
Figures and figure supplements

Single amino acid residue mediates reciprocal specificity in two mosquito odorant receptors

Flavia P Franco *et al.*

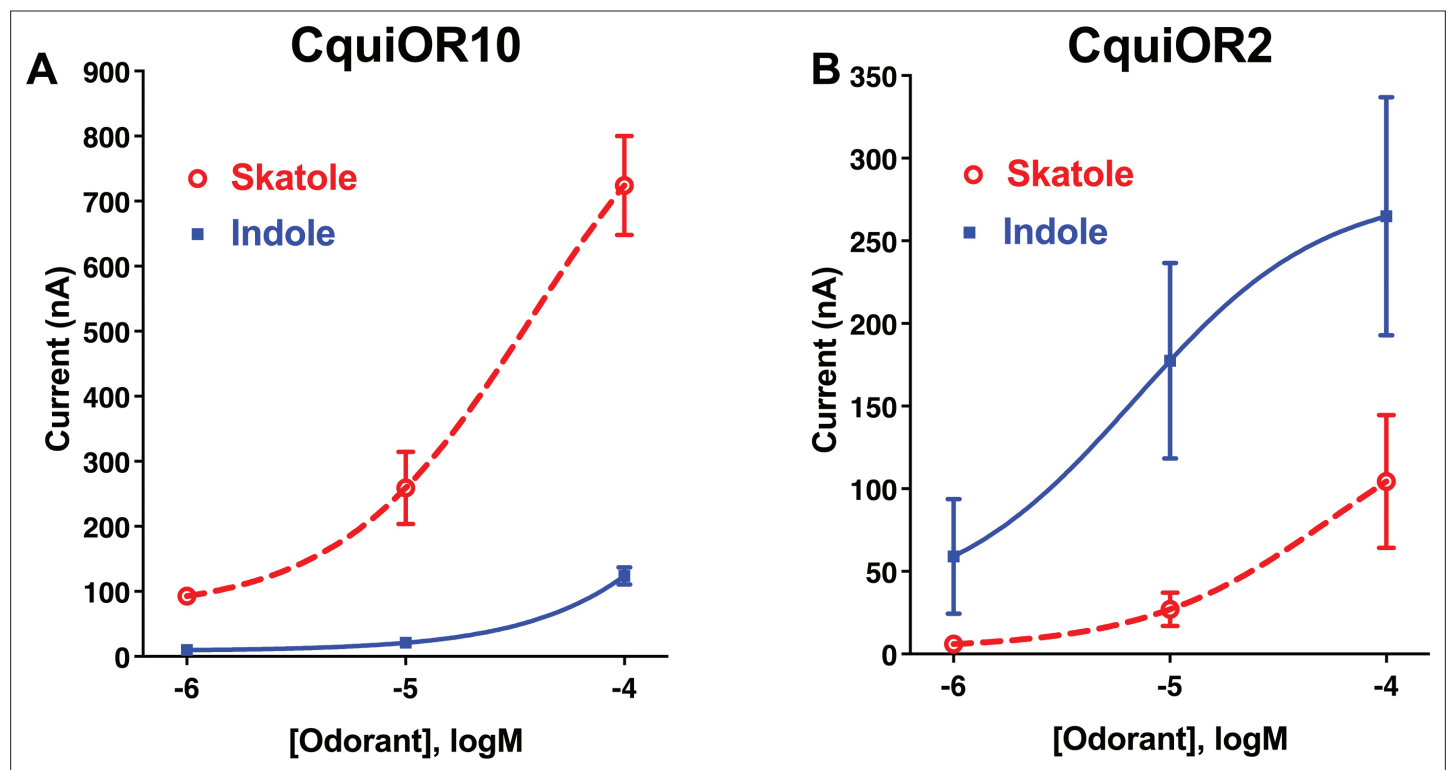


Figure 1. Concentration–response analysis for activation of wildtype odorant receptors (ORs) by skatole and indole. (A) CquiOR10 and (B) CquiOR2. Lines were obtained with nonlinear fit. Bars represent SEM. $n = 4$ –5.

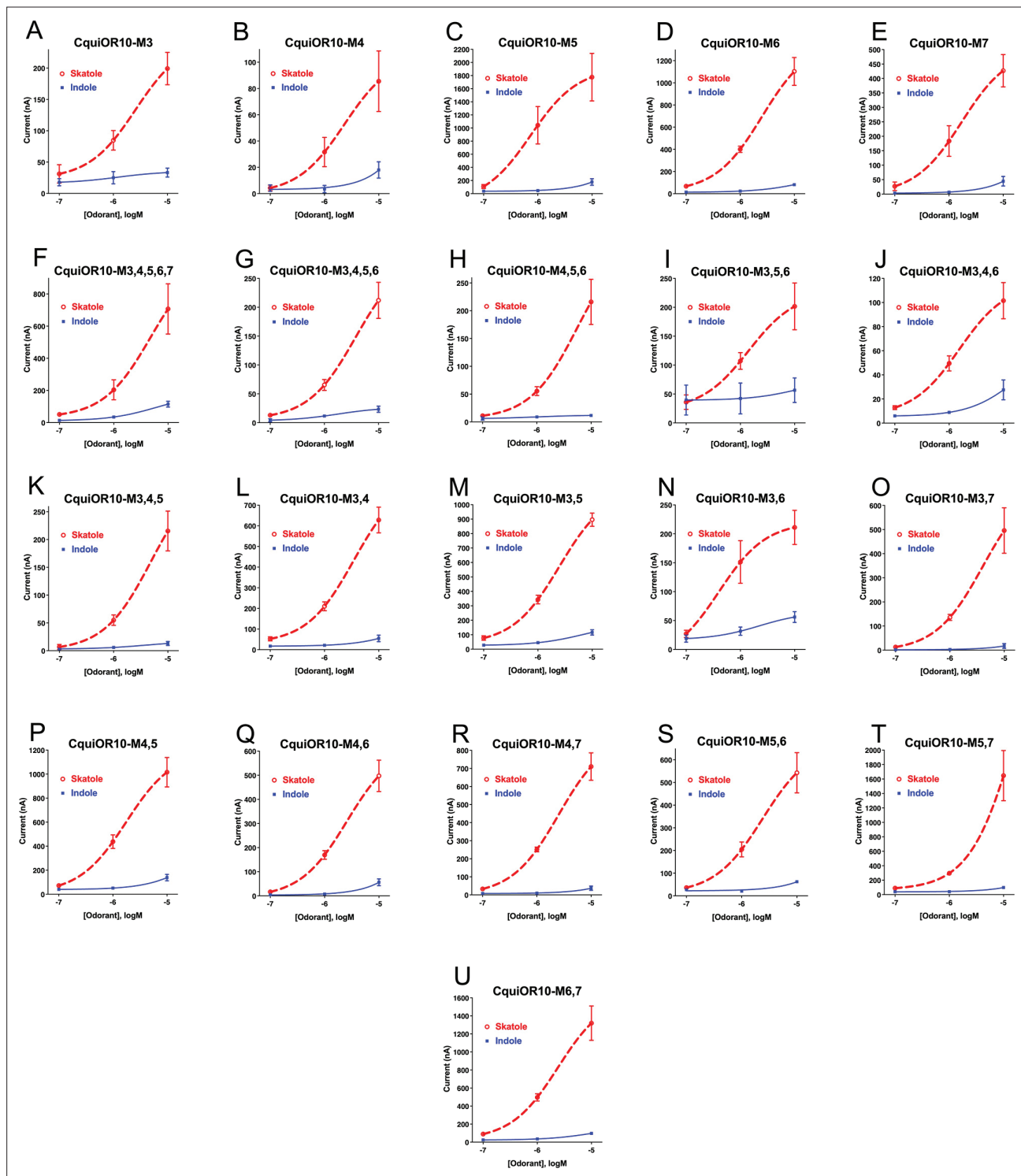


Figure 1—figure supplement 1. Concentration–response analysis for wildtype and chimeric odorant receptors (ORs). (A) CquiOR10^{M3}; (B) CquiOR10^{M4}; (C) CquiOR10^{M5}; (D) CquiOR10^{M6}; (E) CquiOR10^{M7}; (F) CquiOR10^{M3,4,5,6,7}; (G) CquiOR10^{M3,4,5,6}; (H) CquiOR10^{M4,5,6}; (I) CquiOR10^{M3,5,6}; (J) CquiOR10^{M3,4,6}; (K) CquiOR10^{M3,4,5}; (L) CquiOR10^{M3,4}; (M) CquiOR10^{M3,5}; (N) CquiOR10^{M3,6}; (O) CquiOR10^{M3,7}; (P) CquiOR10^{M4,5}; (Q) CquiOR10^{M4,6}; (R) CquiOR10^{M4,7}; (S) CquiOR10^{M5,6}; (T) CquiOR10^{M5,7}; and (U) CquiOR10^{M6,7}. Lines were obtained with nonlinear fit. Bars represent SEM. *n* = 3.

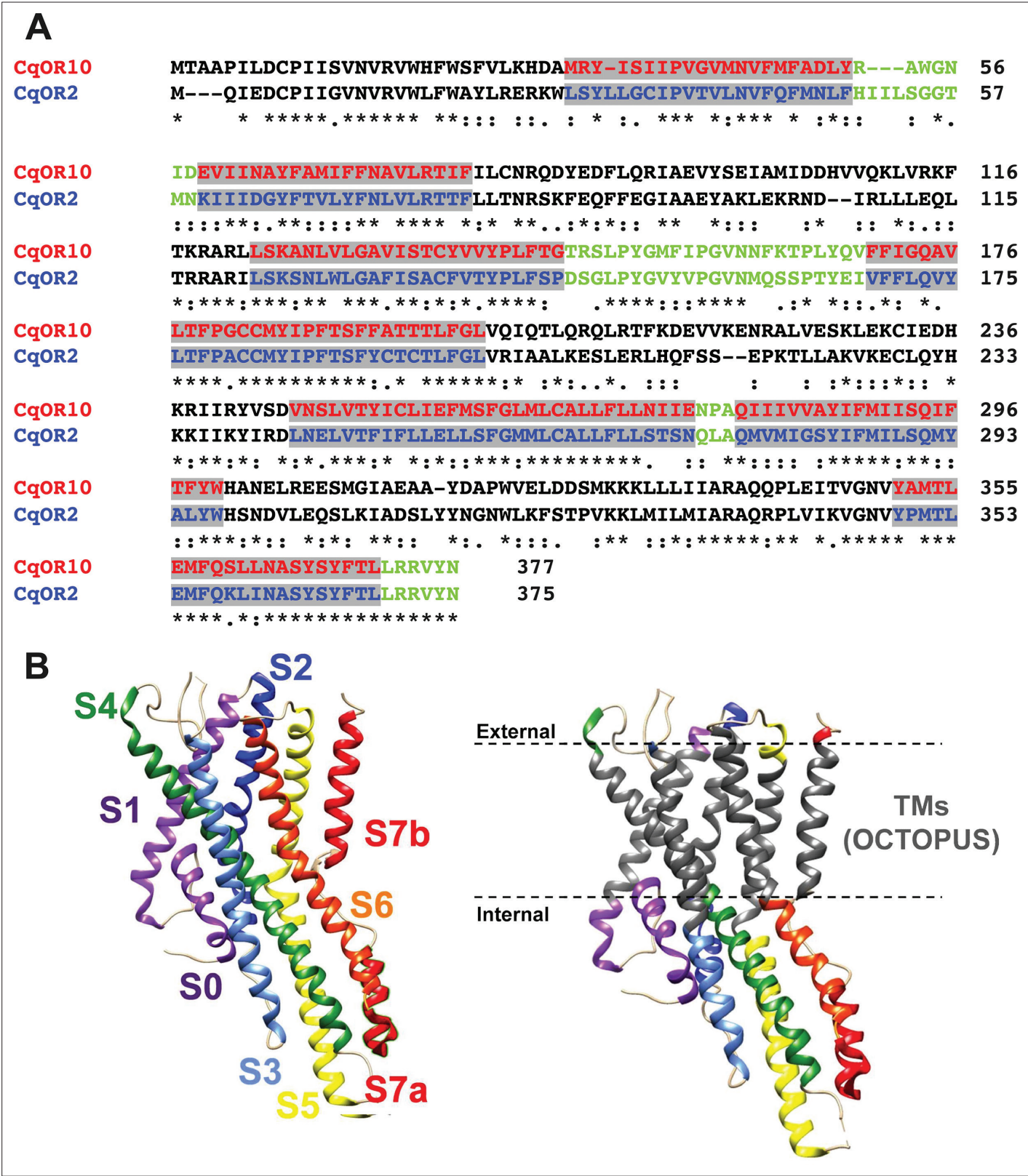


Figure 2. Alignment of the amino acid sequences of CquiOR10 and CquiOR2 highlighting the predicted transmembrane (TM) domains and a comparison of predicted and experimentally determined TM domains of the odorant receptor coreceptor, AbakOrco. (A) CqOR10 and CqOR2 are abbreviations for CquiOR10 and CquiOR2, respectively. The TM domains, predicted by OCTOPUS, are displayed in red and blue for CquiOR10 and CquiOR2, respectively. The sequences of the N-terminus and the intracellular loops are displayed in black, and the C-terminus and extracellular loops

Figure 2 continued on next page

Figure 2 continued

in green. **(B)** Left: the cryo-EM structure of AbakOrco (PDB, 6C70) displayed in rainbow color using UCSF Chimera (**Pettersen et al., 2004**). Right: the predicted TM domains (right) are displayed in gray. The dashed lines represent the membrane boundaries.

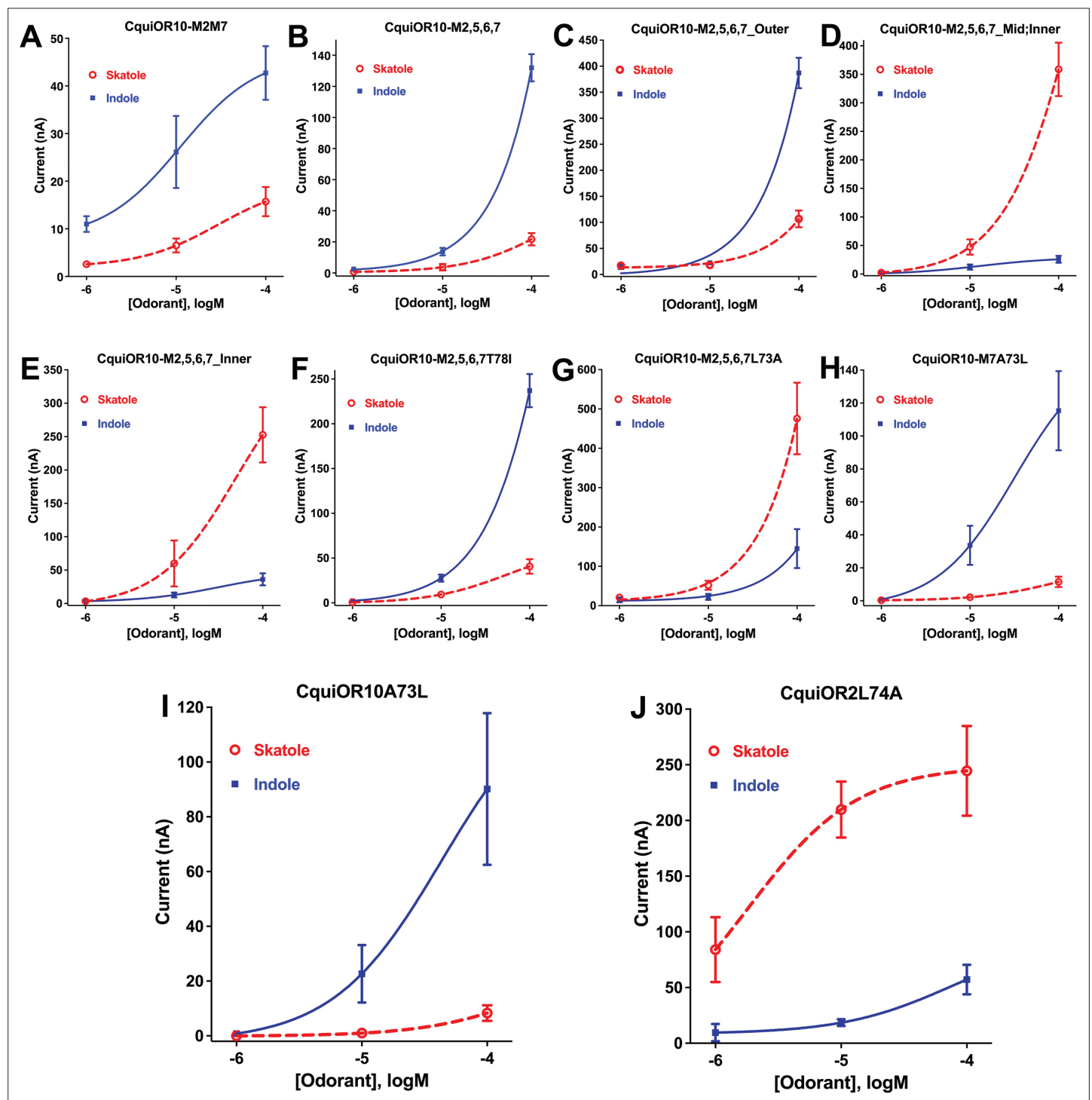


Figure 3. Concentration–response curves obtained with chimeric odorant receptors (ORs) stimulated with skatole and indole. (A) CuiOR10^{M2,7}; (B) CuiOR10^{M2,5,6,7}; (C) CuiOR10^{M2,5,6,7}_Outer; (D) CuiOR10^{M2,5,6,7}_Mid;Inner; (E) CuiOR10^{M2,5,6,7}_Inner; (F) CuiOR10^{M2,5,6,7}T78I; (G) CuiOR10^{M2,5,6,7}L73A; (H) CuiOR10^{M7}A73L; (I) CuiOR10A73L; (J) CuiOR2L74A. Lines were obtained with nonlinear fit. Bars represent SEM. The number of replicates (n) were 7, 4, 5, 5, 4, 3, 9, 7, 6, and 5, respectively.

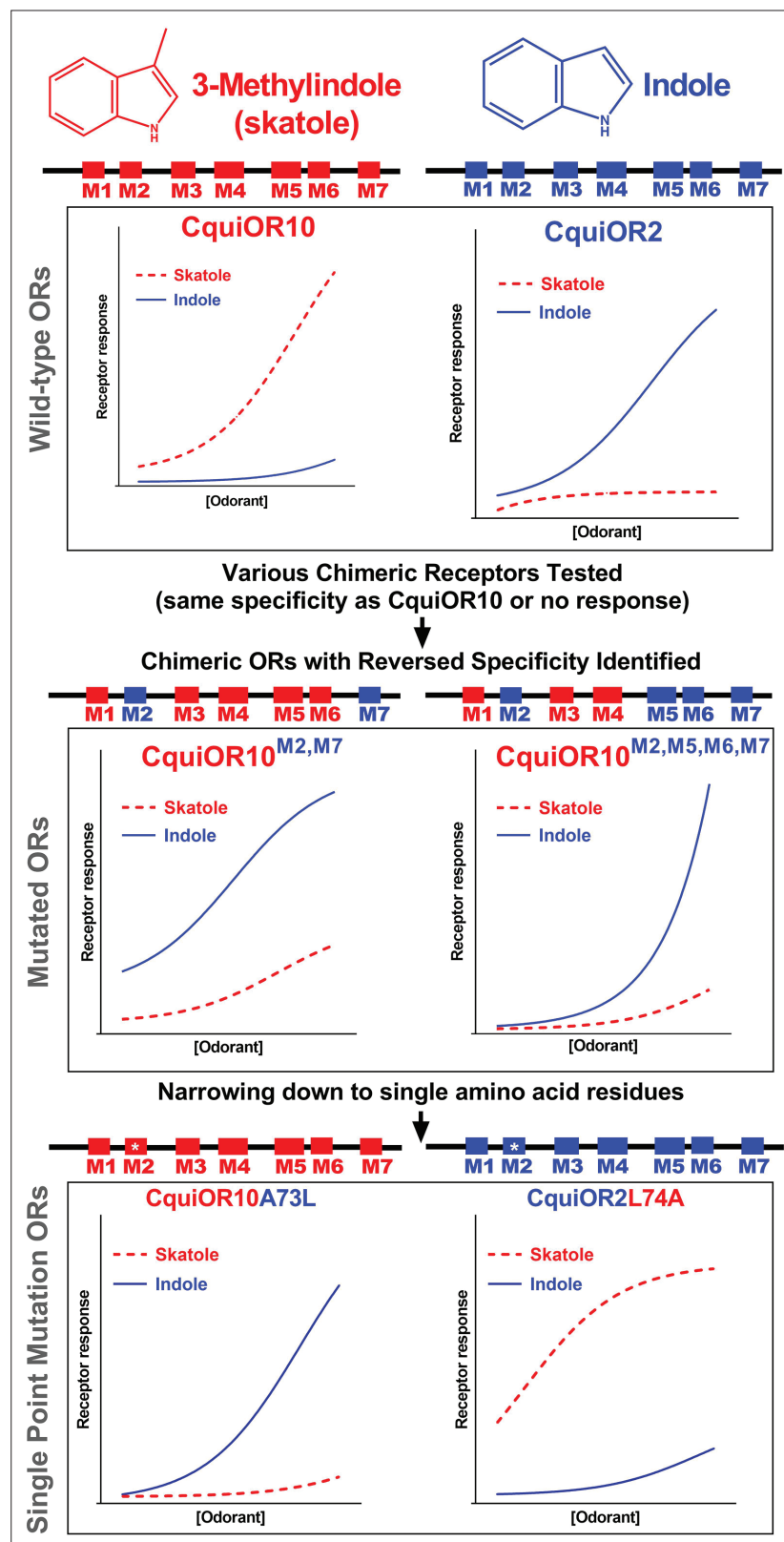


Figure 3—figure supplement 1. Schematic view of the workflow.

	57	73	116	Selective to
CquiOR10	↓	↓	↓	
	ID	EVIIINAYFAMIFFNAVLRTIF	FILCNRQDYEDFLQRIAEVYSEIAMIDDHVVQKLVRKF	Skatole
CquiOR10M ^{2,5,6,7}				
	ID	KIIIDGYFTVLYFNLVLR	TTFILCNRQDYEDFLQRIAEVYSEIAMIDDHVVQKLVRKF	Indole
		Outer Mid Inner		
CquiOR10M ^{2,5,6,7} _Outer	ID	EVIIINAYFTVLYFNLVLR	TTFILCNRQDYEDFLQRIAEVYSEIAMIDDHVVQKLVRKF	Indole
CquiOR10M ^{2,5,6,7} _Mid+Inner	ID	KIIIDGYFAMIFFNAVLRTIF	FILCNRQDYEDFLQRIAEVYSEIAMIDDHVVQKLVRKF	Skatole
CquiOR10M ^{2,5,6,7} _Inner	ID	KIIIDGYFTVLYFNAVLRTIF	FILCNRQDYEDFLQRIAEVYSEIAMIDDHVVQKLVRKF	Skatole
CquiOR10M ^{2,5,6,7} _T78I	ID	KIIIDGYFTVLYFNLVLR	TTFILCNRQDYEDFLQRIAEVYSEIAMIDDHVVQKLVRKF	Indole
CquiOR10M ^{2,5,6,7} _L73A	ID	KIIIDGYFTVLYFNAVLRTIF	FILCNRQDYEDFLQRIAEVYSEIAMIDDHVVQKLVRKF	Skatole

Figure 4. Partial sequences of CquiOR10 and chimeric odorant receptors (ORs) highlighting transmembrane domain-2 (TM2). The two last residues of the extracellular loop-1 (Ile-57 and Asp-58) appear in the N-terminus. The TM2 was divided into the arbitrary segments outer, middle (mid), and inner to identify specificity determinants.

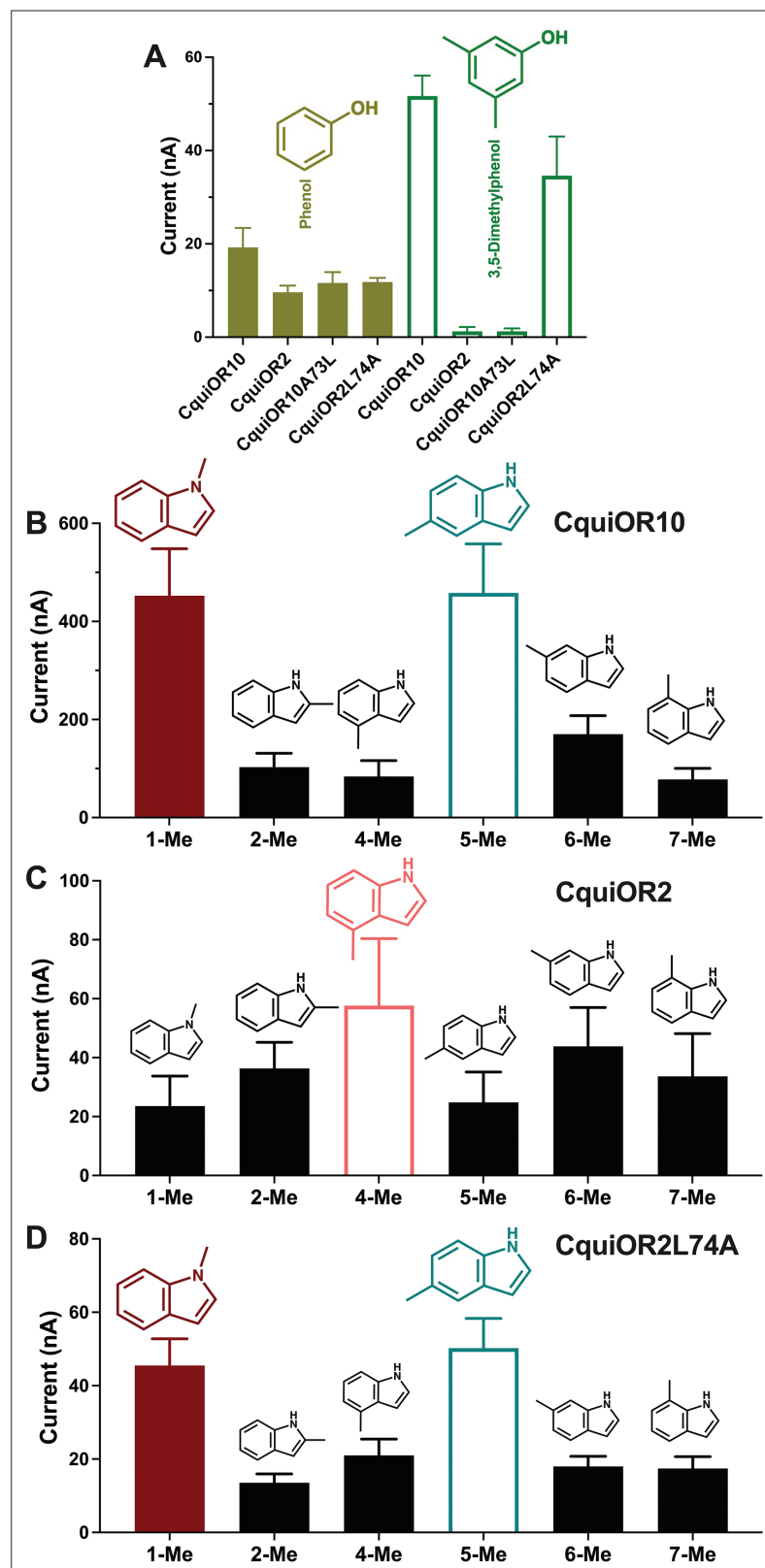


Figure 5. Quantification of wildtype and chimeric receptors to phenol and 2,3-dimethylphenol, and methylindoles. (A) Each receptor was co-expressed with CquiOrco in *Xenopus* oocytes and stimulated with the phenolic compounds at 1 mM. $n = 3-5$. (B) CquiOR10/CquiOrco-, (C) CquiOR2/CquiOrco-, and (D) CquiOR2L74A-expressing oocytes were stimulated with 100 μ M of the specified methylindoles. $n = 9-11$. Bars represent SEM.

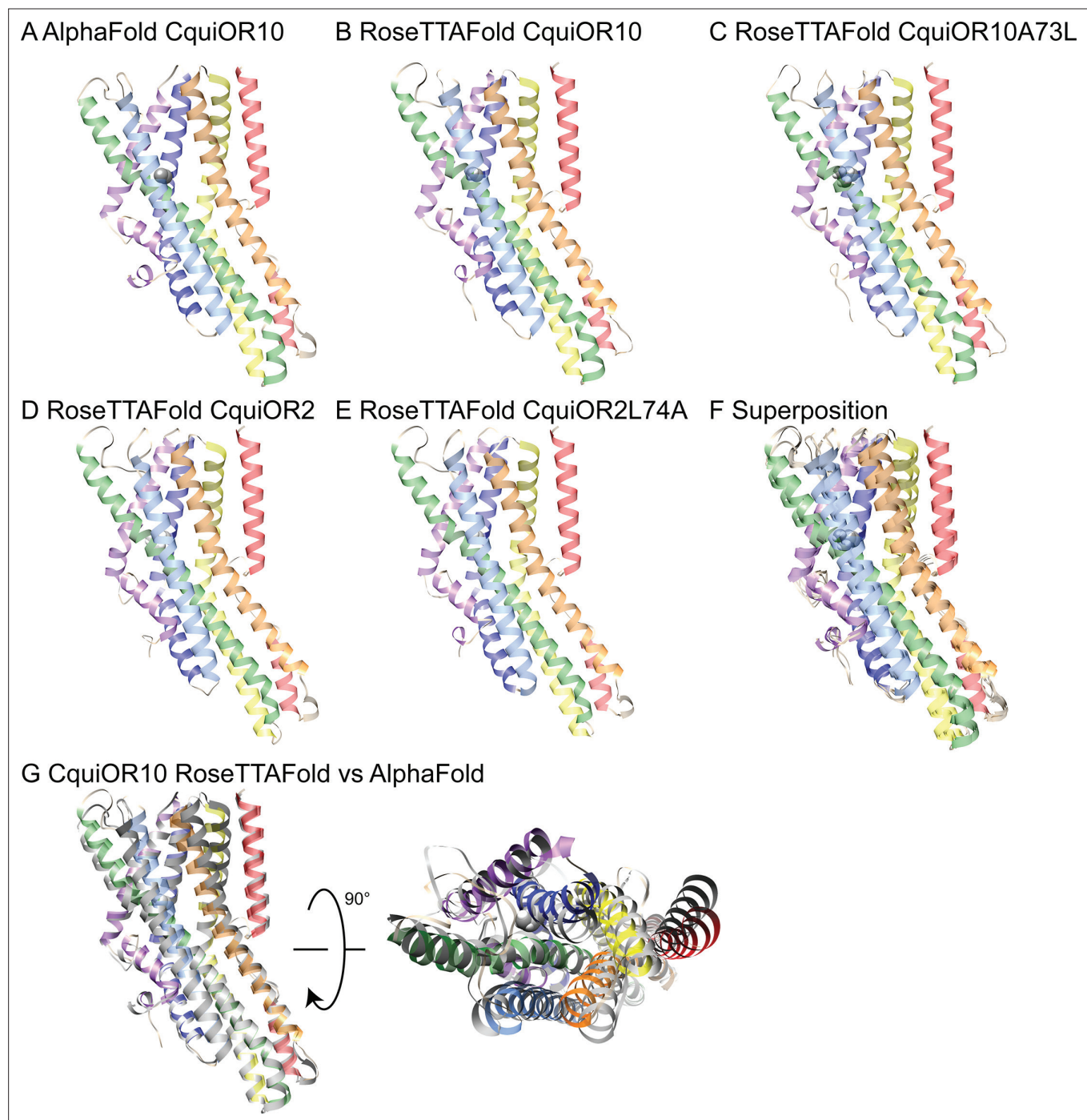
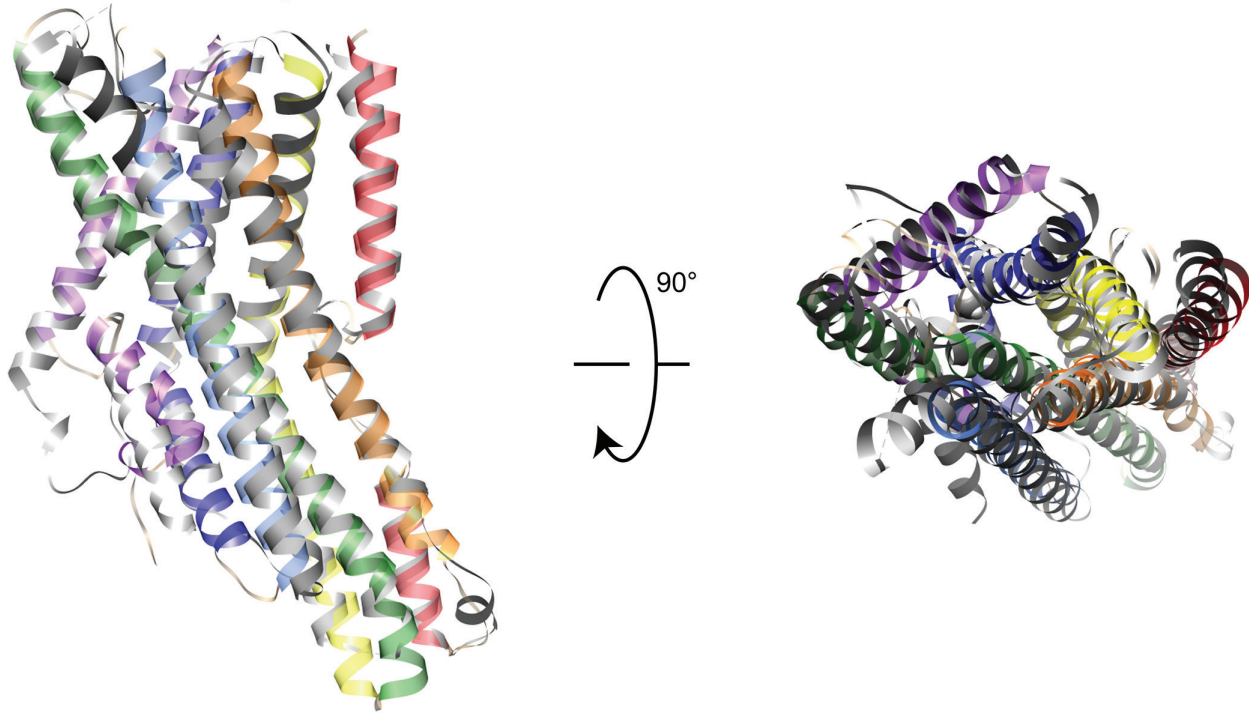


Figure 6. AlphaFold and RoseTTAFold models. Structural models of CquiOR10 (**A**, **B**), CquiOR10A73L (**C**), CquiOR2 (**D**), and CquiOR2L74A (**E**) with AlphaFold (**A**) and RoseTTAFold (**B–E**) structure prediction methods. Superposition of all RoseTTAFold models (**F**) resulted in transmembrane helix root mean square deviation (RMSD) of 0.8 Å when aligned with RoseTTAFold CquiOR10. (**G**) The transmembrane helix RMSD of CquiOR10 RoseTTAFold (rainbow) vs. AlphaFold (gray) was 1.7 Å. Loops were not included in RMSD calculation due to inherent flexibility during structure prediction.

CquiOR10	1	-----	0
MhraOR5	1	GPGRAKIDVDSVDHTDDYIHLRKWIKRIGIILRISGHWPFRLPHEKRNQH	50
CquiOR10	1	-----	0
MhraOR5	51	KSKFRQVYSCLVITLGFITCSCYICIGLCLSEISIAQALNNITVTSYFLQSC	100
CquiOR10	1	-----MTAAPILDCPIISVN	15
MhraOR5	101	VCYVSFIINSRKLETLENYLFENEVVGCPRGYKMSSIKTTFLRCKFVAFS	150
CquiOR10	16	VRVWHFWSFVLKHDAMRYISIIIPVGMNVFMFAD-----LYRAWGN	56
MhraOR5	151	LGILSFFGWLM-----WTLPLAVLVVDGATGGGNQTSRFEAWYP	193
CquiOR10	57	ID-----EVI-INAYFAMIFFNAV-----LRTIFIL----CNRQ	85
MhraOR5	194	FDTTTSPMNEVIAIYEAVAMIFLITAPMSSDIMFCVLMIFIVEHLKCLGM	243
CquiOR10	86	DYEDFLQRIAEVYSEIAMIDDHVQKLVRKFTKRARLLSKANLVLGAVIS	135
MhraOR5	244	AIECTLKGISTNQHQNIGFDDSVSDVNVQR-----RIVIGK---	279
CquiOR10	136	TCYVVYPLFTGTRSLPYGMFIPGVNFKTPLYQVFFIGQAVLTFPGCCMY	185
MhraOR5	280	-----ESPIQSI-----H	287
CquiOR10	186	IPFTSFFATTTLFGLVQIQTLQRLRTFKDEVVKENR-----ALVES---	227
MhraOR5	288	VP-----IKECSRQ---SSDAVFREKRHGTHHQIIRSHNY	319
CquiOR10	228	----KLEKCIEDHKRIIRYVSDVNSLVTYICLIEFMSFGLMLCALLFLLN	273
MhraOR5	320	TDATSLCNIVDSHVKIYRTMEIVQSVYSSYFATLFFTSCLAVCALAYFLA	369
CquiOR10	274	IIENP-AQIIIVVAYIFMIISQIFTFYWHANELREESMGIAEAAAYDAPWV	322
MhraOR5	370	ATSTSFTRVPGMVLYLMYIFLRIFLLCLLATEVAEQGLNLCHAGYSSKLV	419
CquiOR10	323	ELDDSMKKKLLLIARAQQPLEITVGNVYAMTLEMFQSLNLSYSYFTLL	372
MhraOR5	420	LASDHVRSTIQAIATRAQIPLSITGARFFTVNLSFLASMAGVMLTYFIVL	469
CquiOR10	373	RRVYN----- 377	
MhraOR5	470	LQV-NAKPKP 478	

Figure 6—figure supplement 1. Pairwise alignment of CquiOR10 and MhraOR5.

A MhraOR5 vs CquiOR10 RoseTTAFold



B MhraOR5 vs CquiOR10 AlphaFold

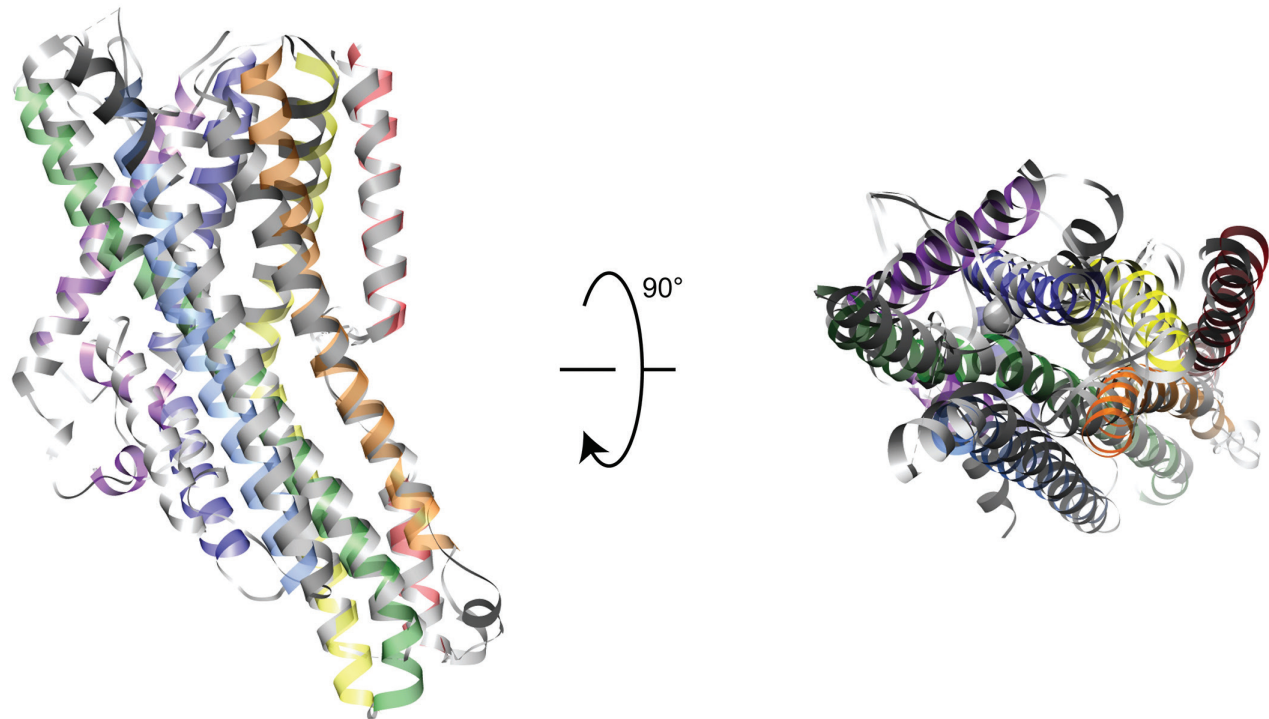


Figure 6—figure supplement 2. Overlay of MhraOR5 structure and CquiOR10 models. (A) RoseTTAFold and (B) AlphaFold models for CquiOR10.

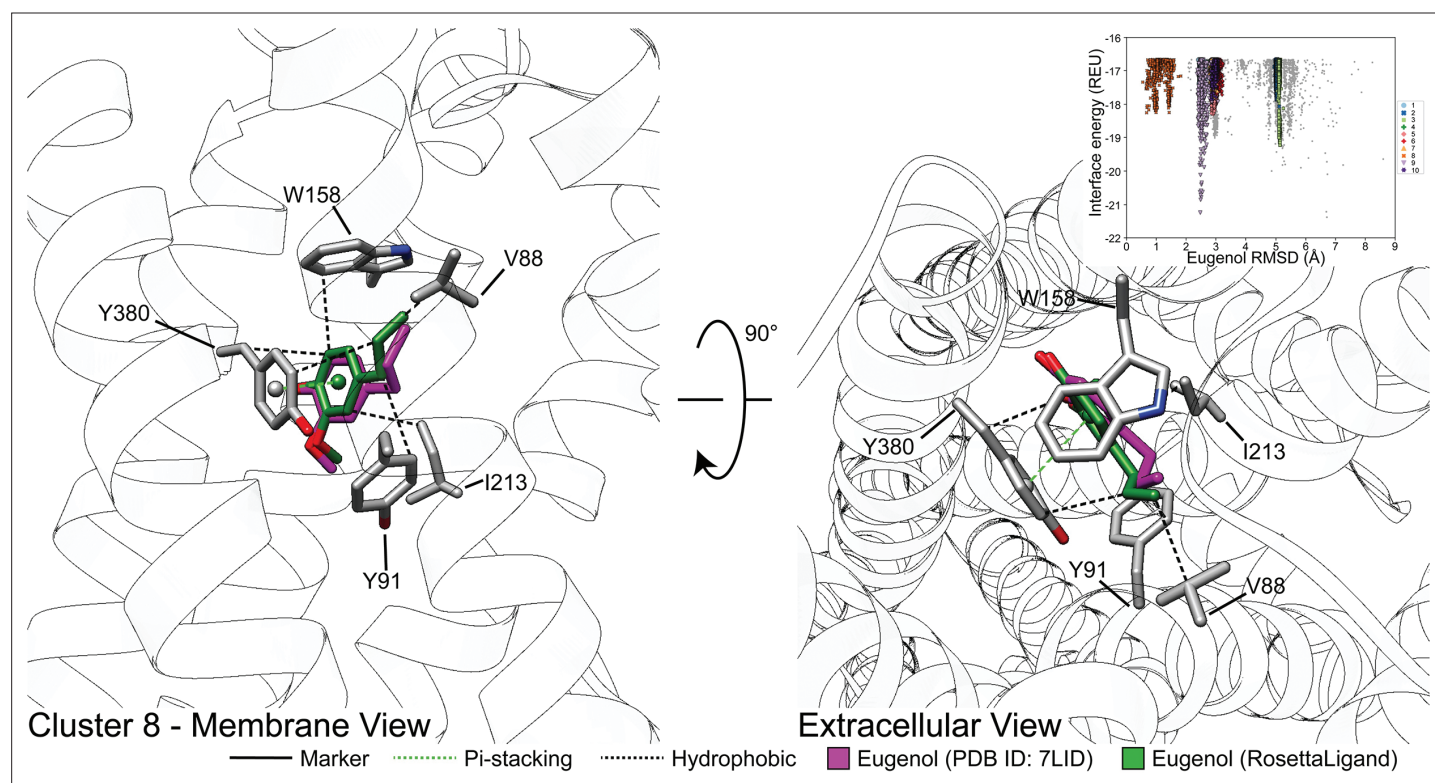


Figure 6—figure supplement 3. Representative model of docked eugenol with MhraOR5.

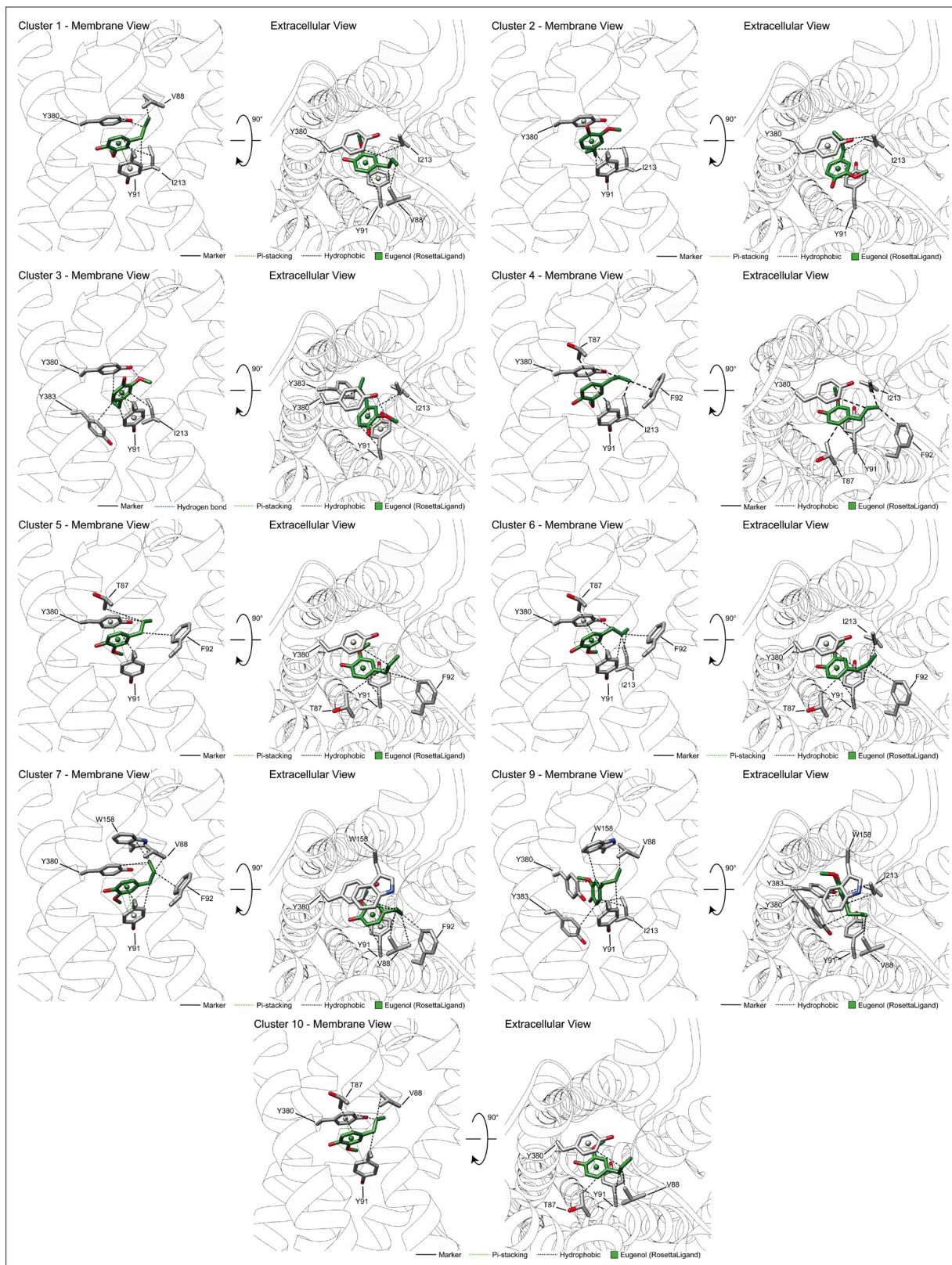


Figure 6—figure supplement 4. Additional clusters of eugenol docked to MhraOR5.

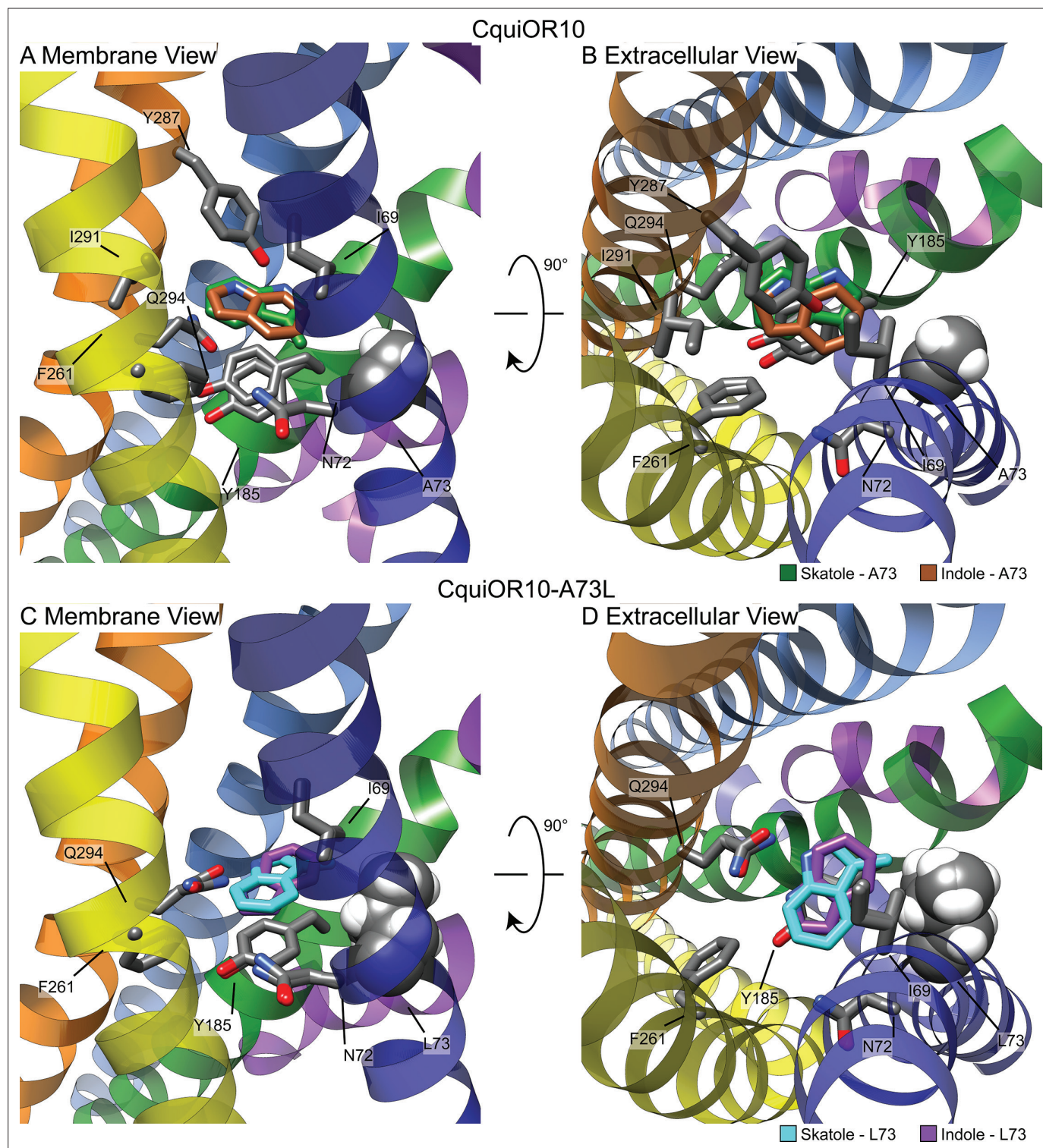


Figure 7. Representative models of docked skatole and indole in complex with CquiOR10 and CquiOR10A73L using RosettaLigand. Each model shown is the lowest interface-energy model from the 10 largest clusters of each docking study. CquiOR10 – skatole (forest green), CquiOR10 – indole (brown), CquiOR10A73L – skatole (light blue), and CquiOR10A73L – indole (purple). Atoms that are not indole/skatole carbon atoms are color-coded by atom type: carbon (gray), nitrogen (dark blue), and oxygen (red). Ala-73 and Leu-73 indicated with space-filling representation. (A, B) and (C, D) Membrane and extracellular views for CquiOR10 and CquiOR10A73L, respectively.

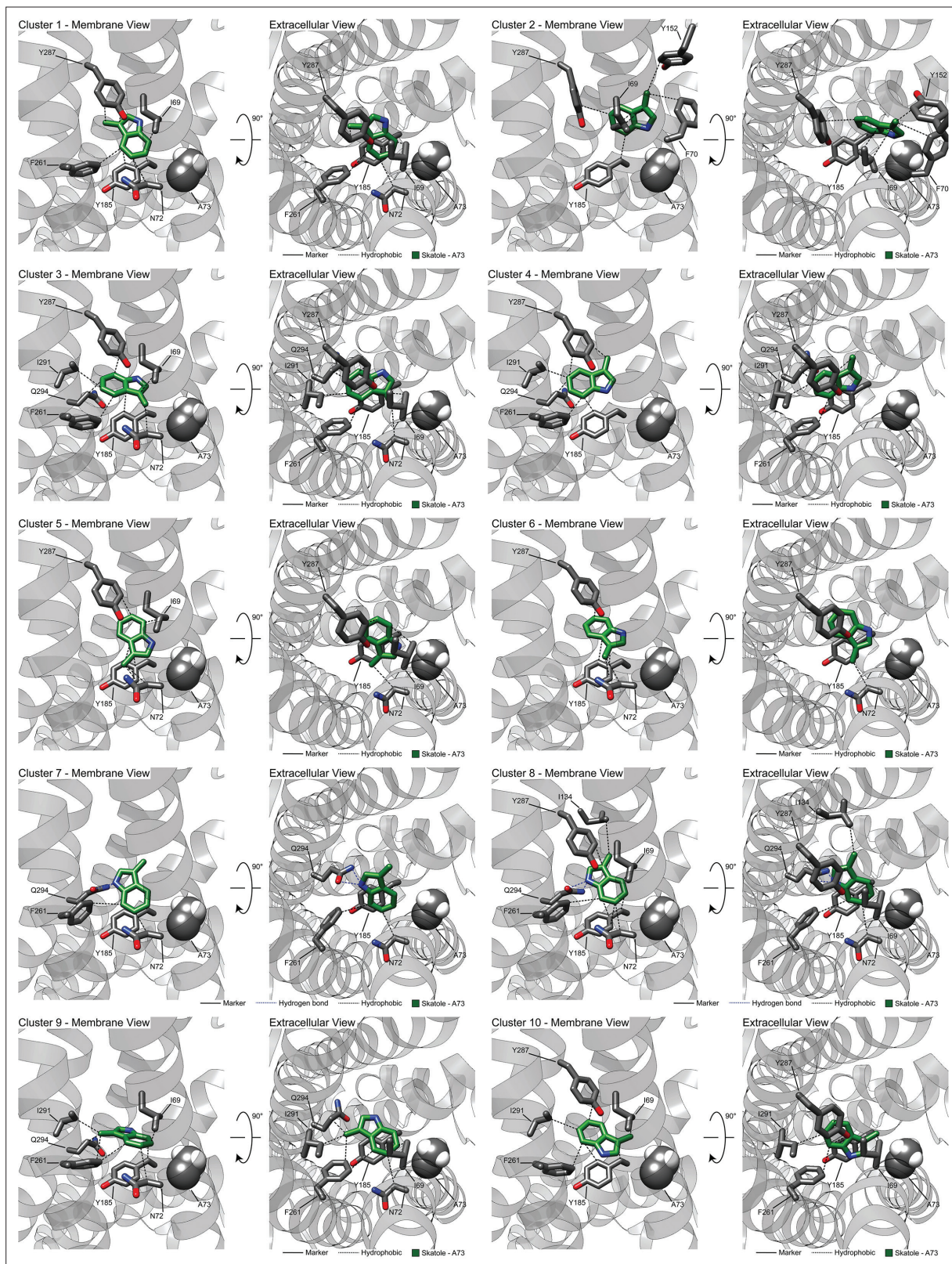


Figure 7—figure supplement 1. Clusters from RosettaLigand docking of skatole or indole to CquiOR10 or CquiOR10A73L.

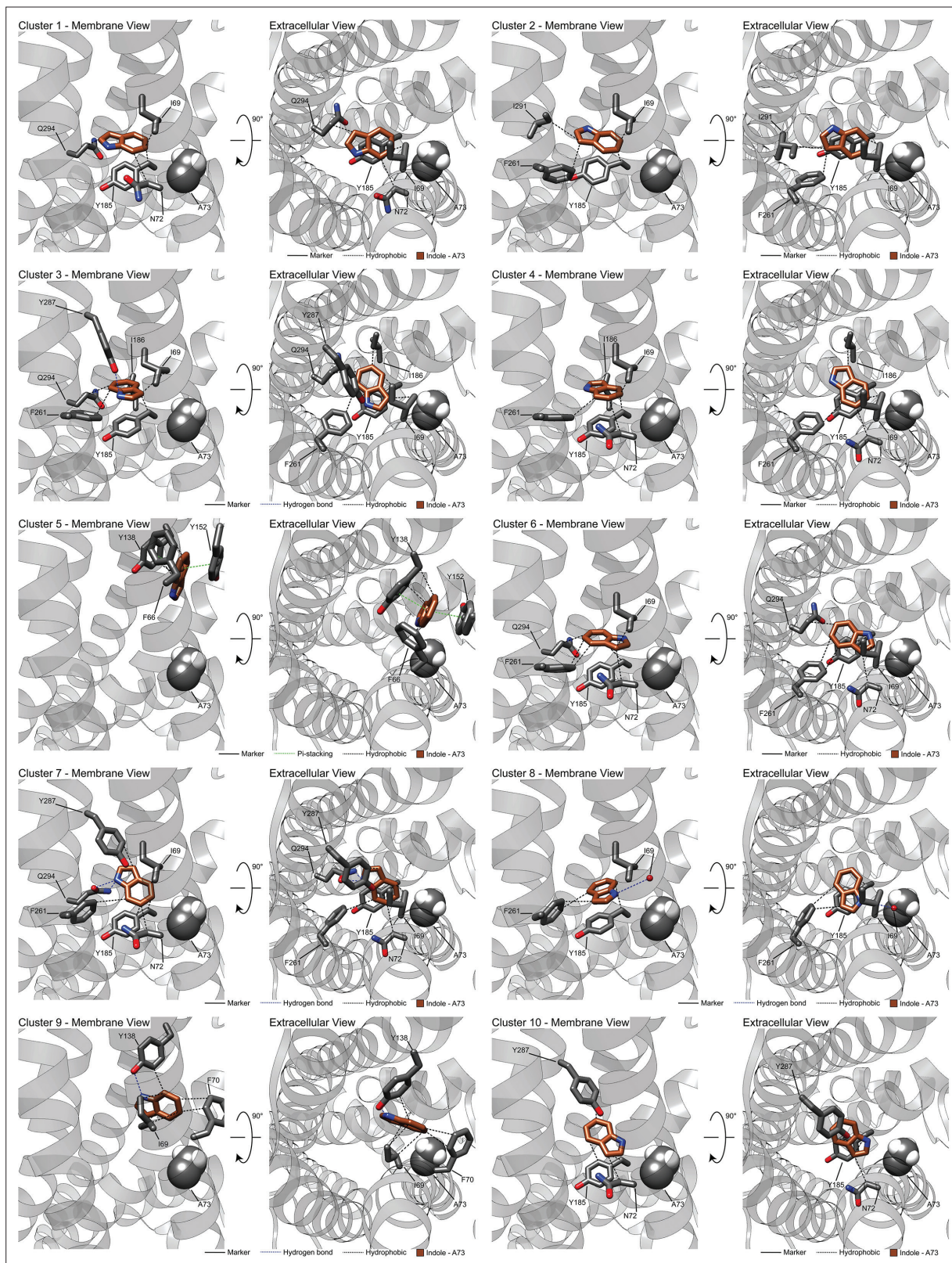
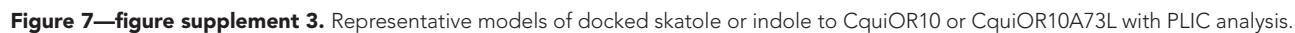


Figure 7—figure supplement 2. Zoom-out view of CquiOR10 or CquiOR10A73L complexed to skatole or indole.



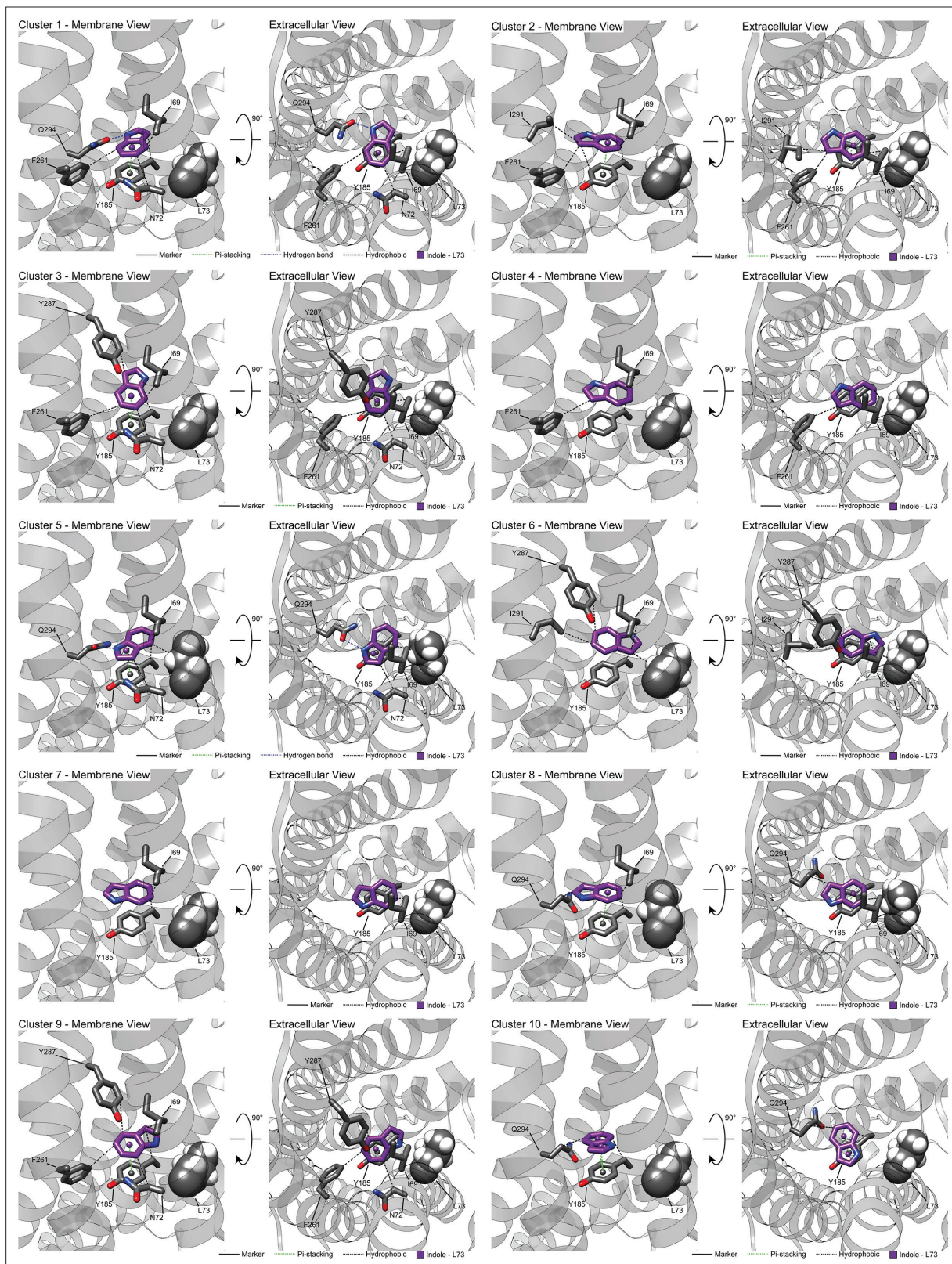


Figure 7—figure supplement 4. Superimposition of all OR-skatole and OR-indole clusters. OR: odorant receptor.

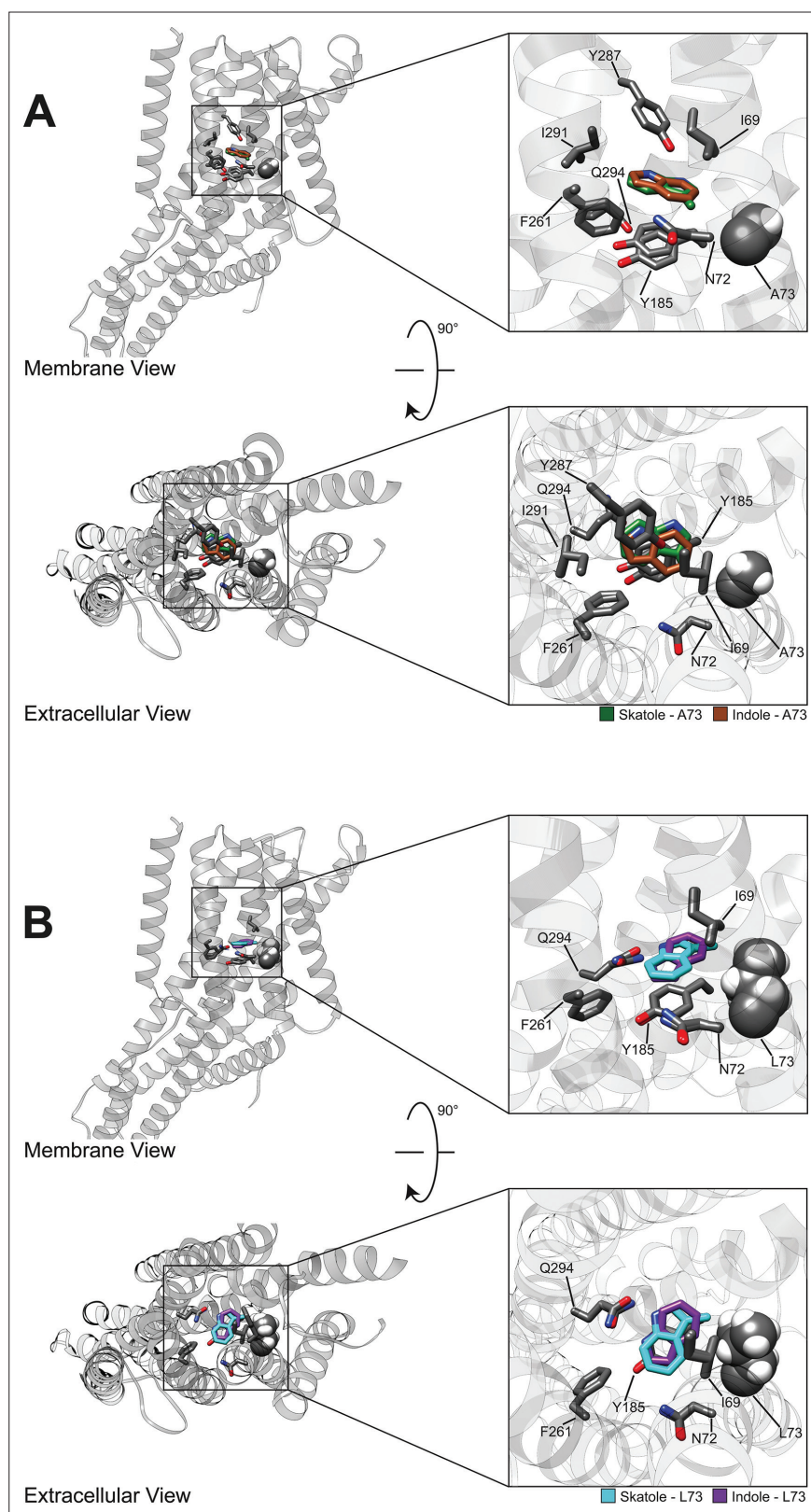


Figure 7—figure supplement 5. Example of sampling from ligand docking. (A) CquiOR10 and (B) CquiOR10A73L.

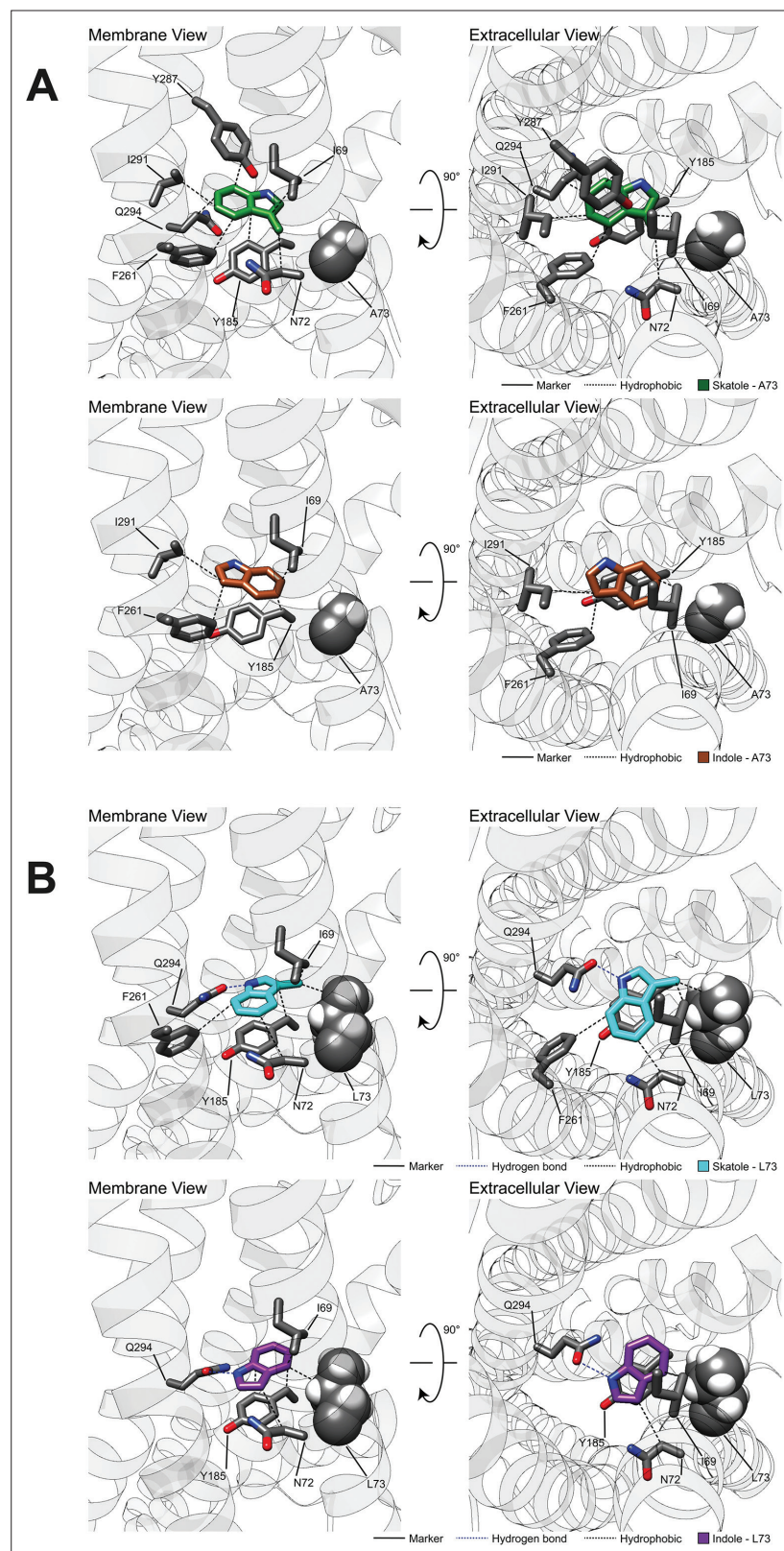


Figure 7—figure supplement 6. Representative RosettaLigand docking of skatole and indole to (A) CquiOR10 and (B) CquiOR10A73L with PLIP analysis. The representative is the lowest interface-scoring energy model from the 10 most frequent clusters of each test case. Hydrogen bond and π - π stacking interactions were filtered by previously reported bond distances (Bissantz et al., 2010).

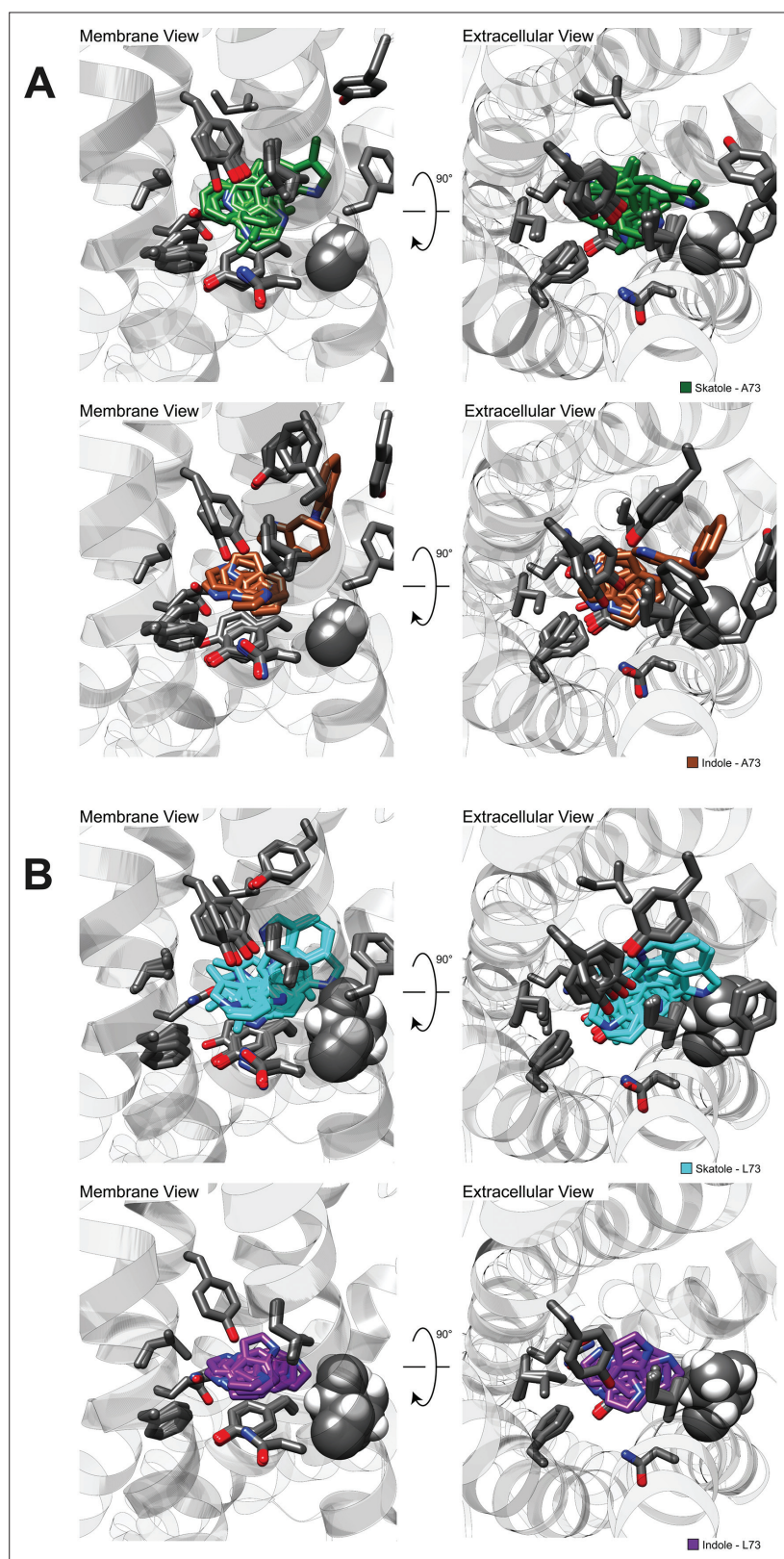


Figure 7—figure supplement 7. Superposition of all clusters of skatole and indole docked to (A) CquiOR10 and (B) CquiOR10-A73L.

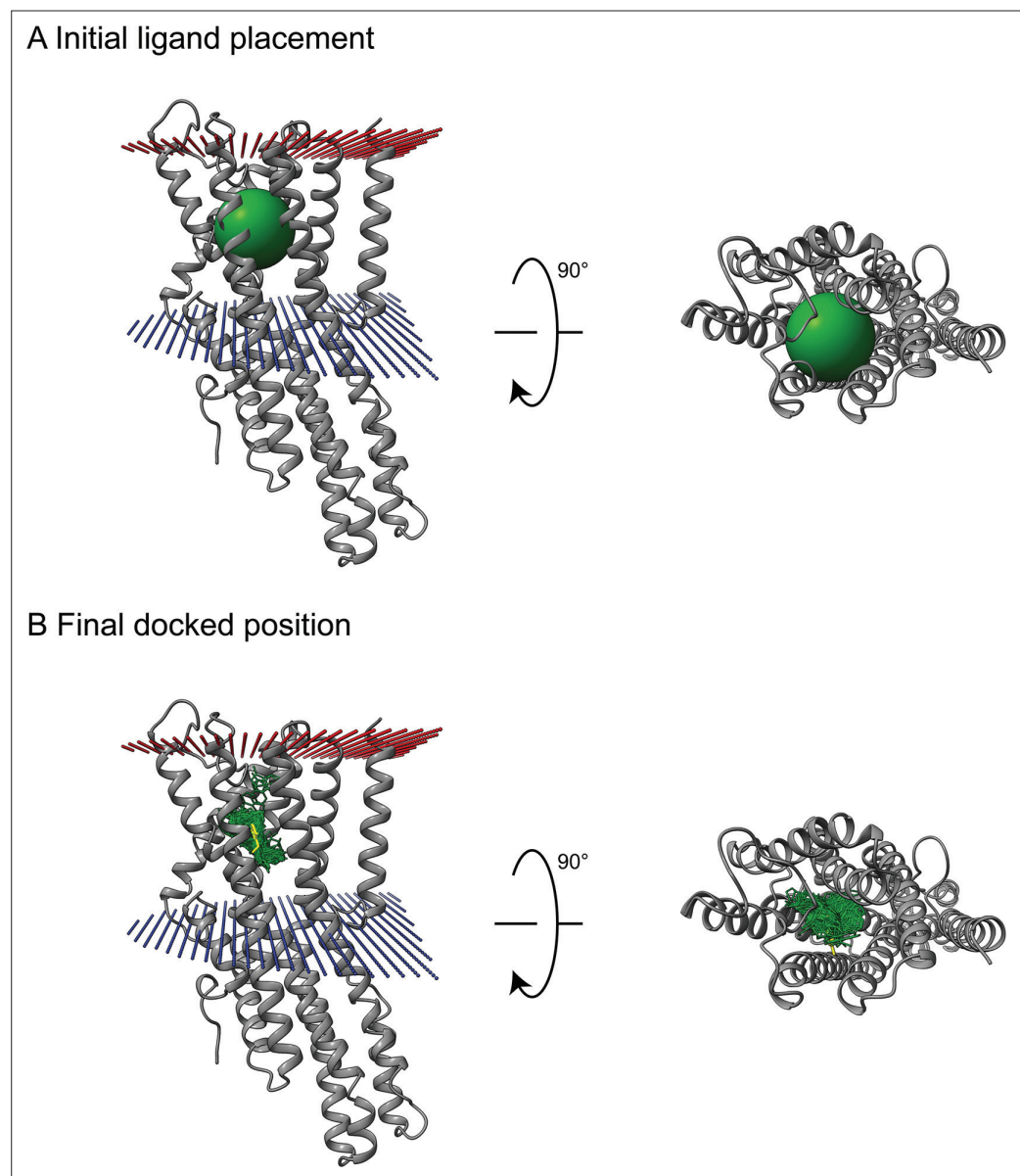


Figure 7—figure supplement 8. Example of sampling from ligand docking. **(A)** Odorants docked to CquiOR (grey) were positioned relative to eugenol from MhraOR5 (PDB 7LID) and then randomly rotated/translated within 7 Å as a starting position for docking. The green sphere represents the 7 Å sampling boundary. **(B)** An example demonstrating the sampling of skatole (green) docked to CquiOR10 after docking with eugenol (yellow) as a positional reference. Red: extracellular membrane boundary. Blue: cytoplasmic membrane boundary.

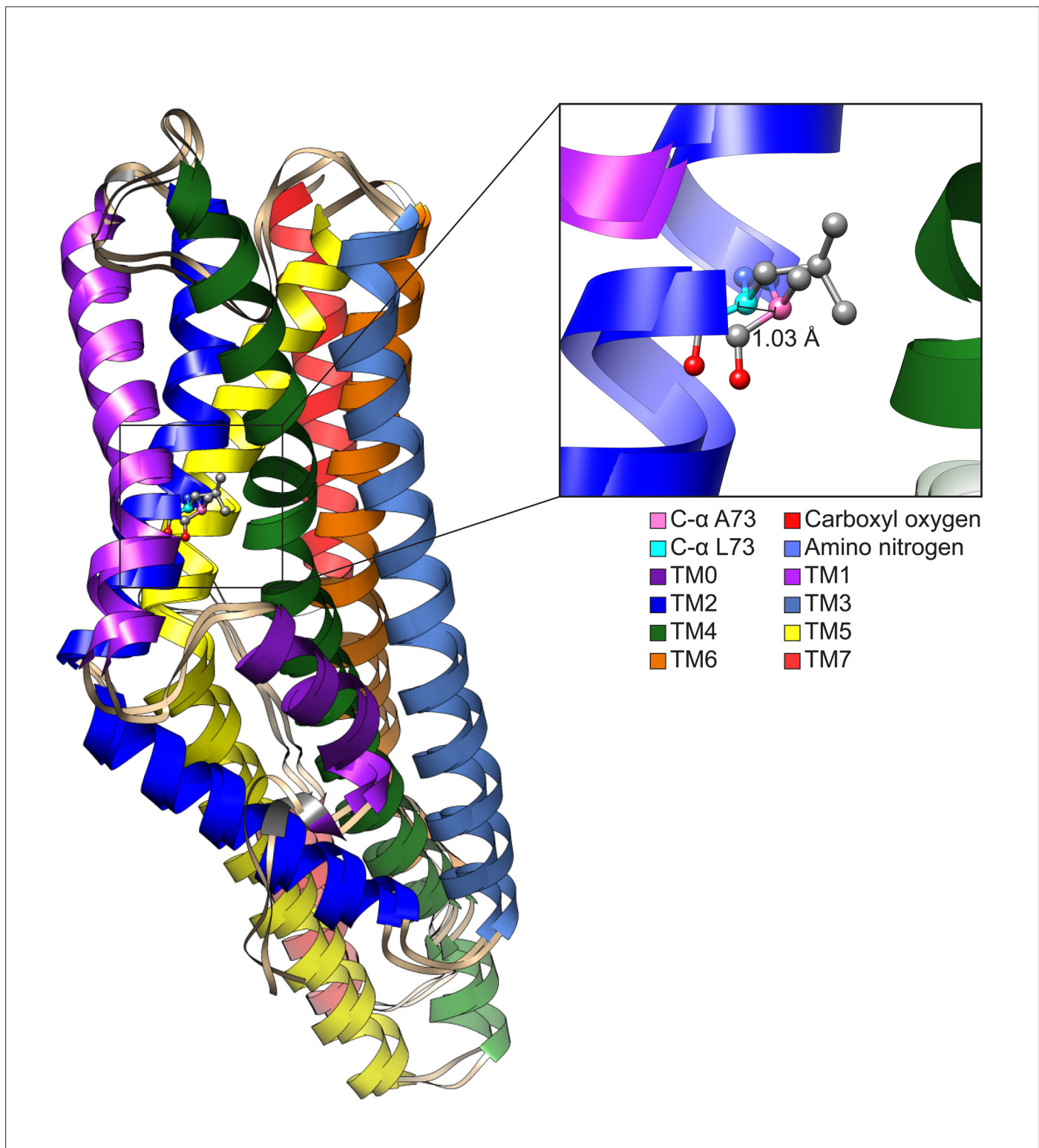


Figure 8. Comparison of CquiOR10 and CquiOR10A73L models. An approximate 1 Å α -carbon outward shift of Leu-73 (forest green) in CquiOR10 model relative to Ala-73 (light blue) in CquiOR10A73L model. Models were superimposed using the TM7b region. Residue 73 amino nitrogen is colored in dark blue, and carboxyl oxygen is colored in red in each model.

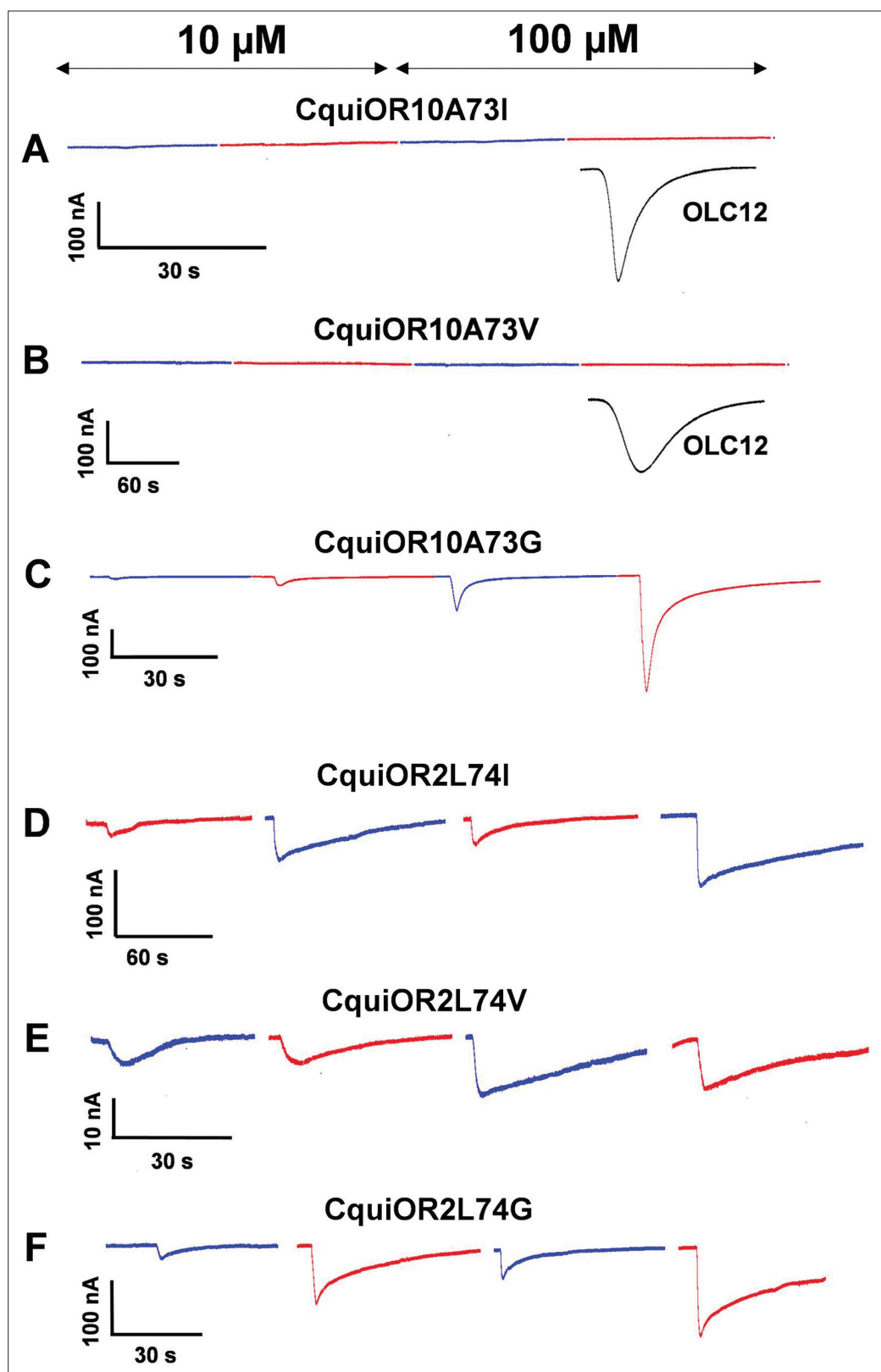


Figure 8—figure supplement 1. Effect of single-point mutations around A73. (A-C) CquiOR10 mutants. (D-F) CquiOR2 mutants.

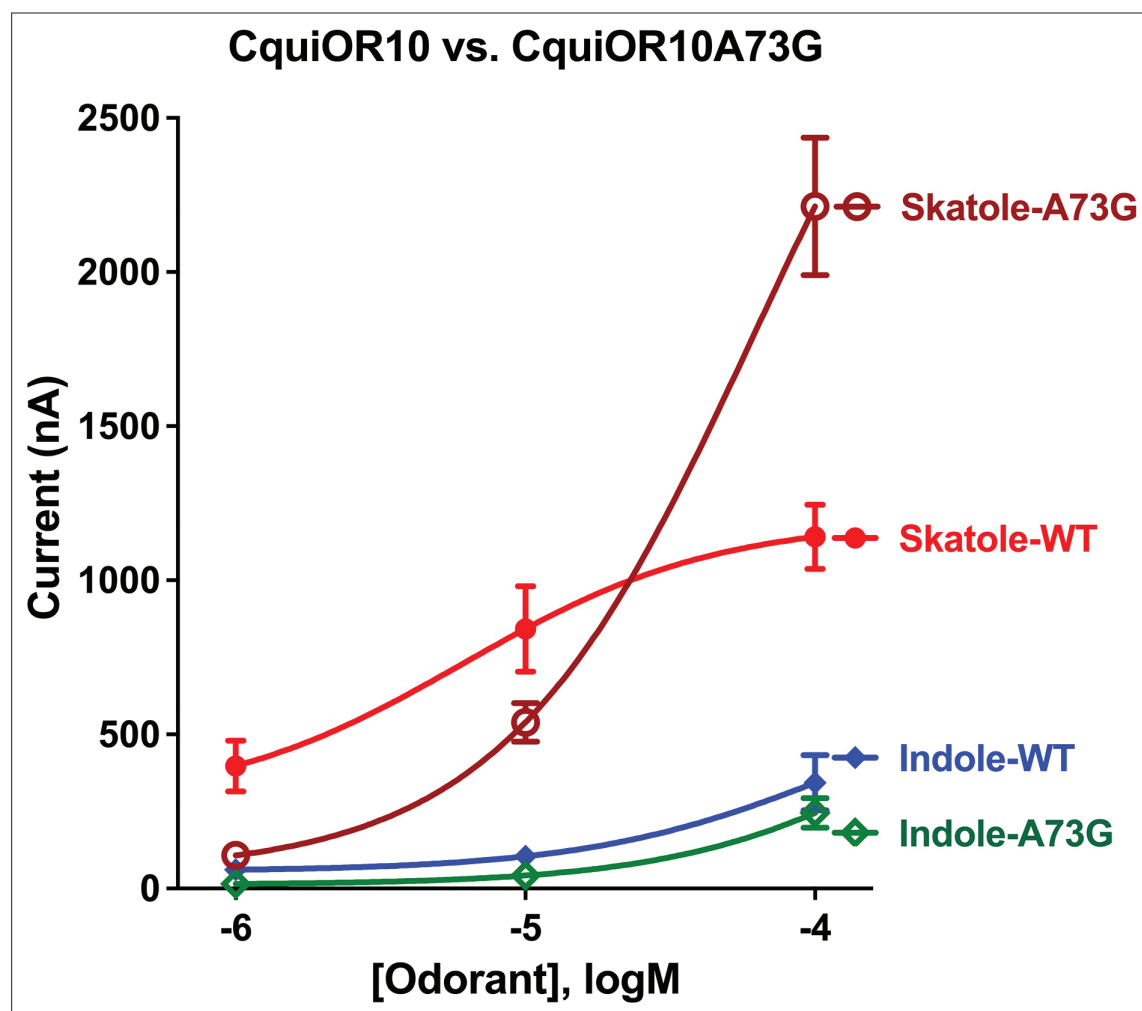


Figure 8—figure supplement 2. Quantification of single-point mutations around A73.

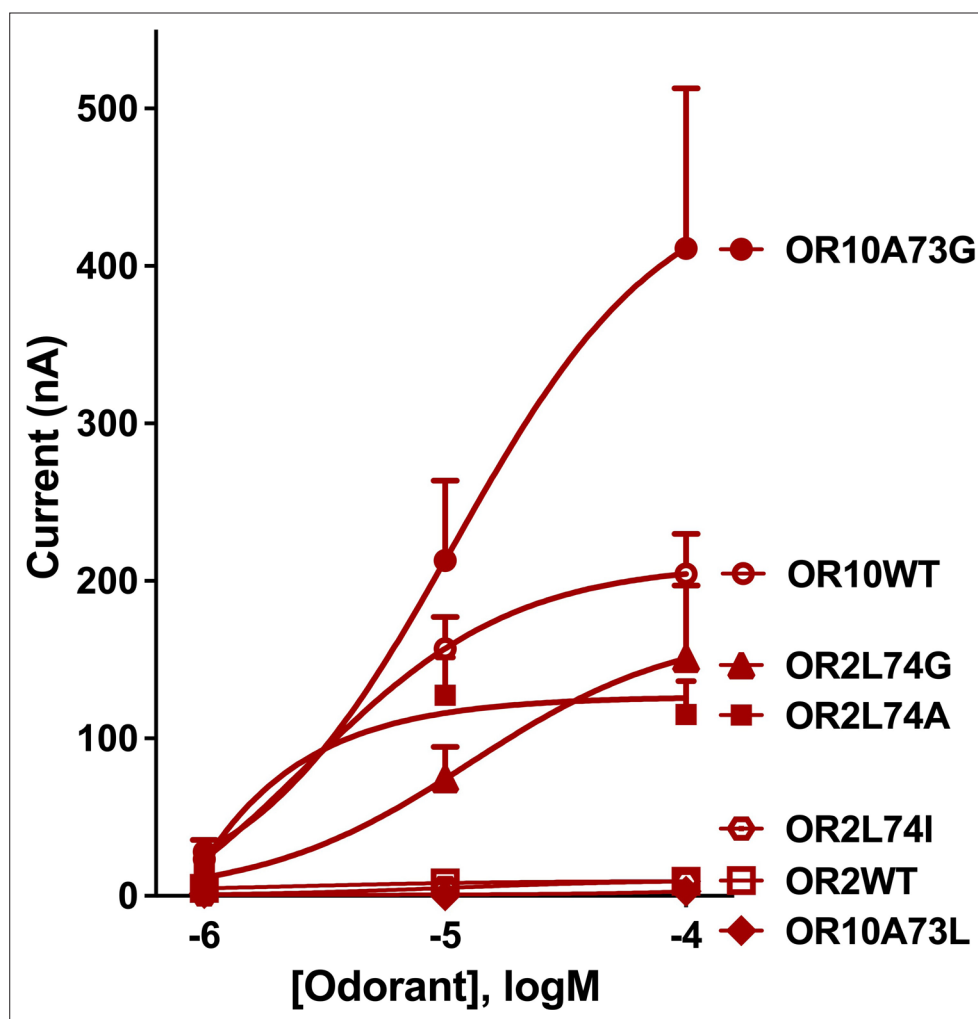


Figure 9. Concentration-dependent responses elicited by 3-ethylindole in oocytes co-expressing CquiOrco with CquiOR10, CquiOR2, or single-point mutants. Bars represent SEM ($n = 4-10$).

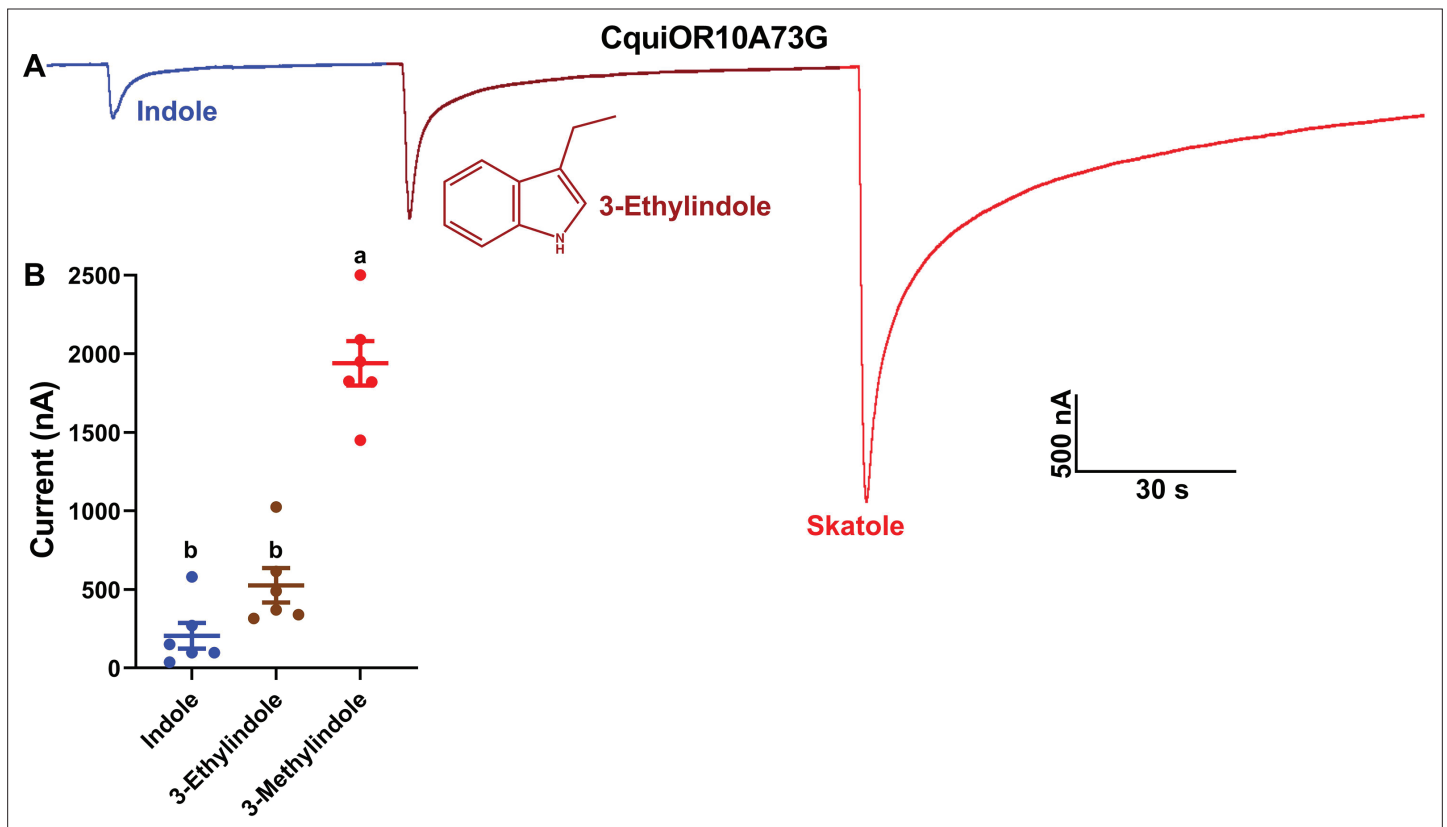


Figure 9—figure supplement 1. Representative trace of the responses of CquiOR10A73G/CquiOrco-expressing oocyte to indole, skatole, and 3-ethylindole (brown). (A) Representative trace recorded after challenging an oocyte with the three odorants at the same dose (100 μ M). (B) Quantification of responses from six different oocytes. Columns with the same letter are not significantly different (Repeated measures, one-way ANOVA).