	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	Q8UVK2	SPT6H_DANRE	Danio rerio	Transcription elongation factor SPT6	26.412228	NaN	S90;T1522;S1525	40044042	MSDFIESEAEESEEEFEEKDLKPKKT QRFMEEDEEEEEENTEDQDEHGNL RGLIDDDDVEEEEEEERGEPPAGED SDSGEEVRHRRRKRSFDDYLDDDDL DLIEENLGVKVKRRKKKYSRVKTMD DEGDDDDEKDLIADEIFTGDGDGEG EVEDGEAVDTLHPRDDEEEEDDEES DIDDFIVDDDGQPITKKKGKKFSGYT DAALQEAQEIFGGDFDFAEFDTEAY DHAEEEEEDQDDESWDRPKKQTKR RVSRRSIFEIYEPSELESSHMTDQDN EIRSTDMPERFQLRAIPVKPAEDDEL EEEAEWIYRNAFSTPTISMQESTDYL DRGTTTNFSRKGPSTIAKIKEALNFM RNQHFEVPFIAFYRKEYVEPELNIND LWKVWQWDEKWTQLKTRKQNLTR LFQRMQSYQFEQISADPDKPLADST RPLDTADMERLKDVQSIDELGDVYN HFLLYYGRDIPKMQNAAKGGKKKLK KIKEVSEEDGEEAEVEEEEEEEEQK GPDLKQASRRDMYSICQSAGLDGLA KKFGLTPEQFGENLRDSYQRHETEQ FPAEPLELAKDYVCSQFNTPEAVLEG ARYMVAMQIAREPLVRHVLRQTFQE RAKINIKPTKKGKKDVDEAHFAYSFK YLKNKPVKELSGDQFLKMCLAEEEG LLAIDICIDLVGVKGYGDQTYFDEIKQ FYYRDEFSHQVQEWNKQRTLAIERS LQQFLYPQMAKELKNKLIAEAKDNI VKSCCKKLYNWLKVAPYRPDQQVEE DDDLMDESQGKGIRVLGVAFASGRD TPVFCSLINGEGEVVDFLRLPYFLKR RNAWREDEREKKQQDVENLKKFLL SKKPHVVAVSGENRDAHMVMEDIK RTISELEQNSSLPVVGVELVDNELAV LYMNSKKSEADFRDYPPLLRQAVSV ARKIQDPLVEFAQVCSTDDDILCLKL HPLQEHVVKEELLSALYCEFINRVN EVGVDVNRAIAHPYTQSLVQYICGLG PRKGSHLLKILKQNNTRLENRTQLV TMCHMGPKVFINCAGFIKIDTASLG DSTDSYIEVLDGSRVHPETYEWARK MAVDALEYDESAEDANPAGALEEIL ENPERLKDLDLDAFAEELERQGYGN KGITLYDIRAELSCRYKDLRAPYRPP NTEEVFNMLTKETPETFYIGKLITCV VTNIAHRRPQGESYDQAIRNDETGL WQCPFCQQDNFPELSEVWNHFDSG SCPGQAIGVRTRLDNAVMGFIPTKFL SDKVVKHPEERVKPGMTVHCRIMKI DIEKFNVDLTCRTSDLSDKNNEWKL PKDTYYDFDAETDDVKQEEEQKKKQ QRTTYIKRVIAHPSFHNINFKQAEKM MESMDQGDVVIRPSSKGENHLTVT WKVADGIYQHVDVREEGKENAFSLG HTLWINTEEFEDLDEITARYVQPMA AFARDLLGHKYFHECNGGDRKKME ELLVRTKKEKPTFIPYYISACRDLPGK FLLGYQPRGKPRIEYVTITPDGFRYRS QIFPTVNGLFRWFKDHYQDPVPGVT PASSRTRTPASVNATPANINIADLTR AVNSLPRNMTSQMFNAIAAVTGQG QNPNTTPAQWASSQYGYSGGSSAG GGGGSSSAYHVFATPQQPMATPLMT PSYSYTTPGQQQAMTTPQYPSSTPQS SHGHHQHSSSTPSSSSSRVRTPQPK ASSHTAVDWGKMAEQWLQEKEAER RKQKTPRMTPRPSPSPMIESTPMSIA GDATPLLDEMDR	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	None