

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extrace region
P32790	SLA1_YEAST	Saccharomyces cerevisiae	Actin cytoskeleton-regulatory complex protein SLA1	24.475439	NaN	S447;S449;S454;S799;T831;T858;T887;T904;T984;T993;S996;T1075	33229814	MTVFLGIYRAVYAYEPQTPEELAIQE DDLLYLLQKSDIDDWWTVKKRVIGS DSEEPVGLVPSTYIEEAPVLKKVRAIY DYEQVQNADEELTFHENDVFDVFD DKDADWLLVKSTVSNFEGFIPGNYV EPENGSTSKQEQAPAAAEAPAATPA AAPASAAVLPFNFLPPPQHNDRARM MQSKEDQAPDEDEEGPPPAMPARP TATTETTDATAAAVRSRTRLSYSDND NDDEEDDYNNNSNSNVGNHEYNT EYHSWNVTEIEGRKKKKAKLSIGNN KINFIPQKGTPEHEWSIDKLVSYDNEK KHMFLFVDPYRSLELHTGNTTTC EIMNIIGEYKGASRDPGLREVEMAS KSKKRGIVQYDFMAESQDELTIKSG DKVYILDDKSKDWWMCQLVDSGK SGLVPAQFIEPVRDKKHTESTASGIIK SIKKNFTKSPSRSRSRSRKSNANAS WKDDELQNDVVGSAAGKRSRKSLL SSHKKNSSATKDFPNPKSRLWVDR SGTFKVDAAEFIGCAKGIHLHKANG VKIAVAADKLSNEDLAYVEKITGFSL EKFKANDGSSSRGTDSRDSERERRR RLKEQEEKERDRRLKERELYELKKA RELLDEERSRLQEKELPPIKPPRPTS TTSVPNTTSVPPAESNNNNSSNKY DWFEFFLNCGVDVSNQRYTINFDR EQLTEDMMPDINNMLRITLGLREG DIVRVMKHLDKKFGRENIASIPTNAT GNMFSQPDGSLNVATSPETSLPQQL LPQTTSPAQTAPSTSAETDDAWTVK PASKESNLLSKKSEFTGSMQDLLD LQPLEPKAAAATPEPNLKDLEPVKT GGTTVPAAPVSSAPVSSAPAPLDPFK TGGNNILPLSTGFVMMPMITGGDM LPMQRTGGFVVPQTTFGMQSQVTG GILPVQKTGNLIPISNTGGAMMPQ TTFGAAATVLPQKTTGGGLPIATTG GAQFPQTSFNVGQQQLPTGSILPV QKTANGLISANTGVSMPTVQRTGGT MIPQTSFGVSQQLTGGAMMTQPON TGSAMMPQTSFNAPQITGGAMMP QTSFNALPQVTGGAMMPLQRTGGA LNTFNTGGAMIPQTSFSSQAQNTGG FRPQSQFGLTLQKTGGIAPLNQNF TGGAMNTLSTGGVLLQQQPQTMNT FNTGGVMQELQMMTTFNTGGAMQ QPQMMNTFNTDGIMQQPQMMNTF NTGGAMQQPQQALQNQPTGFQFG NGPQQSRQANIFNATASNPFQF	None	None	None	None	None	None	None	None	

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