	UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochndrion	endoplasmic reticulum	golgi apparatus	plasm membr
0	Q8TCU6	PREX1_HUMAN	Homo sapiens	Phosphatidylinositol 3,4,5-trisphosphate-dependent Rac exchanger 1 protein	28.908624	T985;S987;S1382	S319;S1001;S1195;S1200	35132862;29351928	MEAPSGSEPGGDGAGDCAHPDPRA PGAAAPSSGPGPCAAARESERQLRL RLCVLNEILGTERDYVGTLRFLQSAF LHRIRQNVADSVEKGLTEENVKVLF SNIEDILEVHKDFLAALEYCLHPEPQ SQHELGNVFLKFKDKFCVYEEYCSN HEKALRLLVELNKIPTVRAFLLSCML LGGRKTTDIPLEGYLLSPIQRICKYPL LLKELAKRTPGKHPDHPAVQSALQA MKTVCSNINETKRQMEKLEALEQL QSHIEGWEGSNLTDICTQLLLQGTL LKISAGNIQERAFFLFDNLLVYCKRK SRVTGSKKSTKRTKSINGSLYIFRGRI NTEVMEVENVEDGTADYHSNGYTV TNGWKIHNTAKNKWFVCMAKTAEE KQKWLDAIIREREQRESLKLGMERD AYVMIAEKGEKLYHMMMNKKVNLI KDRRRKLSTVPKCFLGNEFVAWLLE IGEISKTEEGVNLGQALLENGIIHHV SDKHQFKNEQVMYRFRYDDGTYKA RSELEDIMSKGVRLYCRLHSLYTPVI KDRDYHLKTYKSVLPGSKLVDWLLA QGDCQTREEAVALGVGLCNNGFMH HVLEKSEFRDESQYFRFHADEEME GTSSKNKQLRNDFKLVENILAKRLLI LPQEEDYGFDIEEKNKAVVVKSVQR GSLAEVAGLQVGRKIYSINEDLVFLR PFSEVESILNQSFCSRRPLRLLVATK AKEIIKIPDQPDTLCFQIRGAAPPYVY AVGRGSEAMAAGLCAGQCILKVNGS NVMNDGAPEVLEHFQAFRSRREEA LGLYQWIYHTHEDAQEARASQEAST EDPSGEQAQEEDQADSAFPLLSLGP RLSLCEDSPMVTLTVDNVHLEHGVV YEYVSTAGVRCHVLEKIVEPRGCFGL TAKILEAFAANDSVFVENCRRLMAL SSAIVTMPHFEFRNICDTKLESIGQR IACYQEFAAQLKSRVSPPFKQAPLEP HPLCGLDFCPTNCHINLMEVSYPKT TPSVGRSFSIRFGRKPSLIGLDPEQG HLNPMSYTQHCITTMAAPSWKCLPA AEGDPQGQGLHDGSFGPASGTLGQ EDRGLSFLLKQEDREIQDAYLQLFTK LDVALKEMKQYVTQINRLLSTITEPT SGGSCDASLAEEASSLPLVSEESEM DRSDHGGIKKVCFKVAEEDQEDSGH DTMSYRDSYSECNSNRDSVLSYTSV RSNSSYLGSDEMGSGDELPCDMRIP SDKQDKLHGCLEHLFNQVDSINALL KGPVMSRAFEETKHFPMNHSLQEF KQKEECTIRGRSLIQISIQEDPWNLP NSIKTLVDNIQRYVEDGKNQLLLALL KCTDTELQLRRDAIFCQALVAAVCTF SKQLLAALGYRYNNNGEYEESSRDA SRKWLEQVAATGVLLHCQSLLSPAT VKEERTMLEDIWVTLSELDNVTFSF KQLDENYVANTNVFYHIEGSRQALK VIFYLDSYHFSKLPSRLEGGASLRLH TALFTKVLENVEGLPSPGSQAAEDL QQDINAQSLEKVQQYYRKLRAFYLE RSNLPTDASTTAVKIDQLIRPINALDE LCRLMKSFVHPKPGAAGSVGAGLIPI SSELCYRLGACQMVMCGTGMQRST LSVSLEQAAILARSHGLLPKCIMQAT DIMRKQGPRVEILAKNLRVKDQMPQ GAPRLYRLCQPPVDGDL	True	True	5.0	3.251	1.35	1.158	1.076	5.0