

| UniprotKB ID | Entry name | organism | full name | oglcnacscore | oglcnac sites | phosphorylation sites | PMIDS | sequence | intracellular | extracellular | cytosol | nucleus | mitochondrion |
|--------------|-------------|--------------|-----------------------------------|--------------|--|--|--|--|---------------|---------------|---------|---------|---------------|
| Q7Z6E9 | RBBP6_HUMAN | Homo sapiens | E3 ubiquitin-protein ligase RBBP6 | 7.426989 | T374;S375;T487;T488;T631;S1442;S1444;S1446;S1703 | S244;S245;S246;S247;S360;S516;S768;S770;S772;S780;S815;S861;S873;S957;T984;S1179;S1221;T1271;S1277;S1328;S1341;S1347;T1468;S1646;S1648;S1651 | 38665916;34019948;28657654;33214551;30379171;23301498;39531497;32119511;35138101;40596516;29351928;37217939;38253038;39534244;35254053 | MSCVHYKFFSSKLNVDYVTFDGLHISLCDLKKQIMGREKKAADCDLQITNAQTKEEYTDNALIPKNSVIVRRIPGGVKSTSKTYVISRTEPAMATTKAIDDSSASISLAQLTKTANLAEANASEEDKIKAMMSQSGHEYDPINYMKKPLGPPPSYTCFRCGKPGHYIKNCPTNGDKNFESGPRIKKSTGIPRSFMMEVKDPNMKGAMLTNTGKYAIFTIDA EAYAI GKKEKPPFLPEEPSSSSEEDDPIPELLCLICKDIMTDAVVIPCCGNSYCDECIRTALLESDEHTCPTCHQNDVSPDALIANKFLRQAVNNFKNETGYTKRLRKQLPPPPPPPPRPLIQRNLQPLMRSPISRQODPLMIPVTSSSTHPAPSLSLTSNQSSLAPPVSGNPSAPAPVPDITATVSIHVHSEKSDGPPRDSNDKILPAAALASEHSGTSSIAITALEEKGYQVPVLGTPSLLGQSLHGLIPIITGPVRINTARPGGGRPGWEHSNKLGYLVSPPOQIRRGERSCYRSINRGRHHSERSQRTQGPSLPATPVFVPPPPPLYP PPPHTLPLPPGVPPQFSPQFPPGQP PPAGYSVPPGFPAPANLSTPWVSSGVQTAHSNTIPTTQAPPLSREEFYREQRRLEEEKSKLDEFNDFAKELMEYKKIQKERRRSFSRSKSPYSGSSYSRSSYTSKRSRSGSTRSRSYRSFSRSHRSYRSRPPYPRRGKSRNYSRSHGYHRSRSPYRRYHSRSPQAFRGGQSPNKRNVPGETEREYFNRYREVPPPYDMKAYYGRSVDFRDPFEKERYREWERKYREWYKYKGYAGAQPRPSANRENFSPERFLPLNIRNSPFTGRREDYVGGQSHRSRNIKS NYPEKLSARDGHNQKDNTKSKEKESENAPGDGKGNKHKHRKRRKGESEGLNPELLETSRKSREPTGVEENKTDSLFLVPSRDDATPVRDEPMDAESITFKSVSEKDKRERDKPKAKGDKTKRKNDGSAVSKKENIVKPAKGPOEKVDGERERSRSEPPIKKAKEETPKTDN TKSSSSQKDEKITGTPRKAHKSASKEHQETKPVKEEKVKDYKDVKSEKLTTKEEKAKKPNKPLDNKGEKRRKRTEEKGVKDFESSMKISKLEVTEIVKPSPKRKMPEPTEKMDRTPEKDKISLSAPAKKIKLNRETGKIGSTE NISNTKEPSEKLESTSSKVKQEKVKGKVRRTKVTGTEGSSSTLVDTSTSTSGSPVRKSEKTDTRKRTVIKTMEEYNNDNTAPAEDVIIMIQVPQSKWDKDDFESEEDVKSTQPISSVGKPAVIKNVSTKPSNIVKYPEKESPEKIQKFTKDVSHIIQHEVKSSKNSASSEKGTKDRDYSVLEKENPEKRKNSTQPEKESNLDRLNEQGNFKLSQSSKEARTSDKHDSTRASSNKDFTPNRDKKTDDYDTREYSSSKRRDEKNELTRRKDPSRNKDSASGQKNKPREERDLPKKGTGDSKKSNSPSRDRKPHDHKATYDTKRPNEETKSVDKNPCKDREKHVLEARNNKESGKLLYLNPPEQVEKEQITGQIDKSTVKKPQLSHSSRLSSDLTRETDEAAFEFDYNESSSESNVSVKEEESGNISKDLKDKIVEKAKESLDATAVVQVGISRNQSHSSPSVPSRSHSPSGSQTRSHSSASSAESQSKKKKKKKEKSKKHKHKHKHKHKHAGTEVELEKSQKHKKKKKSKKNKDKKEKEKEDDQKVKSVTV | True | False | 4.3 | 5.0 | False |