	UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochndr
0	Q9NZM3	ITSN2_HUMAN	Homo sapiens	Intersectin-2	15.158655	S126;T138;S139;S183;S184;S185;T186;S191;S192;S210;S216;S218;T220;S222;T223;S225;S230	S110;S210;S230;T553;T573;T882;S884;S889;T968	34725712;38665916;34019948;33214551;30379171;31492838;30059200;23301498;29237092;39531497;40307207;30620550;32119511;35138101;35132862;29351928;40596516;35254053	MMAQFPTAMNGGPNMWAITSEER TKHDRQFDNLKPSGGYITGDQARNF FLQSGLPAPVLAEIWALSDLNKDGK MDQQEFSIAMKLIKLKLQGQQLPVV LPPIMKQPPMFSPLISARFGMGSMP NLSIPQPLPPAAPITSLSSATSGTNLP PLMMPTPLVPSVSTSSLPNGTASLIQ PLPIPYSSSTLPHGSSYSLMMGGFG GASIQKAQSLIDLGSSSSTSSTASLSG NSPKTGTSEWAVPQPTRLKYRQKFN TLDKSMSGYLSGFQARNALLQSNLS QTQLATIWTLADVDGDGQLKAEEFIL AMHLTDMAKAGQPLPLTLPPELVPP SFRGGKQIDSINGTLPSYQKMQEEE PQKKLPVTFEDKRKANYERGNMELE KRRQALMEQQQREAERKAQKEKEE WERKQRELQEQEWKKQLELEKRLE KQRELERQREEERRKDIERREAAKQ ELERQRRLEWERIRRQELLNQKNRE QEEIVRLNSKKKNLHLELEALNGKH QQISGRLQDVRLKKQTQKTELEVLD KQCDLEIMEIKQLQQELQEYQNKLIY LVPEKQLLNERIKNMQFSNTPDSGV SLLHKKSLEKEELCQRLKEQLDALE KETASKLSEMDSFNNQLKCGNMDD SVLQCLLSLLSCLNNLFLLLKELRET YNTQQLALEQLYKIKRDKLKEIERKR LELMQKKKLEDEAARKAKQGKENL WKENLRKEEEEKQKRLQEEKTQEKI QEEERKAEEKQRKDKDTLKAEEKKR ETASVLVNYRALYPFEARNHDEMSF NSGDIIQVDEKTVGEPGWLYGSFQG NFGWFPCNYVEKMPSSENEKAVSP KKALLPPTVSLSATSTSSEPLSSNQP ASVTDYQNVSFSNLTVNTSWQKKSA FTRTVSPGSVSPIHGQGQVVENLKA QALCSWTAKKDNHLNFSKHDIITVL EQQENWWFGEVHGGRGWFPKSYV KIIPGSEVKREEPEALYAAVNKKPTS AAYSVGEEYIALYPYSSVEPGDLTFTE GEEILVTQKDGEWWTGSIGDRSGIF PSNYVKPKDQESFGSASKSGASNKK PEIAQVTSAYVASGSEQLSLAPGQLIL ILKKNTSGWWQGELQARGKKRQKG WFPASHVKLLGPSSERATPAFHPVC QVIAMYDYAANNEDELSFSKGQLIN VMNKDDPDWWQGEINGVTGLFPSN YVKMTTDSDPSQQWCADLQTLDTM QPIERKRQGYIHELIQTEERYMADLQ LVVEVFQKRMAESGFLTEGEMALIF VNWKELIMSNTKLLKALRVRKKTGG EKMPVQMIGDILAAELSHMQAYIRF CSCQLNGAALLQQKTDEDTDFKEFL KKLASDPRCKGMPLSSFLLKPMQRI TRYPLLIRSILENTPESHADHSSLKL ALERAEELCSQVNEGVREKENSDRL EWIQAHVQCEGLAEQLIFNSLTNCL GPRKLLHSGKLYKTKSNKELHGFLF NDFLLLTYMVKQFAVSSGSEKLFSS KSNAQFKMYKTPIFLNEVLVKLPTDP SSDEPVFHISHIDRVYTLRTDNINER TAWVQKIKAASEQYIDTEKKKREKAY QARSQKTSGIGRLMVHVIEATELKA CKPNGKSNPYCEISMGSQSYTTRTIQ DTLNPKWNFNCQFFIKDLYQDVLCL TLFDRDQFSPDDFLGRTEIPVAKIRT EQESKGPMTRRLLLHEVPTGEVWV RFDLQLFEQKTLL	True	False	4.351	1.547	False