	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	extracellular region
0	Q6ZVL6	K154L_HUMAN	Homo sapiens	UPF0606 protein KIAA1549L	27.086674	T1646	NaN	28657654	MDHTASQNAQDLIGIPHLGVSGSST KWHSELSPTEGPHSAGSSTPGFLSP MAELSHPSPPPPALGSLLQLPDGSPS WSMLEVASGPASTQQIKAGVPGRVH NGVSLPTFKNTETATHEAEPPLFQT AESGAIEMTSRKLASATANDSANPL HLSAAPENSRGPALSAEHTSSLVPSL HITTLGQEQAILSGAVPASPSTGTAD FPSILTFLQPTENHASPSPVPEMPTL PAEGSDGSPPATRDLLLSSKVPNLLS TSWTFPRWKKDSVTAILGKNEEANV TIPLQAFPRKEVLSLHTVNGFVSDFS TGSVSSPIITAPRTNPLPSGPPLPSILS IQATQTVFPSLGFSSTKPEAYAAAVD HSGLPASASKQVRASPSSMDVYDSL TIGDMKKPATTDVFWSSLSAETGSL STESIISGLQQQTNYDLNGHTISTTS WETHLAPTAPPNGLTSAADAIKSQD FKDTAGHSVTAEGFSIQDLVLGTSIE QPVQQSDMTMVGSHIDLWPTSNNN HSRDFQTAEVAYYSPTTRHSVSHPQ LQLPNQPAHPLLLTSPGPTSTGSLQE MLSDGTDTGSEISSDINSSPERNAST PFQNILGYHSAAESSISTSVFPRTSSR VLRASQHPKKWTADTVSSKVQPTAA AAVTLFLRKSSPPALSAALVAKGTSS SPLAVASGPAKSSSMTTLAKNVTNK AASGPKRTPGAVHTAFPFTPTYMYA RTGHTTSTHTAMQGNMDTASGLLS TTYLPRKPQAMHTGLPNPTNLEMPR ASTPRPLTVTAALTSITASVKATRLPP LRAENTDAVLPAASAAVVTTGKMAS NLECQMSSKLLVKTVLFLTQRRVQI SESLKFSIAKGLTQALRKAFHQNDV SAHVDILEYSHNVTVGYYATKGKLVY LPAVVIEMLGVYGVSNVTADLKQHT PHLQSVAVLASPWNPQPAGYFQLKT VLQFVSQADNIQSCKFAQTMEQRLQ KAFQDAERKVLNTKSNLTIQIVSTSN ASQAVTLVYVVGNQSTFLNGTVASS LLSQLSAELVGFYLTYPPLTIAEPLEY PNLDISETTRDYWVITVLQGVDNSLV GLHNQSFARVMEQRLAQLFMMSQ QQGRRFKRATTLGSYTVQMVKMQR VPGPKDPAELTYYTLYNGKPLLGTAA AKILSTIDSQRMALTLHHVVLLQADP VVKNPPNNLWIIAAVLAPIAVVTVIIII ITAVLCRKNKNDFKPDTMINLPQRA KPVQGFDYAKQHLGQQGADEEVIPV TQETVVLPLPIRDAPQERDVAQDGST IKTAKSTETRKSRSPSENGSVISNES GKPSSGRRSPQNVMAQQKVTKEEA RKRNVPASDEEEGAVLFDNSSKVAA EPFDTSSGSVQLIAIKPTALPMVPPTS DRSQESSAVLNGEVNKALKQKSDIE HYRNKLRLKAKRKGYYDFPAVETSK GLTERKKMYEKAPKEMEHVLDPDS ELCAPFTESKNRQQMKNSVYRSRQS LNSPSPGETEMDLLVTRERPRRGIR NSGYDTEPEIIEETNIDRVPEPRGYS RSRQVKGHSETSTLSSQPSIDEVRQ QMHMLLEEAFSLASAGHAGQSRHQ EAYGSAQHLPYSEVVTSAPGTMTRP RAGVQWVPTYRPEMYQYSLPRPAYR FSQLPEMVMGSPPPPVPPRTGPVAV ASLRRSTSDIGSKTRMAESTGPEPAQ LHDSASFTQMSRGPVSVTQLDQSAL NYSGNTVPAVFAIPAANRPGFTGYFI PTPPSSYRNQAWMSYAGENELPSQ WADSVPLPGYIEAYPRSRYPQSSPSR LPRQYSQPANLHPSLEQAPAPSTAAS QQSLAENDPSDAPLTNISTAALVKAI REEVAKLAKKQTDMFEFQV	None	None	None	None	None	None	None	None	None