

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
P46013	KI67_HUMAN	Homo sapiens	Proliferation marker protein Ki-67	12.840854	T167;S289;S380;T772;T848;T852;T858;S859;T912;S951;S1736;S2344;S2588;S2738	S125;S128;S166;S264;S296;S308;T328;T347;S352;S357;S374;T401;S411;S538;T543;S579;S584;S648;T761;S859;T1017;S1071;T1091;S1098;T1111;S1131;T1139;S1142;T1167;S1169;T1176;T1193;S1207;T1233;S1253;S1256;T1261;T1298;T1315;T1327;S1329;T1335;T1355;S1376;T1383;S1386;T1420;T1437;S1496;T1503;S1506;T1540;T1552;T1557;T1569;S1571;S1617;S1679;S1689;T1719;S1721;S1740;T1747;T1764;T1784;T1801;S1815;T1841;S1861;S1864;T1869;T1897;T1906;T1923;S1937;T1963;S1983;T2028;T2065;S2072;T2085;S2105;T2113;S2116;S2135;T2146;T2163;T2203;S2223;T2231;T2233;S2239;T2259;S2261;T2268;T2285;T2325;T2328;T2333;S2344;T2352;T2389;S2395;T2406;S2420;T2426;T2446;S2466;S2505;S2528;S2588;S2638;S2708;S2827;S2828;S2838;S3041;S3128	33214551;32574038;35254053;30379171;35083852;34725712;38253038;35132862;30620550;26853435;32119511;33465208;30059200;37217939;34019948;34846842;23301498;20305658	MWPTRRLVTIKRSGVDGPHFPLSLSTCLFGRGIECDIRIQLPVVSKQHCKIEIHEQEAAILHNFSTNPTQVNGSVIDE PVRLKHGVDVITIDRSFRYENESLQN GRKSTEFPRKIREQEPARRVSRSSFS SDPDEKAQDSKAYSKITEGKVSQGNP QVHIKNVKEDSTADDSKDSVAQGT NVHSSEHAGRNGRANAADPISGDFK EISSVKLVSRYGELKSVPTTQCLDNS KNKNEPFWKLYESVKKELDVKSQKE NVLQYCRKSGLQTDYATEKESADGL QGETQLLVSRKSRPKSGGSGHVAE PASPEQELDQNKGGKRDVSVQTPS KAVGAFPLYEPAKMKTPVQVQQQ NSPKQHKNKDLTYTTGRRESVNLGKS EGFKAGDKTLTPRKLSTRNRTPAKV EDAADSATKPENLSSKTRGSIPTDVE VLPTETIHNPEPFLTLWLTOVERKIQ KDSLSKPEKLGTTAGQMCSGLPGLS SVDINNFQDSINESEGIPLKRRRVSF GGHLRPELFDENLPPNTPKRGAEAP TKRKSVMHTPPVVKKIIKEQPQPSG KQESGSEIHVEVKAQSLVISPPAPSP RKTPVASDQRRRSCKTAPASSKSKSQ TEVPKRGGKSGNLPKRVSISRSQ HDILQMICKRRSGASEANLIVAKS WADVVKLGAKQTQTKVIKHGPQRS MNRQRORPATPKKPVGEVHSQFST GHANSPCTIIIGKAHTEKVHVPARPY RVLNNFISNQKMDFKEDLSGIAEMF KTPVKEQPQLTSTCHIAISNSENLLG KQFQGTDSGEEPLLPTSESFQGNVF FSAQNAAKQPSDKCSASPLRRQCI RENGNVAKTPRNTYKMTSLETKTSD TETEPSKTVSTANRSGRSTEFNRNIQK LPVESKSEETNTEIVECILKRGQKAT LLQRRREGEMKEIERPFETYKENIEL KENDEKMKAMKRSRTWGQKCAPM SDLTDLKSLPDTELMKDTARGQNLL QTQDHAKAPKSEKGIKMKPCQSLQ PEPINTPTHTKQQLKASLGKVGVKE ELLAVGKFTRTSGETTHTHREPADG GKSIRTFKESPKQILDPAARVTGMKK WPRTPKEEAQSLEDLAGFKELFQTP GPSEESMTDEKTTKIACKSPPPESVD TPTSTKQWPKRSLRKADVEEFLAL RKLTPSAGKAMLTPKAGGDEKDIK AFMGTPVQKLDLAGTLPGSKRQLQT PKEKAQALEDLAGFKELFQTPGHTE ELVAAGKTTKIPCDSPQSDPVDTPTS TKQRPKRSIRKADVEGELLACRNL PSAGKAMHTPKPSVGEEDIIIFVGT PVQKLDLTENLTGSKRRPQTPKEEA QALEDLTGFKELFQTPGHTEEAVAA GKTTKMPCESSPPESADTPTSTRRQ PKTPLEKRDVQKELSALKKLTQTSGE THTTDKVPGGEDKSINAFRETAQKQ LDPAASVTGSKRHPKTEKAQPLED LAGLKELFQTPVCTDKPTTHEKTTKI ACRSQDPVDTPSSKPSKRSRSLRK VDVEEFFALRKRTPSAGKAMHTPK PAVSGEKNIYAFMGTPVQKLDLTEN LTGSKRRLQTPKEKAQALEDLAGFK

ELFQTRGHTTEESMTNDKTAKVACKS  
SQDPDPKNPASSKRRLKTSLGKVG  
KEELLAVGKLTQTSGETTHTHTPT  
GDGKSMKAFMESPKQILDSAAASLTG  
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PKQILDPAASVTGSRRLRTRKEKAR  
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PVEEESRRRRPRAPKEKAQPLEDLA  
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ESPPELVVDTTASTKRHLRTRVQKV  
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SRRRPRAPRESAQAIEDLAGFKDPAA  
GHTEESMTDDKTTKIPCKSSPELED  
TATSSKRRRPRTRAQKVEVKEELLAV  
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KRLRCMPAPEEIVEELPASKQORVAP  
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NKGISLRSRRQNKTEAEQQITEVFVL  
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