

UniprotKB ID	Entry name	organism	full name	oglcnaescore	oglcnaesites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus
Q92922	SMRC1_HUMAN	Homo sapiens	SWI/SNF complex subunit SMARCC1	20.91903	T603	S310;S328;S330;T335;S350;S357;T398;S573;S822;S825	23301498;20305658;33214551;40596516;38665916;21740066;32119511;40914422;34019948;35138101;28510447;33465208	MAAAAGGGGPGTAVGATGSGIAAAA AGLAVYRRKDGGPATKFWESPETVS QLDSVRVWLGKHYKVVHADAPT KTLAGLVVQLLQFQEDAFGKHVTNP AFTKLPACFMDFKAGGALCHILGA AYKYKNEQGWRRFDLQNPSPRMDRN VEMFMNIEKTLVQNNCLTRPNIYLIP DIDLKLANLKDIIKRHQGTFDEKS KASHHIYPYSSQDDEEWRPVMRK EKQVLVHWGFYSDSYDTVWHSNDV DAEIEDPPIPEKPKVHVWILDTDI FNEWMNEEDYEVDENRKPVSFRQR ISTKNEEPVRSPEERRDRKASANARK RKHSPPPPPTPTESRKSGKGGQA SLYGKRRSQEEDQEDLTKDMED PTPVPNIEEVLFPKNVNLKKDSENTP VKGGTVADLDEQDEETVTAGGKEDE DPAKGDQSRVLDLGEDNVTEQTNHI IIPSYASWFYDNCIHIERRALPEFFN GKNKSKTPEIYLAYRNFMDTYRLNP QEYLSTACRRNLTDGVCAMVRVHA FLEQWGLVNYQVDPESRPMAMGPP PTPHFNVLADTPSGLVPLHLRSPQV PAAQQMLNFPEKNKEKPVDLQNF LRTDIYSKKTAKSKGASAGREWTE QETLLLEALEMYKDDWNKVSEHV GSRTQDECILHFLRLPIEDPYLENSD ASLGPLAYQVPVFSQSGNPMSTVA FLASVVDPRVASAAAKALEEFSRVR EEVPLELVEAHVKKVQEAARASGKV DPTYGLESSCIAGTGPDEPEKLEGAE EEKMEADPDGQQPEKAENKVENET DEGDKAQDGENEKNSEKQDSEVS EDTKSEEKETEENKELDTDCERES DTGKKKVEHEISEGNVATAAAAAA SAATKAKHLAAVEERKIKSLVALLVE TQMKKLEIKLRHFEELETIMDREKE ALEQQRQQLLTERQNFHMEQLKYA ELRARQQMEQQHGGQNPQQAQHQ SGGPGGLAPLGAAGHPGMMMPHQPP PYPLMHHQMPHPHPQPGQIPGPGS MMPGQHMPGRMIPTVAANIHPGSGS GTPPPGMPMPGNILGPRVPLTAPN GMYPPPPQPPPPPPADGVPPPPA PGPPASAAP	True	False	1.441	5.0	1.557	1.056	0.603