

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?7tmrlst.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.

	1.30	
bOPSD	35	WQFSMLAAYMFLIMLGFPINFLTLYVTVQHKKLR
hD2DR	32	PHYNYATLLTLLIAVIVFGNVLVCMVVSREKALQ
hB2AR	31	VWVVGMIIVMSLIVLAIVFGNVLVITAIKFERLQ
hACM1	23	WQVAFIGITGLLSLATVTGNLLVLISFKVNTLQ
hOPRK	57	AIPVITAVYSVVFVVLVGNLSLVMFVIRYTKMK
hNK1R	30	WQIVLWAAAYTVIVVTSVVGNVVVMWIIIAHKMR
hTSHR	412	MGYKFLRIVVWFVSLALLGNVFLILLTSHYKL
	2.38	
bOPSD	71	PLNYILLNLAVADLFMVFGGFTTLYTSLH
hD2DR	68	TTNYLIVSLAVADLVATLVMPVWVYLEV
hB2AR	67	VTNYFITSLACADLVMLAVVPGAAILM
hACM1	59	VNNYFLLSLACADLIIGTFSMNLYTTLLM
hOPRK	93	ATNIYIFNLALADALVTTMPFQSTVYLMN
hNK1R	66	VTNYFLVNLAFEAASMAAFNTVNFYAVH
hTSHR	448	VPRFLMCNLAFADFCMGMYLLLIASVDLYT
	3.22	
bOPSD	107	PTGCNLEGFFATLGGEIALWSLVLAIERVYVVC
hD2DR	104	RIHCDIFVTLDVMMCTASILNLCAISIDRYTAVAM
hB2AR	103	NFWCEFWTSIDVLCVTASIELTLCVIAVDYFAITS
hACM1	95	TLACDLWLALDYVASNASVMNLLISFDYFVSVTR
hOPRK	128	DVLCIKIVISIDYNNMFTSIFTLTMMSVDRYIAVCH
hNK1R	102	LFYCKFHNFFPIAAVFASISMTAVAFDRYMAIIH
hTSHR	491	GPCCNTAGFFTTFASELSVYTLTVITLERWYAITF
	4.38	
bOPSD	149	GENHAIMGVAFTVMALACAAPPLV
hD2DR	148	SKRRVTVMISIVVWLSFTISCPLLF
hB2AR	146	TKNKAIVIIIMVWIVSGLTSFLPIQ
hACM1	138	TPRRAALMIGLAWLVSVFLWAPAIL
hOPRK	171	TPLKAKIINICIWLLSSSVGISAI
hNK1R	143	SATATKVVICVIVWLALLAFPOGY
hTSHR	534	RLRHACAIMVGGVCCFLALLPLV
	5.35	
bOPSD	200	NESFVIYMFVHFIIPLIVIFFCYGQLVFTVKEAAAQ
hD2DR	186	NPAFVYSSIVSFVVPFIVTLVYIKIYIVLRRRRKV
hB2AR	196	NQAYAIASSIVSFVPLVIMVFVYSRVFQEAQRQLQKI
hACM1	185	QPIITFGTAMAFYLPVTVMCTLYWRIYRETNRRREL
hOPRK	223	DLFMKICVFIFAFVIVPLIIIVCYTLMILRLKSVRLLS
hNK1R	193	EKVYHICVTVLIYFLPLLVIYGYATTVVGITLWASEIPG
hTSHR	578	LALAYIVFVLTNLIVAFVIVCCYVKIYITVRNP----
	6.23	
bOPSD	240	SATTQKAEKEVTRMVIIMVIAFLICWLPYAGVAFYIFT
hD2DR	361	RKLSQQKEKKATQMLAIVLGVFLICWLPFFITHILNIH
hB2AR	261	SSKFCLEKHKALKTGLIIMGTFTLCWLPFFIVNIVHVI
hACM1	353	KTFSLVKEKKAARTLSAILLAFILTWTPYINIMVLVSTF
hOPRK	262	SREKDRNLRRITRLVLVVAVFVVCWTPPIHIFILVEAL
hNK1R	236	YHEQVSARKKVVKMIVVVCTFAICWLPFFHIFLLPYI
hTSHR	612	QYNPGDKDKIAKRMVLIPTDFICMAPISFYALSAIL
	7.33	
bOPSD	286	IFMTIPAFFAKTSVAVNPVYIMMNKQFRNCMVTTLCC
hD2DR	406	VLYSAFTWLGYNVSAVNPVYITFNIIEFRKAPFLKILHC
hB2AR	306	EVYILLNWIGYVNSGFNPLIYCRS-PDFRIAFQELLCL
hACM1	398	TLWELGYWLCYVNSTINPMCYALCNKAFRDTFRLLLLC
hOPRK	310	SSYFFICIALGYTNSSLNPILYAFLDENFKRCFRDFCFP
hNK1R	285	QVYLAIMWLAMSSTMYNPVYICCLNDRFLRGFKHAFRC
hTSHR	658	NSKILLVLFYPLNSCANPFLYAIPTKAFQRDVFILLSK

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?7tmrlst.txt>. h, human; b, bovine.