**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
Figure S3. Prediction of transmembrane helices.
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/](http://pymol.org/))