	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
	Q9GPN8	Q9GPN8_DROME	Drosophila melanogaster	Dynein axonemal heavy chain 2	28.06426	T2121;T2124	NaN	40245499	PTFVSQLIPRTIHLIRFIWLNSEQYNR RDLITGIFRNLSNQIIRFCTEKVNVE KILSGSSRFGIKICNMCIDCCLTYKGI YDIMSKTHAKINIRIGWSLDNAMIFN HVDAFMERLNDVIDICESMMVFGR LDESESIPKPQFGGTSGTEFEATADN VENEFLVTLTALCTDSKEIILNVHKN EWYEEVIKYRRTVQSMEETVQRLMS NVFQHICNVEEALESLNVMIFYSYR STIRKTFLRQVSSAWVFFSNEIDSSV HMLMDRSKMHESWVPYYASRALGY RVHLDRLVWLCNRLNSSDWLPNVS EASVVLKKFESVRREFDKEVKKSFD EWQKNCCSLLLNQKLDRYLLIRSKK KKGLIECNIDRTILTICEQAQHFERL GLGVPGMVRKIYEKHETLRFVYNSV VQVCLNYNHILSALSEQERKLFRALI QACDRKIAPGVFKLTYGGELSDAYIA DCAKHTNKLQETMDIYKRAIQNIAR FCEKICDTPMLKFNFSGAVTISIFEN HLSSYLRRVSNILRGFYSTITDLIFAV FKEFQAVIEDMPIEWYGFVNVFDDM LATAFLTSSKNSLNMLTNALHRDPD MAAAPILVMESDVRERCIVLTPDIDV IANLLSGYIDRIHNILEQFPRIGIKMK LPKEHQYESFSKAFLEDSESTQLICN IEAEINHEREEIDGYITFWNSHRML WETTELEFTKRVKATQMTADIFEASI EYYSAMADDISYVDAITHVYFILMNQ NYIKSSILDCIEKWQALNIKILLSHSF SLIRAIYRYMRKNERKMMMVPRTLK ESLLAKQFFERIINEVPLKQAGFPPT LELFAILDKYQVEIPEEIRVKVIGLEA AWHHYLKRLGEADEMLDNNREEFK KILVQQAEKFKIILKEFLDDFFLKLPT SANINPRIALKFLRIIALKIEDCFTFEE SLMRDLAVFNVNQPESIDLRKLDFE VRIVKNIWELIFEWQTNWEGWKKG YFWKMNINEMEDTALNLYKEFTTL NKKFYDRHWEMLEATTKNVDSFRR TLPLITALKNPCMRERHWNRVRDVI HVNFDENSKNFTLELIINLDFQAFS EDIQDISNSATMELQIENSIKNIATIW KKQSFEMAFYHDGIYRIKNVEDCFQ LLEEHMVQISAMKATRFVEPFITIVD YWEKTLSYISETLEKGLTVQRQWLYL ENIFQGDDIRKQLPEEAKRFATITEE FRTISSKMFQAKTAVKATNLRPPPFL LNRFSRMDERLELIQRALEIYLEAKR QLFPRFYFISNDDLLEILGNSKRPDL VQTHLKKLFDNLYKLELKRVGKTLS RWQASGMHSDDGEYVEFMMVIYID GPSERWLKQVEEYMLVVMKEMLKL TRGSLKKLVGNREKWISLWPGQMV LTTAQIQWTTECTRSLIHCSMVDQK KPLRKLKKKQIKVLSKLSEMSRKDLT KTMRLKVNTLITLEIHGRDVIERMYK SNCKDTGHFEWFSQLRFYWHRESE LCVIRQTNTEHWYGYEYTGNSGRLV ITPLTDRCYITLTTALHLHRGGSPKG PAGTGKTETVKDLGKALGIWVIVTNC SEGLDYKSIGKNFSGLAQSGCWGCF DEFNRINIEVLSVVAQQIMSIMAALS TKALELMFEGQMIKLKHTVGLFITM NPGYAGRTELPDNLKSMFRPISMM VPDNIIIAENLLFSDGFTNTRNLARK VYTLYELAKQQLSKQYHYDFGLRSM VALLRYAGRKRRQLPNTTEEEIVYLA MKDMNVARLTANDLPLFNGIMSDI FPGVSLPTIDYSEFNIAIYEEFREAGL QPITIAVKKVIELFETKNSRHSVMIIG DTGTAKSVTWRTLQNCFYRMNSQR FSGWEAVTVYPVNPKALNLAELYGE YNLSTGEWLDGVLSSIMRIICGDEEP TQKWLLFDGPVDAVWIENMNSVMD DNKLLTLVNSERITMPVQVSLLFEV GDLAVASPATVSRCGMVYNDYNDW GWKPFVNSWLQRLRIKEFADFLRIH	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	None

								FYVFVEEDTAAARIIREGGGVYIRSLF LEGGGWLRKNQCLQDPLPMELICPL PVIHFKPVENLKKRCRGVYQCPAYYY PVRSGSFVIAVDLKSGNEKADYWIKR GTALLLSLAN									