	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	P27692	SPT5_YEAST	Saccharomyces cerevisiae	Transcription elongation factor SPT5	24.475439	NaN	T35;T133;S136;S188;S219	33229814	MSDNSDTNVSMQDHDQQFADPVV VPQSTDTKDENTSDKDTVDSGNVTT TESTERAESTSNIPPLDGEEKEAKSE PQQPEDNAETAATEQVSSSNGPATD DAQATLNTDSSEANEIVKKEEGSDE RKRPREEDTKNSDGDTKDEGDNKD EDDDEDDDDDDDDEDDDDEAPTKR RRQERNRFLDIEAEVSDDEDEDEDE EDSELVREGFITHGDDEDDEASAPG ARRDDRLHRQLDQDLNKTSEEDAQ RLAKELRERYGRSSSKQYRAAAQDG YVPQRFLLPSVDTATIWGVRCRPGKE KELIRKLLKKKFNLDRAMGKKKLKIL SIFQRDNYTGRIYIEAPKQSVIEKFCN GVPDIYISQKLLIPVQELPLLLKPNKS DDVALEEGSYVRIKRGIYKGDLAMV DQISENNLEVMLKIVPRLDYGKFDEI DPTTQQRKSRRPTFAHRAPPQLFNP TMALRLDQANLYKRDDRHFTYKNE DYIDGYLYKSFRIQHVETKNIQPTVE ELARFGSKEGAVDLTSVSQSIKKAQA AKVTFQPGDRIEVLNGEQRGSKGIVT RTTKDIATIKLNGFTTPLEFPISTLRKI FEPGDHVTVINGEHQGDAGLVLMV EQGQVTFMSTQTSREVTITANNLSK SIDTTATSSEYALHDIVELSAKNVACI IQAGHDIFKVIDETGKVSTITKGSILS KINTARARVSSVDANGNEIKIGDTIV EKVGSRREGQVLYIQTQQIFVVSKKI VENAGVFVVNPSNVEAVASKDNML SNKMDLSKMNPEIISKMGPPSSKTF QQPIQSRGGREVALGKTVRIRSAGYK GQLGIVKDVNGDKATVELHSKNKHI TIDKHKLTYYNREGGEGITYDELVNR RGRVPQARMGPSYVSAPRNMATGGI AAGAAATSSGLSGGMTPGWSSFDG GKTPAVNAHGGSGGGGVSSWGGAS TWGGQGNGGASAWGGAGGGASAW GGQGTGATSTWGGASAWGNKSSW GGASTWASGGESNGAMSTWGGTG DRSAYGGASTWGGNNNNKSTRDGG ASAWGNQDDGNRSAWNNQGNKSN YGGNSTWGGH	None	None	None	None	None	None	None	None	None