

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
Q7KZ85	SPT6H_HUMAN	Homo sapiens	Transcription elongation factor SPT6	21.313037	S125;T1523;S1525;S1526;S1527;S1528;T1532;S1535;T1539	S7;S12;S73;S78;S91;S125;S267;T1515;T1523;S1526;S1528;T1532;S1535;T1539;T1697;S1701;S1703;T1709;T1718	29351928;33214551;26853435;30059200;30620550;29237092;35254053;28657654;34725712;32574038;30379171;31492838;32119511;35289036;35138101;25367160;28510447;35132862;34019948	MSDFVESEAEFESEEEYNDGEGVVPRTTKKFVEEEDDDDEEEENLDDQDEQGNLKGFINDDDDDEDEGEEDGSDSGDSEDDVGHKKRRTSFDDRLEDDDFDLIEENLGVKVKRGQKYRRVKMSDDEDDDEEEYGKEEHEKEAIAE EIFQDGEGEEGQEAMEAPMAPPEEE EEDDEESDIDDFIVDDDGQPLKKPK WRKKLPGYTDAALQEAQEIFGVDFD YDEFEKYNEYDEELEEEYEDDEA EGEIRVRPKTTTKRVSRRSIFEMYE PSELESSHLTDQDNEIRATDLPERFQ LRSIPVKGAEDELEEEADWIYRNAF ATPTISLQESCDYLDRGQPASSFSRK GPSTIQKIKEALGFMRNQHFVFPFIA FYRKEYVEPELHINDLWRVWQWDE KWTQLRIRKENLTRLFEKMQAYQYE QISADPKPLADGIRALDTTDMERLK DVQSMDELKDVYNHFLLYGRDIPK MQNAAKASRKKLKRVEEGDEEGE GDEAEDEEQRGPELKQASRRDMYTI CQSAGLDGLAKKFGLTPEQFGENLR DSYQRHETEQFPAEPELELAKDYVCS QFPTPEAVLEGARYMVALQIAREPLV RQVLRQTFQERAKLNITPTKKGRKD VDEAHYAYSFKYLKNKPVKELRDDQ FLKICLAEDEGLLTTDISIDLKGVEGY GNDQTYFEEIKQFYRDEFHQVQE WNRQRTMAIERALQQFLYVQMAKE LKNKLLAEKEYVIKACSRKLYNWL RVAPYRPDQQVEEDDDFMDENQGK GIRVLGIAFSSARDHPVFCALVNGEG EVTDFLRLPHFTKRRTAWREEEREK KAQDIETLKKFLLNKKPHVVTVAGE NRDAQMLIEDVKRIVHELDQGOQLS SIGVELVDNELAILYMNSKKSEAEFR DYPPVLRQAVSLARRIQDPLIEFAQV CSSDEDILCLKFHPLQEHVVKELL NALYCFINRVNEVGVDVNRAIAHP YSQALIQYVCGLGPRKGTHLLKILKQ NNTRLESRTQLVTMCHMGPKVFM NCAGFLKIDTASLGDSTDSYIEVLDG SRVHPETYEWARKMAVDALEYDESA EDANPAGALEEILENPERLKDLDLDAFAEELERQGYGDKHITLYDIRAELS CRYKDLRTAYRSPNTEEIFNMLTKE TPETFYIGKLIICNVTGIAHRRPQGES YDQAIRNDETFGLWQCPFCQQDNFPELSEVWNHFDGSGCPGQAIGVKTRL DNGVTGFIPTKFLSDKVVKRPEERVK VGMITVHCRIMKIDIEKFSADLTCRTS DLMDRNNEWKLPKDTYYDFDAEAAA DHKQEEDMKRKKQRTTYIKRVIAHP SFHNINFKQAEKMMETMDQGDVII RPSSKGENHLTVTWKVS DGIYQHVD VREEGKENAFSLGATLWINSEEFED LDEIVARYVQPMASFARDLLNHKYY QDCSGGDRKKLEELLIKTKKEKPTFI PYFICACKELPGKFLLYGQPRGKPRI EYVTVTPEGFRYRGQIFPTVNLFR WFKDHYQDPVPGITPSSSRTRTPAS INATPANINLADLTRAVNALPQNMT SQMFSIAAAVTQGGQNPATPAQW ASSQYGYGGSSAYHVFPPTAQ

