PG03

GENERIC G PROTEIN-COUPLED RECEPTOR RESIDUE NUMBERING - ALIGNING TOPOLOGY MAPS WHILE MINDING THE GAPS

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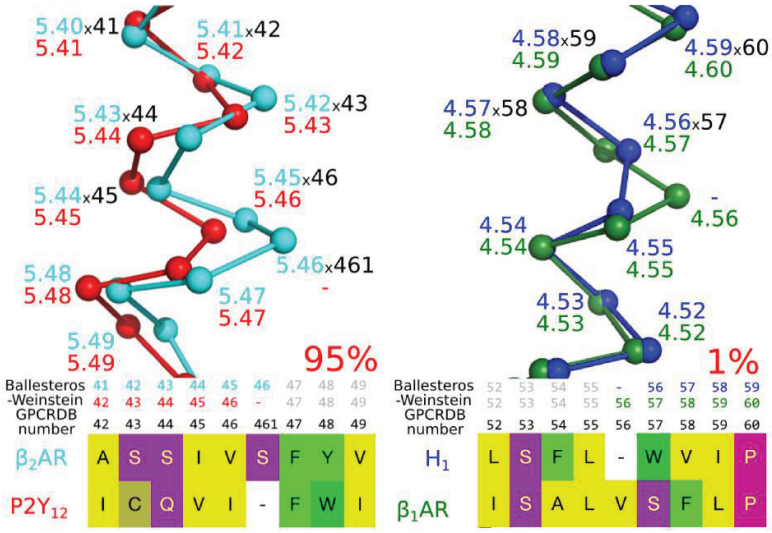

Generic GPCR residue numbers denote the corresponding residues within receptors of interest to facilitate comparisons of e.g. mutational effects, ligand interactions and structural motifs. Their utility is illustrated by the more than 1100 citations for the most commonly used scheme of Ballesteros and Weinstein [1] for class A GPCRs. The first crystal structures for the other classes B, C and F now put the spotlight on how to assign residue numbers within and across these classes. Furthermore, as we entered the structural era, we found that GPCR helices contain frequent bulges and constrictions that offset the generic residue numbers [2].

Here, we provide recommendations for the use of generic GPCR numbering schemes. Moreover, we introduce a complementary structure-based scheme to take proper care of the helical bulges and constrictions. Finally, GPCRDB [3] has been equipped with user-friendly retrieval of the first comprehensive crystal structure-based sequence alignments and tools to assign generic residue numbers to any receptor sequence or structure.

References:

1.) Ballesteros, J., Weinstein, H., Methods Neurosci., **1995**, *25*, 366-428.

2.) van der Kant, R., Vriend, G., Int. J. Mol. Sci., **2014**, *15*, 7841-7864.

3.) Isberg, V. et al., Nucleic Acids Res., **2014**, *42*, 422-425.