

| UniprotKB ID | Entry name | organism | full name | oglcnacscore | oglcnac sites | phosphorylation sites | PMIDS | sequence |
|--------------|-------------|--------------------------|--------------------------------------|--------------|---------------|-----------------------|----------|---|
| Q7LHG5 | YI31B_YEAST | Saccharomyces cerevisiae | Transposon Ty3-I Gag-Pol polyprotein | 9.365641 | NaN | NaN | 33229814 | MSFMDQIPGGGNYPKLPVECLPNFP IQPSLTFRGRNDSHKLNKFNISEIMLN MSMISWPNDASRIVYCRRHLLNPAA QWANDFVQEQGILEITFDTFIQGLYQ HFYKPPDINKIFNAITQLSEAKLGIER LNQRFRKIWDRMPPDFMTEKAAIM TYTRLLTKETYNIVRMHKPETLKDA MEEAYQTTALTERFFPGFELDADGD TIIGATTHLQEEYDSYDSEDNLTQN RYVHTVRTRRSYNKPMNHRNRRN NNASREECIKNRLCFYCKKEGHRLN ECRARKAVLTDLELESKDQOTLFIKT LPIVHYAIPEMDNTAEKTIKIQNTKV KTLFDSGSPTSFIRRDIVELLKYEIYE TPPLRFRGFVATKSAVTSEAVTIDLKI NDLQITLAAYILDNMDYQLLIGNPIL RRYPKILHTVLNTRRESPDSLKPKTYR SETVNNVRTYSAGNRGNPRNIKLSF APTILEATDPKSAGNRGNPRNTKLSL APTILEATDPKSAGNRGDSRTKLSL ATTPPAIDPLTTLDNPGSTQSTFAQ FPIPEEASILEEDGKYSNVVSTIQSVE PNATDHSNKDTFCTLPVWLQQKYR EIIRNDLPPRPADINNIPVKHDIEIKP GARLPRLQPYHVTEKNEQEINKIVQ KLLDNKFIVPSKSPCSSPVVLVPPKKD GTFRLCVDYRTLKATISDPFPLPRI DNLLSRIGNAQIFTTLDLHSGYHQIP MEPKDRYKTAFTVTPSGKYEYTVMPF GLVNAPSTFARYMADTFRDLRFVNV YLDDILIFSESPPEHWHKHLDTVLERL KNENLIVKKKCKFASEETEFLGYSI GIQKIAPLQHKCAAIRDFTPKTVKQ AQRFLGMINYYRRFIPNCSKIAQPIQ LFICDKSQWTEKQDKAIEKLKAALC NSPVLVPFNNKANYRLTTDASKDGI GAVLEEVDNKNKLVGVVGYFSKSLE SAQKNYPAGELELLGIKALHHFRYM LHGKHFTLRDTHISLLSLQNKNEPA RRVQRWLDLATYDFTLEYLAGPKN VVADAISRAIYTITPETS RPIDTESWK SYYKSDPLCSAVLIHMKELTQHNVT PEDMSAFRSYQKKLELSETFRKNYS LEDEMIYYQDRLVVPIKQONAVMRL YHDHTLFGGHFGVTVTLAKISPIYYW PKLQHSIIQYIRTCVQCQLIKSHRPRL HGLLQPLPIAEGRWLDISMDFVTGL PPTSNNLNMILVVDRFSKRAHFIAT RKTLDATQLIDLLFRYIFSYHGFRTI |

