

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.

	1.30	
bOPSD	35	WQFSMLAAYMFLIMLGFPINFLTLYVTVQHKKLK
hD2DR	32	PHYNY ATLLTLLIAVIVFGNVLVCM AVSREKALQ
hB2AR	31	VWVVGMI VMSLIVLAIVFGNVLVITAI KFERLQ
hACM1	23	WQVAFIGIT TGLLSLATVTGNLLVLIS FKVNTELK
hOPRK	57	AIPVITAVSVV FVGLVGNLSLVMFVI IRYTKMK
hNK1R	30	WQIVLWAAAYT VIVVTSVVGNVVMWII LAHKMR
hTSHR	412	MGYKFLRIVV WFVSLALLGNVFLILLT SHYKL
	2.38	
bOPSD	71	PLNYILLNLAVADLF FMVFGGFTTLY TSLSH
hD2DR	68	TTNYLIVSL AVADLLVATLVMPWV VYLEVV
hB2AR	67	VTNYFITSLACADLV MGLAVVPFGAA HILM
hACM1	59	VNNYFLLSLACADLI IGTFSMNLYTT YLLM
hOPRK	93	ATNIYIFNLALADAL VTTTTPFQSTV YLMN
hNK1R	66	VTNYFLVNLAF AEASMAAFNTVNFT YAVH
hTSHR	448	VPRFLMCNLAFAD FCMGMYLLLIAS VDLYT
	3.22	
bOPSD	107	PTGCNLEGFFATLGGEIAL WSLVLAIER YVVVCK
hD2DR	104	RIHCDI FVTLDVMMCTASILNLCAIS IDRYTAVAM
hB2AR	103	NFWCEFWTSIDVLC VTASIELCVIA VDYFAITS
hACM1	95	TLACDLWLALDY VASNASVMNLLIS DFRYFSVTR
hOPRK	128	DVLC KIVISIDYNNMFTSIFTLT MMSVDRIYAVCH
hNK1R	102	LFYCKFHNFFPIA AVFASIYSMTA VAFDRYMAIIH
hTSHR	491	GPCCNTAGF FTVFASELSVYTLT VITLERWYAITF
	4.38	
bOPSD	149	GENHAIMGVAFT VMALACAAPPLV
hD2DR	148	SKRRVT VMISIVVWLSFTIS CPLLF
hB2AR	146	TKNKARV IILMVIVSGLTS FLPIQ
hACM1	138	TPRRALMIGLAW LVSFVLWAPAIL
hOPRK	171	TPLKAKI INICIWLLSSSVGISAIV
hNK1R	143	SATATKVVIC VIWVLALLAF PQGY
hTSHR	534	RLRHACAIMV GGVCCFLALLPLV
	5.35	
bOPSD	200	NESFVIYMFV HFIIPLVIFFCY QGLVFTVKEAAAQ
hD2DR	186	N PAFVYSSIVSFVVPFIVTLLVY IKIYIVLRRRRKV
hB2AR	196	NQ AYAIASSIVSFV VPLVIMVFVYSRVFQEAQRQLQKI
hACM1	185	QPIITFGTAM AAYFLPVTVMCTLY WRIYRETNRRREL
hOPRK	223	DLFMKICV FIFAFVIVLIIIVCY TLMLRLKSVRLLS
hNK1R	193	EKVYHICVT VLIYFLPLLVI GYAYTVVGITLWASEIPG
hTSHR	578	LALAYIVF VLTLNIVAFVIVCCY VKIYITVRNP----
	6.23	
bOPSD	240	SATTQKAEKEV TRMVIIMVIAFLIC WLPYAGVAFYIFT
hD2DR	361	RKLSQKEK KATQMLAIVLGVFICWLP FFITHILNIH
hB2AR	261	SSKFC LKEHKALKTGLI MGTF FLCWL FPFFIVNIVHVI
hACM1	353	KTFSLVKEK KAARTLSAILLAFIL TWTPYINIMVLVSTF
hOPRK	262	SREKDRNL RRLTRLVLVVAVFV VCWTPIHIFILVEAL
hNK1R	236	YHEQVSAKR KVVKMIVVVCTFAIC WLFPFFHIFLLPYI
hTSHR	612	QYNPGDK DTKIAKRM AVLIFTDFICMAPISFYALSAIL
	7.33	
bOPSD	286	IFMTIPAFFAK TSAVYNPVIYIMN KQFRNCMVTTLCC
hD2DR	406	VLYSA FTWLGYN SAVNPIIY TFNIE FRKAPFLKILHC
hB2AR	306	EVYILLN WIGYVNSGFN PLIYCRS-PDFRIAFQELLCL
hACM1	398	TLWELGY WLCYVNSTIN PMCYALCNKAFRDTFRLLLLC
hOPRK	310	SSYFFC IALGYTNSSLNPILYA FLDENFKRCFRDFCFP
hNK1R	285	QVYLAIM WLAMSSTMYNP IYCC LNDR FRFGFKHAFRC
hTSHR	658	NSKILLV LFYPLNSCANPFLYAIFT KAFQRDVFILLSK

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.