

Amino acid sequence alignment of vertebrate chemokine receptors.

Amino acid sequences were aligned by using MUSCLE with gap open and extension penalty of 8 and 2, respectively. Conserved TxP, DRY, CWxP, and NPxxY(x)5,6F motifs are indicated with red letters. Letters highlighted with green and gray colors are the most conserved residues in each transmembrane region and the other evolutionary conserved residues, respectively.

The cysteine residues that are assumed to be involved in disulfide bonds are highlighted with blue colors. Helix regions are underlined in human CXCR1.

(MUSCLE: Edgar, R. C. 2004. MUSCLE: multiple sequence alignment with high accuracy and high throughput. Nucleic Acids Res. 32:1792-1797)

Species:

hsa, *Homo sapiens* (human); mus, *Mus musculus* (mouse); bta, *Bos taurus* (cow); laf, *Loxodonta africana* (elephant); mdo, *Monodelphis domestica* (opossum); meu, *Macropus eugenii* (wallaby); can, *Oryctolophus anatinus* (platypus); gga, *Gallus gallus* (chicken); tgu, *Taeniopterygia guttata* (zebra finch); apl, *Anas platyrhynchos* (duck); aca, *Anolis carolinensis* (anole lizard); xtr, *Xenopus tropicalis* (Xenopus); xlz, *Xenopus laevis*; dre, *Danio rerio* (zebrafish); ola, *Oryzias latipes* (medaka); tnl, *Tetraodon nigroviridis* (Tetraodon); tru, *Takifugu rubripes* (Fugu); gac, *Gasterosteus aculeatus* (stickleback); cmi, *Callorhinchus milii* (elephant shark); pma, *Petromyzon marinus* (sea lamprey)

Amino acid sequences of *Xenopus laevis* and *Takifugu rubripes* (Fugu) were used to complement those of the *Xenopus tropicalis* (Xenopus) and *Tetraodon nigroviridis* (Tetraodon), respectively.

Genome sequence versions:

Human, GRCh37, Feb 2009; Mouse, NCBI37, Apr 2007; Cow, IM3.1, Nov 2009; Elephant, lowAff3 Jul 2009; Opossum, macDomb, Oct 2006; Wallaby, Meu\_1.0, Dec 2008; Platypus, QNNA5, Dec 2005

Chicken, GalGal4, Nov 2011; Zebra finch, TaenGut3.2.4, Aug 2008; Duck, BGI\_duck\_1.0, Apr 2013; Anole lizard, AnoCar2.0, May 2010; Xenopus, JGI 4.2, Nov 2009

Medaka, HdR, Oct 2005; Stickleback, BRAD S1, Feb 2006; Zebrafish, Zv9, Apr 2010; Tetraodon, TETRAZOO 8.0, Mar 2007; Elephant shark, whole genome shotgun sequences9; Sea lamprey, Pmarinus\_7.0, Jan 2011



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