

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
Q80TN7	NAV3_MOUSE	Mus musculus	Neuron navigator 3	40.720439	S1210	S1462;S1466	22517741;35822049;22645316	MPVLGVASKLRQPAVGGPKPVHAALP IPNLGISVSRRCSSRPLEFATPERSM LSCQLTLKSTCEFGKALQGTAKEI EDSKIYTDWANHYLAKSGHKRLIKD LQQDIADGVLADIIQHIANEKVEDIN GCPRSQSQMIENVVCLSLAARGV NVQGLSAEEIRNGNLKAILGLFFSLS RYKQQQHHQQQYYQSLVELQQRVT HTAPQSEASQAKTQODMOSSLTARY AAQSKHSGIATSQKKPTRLPGPSRV AASSNKAQGASNLNRRSQSFNSID KNKPPNYANGNEKDSKPGQPSSGI NGNTQPPSTSGQPPASAIPSPSASKP WRSKSMNVKHSATSTMLTVKQPSP ATSPTPSSDRLKPPVTEGVKSAPSGQ KSMLEKFKLVNARTALRPPQAPSSG PNDGGREDDAFSESGEMEGFNSSL NSGGSTNSSPKVSPKLTTPPKAGSKN FSNKKSLQPKKEKEKTRDKNKACA EKSGKEEKDQVTTAAAPKKTSKIASL IPKGSKTAALKESLIPSSSGIPKPGS KVPTPKQTISPASAASEKEKFRTSK GSSSQAFPKAITAEKASTPSLSTPLD GREAGQASPSVCMQVTHSSGQSP GNGAVQLPQQQHSHPNATVAPFI YRAHSENEGTLPPADSCTSPTKMD SSYKTKAQCLEEISGEDPEARRMR TVKNIADLRQNLLETMSLRGTQIS HSTLETTFDTTVTEVNGRAIPNLTS RSPMTWRLGQACPRLQAGDAPSM GAGYSRSGTSRFIHTDPSRFMYTTP RRAAVSRLGNMSQIDMSEKASSDLD VSSEVDVGGYMSDGDILGKSLRADD INSGYMTDGGNLNLYTRSLNRPDTA TSRDVIQRGVHDVTVDADSWDDSSS VSSGLSDTLNISTDDLNTSSISSYS NITVPSRKNTQLKTDAEKRSTTDET WDSPEELKKAEGDCDSHGDAKAW KGATSGLAEDSEKTGQKASLSVST GSWRRGMSAQGGTPATAROKTSTS ALKTPGKTDDAKASEKGTPLKGS LQRSPSDAGKSSGDEGKPPSGIGR STASSSFGYKPSGVGASTMITSSGA TTSGSATLGKIPKSAAGGKSNAGR KTSLDGSONQDDVVLVHSSKTTLQY RSLRPPSKSSTSGIPGRGGHRSSTSS IDSNVSSKSAGATTSKLEPTKIGSG RSSPVTVNQTDKEKEKVAVSDSESV SLSGSPKSSPTASACGTQGLRQPGS KYPDIASPTFRRLFGAKAGGKSASAP NTEGAKSSSVLSPSTSLARQGSLES PSSGTGSMGAGGLSGSSPLFNKP SDLTTDVISLSHSLASSPASVHSFTS GGLVWAANLSSSAGSKDTPSYQSM TSLHTSSESIDLPLSHHGSLSGLTTG THEVQSLLMRTGSRVSTLSEMQLD RNTLPKKGLRYTPSSRQANQEEGKE WLRSHSTGGLQDTGNQSPVSPSA MSSSATGKYHFSNLVSPNTLSQFNL PAPSMRSSSIPAQDSSFDLYDDAQ LCGATSLEERPRAVSHSGSFRDSM EEVHGSSLVSTSSLYSTAEKKAH SEQIHLRRELVASQEKVATLTSQLS ANAHLVAAPFKSLGNMTGRLQSLT MTAEQKESELIELRETIEMLKAQNS AAQAAIQGALNGPDHPPKDLRIRRO HSSSEVSSINSATSHSSIGSGNDADS KKKKKNWLRSSFKQAFGKKKSTKP PSSHSDIEELTSSLPASPPLPHNAG ESGSSMKPSQASAIACECTEAEAEI ILQLKSELREKELKTLDIRLEALSSA HHLQIREAMNRMQNEIEILKAEN DRLKAETGNTAKPARPPSDSSSTASS SSSRQSLGSLNLLNITESVTSDILL DDTGDATGHKDGSRVKIIVSISKGYG RAKDQKSQAYLIGSIGVSGTKWDV LDGVIRRLFKYVFRIDTSSSLGLSS DCIASYICIGDLIRSHNLEVPPELLCG YLVGDNNIITVNLKGVENSLLDSFVF DTLIPKPIQRYFNLLMEHHRILSGP	None	None	None	None	None	None	None		

