

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma mem
Q62383	SPT6H_MOUSE	Mus musculus	Transcription elongation factor SPT6	27.004857	S1526;T1532	S7;S12;S73;S78;S91;S125;S267;T1515;T1523;S1526;T1532;S1535;T1539;T1697;S1701;S1703;T1709;T1718	39627609;36852467	MSDFVESEAESEEEYHNHEGEVVR VTKKFVEEEDDDDEEEENLDDQD ERGNLKFINDDDDEEEGEEDEGS DSGSEDDVGHKKRKRPSFDRLE DDDFDLIEENLGVKVRGQKYRRVK KMSDDDEDEEEYGKEEHEKEAIA GEIFQDEEGEEQEAVEAPMAPPDE EEFDEESDIDDIVDDDGQPLKPK KWRKCLPGYTDALQEAQEIFGVDF DYDEFEKYNEYDEELEEYEDDE TEGEIRVRPKTTKKRVSRRSIFEMY EPSELESSHLTDQDNEIRATDLPERF QLRSIPVKAEDDELEEEADWIYRN AFATPTISLQDSCDYLDRGQPTSSFS RKGSTVQKIKEALGFMRNQHFEVP FIAFYRKEYVEPELHINDLWRVWQW DEKWTQLRIRKENLIRLFEKMQAYQ YEQISADPKPLADGIRALDITDMER LKDVQSMDELKDVYNHFLYYGRDI PKMQNAAKASRKKLKRKEDGDEEG EGEEAEDEEQRGPELKQASRRDMY TICQSAGLDGLAKFGLTPEQFGEN LRDSYQRHETEQFPAEPELEAKDYV CSQFPTPEAVLEGARYMVALQIAREP LVRQVLRQTFQERAKLNITPTKKGR KDVDEAHYAYSFKYLKKNPKVKELRD DQFLKIGLAEDEGLLTIIDISDMKGV EGYNDQTYFEEIKQFYRDEFHQ VQEWNRQRTMAIERALQQLVYQV AKELKNKLLAEARESVMKACSRKLY NWLRVAPYRPDQVVEEDDFMDEN QGGIRVLGIAFSSARDHPVFCALVN GEGEVTDFLRLPHFTKRRTAWREEE REKKAQDIETLKKFLVNKKPHVVTIA GENRDAQMLTEDVKRIVHELDQGG QLSSIGVELVDNELAILYMNSKKSEA EFRDYPPVLRQAVSLARRIQDPLIEF AQVCSSEDDILCLKFHPLQEHVVKE ELLNALYCEFINRVNEVGVDVNRAIA HPYSQALIQYVCGLGRKGTLLKIL KQNNTRLESRTLVTMCHMGPKVF MNCAGFLKIDTASLGDSTDSYIEVLD GSRVHPETYEWARKMAVDALEYDE SAEDANPAGALEEILENPERLKDLLD DAFAEELERQGYGDKHITLYDIRAEL SCRYKDLRTAYRSPNTEEIFNMLTK ETPETFYIGKLIICNVGIAHRRPQGE SYDQAIRNDETLWQCFPCQODNF PELSEVWNHFDGSGSCQAIQVKT LDNGVTGFIPTKFLSDKVVRPEERV KVGMTVHCRIMKIDIEKFSADLTCRT SDLMDRNNNEWKLPKDTYYDFDAEA ADHKQEEEDMKRKRRTTYIKRVIAH PSFHNINFKQAEKMMETMDQGDVII RPSSKGENHLTVTKVSAGIYQHVD VREEGKENAFSLGATLWINSEEFED LDEIVARYVQPMASFARDLLNHKYY QDCSGGDRKKLEELLIKTKEKPTFI PYFICACKELPGKFLLYGQPRGKPRI EYVTVPEGFRYRGQIFPTVNGLFR WFKDHYQDPVPGITPSSSNRTRTPA SINATPANINLADLTRAVNALPONM TSQMFSAIAAVTGQGNPNATPAQ WASSQYGGGGSSAYHVFPPTPA QQPVATPLMTPSYSYTTSPQITTPQ YHQQLASTTPQSTQAQPPSSSSRQ RQQPKSNSHAAIDWGMMAEQWL QEKEAERRKQKRLTPRPSPSMIE STPMSIAGDATPLLEMDR	True	False	2.287	4.46	1.767	0.998	False	0.922