

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
Q8IWX3	ANKH1_HUMAN	Homo sapiens	Ankyrin repeat and KH domain-containing protein 1	31.649298	S622;S1364;T1653;S1656;S1787;S1793;S1794;T1798;T1799;S1802;S1803;T1813;T1816;S1817;T1820;T1821;S1823;T1824;T1837;S1846;S2098;S2338;S2357;S2398	S101;S105;S803;S1540;T1553;S1632;T1653	21740066;35254053;30397120;23301498;30379171;28657654;31492838;33214551;34725712;30620550;27655845;35289036;20305658;29351928;34019948;28510447;29237092;35132862;35138101;30059200;22661428;28604694;32119511	MLTDSGGGGTSFEEDLDSVAPRSAPAGASEPPPPGGVGLGIRTVRLFGEAGPASGVGSSGGGGSGTGGGDAALDFKLA AAVLRTGGGGGASGSDEDEVSEVESFILDQEDLDNPNVLTSEIFLSSTAEGADLRTVDPETQARLEALLEAA GIGKLTADGKAFADPEVLRRLTSSVSCALDEAAAALTRMKAENSHNAGQVDTRSLAEACSDGDVNAVRLKLLDEGRSVNEHTEEGESLLCLACSAGYYELAQVLLAMHANVEDRGNKGDITPLMAASSGGYLDIVKLLLLHDADVNSQSATGNTALTYACAGGFVDIVKVLNNEGANIEDHNEGHGHTPLMEAASAGHVEVARVLLDHGAGINTHSNEFKESALTLACYKGHLDMVRFLLEAGADQEHKTDEMHTALMEACMDGHVEVARLLDLSGAQVNMPPADSFESPLTLAACGHHVELAALLIERGANLEEVNDEGYTPLMEAAAREGHEEMVALLLAQGANINAQTEETQETALTACCGGFSEVADFLIKAGADIELGCSTPLMEASQEGHLELVKYLASGANVHATTATGDTALTYACENGHTDADVLLQAGADLEHESEGGRTPLMKAARAGHLCTVQFLISKGANVNRATANNDHTVVSACAGGHLAVVELL AHGADPTHRLKDGSTMLIEAAKGGHTNVVSYLLDYPNNVLSVPTTDVSQLPPPSQDQSQVPRVPTHLAMVVPQEPDRTSQENSPALLGVQKGTSKQKSSSLQVADQDLLPSFHPYQPLECIVEETEGKLNELGQRISAIEKALKSLELIQGEPLNKDKIEELKKNREEQVQKKKILKELQKVERQLQMKTQQQFTKEYLETKGQKDTVSLHQQCShRGVFPEGEGDGSLPEDHFSSELQVD TILFKDNDVDDEQQSPPSAEQIDFVPVQPLSSPQCNFSSDLGSNGTNSLELQKVSNGNQIVGQPQIAITGHDQGLLVQEPDGLMVATPAQTLTDLDDLIAAVSTRVPTGSNSSSQTECLTPESCSQTTSNVASQSMPPVYPSVDIDAHTESNHDTALTACAGGHEELVSVLIARDAKIEHRDKKGFPLILAATAGHVGVEILLDKGGDIEAQSERTKDTPLSLACSGGRQEVVDLLARGANKEHRNVSDYTPLSLAASGGYVNIKILLNAGAEINSRTGSKLGISPLMLAAMNGHVPAVKLLLDMGSDINAQIETNRNTALTLACFQGRAEVVSLLDLDRKANVEHRAKTGLTPLMEAASGGYAEVGRVLLDKGADV NAPPVSSRDALTIAADKGHYKFCELLIHRGAHIDVRNKKGNTPPLWLASNGGHFDVVQLLVQAGADVDAADNRKITPLMSAFRKGHVQVYLVKEVNQFPSDIECMRYIATITDKELLKCKHQCVETIVKAKDQQAEEANKNASILKELDLEKSREESRKQALAAKREKREKRRKKKKEEQKRKQEEDEENKPKENSELPEDEEENDEVEQEVPIEPPSATTTTTIGISATSATFTNVFGKKRANVVTTPSTNRKNKKNKTKETPPTAHLILPEQHMSLAQQKADKNKINGEP

RGGGAGGNSDSDNLDSTDCNSESS
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KYVN