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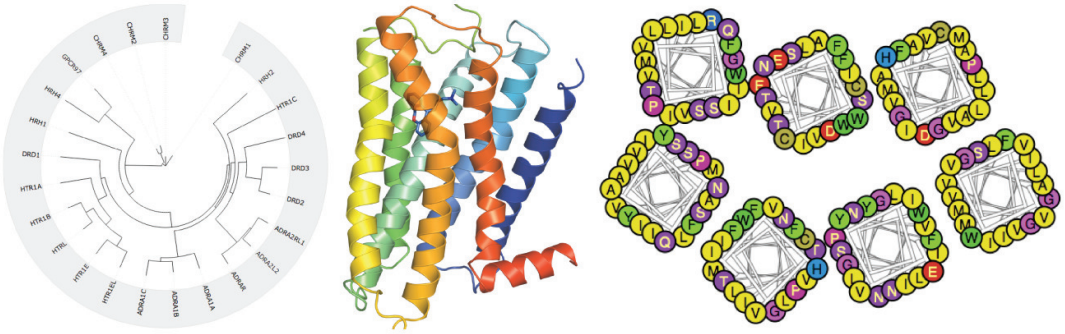
GPCRDB: GPCR DATA, DIAGRAMS AND TOOLS

Vignir Isberg[1], Bas Vroling[2], Stefan Mordalski[3], Alexander Hauser[1], Rob van der Kant[4], Gerrit Vriend[4] and David E. Gloriam[1]

1. Dept of Drug Design and Pharmacology, Univ. of Copenhagen, Jagtvej 162, 2100, Denmark
2. Bio-Prodict B.V., Castellastraat 116, 6512 EZ, Nijmegen, The Netherlands
3. Institute of Pharmacology Polish Academy of Sciences, 12 Smetna St, Krakow, Poland
4. Radboudumc Nijmegen Medical Centre, Geert Grooteplein Zuid 26-28, 6525 GA,The Netherlands



GPCRDB (gpcr.org/7tm) has been a popular resource for the G protein-coupled receptors community for the past 20 years and obtained more than 1000 citations [1-5]. GPCRDB contains experimental data on crystal structures, mutations and oligomers, as well as computationally derived sequence alignments and homology models. The latest release has added user-friendly web browser tools and diagrams for downloaded for publication (tools.gpcr.org).

NEW GPCRDB FEATURE HIGHLIGHTS	**Diagrams**	• Interactive residue snake- and helix box plots • Phylogenetic trees based on any subsequence
	Data	• Structure-based sequence alignments and 3D models • Sequence conservation statistics for alignments • Generic residue numbering of sequences and structures
	Tools	• Crystal structure browser with annotations • Ligand off-target prediction by binding sequence motif search • Receptor similarities based on any subsequence

References:

1.) Horn, F. et al. Nucleic Acids Res., **1998**, *26*, 275-279.
2.) Horn, F. et al. Nucleic Acids Res., **2003**, *31*, 294-297.
3.) Horn, F. et al. Nucleic Acids Res., **2001**, *29*, 346-349.
4.) Vroling, B. et al. Nucleic Acids Res., **2011**, *39*, 309-319.
5.) Isberg, V. et al. Nucleic Acids Res., **2014**, *42*, 422-425.