

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
B2RU80	PTPRB_MOUSE	Mus musculus	Receptor-type tyrosine-protein phosphatase beta	25.685855	NaN	T1982	39627609	MLRHGALTALWITLSVVOQTGVAEQV KCNFTLLESRVSSLSASIQRWTFASP CNFSLIYSSDTS GPMWCHPIRIDNFT YGCNPKDLQAGTVYNFRIVSLDGEE STLVLQTDPLPPARFEVNRKASTT LQVRWTPSSGKVS WYEVQLFDHNN QKIQEVQVQESTTWSQYTFNLNTEG NSYKVAITAVS GEKRSFPVYINGSTV PSPVKDLGISPNPNLSLLISWSRSGSN VEQYRLVLMDKGAIQDNTNVDRRDT SYAFHELTPGHLYNLTIVTMASGLQ NSRWKLVRTAPMEVSNLKVTNDGR LTSLNVKWKQPPGDVDSYSITLSHQ GTIKESKTLAPPVTEQFKDLVPGRL YQVTISCSIGELSAEKSAAGRTPPEK VRNLVSYNEIWMKSFVNWTPPAG DWEHYRIVLFNESLVLNNTTVGKEE THYALDGLELIPGRQYIEIVIVESGN LRNSERCQGRTPVLA VLQVRVKHAN ETSLGITWRAPLGEWEKYIISLMDRE LLVIHKSLSKDAKEFTFTDLMPPGRN YKATVTSMSGDLKQSSSIKGRTPVA QVTDLHVNNQGMTSSLFTNWTKAL GDVEFYQVLLIHENVVVKNESVSSD TSRYSFRALKPGSLYSVVVTVSGGI SSRQVVAEGRTVPSSVSGVTVNNNSG RNDYLSVSWLPAPGEVDHYVVSLSH EGKVDQFLIIAKSVSECSFSSLTPGR LYNVTVTTKSGNYASHSFTEERTVP DKVQGISVNSARS DYLVKVSWWHAT GDFDHYEVTIKNRESFIQTKTIPKSE NECEFIELVPGRLYSVTVSTKSGOYE ASEQGTGRTIPEPVKDLTLLNRSTED LHVTWSRANGDVQYEVQLLFNDM KVFPPIHLVNTATEYKFTALTPGRHY KILVLTISGDVQOSAFIEGLTVPSTVK NIHISANGATDRMLMVTWSPGGGDVD SYVVS AFRQDEKVD SQTIPKHASEH TFHRLEAGAKYRIAVSVSGSLRNQI DALGQTVPASVQGVVAANAYSSNSL TVSWQKALGVAERYDILLNENGLL LSNVSE PATARQH K FEDLTPGKKYK MQILTVSGGLFSKESQAEGRTPPAA VTNLRITENSSRYLSFGWTASEGELS WYNIFLYNPDRTLQERAQVDPLVQS FSFQNLQGRMYKMVIIVTSHGELSN ESFIFGRTPVAAVNHKLGSHRNTTD SLWFSWSPASGDFDFYELILYNPNG TKKENWKEKDVTEWRFQGLVPGRK YTLVYVTHSGDLSNKVTGEGRTAPS PPSLLSFADVANTSLAITWKGPPDW TDYDNFELQWFPGDALTIFNPYSSR KSEGRIVYGLHPGRSYQFSVKTVSGD SWKTYSKPISGSRVTRKPKIQNLHCR PQNSTAIACSWIPPDSDFDGYSIECR KMDTQEIIEFSR KLEKEKSLNIMML VPHKRYLVSIVQSAGMTSEVVES TITMIDRPPQPPHIRVNEKDVLSKS SINFVNC SWFSDTNGAVKYFAVVV READSMDELKPEQHPLPSYLEYRH NASIRVYQTN YFASKCAESPDSSSKS FNIKLGAE MDSLGGKCDPSQKFC GPLKPHTAYRISIRAF TQLFDEDLKE FTKPLYSDTFFSMPITTESEPLFGVIE GVSAGLFLIGMLVALVAFFICRQKAS HSRERPSARLSIRDRPLSVHLNLG QKGNRKTSCPIKINQFEGHFMKLQA DSNYLLSKEYEDLKDVGRSQSCDIAL LPENRGKNRYN NLPYDASRVKLCN VDDDP CSDYINASYIPGNFRREYIA TQGPLPGTKDDFWKMAWEQNVHNI VMVTVQCVKGRVKCDHYWPAQDQD LYYGD LILQM VSES VLP EW TIREFKI CSEEQ LDAHRLIRHFHYTVVDPDHGV PETTQSLIQFVRTVRDYINRSPGAGP TVVHCSAGVGRGTGFVALDRILQQL	False	False	2.148	1.908	2.124	1.451	1.044	3.575	2.461

