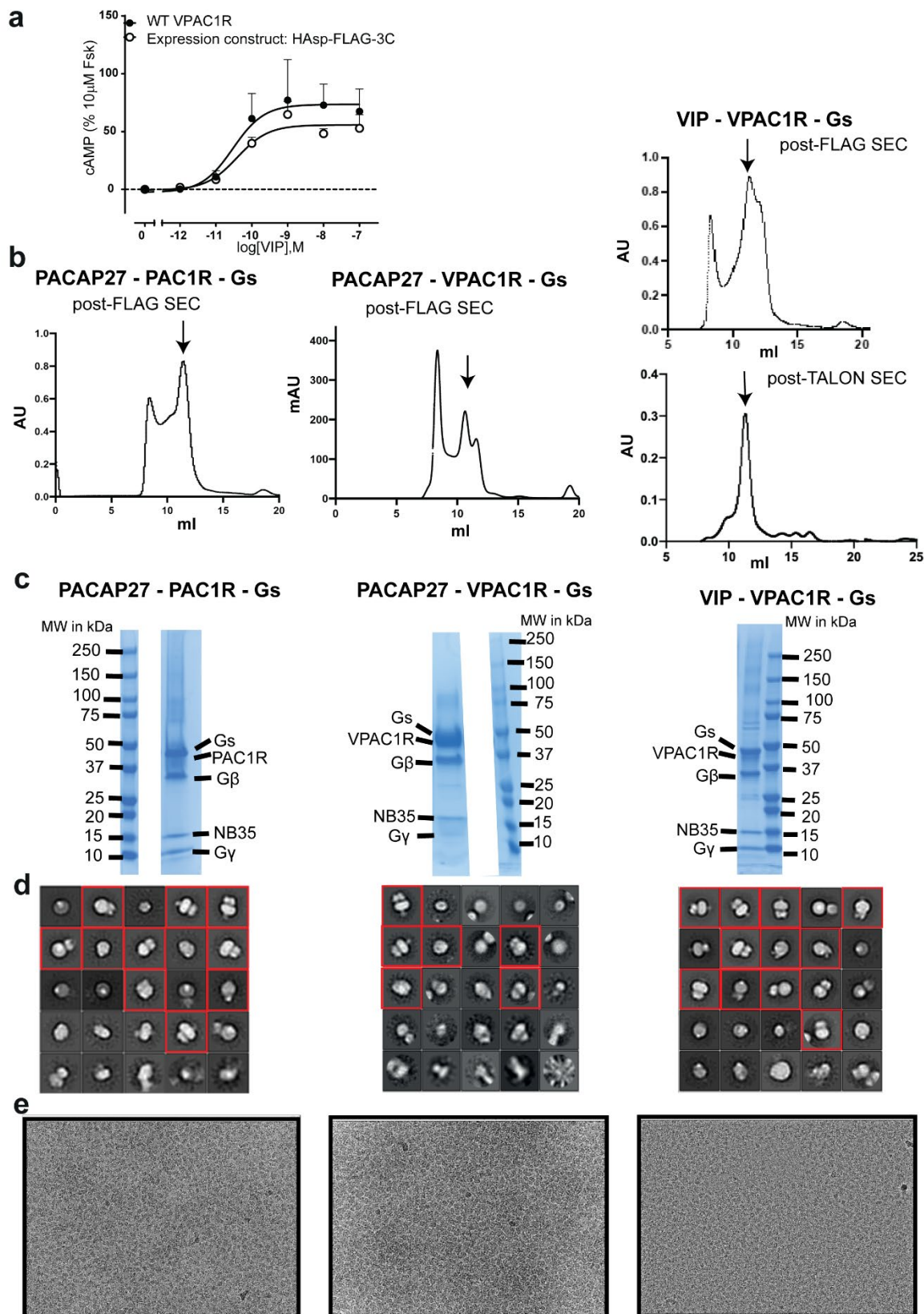
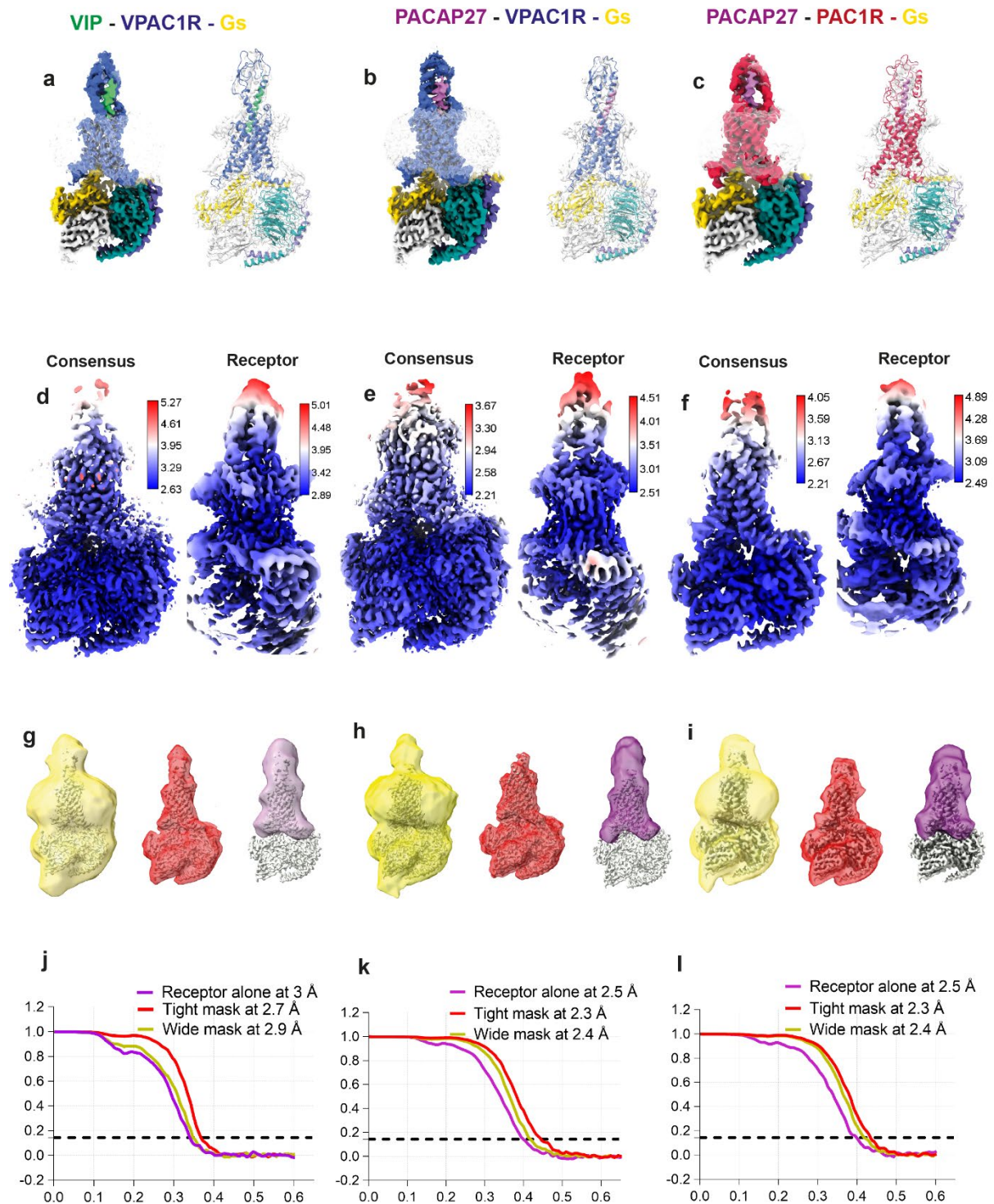


Supplementary Information
Understanding VPAC receptor family peptide binding and selectivity

Piper et al.

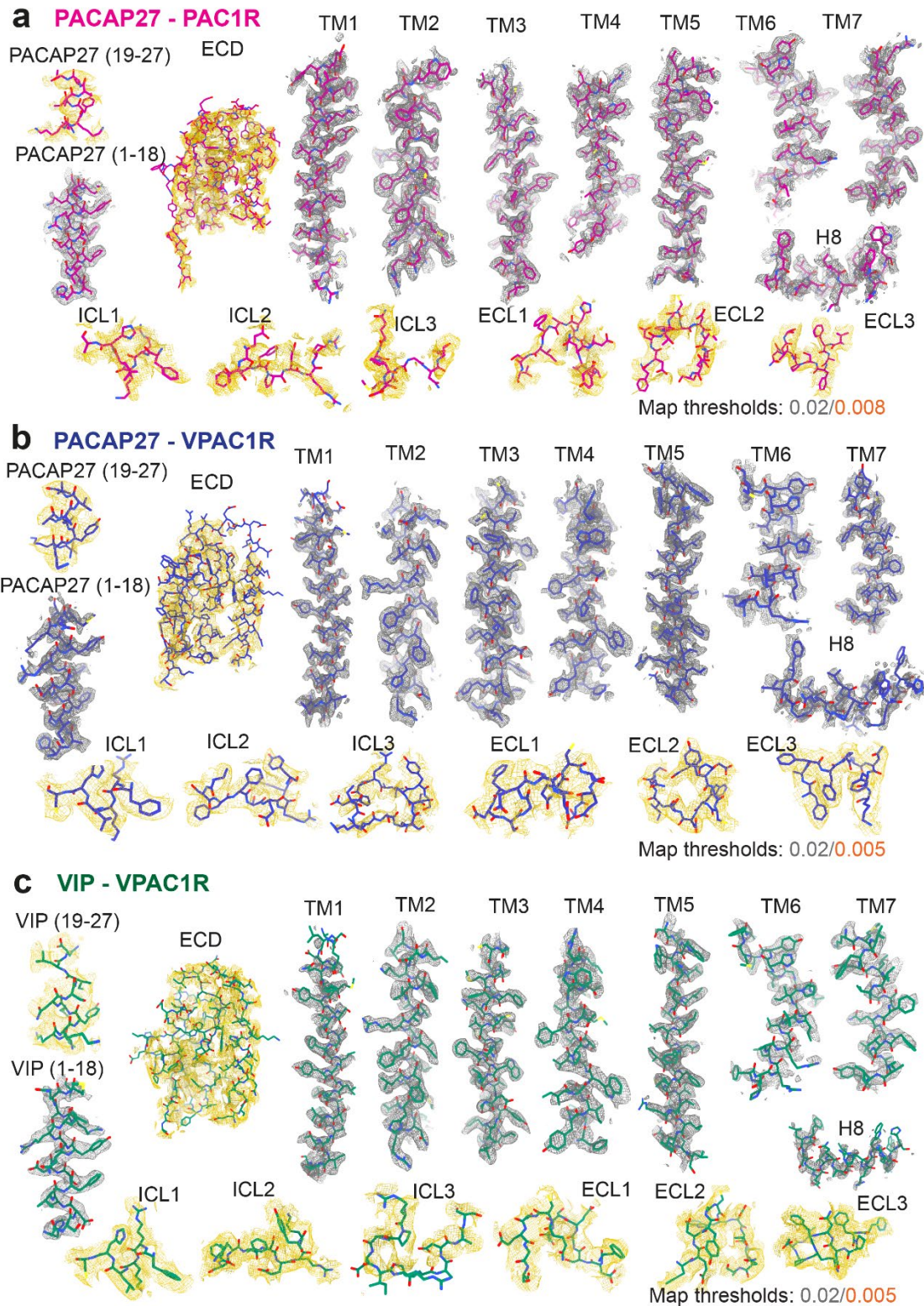


Supplementary Figure 1. Complex purification and quality control. a: cAMP accumulation data for the VPAC1R expression construct used in this study (white circles), in comparison with the wild-type construct (black circles), in response to VIP. Data are presented as mean+SEM of 3 independent experiments. HAsp: HA signal peptide. FLAG, HIS: Purification tags. 3C: 3C protease cleavage site. b: Size-exclusion chromatography (SEC) trace of the PAC1R-PACAP27-Gs, VPAC1R-PACAP27-Gs and VPAC1R-VIP-Gs complex purifications, with the complex peak eluting at ~11-13 ml (indicated by arrows). For the VPAC1R-VIP sample, two size-exclusion chromatography steps were conducted, after FLAG resin elution (1.) and after Talon resin elution (2.). c: Coomassie-stained SDS-PAGE of the complex sample used for cryo-EM imaging, showing bands of all complex components (protein marker molecular weight indicated in kilodalton (kDa)): Dominant-negative G α s subunit (Gs), receptor VPAC1R (right and middle) or PAC1R (left), G β subunit, G γ subunit and Nanobody 35 (NB35). Uncropped Coomassie-stained SDS-PAGE are available at the end of this Supplementary Information file (below). d: Negative-stain TEM 2D classification of complex sample used for cryo-EM imaging, with 2D classes of complexes framed in red. e: Representative micrographs for each data collection/complex, at around 1 μ m defocus, displayed using a lowpass filter (20 Å). The complex purification and data collection for each structure obtained in this manuscript was performed once (n=1).



Supplementary Figure 2. Cryo-EM maps and models of active, Gs-coupled PACAP family complexes. Complexes of VPAC1R-VIP-Gs (a,d,g,j), VPAC1R-PACAP27-Gs (b,e,h,k) and PAC1R-PACAP27-Gs (c,f,l,i) are separated by columns and different subunit colouring. a-c: Consensus map and model fit of the receptor-peptide complexes with coloured map surface (left) and transparent map and ribbon model (right). Colours: VIP: spring green, PACAP27: orchid, PAC1R: red, VPAC1R: royal blue, Gs: goldenrod, G β : dark cyan, G γ : slate blue, Nanobody35: white. d-f: Consensus map (left) and receptor-focused map (right) coloured by resolution (blue: high, red: low). g-i: Consensus wide mask (yellow), consensus tight mask (red) and receptor-focused mask (purple) applied during 3D refinement and/or post-

processing. j-l: Fourier-shell correlation (FSC) curves indicating the resolution determined using the gold-standard 0.143 cut-off, for the masked, post-processed maps, coloured according to mask applied (see g-i). Purple: receptor-alone focus; red: tight mask (without micelle and α -helical domain); yellow: wide mask.

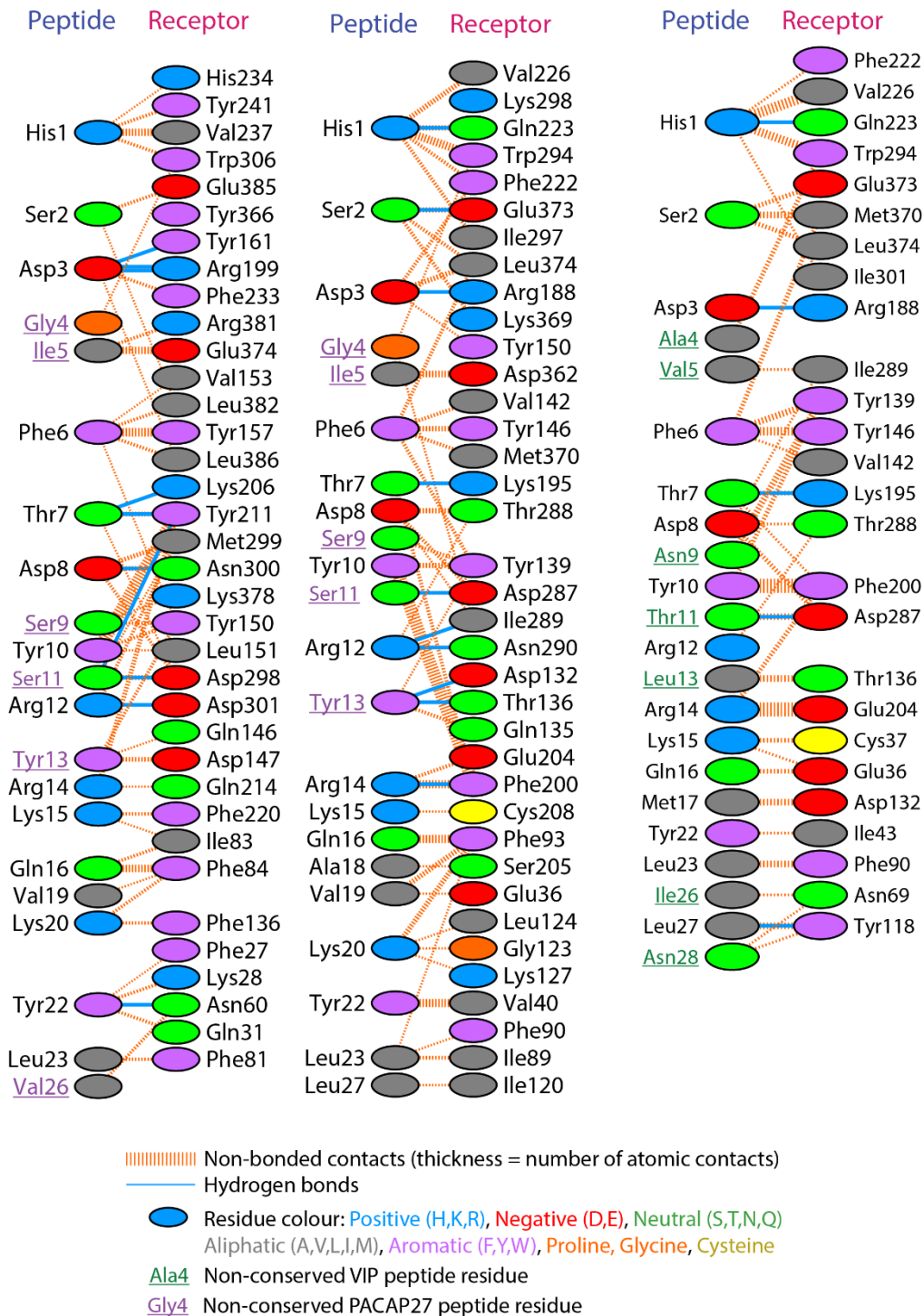


Supplementary Figure 3. Model fit into cryo-EM maps. Maps are displayed as mesh at the indicated volume map threshold in ChimeraX, using the tool 'Surface Zone' with 2 Å radius. The receptor-alone focused map (yellow) was used to build the ECD, peptide C-terminus as well as ECLs and ICLs. The higher resolution consensus map (grey) was used for the TMs, H8 and peptide N-terminus. Models are shown as stick in atom representation. a: PAC1R-PACAP27 (pink), b: VPAC1R-PACAP27 (blue) and c: VPAC1R-VIP (green).

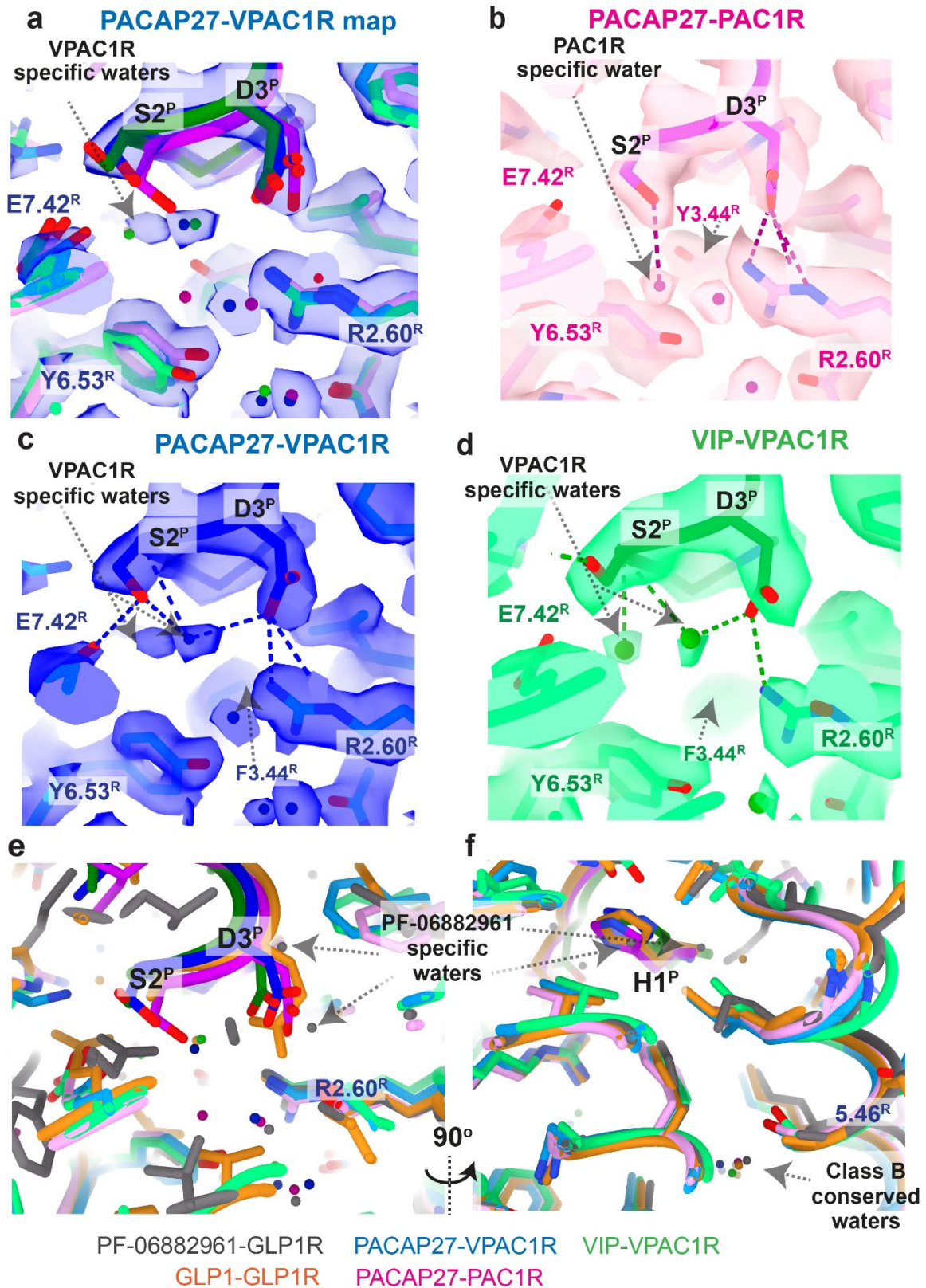
PAC1-PACAP27-Gs

VPAC-PACAP27-Gs

VPAC-VIP-Gs



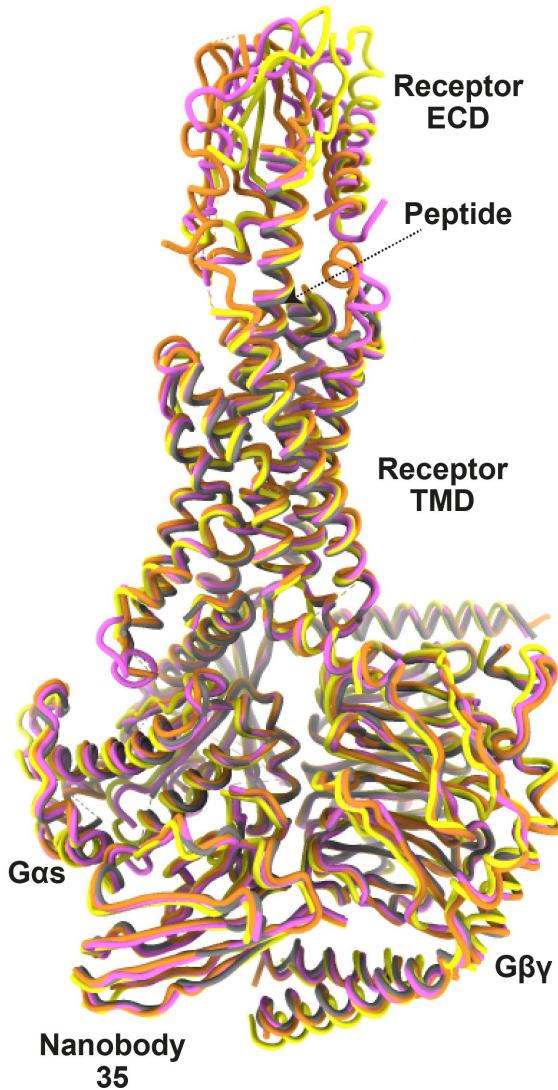
Supplementary Figure 4. Peptide-receptor interaction table. List of generic, van-der-Waals contacts (non-bonded, dotted orange lines) and hydrogen bonds (blue lines) of PAC1R-PACAP27, VPAC1R-PACAP27 and VPAC1R-VIP from the static experimental cryo-EM structures created using Dimplot in Ligplot/LigPlus software. Peptide residues that differ between VIP and PACAP27 are coloured in green and purple, respectively. Residues are represented as oval circles and coloured by residue property/group (positive: blue, negative: red, neutral: green, aliphatic: grey, aromatic: purple, Pro/Gly: orange, Cys: yellow).



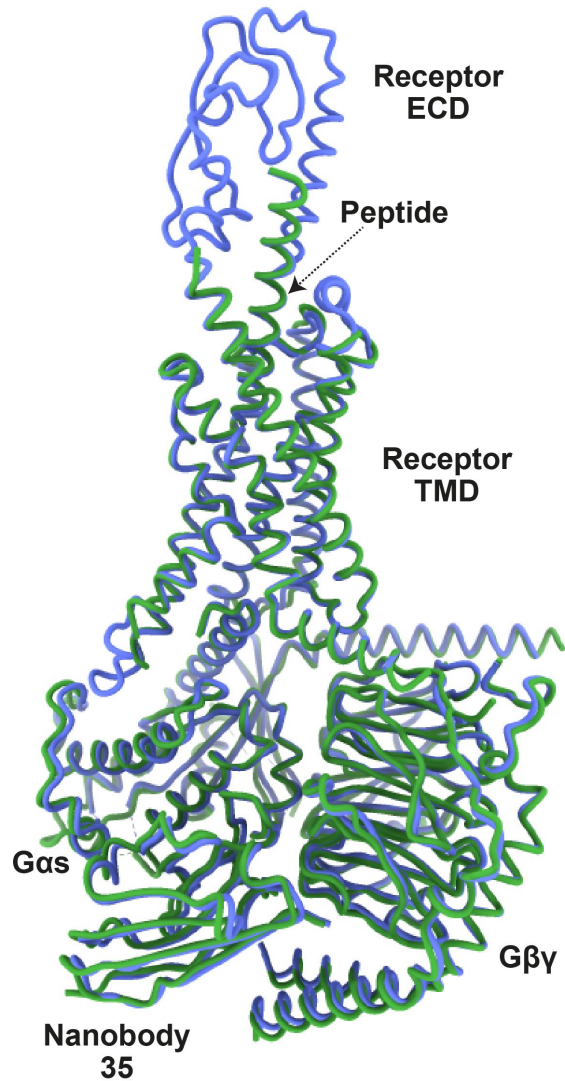
Supplementary Figure 5. Water network near the peptide N-terminus (S2-D3 residues) in the cryo-EM maps. The receptor backbone and peptide backbone are shown in ribbon format, with sidechains displayed in stick format, showing a zoomed-in side view of the map and model environment of the S2-D3 peptide residues. Water molecules are shown as single spheres. PAC1R-PACAP27 is shown in pink-dark pink, VPAC1R-PACAP27 in blue-dark blue

and VPAC1R-VIP in green-dark green, with the cryo-EM consensus maps (post-processed, auto B-factor sharpened with visible densities for water molecules) in the receptor colours shown in transparent. H-bonds involving receptor and peptide residues or waters are shown as dotted lines. Receptor residues are numbered according to the Wootten et al, class B1 scheme. a: Overlay of receptor-aligned models of PAC1R-PACAP27, VPAC1R-VIP and VPAC1R-PACAP27 with the VPAC1R-PACAP27 map (blue transparent) as reference. b-d: Models in their respective maps, of PAC1R-PACAP27 (pink, b), VPAC1R-PACAP27 (blue, c) and VPAC1R-VIP (green, d). e-f: Water network near the peptide N-terminus of GLP1R-GLP1 (orange, PDB 6X18) and below the small molecule binding side of GLP1R-PF-06882961 (grey, PDB 6X1A) as well as PAC1R-PACAP27 (pink), VPAC1R-VIP (green) and VPAC1R-PACAP27 (blue).

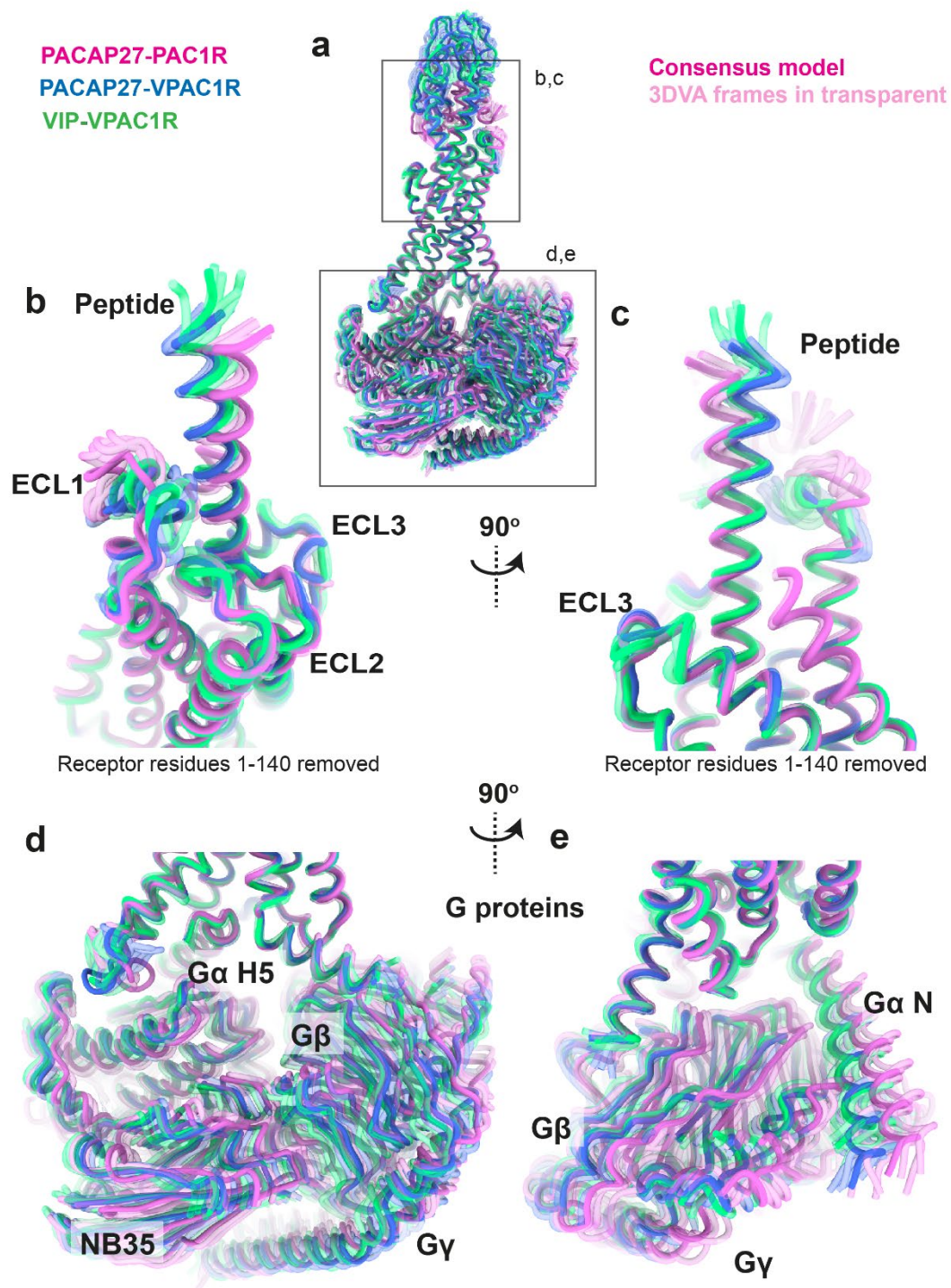
a PACAP27-PAC1R (this study)
PACAP38-PAC1R (PDB: 6M1I)
PACAP38-PAC1R (PDB: 6LPB)
PACAP38-PAC1R (PDB: 6P9Y)



b PACAP27-VPAC1R (this study)
PACAP27-VPAC1R nanobit (6VN7)

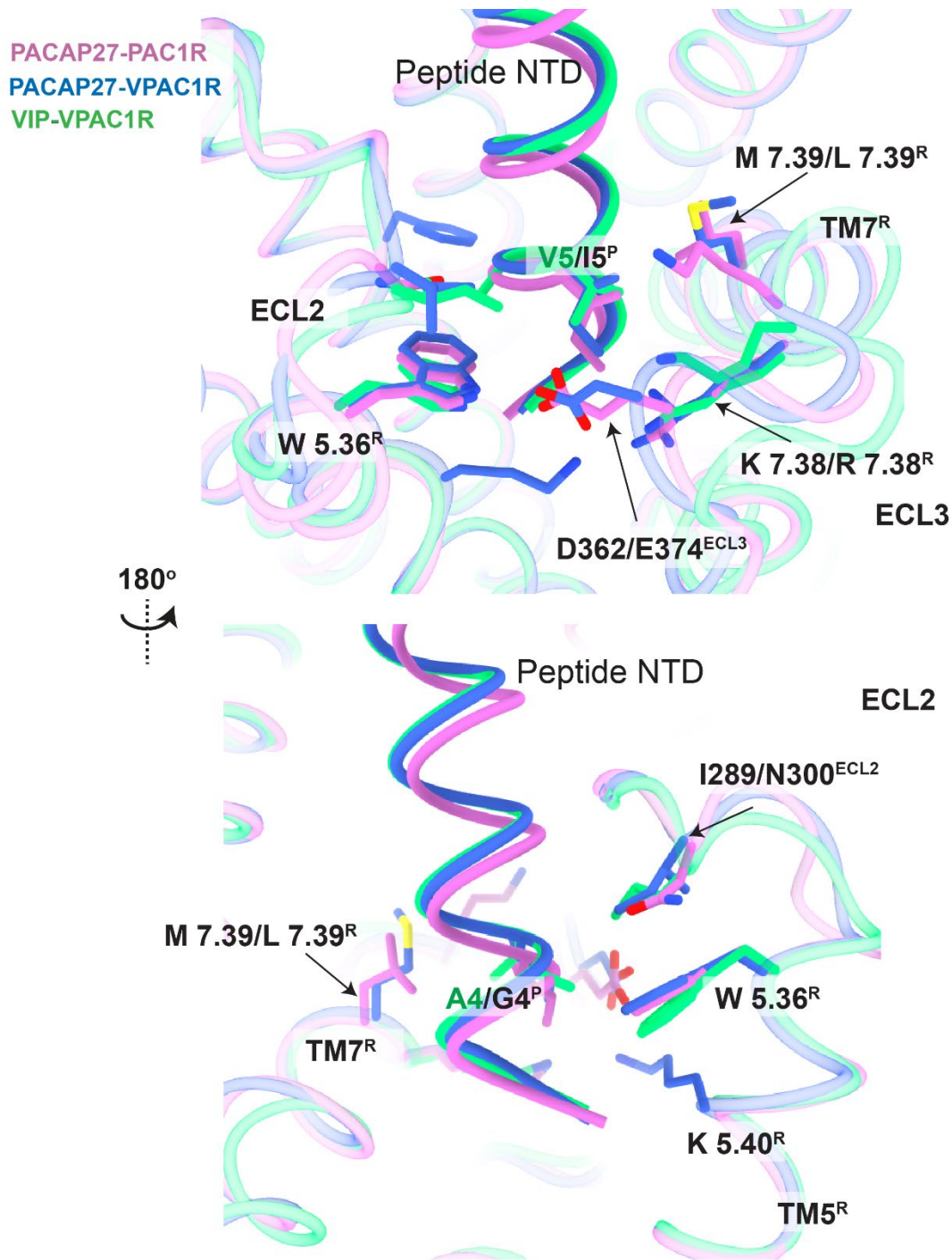


Supplementary Figure 6. Overlay of published PAC1R-PACAP38 and VPAC1R-PACAP27 with structures determined in this study. Models are shown as backbones in ribbon/licorice format. a: PAC1R-PACAP27 (pink) overlaid with available published structures of PAC1R-PACAP38 (PDB 6M1I, orange; PDB 6LPB, yellow; PDB 6P9Y, grey). b: VPAC1R-PACAP27 (blue) overlaid with available published structure of VPAC1R-PACAP27 using the nanobit technology (PDB 6VN7, green).



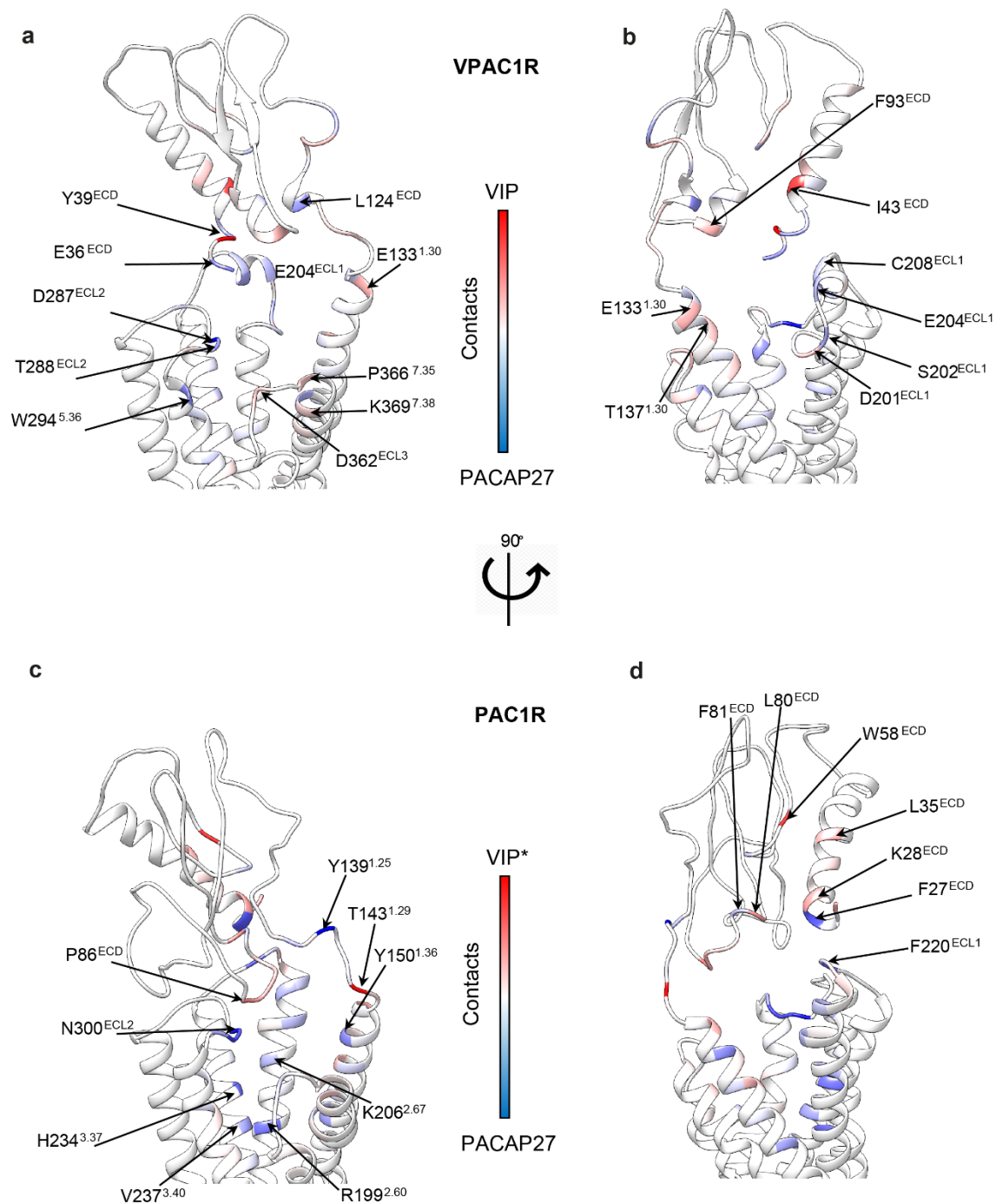
Supplementary Figure 7. Overlay of 3DVA frames aligned by receptor chains. VPAC1R-VIP (green), VPAC1R-PACAP27 (blue) and PAC1R-PACAP27 (pink) frames derived from the cryoSPARC 3D variability analysis (3DVA) were aligned by receptor chains and shown in transparent together with their respective static consensus structure (not transparent). Models are shown as backbones in ribbon/licorice format. The receptor-aligned models show offsets and variability in the peptide C-terminus, ECD as well as G proteins. a: Overview of entire

complex. b-c: Zoom of the peptide and ECLs (with ECD residues removed) as front (b) and side view (c). d-e: Zoom of the G proteins as front (d) and side view (e).

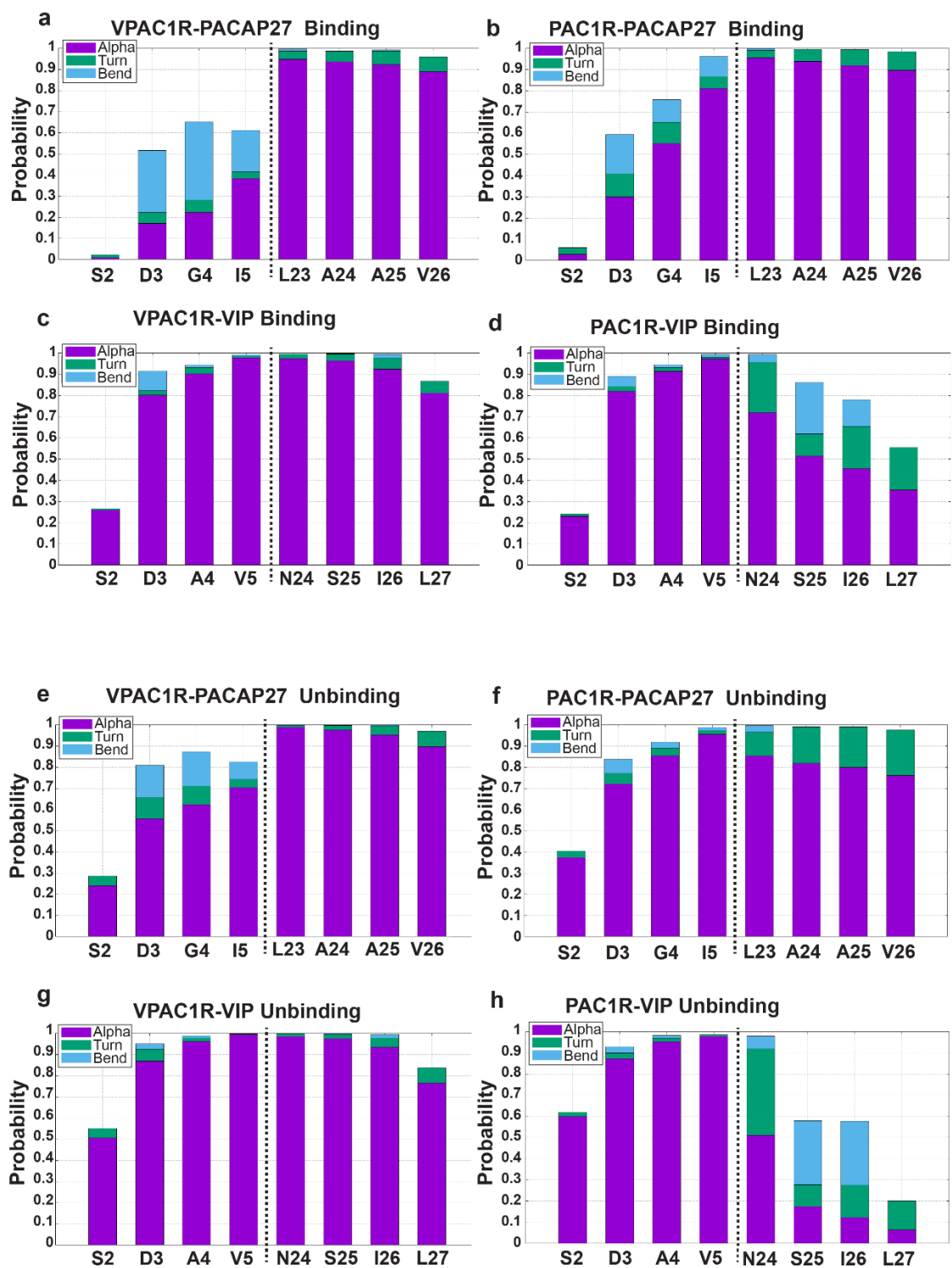


Receptor residues within 4 Å of peptide residues 4 and 5 shown as stick

Supplementary Figure 8. Contacts around peptide residues 4 and 5, based on the static experimental structures. Models are shown as backbones in ribbon format, with receptor residues within 4 Å of the peptide residues A4^{VIP}/G4^{PACAP27} and V5^{VIP}/I5^{PACAP27} shown as stick. Models are shown as front (top) and side view (bottom). Receptor residues are numbered according to the Wootten et al, class B1 scheme. Colour of models: VPAC1R-VIP (green), VPAC1R-PACAP27 (blue) and PAC1R-PACAP27 (pink).

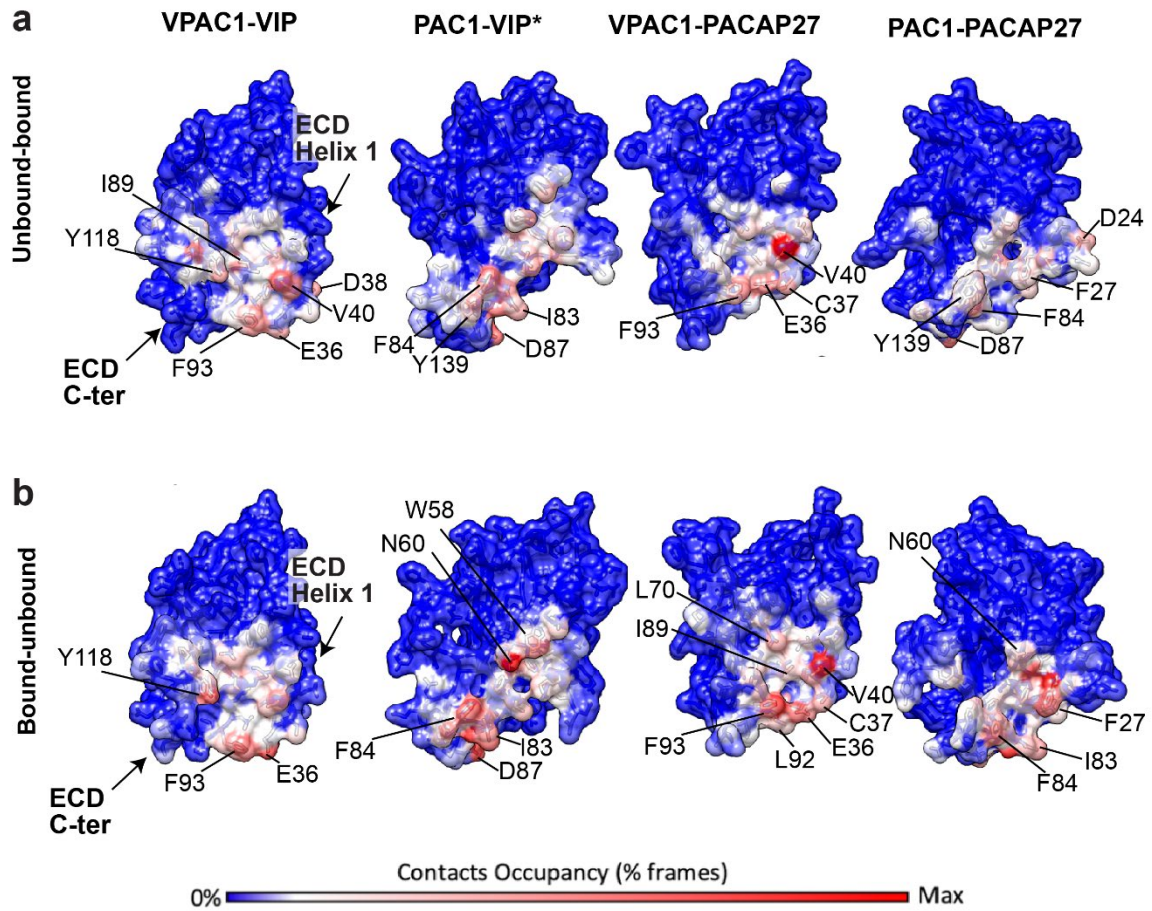


Supplementary Figure 9. Comparison of the generic contacts between PAC1R or VPAC1R and PACAP27 or VIP during MD simulations performed, on the PAC1R-PACAP27, PAC1R-VIP (homology model), VPAC1R-VIP, and VPAC1R-PACAP27 complexes. Residues more involved in contacts with PACAP27 are shown as blue backbone colouring, while residues more involved in contacts with VIP are shown as red backbone colouring. ab: Two-side view of VPAC1R (ribbon representation). c-d: Two-side view of PAC1R (ribbon representation). The PAC1-VIP complex was homology modelled (as indicated by asterisk *) and the MD simulations did not consider the full-length Gs protein (only the G α H5 was retained). Receptor residues are numbered according to the Wootten et al, class B1 scheme.



Supplementary Figure 10. DSSP analysis of the peptide residues in position 2-5 (N-terminus) and 23-26/27 (C-terminus) during peptide binding (a-d) and unbinding (e-h) MD simulations. MD simulations were performed on the PAC1R-PACAP27, PAC1R-VIP (homology model), VPAC1R-VIP, and VPAC1R-PACAP27 complexes. Probability of secondary structure of the peptide termini is displayed as height of bar graphs with α helix (purple), turn (green) and bend (blue).

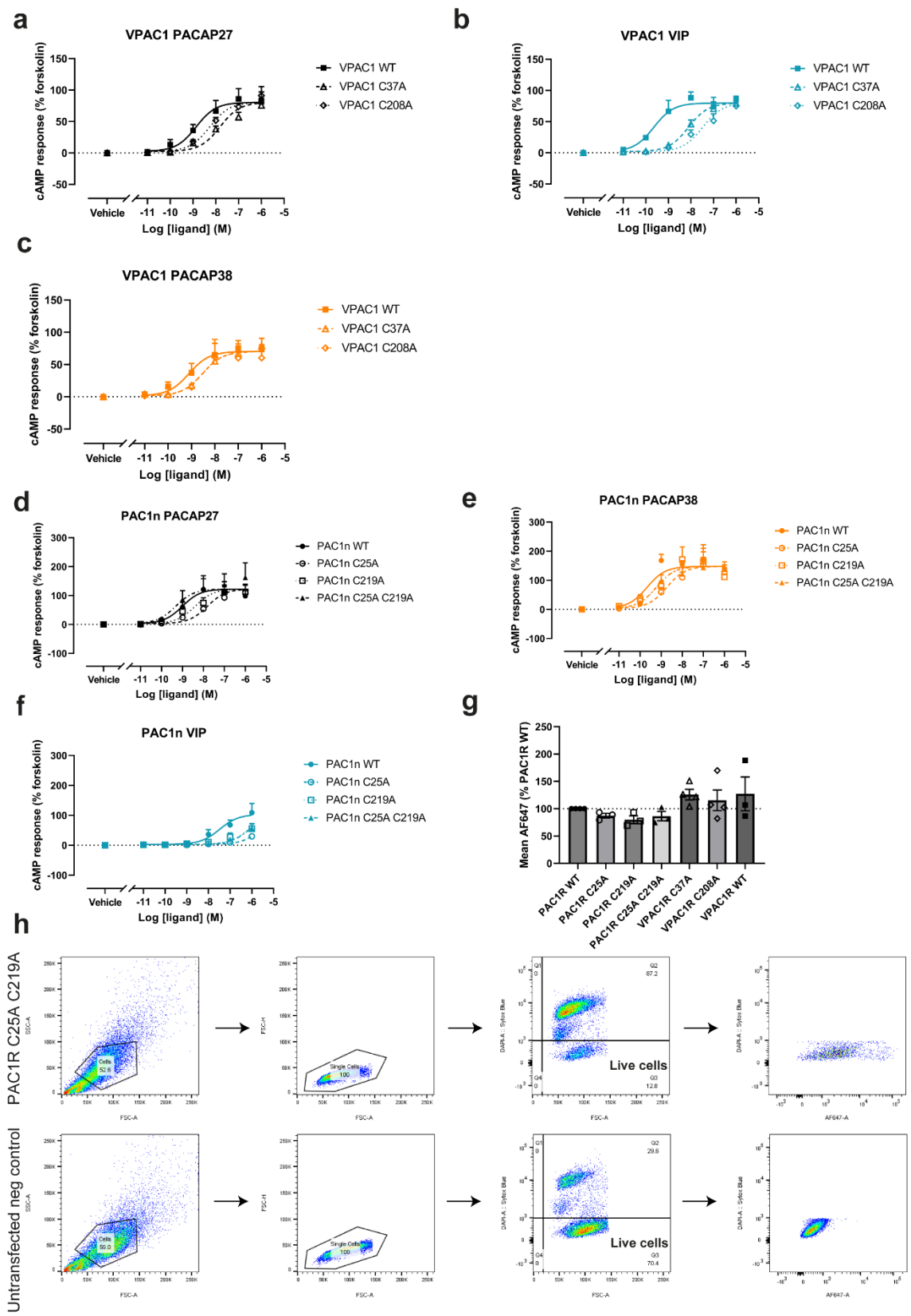
ECD side view (residues 36-129^{VPAC1R}/24-139^{PAC1R})



Supplementary Figure 11. Contacts occupancies based on unbinding and binding MD simulations comparing contacts between the peptides VIP and PACAP27 and receptors PAC1R and VPAC1R. MD simulations were performed on the experimental PAC1R-PACAP27, VPAC1R-VIP and VPAC1R-PACAP27 complexes as well as the PAC1R-VIP (homology model, as indicated by asterisk *). The total occupancy (% MD frames) for each atom is plotted on the surface of the receptor ECD (a,b) according to a colour scale from 0 % contacts occupancy = blue to maximum contacts occupancy = red. a,b: Side view of receptors PAC1R and VPAC1R (surface representation), showing only the ECD residues (36-129^{VPAC1R}/24-139^{PAC1R}) with occupancies plotted based on the binding simulation (a) or unbinding simulation (b). The PAC1-VIP complex was homology modelled (as indicated by asterisk *)

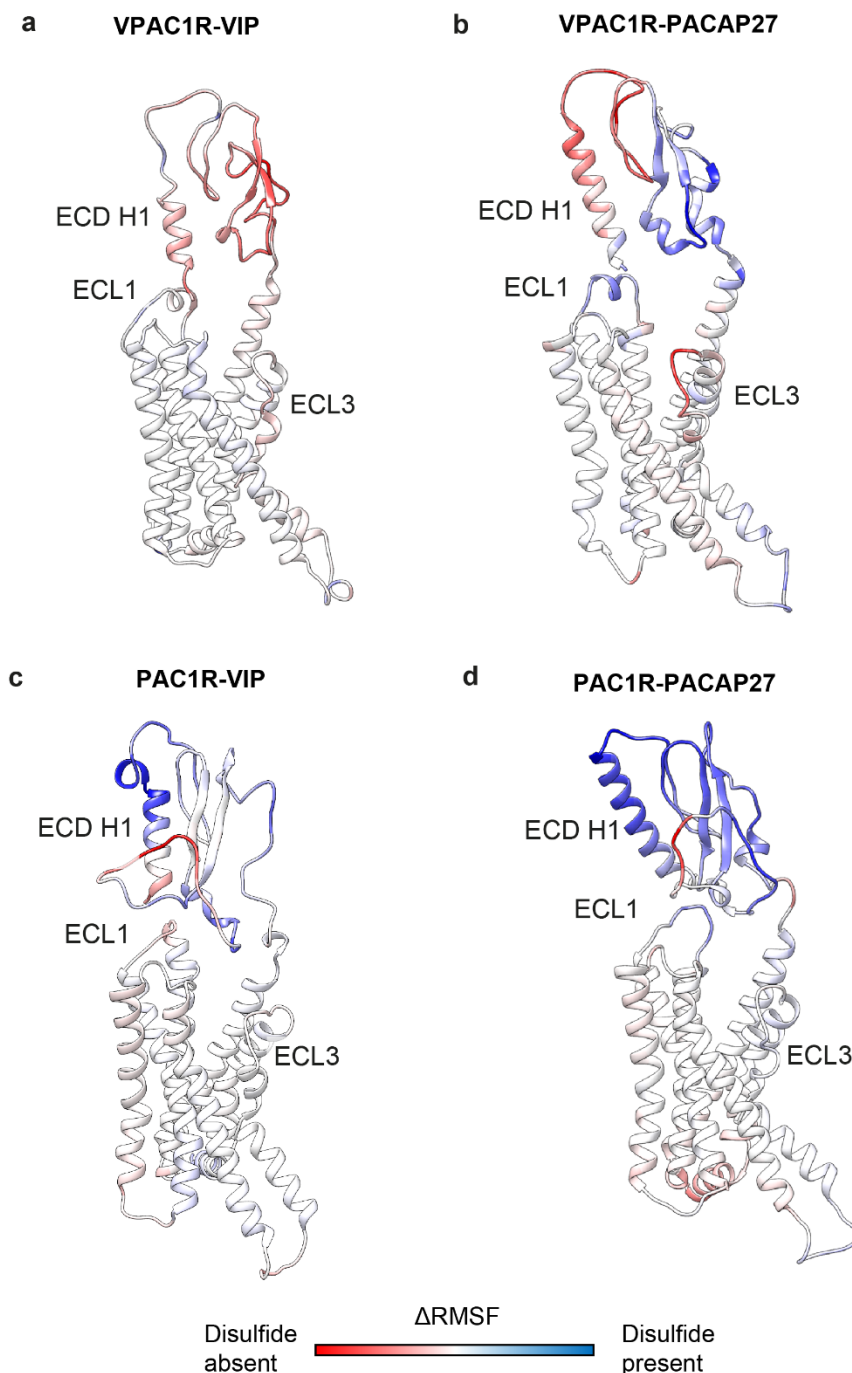


Supplementary Figure 12. MM-GBSA binding energies per peptide residues of VPAC and PAC1 receptor complexes without the ECD-ECL1 disulfide bond (a) and with the disulfide bond present (b). Bar graphs represent peptide residues binding energies in Kcal/mol in the experimental structures of PAC1R-PACAP27 (black), VPAC1R-PACAP27 (green), VPAC1R-VIP (blue), and homology modelled PAC1R-VIP complex (yellow, indicated by asterisk*). MM-GBSA: Molecular Mechanics-Generalized Born Surface Area.

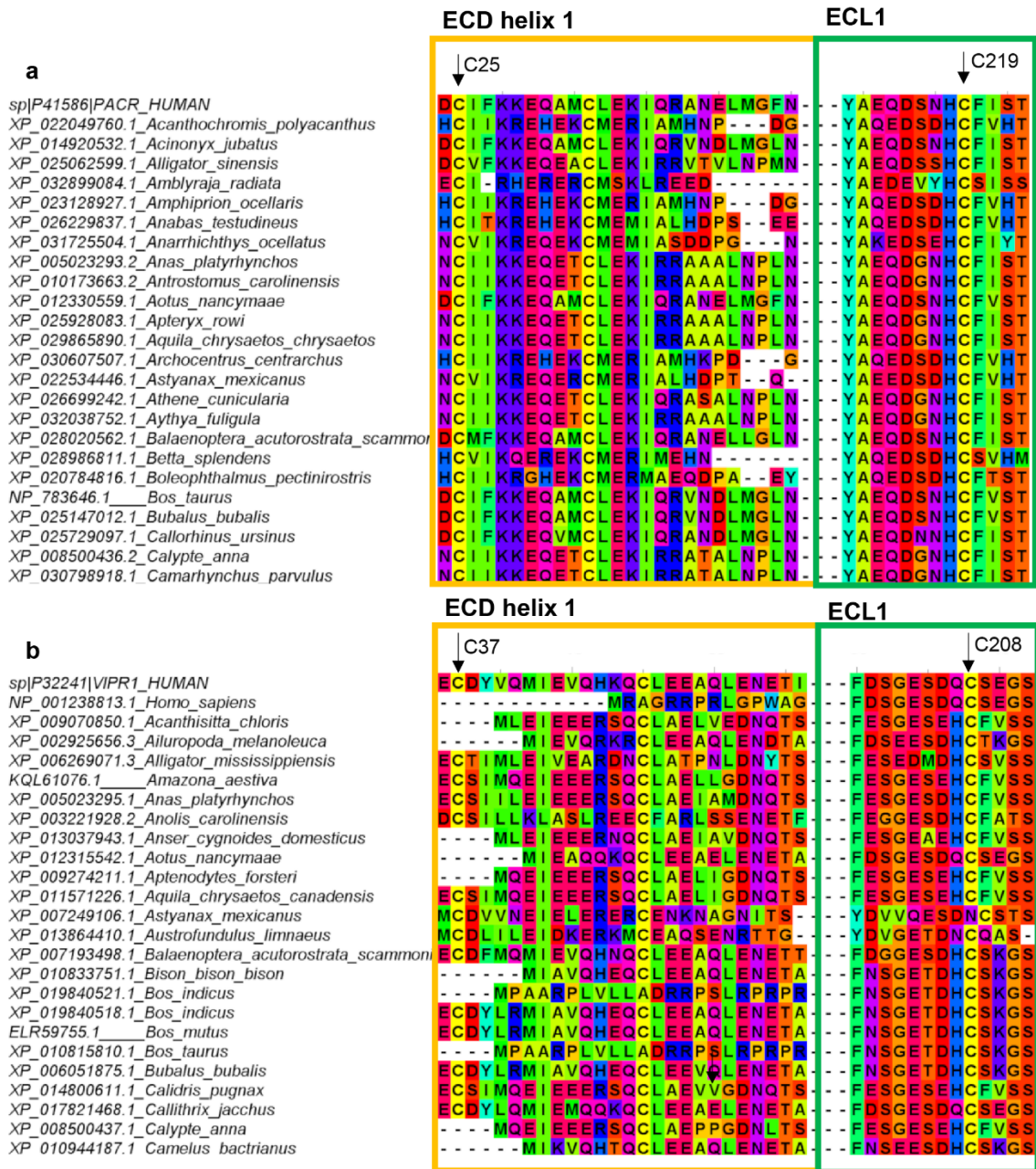


Supplementary Figure 13. Pharmacological analysis of cysteine mutants in cAMP accumulation assay. a-c: Concentration–response data for VPAC1R wild type (WT), C37A,

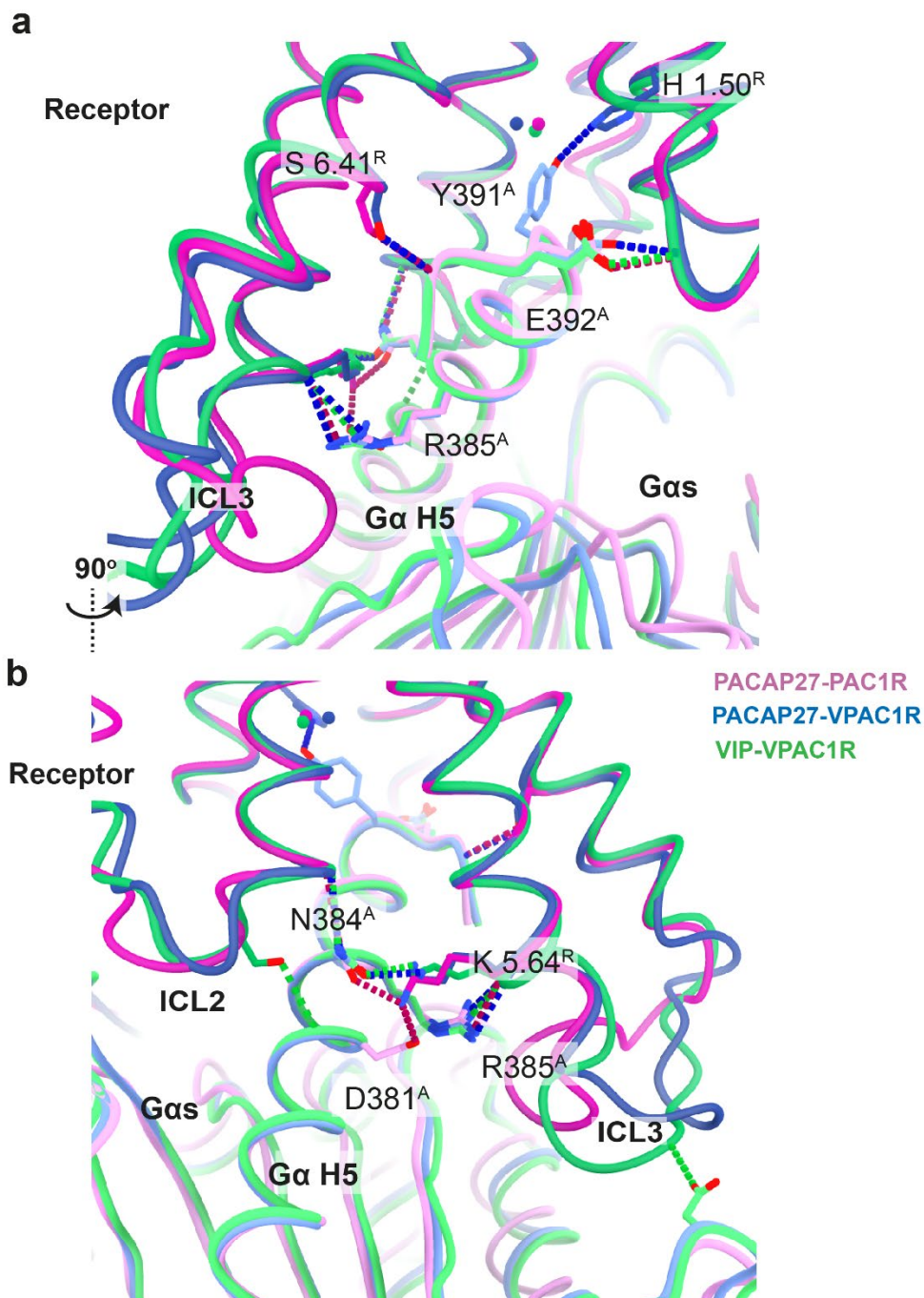
C208A with PACAP27 (a, black), VIP (b, cyan) and PACAP38 (c, orange). d-f: Concentration–response data for PAC1R WT, C25A, C219A and C25A/C219A with PACAP27 (d, black), PACAP38 (e, orange) and VIP (f, cyan). G: FACS analysis of cell surface expression of Flag tagged wild type and mutants used in the cAMP assays. Mean fluorescence reading (mean AF647) is displayed as scatter plot with bar graphs indicating the average, normalised to untransfected COS-7 control (=0%) and PAC1R wild type expression (=100%). Data in a-g are mean \pm SEM of 3 independent experiments, with the exception of WT PAC1R, VPAC1 C37A and VPAC1R C208A in panel g, which are mean \pm SEM of 4 independent experiments. Data were analysed using a one-way ANOVA and Dunnett's post-hoc test with control group being the WT receptor; expression of mutant receptors and WT VPAC1R were not statistically different from the WT PAC1R. h: Gating strategy used for receptor surface expression analysis. Example for PAC1nR C25A C219A (top row) and untransfected COS7 negative control (bottom row). Gating was for single live COS7 cells. Sytox blue was used to discriminate live and dead cells. AF647 levels shown for single live COS7 cells (right column). Source data for panels a-g are provided in the Source Data file.



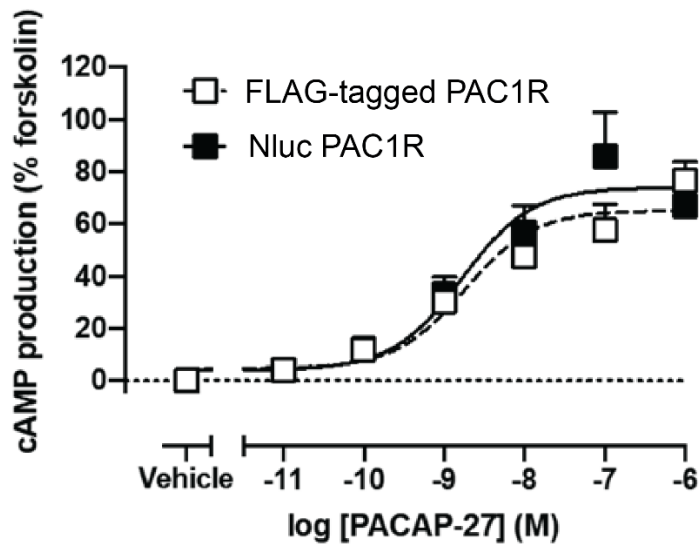
Supplementary Figure 14. RMSF colouring of complexes comparing presence and absence of the ECD-ECL1 disulphide bond during the MD equilibrium simulations. Comparison of the RMSF differences during the MD equilibrium simulations between presence and absence of the ECD-ECL1 disulphide bond performed, on the VPAC1R-VIP (a), VPAC1R-PACAP27 (b), PAC1R-VIP (c) (homology model), and PAC1R-PACAP27 (d). Disulphide bond was either modelled or not modelled between C25^{ECD} - C219^{ECL1} of PAC1R or C37^{ECD} - C208^{ECL1} of VPAC1R. Residues with higher RMSF differences with the disulphide present are shown as blue backbone colouring, while residues with higher RMSF differences with the disulphide bond absent are shown as red backbone colouring, meaning higher structure fluctuations in the presence of the disulphide are coloured in blue, whereas higher structure fluctuations in the absence of the disulphide are coloured in red.



Supplementary Figure 15. PAC1R and VPAC1R multiple sequence alignment for H1 of the ECD (first 41 organisms out of 195). The alignments of PAC1R (a) and VPAC1R (b) show the N-terminal residues of the ECD for PAC1R in different organisms, with a high conservation of the cysteines within the ECD H1 and ECL1 (yellow background, column is highlighted with a blue arrow). The human sequence of PAC1R is shown in the top row (Uniprot ID: P41586).



Supplementary Figure 16. Hydrogen bonds between G α s protein (chain A) and receptor (chain R) residues in the static structures. The G α s backbone is displayed in transparent in ribbon format and receptor backbone in ribbon format, with sidechains that are involved in H-bonds displayed in stick format. PACAP27-PAC1R-Gs is shown in dark pink - pink, PACAP27-VPAC1R-Gs in dark blue - blue and VIP-VPAC1R-Gs in dark green - green. A: Interactions of the Gs protein and the receptor shown as front view (H5/C-terminus of Gs). B: Interactions of the Gs protein and the receptor shown as back view. H-bonds between peptide and receptor are displayed as dotted lines. H-bonds involving backbones, and not sidechains, are labelled as 'bb'. Receptor residues are numbered according to the Wootten et al, class B1 scheme. Gs residues are labelled according to the residue number.



Supplementary Figure 17. Validation of Nanoluc-PAC1R construct for NanoBRET competition binding assay. PACAP27-induced cAMP accumulation comparing N-terminally fused Nanoluc (Nluc)-PAC1R (black squares) to the FLAG tagged PAC1R (white squares). cAMP production is shown as a % of the response to 100 μ M forskolin. Data are mean + S.E.M of 4 independent experiments. Source data are provided in the Source Data file.

Supplementary Tables

Supplementary Table 1: Root-mean square deviation (RMSD) of the PAC1R-PACAP27 in this paper compared to (see overlay in Supplementary Figure 6). RMSD calculated using the matchmaker tool in ChimeraX, measuring RMSD between pruned atom pairs and all atom pairs in Å.

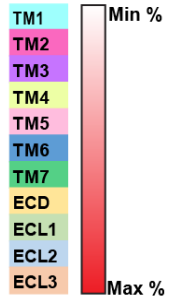
Template	Published PDB (PAC1R-PACAP38)	Chain	RMSD (Å) (pruned)	RMSD (Å) (all)
PAC1R-PACAP27 (this study)	6M1I	Receptor	0.869	2.674
PAC1R-PACAP27 (this study)	6LPB	Receptor	0.719	2.439
PAC1R-PACAP27 (this study)	6P9Y	Receptor	0.589	0.758
PAC1R-PACAP27 (this study)	6M1I	Peptide	0.742	0.742
PAC1R-PACAP27 (this study)	6LPB	Peptide	0.388	0.388
PAC1R-PACAP27 (this study)	6P9Y	Peptide	0.444	0.444
Template	Published PDB (VPAC1R-PACAP27)	Chain	RMSD (Å) (pruned)	RMSD (Å) (all)
VPAC1R-PACAP27 (this study)	6VN7	Receptor	0.753	0.912
VPAC1R-PACAP27 (this study)	6VN7	Peptide	0.304	0.304
VPAC1R-PACAP27 (this study)	6VN7	Gs	0.686	0.768

Supplementary Table 2: Equilibrium MD simulation details. Summary of the equilibrium MD simulations performed.

Complex	# and Duration MD Replicas	Notes
PAC1R:PACAP27:Gs:Nb35	4 x 500 ns (2 μ s)	
VPAC1R:VIP:Gs:Nb35	4 x 500 ns (2 μ s)	
VPAC1R:PACAP27:Gs:Nb35	4 x 500 ns (2 μ s)	
PAC1R:VIP:Gs(H5)	4 x 1000 ns (4 μ s)	Homology-modelled; Gs α H5 only

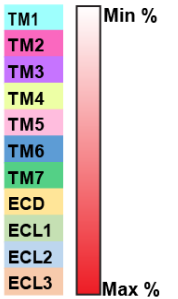
Supplementary Table 3: Generic contacts between receptor and peptide residues during MD equilibrium simulations, with ECD-ECL1 disulphide bond absent (left) and disulphide bond present (right). Columns are sorted by peptide residues and highest to lowest occupancy. Contacts are shown as occupancy of MD frames (in percent), and background is coloured on a scale with highest occupancy in red and lowest occupancy in white. Receptor residues are labelled according to the Wootten numbering system and background is coloured by residue position (TMs, ECLs and ECD, see legend). The PAC1R-VIP simulation is based on a homology model and did not have the full Gs modelled, only the H5 was retained.

MD generic contacts (disulphide bond in ECD-ECL1 absent)				MD generic contacts (disulphide bond in ECD-ECL1 present)			
VPAC1:VIP:Gs	VPAC1:PACAP27:Gs	PAC1:PACAP27:Gs	PAC1:VIP	VPAC1:VIP:Gs	VPAC1:PACAP27:Gs	PAC1:PACAP27:Gs	PAC1:VIP
E373 ^{7.42} H1 99.4	E373 ^{7.42} H1 89.3	E374 ^{ECL3} H1 74.0	E374 ^{ECL3} H1 74.5	E373 ^{7.42} H1 91.4	W294 ^{5.36} H1 73.0	Y241 ^{3.44} H1 68.7	E385 ^{7.42} H1 66.7
V226 ^{3.40} H1 46.3	W294 ^{5.36} H1 73.3	V237 ^{3.40} H1 63.0	W306 ^{5.36} H1 43.3	I301 ^{5.43} H1 34.9	I301 ^{5.43} H1 63.5	E385 ^{7.42} H1 65.6	V237 ^{3.40} H1 50.6
W294 ^{5.36} H1 29.9	I301 ^{5.43} H1 57.1		K310 ^{5.40} H1 25.6	D362 ^{ECL3} H1 34.3	E373 ^{7.42} H1 62.0	V313 ^{5.43} H1 49.5	E374 ^{ECL3} H1 46.4
D362 ^{ECL3} H1 29.3	V226 ^{3.40} H1 43.3			K295 ^{5.40} H1 29.5	V226 ^{3.40} H1 54.8	V237 ^{3.40} H1 39.8	V313 ^{5.43} H1 44.8
I301 ^{5.43} H1 26.8							Y241 ^{3.44} H1 29.8
E373 ^{7.42} S2 98.7	E373 ^{7.42} S2 99.5	E385 ^{7.42} S2 71.9	E385 ^{7.42} S2 81.6	E373 ^{7.42} S2 99.7	E373 ^{7.42} S2 99.5	E385 ^{7.42} S2 79.1	E385 ^{7.42} S2 81.5
M370 ^{7.39} S2 48.6	M370 ^{7.39} S2 74.0	L386 ^{7.43} S2 66.0	L382 ^{7.39} S2 76.0	M370 ^{7.39} S2 56.8	K369 ^{7.38} S2 56.0	L386 ^{7.43} S2 68.5	L386 ^{7.43} S2 63.9
K369 ^{7.38} S2 43.3	L374 ^{7.43} S2 40.8	L382 ^{7.39} S2 62.6	L386 ^{7.43} S2 35.4	L374 ^{7.43} S2 46.6	L374 ^{7.43} S2 43.3	L382 ^{7.39} S2 60.6	L382 ^{7.39} S2 46.6
				K369 ^{7.38} S2 45.7	M370 ^{7.39} S2 42.0		
L374 ^{7.43} D3 56.6	R188 ^{2.60} D3 77.0	R199 ^{2.60} D3 94.9	L386 ^{7.43} D3 37.4	L374 ^{7.43} D3 54.9	R188 ^{2.60} D3 81.1	R199 ^{2.60} D3 93.5	R199 ^{2.60} D3 91.8
R188 ^{2.60} D3 43.7	F222 ^{3.36} D3 46.0	Y161 ^{1.47} D3 68.4	Y157 ^{1.43} D3 29.0	R188 ^{2.60} D3 45.9	L374 ^{7.43} D3 59.7	Y161 ^{1.47} D3 75.3	Y161 ^{1.47} D3 67.7
F222 ^{3.36} D3 37.3	L374 ^{7.43} D3 43.9	F233 ^{3.36} D3 63.5		F222 ^{3.36} D3 30.8	F222 ^{3.36} D3 55.8	F233 ^{3.36} D3 46.0	F233 ^{3.36} D3 52.8
		L386 ^{7.43} D3 44.7				L386 ^{7.43} D3 31.7	L386 ^{7.43} D3 29.0
I289 ^{ECL2} A4 50.8	I289 ^{ECL2} G4 48.3	N300 ^{ECL2} G4 29.2	M299 ^{ECL2} A4 34.1	W294 ^{5.36} A4 37.8	I289 ^{ECL2} G4 52.3		W306 ^{5.36} A4 30.8
W294 ^{5.36} A4 31.8	W294 ^{5.36} G4 35.7			I289 ^{ECL2} A4 36.5	W294 ^{5.36} G4 30.0		
I289 ^{ECL2} V5 29.1	M370 ^{7.39} I5 35.9	L382 ^{7.39} I5 56.5	L382 ^{7.39} V5 44.7	D362 ^{ECL3} V5 44.6	D362 ^{ECL3} I5 44.1	L382 ^{7.39} I5 40.5	L382 ^{7.39} V5 41.3
	W294 ^{5.36} I5 33.9	E374 ^{ECL3} I5 45.8			W294 ^{5.36} I5 33.8		E374 ^{ECL3} V5 27.7
	I289 ^{ECL2} I5 30.0	W306 ^{5.36} I5 36.0			I289 ^{ECL2} I5 28.2		
Y139 ^{1.36} F6 89.5	L374 ^{7.43} F6 76.5	Y153 ^{1.39} F6 85.8	Y150 ^{1.36} F6 69.3	Y139 ^{1.36} F6 83.4	L374 ^{7.43} F6 80.5	Y157 ^{1.43} F6 87.2	Y150 ^{1.36} F6 73.4
L374 ^{7.43} F6 72.8	V142 ^{1.39} F6 67.8	Y157 ^{1.43} F6 82.8	L386 ^{7.43} F6 65.3	L374 ^{7.43} F6 68.5	Y139 ^{1.36} F6 73.3	V153 ^{1.39} F6 86.2	L386 ^{7.43} F6 72.5
V142 ^{1.39} F6 58.1	Y146 ^{1.43} F6 66.3	Y150 ^{1.36} F6 79.4	V153 ^{1.39} F6 60.0	V142 ^{1.39} F6 63.5	Y146 ^{1.43} F6 71.2	Y150 ^{1.36} F6 77.6	Y157 ^{1.43} F6 71.3
M370 ^{7.39} F6 57.3	Y139 ^{1.36} F6 64.8	L386 ^{7.43} F6 58.2	Y157 ^{1.43} F6 37.5	M370 ^{7.39} F6 57.2	V142 ^{1.39} F6 68.2	L386 ^{7.43} F6 40.8	V153 ^{1.39} F6 54.9
Y146 ^{1.43} F6 46.9	M370 ^{7.39} F6 59.1		K154 ^{1.40} F6 30.0	Y146 ^{1.43} F6 43.9	M370 ^{7.39} F6 66.7		
K195 ^{2.67} T7 58.4	K195 ^{2.67} T7 60.7	K206 ^{2.67} T7 85.5	K206 ^{2.67} T7 40.1	K195 ^{2.67} T7 51.0	K195 ^{2.67} T7 68.4	K206 ^{2.67} T7 86.3	K206 ^{2.67} T7 87.0
L199 ^{2.71} T7 52.2	L199 ^{2.71} T7 48.9	Y211 ^{ECL1} T7 40.4	Y211 ^{ECL1} T7 37.1	L199 ^{2.71} T7 31.1	F200 ^{ECL1} T7 39.4	F233 ^{3.36} T7 42.0	F233 ^{3.36} T7 33.4
F200 ^{ECL1} T7 26.3	F222 ^{3.36} T7 34.2	F233 ^{3.36} T7 30.8	L210 ^{2.71} T7 27.5		F222 ^{3.36} T7 35.6	L210 ^{2.71} T7 40.6	L210 ^{2.71} T7 28.1
F200 ^{ECL1} T7 26.3	F200 ^{ECL1} T7 25.5				L199 ^{2.71} T7 25.3	Y211 ^{ECL1} T7 28.2	
I289 ^{ECL2} D8 62.1	T288 ^{ECL1} D8 84.5	N300 ^{ECL2} D8 85.8	M299 ^{ECL2} D8 30.0	I289 ^{ECL2} D8 53.1	I289 ^{ECL2} D8 90.7	N300 ^{ECL2} D8 80.8	
T288 ^{ECL2} D8 39.5	I289 ^{ECL1} D8 84.4	M299 ^{ECL2} D8 80.3		T288 ^{ECL2} D8 38.3	T288 ^{ECL2} D8 90.6	M299 ^{ECL2} D8 47.6	
	D287 ^{ECL2} D8 30.2	D298 ^{ECL2} D8 41.9			D287 ^{ECL2} D8 39.1		
Y139 ^{1.36} N9 52.0	Y139 ^{1.36} S9 76.9	Y150 ^{1.36} S9 76.5	Y150 ^{1.36} N9 65.0	Y139 ^{1.36} N9 68.2	Y139 ^{1.36} S9 72.5	Y150 ^{1.36} S9 59.6	Y150 ^{1.36} N9 52.9
			D87 ^{ECD} N9 27.2				
Y139 ^{1.36} Y10 84.8	F200 ^{ECL1} Y10 85.5	Y150 ^{1.36} Y10 83.8	Y150 ^{1.36} Y10 69.8	Y139 ^{1.36} Y10 79.2	F200 ^{ECL1} Y10 85.1	Y150 ^{1.36} Y10 92.2	Y211 ^{ECL1} Y10 72.8
F200 ^{ECL1} Y10 74.6	Y139 ^{1.36} Y10 81.3	Y211 ^{ECL1} Y10 72.0	Y211 ^{ECL1} Y10 65.1	F200 ^{ECL1} Y10 70.7	Y139 ^{1.36} Y10 80.1	Y211 ^{ECL1} Y10 92.1	Y150 ^{1.36} Y10 67.5
G140 ^{1.37} Y10 33.0	K143 ^{1.40} Y10 33.3		K154 ^{1.40} Y10 36.6	K143 ^{1.40} Y10 33.8	K143 ^{1.40} Y10 29.3		K154 ^{1.40} Y10 39.0
F200 ^{ECL1} T11 50.5	D287 ^{ECL2} S11 93.0	D298 ^{ECL2} S11 79.8		D287 ^{ECL2} T11 47.3	D287 ^{ECL2} S11 94.6	D298 ^{ECL2} S11 68.8	Y211 ^{ECL1} T11 79.5
	F200 ^{ECL1} S11 42.2	Y211 ^{ECL1} S11 61.0		F200 ^{ECL1} T11 39.2	F200 ^{ECL1} S11 63.0	Y211 ^{ECL1} S11 38.0	D298 ^{ECL2} T11 36.9
		M299 ^{ECL2} S11 40.4				M299 ^{ECL2} S11 27.8	
T288 ^{ECL2} R12 28.6	E36 ^{ECD} R12 63.7	M299 ^{ECL2} R12 68.0	I83 ^{ECD} R12 73.3	E36 ^{ECD} R12 42.2	T288 ^{ECL2} R12 51.9	M299 ^{ECL2} R12 54.0	D87 ^{ECD} R12 65.3
	T288 ^{ECL2} R12 31.5	D301 ^{ECL2} R12 60.1	D87 ^{ECD} R12 55.4			F84 ^{ECD} R12 31.1	I83 ^{ECD} R12 36.4
			N85 ^{ECD} R12 48.3				M299 ^{ECL2} R12 35.1
			F84 ^{ECD} R12 39.3				
T136 ^{1.33} L13 74.5	T136 ^{1.33} Y13 84.1	Y150 ^{1.36} Y13 95.7	Q146 ^{1.32} L13 56.9	T136 ^{1.33} L13 67.9	Y139 ^{1.36} Y13 79.1	Y150 ^{1.36} Y13 92.6	T143 ^{1.29} L13 59.0
Y139 ^{1.36} L13 64.6	Y139 ^{1.36} Y13 81.9	D147 ^{1.33} Y13 92.0	Y150 ^{1.36} L13 55.2	Y139 ^{1.36} L13 52.8	T136 ^{1.33} Y13 78.4	D147 ^{1.33} Y13 84.1	Q146 ^{1.32} L13 56.3
D132 ^{1.29} L13 48.1	Q135 ^{1.32} Y13 54.9	Q146 ^{1.32} Y13 64.3	D147 ^{1.33} L13 47.8	Q135 ^{1.35} L13 46.7	D132 ^{1.29} Y13 52.7	Q146 ^{1.32} Y13 74.3	Y150 ^{1.36} L13 54.8
Q135 ^{1.35} L13 47.2	D132 ^{1.29} Y13 48.4	T143 ^{1.29} Y13 31.7	T143 ^{1.29} L13 43.0	D132 ^{1.29} L13 37.7	Q135 ^{1.32} Y13 51.9	T143 ^{1.29} Y13 30.0	D147 ^{1.33} L13 47.2



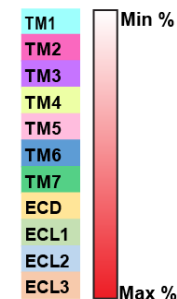
Supplementary Table 4: Hydrogen bonds between receptor and peptide residues during MD equilibrium simulations, with ECD-ECL1 disulphide bond absent (left) and disulphide bond present (right). Columns are sorted by peptide residues and highest to lowest occupancy. Contacts are shown as occupancy of MD frames (in percent), and background is coloured on a scale with highest occupancy in red and lowest occupancy in white. Receptor residues are labelled according to the Wootten numbering system and background is coloured by residue position (TMs, ECLs and ECD, see legend). The PAC1R-VIP simulation is based on a homology model and did not have the full Gs modelled, only the H5 was retained.

MD H-bonds (disulphide bond in ECD-ECL1 absent)				MD H-bonds (disulphide bond in ECD-ECL1 present)																						
VPAC1:VIP:Gs		VPAC1:PACAP27:Gs		PAC1:PACAP27:Gs		PAC1:VIP		VPAC1:VIP:Gs		VPAC1:PACAP27:Gs		PAC1:PACAP27:Gs		PAC1:VIP												
W294 ^{5.36}	H1	10.6		Y241 ^{3.44}	H1	17.2	E374 ^{ECL3}	H1	25.9	E373 ^{7.42}	H1	11.1	Y241 ^{3.44}	H1	33.9	E374 ^{ECL3}	H1	20.2								
Q223 ^{3.37}	H1	10.3		H234 ^{3.37}	H1	11.3				D362 ^{ECL3}	H1	7.8				Y241 ^{3.44}	H1	15.3								
E373 ^{7.42}	H1	7.4		E374 ^{ECL3}	H1	9.0																				
K298 ^{5.40}	H1	5.8																								
E373 ^{7.42}	S2	94.2	E373 ^{7.42}	S2	92.9	E385 ^{7.42}	S2	5.4	E385 ^{7.42}	S2	28.8	E373 ^{7.42}	S2	85.5	E373 ^{7.42}	S2	94.4	E385 ^{7.42}	S2	34.3	E385 ^{7.42}	S2	22.9			
K369 ^{7.38}	S2	6.4	K369 ^{7.38}	S2	7.2							K369 ^{7.38}	S2	17.1												
R188 ^{2.60}	D3	43.0	R188 ^{2.60}	D3	73.8	R199 ^{2.60}	D3	92.4	Y157 ^{1.43}	D3	25.8	R188 ^{2.60}	D3	43.1	R188 ^{2.60}	D3	79.7	R199 ^{2.60}	D3	92.0	R199 ^{2.60}	D3	90.1			
				Y161 ^{1.47}	D3	56.3						Y161 ^{1.47}	D3	13.6				Y161 ^{1.47}	D3	63.8	Y161 ^{1.47}	D3	57.8			
												Y161 ^{1.47}	D3	6.7				Y241 ^{3.44}	D3	5.4	Y157 ^{1.43}	D3	19.2			
K195 ^{2.67}	T7	49.8	K195 ^{2.67}	T7	48.1	K206 ^{2.67}	T7	54.7	K206 ^{2.67}	T7	32.8	K195 ^{2.67}	T7	43.0	K195 ^{2.67}	T7	47.3	K206 ^{2.67}	T7	61.9	K206 ^{2.67}	T7	48.2			
T288 ^{ECL2}	D8	37.4	T288 ^{ECL2}	D8	31.1	N300 ^{ECL2}	D8	6.1				T288 ^{ECL2}	D8	35.4	T288 ^{ECL2}	D8	58.5	N300 ^{ECL2}	D8	28.6						
																		W306 ^{5.36}	D8	7.8						
Y139 ^{1.36}	N9	22.9	Y139 ^{1.36}	S9	50.1	Y150 ^{1.36}	S9	48.2	Y150 ^{1.36}	N9	20.4	Y139 ^{1.36}	N9	26.8	Y139 ^{1.36}	S9	41.9	Y150 ^{1.36}	S9	46.1	N375 ^{ECL3}	N9	17.8			
N363 ^{ECL3}	N9	7.8				K378 ^{7.35}	S9	20.0	D87 ^{ECD}	N9	8.3	N363 ^{ECL3}	N9	9.2	D201 ^{ECL1}	Y10	6.5	K378 ^{7.35}	S9	6.7	Y150 ^{1.36}	N9	16.9			
									D147 ^{1.33}	Y10	18.8										D147 ^{1.33}	Y10	10.5			
D287 ^{ECL2}	T11	5.0	D287 ^{ECL2}	S11	82.5	D298 ^{ECL2}	S11	65.8	Y211 ^{ECL1}	T11	6.5	D287 ^{ECL2}	T11	33.4	D287 ^{ECL2}	S11	90.4	D298 ^{ECL2}	S11	21.2	Y211 ^{ECL1}	T11	55.1			
			Q207 ^{ECL1}	S11	4.2	Y211 ^{ECL1}	S11	32.5										Y211 ^{ECL1}	S11	12.5						
E36 ^{ECD}	R12	14.9	E36 ^{ECD}	R12	61.5	D301 ^{ECL2}	R12	59.7	D87 ^{ECD}	R12	53.2	E36 ^{ECD}	R12	34.2	N290 ^{5.32}	R12	8.1	D301 ^{ECL2}	R12	18.2	D87 ^{ECD}	R12	64.9			
T288 ^{ECL2}	R12	10.2				D87 ^{ECD}	R12	12.9													D301 ^{ECL2}	R12	7.3			
N290 ^{ECL2}	R12	7.4																								
			T136 ^{1.33}	Y13	50.6	D147 ^{1.33}	Y13	86.6										T136 ^{1.33}	Y13	44.9	D147 ^{1.33}	Y13	78.9			
			D132 ^{1.29}	Y13	21.4	T143 ^{1.29}	Y13	6.0										D132 ^{1.29}	Y13	21.7						
E204 ^{ECL1}	R14	30.0	E204 ^{ECL1}	R14	49.3	D215 ^{ECL1}	R14	97.6	D215 ^{ECL1}	R14	72.3	E204 ^{ECL1}	R14	59.7	E210 ^{ECL1}	R14	29.1	D215 ^{ECL1}	R14	33.0	D215 ^{ECL1}	R14	67.2			
Q207 ^{ECL1}	R14	9.1				Q214 ^{ECL1}	R14	14.2	D147 ^{1.33}	R14	22.9	Q207 ^{ECL1}	R14	32.6	E204 ^{ECL1}	R14	15.5	E213 ^{ECL1}	R14	26.6	D147 ^{1.33}	R14	53.6			
																		S205 ^{ECL1}	R14	13.3	D147 ^{1.33}	R14	15.1			
																		D201 ^{ECL1}	R14	6.7	D298 ^{ECL2}	R14	15.0			
E36 ^{ECD}	K15	13.4	D287 ^{ECL2}	K15	44.2	D298 ^{ECL2}	K15	38.0	D24 ^{ECD}	K15	16.4	D287 ^{ECL2}	K15	63.8	E36 ^{ECD}	K15	34.2	D298 ^{ECL2}	K15	53.3	D298 ^{ECL2}	K15	77.1			
D206 ^{ECL1}	K15	6.5	Q207 ^{ECL1}	K15	28.5							E36 ^{ECD}	K15	59.3	E210 ^{ECL1}	K15	15.3									
D38 ^{ECD}	K15	5.8	E36 ^{ECD}	K15	11.0												D287 ^{ECL2}	K15	14.9							
																	Y283 ^{ECL2}	K15	8.0							
Y39 ^{ECD}	Q16	22.3	E36 ^{ECD}	Q16	15.9	N85 ^{ECD}	Q16	9.9	T143 ^{1.29}	Q16	15.4				E36 ^{ECD}	Q16	15.6									
D132 ^{1.29}	Q16	10.7							Y139 ^{1.25}	Q16	5.6										N85 ^{ECD}	Q16	13.2			
D132 ^{1.29}	K20	29.3	D132 ^{1.29}	K20	69.5	D137 ^{ECD}	K20	36.2	E138 ^{ECD}	K20	51.7	D132 ^{1.29}	K20	35.7	D132 ^{1.29}	K20	63.7	D132 ^{ECD}	K20	6.5	S141 ^{1.27}	Q16	5.1			
E133 ^{1.30}	K20	19.7				E142 ^{1.28}	K20	7.6	T143 ^{1.29}	K20	9.8	D126 ^{ECD}	K20	14.4							E138 ^{ECD}	K20	27.3			
D126 ^{ECD}	K20	15.3									E133 ^{1.30}	K20	7.8								E140 ^{1.26}	K20	25.6			
D125 ^{ECD}	K20	9.5																			T143 ^{1.29}	K20	14.2			
																					D137 ^{ECD}	K20	8.1			
																					E142 ^{1.28}	K20	5.2			
E204 ^{ECL1}	K21	48.2	E204 ^{ECL1}	K21	32.4							E204 ^{ECL1}	K21	35.7	E204 ^{ECL1}	K21	41.0	E213 ^{ECL1}	K21	15.9	D215 ^{ECL1}	K21	27.4			
												D206 ^{ECL1}	K21	6.7	D206 ^{ECL1}	K21	38.0	D215 ^{ECL1}	K21	13.8	H218 ^{ECL1}	K21	6.0			
												S205 ^{ECL1}	K21	6.3				E142 ^{1.28}	K21	5.1						
E44 ^{ECD}	Y22	28.5	E44 ^{ECD}	Y22	44.1	N60 ^{ECD}	Y22	5.6				E44 ^{ECD}	Y22	15.4	E44 ^{ECD}	Y22	42.0									
			Q41 ^{ECD}	Y22	7.9										Q41 ^{ECD}	Y22	5.0					Q31 ^{ECD}	Y22	10.6		
Y118 ^{ECD}	N24	17.9																					D137 ^{ECD}	N24	10.2	
																								K28 ^{ECD}	S25	12.5
			E114 ^{ECD}	L27	4.3																					



Supplementary Table 5: Water bridges between receptor and peptide residues during MD equilibrium simulations. Columns are sorted by peptide residues and highest to lowest occupancy. Contacts are shown as occupancy of MD frames (in percent), and background is coloured on a scale with highest occupancy in red and lowest occupancy in white. Receptor residues are labelled according to the Wootten numbering system and background is coloured by residue position (TMs, ECLs and ECD, see legend). The PAC1R-VIP simulation is based on a homology model and did not have the full Gs modelled, only the H5 was retained. The ECD-ECL1 disulphide bond was present for the PAC1R-VIP simulation (right column), and absent for all other simulations. (b) indicates interactions with the backbone.

Water bridge occupancy (% MD Frames)										
	VPAC1R-VIP		VPAC1R-PACAP27		PAC1R-PACAP27		PAC1R-VIP		PAC1R-VIP + disulf	
His1	R188 ^{2.60}	30	Q223 ^{3.37}	46.1	E374 ^{ECL3}	39.8	E374 ^{ECL3}	66.5	E374 ^{ECL3}	58.1
	E373 ^{7.42}	29.9	D362 ^{ECL3}	18.2	H234 ^{3.37}	25.2	E385 ^{7.42}	27.7	E385 ^{7.42}	46.7
	D362 ^{ECL3}	27.6	E373 ^{7.42}	15.9	E385 ^{7.42}	21.1	Y241 ^{3.44}	13.8	Y241 ^{3.44}	31.2
	Q223 ^{3.37}	20.4	Y354 ^{6.53}	11.7	R199 ^{2.60}	18.7	F369 ^{6.56}	10.5	R381 ^{7.38}	16.1
	Y354 ^{6.53}	15.9	R188 ^{2.60}	9	W306 ^{5.36}	18.7	H234 ^{3.37}	9.4	H234 ^{3.37}	11.7
	K369 ^{7.38}	9.6	K369 ^{7.38}	8.4	Y241 ^{3.44}	13.9	S372 ^{6.59}	6.9	F369 ^{6.56}	11.5
	F357 ^{6.56}	6.2	F357 ^{6.56}	5.2	N300 ^{ECL2}	6.4	Y366 ^{6.53}	6.9	Y366 ^{6.53}	11
					I309 ^{5.39} (b)	5.1	I309 ^{5.39} (b)	6.6	R199 ^{2.60}	6.3
							R381 ^{7.38}	6.5		
							W306 ^{5.36}	6.4		
Ser2	E373 ^{7.42}	46.3	E373 ^{7.42}	21.5	E385 ^{7.42}	74.8	E385 ^{7.42}	78.1	E385 ^{7.42}	69.2
	D362 ^{ECL3}	9.1	K369 ^{7.38}	13.8	Y241 ^{3.44}	25.1			R199 ^{2.60}	16.9
	K369 ^{7.38}	8.4	D362 ^{ECL3}	6.2	R199 ^{2.60}	25.1			Y241 ^{3.44}	12.1
					Y366 ^{6.53}	6.9			Y161 ^{1.47}	10.2
Asp3	E373 ^{7.42}	70.5	R188 ^{2.60}	92.1	R199 ^{2.60}	62.7	Y161 ^{1.47}	61.1	R199 ^{2.60}	59.4
	R188 ^{2.60}	66.1	E373 ^{7.42}	65.2	Y161 ^{1.47}	53	R199 ^{2.60}	53	Y161 ^{1.47}	56.2
	Y150 ^{1.47}	62.4	Y150 ^{1.47}	55.3	K206 ^{2.67}	22.1	K206 ^{2.67}	35.1	L386 ^{7.43} (b)	17.7
	K195 ^{2.67}	26.9	K195 ^{2.67}	9.4	L386 ^{7.43} (b)	21.1	Y157 ^{1.43}	20.7	Y241 ^{3.44}	16.1
	Y146 ^{1.43}	7.9	L374 ^{7.43}	8.2	Y241 ^{3.44}	18.3	E385 ^{7.42}	10.1	Y157 ^{1.43}	7.7
			Y354 ^{6.53}	5.8	S390 ^{7.47}	6.8				

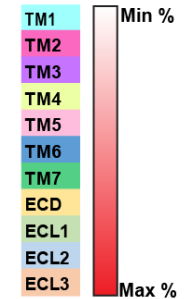


Supplementary Table 6: Non-equilibrium MD simulation details. Summary of the non-equilibrium MD simulations performed.

Complex	Unbinding (well-tempered MetaD) # Replicas	SuMD Binding # Replicas	Analyzed Unbinding/Binding Total Path Sampling
PAC1R:VIP:Gs(H5)	4	12	3.04 μ s / 3.10 μ s
PAC1R:PACAP27:Gs(H5)	4	12	3.04 μ s / 2.64 μ s
VPAC1R:VIP:Gs(H5)	4	12	3.12 μ s / 2.46 μ s
VPAC1R:PACAP27:Gs(H5)	4	12	3.01 μ s / 2.34 μ s

Supplementary Table 7: Contacts between receptor and peptide residues during MD partial binding and unbinding simulations. Columns are sorted by peptide residues and highest to lowest occupancy. Contacts are shown as occupancy of MD frames (in percent), and background is coloured on a scale with highest occupancy in red and lowest occupancy in white. Receptor residues are labelled according to the Wootten numbering system and background is coloured by residue position (TMs, ECLs and ECD, see legend).

Contacts Partial Binding				Contacts Partial Unbinding																
PACAP27-PAC1R		PACAP27-VPAC1R		VIP-VPAC1R		VIP-PAC1R		PACAP27-PAC1R		PACAP27-VPAC1R		VIP-VPAC1R		VIP-PAC1R						
H1	D301 ^{ECL2}	10.0				H1	D362 ^{ECL3}	10.8	H1	E374 ^{ECL3}	22.6	H1	E373 ^{7.42}	12.5	H1	E374 ^{ECL3}	25.9			
H1	M299 ^{ECL2}	7.3				H1	K367 ^{7.36}	7.3	H1	W306 ^{5.36}	22.4	H1	D365 ^{ECL3}	12.3	H1	W306 ^{5.36}	16.7			
H1	T294 ^{ECL2}	4.9				H1	P366 ^{7.35}	6.6	H1	D298 ^{ECL2}	7.1	H1	W294 ^{5.36}	8.1	H1	N300 ^{ECL2}	9.5			
H1	N375 ^{ECL3}	4.3				H1	K365 ^{7.34}	6.5	H1	E374 ^{ECL3}	6.5	H1	E367 ^{7.36}	7.0	H1	D215 ^{ECL1}	8.9			
H1	D292 ^{4.68}	4.3				H1	F280 ^{4.67}	6.5	H1	D147 ^{1.33}	5.4	H1	K369 ^{ECL2}	9.5	H1	K365 ^{7.34}	8.6			
H1	D293 ^{ECL2}	3.5				H1	S292 ^{5.34}	4.3	H1	N300 ^{ECL2}	5.1	H1	D301 ^{ECL2}	8.0	H1	E367 ^{7.36}	7.1			
H1	E374 ^{ECL3}	3.5				H1	E281 ^{4.68}	3.8	H1	W306 ^{5.36}	4.5	H1	I289 ^{ECL2}	7.7	H1	K369 ^{7.38}	6.8			
H1	K378 ^{7.35}	3.2				H1	P361 ^{ECL3}	3.2	H1	D215 ^{ECL1}	4.3	H1	P366 ^{7.35}	5.4	H1	I289 ^{ECL2}	6.3			
						H1	Q135 ^{1.32}	3.1	H1	E91 ^{ECD}	4.2	H1	I301 ^{5.43}	5.0	H1	I301 ^{5.43}	4.4			
									H1	W90 ^{ECD}	3.8	H1	N363 ^{ECL3}	3.9	H1	Q135 ^{1.32}	4.3			
									H1	F220 ^{ECL1}	3.4	H1	Y241 ^{3.44}	4.5	H1	Y139 ^{1.36}	3.9			
									H1	E385 ^{7.42}	3.0	H1	K310 ^{5.40}	3.0	H1	D362 ^{ECL3}	3.7			
									H1	H218 ^{ECL1}	2.4	H1	R381 ^{7.38}	2.6	H1	V226 ^{3.40}	3.1			
									H1	C219 ^{ECL1}	2.1	H1	D298 ^{ECL2}	2.1	H1	Q223 ^{3.37}	2.6			
									H1	Y150 ^{1.36}	2.0				H1	Y354 ^{6.53}	2.5			
															H1	L382 ^{7.39}	2.3			
															H1	C219 ^{ECL1}	2.1			
S2	M299 ^{ECL2}	6.3		S2	N363 ^{ECL3}	6.2			S2	F280 ^{4.67}	6.8	S2	L382 ^{7.39}	17.7	S2	E373 ^{7.42}	21.3	S2	L382 ^{7.39}	24.5
S2	D301 ^{ECL2}	5.8							S2	P366 ^{7.35}	5.4	S2	E385 ^{7.42}	13.5	S2	M370 ^{7.39}	17.3	S2	E385 ^{7.42}	21.5
S2	N375 ^{ECL3}	2.6							S2	E374 ^{ECL3}	3.6	S2	L386 ^{7.43}	10.8	S2	K369 ^{7.38}	13.9	S2	L386 ^{7.43}	15.0
									S2	D147 ^{1.33}	2.6	S2	K378 ^{7.35}	8.4	S2	E367 ^{7.36}	7.2	S2	E374 ^{ECL3}	5.5
									S2	N300 ^{ECL2}	2.5	S2	E374 ^{ECL3}	8.3	S2	Y139 ^{1.36}	6.9	S2	E374 ^{ECL3}	5.5
									S2	K378 ^{7.35}	2.3	S2	N375 ^{ECL3}	6.8	S2	Q135 ^{1.32}	4.4	S2	E374 ^{ECL3}	5.5
												S2	R199 ^{2.60}	3.3	S2	P366 ^{7.35}	4.0	S2	E374 ^{ECL3}	5.5
												S2	R381 ^{7.38}	3.0	S2	L374 ^{7.43}	3.9	S2	E374 ^{ECL3}	5.5
D3	K378 ^{7.35}	10.7		D3	N363 ^{ECL3}	8.6			D3	K365 ^{7.34}	14.4	D3	K378 ^{7.35}	13.5	D3	L374 ^{7.43}	6.4	D3	K206 ^{2.67}	10.5
D3	T294 ^{ECL2}	4.7		D3	N290 ^{5.32}	6.7			D3	K369 ^{7.38}	7.6	D3	R199 ^{2.60}	10.5	D3	Y139 ^{1.36}	5.0	D3	L386 ^{7.43}	9.7
D3	N375 ^{ECL3}	4.4							D3	F280 ^{4.67}	4.9	D3	F233 ^{3.36}	8.8	D3	N290 ^{5.32}	3.8	D3	R199 ^{2.60}	6.7
D3	M299 ^{ECL2}	3.0							D3	Y283 ^{ECL2}	4.7	D3	Y161 ^{1.47}	7.5	D3	I289 ^{ECL2}	3.7	D3	Y211 ^{ECL1}	6.7
D3	D293 ^{ECL2}	2.2							D3	M370 ^{7.39}	4.5	D3	M299 ^{ECL2}	7.1	D3	M370 ^{7.39}	3.7	D3	F233 ^{3.36}	6.6
									D3	D282 ^{ECL2}	3.1	D3	L386 ^{7.43}	5.5	D3	P366 ^{7.35}	3.3	D3	K154 ^{1.40}	6.4
									D3	P366 ^{7.35}	3.0	D3	K206 ^{2.67}	4.1	D3			D3	Y161 ^{1.47}	3.3
												D3	Y211 ^{ECL1}	3.0	D3			D3	Y157 ^{1.43}	2.2
												D3	D301 ^{ECL2}	2.4						
												D3	L382 ^{7.39}	2.3						
												D3	N375 ^{ECL3}	2.1						
G4	M299 ^{ECL2}	4.7		G4	N363 ^{ECL3}	9.4			G4	K378 ^{7.35}	2.8	G4	M299 ^{ECL2}	21.2	G4	I289 ^{ECL2}	11.0	A4	M299 ^{ECL2}	11.0
									A4	M299 ^{ECL2}	2.6	G4	D298 ^{ECL2}	5.0	G4	N290 ^{5.32}	4.5	A4	W306 ^{5.36}	6.1
									A4	N300 ^{ECL2}	2.5	G4	D301 ^{ECL2}	3.2	I5	Q135 ^{1.32}	6.2	A4	N300 ^{ECL2}	5.1
									A4	R379 ^{7.36}	2.1	G4	N300 ^{ECL2}	2.8	A4	W294 ^{5.36}	4.5	A4	Y211 ^{ECL1}	2.4
												G4	W306 ^{5.36}	2.4						
I5	R379 ^{7.36}	6.3		I5	N363 ^{ECL3}	7.2			I5	Y139 ^{1.36}	3.0	V5	W90 ^{ECD}	7.3	I5	D362 ^{ECL3}	5.5	V5	L382 ^{7.39}	13.1
I5	K378 ^{7.35}	4.8		I5	C208 ^{ECL1}	4.8			V5	S141 ^{1.27}	4.7	V5	Y150 ^{1.36}	4.7	I5	C208 ^{ECL1}	4.7	V5	K378 ^{7.35}	6.5
I5	L382 ^{7.39}	4.4		I5	I289 ^{ECL2}	4.7			V5	N375 ^{ECL3}	3.8	I5	K378 ^{7.35}	3.4	I5	M370 ^{7.39}	4.5	V5	E374 ^{ECL3}	6.1
I5	N375 ^{ECL3}	2.8							V5	L382 ^{7.39}	3.7	I5	E374 ^{ECL3}	3.2	I5	Y283 ^{ECL2}	4.5	V5	N375 ^{ECL3}	3.8
I5	M299 ^{ECL2}	2.4							V5	E91 ^{ECD}	3.3	I5	N375 ^{ECL3}	3.1	I5	L92 ^{ECD}	4.3	V5	W306 ^{5.36}	2.6
									V5	K378 ^{7.35}	3.3	I5	M299 ^{ECL2}	2.8	I5	I289 ^{ECL2}	4.2	V5	R379 ^{7.36}	2.3
									V5	Y150 ^{1.36}	2.5	I5	W306 ^{5.36}	2.1	I5	N363 ^{ECL3}	4.0			
									V5	R379 ^{7.36}	2.3									

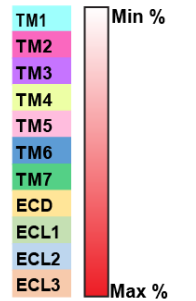


Supplementary Table 7 continued

Contacts Partial Binding				Contacts Partial Unbinding																											
PACAP27-PAC1R		PACAP27-VPAC1R		VIP-VPAC1R		VIP-PAC1R		PACAP27-PAC1R		PACAP27-VPAC1R		VIP-VPAC1R		VIP-PAC1R																	
L27	F136 ^{ECD}	27.7		L27	L70 ^{ECD}	38.8		L27	P119 ^{ECD}	20.0		L27	W58 ^{ECD}	40.0		L27	F131 ^{ECD}	25.1		L27	L70 ^{ECD}	32.7		L27	P119 ^{ECD}	25.8		L27	W58 ^{ECD}	48.3	
L27	N60 ^{ECD}	23.5		L27	T71 ^{ECD}	18.7		L27	L113 ^{ECD}	18.5		L27	N60 ^{ECD}	19.9		L27	Y130 ^{ECD}	14.9		L27	N69 ^{ECD}	22.7		L27	L70 ^{ECD}	22.1		L27	L35 ^{ECD}	23.3	
L27	I61 ^{ECD}	20.0		L27	F90 ^{ECD}	18.1		L27	P117 ^{ECD}	18.2		L27	K28 ^{ECD}	17.7		L27	Y139 ^{1.25}	12.9		L27	L124 ^{ECD}	16.7		L27	Y118 ^{ECD}	22.0		L27	K28 ^{ECD}	11.2	
L27	Y139 ^{1.25}	12.6		L27	N69 ^{ECD}	17.9		L27	Y118 ^{ECD}	15.7		L27	Q31 ^{ECD}	12.8		L27	F136 ^{ECD}	9.6		L27	P117 ^{ECD}	13.4		L27	I120 ^{ECD}	14.9		L27	N60 ^{ECD}	9.3	
L27	D137 ^{ECD}	10.6		L27	A121 ^{ECD}	17.2		L27	L70 ^{ECD}	15.2		L27	L35 ^{ECD}	12.6		L27	F127 ^{ECD}	8.1		L27	H47 ^{ECD}	12.3		L27	W67 ^{ECD}	11.9		L27	Q31 ^{ECD}	7.6	
L27	F81 ^{ECD}	10.1		L27	H47 ^{ECD}	16.5		L27	W110 ^{ECD}	13.9		L27	A32 ^{ECD}	6.5		L27	F84 ^{ECD}	5.6		L27	I120 ^{ECD}	12.0		L27	L113 ^{ECD}	9.9		L27	A32 ^{ECD}	7.4	
L27	F27 ^{ECD}	9.5		L27	L124 ^{ECD}	14.9		L27	H112 ^{ECD}	11.3		L27	F27 ^{ECD}	6.1		L27	N60 ^{ECD}	4.8		L27	A121 ^{ECD}	11.0		L27	P117 ^{ECD}	7.2					
L27	F131 ^{ECD}	9.2		L27	I120 ^{ECD}	13.7		L27	W67 ^{ECD}	6.3						L27	I61 ^{ECD}	3.0		L27	T71 ^{ECD}	9.5		L27	P115 ^{ECD}	5.6					
L27	E138 ^{ECD}	7.9		L27	P117 ^{ECD}	10.0		L27	I120 ^{ECD}	5.6						L27	H129 ^{ECD}	2.4		L27	F90 ^{ECD}	8.9		L27	N69 ^{ECD}	4.4					
L27	K28 ^{ECD}	6.2		L27	I43 ^{ECD}	6.7		L27	P115 ^{ECD}	4.9										L27	P115 ^{ECD}	6.7		L27	E114 ^{ECD}	3.2					
L27	Y130 ^{ECD}	6.1						L27	G116 ^{ECD}	3.8										L27	I43 ^{ECD}	5.6		L27	W110 ^{ECD}	2.7					
L27	L80 ^{ECD}	5.3						L27	T111 ^{ECD}	3.5										L27	G116 ^{ECD}	4.7									
																				L27	W67 ^{ECD}	3.8									
								N28	C208 ^{ECL1}	12.3		N28	K28 ^{ECD}	19.4						N28	Y118 ^{ECD}	3.9		N28	W58 ^{ECD}	40.0					
								N28	H112 ^{ECD}	10.0		N28	W58 ^{ECD}	17.2						N28	P115 ^{ECD}	3.8		N28	L35 ^{ECD}	20.7					
								N28	P117 ^{ECD}	9.3		N28	N60 ^{ECD}	8.3						N28	P117 ^{ECD}	3.8		N28	K28 ^{ECD}	16.6					
								N28	L113 ^{ECD}	9.1		N28	Q31 ^{ECD}	7.8						N28	P119 ^{ECD}	3.6		N28	Q31 ^{ECD}	11.1					
								N28	P115 ^{ECD}	8.1		N28	L35 ^{ECD}	6.2										N28	N60 ^{ECD}	8.3					
								N28	S205 ^{ECL1}	5.3		N28	F27 ^{ECD}	4.8										N28	A32 ^{ECD}	7.6					
								N28	Y118 ^{ECD}	4.4		N28	A32 ^{ECD}	4.5										N28	F27 ^{ECD}	4.0					
								N28	P119 ^{ECD}	3.8		N28	D24 ^{ECD}	2.5										N28	C25 ^{ECD}	2.1					
								N28	S209 ^{ECL1}	3.7																					
								N28	Q207 ^{ECL1}	3.4																					
								N28	G116 ^{ECD}	3.0																					

Supplementary Table 8: Hydrogen bonds between receptor and peptide residues during MD partial binding and unbinding simulations. Columns are sorted by peptide residues and highest to lowest occupancy. Contacts are shown as occupancy of MD frames (in percent), and background is coloured on a scale with highest occupancy in red and lowest occupancy in white. Receptor residues are labelled according to the Wootten numbering system and background is coloured by residue position (TMs, ECLs and ECD, see legend).

Hydrogen bonds partial binding				Hydrogen bonds partial unbinding																				
PACAP27-PAC1R		PACAP27-VPAC1R		VIP-VPAC1R		VIP-PAC1R		PACAP27-PAC1R		PACAP27-VPAC1R		VIP-VPAC1R		VIP-PAC1R										
H1	D301 ^{ECL2}	4.3				H1	D362 ^{ECL3}	4.5	H1	E91 ^{ECD}	3.7	H1	N300 ^{ECL2}	8.0	H1	W294 ^{5.36}	5.3	H1	W294 ^{5.36}	3.9	H1	N300 ^{ECL2}	4.9	
						H1	E367 ^{7.36}	2.4	H1	N300 ^{ECL2}	3.5	H1	E374 ^{ECL3}	5.9	H1	E367 ^{7.36}	2.7	H1	K298 ^{5.40}	3.6	H1	E374 ^{ECL3}	4.1	
									H1	N375 ^{ECL3}	3.2	H1	Y241 ^{3.44}	3.8	H1	K369 ^{7.38}	2.6	H1	K369 ^{7.38}	2.2	H1	D215 ^{ECL1}	2.6	
									H1	E374 ^{ECL3}	1.4	H1	W306 ^{5.36}	2.8	H1	K298 ^{5.40}	2.5	H1	Q223 ^{3.37}	2.0	H1	W306 ^{5.36}	1.7	
									H1	D147 ^{1.33}	1.3	H1	D301 ^{ECL2}	1.2	H1	D362 ^{ECL3}	2.3				H1	K310 ^{5.40}	1.6	
									H1	E385 ^{7.42}	1.2	H1	K310 ^{5.40}	1.0	H1	E374 ^{ECL3}	2.1				H1	K310 ^{5.40}	1.7	
														H1	T303 ^{5.33}	1.0				H1	N375 ^{ECL3}	1.1		
S2	D298 ^{ECL2}	1.0				S2	D362 ^{ECL3}	1.3	S2	E91 ^{ECD}	4.0	S2	E385 ^{7.42}	5.2	S2	E374 ^{ECL3}	15.7	S2	E374 ^{ECL3}	18.0	S2	E385 ^{7.42}	5.9	
S2	D301 ^{ECL2}	2.9							S2	E374 ^{ECL3}	2.4	S2	K378 ^{7.35}	4.1	S2	E367 ^{7.36}	5.0	S2	K369 ^{7.38}	4.5	S2	E374 ^{ECL3}	2.3	
									S2	N300 ^{ECL2}	1.4	S2	N375 ^{ECL3}	2.8	S2	Y139 ^{1.36}	3.7				S2	E374 ^{ECL3}	2.3	
									S2	D147 ^{1.33}	1.3	S2	E374 ^{ECL3}	2.7	S2	K369 ^{7.38}	2.7				S2	D215 ^{ECL1}	1.7	
														S2	D362 ^{ECL3}	1.0								
D3	K378 ^{7.35}	7.9		D3	N290 ^{5.32}	1.7	D3	K365 ^{7.34}	9.0	D3	K310 ^{5.40}	6.2	D3	K378 ^{7.35}	12.8	D3	R188 ^{2.60}	2.5	D3	R188 ^{2.60}	5.1	D3	K206 ^{2.67}	10.2
D3	T294 ^{ECL2}	2.1		D3	N363 ^{ECL3}	1.2	D3	K369 ^{7.38}	7.5	D3	W306 ^{5.36}	4.6	D3	R199 ^{2.60}	10.4	D3	K369 ^{7.38}	2.0	D3	Y139 ^{1.36}	3.4	D3	R199 ^{2.60}	6.5
D3	R379 ^{7.36}	1.5		D3	T288 ^{ECL2}	1.0				D3	K206 ^{2.67}	2.2	D3	Y161 ^{1.47}	6.5	D3	K195 ^{2.67}	1.9	D3	K195 ^{2.67}	1.9	D3	K154 ^{1.40}	6.4
									D3	K378 ^{7.35}	2.0	D3	K206 ^{2.67}	4.0	D3	N290 ^{5.32}	1.5	D3	N290 ^{5.32}	1.5	D3	Y211 ^{ECL1}	2.3	
									D3	K154 ^{1.40}	1.1	D3	R379 ^{7.36}	1.5	D3	Y139 ^{1.36}	1.3				D3	Y161 ^{1.47}	1.6	
																					D3	Y157 ^{1.43}	1.5	
T7	Y150 ^{1.36}	1.8		T7	N290 ^{5.32}	1.7	T7	Y283 ^{ECL2}	1.5				T7	K206 ^{2.67}	6.5	T7	K195 ^{2.67}	1.9	T7	K195 ^{2.67}	6.0	T7	K206 ^{2.67}	5.8
T7	T294 ^{ECL2}	1.0										T7	D298 ^{ECL2}	5.9	T7	Y139 ^{1.36}	1.2				T7	Y211 ^{ECL1}	4.9	
				D8	T288 ^{ECL2}	3.0	D8	T288 ^{ECL2}	2.6	D8	R379 ^{7.36}	5.1				D8	T288 ^{ECL2}	6.4	D8	T288 ^{ECL2}	15.5	D8	R379 ^{7.36}	1.4
				D8	Y283 ^{ECL2}	1.4	D8	N290 ^{5.32}	1.6	D8	K378 ^{7.35}	3.6				D8	K127 ^{ECD}	6.1						
S9	D147 ^{1.33}	9.7		S9	D132 ^{1.29}	10.0	N9	Y283 ^{ECL2}	5.1	N9	Y139 ^{1.25}	3.5	S9	Y150 ^{1.36}	13.6	S9	Y139 ^{1.36}	8.9	N9	Y139 ^{1.36}	11.8	N9	Y150 ^{1.36}	9.9
S9	Y150 ^{1.36}	1.2		S9	Y139 ^{1.36}	3.6	N9	Y139 ^{1.36}	1.6	N9	S141 ^{1.27}	2.4	S9	E142 ^{1.28}	2.6	S9	D132 ^{1.29}	7.6	N9	D132 ^{1.29}	3.8	N9	K378 ^{7.35}	2.3
				S9	Q135 ^{1.32}	1.7	N9	D132 ^{1.29}	1.3	N9	R379 ^{7.36}	1.7				S9	E36 ^{ECD}	2.6				N9	R379 ^{7.36}	2.2
				S9	E36 ^{ECD}	1.7				N9	Q146 ^{1.32}	1.4										N9	Q146 ^{1.32}	1.3
																						N9	N375 ^{ECL3}	1.2
																						N9	S141 ^{1.27}	1.0
Y10	D215 ^{ECL1}	9.1		Y10	D132 ^{1.29}	4.0	Y10	D206 ^{ECL1}	2.9	Y10	D215 ^{ECL1}	5.1	Y10	D215 ^{ECL1}	8.1	Y10	D132 ^{1.29}	4.7				Y10	D147 ^{1.33}	16.4
Y10	Q214 ^{ECL1}	2.0		Y10	E36 ^{ECD}	3.7	Y10	E210 ^{ECL1}	2.2	Y10	D298 ^{ECL2}	1.9	Y10	D147 ^{1.33}	3.9	Y10	D201 ^{ECL1}	3.3				Y10	D215 ^{ECL1}	1.1
Y10	E140 ^{1.26}	1.5		Y10	D287 ^{ECL2}	2.7	Y10	D287 ^{ECL2}	1.4				Y10	Y211 ^{ECL1}	2.3	Y10	Y39 ^{ECD}	2.1						
				Y10	Q207 ^{ECL1}	2.2	Y10	N290 ^{5.32}	1.1							Y10	E204 ^{ECL1}	1.8						
				Y10	E133 ^{1.30}	2.2									Y10	S205 ^{ECL1}	1.3							
															Y10	T136 ^{1.33}	1.3							
															Y10	Q207 ^{ECL1}	1.2							
S11	H218 ^{ECL1}	2.4		S11	E204 ^{ECL1}	2.3	T11	T288 ^{ECL2}	1.5				S11	Y211 ^{ECL1}	6.3	S11	D287 ^{ECL2}	10.0	T11	D287 ^{ECL2}	15.5			
S11	N217 ^{ECL1}	1.3		S11	Q207 ^{ECL1}	2.2						S11	D298 ^{ECL2}	3.6	S11	Q207 ^{ECL1}	3.2							
S11	Q214 ^{ECL1}	1.1																						
R12	D87 ^{ECD}	36.6		R12	E36 ^{ECD}	40.1	R12	E36 ^{ECD}	22.8	R12	D87 ^{ECD}	53.1	R12	D87 ^{ECD}	28.6	R12	D132 ^{1.29}	14.0	R12	E36 ^{ECD}	29.4	R12	D87 ^{ECD}	64.5
R12	D147 ^{1.33}	9.4		R12	D132 ^{1.29}	16.2	R12	D132 ^{1.29}	7.3	R12	D147 ^{1.33}	7.2	R12	D301 ^{ECL2}	9.0	R12	D287 ^{ECL2}	12.7	R12	D287 ^{ECL2}	4.7	R12	Y139 ^{1.25}	1.5
				R12	D287 ^{ECL2}	6.0	R12	Y39 ^{ECD}	5.1	R12	E140 ^{1.26}	3.0	R12	E142 ^{1.28}	4.7	R12	E36 ^{ECD}	11.4	R12	D132 ^{1.29}	3.4	R12	E140 ^{1.26}	1.2
				R12	E210 ^{ECL1}	3.2	R12	D38 ^{ECD}	1.0	R12	D110 ^{ECD}	2.0				R12	N290 ^{5.32}	2.3						
				R12	Q207 ^{ECL1}	1.7				R12	E142 ^{1.28}	1.9				R12	E210 ^{ECL1}	1.0						
				R12	E204 ^{ECL1}	1.3				R12	R82 ^{ECD}	1.2												
										R12	D145 ^{1.31}	1.0												



Supplementary Table 8 continued

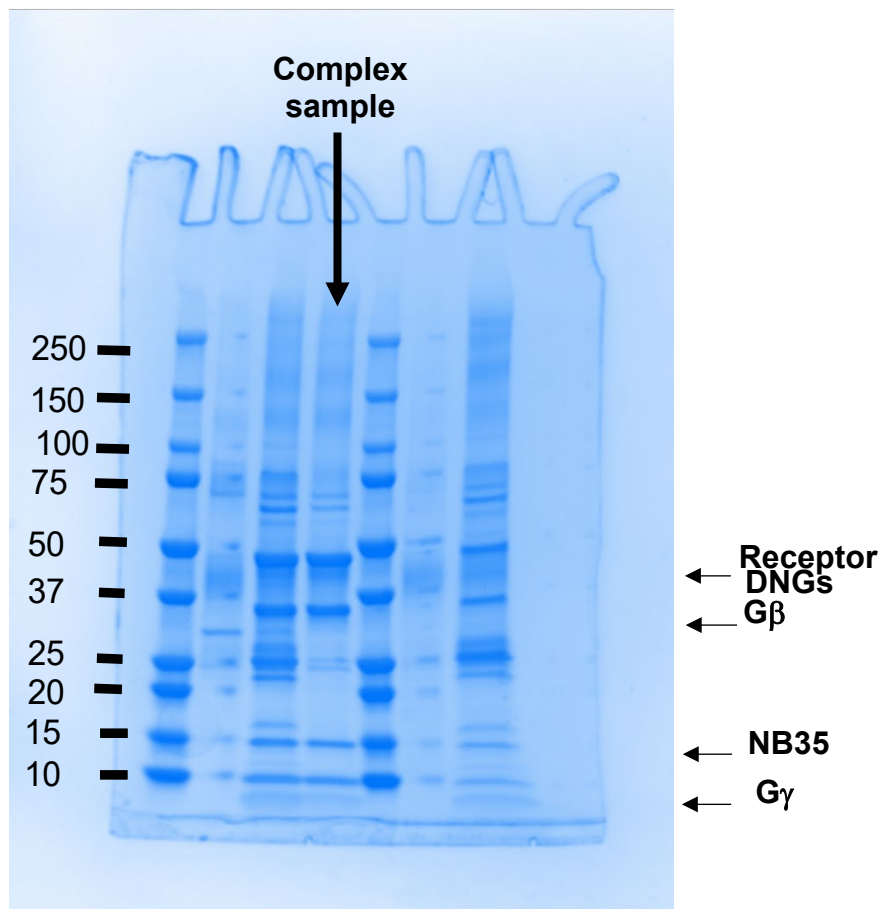
Hydrogen bonds partial binding				Hydrogen bonds partial unbinding																											
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Y13	D87 ^{ECD}	16.1		Y13	E133 ^{1.30}	8.8				Y13	D147 ^{1.33}	26.6		Y13	T136 ^{1.33}	14.5															
Y13	D147 ^{1.33}	4.2		Y13	D132 ^{1.29}	3.8				Y13	E142 ^{1.28}	1.2		Y13	D132 ^{1.29}	14.3															
Y13	D215 ^{ECD}	1.3		Y13	T136 ^{1.33}	1.8				Y13	E140 ^{1.26}	1.0		Y13	E133 ^{1.30}	1.5															
Y13	S141 ^{1.27}	1.2												Y13	E204 ^{ECD}	1.3															
										Y13	S130 ^{1.27}	1.3																			
R14	D215 ^{ECD}	22.2		R14	E204 ^{ECD}	39.0		R14	D287 ^{ECD}	18.1		R14	D215 ^{ECD}	9.6		R14	E204 ^{ECD}	58.3		R14	E204 ^{ECD}	17.5		R14	D215 ^{ECD}	29.7					
R14	D24 ^{ECD}	22.2		R14	E133 ^{1.30}	8.9		R14	E210 ^{ECD}	11.5		R14	D147 ^{1.33}	2.6		R14	D132 ^{1.29}	4.6		R14	Q207 ^{ECD}	9.0		R14	D147 ^{1.33}	13.2					
R14	E142 ^{1.28}	20.1		R14	D287 ^{ECD}	7.1		R14	E204 ^{ECD}	8.8		R14	D298 ^{ECD}	1.2		R14	Q214 ^{ECD}	2.1		R14	E133 ^{1.30}	3.8		R14	D132 ^{1.29}	7.3		R14	D145 ^{1.31}	3.9	
R14	Q214 ^{ECD}	6.2		R14	Q207 ^{ECD}	4.2		R14	D196 ^{2.68}	4.0		R14	H218 ^{ECD}	1.0		R14	E142 ^{1.28}	1.7		R14	Q207 ^{ECD}	1.4		R14	D287 ^{ECD}	5.6		R14	E142 ^{1.28}	1.5	
R14	D147 ^{1.33}	5.1		R14	E210 ^{ECD}	2.0		R14	S202 ^{ECD}	3.1						R14	E36 ^{ECD}	1.2		R14	E210 ^{ECD}	2.0									
R14	E140 ^{1.26}	4.8		R14	D132 ^{1.29}	1.3		R14	E36 ^{ECD}	1.7																					
R14	H218 ^{ECD}	4.5																													
K15	D24 ^{ECD}	8.5		K15	E36 ^{ECD}	39.9		K15	D38 ^{ECD}	53.3		K15	D24 ^{ECD}	4.8		K15	E36 ^{ECD}	39.7		K15	E36 ^{ECD}	40.6		K15	D298 ^{ECD}	2.5					
K15	N217 ^{ECD}	2.0		K15	E210 ^{ECD}	6.0		K15	E36 ^{ECD}	14.9		K15	E79 ^{ECD}	3.7						K15	D287 ^{ECD}	31.6		K15	E79 ^{ECD}	1.0					
K15	H218 ^{ECD}	1.0		K15	E204 ^{ECD}	5.3		K15	D287 ^{ECD}	7.3		K15	D215 ^{ECD}	3.3		K15	D287 ^{ECD}	5.6		K15	D38 ^{ECD}	3.8									
								K15	H218 ^{ECD}	1.2						K15	Q207 ^{ECD}	4.2		K15	E210 ^{ECD}	2.2									
Q16	Y139 ^{1.25}	5.5		Q16	E36 ^{ECD}	13.6		Q16	Y118 ^{ECD}	7.9		Q16	Y139 ^{1.25}	8.1		Q16	E36 ^{ECD}	10.2		Q16	K127 ^{ECD}	6.1		Q16	Y139 ^{1.25}	11.0					
				Q16	D132 ^{1.29}	3.2						Q16	S141 ^{1.27}	1.7		Q16	K127 ^{ECD}	3.3		Q16	D132 ^{1.29}	4.9		Q16	T143 ^{1.29}	2.5					
				Q16	T136 ^{1.33}	1.2						Q16	E138 ^{ECD}	1.0		Q16	Y39 ^{ECD}	2.4		Q16	E36 ^{ECD}	3.0		Q16	S141 ^{1.27}	2.0					
				Q16	S130 ^{1.27}	1.1						Q16	E140 ^{1.26}	1.0						Q16	Q146 ^{1.32}	1.4									
K20	E138 ^{ECD}	28.3		K20	E133 ^{1.30}	14.8		K20	E204 ^{ECD}	11.1		K20	D137 ^{ECD}	19.8		K20	E140 ^{1.26}	23.1		K20	D132 ^{1.29}	18.6		K20	D137 ^{ECD}	14.8					
K20	E140 ^{1.26}	13.8		K20	D132 ^{1.29}	9.6		K20	D206 ^{ECD}	9.3		K20	E142 ^{1.28}	11.1		K20	E138 ^{ECD}	9.9		K20	E133 ^{1.30}	5.1		K20	E133 ^{1.30}	3.2		K20	E142 ^{1.28}	7.0	
K20	D147 ^{1.33}	4.6		K20	D125 ^{ECD}	5.4		K20	S205 ^{ECD}	6.6		K20	E138 ^{ECD}	10.2		K20	E142 ^{1.28}	8.5		K20	D125 ^{ECD}	4.1		K20	E204 ^{ECD}	2.7		K20	T143 ^{1.29}	3.9	
K20	E142 ^{1.28}	4.0						K20	E210 ^{ECD}	1.2		K20	E140 ^{1.26}	4.3		K20	D126 ^{ECD}	1.4		K20	Y118 ^{ECD}	2.2		K20	E138 ^{ECD}	2.7					
K20	S141 ^{1.27}	1.0						K20	S141 ^{1.27}	2.3		K20	S141 ^{1.27}	2.3		K20	D126 ^{ECD}	2.1		K20	D126 ^{ECD}	2.1		K20	Y139 ^{1.25}	2.2					
																				K20	E140 ^{1.26}	1.1									
K21	E142 ^{1.28}	21.7		K21	E204 ^{ECD}	25.3		K21	E204 ^{ECD}	16.3		K21	D215 ^{ECD}	1.9		K21	E204 ^{ECD}	36.0		K21	E204 ^{ECD}	61.9		K21	D145 ^{1.31}	2.1					
K21	D147 ^{1.33}	17.3		K21	D201 ^{ECD}	5.7		K21	D287 ^{ECD}	11.0		K21	E142 ^{1.28}	1.0		K21	E133 ^{1.30}	4.6		K21	D201 ^{ECD}	2.9									
K21	E140 ^{1.26}	14.9						K21	E210 ^{ECD}	8.6		K21	H218 ^{ECD}	3.4		K21	D132 ^{1.29}	1.9		K21	E210 ^{ECD}	2.6									
K21	H218 ^{ECD}	8.2						K21	D206 ^{ECD}	6.7		K21	E140 ^{1.26}	1.4						K21	S205 ^{ECD}	2.6									
K21	D215 ^{ECD}	7.9						K21	Q207 ^{ECD}	1.6		K21	E213 ^{ECD}	1.4																	
K21	D24 ^{ECD}	2.1						K21	S202 ^{ECD}	1.1																					
K21	E138 ^{ECD}	1.1																													
Y22	Q31 ^{ECD}	7.8		Y22	E44 ^{ECD}	34.8		Y22	E44 ^{ECD}	17.4		Y22	Q31 ^{ECD}	2.9		Y22	E44 ^{ECD}	22.4		Y22	E44 ^{ECD}	21.3		Y22	Q31 ^{ECD}	11.9					
Y22	D24 ^{ECD}	6.8		Y22	Q41 ^{ECD}	8.8		Y22	H47 ^{ECD}	12.9		Y22	D24 ^{ECD}	1.6		Y22	Q41 ^{ECD}	6.2		Y22	Q41 ^{ECD}	6.2		Y22	D24 ^{ECD}	1.4					
Y22	E30 ^{ECD}	2.0						Y22	E36 ^{ECD}	3.3		Y22	Q31 ^{ECD}	6.9		Y22	E36 ^{ECD}	4.1													
Y22	N60 ^{ECD}	1.1																													
								N24	Y118 ^{ECD}	8.1		N24	N60 ^{ECD}	1.2						N24	Y118 ^{ECD}	15.5		N24	N60 ^{ECD}	1.1					
								N24	E204 ^{ECD}	3.2		N24	Y139 ^{1.25}	1.2																	
												S25	K28 ^{ECD}	7.1																	
																				S25	K28 ^{ECD}	5.6									
																				S25	N60 ^{ECD}	1.5									
								N28	S205 ^{ECD}	1.6		N28	K28 ^{ECD}	2.5																	
								N28	N60 ^{ECD}	2.2		N28	N60 ^{ECD}	2.2																	
								N28	D24 ^{ECD}	1.2		N28	D24 ^{ECD}	1.2																	

Supplementary Table 9: MM-GBSA binding energy of PACAP27 or VIP in complex to VPAC1 or PAC1. Results refer to equilibrium simulations **without the disulphide** and **in the presence of the disulphide** bond between ECD and ECL1. Asterisk refers to the homology modelled PAC1R-VIP complex.

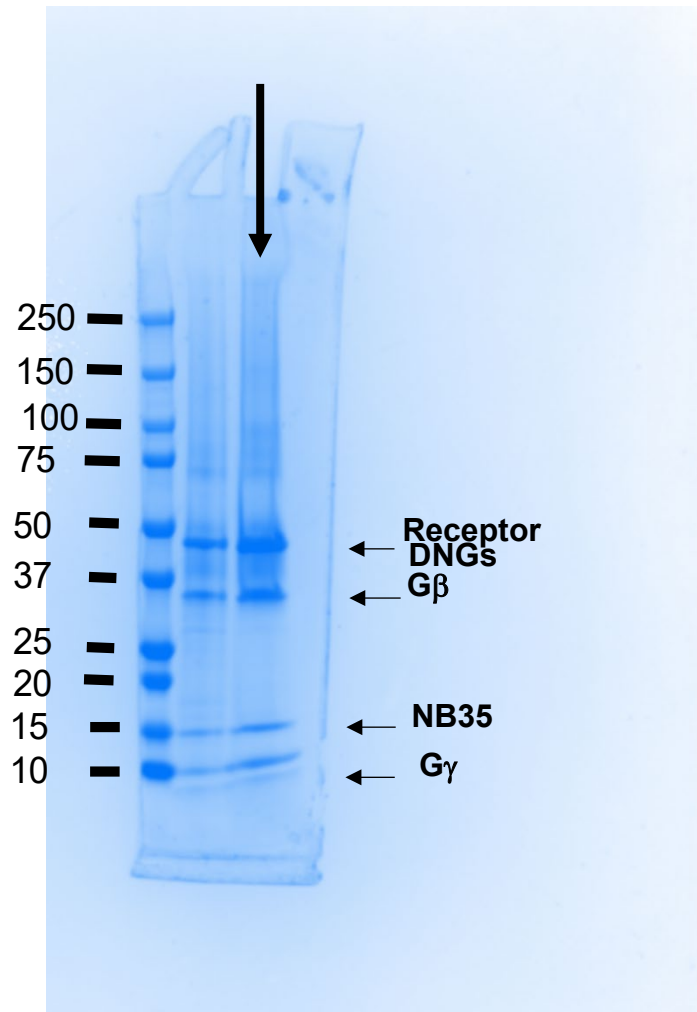
Without disulfide		
Receptor	Agonist	MM-GBSA Binding Energy (Kcal/mol)
VPAC1	PACAP27	-112.18 ± 15.40
PAC1	PACAP27	-99.09 ± 16.13
VPAC1	VIP	-91.25 ± 14.02
PAC1*	VIP*	-77.52 ± 15.29

With disulfide		
Receptor	Agonist	MM-GBSA Binding Energy (Kcal/mol)
VPAC1	PACAP27	-96.82 ± 15.68
PAC1	PACAP27	-90.49 ± 15.47
VPAC1	VIP	-109.41 ± 20.73
PAC1*	VIP*	-99.78 ± 26.48

Source Data for Supplementary Information file: Uncropped Coomassie-stained SDS-PAGE of the complex samples used for cryo-EM imaging (cropped gels shown in Supplementary Figure 1)



PAC1R-PACAP27



VPAC1R-PACAP27

