Correction to "Structural mimicry in G protein-coupled receptors: implications of the high-resolution structure of rhodopsin for structure-function analysis of rhodopsin-like receptors"

In the above article [Ballesteros JA, Shi L, and Javitch JA (2001) *Mol Pharmacol* **60:**1–19], an internet URL in Table 1 was typeset incorrectly. The correct URL is: http://www.expasy.ch/cgi-bin/lists?7tmrlist.txt.

In addition, Fig. 1 contains an error in the alignment of TM5 of the TSH receptor. The authors regret this error and apologize for any confusion or inconvenience it may have caused. The corrected figure appears below.

Fig. 1. Sequence alignment of the transmembrane domain and relevant adjacent residues in selected receptors. Yellow represents residues in the dopamine D2 receptor found in SCAM studies to be accessible and protected. Orange represents accessible residues that were not protected or for which protection was not measured because of small effect size. The overscored regions represent the α-helical domains in rhodopsin. The most conserved residues (X.50) in each TM are indicated by arrows, and the index number of the first residue in each TM of the alignment is indicated. The residue numbers of the first residues in each TM of each indicated receptor are shown to the right of the receptor names. Receptor names are abbreviated according to their SWISS-PROT Annotated Protein Sequence Database entry names: http://www.expasy.ch/cgi-bin/lists?7tmrlist.txt. h, human; b, bovine.

Downloaded from molpharm.aspetjournals.org at ASPET Journals on April 17, 2024