

| UniprotKB ID | Entry name | organism     | full name                      | oglcnacscore | oglcnac sites                                      | phosphorylation sites   | PMIDS  | sequence   |
|--------------|------------|--------------|--------------------------------|--------------|--|---|--|--|
| P46100       | ATRX_HUMAN | Homo sapiens | Transcriptional regulator ATRX | 17.099485    | S9;T13;S52;T578;T591;S594;S703;T792;S804;S933;S978 | S25;S34;T89;S92;S112;S213;S316;T591;S594;S598;S634;T674;S675;S677;S729;S731;S784;S819;S849;S850;S875;S876;S889;S962;S974;T977;S1011;S1012;S1013;S1061;T1063;S1244;S1245;S1253;S1322;S1324;S1326;S1348;S1352;S1527;T1529;S1906;S1913;S1992;S1996;S2220 | 37217939;28510447;35254053;35289036;33465208;23301498;28657654 | MTAEPMSSEKLNLTIVQKLHDFLAH<br>SSEESEETSSPPRLAMNQNTDKISG<br>SGSNSDMMENSKEEGTSSSEKSKS<br>SGSSRSKRKPSIVTKYVESDDEKPLD<br>DETVDNEDASNENSENDITMQSLPK<br>GTVIVQPEPVLNEDKDDFKGPEFRS<br>RSKMKTENLKKRGEDGLHGIVSCTA<br>CGQQVNHFKQKDSIYRHPSLQVLICK<br>NCFKYMSDDISRDSDGMDEQCRW<br>CAEGGNLICCDFCHNAFCKKILRN<br>LGRKELSTIMDENNQWYCYICHPEP<br>LLDLVTACNSVFENLEQLLQONKKK<br>IKVDSEKSNKVYEHTSRFSPKKTSSN<br>CNGEKKLDDSCSGSVTYSYSALIVP<br>KEMIKKAKKLIETTANMNSSYVKFL<br>KQATDNSEISSATKLRQLKAFKSVLA<br>DIKKAHLALEEDLNSEFRAMDANK<br>EKNTKEHKVIDAKFETKARKGEKPC<br>ALEKKDISKSEAKLSRKQVDSEHMH<br>QNVPTEEQRTNKSTGGEHKKSDRK<br>EEPQYEPANTSEDLDMDIVSVPSSVP<br>EDIFENLETAMEVQSSVDHQGDGSS<br>GTEQEVESSSVKNLNISSKDNRRGGIKS<br>KTTAKVTKELYVKLTPVLSNSPIKG<br>ADCQEVQDKDGYKSCGLNPKLEKC<br>GLGQENSDNEHLVENEVSLLEESD<br>LRRSPRVKTTPLRRPTETNPVTSNSD<br>EECNETVKEKQKLSVPVRKDKRNS<br>SDSAIDNPKNLPSKQSETVDQN<br>SDSDEMLAILKEVSRMSSSSSDTD<br>INEIHTNHKTLYDLKTQAGKDDKGGK<br>RKRKSSTSGSDFDTKKGKSAKSSIIS<br>KKKRQTQSESSNYDSELEKEIKSMS<br>KIGAARTTKKRIPTKDFDSEDEKH<br>SKKGMDNQGHKNLKTSQEGSSDDA<br>ERKQERETFSSAEGTVDKDTTIMEL<br>RDRLPKKQASASTDGVDKLSGKEE<br>SFTSLEVRKVAETKEKSKHLKTCTCK<br>KVQDGLSDIAEKFLKQDQSDSESD<br>DKKQSKKGTEKKKPSDFKKKVIKM<br>EQQYESSSDGTEKLPEREIEICHFPK<br>GIKQIKNGTTDGEKSKKIRDKTSKK<br>KDELSDYAEKSTGKGDSCDSSDCK<br>SKNGAYGREKKRCKLLGKSSRKRQD<br>CSSSDTEKYSMKEDGCNSSDKRLKR<br>IELRERRNLSSKRNTKEIQSGSSSD<br>AEESSEDNKKKQRTSSKKKAVIVK<br>EKRNLSLRTSTKRKQADITSSSSDI<br>EDDDQNSIGEGSSDEQKIKPVTE<br>VLSSHTGFCQSSGDEALSKSVPTV<br>DDDDDDNDPENRIAKMLLEIKAN<br>LSSDEDEGSSDDEPEEGKRTGKQNE<br>ENPGDEEAKNQNSSESDDSESK<br>KPRYRHLLRHKLTVSDGESGEEKK<br>TKPKEHKEVGRNRRKVSSESDSDS<br>DFQESGVSEEVSESEDEQRPRTSA<br>KKAEEENQRSYKQKKRRRIKVQE<br>DSSSENKSNSEEEEEKEEEEEEE<br>EEEEEEEDNDDSKSPGGRKKIRK<br>ILKDDKLRTEQNALKEEEERRKRIA<br>EREREREKLRVIEIEDASPTKCPITT<br>KLVLDEDEETKEPLVQVHRNMVIKL<br>KPHQVDGVQFMWDCCCESVKKTKK<br>SPGSGCILAHCMGLGKTLQVVSFLH |

TVLLCDKLDLFSTALVVCPLNTALNW  
MNEFEKWQEGKDDKLEVSELAT  
VKRPQERSYMLQRWQEDGGVMIIG  
YEMYRNLAQGRNVKSRKLEIFNKA  
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FDASWNPSYDIQSIFRVYRFGQTKPV  
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ILAE LLQIHKEHIVGYHEHDSLLDHK  
EEEELTEEERKAAWAEYEAEEKGLT  
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GPSQGKSM