

Supplementary Information for

Active state structures of a bistable visual opsin bound to G proteins

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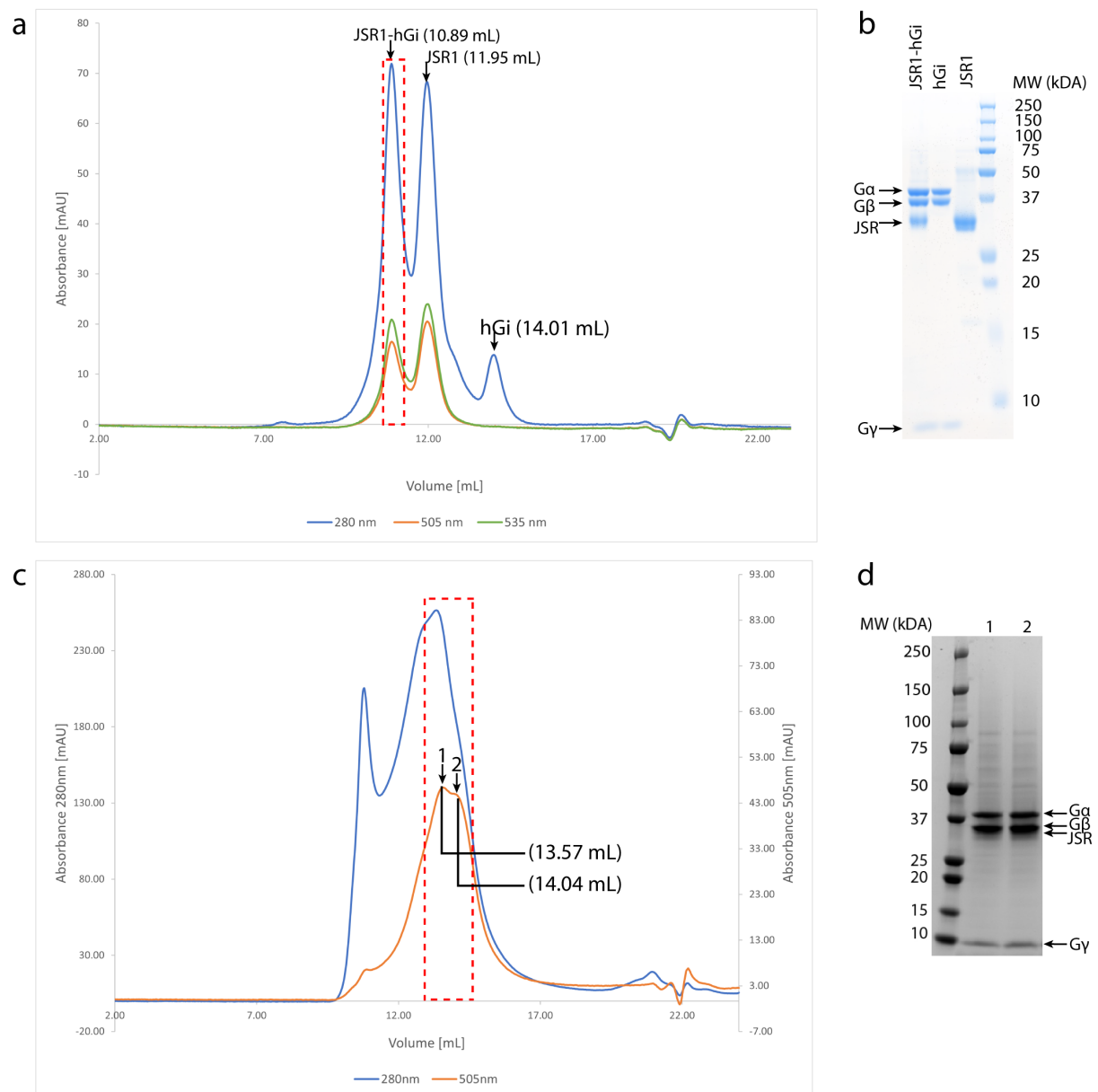
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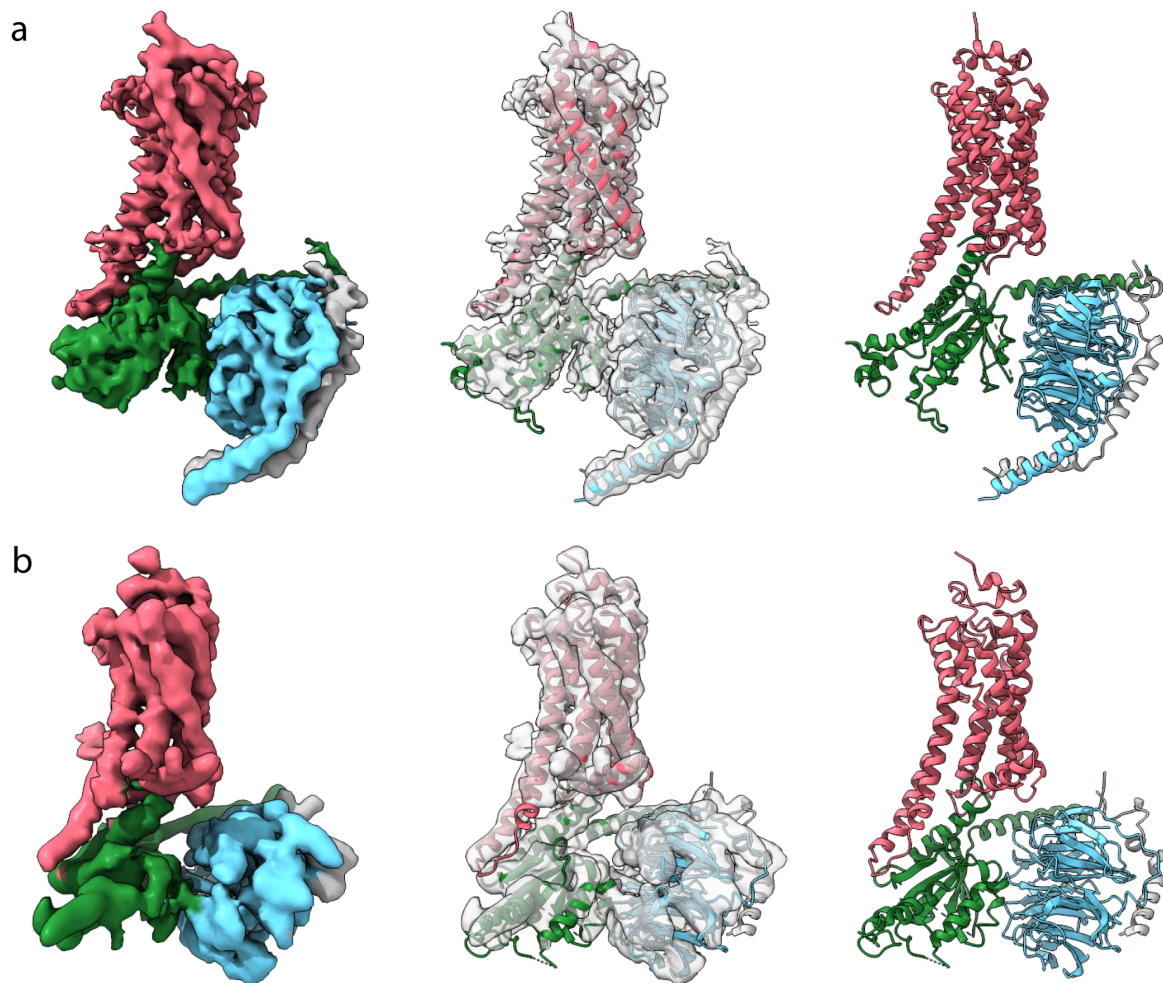
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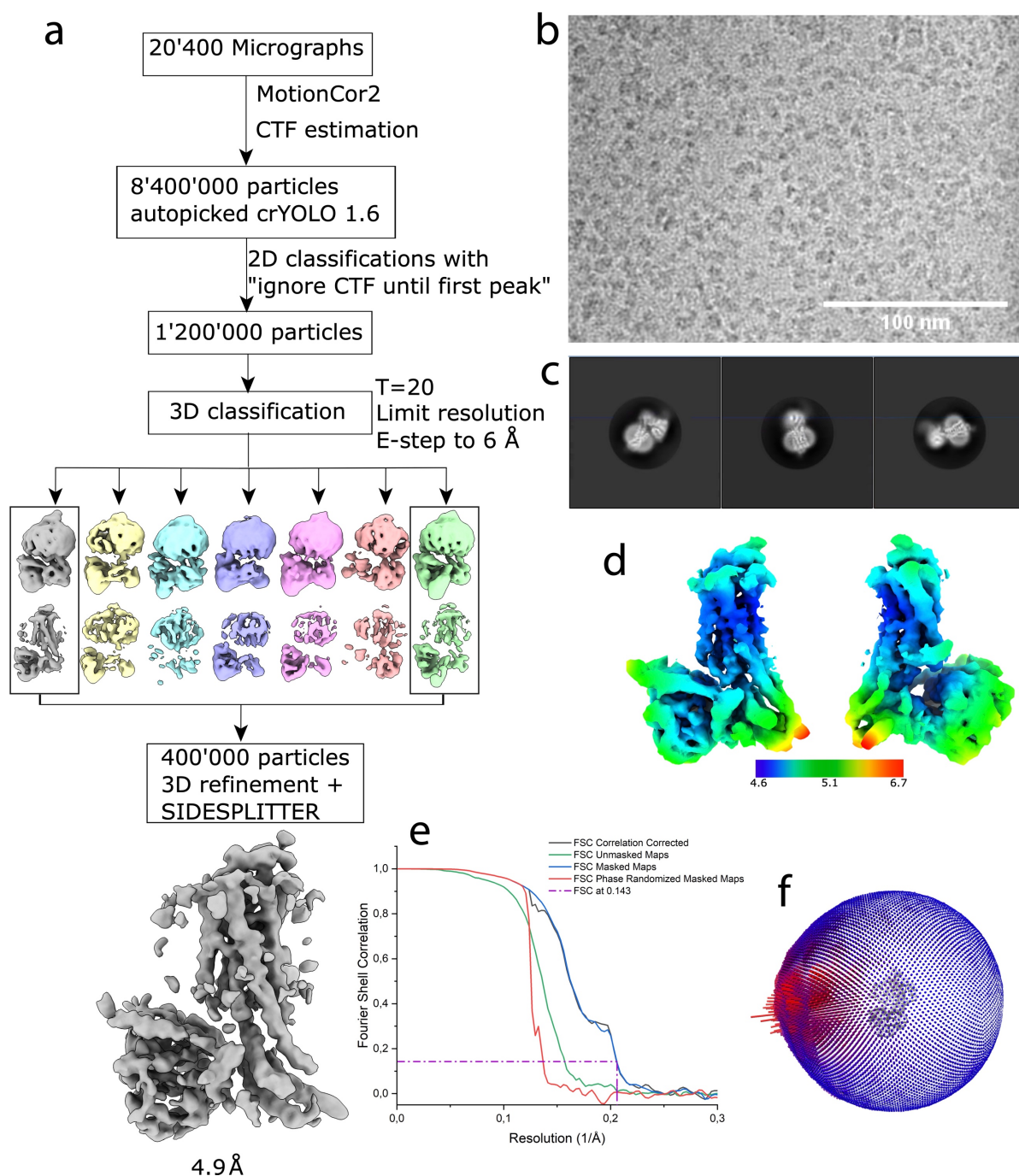
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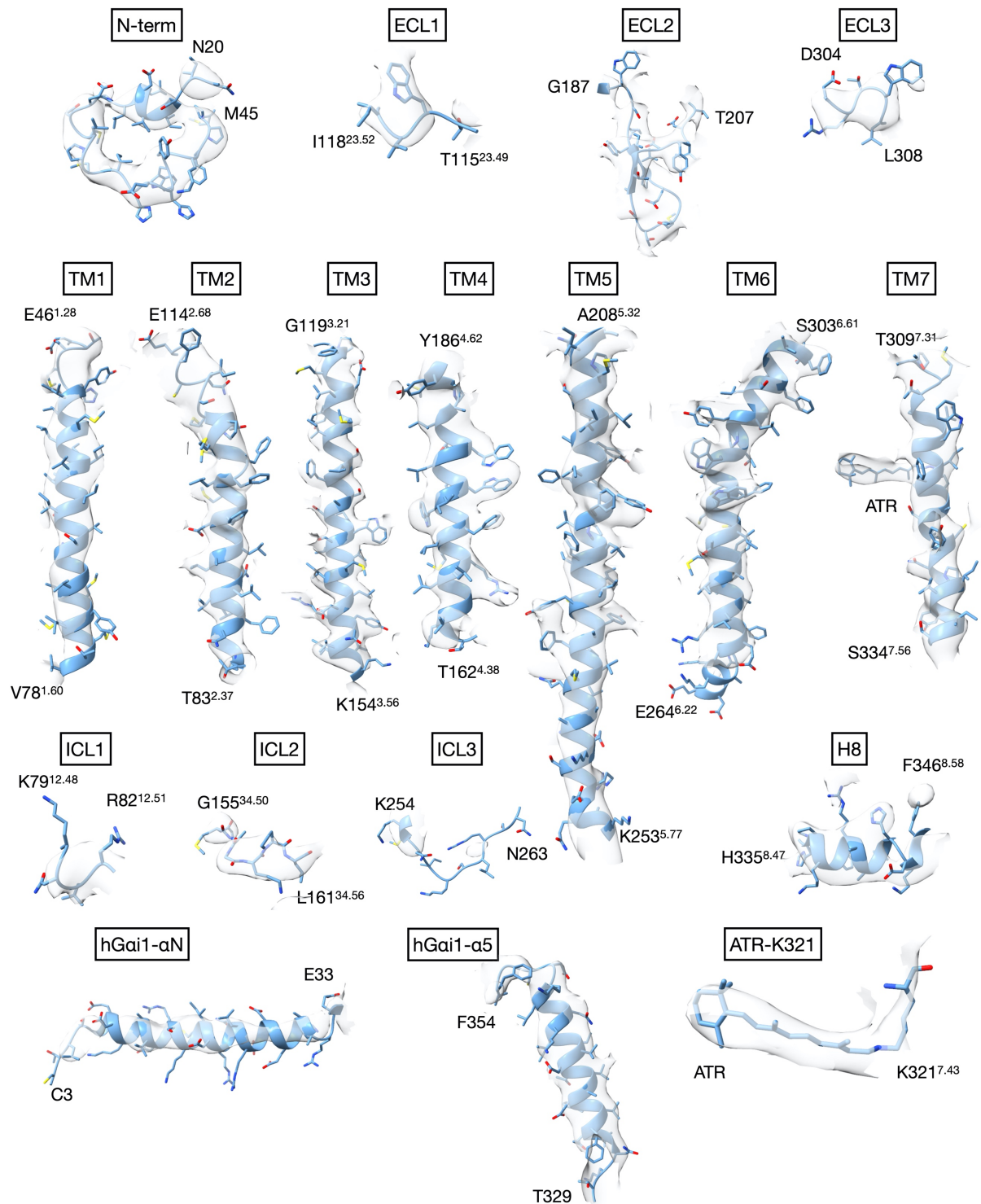
Supplementary Figure 1: SEC and SDS-PAGE of the JSR1-hGi and JSR1-jsGi complexes. **a:** SEC chromatogram of the JSR1-hGi complex. The size exclusion chromatography was performed using a Superdex 200 Increase 10/300 column. Y-axis shows the absorbance in mAU and x-axis shows the volume in mL. The red dashed line marks the fractions collected for freezing on EM grids. **b:** Coomassie stained SDS-PAGE of the three peaks labeled in A. Individual subunits are labeled on the left side and the molecular weight (MW) is indicated on the right side in kDa. **c:** SEC chromatogram of the JSR1-jsGi complex. The SEC profile was recorded using a SRT-C 300 10/300 column. Y-axis shows the absorbance in mAU and x-axis shows the volume in mL. The red dashed line marks the fractions collected for freezing on EM grids. **d:** Coomassie stained SDS-PAGE of the two fractions indicated in C. Left side shows the MW in kDa and individual subunits are labeled on the right side. The bands for Gβ and JSR1 overlap.



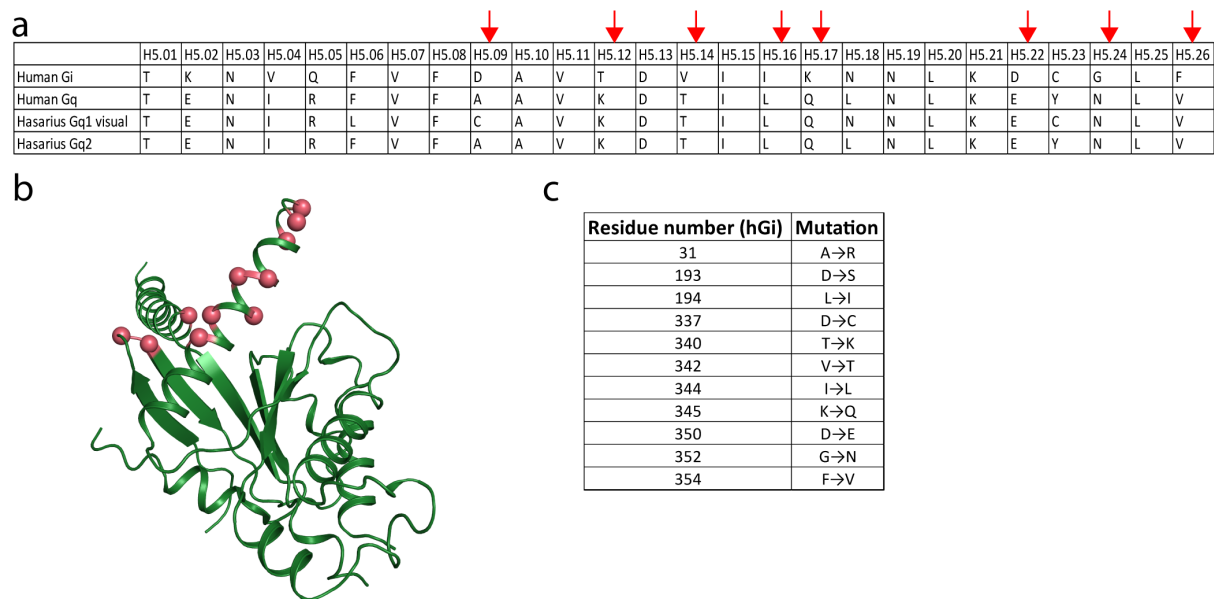
Supplementary Figure 2: Cryo-EM maps and structural model for the JSR1-jsG_{iq_2} complex and the JSR1-hG_i complex. **a:** Left: JSR1-jsG_{iq_2} cryo-EM map colored by subunit. JSR1, jsG_{αiq}, G_β and G_γ subunits are shown in salmon, green, cyan and gray, respectively. Middle: Cryo-EM map is shown in gray and transparent with the model of JSR1-jsG_{iq_2} fitted into the map. Subunits of the model are colored in the same way as the map on the left. Right: Model of the JSR1-jsG_{iq_2} complex shown as cartoon. Subunits are colored as in the left cryo-EM map. **b:** Same figures as in A, colored in the same way, for the JSR1-hG_i complex.



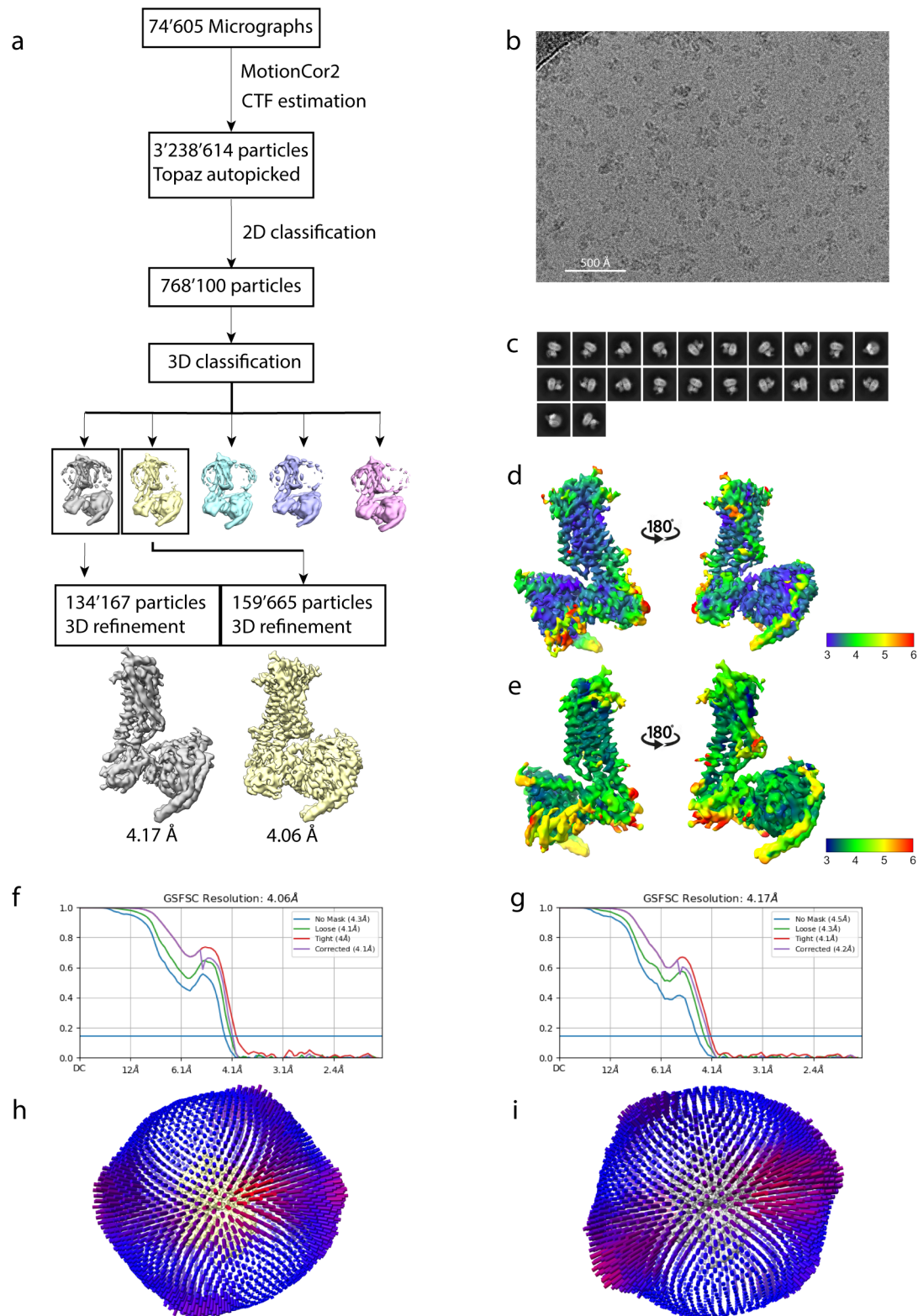
Supplementary Figure 3: Single-particle analysis of the JSR1-hG_i complex. **A:** Single particle data processing workflow for the JSR1-hG_i complex. **B:** Representative micrograph. **C:** 2D class averages for the JSR1-hG_i complex in different orientations. **D:** 4.9 Å JSR1-hG_i complex electron potential map colored by local resolution values. **E:** FSC plot for the JSR1-hG_i complex at 4.9 Å resolution determined at 0.143 cut-off. **F:** 3D Angular distribution of particles.



Supplementary Figure 4: Cryo-EM map quality and model fit of the JSR1-hGai structure. JSR1 is dissected into the N-terminus (N-term), extracellular loops (ECL) 1-3, transmembrane helices (TM) 1-8, helix 8 (H8), and intracellular loops (ICL) 1-3. All-trans retinal (ATR) is shown in two views, one with TM7 and the other with Lys321^{7.43}. The αN and α5 helices of hGai are shown. Protein main chains are displayed in cartoon. Protein side chains and ATR are displayed in stick format with carbon in light blue, nitrogen in dark blue, sulfur in yellow, and oxygen in red.

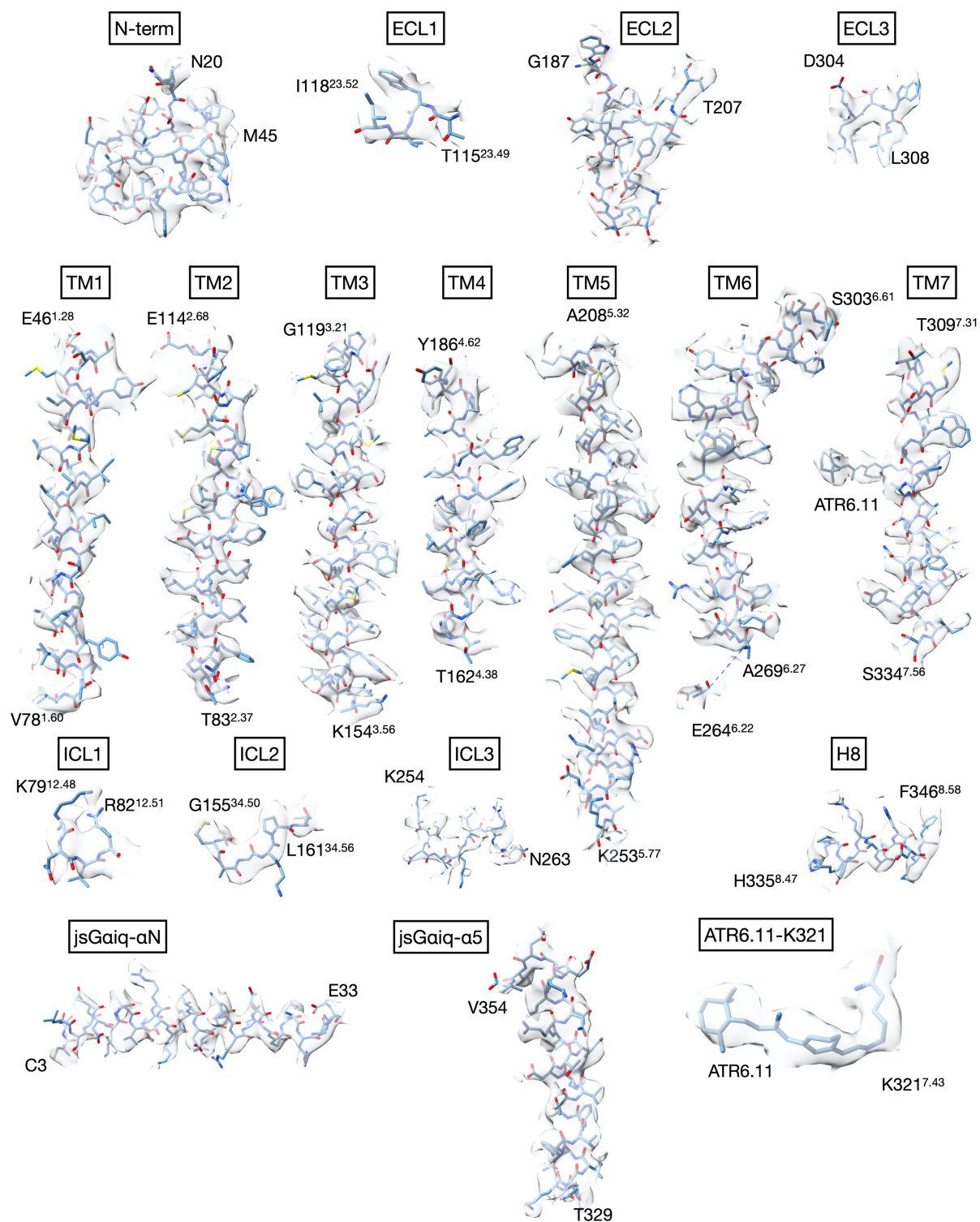


Supplementary Figure 5: Design of chimeric jsG α_{iq} subunit. a: Sequence alignment of the $\alpha 5$ helices of the human G α_i , human G α_q , jumping spider visual G α_{q1} (HaGq1: acc. No. LC799818) and jumping spider G α_{q2} (HaGq2: acc. No. LC799819). **b:** Human G α_i structure from our JSR1-jsG α_{iq_1} complex. Locations where mutations were introduced are marked as red spheres. **c:** Table with the mutations introduced to make the chimeric jsG α_{iq} α subunit using hG α_i as a template.

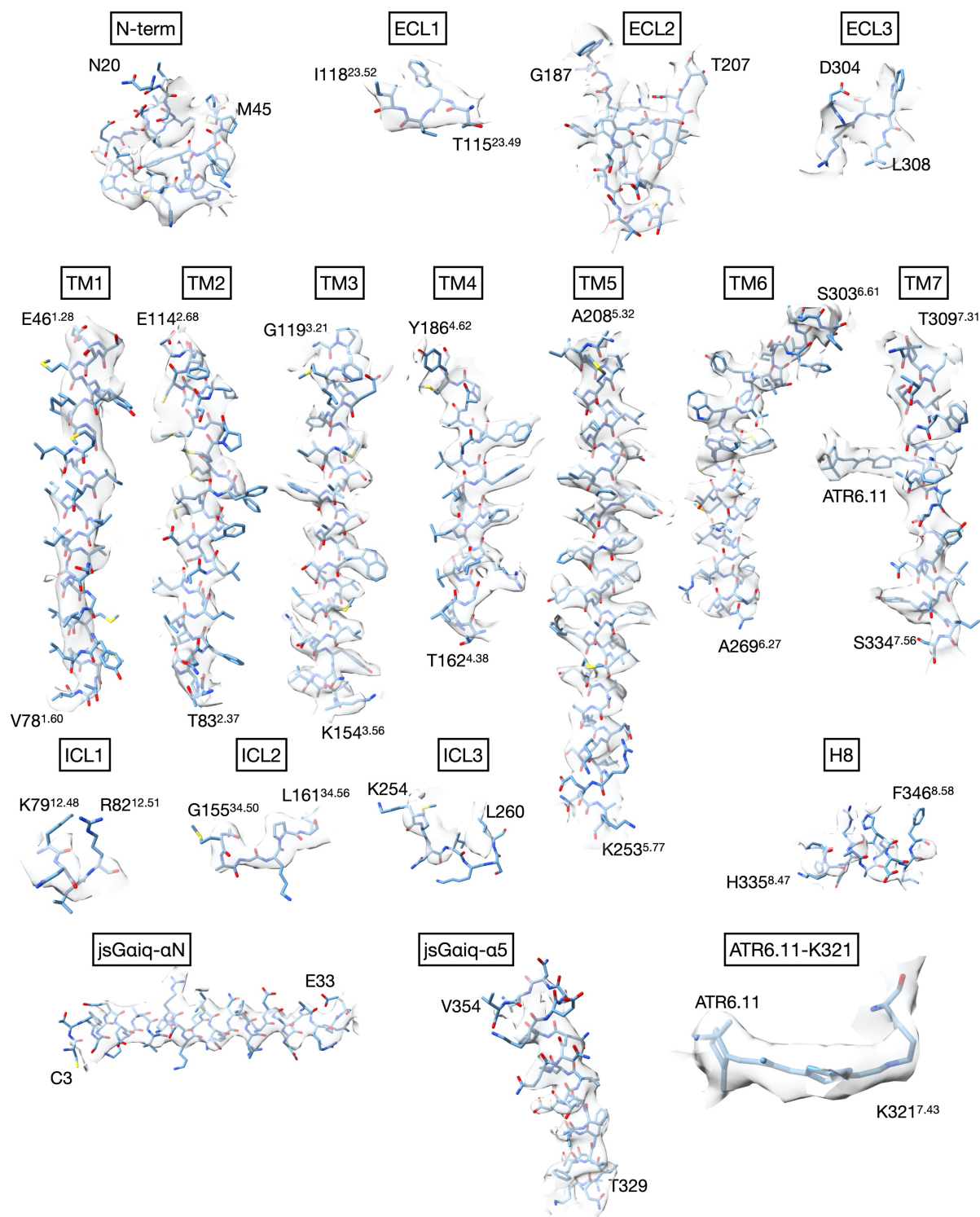


Supplementary Figure 6: Single-particle analysis of the JSR1-jsG_{iq} complex. **a:** Single particle data processing workflow for the JSR1-jsG_{iq} complex. **b:** A representative micrograph taken at a nominal magnification of 165'000 (0.51 Å/pixel). **c:** Selected 2D class averages for the JSR1-jsG_{iq} complex. **d:** 4.1 Å JSR1-jsG_{iq_1} complex electron potential map colored by local resolution values (Local Resolution Estimation, cryoSPARC). **e:** 4.2 Å JSR1-jsG_{iq_2} complex electron potential map colored by local resolution values (Local Resolution Estimation, cryoSPARC). **f:** FSC plot for the JSR1-jsG_{iq_1} complex at 4.1 Å resolution determined by 0.143 cut-off. **g:** FSC plot for the JSR1-jsG_{iq_2} complex at

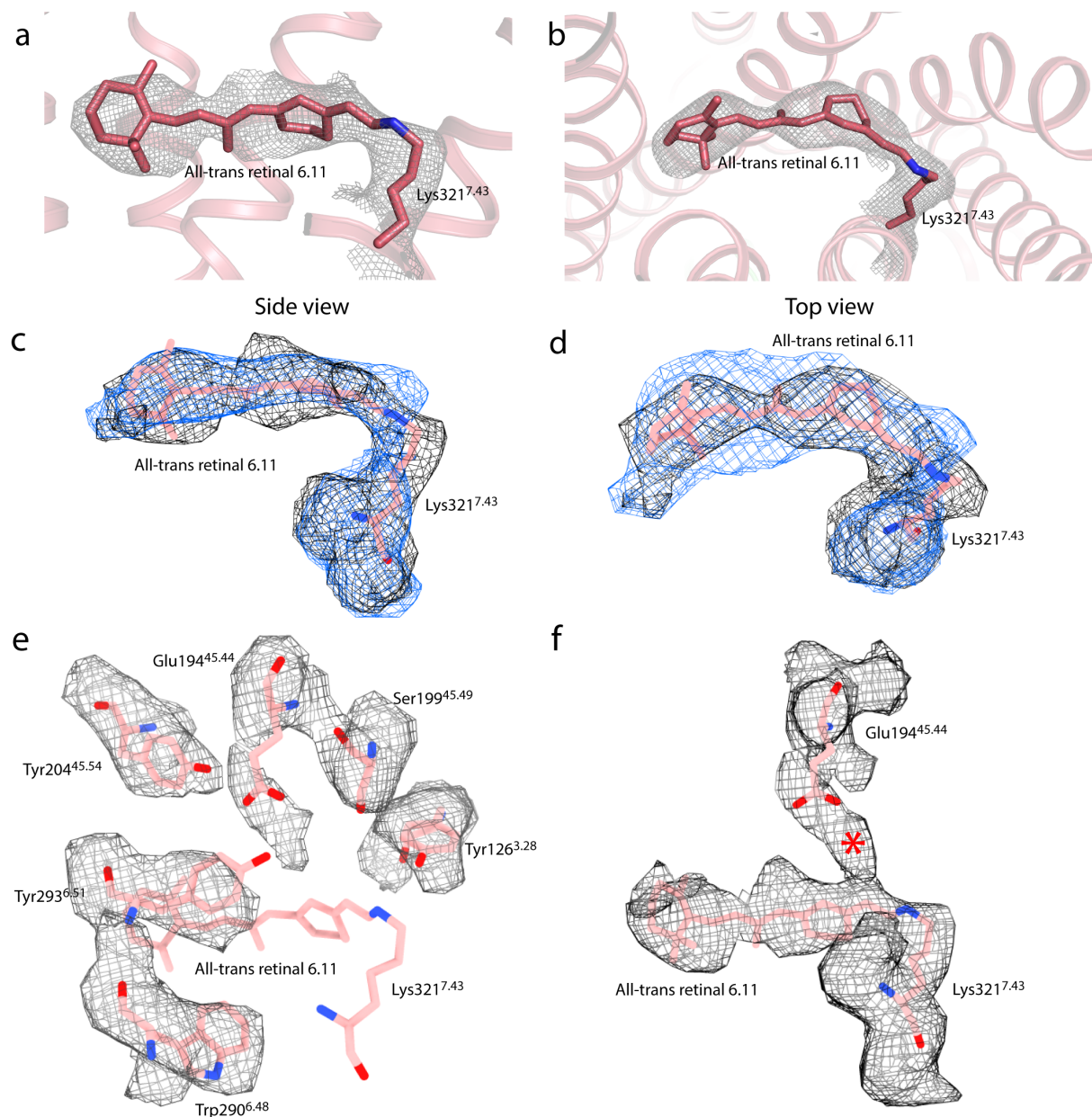
4.2 Å resolution determined by 0.143 cut-off. **h**: 3D angular distribution of the JSR1-jsG_{iq_1} particle set. **l**: 3D angular distribution of the JSR1-jsG_{iq_2} particle set.



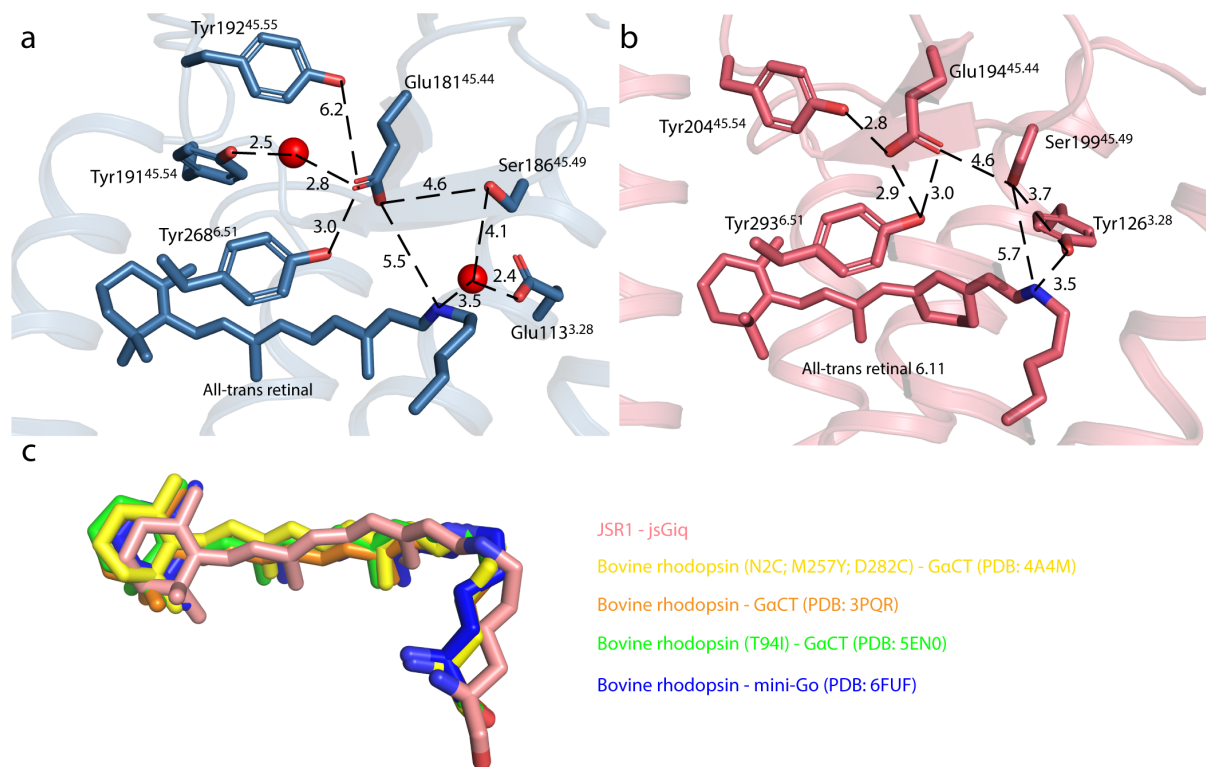
Supplementary Figure 7: Cryo-EM map quality and model fit of the JSR1-jsGaiq₁ structure. JSR1 is dissected into the N-terminus (N-term), extracellular loops (ECL) 1-3, transmembrane helices (TM) 1-8, helix 8 (H8), and intracellular loops (ICL) 1-3. ATR6.11 is shown in two views, one with TM7 and the other with Lys321. The α N and α 5 helices of jsGaiq are shown. Protein residues and ATR6.11 are displayed in stick format with carbon in light blue, nitrogen in dark blue, sulfur in yellow, and oxygen in red.



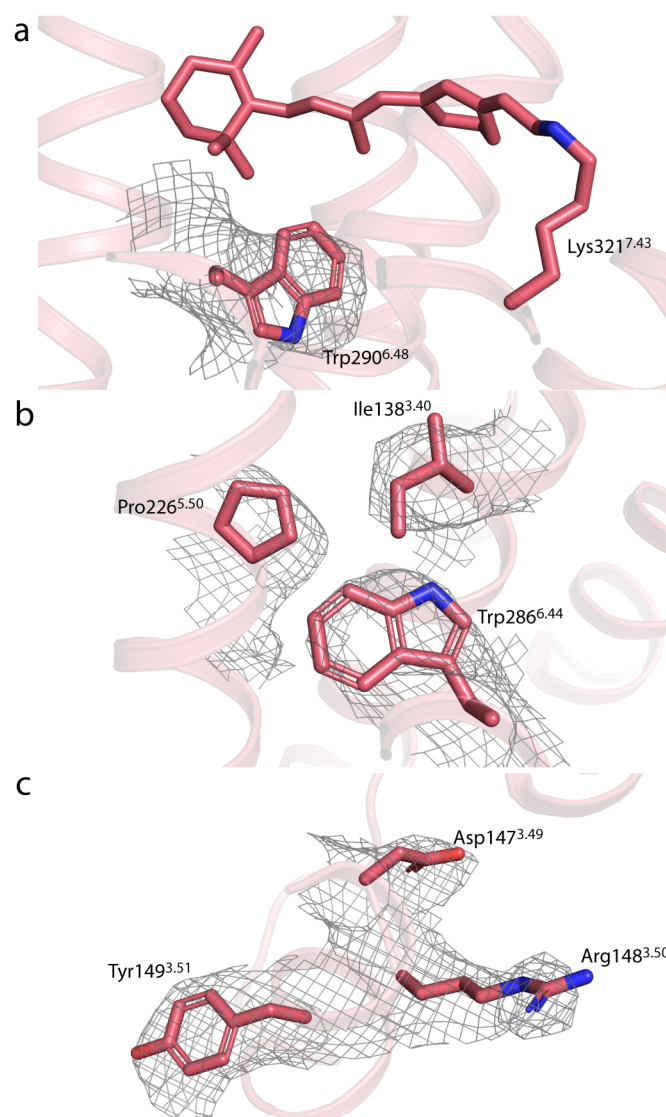
Supplementary Figure 8: Cryo-EM map quality and model fit of the JSR1-jsGaiq₂ structure. JSR1 is dissected into the N-terminus (N-term), extracellular loops (ECL) 1-3, transmembrane helices (TM) 1-8, helix 8 (H8), and intracellular loops (ICL) 1-3. ATR6.11 is shown in two views, one with TM7 and the other with Lys321. The αN and α5 helices of jsGaiq are shown. Protein residues and ATR6.11 are displayed in stick format with carbon in light blue, nitrogen in dark blue, sulfur in yellow, and oxygen in red.



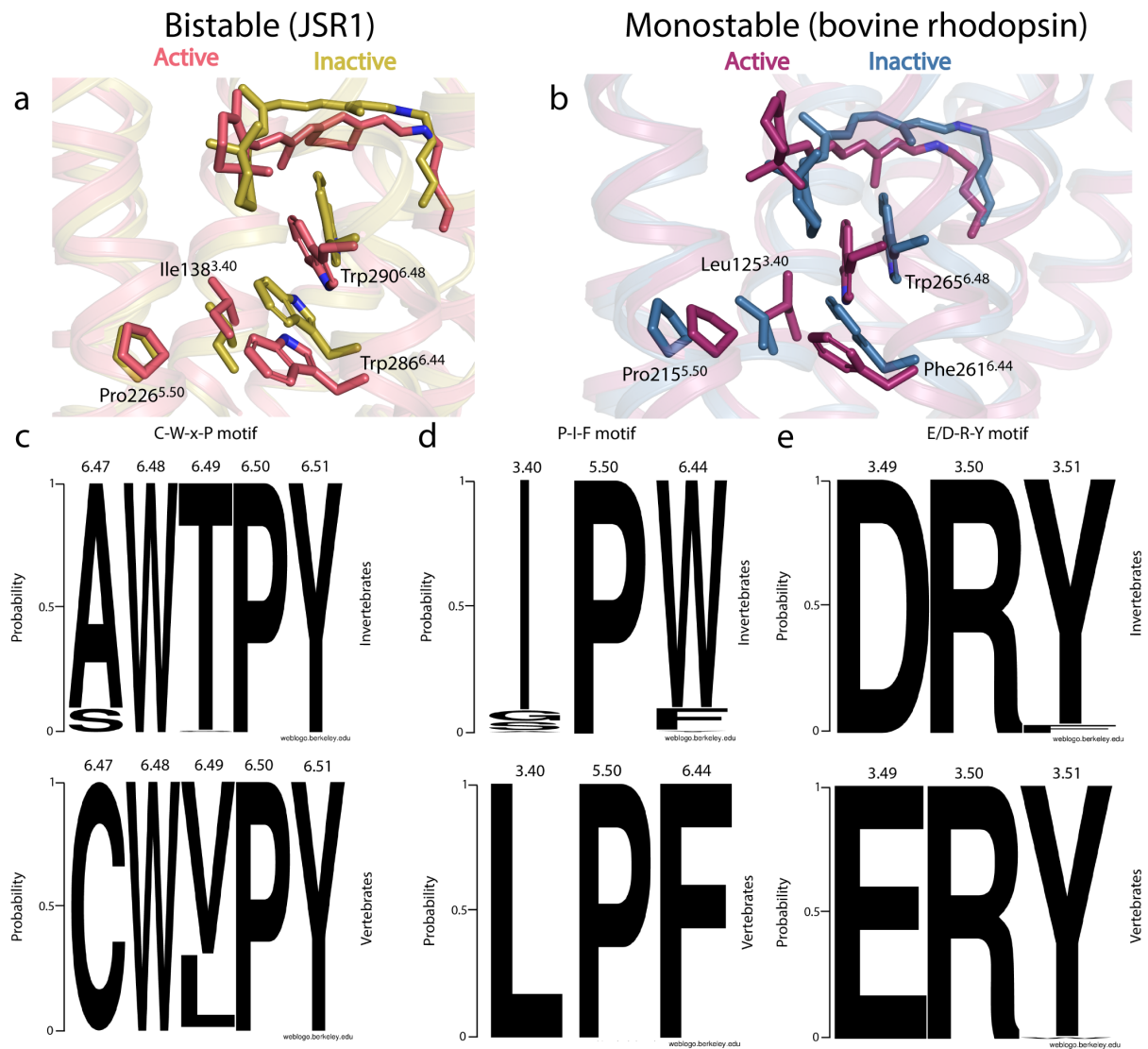
Supplementary Figure 9: All-trans retinal 6.11 with the experimental cryo-EM map and comparison to the all-trans retinal from the JSR1-hGi complex. **a, b:** Visualization of all-trans retinal 6.11 from the JSR1-jsGi_q_1 complex including the experimental cryo-EM map for the Lys321 and all-trans retinal 6.11 shown as a mesh. A shows a side view and B shows a top view from the extracellular side. **c, d:** Overlay of the all-trans retinal 6.11 with the electron density map from the JSR1-jsGi_q_1 complex (black mesh) and the electron density map of all-trans retinal from the JSR1-hGi complex (blue mesh). C shows a side view and D shows a top view from the extracellular side. **e:** Residues in the retinal environment shown with the experimental cryo-EM map overlaid as a mesh. **f:** Counterion (Glu194) and retinal with the Schiff base link with the experimental cryo-EM map overlaid. The red asterisk marks a potential solvent binding site.



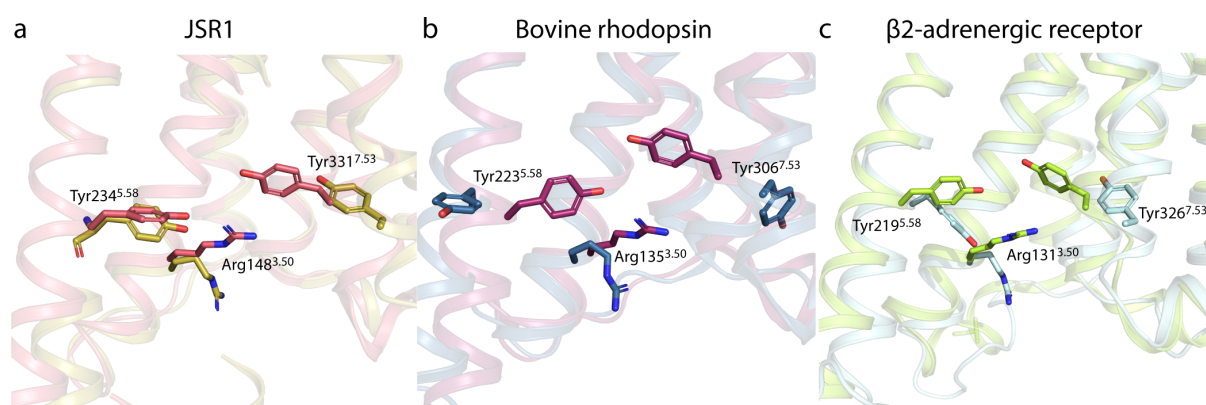
Supplementary Figure 10: Retinal binding site comparison of bovine metarhodopsin-II and active state JSR1. **a:** Retinal environment of bovine metarhodopsin II (PDB 5EN0). Important residues are shown as sticks. Carbon atoms are colored sky blue, nitrogen atoms blue and oxygen atoms red. Water molecules are depicted as red spheres. **b:** All-trans retinal 6.11 environment of the active JSR1. Corresponding residues from A are shown as sticks for JSR1 and carbon atoms are shown in salmon, nitrogen atoms in blue and oxygen atoms in red. **c:** Overlay of the all-trans retinal 6.11 from our JSR1 structure and all-trans retinal from four bovine metarhodopsin II structures (PDB 4A4M (yellow); 3PQR (orange); 5EN0 (green); 6FUF (blue)).



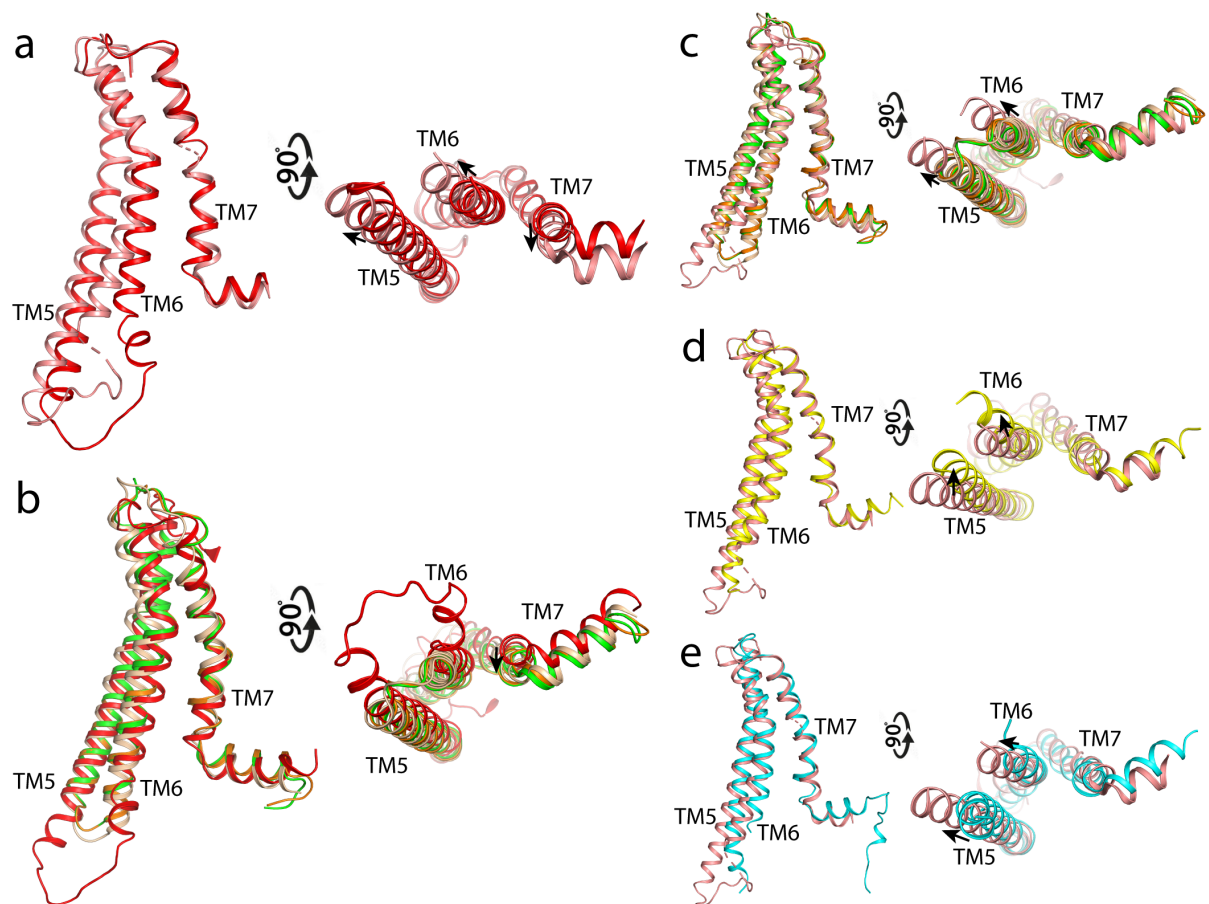
Supplementary Figure 11: Microswitches with experimental cryo-EM map. **a:** Trp290^{6.48} from the C-W-x-P motif shown in stick representation with the experimental map shown as a mesh. **b:** P-I-F motif with side chains shown as sticks and the experimental map shown as a mesh. **c:** D-R-Y motif with side chains shown as sticks and the experimental map shown as a mesh.



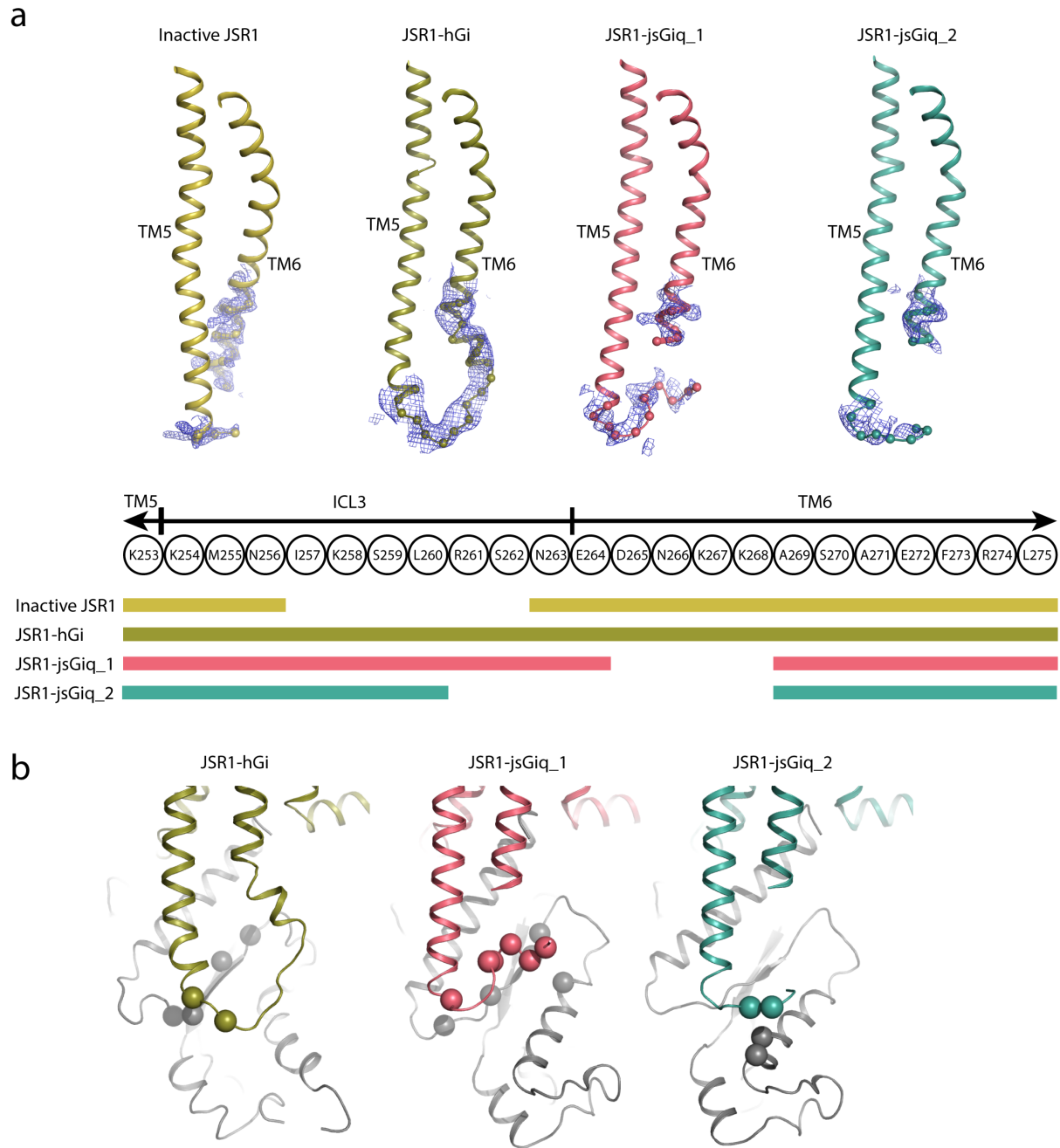
Supplementary Figure 12: Conformational changes upon activation and sequence conservation at the microswitches. **a:** Conformational changes from the retinal isomerization to the P-I-F motif, leading to the outward movement of TM6. Inactive state JSR1 is shown in olive (PDB 6I9K) and active state JSR1 is shown in salmon. **b:** Conformational changes from the retinal isomerization to the P-I-F motif, leading to the outward movement of TM6. Inactive state bovine rhodopsin (PDB 1GZM) is shown in blue and active state bovine metarhodopsin II (PDB 5EN0) is shown in purple. **c:** Sequence conservation of the C-W-x-P motif in invertebrate rhodopsins (top) and vertebrate rhodopsins (bottom). **d:** Sequence conservation of the P-I-F motif in invertebrate rhodopsins (top) and vertebrate rhodopsins (bottom). **e:** Sequence conservation of the E/D-R-Y motif in invertebrate rhodopsins (top) and vertebrate rhodopsins (bottom).



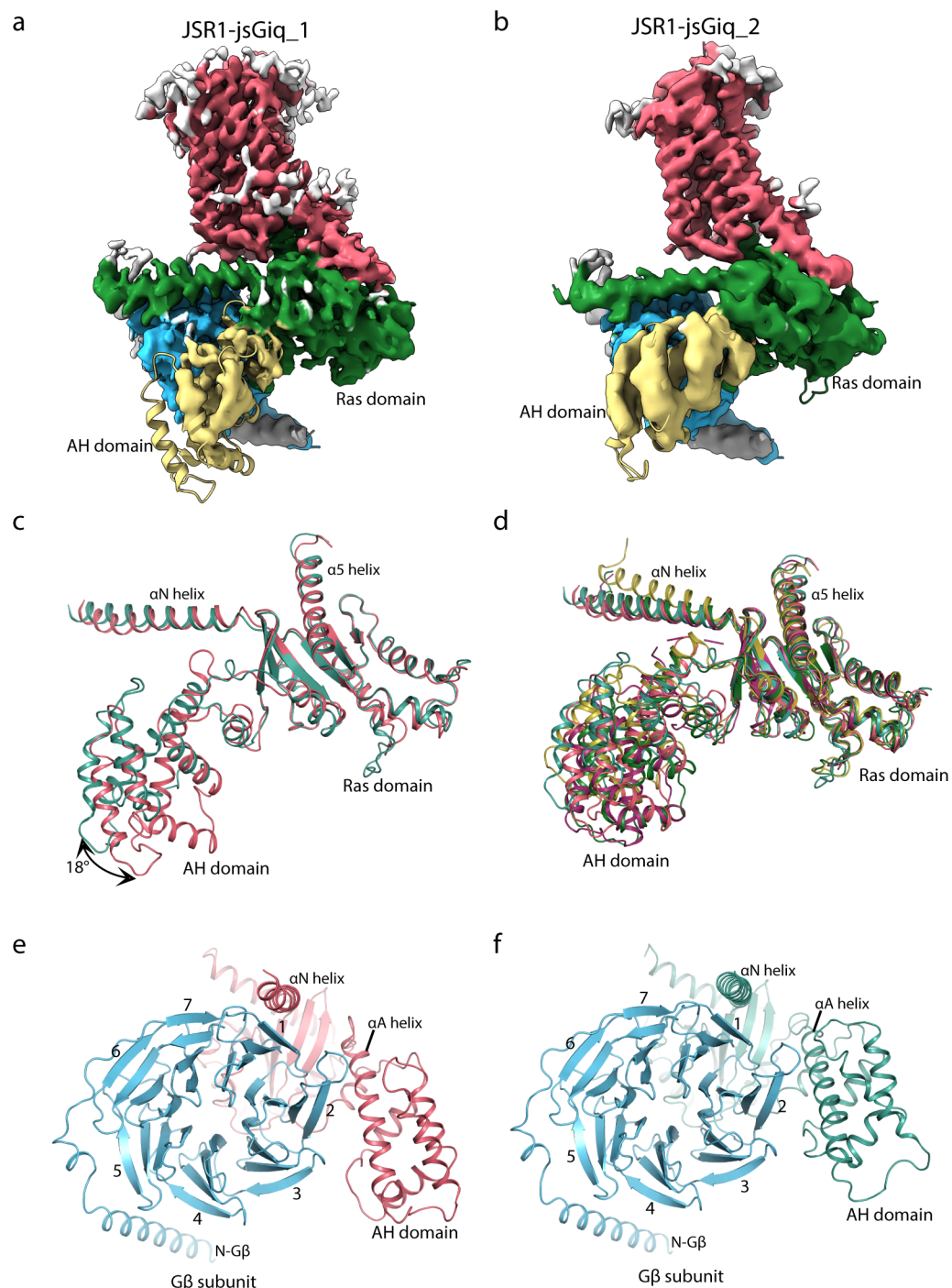
Supplementary Figure 13: Conformational changes of Arg^{3.50}, Tyr^{5.58} and Tyr^{7.53} upon receptor activation. **a:** Inactive JSR1 is shown in yellow and active JSR1 in salmon. Arg148^{3.50}, Tyr234^{5.58} and Tyr331^{7.53} are shown as sticks in the respective color. Oxygen atoms are shown in red and nitrogen atoms in blue. **b:** Inactive bovine rhodopsin is shown in blue and active bovine rhodopsin in purple. Arg135^{3.50}, Tyr223^{5.58} and Tyr306^{7.53} are shown as sticks in the respective color. Oxygen atoms are shown in red and nitrogen atoms in blue. **c:** Inactive β2-adrenergic receptor is shown in pale cyan and active β2-adrenergic receptor is shown in pale green. Arg131^{3.50}, Tyr219^{5.58} and Tyr326^{7.53} are shown as sticks in the respective color. Oxygen atoms are shown in red and nitrogen atoms in blue.



Supplementary Figure 14: TM5/6 and TM7 relocation comparison. **a:** Overlay of TM5/6/7 of the JSR1-jsG_{iq}_1 complex (salmon) and the JSR1-hG_i complex (red). **b:** Overlay of TM5/6/7 of the JSR1-hG_i complex with bovine metarhodopsin II bound to GαCT (PDB 3PQR (orange); PDB 4A4M (green)) and the rhodopsin-hG_i complex (PDB 6CMO (wheat)). **c:** Overlay of TM5/6/7 of the JSR1-jsG_{iq}_1 complex with bovine metarhodopsin II bound to GαCT (PDB 3PQR (orange); PDB 4A4M (green)) and the rhodopsin-hG_i structure (PDB 6CMO (wheat)). **d:** Overlay of TM5/6/7 of the JSR1-jsG_{iq}_1 complex (salmon) with the β₂-adrenergic receptor-G_s complex (PDB 3SN6 (yellow)). **e:** Overlay of TM5/6/7 of the JSR1-jsG_{iq}_1 complex (salmon) with the M1 receptor-G₁₁ complex (PDB 6OIJ (cyan)).

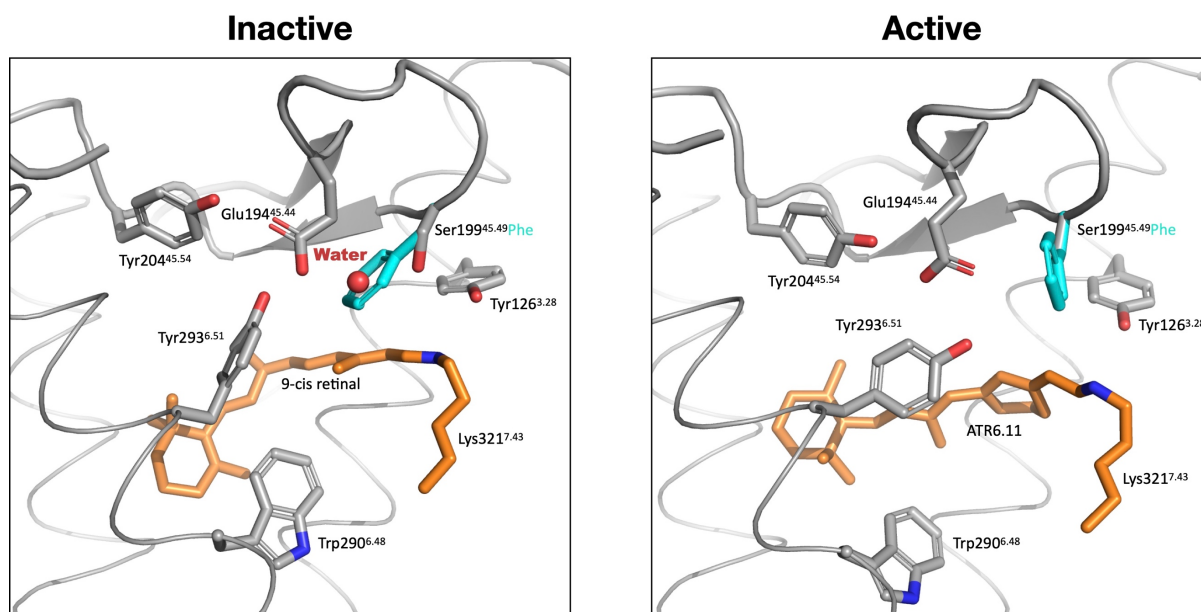


Supplementary Figure 15: Comparison of TM5-ICL3-TM6 in the JSR1 structures. **a:** The top panel shows structures of TM5-ICL3-TM6 of inactive JSR1 (PDB 6I9K), active JSR1 from JSR1-hGi, active JSR1 from JSR1-jsGi_q_1 and active JSR1 from JSR1-jsGi_q_2. The experimental cryo-EM maps are shown for residues 253-275 of JSR1. The bottom panel shows a schematic representation of the residues 253-275. The colored rows show which residues are modeled (solid bar) and missing (no bar) in the respective structures. **b:** Observed contact between JSR1 ICL3 and the $\alpha 4$ - $\beta 6$ region of $G\alpha$. Based on the structural models, carbon α atoms of JSR1 ICL3 residues within 4 Å of the $G\alpha$ $\alpha 4$ - $\beta 6$ region (and vice versa) are shown as spheres. JSR1 is colored in olive (JSR1-hGi), salmon (JSR1-jsGi_q_1) and teal (JSR1-jsGi_q_2), respectively. $G\alpha$ is colored in gray.



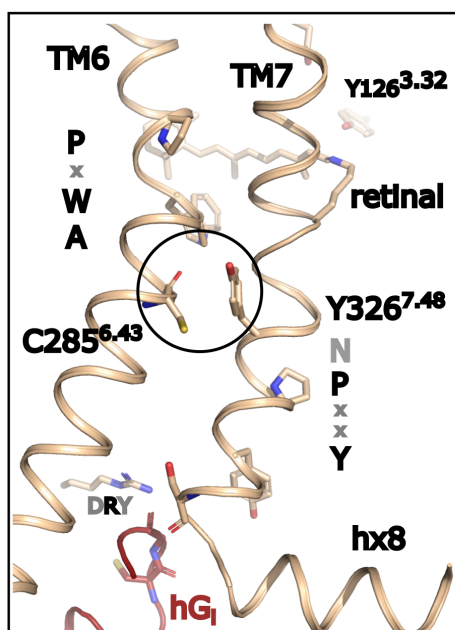
Supplementary Figure 16. **a, b:** Experimental cryo-EM maps of the JSR1-jsG α_{iq} _1 complex (A) and JSR1-jsG α_{iq} _2 (B) overlaid with their models. Specific colors are assigned for JSR1 (salmon), G α Ras domain (green), G α AH domain (yellow), G β (cyan) and G γ (gray). **c:** Structural comparison of the jsG α_{iq} subunit from JSR1-jsG α_{iq} _1 (salmon) and JSR1-jsG α_{iq} _2 (teal). The α -helical domain, α N helix, α 5 helix and the Ras domain are labelled. **d:** Structural comparison of the G α subunit from the JSR1-jsG α_{iq} _1 (salmon), JSR1-jsG α_{iq} _2 (teal), GABA(B) receptor-hG α_i (PDB 7EB2; yellow), NTSR1-hG α_i (PDB 7LOS; purple) and the cannabinoid receptor 2-hG α_i (PDB 6PT0; green) complex structures. The AH domain, α N helix, α 5 helix and the Ras domain are labelled. **e:** Structure of the jsG α_{iq} and G β subunits from JSR1-jsG α_{iq} _1. The G α subunit is colored in salmon and the G β subunit in cyan. The AH domain, α N helix and the α A helix of the jsG α_{iq} are labelled. The numbers of the G β subunit represent the numbering of the β blades according to Wall *et al.*¹ **f:** Structure of the jsG α_{iq} and G β subunits from

JSR1-jsG_{iq}_2. The G α subunit is colored in teal and the G β subunit in cyan. The AH domain, α N helix and the α A helix of the jsG α_{iq} are labelled.

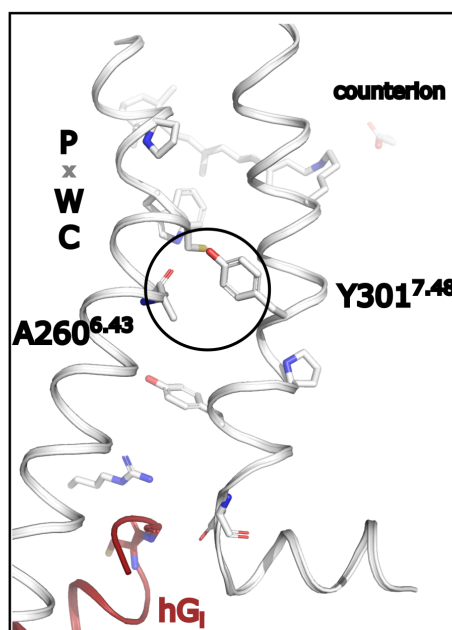


Supplementary Figure 17. Ser199^{45.49} conformation modeled in inactive and active JSR1. In the inactive state, the Schiff base of the Ser199^{45.49}Phe mutant is deprotonated because the bulky aromatic phenylalanine most likely displaces the water molecule that is critical for the hydrogen bond network between the counterion Glu194^{45.44} and the Schiff base. In the active-state JSR1, Ser199^{45.49} changes its rotamer position, if such a change also occurs in Ser199^{45.49}Phe, the phenylalanine side chain would no longer interfere with the hydrogen bond network between Glu194^{45.44} and the Schiff base. The proposed Ser199^{45.49}Phe side chain is shown in cyan. Inactive state JSR1 is represented by PDB 6I9K. The active state JSR1 is adapted from JSR1-jsG_{iq}_1.

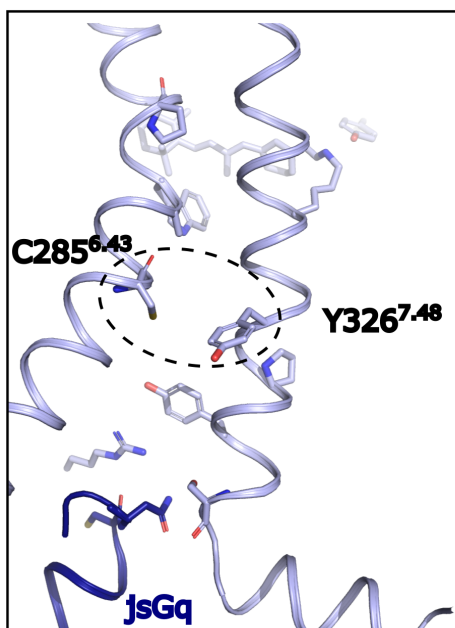
JSR1-hG_i



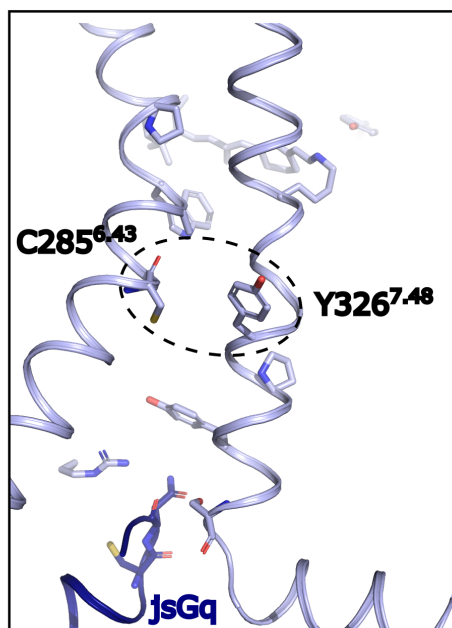
bRHO-hG_i



JSR1-jsG_{iq}_1



JSR1-jsG_{iq}_2



Supplementary Figure 18. Detail of TM6/TM7/H8 in the JSR1-hG_i complex (top left), the two conformations of the JSR1-jsG_{iq} complex (bottom), and the bovine rhodopsin-hG_i complex (top right, PDB 6QNO). Top panels: The packing at the 6.43/7.48 residues (circled) is located right between the A/C-W-x-P motif in TM6 and the N-P-x-x-Y motif in TM7, and is similar in JSR1 and rhodopsin bound to hG_i. In bovine rhodopsin, the packing is stronger, including an inter-helical hydrogen bond. Bottom panels: This packing is looser in jsG_{iq}-bound JSR1.

	JSR1-jsG _{iq} _1 (EMDB-19882) (PDB 9EPP)	JSR1-jsG _{iq} _2 (EMDB-19883) (PDB 9EPQ)	JSR1-hG _i (EMDB-19884) (PDB 9EPR)
Data collection and processing			
Magnification	165'000	165'000	105'000
Voltage (kV)	300	300	300
Electron exposure (e-/Å ²)	70	70	50
Defocus range (µm)	-1.0 to -2.4	-1.0 to -2.4	-0.7 to -2.4
Pixel size (Å)	0.51	0.51	0.85
Symmetry imposed	C1	C1	C1
Initial particle images (no.)	2'964'739	2'964'739	8'400'000
Final particle images (no.)	159'665	134'167	400'000
Map resolution (Å)	4.06	4.17	4.9
FSC threshold	0.143	0.143	0.143
Map resolution range (Å)	n.a.	n.a.	4.6 – 9.0
Refinement			
Initial model used (PDB code)	9EPP	9EPQ	9EPR
Model resolution (Å)	4.3	4.4	6.2
FSC threshold	0.5	0.5	0.5
Model resolution range (Å)	n.a.	n.a.	n.a.
Map sharpening <i>B</i> factor (Å ²)	-162	-206	-229
Model composition			
Non-hydrogen atoms	7482	7489	7046
Protein residues	946	948	890
Ligands	ATR611	ATR611	ATR
<i>B</i> factors (Å ²)			
Protein	76.12	83.33	169.94
Ligand	59.22	41.42	n.a.
R.m.s. deviations			
Bond lengths (Å)	0.004	0.004	0.006
Bond angles (°)	0.718	0.756	1.172
Validation			
MolProbity score	2.10	2.27	2.99
Clashscore	14.16	19.96	12.84
Poor rotamers (%)	1.47	1.72	14.43
Ramachandran plot			
Favored (%)	95.49	95.73	91.87
Allowed (%)	4.40	4.17	7.67
Disallowed (%)	0.11	0.11	0.46

Supplementary Table 1: Cryo-EM data collection, refinement and validation statistics

Residue	R148 (3.50)	V151 (3.53)	I152 (3.54)	M156 (34.51)	A157 (34.52)	P160 (34.55)	I237 (5.61)	H244 (5.68)	L248 (5.72)	Q251 (5.75)	K254 (5.78)	M255 (5.79)	L260 (ICL3)	R261 (ICL3)	S262 (ICL3)	N263 (ICL3)	R274 (6.32)	L275 (6.33)	V278 (6.36)	S334 (7.56)	H335 (8.47)	P336 (8.48)	K337 (8.49)
R31 (G.hns1.02)				Orange	Green																		
E308 (G.H4.16)															Green								
E318 (G.h4s6.12)														Orange		Green							
I319 (G.h4s6.13)															Green								
H322 (G.S6.04)												Green											
C325 (G.s6h5.02)												Green											
Q333 (G.H5.5)										Orange	Green												
F334 (G.H5.6)													Green										
C337 (G.H5.9)										Green													
K340 (G.H5.12)								Green															
D341 (G.H5.13)								Green						Orange									
N347 (G.H5.19)			Green																				
L348 (G.H5.20)			Green																				
K349 (G.H5.21)																						Green	
E350 (G.H5.22)																							Orange
C351 (G.H5.23)	Orange	Green																					
N352 (G.H5.24)	Green																			Orange	Orange	Green	
L353 (G.H5.25)	Green						Green											Green	Green				
V354 (G.H5.26)																	Orange		Green				

Supplementary Table 2: JSR1-jsG_{Iq}_1 interaction table. Top row shows the JSR1 residue number and GPCR numbering. Left column shows the jsG_{Iq} residue number and G protein numbering. Orange fields symbolize polar interactions and green fields residues within 4 Å distance.

Residue	R148 (3.50)	V151 (3.53)	I152 (3.54)	M156 (34.51)	A157 (34.52)	P160 (34.55)	H244 (5.68)	L248 (5.72)	Q251 (5.75)	K254 (5.78)	M255 (5.79)	I257 (ICL3)	K258 (ICL3)	L260 (ICL3)	R274 (6.32)	V278 (6.36)	Y331 (7.53)	S334 (7.56)	H335 (8.47)	P336 (8.48)	K337 (8.49)
R31 (G.hns1.0 2)																					
I194 (G.S3.01)																					
E298 (G.H4.05)																					
A301 (G.H4.08)																					
C337 (G.H5.9)																					
K340 (G.H5.12)																					
D341 (G.H5.13)																					
I343 (G.H5.15)																					
K349 (G.H5.21)																					
E350 (G.H5.22)																					
N352 (G.H5.24)																					
L353 (G.H5.25)																					
V354 (G.H5.26)																					

Supplementary Table 3: JSR1-jsG_{iq}_2 interaction table. Top row shows the JSR1 residue number and GPCR numbering. Left column shows the jsG_{iq} residue number and G protein numbering. Orange fields symbolize polar interactions and green fields residues within 4 Å distance.

Protein	Sequence	Sources
JSR1	MLPHAAKMAARVAGDHDGRNISIVDLLPEDMLPMIHEHWYKFPPME TSMHYILGLMIIVIGIISVSGNGVVMYLMMTVKNLRTPGNFLVLNL ALSDFGMLFFMMPTMSINCFAETWVIGPFMCELYGMIGSLFGSASI WSLVMITLDRYNVIVKGMAGKPLTKVGALLRMLFVWIWSLGTIAP MYGWSRYVPEGSMTSCTIDYIDTAINPMSYLIAYAIFVYFVPLFII IYCYAFIVMQVAAHEKSLREQAKKMKIKSLRSNEDNKKASAEFRLA KVAFMTICCWFMATPYLTLSFLGIFSDRTWLTPTSVWGAIFAKA SACYNPIVYGISHPKYRAALHDKFPCLKCGSDSPKGDASTVAESE KAGEETSQVAPA	Expression in GnTI- deficient HEK293
Human Gα11	MKKHHHHHHHHHENLYFQGGSMGCTLSAEDKAAVERSKMIDRNLR EDGEKAAREVKLLLLLGAGESGKSTIVKQMKIIHEAGYSEEECKQYK AVVYSNTIQSIIAIIIRAMGRLKIDFGDSARADDARQLFVLGAAEE GFMTAELAGVIKRLWKDSGVQACFNRSREYQLNDSAAYYLNDLDRI AQPNYIPTQQDVLRTVKTGTGIVETHFTFKDLHFKMFDVGGQRSER KKWIHCFEGVTAIIFCVALS DYDLVLAEDEEMNRMHESMKLFDSIC NNKWFDTDSIILFLNKKDLFEEKIKKSPLTICYPEYAGSNTYEEAA AYIQCFEDLNKRKDTKEIYTHFTCATDTKNVQFVFDVTDVVIKN NLKDCGLF	Expression in E. coli
jsGαiq	MGCTLSAEDKAAVERSKMIDRNLRDGEKARREVKLLLLLGAGESGK STIVKQMKIIHEAGYSEEECKQYKAVVYSNTIQSIIAIIIRAMGRLK IDFGDSARADDARQLFVLGAAEEGFMTAELAGVIKRLWKDSGVQA CFNRSREYQLNDSAAYYLNDLDRIAQPNYIPTQQDVLRTVKTGTG VETHFTFKSIHFKMFDVGGQRSERKKWIHCFEGVTAIIFCVALS DY DLVLAEDEEMNRMHESMKLFDSICNNKWFDTDSIILFLNKKDLFEE KIKKSPLTICYPEYAGSNTYEEAAAYIQCFEDLNKRKDTKEIYTH FTCATDTKNVQFVFCVAKDTILQNNLKECNLV	Expression in Hi5
Bovine Gβ1	MSELDQLRQAEQLKNQIRDARKACADATLSQITNNIDPVGRIQMR TRRTLGRHLAKIYAMHWGTD S RLLVSASQDGKLI I WDSYTTNKVHA IPLRSSWVMTCAYAPSGNYVACGGLDNICSIYNLKTREGNVRVSRE LAGHTGYLSCCRFLDDNQIVTSSGDTTCALWDIETGQQTTFGTGHT GDVMSLSLAPDTRLFVSGACDASAKLWDVREGMCRQTFGTGHESDIN AICFFPNGNFATGSDDATCRLFDLRADQELMTYSHDNIICGITSV SFSKSGRLLLAGYDDFNCNVWDALKADRAGVLAGHDNRVSLGVTD DGMVATGSWDSFLKIWN	Extraction from Bovine retina
Human Gβ1	MHHHHHHHHHLEVL FQGPSSSGSELDQLRQAEQLKNQIRDARKA CADATLSQITNNIDPVGRIQMRTRRTLGRHLAKIYAMHWGTD S RLL VSASQDGKLI I WDSYTTNKVHA I PLRSSWVMTCAYAPSGNYVACGG LDNICSIYNLKTREGNVRVSREL AGHTGYLSCCRFLDDNQIVTSSG DTTCALWDIETGQQTTFGTGHTGDVMSLSLAPDTRLFVSGACDASA KLWDVREGMCRQTFGTGHESDINAICFFPNGNFATGSDDATCRLFD LRADQELMTYSHDNIICGITSVSFSKSGRLLLAGYDDFNCNVWDAL KADRAGVLAGHDNRVSLGVTD DGMVATGSWDSFLKIWN	Expression in Hi5
Bovine Gγ1	MPVINIEDLTEKDKLKMEVDQLKKEVTLERMLVSKCEEFRDYVEE RSGEDPLVKGIPEDKNPFKELKGGCVIS	Extraction from Bovine retina
Human Gγ2	MASNNTASIAQARKLVEQLKMEANIDRIKVSAAADLMAYCEAHAK EDPLLTPVPA SENPFREKFFCAIL	Expression in Hi5

Supplementary Table 4: Sequences and production sources of JSR1 and G protein subunits.

- 1 Wall, M. A. *et al.* The structure of the G protein heterotrimer Gi alpha 1 beta 1 gamma 2. *Cell* **83**, 1047-1058 (1995).