	UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochndrion	endo retic
0	Q6P4R8	NFRKB_HUMAN	Homo sapiens	Nuclear factor related to kappa-B-binding protein	39.012146	S746;S749;T750;S752;S757;S795;S799;S803;T841;T843;T845;T862;T863;T878;T880;S881;S890;T894;S895;S900;S905;S1027;S1030;S1034;T1045;T1051;S1067;S1080;S1116;S1130;T1141;S1146;S1150;T1151;S1154;S1156;T1157;T1161;S1168;T1169;T1170;S1173;T1174;S1175;T1185;S1189;T1224;T1225;T1263;S1267;T1273;S1275;S1277;S1278;S1282;T1283;T1287;T1288	S228;S298;S351;S1022;S1291	28657654;31492838;34846842;23301498;37340703;34019948;34725712;37217939;20305658;32574038;36240223;21740066;35254053;29237092;29351928;20068230;35138101;30620550;30059200;30379171;22661428;31637018;35132862;33214551;27655845;35289036;32119511;38665916	MDSLDHMLTDPLELGPCGDGHGTR IMEDCLLGGTRVSLPEDLLEDPEIFF DVVSLSTWQEVLSDSQREHLQQFLP QFPEDSAEQQNELILALFSGENFRF GNPLHIAQKLFRDGHFNPEVVKYRQ LCFKSQYKRYLNSQQQYFHRLLKQI LASRSDLLEMARRSGPALPFRQKRP SPSRTPEEREWRTQQRYLKVLREVK EECGDTALSSDEEDLSSWLPSSPAR SPSPAVPLRVVPTLSTTDMKTADKVE LGDSDLKIMLKKHHEKRKHQPDHP DLLTGDLTLNDIMTRVNAGRKGSLA ALYDLAVLKKKVKEKEEKKKKKIKTI KSEAEDLAEPLSSTEGVAPLSQAPSP LAIPAIKEEPLEDLKPCLGINEISSSF FSLLLEILLLESQASLPMLEERVLDW QSSPASSLNSWFSAAPNWAELVLPA LQYLAGESRAVPSSFSPFVEFKEKTQ QWKLLGQSQDNEKELAALFQLWLE TKDQAFCKQENEDSSDATTPVPRVR TDYVVRPSTGEEKRVFQEQERYRYS QPHKAFTFRMHGFESVVGPVKGVF DKETSLNKAREHSLLRSDRPAYVTIL SLVRDAAARLPNGEGTRAEICELLKD SQFLAPDVTSTQVNTVVSGALDRLH YEKDPCVKYDIGRKLWIYLHRDRSEE EFERIHQAQAAAAKARKALQQKPKP PSKVKSSSKESSIKVLSSGPSEQSQM SLSDSSMPPTPVTPVTPTTPALPAIPI SPPPVSAVNKSGPSTVSEPAKSSSGV LLVSSPTMPHLGTMLSPASSQTAPS SQAAARVVSHSGSAGLSQVRVVAQP SLPAVPQQSGGPAQTLPQMPAGPQI RVPATATQTKVVPQTVMATVPVKAQ TTAATVQRPGPGQTGLTVTSLPATAS PVSKPATSSPGTSAPSASTAAVIQNV TGQNIIKQVAITGQLGVKPQTGNSIP LTATNFRIQGKDVLRLPPSSITTDAK GQTVLRITPDMMATLAKSQVTTVKL TQDLFGTGGNTTGKGISATLHVTSN PVHAADSPAKASSASAPSSTPTGTTV VKVTPDLKPTEASSSAFRLMPALGVS VADQKGKSTVASSEAKPAATIRIVQG LGVMPPKAGQTITVATHAKQGASVA SGSGTVHTSAVSLPSMNAAVSKTVA VASGAASTPISISTGAPTVRQVPVSTT VVSTSQAGKLPTRITVPLSVISQPMK GKSVVTAPIIKGNLGANLSGLGRNIIL TTMPAGTKLIAGNKPVSFLTAQQLQ QLQQQGQATQVRIQTVPASHLQQGT ASGSSKAVSTVVVTTAPSPKQAPEQQ	None	None	None	None	None	None