

Figure S1 Sequence alignment of *Schistocerca gregaria* receptor with the crystal structures of hκ-OR (PDB ID: 4DJH). Coloring scheme indicates the degree of similarity at each alignment column. Identical (strong blue background), strongly similar (light blue background), weakly similar (very light blue background) and non-matching residues (white background) are highlighted. Experimentally determined secondary structures for hκ-OR are shown in cartoon are color coded, with helices in red, strands in blue, and coils in beige. The seven transmembrane helices (TM1-TM7) are highlighted and highly conserved residues among Class A GPCRs in hκ-OR and purple are represented in green colored boxes.

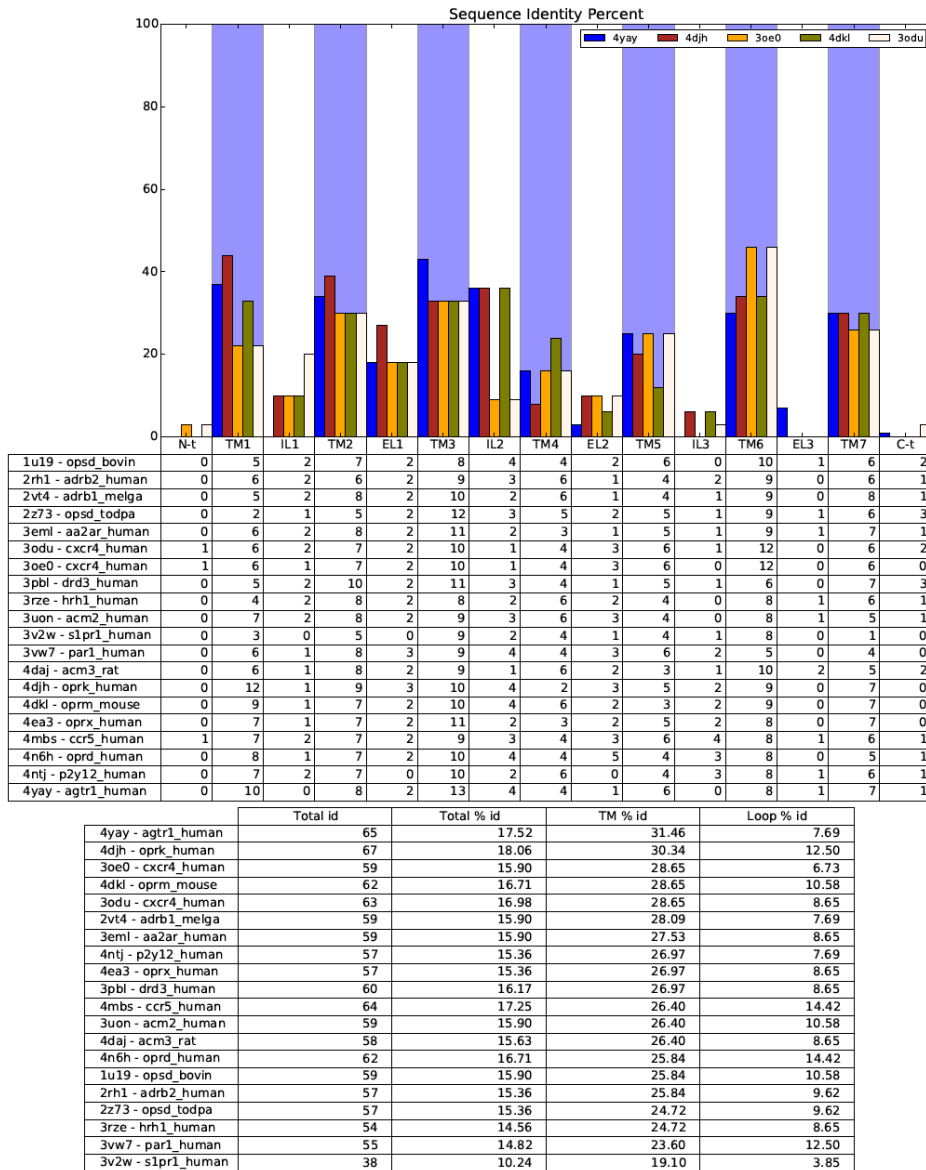
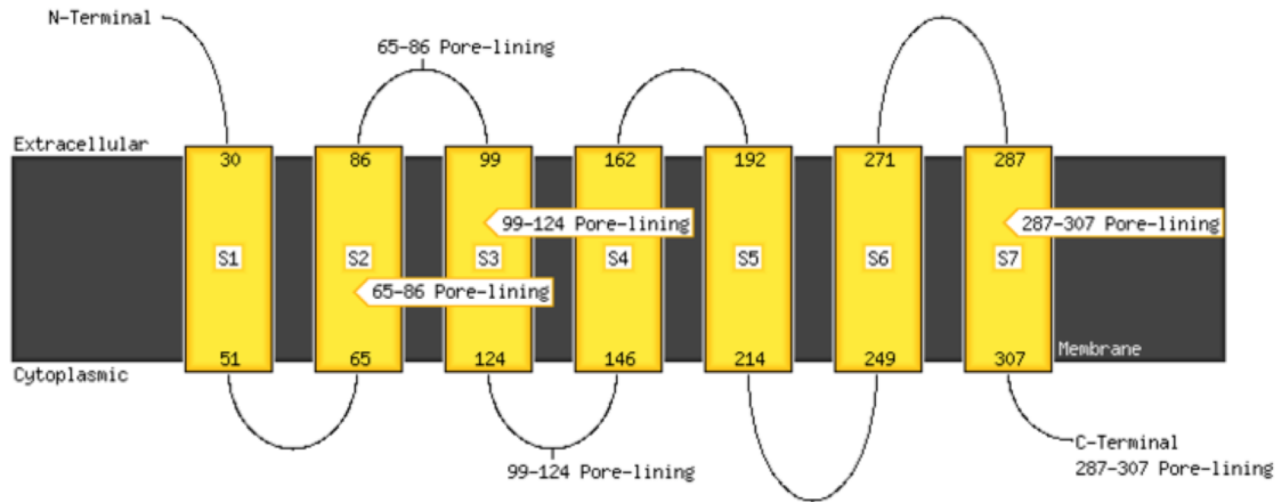


Figure S2 GPCR-ModSim server sequence identity match

MEMSAT-SVM Cartoon

fa724d11-c928-4a24-be1a-7d39ea9a9565.seq.job

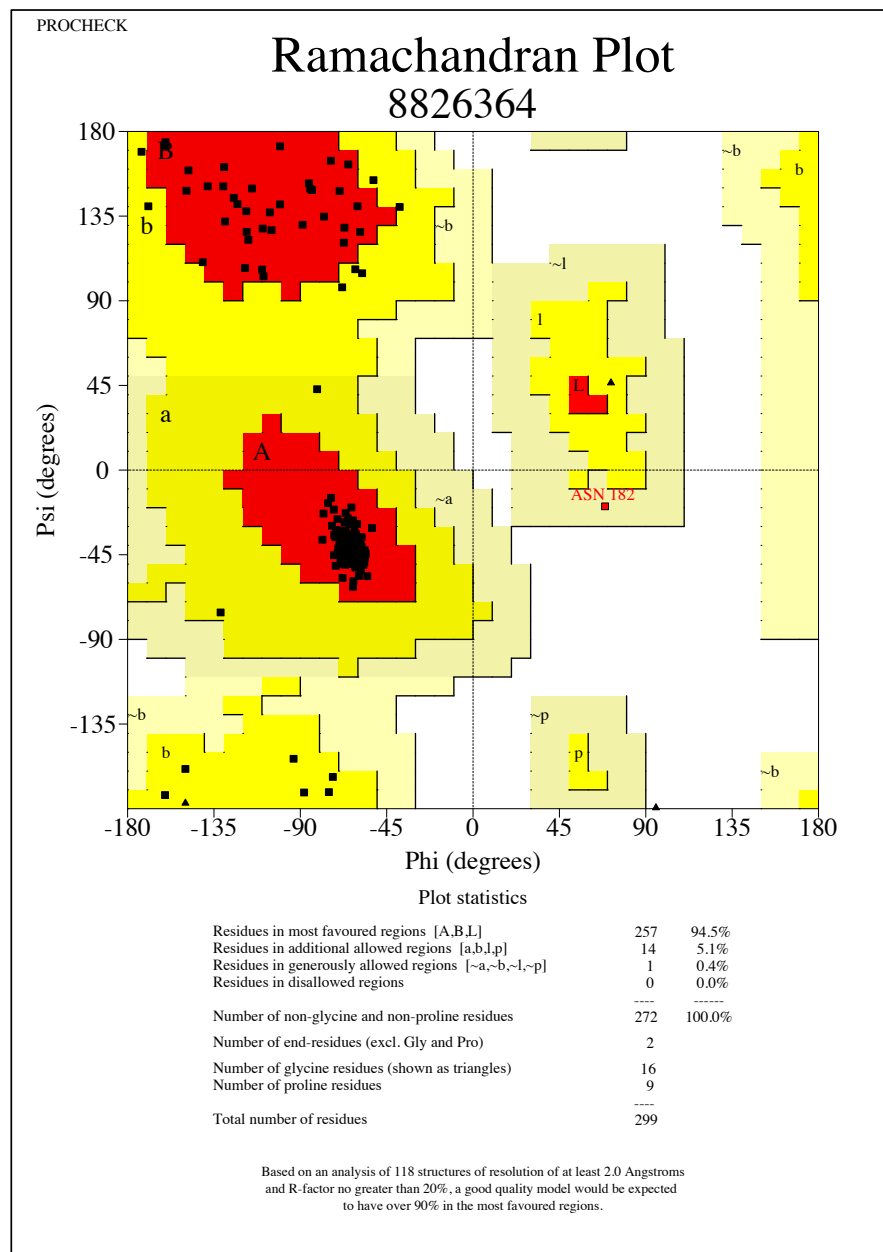


MEMSAT-SVM Prediction

Summary of MEMSAT-SVM Topology Analysis

Signal peptide	Not detected.
Signal score	0
Topology	30-51,65-86,99-124,146-162,192-214,249-271,287-307
Re-entrant helices	Not detected.
Pore-lining helices	65-86,99-124,287-307
Helix count	7
N-terminal	out
Score	10.9748
Pore stoichiometry	1

Figure S3. Prediction of transmembrane helices.



8826364_01.ps

Figure S4. Ramachandran plot analyses of the Schgr-AKHR model from PROCHECK

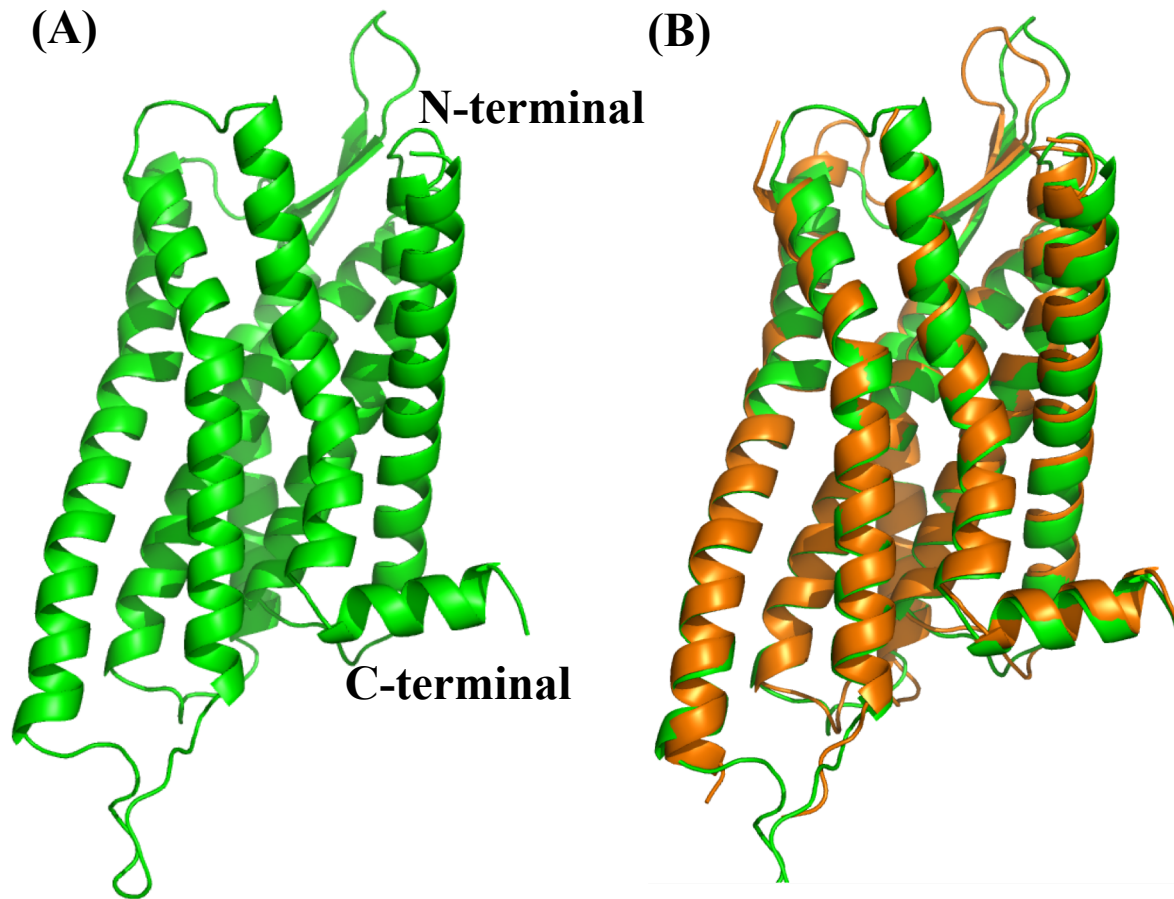


Figure S5. The final 3D structure of *Schistocerca gregaria* (A) and the comparison of *Schistocerca gregaria* model with template structure hκ-OR (orange color). Proteins are shown as ribbon diagram. The figures were made using PyMol (<http://pymol.org/>)