

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
D3ZEH1	D3ZEH1_RAT	Rattus norvegicus	NaN	23.439218	NaN	NaN	38843836	MNLAANRTPRRRRFLPSPSLGQLL RVWGLLSLLPSPARVQAAEQRQVFQ VMEEQPPGTLVGTIPTRPGFTYRLSE SHALFAINSTGALYTTATIDRESLPS DVVNLVVLSSSPTYPTVVRVLRDLN DNAPVFPDPSPVVTFKEDSGSGRQVI LDTATDSDIGSNGVDHRSYRIVRGN EAGRFRLDITLNPSEGAFHLHLVSK GGLDREVTPQYQLLVEVEDKGEPKR RGYLQVNVTVQDINDNPPVFGSSHY QAGVPEDAVVGSSVLQVAAADADEG TNADIRYRLQDEGTPFQMDPETGLIT VREPLDFEARRQYSLTVQATDRGVP SLTGRAEALIQLLDVNDNDPVPVKFR YFPATSRYSVDENAQVGTVVALLTV TDADSPAANGNISVQILGGNEQRHF EVQRSKVPNLSLIKVASALDREIPIS YNLTVSVSDNSGAPPTAEVQARSSV ASLVIFVNDINDHPPVFEQQVYRVNL SEEVPPGSYVSGVSATDGDGSLNAN LRYIVSGNGLGWFFHISEHSGLVTTT AAGGLDRELASQIVLNISARDQGVH PKVSYAQLVVSVDVNDQKPVFSQP EGYEVSVVENAPTGTCELLVLGATDG DLGDNGTVRFSLQEAESDQRLFRLD PVGRLSTISSLDREEQAFYCLLILAT DLGSPQSSSTVQVNVSLLDINDNSP VFYVPQYFAHIQENEPGGSYVTTVSA TDPDMGPNGTVKYISAGDRSRFQI HAKSGVISTKMALDREEKTAYQLQIV ATDGGNLQSPSQAIIVTVLDTQDN PPVFSQAAYSFVVFENVALGYHVGS VSATTMDLNNANISYLITGQDRGMF AMNPVTGQLTTASVIDREEQSFYQL RVVASGGAVTGDVAVNITVKDLNDN APHFLQAVESIDAVENWQAGHSIFQ AKAVDPDEGVNGRVLYSLKQNPKNL FTINEQNGNISLLGLTDVHAGSYQV EIVASDMGVPQLSSSIILTVYVHDVN DNPPVFDQISYEVTLSESEPVNSRFF KVQALDKD SGANGEIAYAITDGNNG EAFGIFPDGQLYIKSELDRELDQDRYV LLVVASDRAVEPLSATVNVTVILEDV NDNRPLFNSTNYTFYFEEEQRAGSF VGKVASVDKDFGPNGEVRYAFEVAQ PDFELHAITGEITNTHKFDRESLMR RRGTAVFSFTVIATDQGLPOPLKDQA TVHVYMKDINDNAPKFLKDFYQATV SETATNLTVLRSASDVDEGNNGL IHYSILKGNRERQFSIDRFSGQVTLV GKLDYEATPAYSLLIQAVDSGTVPLN STCTLSIDILDENDNTPSPFKSTLFV DVLENMRIGELVSSVTATDSDSGVN ADLHYTITGNSNNHGTFSPNTGSIF LAKKLDFFETQSLYKLNITAKDQGRFP RSSTMSVVIHVRDFNDNPPSFPPGD IFKSIVENIPLGTSVISVTAHDPDADI NGQLSYAIIQQMPRGNHFSIDEVKG TIYTSAEIDREFANL FELTVKANDQA VPIETRRYALKNVTLVTDLNDNVPIF ISQNALAADPSAMIGSVLTTIMAADP DEGANGEVEYEIVNGD TDFTVDRY SGDLRVASALVPSQLIYNLIVSATDL GPERRKSTTELTVILQGLDGPVFTQT KYITILKEGEPITNVISIEAASPRGSE APVEYYIVSVRCEEKTVGRLFTIGRQ TGVIQTAAILDREQGA CLYLVDVYAI KSSAFPRTQRAEVEITLQDINDNPPV FPTDTLDTVEENIGDGSKIMQLTA MDADEGANALVYALISGADDSFRI DPESGDLIATKRLDREHRSKYSLLVR ADDGLQSSDMRINITISDVNDHTPR FSRPVYSFDIPEDTTPGSLVAAILATD	False	False	1.31	2.154	1.771	0.188	0.938	4.05	1.502

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RRLAVGSALKIQESLPVHIVANEPLQP  
FQCKCVPGYAGSWCEVDIDECLPAP  
CHNGGTCHNLVGGFSCSCSEGFTG  
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GKYCEKSVTPDTALSLEGKGRLDYH  
MSQSEKREYLLTQSIREATLEPFGV  
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CPQGVCKAGSPGGHVCVQSQGPD  
EISLPLWAVPAIVGSCATALALLVLSL  
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NSETIPSAPLASPEQIEHYDIDNASS  
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YGQALRTSSLHSACPTPNPLSRHSP  
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GTLEMHGDPCCQPGMFNYATRLGRR  
SKSPQAMASHGSRPGSRLKQPIAQIP  
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DREKPVVYTSRMPKLSQVNESDADD  
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NLLNWGPGFGHYVDVFKDLASLPE  
KAAGNEEGKSGAAKPAAKDGAEQY  
V