

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	extra region
Q96QK1	VPS35_HUMAN	Homo sapiens	Vacuolar protein sorting-associated protein 35	18.679725	NaN	S7;S783;T791	33214551;23301498;32870666;35138101;34019948;30397120;26853435;32119511;34725712;35008409;38665916	MPTTQQSPQDEQEKLLEDAIQAVKV QSFQMKRCLDKNKLMALKHASN MLGELRTSMLSPKSYELYMAISDE LHYLEVYLTDEFAGRKVADLYELV QYAGNIIPRLYLLITVGVVYVKSFPQS RKDILKDLVEMCRGVQHPLRGLFLR NYLLQCTRNLDPDEGEPTDEETTGD SDSMDFVLLNFAEMNKLWVRMQH QGHSRDREKRERERQELRILVGTNL VRLSQLEGVNVERYKQIVLTGILEQV VNCRDALAEYLMECHIQVFPDEFH LQTLNPFRLRACAEHLQNVNVKNIIIA LIDRLALFAHREDGPGIPADIKLFDIF SQQVATVIQSRQDMPSEDVVSLOVS LINLAMKCYPRVDYVDKVLTTVEI FNKLNLEHIATSSAVSKELTRLLKIP VDTYNNILTVLKKHFFPLFEYFDYE SRKSMSCYVLSNVLDYNTEIVSQDQ VDSIMNLVSTLIQDQDPDQVDEDPDP EDFADEQSLVGRFIHLRSEDPPDQ YLILNTARKHFGAGGNQRIRFTLPPL VFAAYQLAFRYKENSKVDDKWEKKC QKIFSAHQTIKALAEALPLRLF LQGALAAGEIGFENHETVAYEFMSQ AFSLYEDEISDSKAQLAAITLIIGTFE RMKCFSEENHEPLRTQCALAASKLL KKPDQGRAVSTCAHLFWSGRNTDK NGEELHGGKRVMECLKKALKIANQ CMDPSLQVQLFIEILNRYIFYEKEN DAVTIQLNQLIQKIREDLPNLESSE ETEQINKHFHNTLEHLRRLRESPES EGPIYEGLLI	True	True	5.0	2.753	2.432	2.124	2.924	2.461	4.403