	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	Q12501	YO22B_YEAST	Saccharomyces cerevisiae	Transposon Ty2-OR2 Gag-Pol polyprotein	24.475439	NaN	NaN	33229814	MESQQLHQNPHCPHGSAYASVTSK EVPSNQDPLAVSASNLPEFDRDSTK VNSQEETTPGTSAVPENHHHVSPQP ASVPPPQNGQYQQHGMMTPNKAM ASNWAHYQQPSMMTCSHYQTSPAY YQPDPHYPLPQYIPPLSTSSPDPIDSQ DQHSEVPQAKTKVRNNVLPPHPHTS EENFSTWVKFYIRFLKNSNLGDIIPN DQGEIKRQMTYEEHAYIYNTFQAFA PFHLLPTWVKQILEINYSDILTVLCKS VSKMQTNNQELKDWIALANLEYNG STSADTFEITVSTIIQRLKENNINVSD RLACQLILKGLSGDFKYLRNQYRTKT NMKLSQLFAEIQLIYDENKIMNLNK PSQYKQHSEYKNVSRTSPNTTNTKV TTRNYHRTNSSKPRAAKAHNIATSS KFSRVNNDHINESTVSSQYLSDDNE LSLGQQQKESKPTRTIDSNDELPDH LLIDSGASQTLVRSAHYLHHATPNSE INIVDAQKQDIPINAIGNLHFNFQNG TKTSIKALHTPNIAYDLLSLSELTNQ NITACFTRNTLERSDGTVLAPIVKHG DFYWLSKKYLIPSHISKLTINNVNKS KSVNKYPYPLIHRMLGHANFRSIQK SLKKNAVTYLKESDIEWSNASTYQC PDCLIGKSTKHRHVKGSRLKYQESY EPFQYLHTDIFGPVHHLPKSAPSYFI SFTDEKTRFQWVYPLHDRREESILN VFTSILAFIKNQFNARVLVIQMDRGS EYTNKTLHKFFTNRGITACYTTTADS RAHGVAERLNRTLLNDCRTLLHCSG LPNHLWFSAVEFSTIIRNSLVSPKND KSARQHAGLAGLDITTILPFGQPVIV NNHNPDSKIHPRGIPGYALHPSRNS YGYIIYLPSLKKTVDTTNYVILQNNQT KLDQFDYDTLTFDDDLNRLTAHNQS FIEQNETEQSYDQNTESDHDYQSEI EINSDPLVNDFSSQSLNPLQLDKEP VQKVRAPKEVDADISEYNILPSTIRSR TPHIINKESTEMGGTIESDTTSPRHS STFTARNQKRPGSPNDMIDLTSQDR VNYGLENIKTTRLGGTEEPYIQRNSD TNIKYRTTNSTPSIDDRSSNSDSTTPI ISIETKAACDNTPSIDTDPPEYRSSDH ATPNIMPDKSSKNVTADSILDDLPLP DLTHKSPTDTSDVSKDIPHIHSRQTN SSLGGMDDSNVLTTTKSKKRSLEDN ETEIEVSRDTWNNKNMRSLEPPRSK KRINLIAAIKGVKSIKPVRTTLRYDEAI TYNKDNKEKDRYVEAYHKEISQLLK MNTWDTNKYYDRNDIDPKKVINSM FIFNKKRDGTHKARFVARGDIQHPD TYDSDMQSNTVHHYALMTSLSIALD NDYYITQLDISSAYLYADIKEELYIRP PPHLGLNDKLLRLRKSLYGLKQSGA NWYETIKSYLINCCDMQEVRGWSC VFKNSQVTICLFVDDMILFSKDLNA NKKIITTLKKQYDTKIINLGEGDNEIQ YDILGLEIKYQRSKYMKLGMEKSLTE KLPKLNVPLNPKGKKLRAPGQPGHY IDQDELEIDEDEYKEKVHEMQKLIGL ASYVGYKFRFDLLYYINTLAQHILFPS RQVLDMTYELIQFMWDTRDKQLIW HKNKPTKPDNKLVAISDASYGNQPY YKSQIGNIFLLNGKVIGGKSTKASLT CTSTTEAEIHAVSEAIPLLNNLSHLV QELNKKPIIKGLLTDSRSTISIIKSTNE EKFRNRFFGTKAMRLRDEVSGNNL YVYYIETKKNIADVMTKPLPIKTFKLL TNKWIH	None	None	None	None	None	None	None	None	None