

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
Q68DK2	ZFY26_HUMAN	Homo sapiens	Zinc finger FYVE domain-containing protein 26	22.903221	T929;S2226	S297;S615;S619;S703;S800;S1742;S1764;S1780;S1782	38253038	MNHHPFGKEEAASQKQLFGFFCECLRRGEWLELAQACVQLOEQGGDIPKRVEDILQALVVCNLLRCGGQDINPORVAWVWLLVLEKWLAREKLLPVVFRRKLEFLLLSEDLQGDIPENILEEYELTQTQAVGHVDPDGNPRRESWTPRLSSEAVSVLWDLRLRQSPQAQALLELLLEEDDGTGLCHWPLQNALVDLRKALRALQGPDSVPPGVDAIYGALRTLRCPAEPLGVELHLLCEELLEACRTEGSPLEERLLSCLLHKASRGLLSLYGHTYAEKVTEKPPRATASGKVSPPDHLDPERAMLALFSNPNPAEAWKVAYFYCLSNKHFLEQLVLTALLKKEEDFPNLGCLLDREFRPLSCLLVLLGWTHCQSLSAKRLLQTLHRTQGPCDELLRDACDGLWAHLEVLWEWCIQSSNPIPKRDLLYHLHGGDSHSVLYTLHHLTNLPALREEDVLKLLQKVPKDPQOQEPDAVDAPVPEHLSQCQNLTLYQGFCAKYAIYALCVNSHQHSCQCQCKDSLSEDLASATEPANDLSLSPGAANLFSTYLARCOQYLCVIPDLCLELLENIFSLLLITSADLHPEPHLPEDYAEDDDIEGKSPSGLRSPSESPQHIAHPERKSERGSLGVPKTLAYTMPSHVKAEPKDSYGPHRHSFLDLKHFTSGISGLADEFAIGAFLRLLQEQLEISSRSPPEKPKQESQSCSGSRDGLQSRHLHRLSKVVSEAQWRHKVVTNHRSEEQPSRRYQPA TRHPSLRRGRTRRSQADGRDRGSNPSLESTSELSTSTSEGLSAMSGRNELHSRLHPPHQSLLPMMFSPPELASCILRGNFAEAHQVLTFFNLKSSPSSGELMFMERYQEVIELAQVEHKIENQNSDAGSSTIRRTGSGRSTLQAI GSAAAAGMVFYISDVIDKLLNTSGDPIPMQLQEDFWISTALVEPTAPLREVLEDLSPMAAFDLACSQCQLWKTC KQLETAERLNSLERRGRRIDHVLNADGIRGFPVVLQQISKSLNYLLMSASQTKSESVVEKGGPPRCSTITELLQMCWPSLSEDCVASHHTLSQQLDQVLQSLREALELPEPRTPLSSEVQA AQKAPAEAEHPVQIQTLQKLNKLGKQTPSGSRQMDYLGTFFSYCSTLAAVLLQSLSEPDHVEVKVGNPFVLLQSSSQLVSHLLFERQVPPERLAALLAQENLSLQVQVIVSCCEPLALCSSRQSQTSSLLTRLGTALQLHASHCLDDLPLSTPSSPRITENPTLERKPYSSPRDSSLPALTSALAFKRSRKLATVACLGASPRKVKSPKSLSWKELRGRREVPAAEQVARECERLLEQFPLFEAFLAAWEPLRGSLLQGGQSLAVNLCGWASLSTVLLGLHSPIALDVLSEAFEESLVARDWSRALQLTEVYGRDVEDLSSIKDAVLSCAVACDKEGWQYLPVVKDASLRSRLALQFVDRWPLESCEILAYCISDTAVQEGKCELQRKLAELQVYQKILGLQSPVWCDWQTLRSCCQVEDPSTVMNMILEAQEYELCEFWGCLYP IPREHLISLHQKHLHLERRDHDKALQLLRIPDPTMCLEVEQSLDQH TSLATSHFLANYLTHFYGQLTAVRHREIQALVYVSKILLTPEQHRASYS HLSSNPLFMLEQLLMNMKVDWATVAVQTLQQLLVGQEGFTMDEVDSLLSRYAEKALDFPYPQREKRSDSVIHLQ EIVHQAADPETLPRSPAEFSPAAPP GISSIHSPSLRERSFPPTQPSQEFVPPATPPARHQWVPDETESICMVCCREHFTMFNRRHHCRCRGLVCSSTCKKMVVEGCRENPARVCDQCYSYCNKDVPEEPSEKPEALDSSKNESPPYSFVVRVPKADEVWILDKEEENELVRS EPHYEQAPSASLCAILNLHRDSIACGHQLEHCCLRSKGLTNPEVDAGLLTDIMKQLLFSAKMMFVKAGQSQDLALCDSYISKVDVNLVAAAYRHVPSL	False	False	3.388	3.349	1.495	1.51	1.549	1.27	0.854

