	UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochndrion	endoplasmic reticulum	golgi appara
	A2ARZ3	FSIP2_MOUSE	Mus musculus	Fibrous sheath-interacting protein 2	29.380791	T2310;T2312;S2313;T3270;T4084;S4638	S430	29562282;34105348;34418053	MELYLSACSKTANVAANKAASSTVA EDSQQCVDGRHKTPIPGVGAAQLLD LPLGVKLPMIPGTDTVYFTTNISEKL FRPSYGFNLSDPYCRLLETQYKSLH DPHLRTYYKRKDILRRLKKGGYITSN NKIVCSLRELNKYRQYLTSLKLDFER NYLREQQLISKQLHKLQETSQLPHC SDVTRFQNWLLQDNTHSIKDQERLL RHRYLDMISKELEQLERTAEEQRLL RIDRDERRQREYTRKKLTLRRKIEEE WKTKEMMLLTKIGEDVKREQKIEEQ RRKSREESDRKKQAMLEKKMAYHL QKMQDTGLKDDIGRNGFDYRGQNG TTFESSSKKRKKQFDDIKIVYPDGDQ KAYRGTSGQVSATVNQSQSSSKDVT KVSASSVTYPAEVQNSSSEQKRSEVT KRLSDERGKNSTDDSARESIISTQLS PTRNAKLSQISLDHQKEEKEMKSTW NGGLSKKSSYAGEPGSPTDAPPQGIF SFPVNSNTQQNLQHCLKDKVTSEEL NSIIQNIMTWVVATVTSILYPAITKYE ERVQNNTYPVTDDSDLSSDSSSFCS TCSEGFTYRNYTAKTLPVDPCTFASD MPIKKPPTPLKPPSAHVERTVIDQTY QRQGQSVPSQVNYQKTSLDYQFPKI GSSKSDSHLLTSLETCTKKSKDATTE TESLEISLLYDKKAKAMDQIKNLKNV FVNFKCHLKGETQLILESIFQEIMSD LSQAIPSLSSVTAEVFVDQTETEREE LLSNVDICSVASEIVENMLEKLESAV EKRCVQMFSQEDLSVDIKPSLSTSG DYLSSVETKPSEETLSYTLEPMCDVA DDMVHAILEKLMILASYKKNDVPPE DTTKHFQQTKTEPIHKVHQQTEQKK ASFASDPANQIVKEEIQSLISSIFSQS SLVGYVEEAISTILGYVQTELNNERLI ASEETVVLLQLLDDVLTQLHQQPVK AGVKKPRRPRVRNLSDPEEKYRVTG TRPFNNLKSKRPFPPVNVPGMVLYS EDDDEEIDNFVQSVLDSSFNDEKSS SQEQVPNYWPKKRDTYFESKRSNKL PTKSTFQNKVGSHDWGLKLELSLSS EDIVKTKHCLGQEPSIFSQDQKHQIQ KASENIVKHILTDMLKDMSSDSSSH LGSQTGKGASAFISEKSQGLSDQEW MEQMFSVSEICAFAHEITDSVINILH KASMHIPNTIKNAFTSVHPTHVAPF DTAHTSKETPSKMPFKVWFDSEKK MKYLSSLNMEHEKTSQLRSGKCEP KRVNDITDKITNTIFKRLKLFVCPKL QIGNKSSLIEKSLHSQLSTYTMKIVN IILHAIQSELEINKTKPNLKETDHPKC HKNKGWFTDPNKVVESRVTSVNDD IMESPLLTCICEMISSTNEDKKNTST YTDKTLSTSICESGNFHKQSILSNKQ DKNSFCQLLAKPCLQHSLADEKDFK VSSKLEVLDQIGDTLHEMLGKLTGD HPDPQPSCSHQNTETIDKDPPTMSN TQLISKAILENVLAKLCDVDIDTSIVN SGPKTVPESLDIDNLSFASTMEEMA KCTNIISNIISKIMKDNKEVTKSKAK NDLPTSSKTEIPKEMCPQNLKNIAS DILNMVFAKLEHFASGSVVNVGNLN DENKKEHTVDWECESNSSPADSHD KSLQSTLYSHAKKVSNGILKAIQTEL NMNPPDCKTDKKRSPEETQILTNIV DLILDVVSSDMFAEPESENQSNENY GYRPTYGNFLPGGAESDSFLDDDTQ NKELIRDATSFNEETRTLSTDQMGL ERTLSKIEVKLKEPHRSPIVPIIRNIL NEIFQSALINQLNVFSLSRAHFSGM PQNAPTSSTQTSAHFMDQMMGPLV SDTDVSIVVNDVVRTVFHKLYSAAM TERHVSENRGKTIILSANVSFRECTY GGNAPVSGLNENVCDLQSSWNVDK QIKINVVEDIVQAILGNLETFAASKVE SLFCPQVKFTVPVTLPVMQEEGSLS QALSGKDSYSDNQLPCLVDHGNPE QMDSWYQMSLSKLNIYAKDVARKIL QGIKHELDKEQESPLLTNNIVVSENI	None	None	None	None	None	None	None

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									KITSKILHSIQEFISKSKIKVVQPVKES EAVPSADKAAIEKVVNSVYTNLLKH CGSPTSAFEDLMRKSDVISDIIGFSM VKEISNSEFQPQAEEELSSSELALEA VKIMEKVVKIIDELKSQEKPASITDV MLDSRVLEEALALFLAKLVKTPGPAS KDTTSLTKPELNKIASQLTKSVTAEIS KSNISLVESNHEEQSLDPENIEVISQ VVESVYSNVVKQSGTENELSDIKGT KKAFPKKVASLIVDGVSSVPSCRVIT ESSYTAAHGDLDTNRIIEKAQKHAAL MSSDSDKDSKKELEDEFPVRIVPHV RNKPLRIDPNIVSDHLAVISMKTQPL ETLQMDCLKRTGCSIAELRRNSIRGI GPSSTDVSEMGTRQKERRISLDRTG RLDVKPLEAVGRNSFQNVRRPDITR VELLKDINNKTDLIIRLVAHDIGRKE SDSSLSEGMVSDEEEVVLGEVVGDQ CLRKISGGRVQQVKKSAESHVVSSK TATSTSNLKRFLALSKCCQPTSGENI ESIEESGIQIMDPNKAYVKRAAAELD MPSCKSLAEETTSRDKLQYKEEEILA SEPTHYFIHRIMSTSSYNQEDLISGE AEEFLPDAKANALEESCQEPQEGNS NSLEFVTIYKGSKHIAGSARLSKEHV SEMPRSSISKQGSRVLAKVSSTLSKV FSRSSGSIPKSSSPPHQDKR							