

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	extracellular region
D3YXG0	HMCN1_MOUSE	Mus musculus	Hemicentin-1	25.019509	S351;S2875	NaN	34418053	MIAQEVVHTVFLVALFRSSLAGDGT PQESRAEIEPEGASTLAFVFDVTGS MYDDLQVIEGASKILETSLKRPKRP LYNFALVPPHDPEIGPVITITDPKKF QYELRELYVQGGGDCPEMSIGAIIA LEISLPGSFYVFTDARSKDYRLTHEV LQLIQKQSQVVFVLTGDCDDRNHI GYKVYEEIASTSSGQVPHLDKQVNH EVLKWVEEAVQASKVHLLSTDHLEH AVNTWKIPFDPSLKEVTVSLGSPSPV IEIRNPFGLIKKGFGLNELLNIHNS AKVVNVKEPEAGMWTVKTSSSGRH SVRITGLSTIDFRAGFSRKPITLDFKKT MSRPVQGIPTYVLLNTSGISSPARVD RLELLSISGGSLKTIPIVKHYDPDKPY GIWNISDFIPPDEAFFLKVTGYDKDG YLFQRVSSVSFSSIVPDAPKVTMPTR TLGYLQPGQILCSVESFLPFTLSFM RDGIALGVDQYLRESASVNWDFTKV TLDSEGFYDCLAVSSAGTGRAQTFDD VSEPPPIQLPNNVTVTPGERAVLAC LVISAVDYNLTWQRSGRDIRLADSAR IRTLANLSLELRVSVKIGDAGEYRCVV SSEGSAASVFLTVQEKPKVTVMVP KNQSFYGGSEISIMCSATGYPKPKIV WTMNEFMFMGSHRYRMTSEGLFI KNAVPKDAGTYACLASNAAGTDKQT STLRYIEAPKLVEQSELLVALGDDT VMECKTSGIPPPQVKWFKGDLELRP STFLSIDPLVGLLKIQETQDLDAGDY TCVAINEAGRATGRLLDVGSPPVFI QEPSDVAVEIGSNVTLPCYVQGYPEP KIKWRRLDNMPVFSRPFVSFISQL RTGALFISNLWASDKGTYICEAENQ FGKIQSQTIVTVTGLVAPLIGISPSMA SVIEGQPLTLPCTLLAGNPIPERRWM KNSAMLVQNPYITVRSDGSLHIERV RLQDGGKYTCVASNVAGTNNKITSV AVHVLPSIQHGQQILSTIEGVPTLPL CRASGIPKPSITWSKKGELISTSSAKF SAGADGSLYVSPGSEESGEYICTAT NAAGYAKRKVQLTVYVPRVFGDQR GLSQDKPVEISVLAGEAAILPCEAKS LPPPIITWAKDSQLISPFSPRHTFLPS GSMKITETRVSDSGMYLCVATNIAG NVTQSVKLSVHVPPKIQHGNRHIKV QVGQRVDILCNAHGSPPPVTWFKS GRPFLDGAQHPGSPDGLSIEQAVIS DAGVYTCAATNIAGSDEAEVTLHVQ EPPSVEDLQPPFNTPFQERLANQRIE FPCPAKGTPKPTIKWLHNGREVTGQ EPGVSILEDGALLVIASVTPHNNGEY ICVAVNEAGTTERKYNLKVHVPPVIR DKEHVTNVSVLTSQLASLYCEVEGT PSPVITWYKDDIQVTESSVQIVNNG KILKLFKVSAAEDAGRYSCKAINIAGTS QKDFSVNLVPPSILGASSPSESVV LNHNVTLOCPGTGVPPAIHWFKDG KPLFLGDPNIELSDRGQSLHLRNAR RSDKGRYQCTVSNAAAGQAKDIKLT VYVPPSIKGGNITTEISALLNSIVKLE CETRGLPVPAITWYKDGQVVTSSQ ALYIDKGQLLHIQRAQVSDSATYTC AANVAGTAEKSFHVDIYVPTIEGDL TAPSNKQVIIGQSLILECKAAGNPPPI LTWLKDGVPVKASDNHIEAGGKKL EILSALEVDRGOYICVATSVAGEREIK YEVVVLVPPAVEGGEETSIFIVLANN LLELDCQVSGSPPPTIMWLKGGQLI DERDGFKILLNGRKLVIAQAQVSDT GLYQCVATNIAGDHRKEFEVTVHVP PTIKSSDLPEKTVVRYKPVTLQCIAN GIPNPSITWLKDDQPVNTAHGNLKI QSSGRVLQIAKALLEDAGRYTCVATN AAGEAHQHTQLHVHEPPSLDDAGK MRNETVVVNNPIQLECKATGKPLPV ITWYKDSHPLSGSASAAFLKRGQVL	False	True	1.09	1.707	1.373	1.075	0.784	4.367	5.0

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