	UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochndrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extr regi
0	Q8N201	INT1_HUMAN	Homo sapiens	Integrator complex subunit 1	24.902576	S995	S13;T83;S87;S307;S924;S1318;S1326;S1327;S1395	40596516;38253038	MNRAKPTTVRRPSAAAKPSGHPPPG DFIALGSKGQANESKTASTLLKPAPS GLPSERKRDAAAALSSASALTGLTKR PKLSSTPPLSALGRLAEAAVAEKRAI SPSIKEPSVVPIEVLPTVLLDEIEAAE LEGNDDRIEGVLCGAVKQLKVTRAK PDSTLYLSLMYLAKIKPNIFATEGVIE ALCSLLRRDASINFKAKGNSLVSVLA CNLLMAAYEEDENWPEIFVKVYIED SLGERIWVDSPHCKTFVDNIQTAFN TRMPPRSVLLQGEAGRVAGDLGAGS SPHPSLTEEEDSQTELLIAEEKLSPE QEGQLMPRYEELAESVEEYVLDMLR DQLNRRQPIDNVSRNLLRLLTSTCG YKEVRLLAVQKLEMWLQNPKLTRPA QDLLMSVCMNCNTHGSEDMDVISH LIKIRLKPKVLLNHFMLCIRELLSAH KDNLGTTIKLVIFNELSSARNPNNM QVLYTALQHSSELAPKFLAMVFQDL LTNKDDYLRASRALLREIIKQTKHEI NFQAFCLGLMQERKEPQYLEMEFK ERFVVHITDVLAVSMMLGITAQVKE AGIAWDKGEKRNLEVLRSFQNQIAA IQRDAVWWLHTVVPSISKLAPKDYV HCLHKVLFTEQPETYYKWDNWPPE SDRNFFLRLCSEVPILEDTLMRILVI GLSRELPLGPADAMELADHLVKRAA AVQADDVEVLKVGRTQLIDAVLNLC TYHHPENIQLPPGYQPPNLAISTLYW KAWPLLLVVAAFNPENIGLAAWEEY PTLKMLMEMVMTNNYSYPPCTLTD EETRTEMLNRELQTAQREKQEILAF EGHLAAASTKQTITESSSLLLSQLTS LDPQGPPRRPPPHILDQVKSLNQSL RLGHLLCRSRNPDFLLHIIQRQASSQ SMPWLADLVQSSEGSLDVLPVQCLC EFLLHDAVDDAASGEEDDEGESKEQ KAKKRQRQQKQRQLLGRLQDLLLGP KADEQTTCEVLDYFLRRLGSSQVAS RVLAMKGLSLVLSEGSLRDGEEKEP PMEEDVGDTDVLQGYQWLLRDLPR LPLFDSVRSTTALALQQAIHMETDP QTISAYLIYLSQHTPVEEQAQHSDLA LDVARLVVERSTIMSHLFSKLSPSAA SDAVLSALLSIFSRYVRRMRQSKEGE EVYSWSESQDQVFLRWSSGETATM HILVVHAMVILLTLGPPRADDSEFQA LLDIWFPEEKPLPTAFLVDTSEEALL LPDWLKLRMIRSEVLRLVDAALQDL EPQQLLLFVQSFGIPVSSMSKLLQFL DQAVAHDPQTLEQNIMDKNYMAHL VEVQHERGASGGQTFHSLLTASLPP RRDSTEAPKPKSSPEQPIGQGRIRVG TQLRVLGPEDDLAGMFLQIFPLSPDP RWQSSSPRPVALALQQALGQELARV VQGSPEVPGITVRVLQALATLLSSPH GGALVMSMHRSHFLACPLLRQLCQ YQRCVPQDTGFSSLFLKVLLQMLQW LDSPGVEGGPLRAQLRMLASQASAG RRLSDVRGGLLRLAEALAFRQDLEV VSSTVRAVIATLRSGEQCSVEPDLIS KVLQGLIEVRSPHLEELLTAFFSATA DAASPFPACKPVVVVSSLLLQEEEPL AGGKPGADGGSLEAVRLGPSSGLLV DWLEMLDPEVVSSCPDLQLRLLFSR RKGKGQAQVPSFRPYLLTLFTHQSS WPTLHQCIRVLLGKSREQRFDPSAS LDFLWACIHVPRIWQGRDQRTPQKR REELVLRVQGPELISLVELILAEAETR SQDGDTAACSLIQARLPLLLSCCCGD DESVRKVTEHLSGCIQQWGDSVLGR RCRDLLLQLYLQRPELRVPVPEVLLH SEGAASSSVCKLDGLIHRFITLLADT SDSRALENRGADASMACRKLAVAH PLLLLRHLPMIAALLHGRTHLNFQE FRQQNHLSCFLHVLGLLELLQPHVF RSEHQGALWDCLLSFIRLLLNYRKS SRHLAAFINKFVQFIHKYITYNAPAAI SFLQKHADPLHDLSFDNSDLVMLKS LLAGLSLPSRDDRTDRGLDEEGEEE	True	False	1.891	5.0	False	False	False	2.625	Fals

									SSAGSLPLVSVSLFTPLTAAEMAPYM KRLSRGQTVEDLLEVLSDIDEMSRR RPEILSFFSTNLQRLMSSAEECCRN LAFSLALRSMQNSPSIAAAFLPTFMY CLGSQDFEVVQTALRNLPEYALLCQ EHAAVLLHRAFLVGMYGQMDPSAQI SEALRILHMEAVM									