

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
P98161	PKD1_HUMAN	Homo sapiens	Polycystin-1	24.917859	NaN	S4166	28411811	MPPAAPARLALALGLGLWLGALAGG PGRGCGPEPCLCGPAPGAACRVN CSGRGLRTLGPALRIPADATALDVSH NLLRALDVGLLANLSALAELDISNN KISTLEEGIFANLFLNLEINLSGNPF ECDCLAWLPRWAEQQVRRVQPE AATCAGPGSLAGQPLLGIPLLDGCG EEYVACLPDNSSGTVAAVSFSAAHE GLLQPEACSAFCFSTGQGLAALSEQ GWCLCGAAQPSSASFACLSLCSGPP PPPAPTCRGPILLQHVFPASPGATLV GPHGPLASGQLAAAFHIAAPLVTATR WDFGDGSAEVDAAAGPAASHRYVLP GRYHVTAVLALGAGSALLGTDVQVE AAPAALELVCPSSVQSDSLDLSIQN RGGSGLEAAYSIVALGEEPAPARVHPL CPSDTEIFPGNGHCYRLVVEKAAWL QAQEQCQAWAGAALAMVDSPAVQR FLVSRVTRSLDVWIGFSTVQGVVEG PAPQGEAFSLESCQNWLPGEPPHAT AEHCVRLGPTGWCNTDLCSAPHSYV CELQPGGFPVQDAENLLVGPSPGDLQ GPLTPLAQDGLSAPHEPVEVMVFP GLRLSREAFLLTAEFGTQELRRPAQL RLQVYRLLSTAGTPENGSEPERSPD NRTQLAPACMPGGRWCPCGANICLPL DASCHPQACANGCTSGPGLPGAPYA LWREFLFSVPAGPPAQYSVTLHGQD VLMPLPGDLVGLQHDAGPGALLHCSP APGHPPRAPYLSANASSWLPPLPA QLEGTWACPACALRLLAATEQLTVL LGLRPNPGLRPLGRYEVRAEAVGNV SRHNLSCSFDVVPVAGLRVIYPAPR DGRLYVPTNGSALVLQVDSGANATA TARWPGGSVSARFENVCPALVATFV PGCPWETNDTLFSVVALPWLSEGEH VVDVVENSASRANLSLRVTAEEPIC GLRATPSPEARVLQGVLVRYSPVVEA GSDMVFRWTINDKQSLTFQNVVFN VIYQSAAVFKLSLTASNHVSNTVNY NVTVERMNRMQGLQVSTVPAVLSP NATLALTAGVLVDSAVEVAFLWTFG DGEQALHQFQPPYNESFPVDPDPSVA QVLVEHNVMHYAAPGEYLLTVLAS NAFENLTQQVPVSVRASLPSVAVGV SDGVLVAGRPVTFYPHPLSPGGVLY TWFDFGDSPLTQSQPAANHTYASR GTYHVRLEVNNTVSGAAAQADVRF EELRGLSVDMSLAVEQAPVVVSAA VQTDGNITWTFDMGDGTVLSGPEAT VEHVYLRANCTVTVGAASPAGHLA RSLHVLVFLVLELVREPAACIPTQPD ARLTAYVTGNPAHYLFDWTFGDGSS NTTVRGCPTVTHNFTRSGTFPLALV LSSRVNRAHYFTSICVEPEVGNVTLQ PERQFVQLGDEAWLVACAWPPFPYR YTWDFGTAAAPTRARGPEVTFIYRD PGSYLVTVTASNISAANDSALVEVQ EPVLVTSIKVNGSLGLELQQPFLFSA VGRGRPASLWLDGDDGWLEGPEV THAYNSTGDFTVRVAGWNEVSRSE AWLNVTVKRRVRGLVNASRTVVPL NGSVSFSSTLEAGSDVRYSWVLCDR CTPIPGGPTISYTFRSVGTFNHVTAE NEVGSAQDSIFVYVQLIEGLQVVGG GRYFPTNHTVQLQAVVRDGTNVSYS WTAWRDRGPALAGSGKGFSLTVLEA GTYHVQLRATNMLGSAWADCTMDF VEPVGWLMAASPMPAAVNTSVTSL AELAGGSGVVYTWLEEGLSWETSE PFTTHSFPTPLHLVMTAGNPLGS ANATVEVDVQVPVSLSIRASEPGGS FVAAGSSVPFWQLATGTNVSWCW AVPGGSSKRGPHVTMVFPDAGTFSI RLNASNAVSWVSATYNLTAEEPIVG	False	True	2.142	3.847	1.767	4.45	4.313	5.0	5.0

LVLWASSKVVAPGQVLVHFQILLAAG  
 SAVTFRLQVGGANPEVLPGPRFSHS  
 FPRVGDHVVSVRGKNHVSWAAQAV  
 RIVVLEAVSGLQVPCNCEPFIATGTE  
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 GLHAEQAFVGMKSDFLDSSKSLV  
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 LQLHNWLDNRSRAVLELTRYSPAV

