	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	Q9UM73	ALK_HUMAN	Homo sapiens	ALK tyrosine kinase receptor	21.366884	NaN	T1078;T1092;T1096;T1131;T1278;T1507;T1604	28510447	MGAIGLLWLLPLLLSTAAVGSGMGT GQRAGSPAAGPPLQPREPLSYSRLQ RKSLAVDFVVPSLFRVYARDLLLPPS SSELKAGRPEARGSLALDCAPLLRLL GPAPGVSWTAGSPAPAEARTLSRVL KGGSVRKLRRAKQLVLELGEEAILEG CVGPPGEAAVGLLQFNLSELFSWWI RQGEGRLRIRLMPEKKASEVGREGR LSAAIRASQPRLLFQIFGTGHSSLES PTNMPSPSPDYFTWNLTWIMKDSFP FLSHRSRYGLECSFDFPCELEYSPPL HDLRNQSWSWRRIPSEEASQMDLL DGPGAERSKEMPRGSFLLLNTSADS KHTILSPWMRSSSEHCTLAVSVHRH LQPSGRYIAQLLPHNEAAREILLMPT PGKHGWTVLQGRIGRPDNPFRVALE YISSGNRSLSAVDFFALKNCSEGTSP GSKMALQSSFTCWNGTVLQLGQAC DFHQDCAQGEDESQMCRKLPVGFY CNFEDGFCGWTQGTLSPHTPQWQV RTLKDARFQDHQDHALLLSTTDVPA SESATVTSATFPAPIKSSPCELRMSW LIRGVLRGNVSLVLVENKTGKEQGR MVWHVAAYEGLSLWQWMVLPLLD VSDRFWLQMVAWWGQGSRAIVAFD NISISLDCYLTISGEDKILQNTAPKSR NLFERNPNKELKPGENSPRQTPIFD PTVHWLFTTCGASGPHGPTQAQCN NAYQNSNLSVEVGSEGPLKGIQIWK VPATDTYSISGYGAAGGKGGKNTMM RSHGVSVLGIFNLEKDDMLYILVGQ QGEDACPSTNQLIQKVCIGENNVIEE EIRVNRSVHEWAGGGGGGGGATYV FKMKDGVPVPLIIAAGGGGRAYGAK TDTFHPERLENNSSVLGLNGNSGAA GGGGGWNDNTSLLWAGKSLQEGAT GGHSCPQAMKKWGWETRGGFGGG GGGCSSGGGGGGYIGGNAASNNDP EMDGEDGVSFISPLGILYTPALKVME GHGEVNIKHYLNCSHCEVDECHMD PESHKVICFCDHGTVLAEDGVSCIVS PTPEPHLPLSLILSVVTSALVAALVLA FSGIMIVYRRKHQELQAMQMELQSP EYKLSKLRTSTIMTDYNPNYCFAGKT SSISDLKEVPRKNITLIRGLGHGAFG EVYEGQVSGMPNDPSPLQVAVKTLP EVCSEQDELDFLMEALIISKFNHQNI VRCIGVSLQSLPRFILLELMAGGDLK SFLRETRPRPSQPSSLAMLDLLHVA RDIACGCQYLEENHFIHRDIAARNC LLTCPGPGRVAKIGDFGMARDIYRAS YYRKGGCAMLPVKWMPPEAFMEGI FTSKTDTWSFGVLLWEIFSLGYMPY PSKSNQEVLEFVTSGGRMDPPKNCP GPVYRIMTQCWQHQPEDRPNFAIIL ERIEYCTQDPDVINTALPIEYGPLVEE EEKVPVRPKDPEGVPPLLVSQQAKR EEERSPAAPPPLPTTSSGKAAKKPTA AEISVRVPRGPAVEGGHVNMAFSQS NPPSELHKVHGSRNKPTSLWNPTY GSWFTEKPTKKNNPIAKKEPHDRGN LGLEGSCTVPPNVATGRLPGASLLLE PSSLTANMKEVPLFRLRHFPCGNVN YGYQQQGLPLEAATAPGAGHYEDTIL KSKNSMNQPGP	False	True	2.716	3.193	2.42	2.642	2.158	5.0	4.647