

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnacsites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
Q12802	AKP13_HUMAN	Homo sapiens	A-kinase anchor protein 13	26.21016	S345	S790;T815;T953;S983;S1489;S1507;S1540;S1565;S1602;S1642;S1645;S1647;S1876;S1895;S1929;T1930;S1932;S1945;S2345;S2398;T2467;S2473;S2563;S2566;S2703;S2709;S2728	29351928	MKLNPPQAPLYGDCVVTVLLAEEDK AEDDVVFLVFLGSLTRHCTSTRKVS SDTLETIAPGHDCCEYKVKVQLCASKE GLPVFVVAEEDFHFVQDEAYDAAQF LATSAGNQALNFTRFLDQSGPPSG DVNSLDKLLVLAFRHLKLPTEWNVL GTDQSLHDAGPRETLMHFAVRLGLL RLTWFLLOKPGGRGALSIIHQEGAT PVSLALERGYHKLHQLLTeenAGEP DSWSSLSYEIPIYGDSCVRHRELDIY TLTSEDSHHEHPFPGDGCCTGPIFK LMNIQQQLMKTNLKQMDSLMPLM MTAQDPSSAPETDQGFLPCAPEPTD PQRLSSSEETESTQCCPGSPVAQTES PCDLSIVEEENTDRSCRKKNKGVE RKGEEVEPAPIVDSGTVSDQDSCLO SLPDCGVKGTGLSSCGNRNEETGT KSSGMPTDQESLSSGDAVLQRDLV MEPGTAQYSSGGELGGISTTNVSTP DTAGEMEHLMPDATVWKNVLQ GGESTKERFENSNIAGASDVHVT SKPVDKISVPNCAPAASLDGNKPAE SSLAFSNEETSTEKTAETETSRSRREE SADAPVDQNSVVPAAAKDKISDGLE PYTLAAGIGEAMSPDLALLGLEED VMPHQNSSETNSSHAQSQKGGSSPIC STTGDDKLCADSACQONTVTSSGDL VAKLCDNIVSESESTTARQPSQDPP DASHCEDPQAHTVTSDFVRDQTQERA DFCPCFKVVDNKGQRKDKVLDKPLTN MLEVVSHPHVVPKMEKELVPDQA VISDSTFLANSFGSESVTKDDALS VPSQKEKGTATPELHTATDYRDGPD GNSNEPDTRFLEDRAVGLTSSSTAA ELQHGMGNTSLTGLGGEHEGPAPP AIPEALNIKNTDSSLQSVGKATLAL DSVLTEEGKLLVVSSEAAQEQDKD KAVTCSSEIKENALSSGTLQEEQRTPP PGQDTQQFHKEKISADCAKDKALQL SNSPGASSAFLKAETEHNKVAPQV SLLTQGGAAQSLVPPGASLATESRQE ALGAEHNSSALLPCLLPDGS DSDA LNCSPSPPLDVGKNTQSQGKTSAC EVSGDVTVDVTGVNALQGMAEPRR ENISHNTQDILIPNVLLSQEKNAVLG LPVALQDKAVTDPQGVGTPPEMIPLD WEKGLKLGADHSCMTMGDAEEAQID DEAHPVLLQPVAKELPTDMELSAHD DGAPAGVREVMRAPPSPGRERSTPSL PCMVSAQDAPLPKGADLIEEAASRIV DAVIEQVKAAGALLTEGEACHMSLS SPELGPLTKGLESAFTEKVSFTFPPGE SLPMGSTPEEATGSLAGCFAGREEP EKIILPVQGPPEAAEMPDVKAEDVD FRASSISEEVAVGSAIATLKMKGQGM TQAINRENWCTIEPCDAASLLASK QSPECENFLDVLGRECTSKQGVVK RESGSDSDFHSPSDDMDSIIFPKPE EEHLACDITGSSSSTDDTASLDRHSS HGS DVSLSQILKPNRSRDRQSLDGF YSHGMGAEGRESESEPADPGDVEE EEMDSITEVPANC SVLRSSMRSLSP FRRH SWPGKNAASDAEMNHRSS MRVLGDVVRPPIHRRSFLEGLTG GAGVGNKPSLSLEVSSANAELRHP FSGEERVDSLVSLEEDLESQREH RMFDQQICHRSKQQGFNYCTSAISS PLTKSISLMTISHPGLDNSRPFHSTF HNNTSANLTESITEENYFLPHSPSK KDSEWKSGTKVSRFTSYIKNMSSS KKSKEKEKEKDIKEKEDSKDKEK DKKTVNGHTFSSIPVVGPISSCSQCM KPFTNKDAYTCANCSAFVHKGCRES LASC AKVMKQPKGSLQAHD TSSLP TVIMRNKPSQPKERPRSAVLLVDET ATTPIFANRRSQSVLSKSVSIQNT GVGN DENMSNTWKFLSHSTDSL NK ISKVNESTESLTDGEGVTDMMNEGOL LGD FEIESKQLEAESWSRIIDSKFLK QQKDVVKRQEVYIELMQTEFHHR	True	False	4.792	4.191	1.591	1.695	1.522	2.023	1.653

TLKIMSGVYSQGMADLLFEQQMV
EKLFPCLDELISHSQFFQRILERKKE
SLVDKSEKNFLIKRIGDVLVNQFSGE
NAERLKKTYGKFCGQHNSVNYFK
DLYAKDKRFQAFVKKMSSSVVRRLL
GIPECILLVTQRITKYPVLFQRILQCT
KDNEVEQEDLAQSLSLVKDVIGAVD
SKVASYEKKVRLNEIYTKTDSKSIMR
MKSQGMFAKEDLKRKKLVRDGSVF
LKNAAGRLEKEVQAVLLTDILVFLQEK
DQKYIFASLDQKSTVISLKKLIVREVA
HEEKGLFLISMGMTPPEMVEVHAS
SKEERNSWIIHQDTINTLNREDEG
IPSENEEKKMLDTRARELKEQLHQ
KDQKILLLEEKEMIFRDMAECSTPL
PEDCSPTHSPRVLFRSNTTEEALKGG
PLMKSAINVEILQGLVSGNLGGTL
GPTVSSPIEQDVVGPVSLPRRAETFG
GFDSHQMNASKGGEKEEGDDGQDL
RRTESDGLKKGANLVFMLKRN
SEQVVQSVVHLYELLSALQGVVLQ
DSYIEDQKLVLSERALTRSLRPSLI
EQEKQRSLEKQRQDLANLQKQQAQ
YLEEKRRREREWEARELEREREAL
LAQREEEVQGGQDLEKEREELQ
KKGTYYDLERLRAAQQLEREQEQ
LRREAERLSQRQTERDLCQVSHPHT
KLMRIPSFPPSPPEPPSPSAPSIKSG
SLDSELSVSPKRNSISRTHKDKGPF
HLSSTSQTNKPEGQSAPASTSAS
TRLFGLTKPEKKEKKKNKTSRSQ
PGDGPASEVSAEGEEIFC