

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
E9PVX6	KI67_MOUSE	Mus musculus	Proliferation marker protein Ki-67	26.422241	T283;T797	S125;S128;S162;S250;S276;S277;S286;S287;T307;T316;S321;S337;S373;S498;S503;S588;T701;S1062;S1114;T1122;S1125;T1150;S1152;T1159;T1175;S1189;T1215;S1235;T1243;T1279;T1295;T1307;T1315;T1335;S1356;T1363;S1366;T1400;T1416;S1469;T1477;S1480;T1513;S1542;S1587;T1684;T1712;S1734;T1766;S1779;T1805;S1825;T1859;T1868;T1884;T1924;S1944;T1989;T2005;T2025;T2045;S2065;T2073;S2076;S2095;S2103;T2106;T2122;T2162;S2182;T2190;S2198;T2218;S2220;T2227;T2243;T2283;S2303;T2311;T2348;S2390;S2392;T2405;S2423;S2425;S2464;S2487;S2545;S2592;S2649;S2768;S2780;S2980;T3021;S3061	22645316;34887587;36852467	MASSAHLVTIKRSGDDGAHFPLSLS SCLFGRSIECDIRIQLPVVSKRHCKIE VKEQEAILYNFSSTNPTQVNGVTIDE PVRLRHGDIITIIDRSFRYEDGNHED GSKPTEFFPGKSLGKEPSRRASRDSF CADPDGEGQDTKASKMTASRRSFVH AKGLSADSPASDGSKNSVSDSSGH VEQHTGRNIVEPTSGDLFKKSRSTG SSYREPKSSPTQSLSNSNEKESPFEK LYQSMKEELDVKSQKSCRKSEPQPD RAAEEsRETQLLVSGRARAKSSGSTP VTAASSPKVGKIWTERWRGGMVVP QTSTETAKMKTPVRHSQQLKDEDSR VTGRRHSVNLDEGEAQVAVHKTVTP GKLATRQAAVEAGDVASPADTPEH SSSKKRSIPAKVEAPSAETQKRLSLT QRLVPGEEKTPKGSFSKPEKLATAAE QTCSGLPGLSSVDISNFGDSINKSEG MPMKRRRVsFGGHLRPELFDENLP PNTPLKRGETPTKRKSLGTHSPAVLK TIIKERPQSPGKQESPGITPPRTNDQ RRRSGRTSSGSKFLCETDIPKKAGRK SGNLPKRASISRSQHILQMICSKR RSGASEANLIVAKSWADVVKLGVKQ TQTKVAKHVPQKQTSKRQRRPSTPK KPTSNLHNQFTTGHANSPCTIVVGR AQIEKVSVPARPYKMLNMLNRKV DFSEDLsGLTEMFKTPVKEKQQQM SDTGSVLSNSANLSERQLQVTNSGD IPEPITTEILGEKVLsSTRNAAKQQSD RYSASPTLRRRSIKHENTVQTPKNV HNITDLEKKTpVSETEPLKTASSVSK LRRSRELRLTLVETMNEKTEAVLAE NTTARHLRGTFREQKVDQQVQDNE NAPQRCKESGELSEGSEKTSARRSS ARKQKPTKDLLGSQMVTQTADYAE LLSQGQGTIQNLEESMHMQNTSISE DQGITEKKVNIIVYATKEKHSPKTPG KKAQPLEGPAGLKEHFETPNPKDKP ITEDRTRVLCKSPQVTTENITTNTKP QTSTSGKKVDMKEESSALTKRIHMP GESRHNPKILKLECEDIKALKQSENE MLTSTVNGSKRTLEKSKKKAQPLED LTCFQELFISPVPTNIIKKIPSKSPHT QPVRTPASTKRLSKTGLSKVDVRQE PSTLGKRTKSPGRAPGTPAPVQEE DSTAFMETPKQKLDfAGNSSGSKRR SRTSKNRSQPLEDLDFQELFQTPA GASDSVTVEESAKISLESSQAEPVKT PASTKRRSKMSLMKVDMKELSILEK QTQSRGRDAGTPAPMQEgNGTTAI METPKQKLDFTGNSTGHKRRPRTPK IRAQPLEDLDFQELFQTPAGANDS

VTVEESAKMSLESSQAEPVKTPAST
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