

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
B9EKR1	PTPRZ_MOUSE	Mus musculus	Receptor-type tyrosine-protein phosphatase zeta	33.64034	NaN	S572;S576;S645;S647;T1681;T1684;S2052	33300544;22645316	MRILQSFACVQLLCLCRLDWAYGY YRQQRKLVEIEIGWSYTGALNQKNW GKKYPICNSPKQSPINIDELTQVNV NLKCLKFQGWKASLENTFIHNTGK TVEINLTNDYYLSGGLSEKVFKASKI TFHWGKCNVSSEGESEHSLEGQKFP LEMQVYCFDADRFSFEEAVKGGKR LRALSILFEVGVENLDYKAIDGTES VSRFGKQAALDPFVLQNLNPNSTDK YYIYNGSLTSPPCDTDTVEWIVFKDTV SISESQLAVFCEVLTMQQSGYVMLM DYLQNNFREQQYKFSRQVFSYTGK EEIHEVVCSEFENVOADPENYTSLL VTWERPRVVYDAMIEKFAVLYQPLA GNDQAKHEFLTDGYODLGAILNLL PNMSYVLQIVAVCSNGLYGKYSQDLI VDMPTEDAELDFPELIGTEEIKKEE EYKDNNEEDTGLNPRDVSVINQIRK KEPQVSTTTHYNHMGTKYNEAKTN RSPTRGSEFSGKSDVPNTSPNSTSQ HVAEFETERGISLPSQTGTLNPPHN VEGTSASLNSGSKTLFIFQMNLSG TAESLNTVPITEYKEVSADVSEENF LTDFKLDTGADSSGSSPSTSTVPFS SDNLSHGYSDDMPEAITVDLKPFG STRNAPEDSAPSGSEESLKDPSLEGS VWFFPGSTDLTQSETGSGRESFLQV NSTDIQIDESRETTEFSPDATVSQD PSVTDMGMPHYSTFAYLPTEVTPQA FTPSSRPLDLAPTINILHSQTTQPVY NGETPLQPSYSSEVFPLATPLLLDNQ TLNTPAASSSDSALHATPVSPSVGV SFESILSSYDDAPLPPFSASFSEM FRHLHTVSQTLQVTSAAERDELSL HASLLVARGDLLEPSLVQYSDVAS HQATTRAADTLGFGSESAVFYKTS MVSQIESPRSDVMHAYSSGPEPSY TVEGSHHVPTVSYSSAMPLHGSVDV SDQGSLLINPSHISMPESSFITPTASL LQPPALSGDGEWGSASSSELLLP DADGLRTLNISSPVSAEFTYTSVF ADGIKPLSKSEMMYGNETELKMSSF SDMAYPSKSTVVPKMSDVVHKWSE SLKETSVSISMKSVFPESLVYPTTK GFEEQVSHVPEIIFPVQPTHASQAS GDTWLKPGLSANSEAAFSDTASREV VHPSTQPLLYEATPFNTEALLQPSF QASDVDTLKKTALPSVSDPILAGTP QVEQSSSVSHPMASESGSSESML HFTSVPILDISPVKVHSTPLQGLTVP HSSKCFSEQGLLKSKSPQVLPFLFS NDEFFQSAHLQVQAYPPKGRHAFV TPVLSIDEQNTLINKLVYSEDIFSST EISITDKVLTGLPTLASDVLSSDTHSV PLGSGPISLTMVSPNRDSDVTTAKLL LPSTATSKLTQSARSDADLVGGGED GDDYDDDDYDDIDRGRFPVNCMS CLPYRESREKVMNDSDTQESSLVDQ SDPISPLLFENTEEENGGTGVTRVDK SPPPSMLPQNHNKGKEDSDIQMGS AVLPHTPGSKAWAVLTSDEESGGQ GTSDSLNDNETSTDFSPDVNEKDT DGVLETDGTGIAPGSPRSSTPSVTSG HSGVNSSEAEASNSHESRIGLAE GLESEKKAIVPLVIVSALTFICLVVLV GILYWRKCFQTAHFYLEDNTSPRVI STPPTPIFISDDIGAIPKHFPHKHAVD LHASNGFTEEFETLKEFYQEVQVQCT ADLGITADSSNHPDNKHKNRVYVIV AYDHSRVKLTQLAEKDGKLDYINA NYVDGYNRPKAYIAAQGPLKSTAED FWRMIWEHNVEVIVMITNLVEKGR RKCDQYVPTDGSEEGSFLVNQKSV QVLAYYTVRNFTLRNKLKKGSKG RSSGRLVTQYHYTQWPDMPVPEYSL PVLAFVRKAAQAKRHAVGPVVHCS AGVGRGTYYVLDLMLQIQHEGTV NIFGFLKHRSQRNYLVQTEEQYVFI HDTLVEAILSKETEVDPDSHIHSYVNT LLIPGPTGKTKLEKQFQLLSQSNILQ	False	True	1.486	2.064	1.672	1.744	1.377	5.0

SDYSTALKQCNREKNRTSSIIIPVERS  
RVGISSLSGEGTDYINASYIMGYYS  
NEFIITQHPLLHTIKDFWRMIWDHN  
AQLVVMIPDGQNMAEDEFVYWPNK  
DEPINCESFKVTLMSEEHKCLSNEE  
KLIVQDFILEATQDDYVLEVRHFQCP  
KWPNPDSPIKTFELISIIKEEAANRD  
GPMIVHDEHGGVTAGTFCALTTLM  
HQLKENAMDVYQVAKMINLMRPG  
VFTDIEQYQFLYKVVLVSLVSTRQEEN  
PSTSLDSNGAALPDGNIAESLESV