P01

GPCRdb Structural Data and Tools for G Protein-Coupled Receptors

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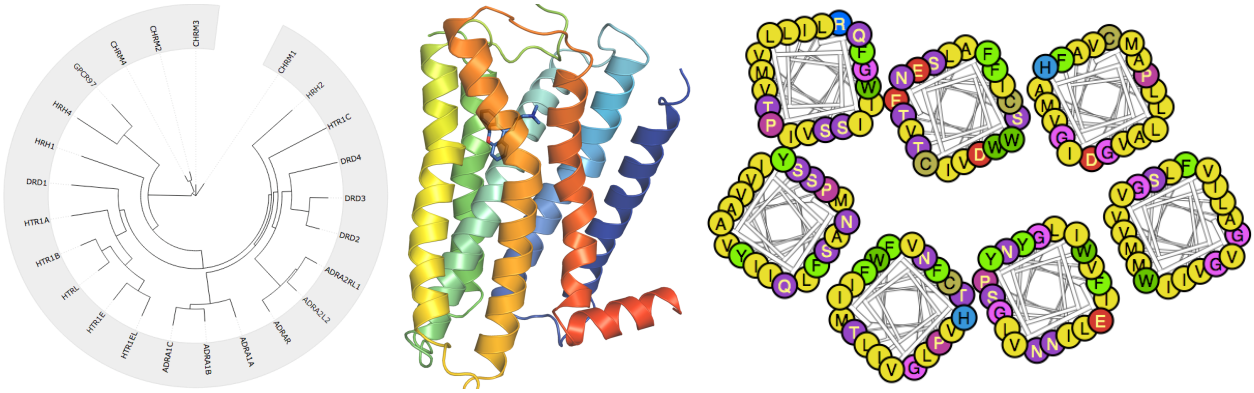

GPCRdb (gpcrdb.org) has been a popular resource for the G protein-coupled receptor community for the past 20 years and today has around 1500 users every month[1]. GPCRdb contains experimental data on crystal structures, mutants, as well as computationally derived sequence alignments and homology models. The latest release has added user-friendly web browser structural tools[2,3].

References: 1) V Isberg *et al.*, Nucleic Acids Res., **2014**, *42*, D422-425; 2) V Isberg *et al.*, Trends Pharmacol. Sci., **2015**, *36*, 22-31; 3) K Fidom *et al.*, Methods, **2015**, *71*, 104-112.

P02

GPCR$_{TM}$: An amino acid substitution matrix for class A G Protein-Coupled Receptors

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Protein sequence alignments and database search methods use standard scoring matrices calculated from amino acid substitution frequencies in general sets of proteins. These general-purpose matrices are not optimal to align accurately sequences with marked compositional biases, such as hydrophobic transmembrane regions found in membrane proteins. In this work, an amino acid substitution matrix (GPCRtm) is calculated for the membrane spanning segments of the G protein-coupled receptor (GPCR) rhodopsin family. The GPCRtm matrix reveals the amino acid compositional bias distinctive of the class A GPCR family and differs from other standard substitution matrices. These membrane receptors, as