	UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochndrion
0	Q8CH77	NAV1_MOUSE	Mus musculus	Neuron navigator 1	52.787615	T157;T537;T543;T617;T619;T621;T625	S93;S145;T162;S197;S202;S299;S311;S315;S365;S394;S455;S477;S479;S493;S531;T537;S544;T547;T575;S651;S752;S756;S762;S799;S810;S998;T1004;T1168;S1179;S1263;S1380	22517741;22645316;40885482;36852467;40021952;34678516;34418053	MLGSSVKSVQPEVELSGGSGSGGDE GADESRGASRKAAAADGRGMLPKR AKAAGGSGSMAKASAAELKVFKSGS VDSRVPGGLPTSNLRKQKSLTNLSF LTDSEKKLQLYEPEWSDDMAKAPKG LGKLGPKGRETPLMSKTLSKSEHSL FQPKGGSTGGAKTPLAPLAPSLGKPS RIPRGPYAEVKPLSKAPEAAVSDDGK SDDELLSSKAKAQKGSGTVPSAKGQ EERAFLKVDPELVVTVLGDLEQLLFS QMLDPESQRKRTVQNVLDLRQNLE ETMSSLRGSQVTHSSLEMPCYDSDD ANPRSVSSLSNRSSPLSWRYGQSSP RLQAGDAPSVGGSCRSEGPPAWYM HGERAHYSHTMPMRSPSKLSHISRL ELVESLDSDEVDLKSGYMSDSDLM GKTMTEDDDITTGWDESSSISSGLS DASDNLSSEEFNASSSLNSLPTTPTA SRRSSTIVLRTDSEKRSLAESGLNWF SESEEKTPKKLEYDSGSLKMEPGTS KWRRERPESCDDASKGGELKKPISL GHPGSLKKGKTPPVAVTSPITHTAQS ALKVAGKPEGKATDKGKLAVKNTGL QRSSSDAGRDRLSDAKKPPSGIARPS TSGSFGYKKPPPATGTATVMQTGSS ATLSKIQKSSGIPVKPVNGRKTSLDV SNSVEPGFLAPGARSNIQYRSLPRPA KSSSMSVTGRGGPRPVSSSIDPSLLS TKQGGLTPSRLKEPSKVASGRSTPAP VNQTDREKEKAKAKAVALDSDNISL KSIGSPESTPKNQASHPPATKLAELP PTPLRATAKSFVKPPSLANLDKVNS NSLDLPSSSDTHASKVPDLHAPSSS TGGPLPSCFTPSPAPILNINSASFSQ GLELMSGFSVPKETRMYPKLSGLHR SMESLQMPMSLPSAFPSSAPIPTPPT APSEEDTEELPWSGSPRAGQLDSSQ RDRNTLPKKGLRYQLQSQEETKERR HSHTAGGLPESDDQAELPSPPALSM SLSAKGQLTNIVSPTAATTPRITRSNS IPTHEAAFELYSGSQMGSTLSLAERP KGMIRSGSFRDPTDDVHGSVLSLAS SASSTYSSAEERMQSEQIRKLRRELE SSQEKVATLTSQLSANANLVAAFEQ SLVNMTSRLRHLAETAEEKDTELLD LRETIDFLKKKNSEAQAVIQGALNAS EATPKELRIKRQNSSDSISSLNSITSH SSIGSSKDADAKKKKKKSWVYELRS SFNKAFSIKKGPKSASSYSDIEEIATP DSSAPSSPKLQHGSTETASPSIKSST SSSVGTEVTETPAHSVPHTRLFQAN EEEEPEKKEVSELRSELWEKEMKLT DIRLEALNSAHQLDQLRETMHNMQ LEVDLLKAENDRLKVAPGPSSGCTP GQVPGSSALSSPRRSLGLALSHPFSP SLTDTDLSPMDGISTCGSKEEVTLRV VVRMPPQHIIKGDLKQQEFFLGCSK VSGKVDWKMLDEAVFQVFKDYISK MDPASTLGLSTESIHGYSLSHVKRVL DAEPPEMPPCRRGVNNISVALKGLK EKCVDSLVFETLIPKPMMQHYISLLL KHRRLVLSGPSGTGKTYLTNRLAEY LVERSGREVTDGIVSTFNMHQQSCK DLQLYLSNLANQIDRETGIGDVPLVI LLDDLSEAGSISELVNGALTCKYHKC PYIIGTTNQPVKMTPNHGLHLSFRM LTFSNNVEPANGFLVRYLRRKLVES DSDVNANKEELLRVLDWVPKLWYH LHTFLEKHSTSDFLIGPCFFLSCPIGI EDFRTWFIDLWNNSIIPYLQEGAKD GIKVHGQKAAWEDPVEWVRDTLPW PSAQQDQSKLYHLPPPSVGPHSTAS PPEDRTVKDSTPNSLDSDPLMAMLL KLQEAANYIESPDRETILDPNLQATL	False	False	1.649	2.187	0.938