

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
Q64605	PTPRS_RAT	Rattus norvegicus	Receptor-type tyrosine-protein phosphatase S	23.439218	NaN	NaN	38843836	MAPTWRPVSVVVGVGLFVLLAR GCLAEPPRFIREPKDQIGVSGGVAS FVCQATGDPKPRVTWNKKGKKNVNS QRFETIDFDESSGAVLRIQPLRTPRD ENVYECVAQNSVGEITVHAKLTVLR EDQLPPGFPNIDMGQPLKVVVERTRT ATMLCAASGNPDPEITWFKDFLPVD PSASNGRIKQLRSGALQIESSEETDQ GKYECVATNSAGVRYSSPANLYVRV RRVAPRFSILPMSHEIMPGGNVNIT CVAVGSPMPYVVKWQGAEDLTPED DMPVGRNVLELTDVKDSANYTCVA MSSLGVIEAVAQITVKSLPKAPGTPV VTENTATSITVTWDSGNPDPVSYVI EYKSKSQDGPYQIKEDITTRYSIGGL SPNSEYEIWVSAVNSIGQGPPESEV TRTGEQAPASAPRNVQARMLSATTM IVQWEEPVEPNGLIRGYRVYYTMEP EHPVGNWQKHNVDDSLTTVGSLL EDETYTVRVLAFSTVGDGPLSDPIQV KTQQGVPGQPMNLRAEAKSETSIGL SWSAPRQESVIKYELLFREGDRGRE VGRTFDPTTAFVVEDLKPNTYAFRL AARSPQGLGAFTAVVRQRTLQAKPS APPQDVKCTSLRSTAILVSWRPPPE THNGALVGYSVRYRPLGSEDDPKE VNNIPPTTQILLEALEKWTEYRVTA VAYTEVGGPESSPVVVRTDEDVPSA PPRKVEAEALNATAIRVLWRSPTPGR QHGGIRGYQVHYVRMEGAEARGPP RIKDIMLADAQEMVITNLQPETAYSI TVAAAYTMKGDGARSKPKVVVTKGAV LGRPTLSVQQTPEGSLARWEPPAD AAEDPVLGYRLQFGREDAAPATLEL AAWERRFAAPAHKGATYVFRLAARG RAGLGEESAALSIPEDAPRGFPQIL GAAGNVSAGSVILRWLPPVPAERN AIIKYTVSVREAGAPGPATETELAAAA QPGAETALTQGLRPETAYELRVRA HTRRGPGFSPPLRYRLARDPVSPK NFKVKMIMKTSVLLSWEFPDNYNS PTPYKIQYNGLTLDVDGRTTKKLITH LKPHTFYNFVLTNRGSSLGGLQQT TARTAFNMLSGKPSVAPKPDNDGSI VVYLPDQSPVTVQNYFIVMVPLRK SRGGQFPILLGSPEDMDLEELIQDLS RLQRRSLRHSRQLEVPRIYAAAFSI LPAVFHHPGNQKQYGGFDNRGLEPG HRYVLFVLAFLQKNEPTFAASPFSDP FQLDNDPDPPIVDGEEGLIHWVGPV AVVFIICVIAILLYKNKPSKRKDEP RTKCLLNADLAPHHPKDPVEMRRI NFQTPGMLSHPPIPITDMAEHMERL KANDSLKLSQEYESIDPGQFTWEH SNLEANKPKNRYANVIAYDHSRVIL QPLEGIMGSDYINANYVDGYRRONA YIATQGPLPETFGDFWRMVWEQRSA TVVMMTRLEEKSRVKCDQYWPNRG TETYGFIQVTLDDTMELATFCVRTFS LHKNGSSEKREVRHFQFTAWPDHG VPEYPTPFLAFLRRVKTCPNDAGPV VVHCSAGVGRGCFVIDAMLERIRT EKTVDVYGHVTLMRSQRNYMVQTE DQYSFIHEALLEAVGCGNTEVPARSL YTYIQKLAQVEPGEHVTGMELEFKR LASSKAHTRFITASLPCNKFKNRLV NILPYESSRVCLQPIRGVEGSDYINA SFIDGYRQQKAYIATQGPLAETTEDF WRALWENNSTIVVMLTKLREMGRE KCHQYWPAERSARYQYFVVDPMAE YNMPQYILREFKVTDARDGQSRTVR QFQFTDWPEQGAPKSGEGFIDFIGQ VHKTKEQFGQDGPISVHCSAGVGRT GVFITLSIVLERMRVYEGVVDIFQTVK VLRTQRPAMVQTEDEYQFCFQAAL	False	True	1.495	1.788	1.392	1.333	1.036	5.0	2.22

