	UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochndrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
0	Q8WZ64	ARAP2_HUMAN	Homo sapiens	Arf-GAP with Rho-GAP domain, ANK repeat and PH domain-containing protein 2	25.476563	S346	T77;S1632	36240223	MSSVSEVNVDIKDFLMSINLEQYLL HFHESGFTTVKDCAAINDSLLQKIGI SPTGHRRRILKQLQIILSKMQDIPIYA NVHKTKKNDDPSKDYHVPSSDQNIC IELSNSGSVQTSSPPQLETVRKNLED SDASVERSQYPQSDDKLSPPKRDFP TAEEPHLNLGSLNDSLFGSDNIKIES LITKKTVDHTVEEQQTEKVKLITENL SKLPNADSECLSFVGCSTSGTNSGN GTNGLLEGSPPSPFFKFQGEMIVND LYVPSSPILAPVRSRSKLVSRPSRSFL LRHRPVPEIPGSTKGVSGSYFRERRN VATSTEKSVAWQNSNEENSSSIFPY GETFLFQRLENSKKRSIKNEFLTQG EALKGEAATATNSFIIKSSIYDNRKE KISEDKVEDIWIPREDKNNFLIDTAS ESEYSTVEECFQSLRRKNSKASKSR TQKALILDSVNRHSYPLSSTSGNADS SAVSSQAISPYACFYGASAKKVKSGW LDKLSPQGKRMFQKRWVKFDGLSIS YYNNEKEMYSKGIIPLSAISTVRVQG DNKFEVVTTQRTFVFRVEKEEERND WISILLNALKSQSLTSQSQAVVTPEK CGYLELRGYKAKIFTVLSGNSVWLC KNEQDFKSGLGITIIPMNVANVKQV DRTVKQSFEIITPYRSFSFTAETEKEK QDWIEAVQQSIAETLSDYEVAEKIWF NESNRSCADCKAPDPDWASINLCVV ICKKCAGQHRSLGPKDSKVRSLKMD ASIWSNELIELFIVIGNKRANDFWAG NLQKDEELHMDSPVEKRKNFITQKY KEGKFRKTLLASLTKEELNKALCAA VVKPDVLETMALLFSGADVMCATGD PVHSTPYLLAKKAGQSLQMEFLYHN KFSDFPQHDIHSEGVLSQESSQSTF LCDFLYQAPSAASKLSSEKKLLEETN KKWCVLEGGFLSYYENDKSTTPNGT ININEVICLAIHKEDFYLNTGPIFIFEI YLPSERVFLFGAETSQAQRKWTEAIA KHFVPLFAENLTEADYDLIGQLFYKD CHALDQWRKGWFAMDKSSLHFCL QMQEVQGDRMHLRRLQELTISTMV QNGEKLDVLLLVEKGRTLYIHGHTK LDFTVWHTAIEKAAGTDGNALQDQQ LSKNDVPIIVNSCIAFVTQYGLGCKYI YQKNGDPLHISELLESFKKDARSFKL RAGKHQLEDVTAVLKSFLSDIDDALL TKELYPYWISALDTQDDKERIKKYGA FIRSLPGVNRATLAAIIEHLYRVQKCS EINHMNAHNLALVFSSCLFQTKGQT SEEVNVIEDLINNYVEIFEVKEDQVK QMDIENSFITKWKDTQVSQAGDLLI EVYVERKEPDCSIIIRISPVMEAEELT NDILAIKNIIPTKGDIWATFEVIENEE LERPLHYKENVLEQVLRWSSLAEPG SAYLVVKRFLTADTIKHCSDRSTLGS IKEGILKIKEEPSKILSGNKFQDRYFV LRDGFLFLYKDVKSSKHDKMFSLSS MKFYRGVKKKMKPPTSWGLTAYSE KHHWHLCCDSSRTQTEWMTSIFIA QHEYDIWPPAGKERKRSITKNPKIGG LPLIPIQHEGNATLARKNIESARAEL ERLRLSEKCDKESVDSSLKERASMV AHCLEHKDDKLRNRPRKHRSFNCL EDTEPEAPLGQPKGHKGLKTLRKTE DRNSKATLDSDHKLPSRVIEELNVV LQRSRTLPKELQDEQILK	None	None	None	None	None	None	None	None	None