	UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochndrion	endoplasmi reticulum
0	Q04690	NF1_MOUSE	Mus musculus	Neurofibromin	28.298582	S676;T782;T2577;T2583	S866;S878;S2190;S2469;T2516;S2517;S2523;S2525;S2545;T2567;S2599;S2804;S2819	33300544;30016717;34418053	MAAHRPVEWVQAVVSRFDEQLPIKT GQQNTHTKVSTEHNKECLINISKYK FSLVISGLTTILKNVNNMRIFGEAAE KNLYLSQLIILDTLEKCLAGQPKDTM RLDETMLVKQLLPEICHFLHTCREG NQHAAELRNSASGVLFSLSCNNFN AVFSRISTRLQELTVCSEDNVDVHDI ELLQYINVDCAKLKRLLKETAFKFKA LKKVAQLAVINSLEKAFWNWVENYP DEFTKLYQIPQTDMAECAEKLFDLV DGFAESTKRKAAVWPLQIILLILCPEI IQDISKDVVDESNINKKLFLDSLRKA LAGHGGSRQLTESAAIACVKLCKAST YINWEDNSVIFLLVQSMVVDLKNLL FNPSKPFSRGSQPADVDLMIDCLVS CFRISPHNNQHFKICLAQNSPSTFH YVLVNSLHRIITNSALDWWPKIDAVY CHSVELRNMFGETLHKAVQGCGAH PAIRMAPSLTFKEKVTSLKFKEKPTD LETRSYKCLLLSMVKLIHADPKLLLC NPRKQGPETQSSTAELITGLVQLVPQ SHMPEVAQEAMEALLVLHQLDSIDL WNPDAPVETFWEISSQMLFYICKKL TSHQMLSSTEILKWLREILICRNKFL LKNKQADRSSCHSLYLYGVGCEMSA TGNTTQMSVDHDEFLRACTPGASLR KGRGNSSMDSTAGCSGTPPICRQAQ TKLEVALYMFLWNPDTEAVLVAMS CFRHLCEEADIRCGVDEVSVHNFLP NYNTFMEFASVSNMMSTGRAALQK RVMALLRRIEHPTAGNIEAWEDTHA KWEQATKLILNYPKAKMEDGQAAES LHKTIVKRRMSHVSGGGSIDLSDTD SLQEWINMTGFLCALGGVCLQQRSS SGLATYSPPMGAVSERKGSMISVMS SEGNIDSPVSRFMDRLLSLMVCNHE KVGLQIRTNVKDLVGLELSPALYPML FNKLKNTISKFFDSQGQVLLSDSNT QFVEQTIAIMKNLLDNHTEGSSEHL GQASIETMMLNLVRYVRVLGNMVH AIQIKTKLCQLVEVMMARRDDLSFC QEMKFRNKMVEYLTDWVMGTSNQ AADDDIKCLTRDLDQASMEAVVSLL AGLPLQPEEGDGVELMEAKSQLFLK YFTLFMNLLNDCSEVEDENAQTGG RKRGMSRRLASLRHCTVLAMSNLL NANVDSGLMHSIGLGYHKDLQTRA TFMEVLTKILQQGTEFDTLAETVLAD RFERLVELVTMMGDQGELPIAMALA NVVPCSQWDELARVLVTLFDSRHLL YQLLWNMFSKEVELADSMQTLFRG NSLASKIMTFCFKVYGATYLQKLLDP LLRVIITSSDWQHVSFEVDPTRLEPS ESLEENQRNLLQMTEKFFHAIISSSS EFPSQLRSVCHCLYQATCHSLLNKA TVKERKENKKSVVSQRFPQNSIGAV GSAMFLRFINPAIVSPYEAGILDKKP PPRIERGLKLMSKVLQSIANHVLFTK EEHMRPFNDFVKSNFDLARRFFLDI ASDCPTSDAVNHSLSFISDGNVLAL HRLLWNNQEKIGQYLSSNRDHKAV GRRPFDKMATLLAYLGPPEHKPVAD THWSSLNLTSSKFEEFMTRHQVHE KEEFKALKTLSIFYQAGTSKAGNPIF YYVARRFKTGQINGDLLIYHVLLTLK PYYAKPYEIVVDLTHTGPSNRFKTDF LSKWFVVFPGFAYDNVSAVYIYNCN SWVREYTKYHERLLTGLKGSKRLIFI DCPGKLAEHIEHEQQKLPAATLALE EDLKVFHNALKLAHKDTKVSIKVGS TAVQVTSAERTKVLGQSVFLNDIYYA SEIEEICLVDENQFTLTIANQGTPLTF MHQECEAIVQSIIHIRTRWELSQPDS IPQHTKIRPKDVPGTLLNIALLNLGS SDPSLRSAAYNLLCALTCTFNLKIEG QLLETSGLCIPANNTLFIVSISKTLAA NEPHLTLEFLEECISGFSKSSIELKH LCLEYMTPWLSNLVRFCKHNDDAK RQRVTAILDKLITMTINEKQMYPSIQ AKIWGSLGQITDLLDVVLDSFIKTSA	True	False	3.869	4.711	2.373	1.924

									TGGLGSIKAEVMADTAVALASGNVK LVSSKVIGRMCKIIDKTCLSPTPTLEQ HLMWDDIAILARYMLMLSFNNSLD VAAHLPYLFHVVTFLVATGPLSLRAS THGLLINIIHSLCTCSQLHFSEETKQ VLRLSLTEFSLPKFYLLFGISKVKSAA VIAFRSSYRDRSFSPGSYERETFALT SLETVTEALLEIMEACMRDIPTCKW LDQWTELAQRFAFQYNPSLQPRALV VFGCISKRVSHGQIKQIIRILSKALES CLKGPDTYNSQVLIESTVIALTKLQP LLNKDSPLHKALFWVAVAVLQLDEV NLYSAGTALLEQNLHTLDSLRIFND KSPEEVFMAIRNPLEWHCKQMDHF VGLNFNSNFNFALVGHLLKGYRHPS PAIVARTVRILHTLLTLVNKHRNCDK FEVNTQSVAYLAALLTVSEEVRSRCS LKHRKSLLLTDISMENVPMDTYPIH HGDPSYRTLKETQPWSSPKGSEGYL AATYPAVGQTSPRARKSMSLDMGQP SQANTKKLLGTRKSFDHLISDTKAPK RQEMESGITTPPKMRRVAETDYEME TQRIPSSQQHPHLRKVSVSESNVLL DEEVLTDPKIQALLLTVLATLVKYTT DEFDQRILYEYLAEASVVFPKVFPVV HNLLDSKINTLLSLCQDPNLLNPIH GIVQSVVYHEESPPQYQTSYLQSFGF NGLWRFAGPFSKQTQIPDYAELIVKF LDALIDTYLPGIDEETSEESLLTPTSP YPPALQSQLSITANLNLSNSMTSLAT SQHSPGLDKENVELSPTAGHCNSG RTRHGSASQVQKQRSAGSFKRNSIK KIV						