

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
P33334	PRP8_YEAST	Saccharomyces cerevisiae	Pre-mRNA-splicing factor 8	9.365641	NaN	NaN	33229814	MSGLPPPPPGFEEDSDLALPPPPPP PGYEIEELDNPMVPSSVNEDTFLPPP PPPPSNFEINAEIIVDFTLPPPPPPG LDELETKAEKKVELHGKRKLDIGKD TFVTRKSRKRAKMTKAKRSNLYT PKAEMPPEHLRKIINTHSDMASKMY NTDKKAFLGALKYLPHAILKLENM PHPWEQAKEVKVLYHTSGAITFVNE TPRVIEPVYTAQWSATWIAMRREKR DRTHFKRMRFPFFDDDEPPLSYEQH IENIEPLDPINPLDSQDDEYVKDWL YDSRPLEEDSKKVNGETSYKKWSFDL PEMSNLYRLSTPLRDEVTDKNYYL FDKKSFFNGKALNNAIPGGPKFEPL YPREEEEDYNEFNSIDRVIFRVPIRS EYKVAFPHLYNSRPRSVRIPWYNNP VSCIIQNDEEYDTPALFFDPSLNPIP HFIDNNSSLNVSNTKENGDFTLPED FAPLLAEEEEELILPNTKDAMSLYHSP FPFNRTKGKMVRAQDVALAKKWFL QHPDEEYPVKVVSQKLLKNYVLN ELHPTLPTNHNKTKLLKSLKNTKYF QOTTIDWVEAGLQLCRQGHNMLNL LIHRKGLTYLHLDYFNFKPTKTLTT KERKKSRLGNSFHLMRELLKMMKL IVDTHVQFRLGNVDAFQLADGIHYIL NHIGQLTGIYRYKYKVMHQIRACKD LKHIYYKFNKNLGGKPGCGFWQPA WRVWLNFLRGTIPLLERIYGNLITRQ FEGRSNEIVKTTTKQRLDAYYDLELR NSVMDDILEMMPESIRQKKARTILO HLSEAWRCWKANIPWDVPGMPAPI KKIERYIKSKADAWVSAAHYNRERI KRGHVEKTMVKKNLGRLTRLWIK NEQERQRQIQKNGPEITPEEATTIFS VMVEWLESRSFSPIFPPLTYKNDTK ILVLALEDLKD VYASKVRLNASEREE LALIEEAYDNPHDTLNRICKYLLTQR VFKPVDITMMENYQNISPVYSVDPL EKITDAYLDQYLWYEAQQRKLFPNW IKPSDSEIPPLL VYKWTQGINNLSEI WDVSRGQSAVLETTLGEMAEKIDF TLLNRLLRLIVDPNIADYITAKNNVI NFKDMSHVNKYGLIRGLKFASFIFQ YYGLVIDLLLQGERATDLGANNP NEFMQFKSKEVEKAHPYRIRLYTRYLD RIYMLFHFEEDEGEELTDEYLAENP DPNFENSIGYNNRKCWPKDSRMRLI RQDVNLGRAVFEIQSRVPTSLTSIK

WENAFVSVYSKNNPNLLFSMCGFE
VRILPRQRMEEVVSNDQGVWDLVD
ERTKQRTAKAYLKVSEEEIKKFDRI
RGILMASGSTTFTKVAKWNTSLISL
FTYFREAIVATEPLLDILVKGETRIQ
RVKLGKLSKMPTRFPPAVFYTPKEL
GGLGMISASHILIPASDLSWSKQTD
GITHFRAGMTHEDKLIPTIFRYITT
WENEF LDSQRVWAEYATKRQEAIQ
QNRRLAFEELEGSWDRGIPRISTLFQ
RDRHTLAYDRGHRIRREFKQYSLER
NSPFWWTNSHHDGKLWNLNAYRT
DVIQALGGIETILEHTLFKGTGFNSW
EGLFWEKASGFEDSMQFKLTHAQ
RTGLSQIPNRRFTLWWSPTINRANV
YVGFLVQLDLTGIFLHGKIPTLKISLI
QIFRAHLWQKIHESIVFDICQILDGE
LDVLQIESVTKETVHPRKSYKMNSS
AADITMESVHEWEVSKPSLLHETND
SFKGLITNKMWFDVQLRYGDYDSH
DISRYVRAKFLDYTTDNVSMYPSPTG
VMIGIDLAYNMYDAYGNWFNGLKPL
IQNSMRTIMKANPALYVLRERIRKGL
QIYQSSVQEPFLNSSNYAELFNNDIK
LFVDDTNVYRVTVHKTFEQNVATKA
INGCIFTLNPKTGHLFLKIIHTSVWA
GQKRLSQLAKWKTAEEVSALVRSPL
KEEQPKQIIVTRKAMLDPLEVHMLD
FPNIAIRPTELRLPFSAA SIDKLSDV
VMKATEPQMVLFN IYDDWLDRISSY
TAFSRLTLLLRALKTNEESAKMILLS
DPTITIKSYHLWPSFTDEQWITIESQ
MRDLILTEYGRKYNVNISALTQTEIK
DILGQNIKAPSVKRQKMAELEAARS
EKQNDEEAAGASTVMKTKTINAQGE
EIVVASADYESQTFSSKNEWKSAI
ANTLLYLRLKNIYVSADDFVEEQNVY
VLPKNLLKKFIEISDVKIQVAAFIYGM
SAKDHPKVKEIKTVVLPQLGHVGS
VQISNIPDIGDLPDTEGLELLGWIHT
QTEELKFMAASEVATHSKLFADKKR
DCIDISIFSTPGSVLSAYNLTDEGYQ
WGEENKDIMNVLSEGFPTFSTHA
QLLSDRITGNFIIPSGNVWNYTFM
GTA FNQEGDYNFKYGIPLEFY NEMH
RPVHFLQFSELAGDEELEAEQIDVFS