

Saccharomyces cerevisiae:

**YBR023C**

MTGLNGDDPDDYYLNLNQDEESLLRSRHSVSGGAPHRQGSVLRPERSRLNPNPDNPHFYAQTQEQMNHLDVLP  
SSTGVNPNATRRSGSLRSKGSVRSKFSGRETDSYLLQDMNTTDDKASVKISDEGVAEDEFKDGDDVDNFEESSTQPI  
NKSILPLRKETNDTLFWQMYCYFITFWAPILAFCGMPKKERQMAWREKVALISVILYIGAIVAFLTFGFTKVCSSS  
KLRLKNNEVSTEFVINGKAYELDTSSRSIQDVEVDSDTLYGPWSDAGKDAFLFQNVNGNCHNLITPKSNSSIPHD  
DDNNLAWYFPCKLKNQDSSKPNFTVENYAGWNCHTSKEDRDAFYGLKSKADVFTWDGIKNSRNLIYVNGDVL  
DLDLLDWLEKDDVDYPVVFDDLKTSNLQGYDLSLVLNNGHERKIARCLSEIIVGEVDSKTVGCIASDVVLYVSLVFLS  
VVIIFIIACYFRWTVARKQGAYIVDNKTMDKHTNDIEDWSNNIQTKAPLKEVDPHLRPPKYSKSLGHKRASTFDLL  
KKHSSKMFQFNESVIDLDTSMSSSLQSSGSYRGMTTMTTQNAWKLSNENKAVHSRNPSTLLPTSSMFWNKATSSP  
VPGSSLIQSLDSTIHPDIVQQPLDFMPYGFPLIHTICFVTCYSEDEEGLRTTLDLSLSTTDYPNSHKLLMVVCDGLIKGS  
GNDKTTPEIALGMMDDFVTPPDEVKPYSYVAVASGSKRHNMAKIYAGFYKYDDSTIPPENQQRVPIITIVKCGTPAE  
QGAAPGNRGRKRSQIILMSFLEKITFDERMTQLEFQLLKNIWQITGLMADFYETVLMVDADTKVFPDALTHMVAE  
MVKDPLIMGLCGETKIANKAQSWVTAIQVFEYIYSHHQAKAFESVFGSVTCLPGCFSMYRIKSPKGSDDGYWVPVLA  
NPDIVERYSDNVTNTLHKKNNLLLGEDRFLSMLKTFPKRKQVFPKAACTIAPDKFKVLLSQRNRWINSTVHNLFE  
LVLIRDLCGTFCFSMQFVIGIELIGTMVLPALCFTIYVIFAVISKPTPVITLVLLAILGLPLIVVITATRWSYLWVMCVYI  
CALPIWNFVLPYAYWKFDDFSWGDTRTIAGGNKKAQDENEGEFDHSHKIKMRTWREFEDEDILNRKEESDSFVA

**YBR038W**

MTRNPFMVEPSNGSPNRRGASNLKSFYANANSNSRWANPSEESLEDSYDQSNVFOGLPASPSRAALRYSPDRRHR  
TQFYRDSAHNSPVAPNRYAANLQESPKRAGEAVIHLSEGSNLYPRDNADLPVDPYHLSPQQPSNNLFGSGRLYSQS  
SKYTMSTTSTTAPSLAEADDEKEKYLTSTTSYDDQSTIFSADTFNETKFELNHPTRQQYVRRANSESKRRMVSDLPPPS  
KKKALLKLDNPIPKGLLDLTPRRNSPEFTEMRYTACTVEPDDFLREGYTLRFAEMNRECQIAICITMYNEDKYSLARTIH  
SIMKNVAHLCKREKSHVWGPNGWKKVSVILISDGRAKVNQGSLDYLAALGVYQEDMAKASVNGDPVKAHIFELT  
QVSINADLDYVSKDIVPVLVFLCKEENKKKINSHRWLFNAFCPVLQPTVVTLVDVGTRLNNTAIYRLWKVDFMDSN  
VAGAAGQIKTMKGKWGLKLFNPLVASQNFYKISNILDKPLESVFGYISVLPGALSAYRYRALKNHEDGTGPLRSYFLG  
ETQEGRDHDVFTANMYLAEDRILCWELVAKRDAKWVLKYVKEATGETDVPEDVSEFISQRRRWLNGAMFAAIYAQL  
HFYQIWKTKHSVVRKFFLHVEFLYQFIQMLFSWFSIANFVLTFFYLAGSMNLVIKHGEALFIFFKYLIFCDLASLFIISMG  
NRPQGAHLFITSMVILSICATYSLICGFVFAFKSLASGTESHKIFVDIVISLLSTYGLYFFSSLMYLDPWHMFTSSIQYFLT  
LPAFTCTLIQIFACNTHDVSWGKSTQESKQLSKAIVVQGPDGKQIVETDWPQEVDDKFKLEIKSRLKEPEFEESGN  
EKQSKNDYRDIRTRIVMIWMLSNLILIMSIIQVFTPDQDNGYLIFILWSVAALAAFRVVGSM AFLFMKYLRIVSYR  
NKVEGSGSWEVSKLDLPNVFHKKG

**YNL192W**

MSDQNNRSRNEYHSNRKNEPSYELQNAHSGLFHSSNEELTNRNQRYTNQNASMGSFTPVQSLQFPEQSQQTNM  
LYNGDDGNNTINDNERDIYGGFVNHHRQRPPATAEYNDVFNNTNSQQLPSEHQYNNVPSYPLPSINVIQTPELIH  
NGSQTMATPIERPFFNENDYYNNRNSRTSPSIASSSDGYADQEARPILEQPNNNMNSGNIPQYHDQPFYNGGY  
HGLQAKDYDDPEGGYIDQRGDDYQINSYLGRNGEMVDPYDYENSLRHMTMPMERREYLHDDSRPVNDGKEELDS  
VKSGYSHRDLGEYDKDDFSRDDEYDDLNTIDKLQFQANGVPASSVSSIGSKESDIIVSNDNLNANRALKRSGTEIRKF  
KLWNGNFVFDSPISKTLDDQYATTTENANTLPNEFKFMRYQAVTCEPNQLAEKNFTVRQLKYLTPRETELMLVVTMY  
NEDHILLGRTRLKGMNDNVKYMVKKNSSTWGPDAWKIVVCIISDGRSKINERSLALLSSLCYQDGFADKDEINEKKV  
AMHVYEHTTMINITNISESEVSLECNQGTVPILQLLFLCKEQNQKINSHRWAFEGFAELLRNIVTLDDAGTMPGKDS  
IYQLWREFRNPVVGACGEIRTDLGRKRVKLLNPLVASQNFYKMSNILDKTTESNFGFITVLPGAFSAYRFEAVRGQ  
PLQKYFYGEIMENEGFHFFSSNMYLAEDRILCFEVVTKKNCNWILKYCRSSYASTDVPERVPEFILQRRRWLNGSFFAS  
VYFCHFYRVWSSGHNIGRKLTLTVEFFYLFFNTLISWFSLSFFLVFRILTVSIALAYHSANVLSVIFLWLYGICTLSTFIL  
SLGNKPKSTEFYVLTVCIFAVMMIYMIFCSIFMSVKSQNILKNDTISFEGLITTEAFRDIVISLSTYCLYLISSIIYLPW  
HMLTSFIQYILLSPSYINVLNIYAFCNVHDLSWGKGTGAMANPLGKINTTEDGTFKMEVLVSSSEIQANYDKYLKVLNDF  
DPKSESRTPEPSYDEKKTGYANVRSVLVIFWVITNFIVAVVLETGGIADYIAMKSISTDDTLETAKKAEIPLMTSKASIYF  
NVILWLVALSALIRFIGCSIYMIIVRFFKVTFR

