	UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochndrion	endoplasmic reticulum	golgi apparatus	plasma membran
0	Q86V15	CASZ1_HUMAN	Homo sapiens	Zinc finger protein castor homolog 1	23.493983	S444;S847;T1472	S720;S721;S981	30379171;32574038;35132862;29485866;38253038	MDLGTAEGTRCTDPPAGKPAMAPK RKGGLKLNAICAKLSRQVVVEKRAD AGSHTEGSPSQPRDQERSGPESGAA RAPRSEEDKRRAVIEKWVNGEYSEE PAPTPVLGRIAREGLELPPEGVYMVQ PQGCSDEEDHAEEPSKDGGALEEK DSDGAASKEDSGPSTRQASGEASSL RDYAASTMTEFLGMFGYDDQNTRD ELARKISFEKLHAGSTPEAATSSMLP TSEDTLSKRARFSKYEEYIRKLKAGE QLSWPAPSTKTEERVGKEVVGTLPG LRLPSSTAHLETKATILPLPSHSSVQ MQNLVARASKYDFFIQKLKTGENLR PQNGSTYKKPSKYDLENVKYLHLFK PGEGSPDMGGAIAFKTGKVGRPSKY DVRGIQKPGPAKVPPTPSLAPAPLAS VPSAPSAPGPGPEPPASLSFNTPEYL KSTFSKTDSITTGTVSTVKNGLPTDK PAVTEDVNIYQKYIARFSGSQHCGHI HCAYQYREHYHCLDPECNYQRFTSK QDVIRHYNMHKKRDNSLQHGFMRF SPLDDCSVYYHGCHLNGKSTHYHC MQVGCNKVYTSTSDVMTHENFHKK NTQLINDGFQRFRATEDCGTADCQF YGQKTTHFHCRRPGCTFTFKNKCDI EKHKSYHIKDDAYAKDGFKKFYKYE ECKYEGCVYSKATNHFHCIRAGCGF TFTSTSQMTSHKRKHERRHIRSSGA LGLPPSLLGAKDTEHEESSNDDLVD FSALSSKNSSLSASPTSQQSSASLAA ATAATEAGPSATKPPNSKISGLLPQG LPGSIPLALALSNSGLPTPTPYFPILA GRGSTSLPVGTPSLLGAVSSGSAASA TPDTPTLVASGAGDSAPVAAASVPAP PASIMERISASKGLISPMMARLAAAA LKPSATFDPGSGQQVTPARFPPAQV KPEPGESTGAPGPHEASQDRSLDLT VKEPSNESNGHAVPANSSLLSSLMN KMSQGNPGLGSLLNIKAEAEGSPAA EPSPFLGKAVKALVQEKLAEPWKVY LRRFGTKDFCDGQCDFLHKAHFHC VVEECGALFSTLDGAIKHANFHFRT EGGAAKGNTEAAFPASAAETKPPMA PSSPPVPPVTTATVSSLEGPAPSPASV PSTPTLLAWKQLASTIPQMPQIPASV PHLPASPLATTSLENAKPQVKPGFLQ FQENDPCLATDCKYANKFHFHCLF GNCKYVCKTSGKAESHCLDHINPN NNLVNVRDQFAYYSLQCLCPNQHC EFRMRGHYHCLRTGCYFVTNITTKL PWHIKKHEKAERRAANGFKYFTKRE ECGRLGCKYNQVNSHFHCIREGCQ FSFLLKHQMTSHARKHMRRMLGK NFDRVPPSQGPPGLMDAETDECMD YTGCSPGAMSSESSTMDRSCSSTPV GNESTAAGNTISMPTASGAKKRFWII EDMSPFGKRRKTASSRKMLDEGMM LEGFRRFDLYEDCKDAACQFSLKVT HYHCTRENCGYKFCGRTHMYKHAQ HHDRVDNLVLDDFKRFKASLSCHF ADCPFSGTSTHFHCLRCRFRCTDST KVTAHRKHHGKQDVISAAGFCQFSS SADCAVPDCKYKLKCSHFHCTFPGC RHTVVGMSQMDSHKRKHEKQERG EPAAEGPAPGPPISLDGSLSLGAEPG SLLFLQSAAAGLGLALGDAGDPGPP DAAAPGPREGAAAAAAAAGESSQED EEEELELPEEEAEDDEDEDDDEDDD DEDDDEDDDDEDLRTDSEESLPEAA AEAAGAGARTPALAALAALGAPGPAP TAASSP	None	None	None	None	None	None	None	None