

UniprotKB ID	Entry name	organism	full name	oglcna score	oglcna sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extract region
Q6P5H2	NEST_MOUSE	Mus musculus	Nestin	32.044098	NaN	S312;T316;S356;S359;T389;S565;S575;S623;S688;S731;S775;S841;S862;S894;S963;S1010;S1021;S1106;S1127;S1177;S1188;S1195;S1216;S1290;S1541;S1565;S1656;S1665;S1745;S1747;S1837;S1860;S1861	22645316;24788674	MEGCVGEESFQMWELNRRLEAYLT RVKTLLEEQNQLLSAELGGLRAGSGD ASWRARADDELAALRVLDQRWRE KHEAEVQRDNLAEELESVAGRCQQ VRLARERTIEEAACSRRALEAEKNAR GWLSTQAAELEERELEALRASHEEER AHLNAQAACTPRRPPAPAHASPIRAP EVEELARRLGEVWRGAVRDYQERVA HMESSLQARERLQAVRGARES LEVQQQLQADDRSLQERREALEQRLE GRWQDRLQATEKFQLAVEALEQEK QGLQSQIAQILEGGQQLAHLKMSLS LEVATYRTLLEAENSRLQTPGRSSQA SLGFDPKLLHFLGIPEDQHLGSVL PVLSPTSFSSPLPNTLETPTVAFKLT QEFLKARTPTLASTPIPPMSEAPYPK NAEVRAQDVPHSLQGGRRQQAPEPL WAEATVPSSTGVLPELEPGGEQPD HFPDDPTSLAPPLNPHHSILEAKDR ESSESRSVSSIFQEEEGQIWELVKKEA ATEVKVENS LAQEIQESGLDTEEIQD SOGPLQMETLEALGDEPLMSLKTQ NHETPGKENCNSSIEENSGTVKSPE KEKQTPKLSLEEKVNAEAKTLENGV LELSKPLGEEPRMEDQELMSPEHT LETVSFLGKENQEVRSSEEQNLES LITFKESQYPLGGPEAEDQMLERL VEKEDQRFPSPPEEQAFRPLEKE NQEPLRFEEAEDQVLERLIEKERQE SLKSPPEEQQAFRLLEKENQEPLR FEDAEDQVLERLIEKERQESLKSPEE EDQQAFRLLEKENQEPLRFEEAEDQ VLERLVEKESQESLKSPEEEDQRTG KPLEKENQESLRSLDENQETIVLLES KNQRPLRSLEVEEEEQRIVKPLEKVS QVSLLESLEKENVQSPRYLEEDDHMI KSILLEDKTHEILGSLEDRNGENFIPP ENETQGSLRPPPEEQQRIVNHLEKE SQEFLRSPEAEVEEVEEVMVRSLEGE NHDPLSSVVKEEQMAESKLENESQ DSRKSLDEDESQETFGSLEKENLES RSLAQDQEEQKLEQETQOPLRAVE DEQMTVNPPEKVDPELPKPLRNDQ EVVRSLDKENQESLVSLEGGMETV KSSSETENIESLETVGECLGRKRSVDT QEPLWSTEVTSSETIEPLEDETQEPLG CVDENQEVLTPLERESQELRSLGKW NPETVESPGGVEDSQOCLEVEEGPE REQHQESLRSLEGEVWELPGSGSQ QRWEDVVEDGEGQASLGATGVET EDKAEHLHRGQGGEEKAVEEGELLQ DAVGEAWSLGSSEPKQRPVPAEPLD DLEGQPEQTGTLEVPVAQGMPEATE QDEDRAGAGEQDSVEVTLGLEAARA GLELEQEVVGLDPRHFAREEAIHP SLGEESVKAKIDQGLEEPGKEPKEA GALDSGIPELPKTSSETLECKGWEEES GEGWEEEAASLETSDHEGSHAPQP RPPKTEEDELQAALTVPKPLLEPC SPIPILTAHELQQAEGIQEAGWQP EAGTEALGRVEDEPEFGRGEIPEGL QDWEEGREDSEADELGETLPDSTPL GLYLKSPASPKEWQAGEQRLFPQGE ARKEGWSPAALAAQGLSDPPEEEQQ GHSDLSSEEFEDLGTASLLPGVP KEVSDHLGQEPVLPQACWDQGGGE SDGFADDEESGEEGEEEDADEEEGA ESGTQWVGPGPSGGVQVQDVTQR GDLEHESVGDGSLWDDGLSAAAAN VLVTALETVSQDSAEPSPGSEGESAS LEGEEQAIDHLDAPQEVTSVVPGA GDTFDISGQGNLESEQVNGRMEN GLEQAEGQVVLHGDEDOGIPLQEQG TLKAPLVGSPVHLGSPQLKFTLSGV DGDSWSSGED	False	False	3.149	3.932	2.63	2.172	2.119	2.785	2.8