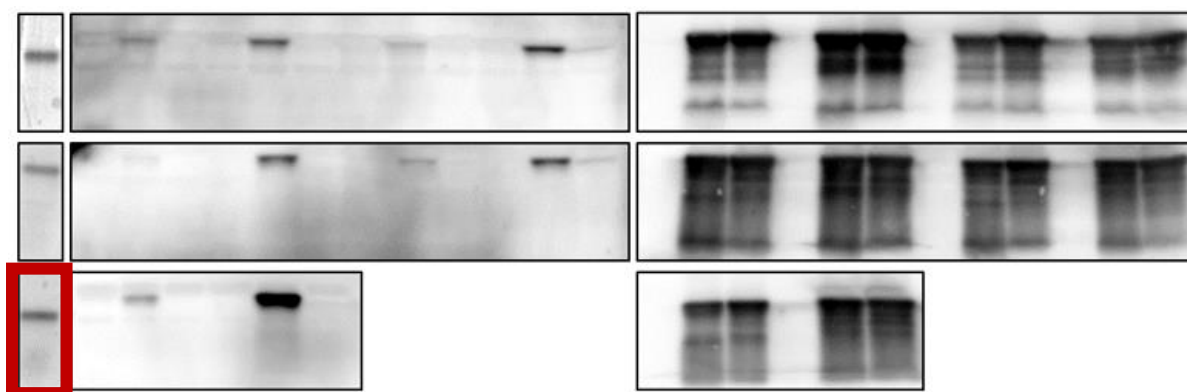


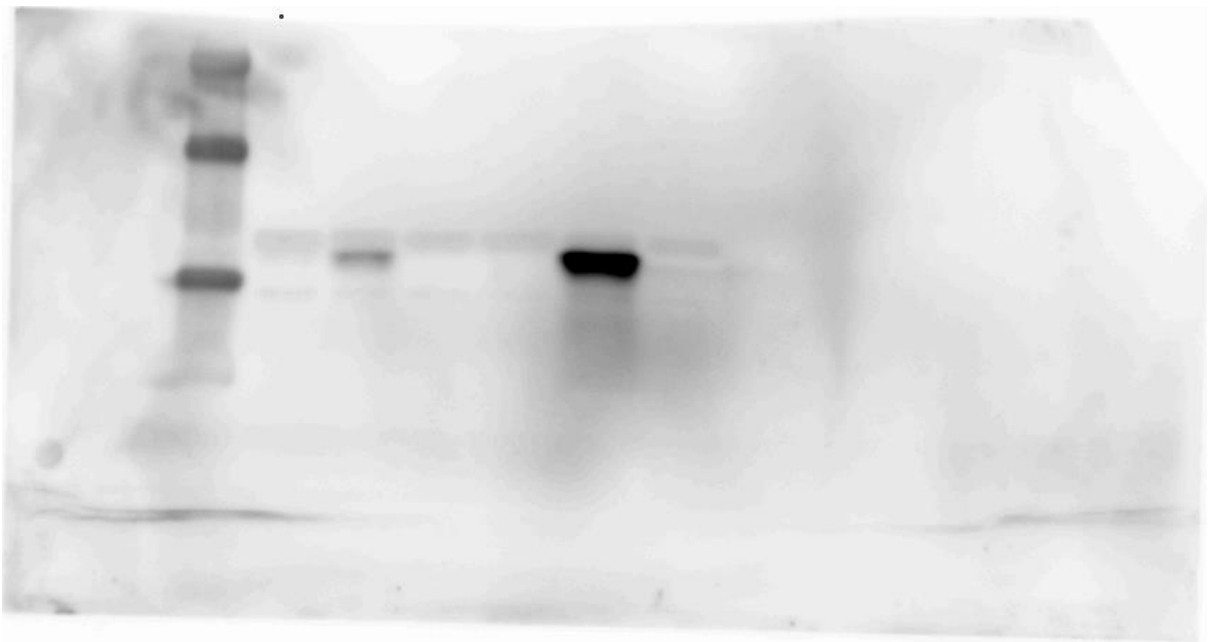
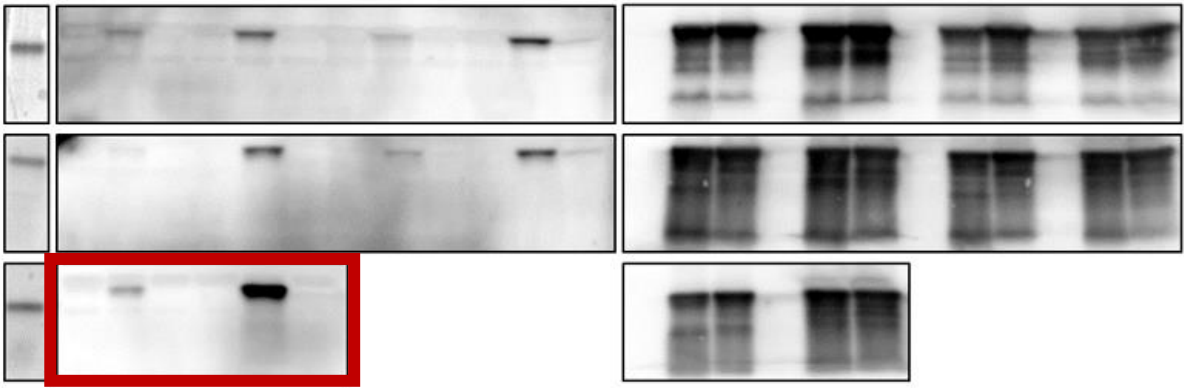


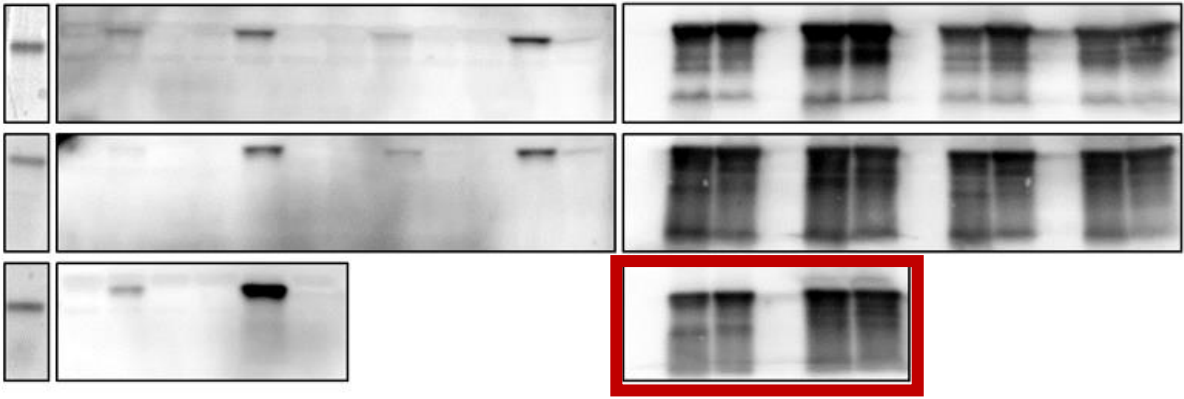












Supplementary Table 1. Data collection, refinement, and validation statistics.

Data collection and scaling	
Spacegroup	P2 ₁ 2 ₁ 2 ₁
Cell parameters	a = 37.484 Å b = 66.700 Å c = 167.167 Å
Wavelength (Å)	0.97625
Resolution (Å)	83.58 – 1.712
Highest resolution bin (Å)	1.902 – 1.712
R _{merge}	0.208 (1.609)
Total number of observations	425239
Number of unique reflections	32524
I/σ(I)	8.5 (1.6)
Completeness (%)	87.5 (42.7)
Multiplicity	13.1 (11.6)
Refinement	
R _{work}	0.200
R _{free}	0.251
Average B factor (Å ²)	
protein	27.6
peptide	29.6
solvent	31.3
Number of atoms	
protein	3237
peptide	43
solvent	171
RMS deviations from ideal	

bond lengths (Å)	0.006
bond angles (°)	1.372
Ramachandran plot	
residues in favored regions (%)	96.7
residues in allowed regions (%)	99.8

Supplementary Table 2. Fitted kinetic parameters for the GCI measurements.

	Figure 5A	Figure 5B	Figure 5C	Figure 5D	Figure 5E	Figure 5F	Figure 5G	Figure 5H	Figure 5I	Figure 5J
Chip	4PCP-PAG	4PCP-PAG	4PCP-PAG	4PCP	4PCP	4PCP	4PCP-STA	4PCP-STA	4PCP-STA	4PCP-STA
Ligand (immobilised)	MJFR14-6-4-2	MJFR14-6-4-2	MJFR14-6-4-2	Fab	Fab	Fab	OLIGO	OLIGO	VLP	VLP
Analyte	MONO	OLIGO	VLP	MONO	OLIGO	VLP	Fab	MJFR14-6-4-2	Fab	MJFR14-6-4-2
k_a , $M^{-1} s^{-1}$	$1.2 (\pm 0.11) \times 10^6$	No dissociation	No dissociation	$2.96 (\pm 0.13) \times 10^5$	No dissociation	$1.00 (\pm 0.06) \times 10^5$	$5.11 (\pm 0.49) \times 10^5$	$2.26 (\pm 0.31) \times 10^6$	$8.45 (\pm 0.99) \times 10^5$	$2.84 (\pm 0.16) \times 10^5$
k_d , s^{-1}	$6.37 (\pm 0.49) \times 10^{-1}$			$8.48 (\pm 0.25) \times 10^{-1}$		$1.89 (\pm 0.17) \times 10^{-2}$	$9.43 (\pm 1.05) \times 10^{-2}$	$8.21 (\pm 1.79)$	$1.16 (\pm 0.11) \times 10^{-1}$	$3.72 (\pm 0.97) \times 10^{-3}$
K_D , μM	0.530			2.861		0.189	0.184		0.136	0.001