

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
Q8IVL0	NAV3_HUMAN	Homo sapiens	Neuron navigator 3	22.982787	S982;S984;S988;S1207;S1209	S1459;S1463	30379171;28657654;35254053	MPVLGVASKLRQPAVGSKPVHTALPI PNLGTGTSQHCSSSRPELETTETESSM LSCQLALKSTCEFGKPKLQKAKE KEDSKIYTDWANHYLAKSGHKRLIK DLQQDIADGVLLAEIHIANEKVEDI NGCPRSQSQMIENVVCLFLAARG VNVQGLSAEEIRNGNLKAILGLFFSL SRYKQQQHQQYYQSLVELQQRV THASPPSEASQAQTQDMQSSLAAR YATQSNHSGIATSQKKPTRLPGPSRV PAAGSSSKVQGNLNRSSQSFNSI DKNKPPNYANGNEKSSKGPQSSS GVNGNVQPPSTAGOPPASAIPSPSAS KPWRSKSMNVKHSATSTMLTVKQS STATSPTSSDRLKPPVSEGVKTAPS GQKSMLEKFKLVNARTALRPPQPPS SGPSDGGKDDDAFSESGEMEGFNS GLNSGGSTNSSPKVSPKLAPPKAGS KNLSNKKSLLOPKKEKEKNRDKNK VCTEKPVKEEKDQVTEMAPKTKSKI ASLIPKGSKTTAAKKESLIPSSSGIPK PGSKVPTVKQITISPGSTASKESEKFR TTKGSPPSLSKIPITMEKASASSCPA PLEGREAGQASPSGSCMTVAQSSG QSTGNGAVQLPQQQHSHPNTATV APFIYRAHSENEGATLPSADSCSTPT KMDLSYSKTAQCLEEISGEDPETR RMRTVKNIALDRQNEETMSSLRGT QISHSTLETTDFSTVTEVNGRTIPN LTSRPTMTWRLGQACPRLQAGDAP SLGAGYPRSGTSRFIHTDPSRFMYTT PLRRAAVSRLGNMSQIDMSEKASSD LDMSSSEVDVGGYMSDGDILGKSLRT DDINSGYMTDGGLNLYTRSLNRIPD TATSRDIIQRGVHDVTVDADSWDDS SSVSSGLSDTLDNISTDDLNTTSSVS SYSNITVPSRKNTQLRTDSEKRSTTD ETWDSPEELKKPEEDFDHSHGDAGG KWKTVSSGLPEDPEKAGQKASLSVS QTGSWRRGMSAQGGAPSRQKAGTS ALKTPGKTDDAKASEKGAFLKGGSS LQRSPSDAGKSSGDEGKPPSGIGR STATSSFGFKKPSGVGSSAMITSSGA TITSGSATLGKIPKSAIAGGKSNAGR KTSLDGSONQDDVVLHVSSKTTLQY RSLRPRPSKSSSTSGIPGRGGHRSSTSS IDSNVSSKSAGATTSKLEPTKIGSG RSSPVTVNQTDKEKEKVAVSDSESV SLSGSPKSSPTASACGAOGLRQPG SKYPDIASPTFRRLFAGAKAGGSASA PNTEGVKSSSVMPSPTTLARQSSL ESPSSGTGSMGSAGGLSGSSSPLFN KPSDLTDDVISLSHSLASSPASVHSF TSGGLVWAANMSSSAGSKDTPSYQ SMTSLHTSSESIDLPLSHHGSLSGLT TGTHEVQSLLMRTGVRSTLSESMQ LDRNTLPKKGLRYTPSSRQANQEEG KEWLRSHSTGGLQDTGNQSPVLSPS AMSSSAAGKYHFNLSVPTNLSQFN LPGPSMMRNSIPAQDSSFPLYDSS QLCGSATSLERPRASHSGSFRDS MEEVHGSSLSLVSSTSSLYSTAEKA HSEQIHKLRRELVASQEKVATLTSQL SANAHLVAAFEKSLGNMTGRLQSLT MTAEQKESELIELRETIEMLKAQNS AAQAAIQGALNGPDHPPKDLRIRRO HSSSEVSSINSATSHSSIGSGNDADS KSKKKKNWVNSRGSSELRSFKQAF GKKKTKPPSSHSDIEELTSSLPAS PKLPHNAGDCGSASMKPSQASASP LVVPPKQRONGPVIYKHSRICECT EAEAEIILQLKSELREKELKLDIRLE ALSSAHHLQIREAMNRMONEIEIL KAENDRLKAETGNTAKPTRPPESS SSTSSSSRQSLGLSLNMLNITEAVS SDILLDDAGDATGHKDRSVKIIVSIS KGYGRAKDQKSQAYLIGSIGVSGKTK WDVLDGVIRRLFKEYVFRIDTSTSLG LSSDCIASYCIGDLIRSHNLEVPPELLP CGYLVGDNNIITVNLKGVENSLSDS	True	False	3.817	4.457	1.591	0.513	0.54	1.3

								FVFDTLIPKPITQRYFNLLMEHHRIL SGPSGTGKTYLANKLAEYVITKSGRK KTEDAIAITFNVDHKSSKELQQYLAN LAEQCSADNNGVELPVVILDNLHH VGSLSDFNGFLNCKYKCPYIIGTM NQCWSSPNLELHHNFRWVLCANH TEPVKGFLGRYLRRLIEIEIERNIRN NDLVKIIDWIPKTWHHLNSFLETHS SSDVTIGPRLFLPCMDVEGSRVWF MDLWNYSLVPYILEAVREGLQMYGK RTPWEDPSKWVLDTPWSSATLPQE SPALLQLRPEDVGYECSSTKEATTS KHIPQTDTEGDPLMNMLKLEAA NYSSTQSCDSESTSHHEDILDSLES TL							
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