

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracell region
Q9Z0R4	ITSN1_MOUSE	Mus musculus	Intersectin-1	36.83566	T718;S884	S203;S318;S334;S335;S685;T890;S894;S895;S897;S971;T977;S979;S988;S1130;T1137;S1638	40885482	MAQFPTPFGGSLDVVAITVEERAKH DQQLSLKPIAGFITGDQARNFFFQS GLPQPVLAQIWAADMNDGRMDQ VEFSIAMKLIKLLKQGYQLPSTLPPV MKQQPVAISSAPAFGIGGIASMPPLT AVAPVPMGSIPIVVGMSPLVSSVPPA AVPPLANGAPPVIQPLPAFAHAAATL PKSSSFSSRSGPGSQLNTKLQKAQSF DVASAPPAEWAIVPQSSRLKYRQLF NSHDKTMSGHLTGPQARTILMQSSL PQAQLASIWNLSIDIDQDGKLTAEEFI LAMHLIDVAMSGQPLPPLVPEYIYP SFRVRSGSGMSVSSSSVDQRLPE EPSSEDEQQPEKKLPVTFEDKKREN FERGSVELEKRRQALLEQQRKEQER LAQLERAEOERKERERQEQERKRQL ELEKQLEKQRELERQREERREKEIE RREAARKRELERQRQLEWERNRRQE LLNQRNKEQEGTVVLKARRKTLEFE LEALNDKKHQLEGLQDIRCRLATO RQEIESTNKSRELRIAEITHLQQQLQ ESQQMLGRLIPEKQILSDQLKQVOQ NSLHRDSLTLKRALEAKELARQQL REQLDEVERETRSKLOEIDVFNQL KELREIHSKQQLQKORSLEAARLKQ KEQERKSLELEKQKEDAQRRVQERD KQWLEHVQQEEQPRPRKPHEEDRL KREDSVRKKEAEERAKPEMQDKQS RLFHHPHQEPAKLATQAPWSTTEKGP LTISAQESVKVYYRALLYPFESRSHD EITIQPGDIVMVEQSOTGEPGWLGG ELKGGTGWFPANYAEKIPENEVPTP AKPVTDLTSAPAPKLALRETPAPLPV TSSEPSTTPNNWADFSTWPSSSNE KPETDNWDTWAAQPSLTVPSAGQL RQSAFTPATATGSSPSPVLGQGEKV EGLQAQALYPWRAKKDNHLNFNKS DVITVLEQQDMWVWFGVQGGQKGW FPKSYVKLISGPRKSTSIDTGPTESP ASLKRVASPAAPKPAIPGEEFIAMTY ESSEQDLDLTFQQGDVIVVTKKDGDW WTGTVGDKSGVFPNSYVRLKDSGS GTAGKTGSLGKKEIAQVIASAAATG PEQLTLAPGQLILIRKKNPGGWWEQ ELQARGKKRQIGWFPANYVLLSPG TSKITPTELPKTAVQPAVCQVIGMYD YTAQNDDLEAFSGQIINVLNKEDP DWWKGEVSGQVGLFSPSNYVCLTD MDPSQQWCSDLHLLDMLTPTERKR QGYIHELIVTEENYVNDLQLVTEIFQ KPLTESELLTEKEVAMIFVNWKELI MCNIKLLKALRVRKMSGKMPVK MIGDILSAQLPHMQPYIRFCSCQLN GAALIQOKTDEAPDFKEFVKRLAMD PRCKGMPSSFILKPMQRVTRYPLII KNILENTPENHPDHSHLKHLEKAE ELCSQVNEGVRKENSRLREWIQA HVQCEGLSEQLVFNVSNTCLGPRKF LHSGKLYKAKSNKELYGFLFNDLFL LTQITKPLGSSGTDKVFSPKSNLQYK MYKTPIFLNEVLVKLPTDPSGDEPIF HISHIDRVYTLRAESINERTAWVQKI KAASELYIETEKKKREKAYLVRQRA TGIGRLMVNVVGGIELKPCRSHGKS NPYCEVTMGSCCHITKTIQDTLNP WNSNCQFFIRDLEQEVLCITVFERD QFSPDDFLGRTEIRVADIKKDGSGK PVTKCLLLHEVPTGEIVRDLQLFD EP	True	True	5.0	4.558	1.402	1.317	1.661	5.0	1.647