	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	ext reg
	M9PGT0	M9PGT0_DROME	Drosophila melanogaster	NaN	28.06426	S223;T608;T609;S688;S691;T701;T702;T825;T832;T892;T894;T895;T896;T899;T900;T901;T902;T903;T2439;S2466;S2482;T2641;T2642;T2807;T2809;T3116;S4303;S4308;T4383;S4388;T4946;T4948;T4952;S4989;T4992;T4993	NaN	40245499	MEVECDLGDIQNEELLRKMWQQSE DSERKRQIRSHLYKLRESRLCNLYR HETDPMSEPNGNGHGNVNTLAGYA GKDPLATSHGDALLDQNFQSLKSKE VRDSTSPTHELRFHSMTLSQPNTTG WDVQTSSEVSPDGRAYRTETLAKTD GVEKLNGGGLAEFKGRNEQRSSAS HQGDDKNFVKQASDSSKTQLQETV VFGDETSGRTEMKMSSTSTSSSSKV VSSSSTVEYGDEPRYLLDNQEKPHK QHQTREWEQDQRRQEQRIQEQRQE QQIRQEQLQRQEEFQRQEQIQRQEQ IQRQEQVQRQQERFTESREQSNSTR NVQTQQHYEENKRYVDMDKASPEY QRHVQHLMEQPGEIISNTVEYPKPN VKMITTVKRLPDGTIVKNKRYETEQL TPSQSHTTHKQTNNQTHNQTRNQV HNQRREQDEQDSQTRDVVDNVEQK HVTESQSFSSVKKSSRRFSTETTSET VEEYDDRDQPTSRVVQKAPTPSYAP PSHSPRQSPAKDFSTHGFPSVRPNK ATQEYPSQRPGIAGEEVVVVRSEKSR QVKQQTSSQRTIETEVVGDDYQEPQ RSPQKLREAPTPSWEQPATRRQPVE EDFSTHGFPSVRTTTTSTRPDQPDG EVLHTSKTVSRNQSANRKTNTERIIE TQVEHPNAPSHSTPRSGSPRRSQPR DDYASSPRGPAGKPSQSRPSNTGGS TTTKTTTTSEPLTRRQLQKEREVDAA HRAFAASLRSSSPADSTTSVGSHHQ TPRSSVSSNRTFRREMREGSHDSQA PSESSRISSTTVTRHTTGGNVTSNTI KTKTTKPVKTASEPRSPTPKAGGSVT TTTTTITTKSSPSPAPASPTTAAPPTS APASSAPPDNKLSQYTYTTTKPGDIF SLPPTTPPTINNEPTLTTTRNTTTTTT TTTTATSDNLQNHPKKSAIEPATDTD SQPIRKVKLSANEAKVVEEAPCVRR QYYQLGNEGENPETPESSGTPANKK PHQMRRPHDEPEPQLRRSSKSPSVE PRQVQRETTFEGRRVSQDREISIDEL ILIEETSGAPGSPKIPSPRAQSPGKPA TRSQSPEKPQPRATPRQSPEKEQPA FKQTHEVYTPSQPEKQFPRARSPEK TPGWTQPQVSPRQSPEKQLPRAQSP EKVPAVRQPSVSPRQSPEKQIPDPKT RDQGPGLPRISPRQSPEKQLPKDVP QKSRQSPEKDLTNQQRREEEIFRSTI TTTQKRTTNNLNEEFITNERDNQNQ PISEKKPQIPANAEPNTKPSETIESPD GGFPSKTTEVEAQPEVKESPTYRKK GLTRRETFEDRCRQILGMEEDGDTQ GTYTERPNNEQEDVNVSHTTIETIQV KIEDCPNDDEDDKPRRVTETYVVRT QPKIKVEEELFVDVTEAEDVEILVNP SKKSPKEEDSPKYPKGPETPKSPRN DQRIPSIPKKGQSPVQFKTEETPRYP QEQERYPKEPETSQYPKESPRNPKE DAETININEETTIVITKEGSKSPSPRW SPSPERRVPKSQQPPSPTASPSVSPV SGRKIPNEVESNFVTEKIIDCRGKTV VEKISQRPRTPSPTTPKKNTKPSQKI PERVPETESEPEKDSESETKKTTSVS VTKTETERRNSRTTKTKQPLPLKEPQ SKVPAGKSPRKDSLTGRKRDSLVEE TRITTTTTTTRQGRKPSDTNGSPSIK DRLRSSPRKQKTSPQQTRTPTPAQT RNPEDDVDGDSSSPDASPTRVGNER RRSSNISVHTEIIIDHMAPKSPKTER RSQGGTGNVPSPIRKLPVTERKESAP VPRVTRRDKAEKVTRSTSENIIKMSG TKPHPEMSSLKPGGDRSRPSKCCTT KTINLSEQRINTATDIEGVIIDIQQAK SSREPSPDRIVPTPVPAELETGKPRY PDVVQEPDDEPRRKPQVTNIPIFEEE SQTYVGCQISELHSSNGIEVDILDNP TVEAPKSLDYPVNTPDTDESLLSVHE KVSRFTHSAEKVKEPKVSAPFSREF DVNAKIPENDDCLLSINQKVDKFLR TAENVIRPTSLPSRPEIERPGLEEIDE	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	No

									ALSEFKKRPSLPNAMDPGTAAPPRQ VYQAPPPPTNISFTYADFPPVRRPQG ASAHNYRSQPCLTSAVDQVEALTNP LGAPLVLTSSNPTYLPPPGSRRFDYIS SPVDVDADSPPNSPTSFMTMPNPTL MTDNTDDDLDLDSDNNMLEYRAET KVMRKPRSQTAVRVADRRNAHMSD DEVYGKNSRAAKSLLYTMKQLGGGP GNASVGNSGQRRQPLTAPSSPKSGC LSPDGRPYQAPLVEPLFPQLSTFEPK RQPQFANSPMSTPPAVSMPSINYQA NPTYTPPRSNQNSNSYLGETNTSYV VTYPLDDSGDEPEPESMATSVSQRL RRTSEHSNASSSLSLGSTSWTANPV HNTVPSVPLDSAMGPPVDRSTKPQV SQPVGPKMPQHVAQKQIPQQLPNQL PQQIPQQLPKQLPQQIPQQLPQQLPQ QLPKQLPQQIPPQLPKQLPQQIPQPE LPQQLPNNLPRHAPKLSSRSHTIQG DSGYENRPLQNRVMSQQTLNSSIIT SNNHTTVQKQQKEQHINELRRKSL GNVLESSQRSTYFEQEYKSSAPPDTP DIVKSSLPKEDAPLLKKFGPPQRHHY MPNSYQSPQLNKQGNSNSTTTSSTS VRSTTVVQQQHHQQQHQQIKPSIVE TPATPQPQVPPEDEIPHNIVFNNVSA FTSMSRRNHEEDSHQGTQSGSRVN RLSKCDSWNQICQLQQTAGPSPAKY NQPGSPGELRRTKSGHSLAVPKLYE AGIDKAQVSEKQRTVAAYFSGQKSPT GGQVEELRTSMTTTTSSRKSAINRT KTSEKLSAAARKSLSSLTTTSNAAQH KSSSSSEQRTETKSKDGGATVTTTTT KVTTRTVSGSAASKNISPLAKFKQLD KQAAAQQAQKSSPTTSTPTTPGGSA QPLFKFTDPALNARAATVKDQLLQW CKHKTQEYENVQINNFSSSWSDGLA FCALIHHFLPDAFDYTTLTKQTRRH NFELAFSVADEKAGIAPLLDVEDMV EMSRPDWKCVFVYVQSIYRRFRNCQ								