	UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
0	Q99NH0	ANR17_MOUSE	Mus musculus	Ankyrin repeat domain-containing protein 17	34.875366	T1821;T1822;T1834;T1997;T2186;S2382;S2388	S15;S42;S152;S799;S1453;S1631;S1692;S1696;S1705;S2038;S2040;S2041;S2043;S2055;S2063;S2373;S2401	30059200;22517741;35822049;22645316;27669760;34678516;29187734	MEKATVPAAAEGEGSPPAAAAVAAP PAAAAAEVGGGARPASSPRGMVRVC DLLLKKKPPQQQQQQQPPHHKAKR NRTCRPPSSSESSSDSDNSGGGGGG GGGGGGGTSSNNSEEEEDDDDEEE EVSEVESFILDQDDLENPMLETASK LLLSGTADGADLRTVDPETQARLEAL LEAAGIGKLSTADGKAFADPEVLRRL TSSVSCALDEAAAALTRMRAESTAN AGQSDNRSLAEACSEGDVNAVRKLL IEGRSVNEHTEEGESLLCLACSAGYY ELAQVLLAMHANVEDRGIKGDITPL MAAANGGHVKIVKLLLAHKADVNA QSSTGNTALTYACAGGYVDVVKVLL ESGASIEDHNENGHTPLMEAGSAG HVEVARLLLENGAGINTHSNEFKES ALTLACYKGHLEMVRFLLEAGADQE HKTDEMHTALMEACMDGHVEVAR LLLDSGAQVNMPADSFESPLTLAAC GGHVELAALLIERGASLEEVNDEGY TPLMEAAREGHEEMVALLLGQGANI NAQTEETQETALTLACCGGFLEVAD FLIKAGADIELGCSTPLMEAAQEGHL ELVKYLLAAGANVHATTATGDTALTY ACENGHTDVADVLLQAGADLEHES EGGRTPLMKAARAGHVCTVQFLISK GANVNRTTANNDHTVLSLACAGGH LAVVELLLAHGADPTHRLKDGSTML IEAAKGGHTSVVCYLLDYPNNLLAAP PPDVTQLTPPSHDLNRAPRVPVQAL PMVVPPQEPDKPPANLAATLPVRSK AASKQKSNSHLPANSQDVQGYITNQ SPESIVEEAQGKLTELEQRIKEAIEK NAQLQSLELAHADQLTKEKIEELNK TREEQIQKKQKILEELQKVERELQLK TQQQLKKQYLEVKAQRIQLQQQQQQ SCQHLGLFTSVGVGEQLSEGDYARL QQVDPVLLKDEPQQTAAQMGFAPIQ PLAMPQALPLATGPLPPGSIANLTEL QGVIVGQPVLGQAQLAGLGQGILTET QQGLMVASPAQTLNDTLDDIMAAVS GRASAMSNTPTHSIAASVSQPQTPTP SPIISPSAMLPIYPAIDIDAQTESNHD TALTLACAGGHEELVQTLLERGASIE HRDKKGFTPLILAATAGHVGVVEILL DNGADIEAQSERTKDTPLSLACSGG RQEVVELLLARGANKEHRNVSDYTP LSLAASGGYVNIIKILLNAGAEINSRT GSKLGISPLMLAAMNGHTAAVKLLL DMGSDINAQIETNRNTALTLACFQG RTEVVSLLLDRKANVEHRAKTGLTP LMEAASGGYAEVGRVLLDKGADVN APPVPSSRDTALTIAADKGHYKFCEL LIGKGAHIDVRNKKGNTPLWLAANG GHLDVVQLLVQATADVDAADNRKIT PLMAAFRKGHVKVVRYLVKEVNQFP SDSECMRYIATITDKEMLKKCHLCM ESIVQAKDRQAAEANKNASILLEELD LEKLREESRRLALAAKREKRKEKRR KKKEEQRRKLEEIEAKNKENFELQA AQEKEKLKVEEEPEVLTEPPSATTTT TIGISATWTTLAGSHGKRNNTITTTS SKRKNRKNKITPENVQIIFDDPLPISY

								SQPEKVNGESKSSSTSESGDSDNM RISSCSDESSNSNSSRKSNNHASAV VTTTMASKKQPSVLVTFPKEERKSV SGKASIKLSETVNEGTSNSLSTCTKS GPSPLSSPNGKLTVASPKRGPKREE GWKEVVRRSKKVSVPSTVISRVIGRG GCNINAIRECTGAHIDIDKQKDKTGD RIITIRGGTESTRQATQLINALIKDPD KEIDELIPKNRLKSSTANSKIGSSAPT TTAANSSLMGIKMTTVALSSTSQTAT ALTVPAISSASTHKTIKNPVNNVRPG FPVSLPLAYPPPQFAHALLAAQTFQQ IRPPRLPMTHFGGTFPPAQSTWGPF PVRPLSPARATNSPKPHMVPRHSNQ NSSGSQVNSAGSLTSSPTTTASSSAS AVPGTTSNGSPSSPSVRRQLFVTVVK TSNATTTTVTTTASNNSTAPTNATYP MPTAKEHYPVSSPSSPSPPAQPGGV SRNSPLDCGSASPNKGASASEQEAS SPPVVEPANSRPPHSSSSSGSSSGH STQQQPPGSVPQEPRPPLQQSQVPS PDVRMTVPPTATSSAPVAVPSTAPVT YPMPQTQMGCSQPPKMEAPAIRPPS HATAAPHKTPAPVQSSSASVLNVNH IKRPHSVPSSVQLPSTLSTQSACQNS VHPANKPVAPNFSAPLPFGPFSTLFE NNPTNAHAFWGGPVVSSQSTPESM LSGKSSYLPNSDPLHQSDTSKAPGF RPPLQRPAPSPSGIVNMDTPYGSVTP SSTHLGNFASSLSGGQMYGPGAPLG GAPLGGAPTAANFNRQHFSPLSLLT PCSSASNESPAQSVSSGVRAPSPAPS SVPLGSEKPSSVSQDRKVPVPIGTER SARIRQTGTSAPSVIGSNLSTSVGHS GIWSFEGIGGNQDKVDWCNPGMGN PMIHRPMSDPGVFSQHQAMERDST GIVTPSGTFHQHVPAGYMDFPKVGS MPFSVYGNAMLPPVAPIADGAGGPI FNGPHSAEPSWNSLIKMVSSSTENN GPQTVWTGPWAPHMNSVHMNQLG