

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	ex re
E9Q4F7	ANR11_MOUSE	Mus musculus	Ankyrin repeat domain-containing protein 11	38.939326	T2030	S276;S408;T410;S411;S838;S1070;T1111;S1114;S1676;S1777;S1832;T1835;T1836;S1837;S1844;S1981;S2139	40997131;36852467	MPKGGCSKTPQOEDFALSNDMVEK QTGKKDKDKVSLTKTPKLRSDGGK EVREERATKRRLPFTVVGANGEQKSD TEKQGPERRKRIKKEPVARKSGLLF MGLSGIRAGYPLSERQVALLMQMT AEESANSPVDTPKHPSQSTVCQKG TPNSASKTKDKVNRNERGETRLHR AAIRGDARRIKELISEGADVNVKDF GWTALHEACNRGYDYIAKQLLAAGA EVNTKGLDDDTPLHDAANNHGYK VKLLLRYGGNPQQSNRKGTPKVA NSPTMVNLLLGKGTYSSEESSTES SEEEADPSFAPSSSDGNNDSSEFE KGLKAKNPEPQKTVTPVKDEYEF DEDEQDRVPPVDDKHLLKDYRK EAKANSFISIPKMEVKSYSKNTLAP KKAHRILSDTSEEDVSVSIGAGEK LRLSAHTMLPGSKARESSSRQOKE KNLKKRKKETKGEVRFGRKSDK FCSSGSESESESEEDDGDVGS CLKGSPLVLKDPFLSFLSASSTSSH GSAVAQKHGSGHTDQHTKHWRD NWKAISSPAWSEVSSLDSSRTGLT SESDCSSESSVESLKPTRRQEH KRGVLQAPSEKRSSFHPCTDGAVP KLDKEGVVKKHKTKHKKHKEK QCSVSQELKLSFTYEDSKQKSD KAILLESDLSTENKLVKHDREHL KKEDKLRMKPEDKDWLFKDEKVL KRIKDANKDMSRAFREDKDRASKAE RERATKDKSPKEEKLRLYKEERKKK SKDRASRLERKNDMKEDLSKEKE KAFKEDKEKLEKLYREDAAFDDY CNKSQFLDHEDTKFSLSDDQQERW FSDLSDSSDFDKGSDSVTDYRD IKNDSVAKLILETVKEDSKEKRDNK IREKRDFKDSFFRKRDRDCLDNSE KRRDQTEKHKSIPLYSEKDKRRE SAEGRRDRRGRIRSEEVHREDLKE CGFESSFKDKSDCFPNLEPWERP HAAREKEDDALEKERKEKGRADKY KEKSSERERSDKSTLDCQKDFE KCFKEKKGKEKHKDIHSDRKA DQLREKKEKVFSSISEDFSERKDDR KGKEKSWYIADIFTDESEDEKDDCV AGSFKATEASDTQRVDGLPEKEEGR EHPSDRHRKSSDRQHTKPRDKEP KEKKDRGASEGGDKKEKMEKIFE KHKEKDKCAERYKDRKERASADS APEKKNKQLPEKVEKHFEDKVK SKHKEKPEKHSRERERKPSRGPDV EKSLLEKLEEEALHDYREDSNDKISE VSSDSFADHGQEPSTLLEVSFSEP PAEDKARDSACLSEKLEREHRHS SSSSKKSHERERAKKEKAEKKEKSE DYKDSISSVRKDAQFEKDFLDAETY GVSYPTKADVEEELDKAIELFSSEK DRSDPEREPAKRIEKELKPYGSSAISI LKEKKEKHEKHEKHEKHEKHEKHEK HVDGFLRHHKDEPKPAADKDNPP NSFKEKSREESLKLSEKLEKKEFKE NTEREKGDSIKMSNGNDKLVPSRDS GKKDSRPREKLLGDGLMMSFER MLSQKLEIEERHRRKERMKQME KMRHRSGDPKLEKKEKPTEDGRKKS LDFPSKALGLDKKVKEPAPTLTTGE SKPHSGPGTESKDWLGGQPLKEVLP ASPRTEQSRPTGVPTPTSVVSCPSYE EVMHTPRTPCSADDPDLVDFDCTD SQHSMPVSTASTSACSPFFDRFSV ASSVVSENAAGQTPTRPISTNLYRSI SVDIRRTPEEEFSAGDKLFRQQSVPA PSSFDSPVQHLLLEKAPLPPVPAEKF ACLSPGYYSPTYGIPSPKVDTLHCPP TAVVSATPPPDVSVFNLPPKSSPSR GELLSPAIEGTLPPDLGLPLDATEDQ QATAAILPQEPSYLEPLDEGPFTTIVIT EPPVEWTHTAEEQGLSSSSLIASASE NPVSWPVGSELMLKSPQRFAPSPKH FCPGESLHSTTPGYSAAEPTYPVSP	True	False	3.33	4.641	1.007	0.619	False	0.867	0.1

GSYPLPAPEPALEEVKDDGGTGAIPVA
ISAAEGAAPYAAPARLESFFSNCKSH
PDAPLDTAPEPTGVTAVAQVEALGPL
ESSFLDSNPSISTLSQVEPVSWHEAF
TSPEDDLDLGPFSLPELPLQAKDASD
VEAEAAKASPVPPAESPPGPTGVLGG
GDVPAPAAEPPAPPQEASQLSTE
PEPSEEPKLDVVLEATVETEVLADDS
APEASISNSVPAPSPPPQQPPGGGDE
EAETEDPSATPCCAPDGPTTDGLAQ
AHNSAEASCVVAAAEGPPGNVQAEA
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SLAEPLKELFKQQAVERGKLRLOHSI
EREKLIVSCEQEILRVHCRAARTIAN
QAVPFSACTMLLDSEVYNMPLESQG
DENKSVRDRFNARQFISWLQDVDD
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PSFYVPMVDVNDDFVLLPA