

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membr
Q9Y566	SHAN1_HUMAN	Homo sapiens	SH3 and multiple ankyrin repeat domains protein 1	27.086674	S1788;T1790;T1794;S1869	T186;S540;S671;S791;S890;S1287;S1436	28657654	MTHSPATSEDEERHSASECEPGESESDSSPDGPRGPRGTRGQGSAGPGLASVRGLQGRSMVDPDDAHFSMMVFRIGIPDLHQTKCLRFNPDATIWTAKQQVLCALSESLODVLNLYGLFPATSRDANFLEEEERLLREYPQSFKEGVPYLEFRYKTRVYKQTNLDEKQLAKLHKTGLKKFLEYVQLGTSKVARLLDKGLDPNYHDSGETPLTLAAQTEGSVEVIRTLCLGGAHIDFRARDGMALHKAACARHCLALTALLDLGGSPNYKDRRGLTLPFHTAMVGGDPRCCCELLFNRAQLGIADENGWQEIHQACQRGHSQHLEHLLFYGAEPGAQNASGNTALHICALYNKETCARILLYRGADKDVKNNNGQTPFQVAVIAGNFELGELIRNHREQDVPFQESPKYAARRRGGPPTGLTVPPALLRANS DTSMALPDWMMVFSAPGAASSGAPGPTSGSQGSSQPSAPTTKLSSGTLRSASSPRGARARSPSRGRHPEDAKRQPRGRPSSSGTPREGPAGGTGGSGGPGGSLGSRRRRKLYSAVPGRSFMVAVKSYQAQAEGEISLSKGEKIKVLSIGEGGFWEQVKGKRVGWFPSDCLEEVANRSQESKQESRSDKAKRFLRHRYTVGSDSFDAPSLMDGIGPGSDYIIKEKTVLLQKDSGFGFVLRGAKAQTPIEEFTPTAFPALQYLESVDEGGVAWRAGLRMGDFLIEVNGQNVVKVGHQRQVVMIRQGGNTLMVKVMVTRHPDMDEAVHKKAPQQAARLPPPTISLRKSMSTSELEEMEYEQQPAPVPSMEKKRTVYQMALNKLDEILAAAQQTISASESPGPGGLASLGKHRPKGFFATESSFDPHHRAQPSYERPSFLPPGPGMLRQKSGAAEDDRPYLAPAMKFSRSLSVPGSEDI PPPPTTSPPEPPYSTPPVPSSSGRLTPSPRGGPFNPGSGGPLPASSPASFDGPSPPDTRVGSREKSLYHSGPLPAHHHPHHHHHHHHAPPQPHHHHAHPHPPEMETGSPDDPPRLALGPQPSLRGWRGGGSPSTPGAPSPSHHGSAGGGGSSSQGPALRYFQLPPRAASAAMYVPARSGRGRKGPLVKQTKVEGEPQKGGGLPPAPSPTPASPQPPPAVAAPSEKNSIPIPTIIKAPSTSSSGRSSQGSSTEAEPTQPEPTGGGGGGSSPSPAPAMSPVPPSPSPVPTPASPSGPATLDFTSQFGAALVGAARREGGWQNEARRRSTLFLSDAGDEDEGGDGLGTGAAPGPRLRHSKSIDEGMFAEPYLRLESAGSGAGYGGYGAGSRAYGGGGSSAFTSFLPPRPLVHPLTGKALDPASPLGLALAAERALKESSEGGGAPQPPRPPSPRYEAPPTPHHHSPHAHHEPVLRLWGPASPDPARRELGYRAGLGSQEKSLPASPAAARRLLHRLPPTAPGVGPLLLQLGTEPPAPHPGVSKPWRSAAPEEPERLPLHVRFLENCQPRAPVTSGRGPSEDGPGVPPSPRRSVPPSPTSPRASEENGLPLLVLPPAPSV DVEDGEFLFVEPLPPPLEFSNSFEKPE SPLTPGP PHPLPDTAPATPLPPVPPAVAAAAPTLDDSTASSLTSYDSEVATLTQGASAPGDPHPGPPAPAAPAPAAPQGPDPDPGTDSDGIEEVDSSSDHPLETISASTLSSLAEAGGGSAGGGGAGAGVASGPELLDITYVAYLDGQAFGGSSTPGPPYPPQLMTPSKLRGRALGASGLRPGPSGGLRDPVPTPTSVTVTGA GTDGLLALRACSGPPTAGVAGGPVAVEPEVPPVPLTASSLPRKLLPWEEGPGPPPPPLPGPLAQPQASALATVKASIISELSSKLQQFGGSSAAGGALPWARGSGGGGDSHHGGASYVPERTSSLQRQLSDDSSQSSLLSKPVSSLFQNWPKPPLPLPTGTGVSP TAAAAPGATSPASSSSTSTRHLQGVFEMRPPLLRRAPSPSLLPASEHKVSPAPRPSLPI	True	True	4.611	3.922	1.411	1.2	0.68	4.66

