

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
B0V2N1	PTPRS_MOUSE	Mus musculus	Receptor-type tyrosine-protein phosphatase S	24.474581	NaN	NaN	33300544	MAPTWSPSVSVVSGPVGFLFVLLAR GCLAEPPRFIREPKDQIGVSGGVAS FVCQATGDPKPRVTWNKKGKKVNS QRFETIDFDESSGAVLRIQPLRTPRD ENVYECVAQNSVGEITIHAKLTVLRE DQLPPGFPNIDMGPQLKVVVERTRTA TMLCAASGNPDPEITWFKDFLPVDP SASNGRIKQLRSGALQIESSEETDQG KYECVATNSAGVRYSSPANLYVRVR RVAPRFSILPMSHEIMPGGNVITCV AVGSPMPYVKWMQGAEDLTPEDDM PVGRNVLELTDVKDSANYTCVAMSS LGVIEAVAQITVKS LPAKGTVPVTE NTATSITVTWDSGNPDPVSYVIEYK SKSQDGPYQIKEDITTRYSIGGLSPN SEYEIWVSAVNSIGQPPSESVVTRT GEQAPASAPRNVQARMLSATTMIVQ WEEPVEPNGLIRGYRVYITMEPEHP VGNWQKHNVDDSLTTVGSLEDE TYTVRVLAFTSVGDGPLSDPIQVKTQ QGVPGQPMNLRAEAKSETSIGLSWS APRQESVIKYELLFREGDRGREVGRT FDPTTAFVVEDLKPNTYAFRLAARS PQGLGAFTAVVRQRTLQAKPSAPPQ DVKCTSLRSTAILVSWRPPPEPTHN GALVGYSVRYRPLGSEDPDPKEVNN IPPTTTQILLEALEKWTEYRVTAVAYT EVGPGPESSVVRTDEDVPSAPPRK VEAEALNATAIRVLWRSPTPGRQH QIRGYQVHYVRMEGAEARGPPRIKDI MLADAQEMVITNLQPETAYSITVAAY TMKGDGARSKPKVVVTKGAVLGRPT LSVQQTPEGSLARWEPPADAEDP VLGYRLQFGREDAAPATLEAAWER RFAAPAHKGATYVFLAARGRAGLG EAAAAALSIPEDAPRGFPQILGAAGN VSAGSVLLRWLPPVPAERNGAIKYT VSVREAGAPGATETELAAAAQPGA ETALTLRGLRPETAYELRVRATRRG PGPFSPPLRYRLARDPVSPKNFKVK MIMKTSVLLSWEFDPNYSPTPYKI QYNGLTLDVDGRTTKKLITHLKPHT FYNFVLTNRGSSLGLQQTVTARTA FNMLSGKPSVAPKPDNDGFIVVYLP DGQSPVTQNYFIVMVPLRKSRRGGQ FPVLLGSPEDMDLEELIQDISRLQRR SLRHSRQLEVP RPYYAARFSILPAVF HPGNQKQYGGFDNRGLEPGHRYVL FVLAVLQKNEPTFAASPFSDPFQLD NPDQPQIVDGEELIWIWVIGPVLAVVF IICVIAILLYKNKPDSKRKDESEPRK CLLNNADLAPHHKDPVEMRRINF QTPGMLSHPPIPITDMAEHMERLKA NDSLKLSQEYESIDPGQOFTWEHSN LEANKPKNRYANVIAYDHSRVLQPL EGIMGSDYINANYVDGYRRQNAYIA TQGPLPETFGDFWRMVWEQRSATV VMMTRLEEKSRKCDQYWPNRGTE TYGFIQVTLTDMELATFCVRTFSLH KNGSSEKREVRHFQFTAWPDHGVP EYPTPFLAFLRRVKTCNPPDAGPIVV HCSAGVGRGTCFVIDAMLERIKTEK TVDVYGHVTLMRSQRNYMVQTEDQ YGFIEALLEAVGCGNTEVPARSLYT YIQKLAQVEPGEHVTGMELEFKRLA SSKAHTRFITASLPCNKFKNRLVNI LPYESSRVCLQPIRGVEGSDYINASF DGYRQKAYIATQGLAETTEDFWR ALWENNSTIVVMLTKLREMGREK HOYWPAERSARYQYFVVDPMAYEN MPQYLREFKVTDARDGQSRVTRQF QFTDWPEQGAPKSGEGFIDFIGQVH KTKEQFGQDGPISVHCSAGVGRGTV FITLSIVLERMRYEGVVDIFQTVKVL RTQRPAMVQTEDEYQFCQAAYEYL GSFDHYAT	False	True	2.945	1.734	1.277	2.519	1.037	5.0	2.581

