

Table S4. Details of homology modeling of yeast proteins

>gi|6319522|ref|NP_009604.1| Homology to rat S11, human S11, and E. coli S17; Rps11bp [Saccharomyces cerevisiae]
MSTELTVQSERAFQKQPHIFNPNPKVKTskRTRKRWYKNAGLGFKTPKTAIEGSYIDKKCPFTGLVSIKGI
LTGTVVSTKMHRTIVIRRAYLHYIPKYNRYEKRRHKNVPVHVSPAFRVQVGDIVTVGQCRPISKTVRFNVV
KVSAAAGKANKQFAKF

Modeled residue range: 69 to 142 based on template [2i00Q](#) (2.80 Å) Sequence Identity [%]: 39 Evaluate: 6.85e-6

>gi|6319726|ref|NP_009808.1| 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase isoenzyme; Aro4p [Saccharomyces cerevisiae]
MSESPMFAANGMPKVNQGAEEEDVRIILGYDPLASALLQVQIPATPTSLETAKRGRREAIDIIITGKDDRVL
VIVGPCSIHDLEAAQYALRLKLLSDELKGLDSIIMRAYLEKPRRTTVGWKGLINDPDVNNTFNINKGLQS
ARQLFVNLTNIGLPIGSEMLDTISPOYLADLVSFGAIGARTTESQLHRELASGLSFPVGFKNGTDGTLNV
AVDACQAAAASHHFMGVTKHGVAAITTTKGNHCFVILRGGKKGTYDAKSVAEAKAQLPAGSNGLMIDY
SHGNSNKDFRNQPKVNDVVEQIANGENAITGVMIESNINEGNQGIPAEGKAGLKYGVSTITDACIGWETT
EDVLRKLAAAARQREVNKK

Modeled residue range: 23 to 369 based on template [1of8B](#) (1.50 Å) Sequence Identity [%]: 99 Evaluate: 0.00e-1

>gi|6319966|ref|NP_010046.1| Ypdlp is an intermediate protein between Slnlp and Ssklp in the phosphorelay reaction.; Ypdlp [Saccharomyces cerevisiae]
MSTIPSEIINWTILNEIISMDDDSDFSKGLIIQFIDQAQTTFMQQRQLDGEKNLTELNDLGHFLKGSS
AALGLQRIAWVCERIQNLGRKMEHFFPNKTELVTLSDKSIIINGINIDEDDEEIKIQVDDKDENSIIYLIL
IAKALNQSRLEFKLARIELSKYYNTNL

Modeled residue range: 2 to 167 based on template [1c02B](#) (1.80 Å) Sequence Identity [%]: 99 Evaluate: 4.73e-75

>gi|6320210|ref|NP_010290.1| Note that the sequence of TRP1 from strain S228C, which is the sequence stored in SGD, contains an ochre mutation at codon 67.; Trp1p [Saccharomyces cerevisiae]
MSVINFTGSSGPLVKVCGQLQSTEEAECALDSADLLGIIICVPNRKRITIDPVIARKISSLVKAYKNSSGTP
KYLGVFVRNQPKEDVLALVNDYGIDIVQLHGDESWQEYQEFGLGLPVIKRLVFPKDCNILLSAASQKPHSF
IPLFDSEAGGTGELLDWNISISDWVGRQESPELHFMLAGGLTPENVGDALRLNGVIGVDVSSGGVETNGVK
DSNKIANFVKNNAK

Modeled residue range: 14 to 223 based on template [1nsjA](#) (2.00 Å) Sequence Identity [%]: 33 Evaluate: 1.28e-19

>gi|6320228|ref|NP_010308.1| Homology to rat S11, human S11, and E. coli S17; Rps11ap [Saccharomyces cerevisiae]
MSTELTVQSERAFQKQPHIFNPNPKVKTskRTRKRWYKNAGLGFKTPKTAIEGSYIDKKCPFTGLVSIKGI
LTGTVVSTKMHRTIVIRRAYLHYIPKYNRYEKRRHKNVPVHVSPAFRVQVGDIVTVGQCRPISKTVRFNVV
KVSAAAGKANKQFAKF

Modeled residue range: 49 to 142 based on template [2i00Q](#) (2.80 Å) Sequence Identity [%]: 39 Evaluate: 6.85e-6

>gi|6320720|ref|NP_010801.1| Glutaredoxin (thioltransferase) (glutathione reductase); Ttr1p [Saccharomyces cerevisiae]
METNFSFDSNLIVIIITLAFATRIIAKRFLSTPKMVSQETVAHVKDLIGQKEVFVAAKTYCPYCKATLST
LFQELNVPKSKALVLELDEMNSNGSEIQDALEEISGQKTVPNVYINGKHIGNSDLETLLKNGKLAIEILKP

VFQ

Modeled residue range: 35 to 126 based on template [2jacA](#) (2.02 Å) Sequence Identity [%]: 67 Evalue: 1.85e-32

>gi|6320796|ref|NP_010875.1| iso-2-cytochrome c; Cyc7p [Saccharomyces cerevisiae]
MAKESTGFKPGSAKKGATLFFKTRCQQCHTIEEGGPNKVGPNLHGIFGRHSGQVKGYSTYTDANINKNVKWD
EDSMSEYL TNPKKYIPGTKMAFAGLKKKEKDRNDLITYMTKAAK

Modeled residue range: 2 to 113 based on template [lyeaA](#) (1.90 Å) Sequence Identity [%]: 100 Evalue: 1.72e-54

>gi|6320998|ref|NP_011077.1| Stationary Phase Induced; strongly expressed during stationary phase, and transcription is dependent on MSN2/MSN4.; Spilp [Saccharomyces cerevisiae]
MLSNAKLLLSLAMASTALGLVSNSSSSVIVVPSSDATIAGNDTATPAPEPSSAAPIFYNSTATATQYEVV
SEFTTYCPEPTTFVTNGATFTVTAPTTLTITNCPCTIEKPTSETSVSSTHDVETNSNAANARAIPGALGL
AGAVMMLL

Modeled with HOMER

Modeled residue range: 18 to 89 based on template [2VC9IA](#) (2.36 Å)
Sequence Identity [%]: 26 PDB Blast Evaluate: 1.0

>gi|6321022|ref|NP_011101.1| Member of a glutaredoxin subfamily in Sc together with GRX3 & GRX5. Significant sequence diff. with the other glutaredoxin subfamily, formed by the previously described GRX1 & GRX2 glutaredoxins (Luikenhuis MBC 9:1081, 1998); Grx4p [Saccharomyces cerevisiae]
MTVVEIKSQDQFTQLTTTNAANKLIVLYFKAQWADPCKTMSQVLEAVSEKVRQEDVRFSLSIDADEHPEIS
DLFEIAAVPYFVFIQNGTIVKEISAADPKFVKSLLEILSNASASLANNAKGPKSTSDEESSGSSDDEEDE
TEEEINARLVKLVQAAPVMLFMKGGSPSEPKCGFSRQLVGLREHQIRFGFFDILRDENVRQSLKKFSDWP
TFPQLYINGEFQGGLDI IKESIEEDPEYFQHALQ

C-term: Modeled residue range: 152 to 230 based on template [1wika](#) (99.9 Å)

Sequence Identity [%]: 58 Evalue: 5.03e-22

N-term: Modeled residue range: 2 to 101 based on template [2j23A](#) (1.41 Å)

Sequence Identity [%]: 36 Evalue: 1.57e-12

>gi|14318471|ref|NP_116606.1| 47 kDa type I transmembrane protein localized to the Golgi; Emp47p [Saccharomyces cerevisiae]
MMLLITMKSTVLLSVFTVLATWAGLLEAHPLGDTSDASKLSSDYSLPDLINARKVPNNWQTGEQASLEEG
RIVLTSKQNSKGLWKLKQGFDLKDSFTMEWTFRSVGYSGQTDGGISFWFVQDSNVPRDKQLYNGFPVNYDG
LQLLVDNNGPLGPTLRGQLNDGQKPVDKTKIYDQSFASCLMGYQDSSVPSTIRVTYDLEDDNLLKVQVDN
KVCFQTRKVRFPSPGSYRIGVTAQNGAVNNAESFEIFKMQFFNGVIEDSLIPNVNAMGQPKLITKYIDQQ
TG KEKLEKTAFDADKDKITNYELYKLDLDRVEGKILANDINALETKLNDVIKVQQELLSFMTTITKQLSS
KPPANNEKGTSTDDAIAEDKENFKDFLSINQKLEKVLVEQEKYREATKRHGQDGPQVDEIARKLMIWLLP
LIFIMLVMAYYTFRIRQEIIKTKLL

Modeled residue range: 28 to 282 based on template [2A6YIA](#) (1.42 Å)

Sequence Identity [%]: 98 Evalue: 4.0 e-50

>gi|14318550|ref|NP_116683.1| Establishment of COhesion; Eco1p [Saccharomyces cerevisiae]
MKARKSQRKAGSKPNLIQSKLQVNNNGSKSNKIVKCDKCEMSYSSTSIEDRAIHEKYHTLQLHGRKWSPNW
GSIVYTERNHSRTVHLSRSTGTITPLNSSPLKSSPSITHQEEKIVYVRPDKSNGEVRAMTEIMTLVNNE
LNAPHDENVIWNSTTEEKGKAFVYIRNDRAVGII IENLYGGNGKTSRGRWMVYDSRRLVQNVYPDFKI
GISRIWVCRTARKLGIATKLIDVARENIVYGEVIPRYQVAWSQPTDSSGGKLASKYNGIMHKSGKLLLPVY

Modeled with HOMER

Modeled residue range: 23 to 98 based on template [1E58IA](#) (1.25 Å)

Sequence Identity [%]: 23 PDB Blast Evaluate: 2.3

>gi|14318558|ref|NP_116691.1| ubiquinol-cytochrome c oxidoreductase subunit 6 (17 kDa); Qcr6p [Saccharomyces cerevisiae]

MGMLELVGEYWEQLKITVVPVAAAEDDDNEQHEEKAAEGEEKEEENGDEDEDEDEDEDDDDDDDEDEEEE
EEEVTDQLEDLREHFKNTEEGKALVHHYEECAERVKIQQQQPGYADLEHKEDCVVEEFFHLQHYLDTATAP
RLFDKLLK

Modeled residue range: 74 to 147 based on template [1ezvH](#) (2.30 Å) Sequence Identity [%]: 100 Evaluate: 5.93e-24

>gi|6321631|ref|NP_011708.1| Glyceraldehyde-3-phosphate dehydrogenase 3; Tdh3p [Saccharomyces cerevisiae]

MVRVAINGFGRIGRLVMRIALSRLNVEVVALNDPFIITNDYAAAYMFKYDSTHGRYAGEVSHDDKHIIVDGGK
KIATYQERDPANLPWGSSNVDIAIDSTGVFKELDTAQKHIDAGAKKVVITAPSSSTAPMFVGMVNEEKYTS
DLKIVSNASCTTNCLAPLAKVINDAFGIEEGLMTTVHSLTATQKTVDGSPHKDWRGGRTASGNIIPSSSTG
AAKAVGKVLPELQKLTGMAFRVPTVDVSVVDLTVKLNKETTIDEIKKVVKAAAEGKLGVLGYTEDAVV
SSDFLGDSSHSSIFDASAGIQLSPKFVKLVSWYDNEYGYSTRVVDLVEHVAKA

Modeled residue range: 1 to 330 based on template [2i5pP](#) (2.30 Å) Sequence Identity [%]: 78 Evaluate: 3.53e-139
{25}

>gi|6321706|ref|NP_011783.1| First enzyme in biosynthetic pathway for folic acid and tetrahydrobiopterin; Fol2p [Saccharomyces cerevisiae]

MHNIQLVQEIERHETPLNIRPTSPYTLNPPVERDGFVSWPSVGTQRRAEETEEEEKERIQRISGAIKTILT
ELGEDVNREGLLDTPQRYAKAMLYFTKGYQTNIMDDVIKNAVFEEHDHDEMIVVRDIEIYSLCEHHLVPPFF
GKVHIGYIPNKKVIGLSKLARLAEMYARRLQVQERLTQIAMALSDILKPLGVAVVMEASHMCMVSRGIQ
KTGSSTVTSCMLGGFRAHKTREEFLTLGRRSI

Modeled residue range: 42 to 238 based on template [1fb1A](#) (3.10 Å) Sequence Identity [%]: 63 Evaluate: 5.73e-65

>gi|6322180|ref|NP_012255.1| Derepression Of Telomeric silencing; Dot5p [Saccharomyces cerevisiae]

MGEALRRSTRIAISKRMLEEEESKLAPISTPEVPKKKIKTGPKHNANQAVVQEANRSSDVNELEIGDPIP
DLSSLNEDNDSISLKKITENNRVVVFFVYPRASTPGCTRQACGFRDNYQELKKYAAVFGLSADSVTSQKK
FQSKQNLPHYLLSDPKREFIGLLGAKKTPLSGSIRSHFIFVDGKLFKRVKISPEVSVNDAKKEVLEVAE
KFKEE

Modeled residue range: 59 to 214 based on template [2a4vA](#) (1.80 Å) Sequence Identity [%]: 98 Evaluate: 1.04e-76

>gi|6322409|ref|NP_012483.1| Glyceraldehyde-3-phosphate dehydrogenase 1; Tdh1p [Saccharomyces cerevisiae]

MIRIAINGFGRIGRLVLRALQQRKIDIEVVAVNDPFIISNDYAAAYMVKYDSTHGRYKGTVSHDDKHIIVIDGV
KIATYQERDPANLPWGSLKIDVAVDSTGVFKELDTAQKHIDAGAKKVVITAPSSSAPMFVVGVNHTKYTP
DKKIVSNASCTTNCLAPLAKVINDAFGIEEGLMTTVHSMATQKTVDGSPHKDWRGGRTASGNIIPSSSTG
AAKAVGKVLPELQKLTGMAFRVPTVDVSVVDLTVKLEKEATYDQIKKAVKAAAEGPMKGVLYTEDAVV
SSDFLGDTHASIFDASAGIQLSPKFVKLISWYDNEYGYSARVVDLIEYVAKA

Modeled residue range: 5 to 325 based on template [2i5pP](#) (2.30 Å) Sequence Identity [%]: 77 Evaluate: 1.23e-139

>gi|6322559|ref|NP_012633.1| ubiquitin hydrolase; Yuh1p [Saccharomyces cerevisiae]
MSGENRAVVPIESNPEVFTNFPAHKLGLKNEWAYFDIYSLTEPELLAFLPRPVKAIVLLFPINEDRKSSTS
QQITSSYDVIWFKQSVKNACGLYAILHLSLNNQSLLEPGSDLDNFKSQSDTSSSKNRFDDVTTDQFVLN
VIKENVQTFSTGQSEAPEATADTNLHYITYVEENGGIFELDGRNLSGPLYLGKSDPTATDLIEQELVRVR
VASYMENANEEDVLFAMLGLGPNWE

Modeled residue range: 6 to 234 based on template [1cmxA](#) (2.25 Å) Sequence Identity [%]: 93 Evalue: 5.16e-114

>gi|7839183|ref|NP_058168.1| Translocase of the inner membrane; mitochondrial intermembrane space protein mediating import and insertion of polytopic inner membrane proteins; Tim8p [Saccharomyces cerevisiae]
MSSLSTSDLASLDDTSKKEIATFLEGENSKQKVQMSIHQFTNICFKKCVESVNSNLSSQEEQCLSNCVN
RFLDTNIRIVNGLQNTR

Modeled residue range: 28 to 86 based on template [3cjhB](#) (2.60 Å) Sequence Identity [%]: 100 Evalue: 4.14e-19

>gi|6322468|ref|NP_012542.1| glyceraldehyde 3-phosphate dehydrogenase; Tdh2p [Saccharomyces cerevisiae]
MVRVAINGFGRIGRLVMRIALQRKNVEVVALNDPFI SNDSAYMFKYDSTHGRYAGEVSHDDKHIIVDGH
KIATFQERDPANLPWASLNIDIAIDSTGVFKELDTAQKHIDAGAKKVVIITAPSSSTAPMFVMGVNEEKYTS
DLKIVSNASCTTNCLAPLAKVINDAFGIEEGLMTTVHSMATQKTVDGPHKDWRRGGRTASGNIIPSSSTG
AAKAVGKVLPELQGLTGMAFRVPTVDVSVVDLTVKLNKETTYDEIKKVVKAAAEGKLGKVLGYTEDAVV
SSDFLGDSSNSIFDAAAAGIQLSPKFKVSVKLVSWYDNEYGYSTRVVDLVEHVAKA

Modeled residue range: 1 to 330 based on template [2i5pP](#) (2.30 Å) Sequence Identity [%]: 78 Evalue: 1.23e-139

>gi|6323103|ref|NP_013175.1| Bud20p [Saccharomyces cerevisiae]
MGRYSVKRYKTKRRTRDLDIYNDLSTKESVQKLLNQPLDETKPGLGQHYCIHCAKYMETAIALKTHLKG
KVHKRRVKELRGVPTYQEVSDAAAAGYNLNKFLNRVQEITQSVGPEKESNEALLKEHLDSTLANVKTTTEPT
LPWAAAADAEANTAAVTEAESTASAST

Modeled residue range: 36 to 95 based on template [1zr9A](#) (99.9 Å) Sequence Identity [%]: 45 Evalue: 6.24e-9

>gi|6323613|ref|NP_013684.1| antioxidant enzyme that provides protection against oxidation systems capable of generating reactive oxygen and sulfur species; Tsalp [Saccharomyces cerevisiae]
MVAQVQKQAPTFFKKTAVVDGVFDEVSLDKYKGYVVLAFIPLAFTFVCPTEIIAFSEAAKKFEEQGAQVL
FASTDSEYSLAWTNIPRKEGGLPINIPLLADTNHSLSRDYGVLEEEGVALRGLFIIDPKGVI RHITI
NDLPVGRNVDEALRLVEAFQWTDKNGTVLPCNWTPGAATIKPTVEDSKEYFEAANK

Modeled residue range: 3 to 195 based on template [1qmvH](#) (1.70 Å) Sequence Identity [%]: 66 Evalue: 1.07e-69

>gi|6324070|ref|NP_014140.1| antioxidant protein and metal homeostasis factor, protects against oxygen toxicity; Atx1p [Saccharomyces cerevisiae]
MAEIKHYQFNVMTCSCGSGAVNKVLTKEPVDVSKIDISLEKQLVDVYTTLPYDFILEKIKKTGKEVRSG
KQL

Modeled residue range: 2 to 73 based on template [1cc7A](#) (1.20 Å) Sequence Identity [%]: 100 Evalue: 4.30e-32

>gi|6324090|ref|NP_014160.1| aminopeptidase of cysteine protease family; bleomycin hydrolase; Lap3p [Saccharomyces cerevisiae]
MLPTSVSRSLYLKTFRSHLLRAPQIVLKRMSSSSIDISKINSWNKEFQSDLTHQLATTVLKKNYNADDALLN
KTRLQKQDNRFVNTVVSTDPVTNQKSSGRCWLFAATNQLRLNLVSELNLKEFELSQAYLFFFYDKLEKA
NYFLDQIVSSADQDIDSRLVQYLLAAPTEDGGQYSMFLNLVKKYGLIPKDLYGDLPYSTTASRKWNSLLT
TKLREFAETLRTALKERSADDSIIIVTLREQMQREIFRLMSLFMDIPPVQPNEQFTWEYVDKDKKIHTIKS
TPLEFASKYAKLDPSTPVSLINDPRHPYGKLIKIDRLGNVLGGDAVIYLNVDNETLSKLVVKRLQNNKAV
FFGSHTPKFMDKKTGVMDIELWNYPAIGYNLPQQKASRIRYHESLMTHAMLITGCHVDETSKLPRLRYRVE
NSWGKDSGKDGLYVMTQKYFEEYCFQIVVDINELPKELASKFTSGKEEPIVLPIWDFPMGALAK

Modeled residue range: 30 to 482 based on template [2e01A](#) (1.73 Å) Sequence Identity [%]: 97 Evaluate: 0.00e-1

>gi|6681849|ref|NP_014237.2| Homology to rat L36a and human L36a; Rpl42ap [Saccharomyces cerevisiae]
MVNVPKTRKTYCKGKTCRKHQHKVTQYKAGKASLFAQGKRRYDRKQSGFGGQTKPVFHKKAKTTKKVVV
RLECVKCKTRAQLTLKRCKHFELGGEKKQKQALQF

Modeled residue range: 2 to 93 based on template [2zkr4](#) (8.70 Å) Sequence Identity [%]: 73 Evaluate: 1.84e-20

>gi|6324639|ref|NP_014708.1| Cytochrome c1; Cyt1p [Saccharomyces cerevisiae]
MFSNLSKRWAQRTLKSKSFYSTATGAASKSGKLTQKLVTAGVAAAAGITASTLLYADSLTAEAMTAAEHGLH
APAYAWSHNGPFETFDHASIRRGYQVYREVCAACHSLDRVAWRTLVGVSHTNEEVRNMAEEFEYDDEPDE
QGPNPKRPGKLSDYIPGPYPNEQAARAANQALPPDLSLIVKARHGGCDYIFSLLTGYPDEPPAGVALPP
GSNYNPYFPGGSIAMARVLFDDMVEYEDGTPATTSQMAKDVTTFLNWCAEPEHDERKRLGLKTVIILSSL
YLLSIWVKKFKWAGIKTRKVFVFNPPKPRK

Modeled residue range: 62 to 307 based on template [1kb9D](#) (2.30 Å) Sequence Identity [%]: 100 Evaluate: 1.76e-145

>gi|6325168|ref|NP_015236.1| serum response factor-like protein that may function downstream of MPK1 (SLT2) MAP-kinase pathway; Rlmlp [Saccharomyces cerevisiae]
MGRRKIEIQRISDDRNRAVTFIKRKAGLFKKAHELSQLCQVDIAVILGNSNTFYEFSSVDTNDLIYHYQ
NDKNLLHEVKDPSDYGDFHKSASVNIQDILLRSSMSNPKSKSNVKGMNQSENNDDENDEDDDDHGNFER
NSNMHSNKKASDKNIPSAHMKLLSPTALISKMDGSEQNKRPENALPPLQHLKRLKPDPLQISRTPQQQQ
QQNISRPYHSSMYNLNQPSSSSSSPSTMDFPKLPSPFQNSSFNGRPPPIISISPNKFSKPF TNASSRTPKQE
HKINNSGSNNNDNSNYTQSPSNSLEDSIQQTVKARRKLSARPVLRVRIPNNNFSSNSAIPSEPPSSASSTS
ANGNSMGSSQIMKENKTSRSSKISPLSASASGPLTLQKGNNGRMVIKLPNANAPNGSNNNGSNNNNHPY
PFGSGSSPLFSATQPYIATPLQPSNIPGGPFQQNTSFLAQRQTQQYQQMSFKKQSQTVPPLTTTLTGRPPS
TFSGPETSNGPPTGSLPSKVFVHDLMSNSPNVSSISMFPDWSMGPNSAKPGNTNPNPGTFPPVQTAVNNGNS
SNISSTNNTNNNNNNNNNNSSNNNSNNGNDNNSNNSNSYSNNEAPVNGAAISEHTTDGDSNNQSNSS
TYDAAATAYNGTGLTPYINTAQTPLGTKFFNFSTDISGEKNSSKI

Modeled residue range: 2 to 69 based on template [legwA](#) (1.50 Å) Sequence Identity [%]: 54 Evaluate: 3.48e-16

>gi|6325198|ref|NP_015266.1| Member of a glutaredoxin subfamily in Sc together with GRX3 & GRX4. Significant sequence diff. with the other glutaredoxin subfamily, formed by the previously described GRX1 & GRX2 glutaredoxins (Luikenhuis MBC 9:1081, 1998); Grx5p [Saccharomyces cerevisiae]
MFLPKFNPPIRSFSPILRAKTLRLRYQNRMYLSTEIRKAIEDAIESAPVVLFMKGTPEFPKCGFSRATIGLL
GNQGVDPKFAAYNVLEDPLELREGIKEFSEWPTIPQLYVNKEFIGGCDVITSMARSGELADLLEEAQALV
PEEEEEETKDR

Modeled residue range: 30 to 148 based on template [1ykaA](#) (99.9 Å) Sequence Identity [%]: 38 Evaluate: 4.23e-20

```
>gi|6325296|ref|NP_015362.1| homologous to ERV1; Erv2p [Saccharomyces cerevisiae]
MKQIVKRSHAIRIVAALGIIGLWMMFFSSNELSIATPGLIKAKSGIDEVQGAEEKNDARLKEIEKQTIMP
LMGDDKVKKEVGRASWKYFHTLLARFPDEPTPEEREKLTFTIGLYAELYPCGECSEYHFVKLIEKYPVQTS
SRTAAAMWGCHIHNKVNEYLKKDIYDCATILEDYDCGCSDSGKRVSLKEEAKQHG
```

Modeled residue range: 74 to 178 based on template [1jr8A](#) (1.50 Å) Sequence Identity [%]: 100 Evaluate: 1.01e-60

```
>gi|6325330|ref|NP_015398.1| Homologous to mammalian phosphotyrosine phosphatase; Ltp1p
[Saccharomyces cerevisiae]
MTIEKPKISVAFICLGNFCRSPMAEAIKFKEVEKANLENRFNKIDSFGTSNYHVGESPDHRTVSIKQHG
VKINHKGKQIKTKHFDEYDYIIGMDESNINNLKKIQPEGSKAKVCLFGDWNTNDGTVQTIIEDPWYGDIQ
DFEYNFKQITYFSKQFLKKEL
```

Modeled residue range: 3 to 161 based on template [1d1qA](#) (1.70 Å) Sequence Identity [%]: 99 Evaluate: 1.04e-85

```
>gi|6319925|ref|NP_010006.1| mitochondrial thioredoxin; Trx3p [Saccharomyces cerevisiae]
MLFYKPVMRMAVRPLKSIRFQSSYTSITKLTNLTEFRNLKIQNDKLVIDFYATWCGPCKMMQPHLTKLIQ
AYPDVRFVKCDVDESPDIAKECEVTAMPTFVLGKDGQLIGKIIGANPTALEKGIKDL
```

Modeled residue range: 27 to 124 based on template [2fa4B](#) (2.38 Å) Sequence Identity [%]: 43 Evaluate: 6.45e-23

```
>gi|6320259|ref|NP_010339.1| ubiquitin-conjugating enzyme, E2; Cdc34p [Saccharomyces cerevisiae]
MSSRKSTASSLLLRQYRELTDPKKAIPSFHIELEDDSNIFTWNIGVMVLNEDSIYHGGFFKAQMRFPEDF
PFSPPQFRFTPAIYHPNVYRDGRLCISILHQSGDPMTEPDAETWSPVQTVESVLSISIVSLEDPNINSP
ANVDAADVDRKNPEQYKQVVKMEVERSKQDIPKGFIMPTSESAYISQSKLDEPESNKDMADNFWYDSDLD
DDENGSVILQDDDYDDGNHHPFEDDDVYNYNDNDDDDERIEFEDDDDDDDSDIDNDSVMDRKQPHKAED
ESEDVEDVERVSKKI
```

Modeled with HOMER.

Modeled residue range: 9 to 170 based on template [1PZVIA](#) (2.52 Å) Sequence identity[%]: 43 PDB Blast Evaluate: 2e-33

```
>gi|6320304|ref|NP_010384.1| Brain Modulosignalin Homolog; Bmh2p [Saccharomyces cerevisiae]
MSQTREDSVYLAKLAEQAERYEEMVENMKAVASSGQELSVEERNLLSVAYKNVIGARRASWRIVSSIEQK
EESKEKSEHQVELIRSYRSKIETELTKISDDILSVLDLHIPSATTGESKVFYKMGDYHRYLAEFSSG
DAREKATNSSLEAYKTASEIATTELPPTHPIRLGLALNFSVFYIEIQNSPKACHLAKQAFDDAIAELDT
LSEESYKDSTLIMQLLRDNLTLWTSDISESGQEDQQQQQQQQQQQQQQQAPAEQTQGEPTK
```

Modeled residue range: 5 to 234 based on template [2br9A](#) (1.75 Å) Sequence Identity [%]: 79 Evaluate: 3.51e-90

```
>gi|6681846|ref|NP_011543.2| Protein essential for mitochondrial biogenesis and cell viability;
Erv1p [Saccharomyces cerevisiae]
MKAIDKMTDNPPEGLSGRKKIYDEDGKPCRSCNTLLDFQYVTGKISNGLKNLSSNGKLAGTGALTGEAS
ELMPGSRTYRKVDPPDVEQLGRSSWTLHLSVAASYPAPQPTDQKQKEMKQFLNIFSHIYPCNCAKDFEKY
IRENAPQVESREELGRWMCEAHNKVNKKLRKPKFDCNFWEKRWKDGWDE
```

Modeled residue range: 84 to 189 based on template [logcB](#) (1.80 Å) Sequence Identity [%]: 47 Evaluate: 5.00e-27

```
>gi|6321648|ref|NP_011725.1| thioredoxin; Trx2p [Saccharomyces cerevisiae]
MVTQLKSASEYDSALASGDKLVVVDFFATWCGPCKMIAPMIEKFAEQYSDAAFYKLDVDEVSDVAQKAEV
SSMPTLIFYKGGKEVTRVVGANPAAIKQAIASNV
```

Modeled residue range: 1 to 104 based on template [2fa4B](#) (2.38 Å) Sequence Identity [%]: 100 Evaluate: 3.32e-48

```
>gi|6323072|ref|NP_013144.1| thioredoxin; Trx1p [Saccharomyces cerevisiae]
MVTQFKTASEFDSAIAQDKLVVVDFFYATWCGPCKMIAPMIEKFAEQYQADFYKLDVDELGDVAQKNEVS
AMPPTLLLFKNGKEVAKVVVGANPAAIKQAIANA
```

Modeled residue range: 1 to 103 based on template [2i9hA](#) (99.9 Å) Sequence Identity [%]: 100 Evaluate: 1.63e-48

```
>gi|6324082|ref|NP_014152.1| Protein required for cell viability; Ynl247wp [Saccharomyces
cerevisiae]
MNI F I K A L R R Y T I M S T P K I V Q P K W K V P T P Q A K E T V L K L Y N S L T R S K V E F I P Q S G N R G V T W Y S C G P T V Y D A
S H M G H A R N Y V S I D I N R R I I Q D Y F G Y D V Q F V Q N V T D I D D K I I L R A R Q N Y L F D N F V K E N D T K F N A T V V D K V K
T A L F Q Y I N K N F T I Q G S E I K T I E E F E T W L S N A D T E T L K L E N P K F P M H V T A V Q N A I E S I T K G D S M D A E V A F E
K V K D V T V P L L D K E L G S T I S N P E I F R Q L P A Y W E Q K F N D D M L S L N V L P P T V T T R V S E Y V P E I I D F V Q K I I D N
G Y A Y A T S D G S V Y F D T L K F D K S P N H D Y A K C Q P W N K G Q L D L I N D G E G S L S N F A D N G K K S N N D F A L W K A S K A G
E P E W E S P W G K G R P G W H I E C S V M A S D I L G S N I D I H S G G I D L A F P H H D N E L A Q S E A R F D N Q Q W I N Y F L H T G H
L H I E G Q K M S K S L K N F I T I Q E A L K K F S P R Q L R L A F A S V Q W N N Q L D F K E S L I H E V K S F E N S M N N F F K T I R A L
K N D A A S A G H I S K K F S P L E K E L L A D F V E S E S K V H S A F C D N L S T P V A L K T L S E L V T K S N T Y I T T A G A A L K I E
P L I A I C S Y I T K I L R I I G F P S R P D N L G W A A Q A G S N D G S L G S L E D T V M P Y V K C L S T F R D D V R S L A I K K A E P K
E F L Q L T D K I R N E D L L N L N V A L D D R N G Q S A L I K F L T N D E K L E I V K L N E E K H A N E L A K K Q K K L E Q Q K L R E Q K
E N E R K Q K A Q I K P Q D M F K D V T L Y S A W D E Q G L P T K D K D G N D I T K S M T K K L K K Q W E Q Q K K L H E E Y F G E D K
```

N-term: Modeled residue range: 35 to 133 based on template [1li5A](#) (2.30 Å)

Sequence Identity [%]: 43 Evaluate: 1.00e-16

C-term: Modeled residue range: 221 to 602 based on template [1u0bB](#) (2.30 Å)

Sequence Identity [%]: 30 Evaluate: 7.04e-49

```
>gi|6324296|ref|NP_014366.1| Synthetic interaction with Whi2; Siw14p [Saccharomyces cerevisiae]
MGLYQAKNDEGSDPKSSSKIDDLIENEAEIIRLIKEDGKLLIDNGDGRDIHNI IQEDKLLSVEFNEVLKR
FHGEEKSDIPRKEFDEDEDDGYDSNEHHQKTIEVMNTLNHVINKEVIPPENF SHVVGEIYRSSFPQENF
SFLHERLKLKLSILVLIPEEYPQENLNF LKLTG I K L Y Q V G M S G N K E P F V N I P S H L L T K A L E I V L N P A N Q P I
L I H C N R G K H R T G C L I G C I R K L Q N W S L T M I F D E Y R R F A F P K A R A L D Q Q F I E M Y D D D E I K R I A S K N N W L P L Q
W
```

Modeled residue range: 116 to 263 based on template [1xriA](#) (3.30 Å) Sequence Identity [%]: 61 Evaluate: 1.81e-50

```
>gi|6324360|ref|NP_014430.1| Similar to ubiquitin-like protein 8 of Arabidopsis thaliana and C.
elegans; Hub1p [Saccharomyces cerevisiae]
MIEVVVNDRLGKKVRVKCLAEDSVGDFKKVLSLQIGTQPKNIVLQKGGSVLKDHI SLEDEYEVHDQTNLEL
YYL
```

Modeled residue range: 1 to 73 based on template [1m94A](#) (99.9 Å) Sequence Identity [%]: 100 Evaluate: 2.44e-31

>gi|6325229|ref|NP_015297.1| acetoacetyl CoA thiolase; Erg10p [Saccharomyces cerevisiae]
MSQNVYIVSTARTPIGSGFQGSLSKTAVELGAVALKGALAKVPELDASKDFDEIIFGNVLSANLGQAPAR
QVALAAGLSNHIVASTVNVKVCASAMKAIILGAQSIKCGNADVAVVAGGCE SMTNAPYYMPAARAGAKFGQT
VLVDGVERDGLNDAYDGLAMGVHAEKCARDWDITREQQDNFAIESYQKSQKSQKEGKFDNEIVPVTIKGF
RGKPDQTQVTKDEEPARLHVEKLR SARTV FQKENGTVTAANASPINDGAAAVILVSEKVLKEKNLKLPLAII
KGWGEAAHQPADFTWAPSLAVPKALKHAGIEDINSVDYFEFNEAFSVVGLVNTKILKLDPSKVN VYGGAV
ALGHPLGCSGARVVVTL LLSILQQEGGKIGVAAICNGGGGASSIVIEKI

Modeled residue range: 3 to 398 based on template [2ib8B](#) (1.85 Å) Sequence Identity [%]: 48 Evaluate: 1.97e-92

>gi|6325255|ref|NP_015323.1| appears to be functionally related to SNF7; Snf8p [Saccharomyces cerevisiae]
MKQFGLAAFDLKD GKYNDV NKTILEKQSVELRDQLMVFQERLVEFAKKNHSELQASPEFRSKFMHMCSS
IGIDPLSLFDRDKHLFTVNDFYEVCLKVIEICRQTKDMNGGVISFQELEKVFHFRKLNVLGDDLEKSIDM
LKSLECFEIFQIRGKKFLRSVPNELTSDQTKILEIC SILGYSSISLLKANLGWEAVRSK SALDEM VANG L
LWIDYQGGAEALYWDPSWITRQL

Modeled residue range: 20 to 232 based on template [1w7pA](#) (3.60 Å) Sequence Identity [%]: 100 Evaluate: 2.05e-119

>gi|6325339|ref|NP_015407.1| S. pombe dim1+ in budding yeast; Dib1p [Saccharomyces cerevisiae]
MASVLLPQLRTGWHVDQAIVTETKRLVVIRFGRKNDRQCMIMDELLSSIAERVRNF AVIYLCDIDEVSDF
DEMYELTDPMTVMFFYHNKHMCDFTGTGNNKLNFI VDDKQEMIDILETIFRGARKNKGLV VSPYDYNHK
RVS

Modeled residue range: 5 to 138 based on template [1svxA](#) (2.35 Å) Sequence Identity [%]: 66 Evaluate: 9.31e-49

>gi|6319498|ref|NP_009580.1| Originally identified as a multicopy suppressor of a respiratory defective mutant; homolog of Sco1p; Sco2p [Saccharomyces cerevisiae]
MLNSSRKYACRSLFRQANVSIKGLFYNGGAYRRGFSTGCCLRSDNKESPSARQPLDRLQLGDEINEPEPI
RTRFFQFSRWKATIALLLLSGGTYAYLSRKRRLLETEKEADANRAYGSVALGGPFNL TDFNGKPFTEENL
KGKFSILYFGF SHCPDICPEELDR LTYWISELDDKDHIKI QPLFISCDPARDTPDVLKEYLSDFHPAII G
LTGTYDQVKSVCCKYKVFYFSTPRDVKPNQDYLV DHSIFFY LIDPEGQFIDALGRNYDEQSGLEKIREQIQ
AYVPKEERERRSKK WYSFIFN

Modeled residue range: 120 to 299 based on template [2b7jB](#) (2.30 Å) Sequence Identity [%]: 68 Evaluate: 1.05e-75

>gi|6319733|ref|NP_009815.1| Riboflavin biosynthesis; Rib5p [Saccharomyces cerevisiae]
MFTGIVECMGTVLENNPYDDSESGGQGV SITIGNAGSILTDCHVGDSI AVNGVCLTVTEFNND SFKVGIS
PETIKRSNVASWIQGTQVNLERAVSQDVRFGGHYVQGHVDTVANIVSRRPEGNSIIFGFQLRDQ EYFKYI
VEKGFICIDGTSLTIIKVDPLSQGGAFYISMIKHTQDNVIMPLK KIGDEVNIEVDLTGKIIEKQILLTLE
NQISKKDSLNTMISNIIIEEKVRNYLNK

Modeled residue range: 1 to 205 based on template [1kz1A](#) (2.10 Å) Sequence Identity [%]: 51 Evaluate: 3.24e-46

>gi|6319741|ref|NP_009823.1| similar to Rab proteins and other small GTP-binding proteins; Ypt10p [Saccharomyces cerevisiae]
MIVKLLQEIQVAQNTEEYDMEATIKVVLLGDSSVGKTSIVTRLKSGKFLAKHAATIGAAFITKTIEVPSN
DSSTEKRIHMEIWDTAGQERYKSLVPMYYRDANIALIVFELGDVSSSLQCAKTW FQDLQDRAQGTQVIIVG
NKYDLVCEEHSGEVTIPAE LQGLPYVA VSAKTGYNFDTLNKIIISLVPESQFKT LSKNNEQGNILEINKK
KSGSGCIC

Modeled residue range: 23 to 179 based on template [1z08D](#) (1.80 Å) Sequence Identity [%]: 42 Evaluate: 1.77e-25

>gi|6319971|ref|NP_010051.1| phosphotyrosine-specific protein phosphatase; Ptp1p [Saccharomyces cerevisiae]
MAAAPWYIRQRDITDLLGKFKFIQNQEDGRLREATNGTVNSRWSLGVSIIEPRNDARNRYVNIIMPYERNRVH
LKTLSGNDYINASYVKVNVPGQSIIEPGYYIATQGPTRKTWDQFWQMCYHNCPLDNIVIVMVTPLVEYNRE
KCYQYWPRGGVDDTVRIASKWESPGGANDMTQFPSDLKIEFVNVHVKVDYYTVTDIKLTPDPLVGPVKT
VHHFYFDLWKDMNKPEEVVPIIMELCAHSHSLNSRGNPIIVHCSAGVGRTGTFIALDHLMDTLDFKNITE
RSRHSDRATEEYTRDLIEQIVLQLRSQRMKMVQTKDQFLFIYHAAKYLNLSLVNQ

Modeled residue range: 47 to 324 based on template [2h4va](#) (1.55 Å) Sequence Identity [%]: 31 Evaluate: 4.46e-32

>gi|6320303|ref|NP_010383.1| Member of a glutaredoxin subfamily in Sc together with GRX4 & GRX5. Sign. sequence diff. with the other glutaredoxin subfamily, formed by the previously described GRX1 & GRX2 glutaredoxins (Luikenhuis MBC 9:1081, 1998); Grx3p [Saccharomyces cerevisiae]
MCSFQVPSAFSFNYSYCYKRHQARYYTAAKLFQEMPVIEINDQEFTYLTTTAAGDKLIVLYFHTSWAE
PCKALKQVFEAISNEPSNSNVSFSLIDADENSEISELFEISAVPYFIIHKGITILKELSGADPKKEYVSLLE
EDCKNSVNSGSSQTHMENANVNEGSHNDEDDDEEEEEETEEQINARLTKLVNAAPVMLFMKGGSPSEPK
CGFSRQLVGLILREHQVRFVGFDFDILRDESVRQNLKFFSEWPTFPQLYINGEFQGGLDIIKESLEEDPDFLQ
HALQS

N-terminal: Modeled residue range: 36 to 135 based on template [2i23B](#) (1.41 Å)

Sequence Identity [%]: 37 Evaluate: 1.40e-14

C-terminal: Modeled residue range: 189 to 270 based on template [1wika](#) (99.9 Å) Sequence Identity [%]: 60 Evaluate: 5.69e-23

>gi|6320389|ref|NP_010469.1| Phosducin-Like Protein; Plp1p [Saccharomyces cerevisiae]
MEDKLDRIYTNVLSNAEKDKHTTVDSDDKSSGEENLDELLNELDRELEDEHFEFLSAYRSERLQQISDHLK
QVKKNVEDDGYGRLQCIDNEADAIQICTKTTMVVIHFELETFGKCQYMNEKLENLAKRYLTTRFIKVNVO
TCPFLVKNLNIKVLFPVVGYYKNGLEKVRVYVGFSKLGNDFNGFDIRRLEQSLAHSGVIEDTFEIRKHSSVN
TERFASTNHDRSESDSLDI

Modeled residue range: 99 to 202 based on template [2dbcA](#) (99.9 Å) Sequence Identity [%]: 28 Evaluate: 4.97e-5

>gi|6320610|ref|NP_010690.1| Disp. for spores & spore viab. - required for dityrosine biosynth. & dityrosine accumul. in outer spore wall (s.w.); s.w. matur. & resist. to ether & lytic enz. mRNA trans. mid/late during s.w. formation; Dit2p [Saccharomyces cerevisiae]
MELLKLLCLILFLTLISYVAFIIVPPLNFPKNIPTIPFYVVFVLPVIFPIDQTELYDLYIRESMEKYGAVK
FFFSGSRWNILVSRSEYLAQIFKDEDTFKASGNQKIPYSALAAAYTGDNVISAYGAVWRNYRNAVTNGLQH
FDDAPIFKNAKILCTLIKNRLLLEGQTSIPMGPLSQRMALDNISQVALGFDFGALTHEKNAFHEHLIRIKK
QIFHPFFLTFPFLDVLPIPSRKKAFKDVVSFRELIVKRVQDELVNNYKFEQTTFAASDLIRAHNNEIIDY
KQLTDNIVIIILVAGHENPQLLFNSSLYLLAKYSNEWQEKLRKEVNGITDPKGLADLPLLNALFLEVVRMY
PPLSTIINRCTTKTCKLGAIEIVIPKGVYVGYNNFGTSHDPKTWGTADDFKPERWGSDIETIRKNWRMAK
NRCAVTGFHGGRRACLGEKLALTEMRISLAEMLKQFRWSLDPWEWEEKLTPAGPLCPLNLKLFNENIME

Modeled residue range: 156 to 481 based on template [1w0gA](#) (2.73 Å) Sequence Identity [%]: 26 Evaluate: 2.94e-15

>gi|6320695|ref|NP_010775.1| Riboflavin biosynthesis; Rib3p [Saccharomyces cerevisiae]
MFTPIDQAIIEHFQKQNFVIVMDDAGRENEGDLICAAENVSTEQMAFLVRHSSGYVCAPMTNAIADKLDLP
LLRTGMKFESNDDDRHGTAITITVDVAQGTGTTGISAHDRSMTCRALADSSSTPKSFLKPGHICPLRAADG
GVLQRRGHTEAGVDLCKLSGLSPVAVIGELVNDDEQGTMMRLNDCQAFGKKHGIPLISIEELAQYLKK

Modeled residue range: 1 to 208 based on template [1tksB](#) (1.60 Å) Sequence Identity [%]: 57 Evaluate: 5.48e-63

>gi|6320726|ref|NP_010806.1| ER protein functionally likely involved in interacting with nascent polypeptides in the ER; Eug1p [*Saccharomyces cerevisiae*]
MQVTTRFISAIVSFCLFASFTLAENSARATPGSDLLVLTEKKFKSFIESHPLVLVEFFAPWCLHSQILRP
HLEEAASILKEHNPVVQIDCEANSMVCLQQTINTYPTLKIFKNGRIFDQVYRQVVKITDEITQYMIQLY
EASVIYLNSEDEIQPYLENATLPVVINRGLTGLNETYQEVALLDAEDYVFLSLLDSEDKSLSIHLPTTE
PILFDGNVDSL VGNSVALTQWLKVVILPYFTDIEPDLFPKYISSNLPPLAYFFYTSEELEDYTDLFTQLG
KENRGQINFIALNSTMFPHHVRFLNMREQFPLFAIHNMNNLKYGLPQLPEEEYAKLEKQPPLDRDMIVQ
LVKDYREGTAKPIVKSEEIPKEQKSNVYKIVGKTHDDIVHDDDKDVLVYKYYATWCIIHSKRFAPYEEIAN
VLASDESVRDKILIAEVDSGANDILSFPVTGYPTIALYPAGNNSKPIIFNKIRNLEDVFEF IKESGTHHI
DGOAIYDKLHQAKDSEVSTEDTVHDEL

Modeled residue range: 24 to 496 based on template [2b5eA](#) (2.40 Å) Sequence Identity [%]: 42 Evaluate: 6.09e-105

>gi|6320808|ref|NP_010887.1| vacuolar ATPase V0 domain subunit c (17 kDa); Cup5p [*Saccharomyces cerevisiae*]
MTELCVYAPFFGAIGCASAIIFTSLGAAYGTAKSGVGICATCVLRPDLDFKNIVPVMAGIIAIYGLVV
SVLVCYSLGQKQALYTGFIQLGAGLSVGLSGLAAGFAIGIVGDAGVRGSSQPPRLFVGMILILIFAENVL
LYGLIVALLLNSRATQDVVC

Modeled residue range: 12 to 150 based on template [2bl2B](#) (2.10 Å) Sequence Identity [%]: 27 Evaluate: 9.13e-9

>gi|6320869|ref|NP_010948.1| probably involved in intra-Golgi transport or in the formation of transport vesicles at the most distal Golgi compartment; Ypt31p [*Saccharomyces cerevisiae*]
MSEEDYGYDYDLLFKIVLIGDSGVGKSNLLSRFTKNEFNMDSKSTIGVEFATRLEIDGKRIKAQIWDTA
GQERYRAITSAYYRGAVGALIVYDISKSSSYENCNHWSLRENNADDNVAVGLIGNKSDLAHLRAVPTEE
SKTFAQENQLLFTETSALNSENVDKAFEEELINTIYQKVSQKQMDLGDSSANGNANGASAPNGPTISLTPT
PNENKKANGNNCC

Modeled residue range: 10 to 183 based on template [2f9mA](#) (1.95 Å) Sequence Identity [%]: 70 Evaluate: 5.45e-67

>gi|6320881|ref|NP_010960.1| peptide Methionine sulfoxide Reductase 1; Mxrlp [*Saccharomyces cerevisiae*]
MSSLISKTIKYDPAKDKLITLACGCFWGTTEHMYRKYLNDRIVDCKVGYANGEESSKKDSPSSVSYKRVCGG
DTDFAEVLQVSYNPKVITLRELTDFFRIHDPPTSNSQGPDKGTQYRSGLFAHSDADLAKELAKIKEEWQP
KWGNKIATVIEPIKNFYDAEEYHQLYLDKNPQGYACPTHYLRM

Modeled residue range: 6 to 174 based on template [1fvaB](#) (1.70 Å) Sequence Identity [%]: 36 Evaluate: 4.50e-23

>gi|6320917|ref|NP_010996.1| Utilizes NADP+ as the preferred coenzyme. Activated by K+.; Ald5p [*Saccharomyces cerevisiae*]
MLSRTRAAAPNSRIFTRSLRLRYSQAPLVRPITLPLNGFTYEQPTGLFINGEFVASKQKKTDFVINPNEE
KITTVYKAMEDDVDEAVAAAKKAFETKWSIVEPEVRAKALFNLADLVEKHQETLAAIESMDNGKSLFCAR
GDVALVSKYLRS CGGWADKIYGNVIDTGKNHFTYSIKEPLGVCQIIPWNFPLLMWSWKIGPALATGNTV
VLKPAETTPLSALFASQLCQEAGIPAGVVNIPGSGRVVGERLSAHPDVKKIAFTGSTATGRHIMKVAAD
TVKKVTLELGGKSPNIVFADADLDKAVKNIAFGIFYNSEVCCAGSRIYIQDQTVYEEVLQKLKDYTESLK
VGDPFDEEVFQGAQTSQKQLHKLIDYVDVAKSEGARLVTTGGARHGSKGYFVKPTVFADVKGDMRIVKEEV
FGPIVTVSKFSTVDEVIAMANDSQYGLAAGIHTNDINKAVDVSKRVKAGTVWINTYNNFHQNVPFGGFGQ
SGIGREMGEAALSNTYQTKSVRIAIDKPIR

Modeled residue range: 46 to 515 based on template [1o04G](#) (1.42 Å) Sequence Identity [%]: 48 Evaluate: 1.73e-131

>gi|6320936|ref|NP_011015.1| vitamin B12-(cobalamin)-independent isozyme of methionine synthase (also called N5-methyltetrahydrofolate homocysteine methyltransferase or 5-methyltetrahydropteroyl triglutamate homocysteine methyltransferase); Met6p [*Saccharomyces cerevisiae*]

```
MVQSAVLGFPFRIGPNRELKKAEGYWNGKITVDELFKVGGKDLRTQNWKLQKEAGVDIIPSNDFSFYDQVL
DLSLLFNVIPDRYTKYDLSPIDTLFAMGRGLQRKATEKAVDVTALEMVKWFDSDNYHYVRPTFSKTTQF
KLNQKQPVDEFLEAKELGIHTRPVLLGVPVSYFLGKADKDSLDEPLSLLEQLLPLYTEILSKLASAGAT
EVQIDEPVLVLDLPANAQAAIKKAYTYFGEQSNLPKITLATYFQTVVFNLDIAIKGLPVAALHVDVFRAPL
QFDEVVAAIGNKQTLVSGIVDGRNIWKNDFKSSAIVNKAIEKLGADRUVVATSSSLHHTPVLDLNNETKL
DAEIKGFFSFATQKLDEVVVIITKNVSGQDVAAALEANAKSVESRGKSKFIHDAAVKARVASIDEKMSRA
APFEQRLPEQQKVFNLPLFPPTTIGSFQTKDIRINRNKFNKGTISAEYEFKINSEIEKVIRFQEEIGL
DVLVHGEPPERNDMVQYFGEQINGYAFVNGWVQSYGSRVYRPPPIVGDLSRPKAMSVKESVYAQSITSKP
VKGMLTGPITCLRWSFPRDDVDQKTQAMQLALALRDEVNDLEAAGIKVIQVDEPALREGLPLREGTERSA
YYTWAAEAFRVATSGVANKTQIHSHFCYSDLDPNHIKALDADVVSIEFSKDDANYIAEFKNYPNHIGLG
LFDIHSRIPRPSKDEFIAKISTILKSYPAEKFWVNPDCGLKTRGWEETRLSLTHMVEAAKYFREQYKN
```

Modeled residue range: 4 to 764 based on template [1u1jA](#) (2.40 Å) Sequence Identity [%]: 47 Evaluate: 0.00e-1

>gi|6320972|ref|NP_011051.1| involved in ubiquitin-mediated protein degradation; Rsp5p [*Saccharomyces cerevisiae*]

```
MPSSISVKLVAAESLYKRDVFRSPDPFAVLTIDGYQTKSTSAAKKTLNPNYWNFTKFDINENSILTIQV
FDQKKFKKKDQGFGLGVVNVVVDLGLHLEDDTATSSGRPREETITRDLKKSNDGMAVSGRLIVVLSKLPS
SSPHSQAPSGHTASSSTNTSSTRNTHSTSHPSRGTAQAVESTLQSGTAAATNTATTSRHS
TNSTSSATRQYSSFEDQYGRLLPPGWERRTDNFGRTYYVDHNTRTTTWKRPTLDQTEAERGNQLNANTELE
RRQHRGRTLPGGSSDNSSVTVQVGGGNSIPPVNGAAAAAFAATGGTTSGLGELPSGWEQRFTEPGRAYFV
DHNTRTTTWVDPRRQYIRTYGPTNTTIQQQPVSQLGPLPSGWEMRLTNTARVYFVDHNTKTTTWDDPRL
PSSLQDNVQYKRFRRKVIYFRSQPALRILPGQCHIKVRRKNIFEDAYQEIIMRQTPEDLKKRLMIKFDG
EEGLDYGGVSREFFFLLSHEMFNPFYCLFEYSAYDNYTIQINPNSGINPEHLNYFKFGRVVGLGVFHRR
FLDAFFVYGALYKMLRKKVVLQDMEGVDAEVYNSLNLNMLENSIDGVLDTFSADDERFGEVTVVDLKPDPG
RNIEVTDGNKKEYVELYQWRIVDRVQEQFKAFMDGFNELIPEDLVTVFDERELELLIGGIAEIDIEDWK
KHTDYRGYQESDEVIQWFVKCVSEWDNEQRARLLQFTTGTSRIPVNGFKDLQGSDDGPRRFTIEKAGEVQQ
LPKSHTCFNRVDLPQYVDYDSMKQKLTlaveetIGFGQE
```

Modeled residue range: 430 to 801 based on template [2oniA](#) (2.20 Å) Sequence Identity [%]: 56 Evaluate: 5.39e-123

>gi|6321025|ref|NP_011104.1| Brain Modulosignalin Homolog; Bmh1p [*Saccharomyces cerevisiae*]

```
MSTSREDSVYLAKLAEQAERYEEMVENMKTVAASSGQELSVEERNLLSVAYKNVIGARRASWRIVSSIEQK
EESKEKSEHQVELICSYRSKIETELTKISDDILSVLDLHLSIPATTGESKVFYKMKGDYHRYLAEFSSG
DAREKATNASLEAYKTASEIATTELPPHTPIRLGLALNFSVFYIEIQNSPKACHLAKQAFDDAIAELDT
LSEESYKDSTLIMQLLRDNLTLWTSMSSESQAEDQQQQQQHQQQQPPAAAEGEAPK
```

Modeled residue range: 5 to 234 based on template [2br9A](#) (1.75 Å) Sequence Identity [%]: 78 Evaluate: 1.59e-89

>gi|14318459|ref|NP_116595.1| SNZ3 proximal ORF, stationary phase induced gene family; Sno3p [*Saccharomyces cerevisiae*]

```
MTVVIGVLALQGAFLIEHVRHVEKCIVENRDFYEKKLSVMTVKDKNQLAQCDALIIPGGESTAMSLIAERT
GFYDDLAYFVHNPSKVTWGTCAGLIYISQQLSNEAKLVKTLNLLKVKVKNRFAFGRQAQSSTRICDFSNFI
PHCNDPFATFIRAPVIEEVLDPEHVQVLYKLDGKNDGGQELIVAAKQKNNILATSFHPELAENDIRFHDW
FIREFVLKNYSK
```

Modeled residue range: 3 to 220 based on template [2abwB](#) (1.62 Å) Sequence Identity [%]: 35 Evaluate: 1.01e-23

>gi|14318463|ref|NP_116599.1| high degree of similarity with the AAD of *P. chrysosporium*; Aad6p [Saccharomyces cerevisiae]
MADLFAPAPEPSTELGRLRVLSKSAGIRVSPLILGGMSIGDAWSEILGSMKERAPELLDAFYEAGGNFI
DTANNYQNEQSEAWIGEMVSRKLRDQIVIA TKFTTDYKKYDVGGGKSANYCGNHKRSLHVSVRDSLRLK
QTDWIDILYVHWWDYMSSIEEVMSLHILVQQARSSIWVCLIRLPLGLFLRQITTLNLMVKPLLASIKVNG
TC

Modeled residue range: 26 to 166 based on template [1pz1A](#) (2.20 Å) Sequence Identity [%]: 32 Evaluate: 1.32e-11

>gi|14318479|ref|NP_116614.1| Involved in cell polarization, endocytosis and other cytoskeletal functions; Act1p [Saccharomyces cerevisiae]
MDSEVAALVIDNGSGMCKAGFAGDDAPRAVFP SIVGRPRHQGIMVGMGQKDSYVGD EAQSKRGILT LRYPI
IEHGIVTNWDDMEKIWHHTFYNELRVAP EHPVLLTEAPMNP KSNREKMTQIMFETFNVP AFYVSIQAVL
SLYSSGRTTGIVLDSGDGVTHVPIYAGFSLPHAILRIDLAGRDLTDYLMKILSERGYSFSTTAEREIVR
DIKEKLCYVALDFEQEMQTAAQSSSIEKSYELPDGQVITIGNERFRAPEALFHPSVLGLESAGIDQTTYN
SIMKCDVDVRKELYGNIVMSGGTTMFPGIAERMQKEITALAPSSMKVKI IAPPERKYSVWIGGSILASLT
TFQQMWISKQEYDESGPSIVHHKCF

Modeled residue range: 4 to 371 based on template [2fxuA](#) (1.35 Å) Sequence Identity [%]: 85 Evaluate: 0.00e-1

>gi|14318481|ref|NP_116616.1| beta subunit of tubulin monomer; involved in chromosome segregation and nuclear migration; Tub2p [Saccharomyces cerevisiae]
MREIIHISTGQCGNQIGAAFWETICGEHGLDFNGTYHGDDIQKERLNVYFNEASSGKWVPRSINVDLEP
GTIDAVRNSAIGNLFRPDNYIFGQSSAGNVWAKGHYTEGAELVDSVMDVIRREAEGCDSLQGFQITHSLG
GGTSGMG TLLISKIREEF PDRMMATFSVLPSPKTS DTVVEPYNATLSVHQ LVEHSD ETCIDNEALYDI
CQRTLKLNQPSYGD LNNLVSSVMSGVT TSLRYPGQLNSDLRKLAVNLVFP PRLHFFMVGYAPLTAIGSQS
FRSLTVPELTQQMFD AKNMMAAADPRNGRYLTVAAFFRGKVS VKEVEDEMHKVKQSKNSDYFVEWIPNNVQ
TAVCSVAPQGLDMAATFIANSTSIQELFKRVGDQFSAMFKRKAFLHWY TSEGMDLEFSEAESNMNDLVS
EYQQYQEATVEDDEEVDENGDFGAPQNQDEPITENFE

Modeled residue range: 2 to 427 based on template [1tvkB](#) (2.89 Å) Sequence Identity [%]: 77 Evaluate: 0.00e-1

>gi|14318551|ref|NP_116684.1| Required for mitosis and sporulation; Cdc14p [Saccharomyces cerevisiae]
MRRSVYLDNTIEFLRGRVYL GAYDYTPEDTDELVFFTVEDAIFYNSFHLDFGPMNIGHLYRFAVIFHEIL
NDPENANKAVVFYSSASTRQRANAACMLCCYMLLVQAWTPHQVLQPLAQVDPPFMPFRDAGYSNADFEIT
IQDVVYGVWRAKEKGLIDLHSFNLESYKEYEHVEFGDFNVLTPDFIAFASPQEDHPKGYLTKSSHLNQF
FKSVLNF FANNVQLVVRLNSHLYNKKH FEDIGIQHLDLIFEDGTCPDLSIVKNFVGA AETIIKRGGKIA
VHCKAGLGRTGCLIGAHLIYTYGFTANECIGFLRFIRPGMVVGPQQHWLYLHQND FREWKYTTTRISLKPS
EAI GGLYPLISLEEYRLQKKKLKDDK RVAQNNIEGELRDLTMTPPSNGHGALSARNSSQPSTANN GSN SF
KSSAVPQTSPGQPRKGQNGSNTIEDINNNRNP TSHANRKVVIESNNSDDESMQDTNGT SNHYPKVSRRKN
DISSASSSRMEDNEPSATNINNAADDTILRQLLPKNRRVTSGRRTTSAAGGIRKISGSIKK

Modeled residue range: 5 to 336 based on template [1ohcA](#) (2.50 Å) Sequence Identity [%]: 37 Evaluate: 1.46e-61

>gi|14318480|ref|NP_116615.1| involved in the secretion pathway at the ER-to-Golgi step; required for sporulation; Ypt1p [Saccharomyces cerevisiae]
MNSEYDYLFKLLLIGNSGVGKSCLLLRFSDDTYTNDYISTIGVDFKIKTVELDGKTVKLQIWDTAGQERF
RTITSSYRGSHGIIIVYDVT DQESFNGVKMWLQEIDRYATSTVLKLLVGNKCDLKD KRVVEYDVAKEFA
DANKMPFLET S ALDSTNVEDAFLTMARQIKESMSQQLNETTQKKEDKGNVNLKGQSLTNTGGGCC

Modeled residue range: 3 to 205 based on template [lukyY](#) (1.50 Å) Sequence Identity [%]: 100 Evaluate: 1.12e-102

>gi|6321228|ref|NP_011305.1| probably involved in intra-Golgi transport or in the formation of transport vesicles at the most distal Golgi compartment; Ypt32p [*Saccharomyces cerevisiae*]
MSNEDYGYDYDYLKIVLIGDSGVGKSNLLSRFTTDEFNIESKSTIGVEFATRTIEVENKKIKAQIWDTA
GQERYRAITSAYYRGAVGALIVYDISKSSSYENCNHWTTELRENADDNVAVGLIGNKSDLAHLRAVPTDE
AKNFAMENQMLFTETSALNSDNVDKAFRELIVAIQVMVSKHQVDLSGSGTNNMGSNGAPKGPPTISLTPAP
KEDKKKKSSNCC

Modeled residue range: 10 to 183 based on template [2f9mA](#) (1.95 Å) Sequence Identity [%]: 70 Evaluate: 3.68e-67

>gi|6321643|ref|NP_011720.1| Required for the biosynthesis of purines, thymidylate, methionine, histidine, pantothenic acid and formylmethionyl-tRNA; Ade3p [*Saccharomyces cerevisiae*]
MAGQVLDGKACAOQFRSNIANEIKSIQGHVPGFAPNLAI IQVGNRPDSATYVRMKRKAEEEAGIVANFIH
LDESATEFEVLRVYDQLNEDPHTHGIIVQLPLPAHLDEDRITSRVLAEKDVGDFGPTNIGELNKKNGHPF
FLPCTPKGIIELHKNVTEIGSRSVVIGRSDIVGSPVAELLKSLNSTVTITHSKTRDIASYLHDADIVV
VAIGQPEFVKGEWFKPRDGTSSDKKTVVIVDGTNYVADPSKKSFGKCVGDVEFNIAIKYVHLITPVPGGV
GPMTVAMLQNTLIAAKRQMEESSKPLQIPPLPLKLLTPVPSDIDISRAQQPKLINQLAQELGIYSHELE
LYGHYKAKISPKVIERLQTRQNGKYILVSGITPTPLGEGKSTTTMGLVQALTAHLGKPAIANVRQPSLGP
TLGVKGAAGGGYSQVIPMDEFNLHLTGDIHAIGAANNLLAAAIDTRMFHETTQKNDAFYNRLVPRKNG
KRFKTPSMQRRNLRLGIQKTNPDDLTPPEINKFARLNIDPDTITIKRVVDINDRMLRQITIGQAPTEKNH
TRVTGFDITVASELMAILALSCKDLRDMKERIGRVVVAADVNRSPVTVEDVGTGAL TALLRDAIKPNLMQ
TLEGTPVLVHAGPFANISIGASSVIADRVALKLVGTEPEAKTEAGYVVTEAGDFDTMGGERRFFNIKCRSS
GLTPNAVVLVATVRALKSHGGAPDVKPGQPLPSAYTEENIEFVEKGAANMCKQIANIKQFGVPVVVAINK
FETDTEGEIAAIRKAALAEAGAFEAVTSNHWAEGGKAIDLAKAVIEASNQPVDFHFLYDVNSSVEDKLT
IVQKMYGGAAIDILPEAQRKIDMYKEQGFGNLPICTIAKTQYSLSHDATLKGVPPTGFTFPIRDVRLSNGAG
YLYALAAEIQTIPLATYAGYMAVEVDDDDGEIDGLF

Modeled residue range: 323 to 944 based on template [1fpmA](#) (3.00 Å) Sequence Identity [%]: 45 Evaluate: 1.32e-137

>gi|6321691|ref|NP_011768.1| functions in the Ada and SAGA (Spt/Ada) complexes to acetylate nucleosomal histones; Gcn5p [*Saccharomyces cerevisiae*]
MVTKHQIEEDHLDGATTDPEVKRVKLENNVEEIQPEQAE TNKQEGTDKENKGKFEKETERIGGSEVVTDV
EKGIVKFEFDGVEYTFKERPSVVEENEGKIEFRVVNNDNTKENMMVLTGLKNIFQKQLPKMPKEYIARLV
YDRSHLSMAVIRKPLTVVGGITYRPFDFKREFAEIVFCAISSTEQVRGYGAHLMNHLKDYVRNTSNIKYFL
TYADNYAIGYFKKQGF TKEITLDSKIWMGYIKDYEGGTLMQCSMLPRI RYLDAGKILLLQEAALRRKIRT
ISKSHIVRPGLEQFKDLNNIKPIDPMTIPGLKEAGWTPEMDALAQRPKRGP HDAAIQNILTELQNHAAAW
PFLQPVNKEEVPDYDFIKEPMDLSTMEIKLESNKYQKMEDFIYDARLVFN NCRMYNGENTSYYKYANRL
EKFFNKNVKEIPEYSHLID

Modeled residue range: 99 to 262 based on template [lyghA](#) (1.90 Å) Sequence Identity [%]: 100 Evaluate: 6.64e-93

>gi|6321832|ref|NP_011908.1| NADP-cytochrome P450 reductase; Ncplp [*Saccharomyces cerevisiae*]
MPFGIDNTDFTVLAGLVLAVLLYVKRNSIKELLSDDGDITAVSSGNRDIAQVV TENNKNYLVLYASQTG
TAEDYAKKFSKELVAKFNLMVMCADVENYDFESLNDVPVIVSIFISTYGE GDFPDGAVNFEDFICNAEAG
ALSNLRYNMFGLGNSTYEFFNGAAKKA EKHL SAAGA IRLGKLG EADDGAGTTDEDYMAWKDSILEVLKDE
LHLDEQEAKFTSQFYTVLNEITDSMSLGEPSAHYLP SHQLNRNADGIQLGPF DLSQPYIAPIVKSRELF
SSNDRNCIHSEFDLSGSNIKYSTGDHLAVWPSNPLEKVEQFLSIFNLDPETIFDLKPLDPTVKVPFPPTPT
TIGAAIKHYLEITGPVSRQLFSSLIQFAPNADVKEKLTLLSKDKDQFAVEITSKYFN IADALKYLSDGAK
WDTVPMQFLVESVPQMTPRYYSISSSSLSEKQTVHVTSIVENFPNPEL PDAPPVVGVTNLLRN IQLAQN
NVNIAETNLPVHYDLNGPRKLFANYKLPVHVRNSNFR LPSNPSTPVIMIGPGTG VAPFRGFIRERVAFLE
SQKKGNNVSLGKHILFYGSRNTDDFLYQDEWPEYAKKLDGSFEMVVAHSRLPNTKKVYVQDKLKDYEDQ

VFEMINNGAFIYVCGDAKGMAGVSTALVGIILSRGKSITTEATELIKMLKTSGRYQEDVW

Modeled residue range: 47 to 691 based on template [2bpoA](#) (2.90 Å) Sequence Identity [%]: 99 Evaluate: 0.00e-1

>gi|6322027|ref|NP_012102.1| nitrilase; Nit1p [Saccharomyces cerevisiae]
MAKHIVAALQIGSCPGSTKDTLKKILSYEKEIKESGAKLVVIPEATLGGYPKGSNFGVYLYRLQEGREE
YAKYLAEAEIEIGNGEKYPEISQLCALSKATDASLVCVGCIERDGTTLTYCTMVYIDPKDGYVVGKHKRLMPTA
GERLIWGGDGSTLPVVDTAAGKIGGAICWENMMPLLRVYAMYKKGVEIWCAPTVDARPI

Modeled residue range: 30 to 192 based on template [1j31C](#) (1.60 Å) Sequence Identity [%]: 32 Evaluate: 3.29e-9

>gi|6323822|ref|NP_013893.1| Expression induced in response to high osmotic stress. NAD+ is preferred coenzyme.; Ald2p [Saccharomyces cerevisiae]
MPTLYTDIEIPQLKISLQPLGLFINNEFCPSSDGKTIETVNPATGEPITSFQAANEKDVVDKAVKAARAA
FDNVWSKTSSEQRGIYLSNLLKLIIEEEQDTLAALETLDAGKPYHSNAKGDLAQILQLTRYFAGSADKFDK
GATIPLTFNKFAYTLKVPFVVAQIVPWNYPPLAMACWKLQGALAAAGNTVIKPAENTSLSLLYFATLIKK
AGFPPGVVNIIVPGYGLVQALASHMDIDKISFTGTSKVGGFVLEASGQSNLKDVTLECGGKSPALVFED
ADLDKAIWDWIAAGIFYNSGQNTANSRVYVQSSYDKFVEKFKETAKKEWDVAGKFDPFDEKCI VGPVIS
STQYDRIKSYIERGKREEKLDMFQTSSEFPIGGAKGYFIPPTIFTDVPQTSKLLQDEIFGPVVVVSKFTNY
DDALKLANDTCYGLASAVFTKDVKKAHMFARDIKAGTVWINSSNDEDVTVPFGGFKMSGIGRELQSGVD
TYLQTKAVHINLSLDN

Modeled residue range: 23 to 506 based on template [1o04G](#) (1.42 Å) Sequence Identity [%]: 48 Evaluate: 1.79e-122

>gi|6681848|ref|NP_012160.2| Mps One Binder; Mob1p [Saccharomyces cerevisiae]
MSFLQNFHISPGQTI RSTRGFKWNTANAANNAGSVSPTKATPHNNTINGNNNNANTINNRADFTNPNVNG
YNESDHGRMSPVLTTPKRHAPPPEQLQNVTDNFNYTPSHQKPFLLQFQAGTTVTHQDIKQIVEMTLGSEGV
LNQAVKLPRGEDENEWLAVHCVDYFNQINMLYGSITEFCSPQTCPRMIATNEYEYLWAFQKGGPPVSVSA
PKYVECLMRWCQDQFDDDESLFP SKVTGTFPEGF IQRVIQPILRRLFRVYAHYCHHFNELLELNLQTVLN
TSFRHFCLFAQEFELLRPADFGPLLELVME LRDR

Modeled residue range: 81 to 313 based on template [2hjnA](#) (2.00 Å) Sequence Identity [%]: 88 Evaluate: 7.94e-116

>gi|6322155|ref|NP_012230.1| capping - addition of actin subunits; Cap2p [Saccharomyces cerevisiae]
MSDAQFDAALDLLRRLNPTTLQENLNNLIELQPNLAQDLLSSVDVPLSTQKDSADSNREYLCCDYNRDID
SFRSPWNTYYPELSPKDLQDSPFP SAPLRKLEILANDSFVYRDLYYEGGISSVYLWDLNEEDFNHDF
AGVVLFFKKNQSDHSNWD SIHVFEVTTSPSSPDSFNRYRVT TTIILHLDKTKTDQNSHMMLSGNLTRQTEKD
IAIDMSRPLDVIFTSHVANLGLSIEDIESQMRNLL ETVYFEKTRDIFHQTKNAAIASSAEEANKDAQAEV
IRGLQSL

Modeled residue range: 2 to 256 based on template [1iznD](#) (2.10 Å) Sequence Identity [%]: 50 Evaluate: 8.43e-60

>gi|6322811|ref|NP_012884.1| Nifu-like protein; Nfulp [Saccharomyces cerevisiae]
MFKSVAKLGKSPIFYLN SQRLIHIKLTTPNENALKFLSTDGEMLQTRGSKSIVIKNTDENLINHSKLAQ
QIFLQCPGVE SLMIGDDFLTINKDRMVHWSIKPEIIDLLTKQLAYGEDVISKEFHAVQEEEEGEGGYKIN
MPKFELTEEDEEVSELIEELIDTRIRPAILEDGGDIDYRGWDPKTGTVYLRQLQGACTSCSSSEVTLKYGI
ESMLKHVYDEVKEVIQIMDPEQEIALKEFDKLEKKLESSKNTSHEK

Modeled residue range: 153 to 230 based on template [1vehA](#) (99.9 Å) Sequence Identity [%]: 55 Evaluate: 7.96e-18

>gi|6323244|ref|NP_013316.1| Product of gene unknown; Cdc123p [Saccharomyces cerevisiae]

MSSQEYTTFFIDIPVTRAQVEHCSYSFWSSLYPKYVPKSIVLKSLPKKFIQYLEQDGIKLPQEENSRSVYT
EEIIRNEDNDYSDWEDDEDTATEFVQEVEPLIDFPPELHQKLDALNELGAVAPKLNWSAPRDATWILPNN
TMKCNEVNELYLLLNASNIMHDLQRAFKGCVDDIKGLKFDLVLRQWCDMNPALFVFRVFNKNAHVGA
TQRDLNYYDYLDLSDTFKDLIDEIVHDVVLPKFPDKSFVLDVYIPRPFNKIFIVDINPFARKTDSLIFS
WNEIAAIAPPKNDVEDYELRLVTRHNTGRFASKEHSENHVPQDLVEASLNPEAIRELTQKWKELLSQQA
EESDSENET

Modeled with Homer

Modeled residue range: 79 to 229 based on template [2potA](#) (1.80 Å) Sequence Identity [%]: 25 PDB Blast Evaluate: 2.2

>gi|6322908|ref|NP_012981.1| ras homolog--GTP binding protein; Rho4p [Saccharomyces cerevisiae]
MNTLLFKRKGNGCNESNIVSQSPSSSNLPESPGTLDEKNLPRLPPTPFARSLSTIPSYEQMKRINKLPD
YHLKIVVVDGAVGKTCLLISYVQGTFFPTDYIPTIFENYVTNIEGPNQIIEELALWDTAGQEEYSRLRPL
SYTNADVLMVCYSVGSKTSKLNVEDLWFPEVKHFCPSTPIMLVGLKSDLYEADNLSDLVEPSSAESLAKR
LGAFQAHIQCSARLKENIDEVFETAIHITLLSDSLYAPREPHTHTIKNPFKRNTTRSDIDSSTGDTSVSISGT
KRLRKNKCIIM

Modeled residue range: 74 to 239 based on template [1s1cB](#) (2.60 Å) Sequence Identity [%]: 51 Evaluate: 3.10e-48

>gi|6322921|ref|NP_012994.1| Hydrophilic protein that acts in conjunction with SNARE proteins in
targeting and fusion of ER to Golgi transport vesicles; Bet3p [Saccharomyces cerevisiae]
MVSTTQSRSLKAMGEEIWKNKTEKINTELFITLYGSIVAQLCQDYERDFNKVNDHLYSMGYNIGCRLLIED
FLARTALPRCENLVKTSEVLSKCAFKIFLNITPNI TNWSHNKDTFSLILDENPLADVFELPMDAMKSLWY
SNILCGVLKGSLEMVQLDCDVFVSDILRGDSQTEIKVKNRILKDEIPIGED

Modeled residue range: 23 to 182 based on template [1wc9A](#) (1.60 Å) Sequence Identity [%]: 58 Evaluate: 9.36e-49

>gi|6323138|ref|NP_013210.1| alkyl hydroperoxide reductase; Ahp1p [Saccharomyces cerevisiae]
MSDLVNKKFPAGDYKFQYIAISQSDADSECKMPQTVESKLI SENKKVIIITGAPAAFSPCTVSHIPGY
INYLDLVLVKEKEVDQVIVVTVDNPFANQAWAKSLGVKDTTHIKFASDPGCAFTKSGIFELAVGDGVYWSG
RWAMVVENGIVTYAAKETNPGTDVTVSSVESVLAHL

Modeled residue range: 47 to 176 based on template [1tp9A](#) (1.62 Å) Sequence Identity [%]: 40 Evaluate: 3.45e-18

>gi|6323224|ref|NP_013296.1| N-myristoyl transferase; Nmt1p [Saccharomyces cerevisiae]
MSEEDKAKKLENLLKLLQLNNDTTSKFTQEQKAMKDHKFWRTQPVKDFDEKVVVEEGPIDKPKTPEDISD
KPLPLLSSFEWCSIDVDNKKQLEDVFLNENYVEDRDAGFRFNKYTKEFFNWALKSPGWKKDWHIGVRVK
ETQKLVAFISAIPVTLGVRGKQVPSVEINFLCVHKQLRSKRLTPVLIKEITRRVKNCDIWHALYTAGIVL
PAPVSTCRYTHRPLNWKKLYEVDFTGLPDGHTTEEDMIAENALPAKTKTAGLRKLLKEDIDQVFELFKRYQ
SRFELIQIFTKKEEFHNFIGEESLPLDKQVIFSYVVEQPDGKITDFFSFYSLPFTILNNTKYKDLGIGYL
YYYATDADFQFKDRFDPKATKALKTRLCELIYDACILAKNANMDVFNALTSQDNTLFLDDLKFGPGDGF
NFYLFNYRAKPIITGGLNPDNSNDIKRRSNVGVVML

Modeled residue range: 34 to 455 based on template [1iicB](#) (2.20 Å) Sequence Identity [%]: 100 Evaluate: 0.00e-1

>gi|6323383|ref|NP_013455.1| Nit protein, nitrilase superfamily member; Nit3p [Saccharomyces
cerevisiae]
MSASKILSQIKVALVQLSGSSPDKMANLQRAATFIERAMKEQPDTKLVVLPECFNSPYSTDQFRKYSEV
INPKPSTSVQFLSNLANKFKIILVGGTIPELDPKTDKIYNTSIFNEDGKLIDKHKRVHLFDVDIPNGI
SFHESETLSPGEKSTTIDTKYKGFVGVICYDMRFPPELAMLSARKGAFAMIYPSAFNTVTVGPLHWHLARS

RAVDNQVYVMLCSPARNLQSSYHAYGHSIVVDPRGKIVAEAGEGEEIIYAELDPEVIESFRQAVPLTKQR
RFDVYSDVNAH

Modeled residue range: 2 to 282 based on template [1f89A](#) (2.40 Å) Sequence Identity [%]: 96 Evaluate: 6.86e-154

>gi|6323609|ref|NP_013680.1| Required for X-ray damage repair & various types of intra- and interchr. mitotic recombination, including HO switching & plasmid exchange. Disp. for premeiotic DNA synthesis, double strand breaks & heteroduplex formation.; Rad52p [*Saccharomyces cerevisiae*]
MAFLSYFATENQQMQRRLPRTAEGSGGFGVLLMNEIMDMDEKKPVFGNHSEDIQTKLDKKGPEYISKR
VGFGTSR IAYIEGWRVINLANQIFGYNGWSTEVKSVVIDFLDERQGKFSIGCTAIVRVTLTSGTYREDIG
YGTVENERRKPAAFERAKKSAVTDALKRSLRGFGNALGNCLYDKDFLAKIDKVKFDPPDFDENNLFRPTD
EISESSRINTLHENQEQQQYPNKRRQLTKVTNTNPDSTKNLVKIENITVSRGTPMMAAPAEANSKNSNKD
TDLKSLDASKQDQDDLLDDSLMFSDDFQDDDLINMGNTNSNVLTTEKDPVVAKQSPTASSNPEAEQITFV
TAKAATSVQNER YIGEESIFDPKYQAQSIRHTVDQTTSKHIPASVLKDKTMTTARDSVYEKFA PKGKQLS
MKNNDKELGPHMLEGAGNQVPRETTPIKTNATAFPAAAPRFAPPSKVVHPNGNGAVPAVPQQRSTREV
GRP KINPLHARKPT

Modeled residue range: 52 to 198 based on template [1h2iP](#) (2.70 Å) Sequence Identity [%]: 52 Evaluate: 2.17e-41

>gi|6323703|ref|NP_013774.1| FET3 encodes a ferro-O₂-oxidoreductase that is part of the high-affinity iron transport system; Fet3p [*Saccharomyces cerevisiae*]
MTNALLSIAVLLFSMLS LAQAETHFNWTTGWDRYRVDGLKSRPVITCNGQFPWPDITVNGKDRVQIYLT
NGMNTNTSMHFHGLFQNGTASMDGVPFLTQCP IAPGSTMLYNFTVDYNVGT YWYHSHTDGQYEDGMKGL
FIIKDDSF PYDYDEELSLSLSEWYHDLVTDLT KSFMSVYNPTGAEP IPQNLIVNNTMNL TWEVQPD TTYL
LRIVNVGGFVSQYFWIEDHEMTVVEIDGITTEKNVTDMLYITVAQRYTVLVHTKNDTDKNFAIMQKFD
MLDVIPSDLQLNATSYMVYNKTAALPTQNYVDSIDNFLDDFYLQPYEKEAIYGE PDHVI TVDVVMDNLKN
GVNYAFFNNITYTAPKVPTLMTVLSSGDQANNSEIYGSNHTF ILEKDEIVEIVLNNQDTGTHPFHLHG
AFQTIQRDRTYDDALGEVPHSFDPDNHPAFPEYPMRRDTLYVRPQSNFVIRFKADNPGVWFFHCHIEWHL
LQGLGLV LVEDPFGIQDAHSQQLSENHLEVCQSCSVATEGNAAAANTLDLTDLTGENVQHAF IPTGFTKKG
IIAMTFSCFAGILGIITIAIYGMMDMEDATEK VIRD LHVDP E VLLNEVDENEERQVNE DRHSTEKHQFLT
KAKRFF

Modeled residue range: 22 to 550 based on template [1zpuC](#) (2.80 Å) Sequence Identity [%]: 100 Evaluate: 0.00e-1

>gi|6323742|ref|NP_013813.1| SNZ1 proximal ORF, stationary phase induced gene; Snolp [*Saccharomyces cerevisiae*]
MHKTHSTMSGKSMKVI GVLALQGAFL EHTNHLKRCLAENDYGIKIEIKTVKTPEDLAQCDALIIPGGEST
SMSLIAQRTGLYPCLYEFVHNPEKVVWGTCAGLIFLSAQLENSALVKTLGLV LKVDVRRNAFGRQAQSFT
QKCDFSNFIPGCDNF PATFIRAPVIERILDPIAVKSLYELPVNGKDVVVAATQNHNI LVT SFHPELADSD
TRFHDFWIRQFVSN

Modeled residue range: 15 to 218 based on template [2ywdA](#) (1.90 Å) Sequence Identity [%]: 38 Evaluate: 1.22e-27

>gi|6323821|ref|NP_013892.1| Expression induced in response to heat shock, oxidative and osmotic stress. NAD⁺ is preferred coenzyme; Ald3p [*Saccharomyces cerevisiae*]
MPTLYTDIEIPQLKISL KQPLGLFINNEFCPSSDGKTIETVNPATGEPITSFQAANEKDVDKAVKAARAA
FDNVWSKTSSEQRGIYLSNLLK LIEEEQDTLAALETLDAGKPFH SNAKQDLAQI IELTRY YAGAVDKFNM
GETIPLTFNKFA YTLKVPFGVVAQIVPWNYP LAMACRKMQGALAAAGNTVI IKPAENTSLSLLYFATLIKK
AGFP PGVVNVIPGYGSVVGKALGTHMDIDKISFTGSTKVGGSVLEASGQSNLKDITLECGGKSPALVFED
ADLDKAI EWVANGIFFNSGQICTANSRVYVQSS IYDKFVEKFKETAKKEWDVAGKFDPFDEK CIVGPVIS
STQYDRIKSYIERGKKEEKLD MFQTSEFP IGGAKGYFIPPTIFTDVPETSKLLRDEIFGPVVVSKFTNY

DDALKLANDTCYGLASAVFTKDVKKAHMFARDIKAGTVWINQTNQEEAKVPPFGGFKMSGIGRESGDTGVD
NYLQIKSVHVDLSLDK

Modeled residue range: 23 to 502 based on template [1o04G](#) (1.42 Å) Sequence Identity [%]: 47 Evaluate: 1.28e-120

>gi|6323873|ref|NP_013944.1| GMP synthase; Gualp [Saccharomyces cerevisiae]
MAAGEQVSNMFDITILVLDVDFGSQYSHLITRRLREFNIYAEMLPCTQKISELGTWPKGVILSGGPYSVYAED
APHVDHAIFFDLNVPILGICYGMQELAWINGKQVGRGDKREYGPATLKVIDDSNSLFGMNDSTVWMSHGD
KLHGLPTGYKTIATSDNSPYCGIVHETKPIYGIQFHPEVTHSTQGKTLKKNFAVDLCHAKQNWTFENFID
TEINRIRKLVGPTAEVIGAVSGGVDSVASKLMTAIGDRFHAILVDNGVLRRLNEAANVKKTLVEGLGIN
LMVVDASEEFLSKLKGVTDPKRRKIIGNTFIHVFEREAEEKIKPKDGKEIQFLLQGTLYPDVIESISFKG
PSQTIKTHHNVGGLLENMMLKLIIEPLRELFKDEVRHLGELLGIPHDLVWRHPPFPGPGIAIRVLGEVTKEQ
VEIARKADNIYIEEIKKAGLYNQISQAFACLLPVKSVGVMGDQRTYDQVIALRAIETTDFMTADWFFFEH
SFLKKVASRIVNEVDGVARVTDITSKPPATVEWE

Modeled residue range: 14 to 525 based on template [1gpmA](#) (2.20 Å) Sequence Identity [%]: 46 Evaluate: 6.04e-142

>gi|6323995|ref|NP_014065.1| SNZ2 proximal ORF, stationary phase induced gene; Sno2p
[Saccharomyces cerevisiae]
MTVVIGVLALQGAFIEHVRHVEKCIVENRDFYEKKLSVMTVKDKNQLAQCDALIIIPGGESTAMSLIAERT
GFYDDLYAFVHNPSKVTWGTACAGMIYISQQLSNEEKLVKTLNLLKVKVKNRFAFGRQAQSSSTRICDFSNFI
PHCNDFPATFIRAPVIEEVLDPHEHVQVLYKLDGKDNQQELIVAAKQKNNILATSFHPELAENDIRFHDW
FIREFVLKNYSK

Modeled residue range: 4 to 212 based on template [2ywdA](#) (1.90 Å) Sequence Identity [%]: 35 Evaluate: 8.95e-24

>gi|6324175|ref|NP_014245.1| membrane-bound casein kinase I homolog; Yck2p [Saccharomyces
cerevisiae]
MSQVQSPLTATNSGLAVNNNTMNSQMPNRSNVRLVNGTLPPSLHVSNNLNHNTGNSASYSQSRDDST
IVGLHYKIGKKIGEGSFGVLFEGTNMINGLPVAIKFEPKTEAPQLKDEYRTYKILAGTPGIPQEYYFGQ
EGLHNILVIDLLGPSLEDLDFWCGRRFSVKTVVQVAVQMITLIEDLHAHDLIYRDIKPDNFIIGRPGQPD
ANKVHLIDFGMAKQYRDPKTKQHIPPYREKKSLSGTARYMSINTHLGREQSRDDMEAMGHVFFYFLRGQL
PWQGLKAPNNKQKYEKIGEKRLTNVYDLAQGLPIQFGRYLEIVRNLSEETPDYEGYRMLLLSVLDDL
ETADGQYDWMKLNNGRGWDLINKKPNLHGYGHPNPPNEKSKRHRSKNHQYSSPDHHHHYNQQQQQQQAQ
AQQAQAQAQVQQQLQQAQAQQANRYQLQPDDSHYDEEREASKLDPTSYEAYQQQTQQKYAQQQKQKQ
QQKSKQFANTGANGQTNKYPYNAQPTANDEQNAKNAQDRNSNKS SKGFFSKLGCC

Modeled residue range: 71 to 359 based on template [1csnA](#) (2.00 Å) Sequence Identity [%]: 67 Evaluate: 5.13e-117

>gi|6324191|ref|NP_014261.1| 70-kDa adenylyl cyclase-associated protein; Srv2p [Saccharomyces
cerevisiae]
MPDSKYTMQGYNLVLLKRLLEEATARLEDVTIYQEGYIQNKLEASKNNKPSDSGADANTTNEPSAENAPE
VEQDPKCI TAFQSYIGENIDPLVELSGKIDTVVLDALQLLKGQFQSQTFLRAAVRSRKPDISSQTFADS
LRPINENI IKLGQLKESNRQSKYFAYLSALSEGAPLFSWVAVDTPVSMVTDKFAAQFWTNRILKEYRES
DPNAVEWVKKFLASFDNLKAYIKEYHTTGVSWKKGDMDFADAMAQSTKNTGATSSPSPASATAAPAPPPP
PPAPPASVFEISNDTPATSSDANKGGIGAVFAELNQGENITKGLKKVDKSQQTHKNPELRQSSTVSSTGS
KSGPPPRPKPSTLKTTRPPRKELVGNKWF IENYENETESLVIDANKDESIFIGKCSQVLVQIKGKVNAI
SLSETESCSVVDSSISGMDVIKSNKFGIQVNHSLPQISIDKSDGGNIYLSKESLNTEIYTSCSTAINVN
LPIGEDDDYVEFPPIPEQMKHSFADGKFKSAVFEHAG

Modeled residue range: 369 to 524 based on template [1k4zB](#) (2.30 Å) Sequence Identity [%]: 100 Evaluate: 2.46e-82

>gi|6324268|ref|NP_014338.1| May participate in nucleolar function during the transition from stationary phase to rapid growth; Nop2p [Saccharomyces cerevisiae]
MGSRRHKNKQAAPPTLEEFQARKEKKANRKLKKGKRPSTTQGDDEVSDRKKKKSKPFFKSRKEEEEVVEED
KDLPEVDLEELSKARKSLFDDEEDDDEAGLVDEELKDEFDLEQEYDYDEDEDNDAHPIFSDDDDDEADLEE
LNAQNMEALSKKLDEEEAEAEAEAEEMELVEAENMQPRADILPTEEQEEMMAQETPNLTSTRTRMIEIVKV
LENFKTLGAEGRSRGEYVDRLLKDI CEYFGYTPFLAEKLFNLFSPAEEFFEANEIARPITIRTNTLKT
RRRDLAQTLVNRGVNLQPIGSWTKVGLQIFDSQVPIGATPEYLAGHYILQAASSFLPVIALDPHENERIL
DMAAAPGGKTTYISAMMKN TGCVFANDANKSRTKSLIANIHR LGCTNTIVCNYDAREFPKVI GGFDRI LL
DAPCSGTGVIGKDQSVKVS RTEKDFIQIPHLQKQLLLSAIDSVDCNSKHGGVIVYSTCSVAVEEDEAVID
YALRKRPNVKLVDTGLAIGKEAFTSYRGKKFHPSVKLARRYYPHTYNVDGFFVAKFQKIGPSSFDDNQAS
AKEKETAARKEALEEGIIHSDFATFEDEEDDKYIEKSVKNNLLKKGVNPKAKRPSNEK

Modeled residue range: 228 to 549 based on template [1ixkA](#) (1.90 Å) Sequence Identity [%]: 36 Evaluate: 2.87e-47

>gi|6324275|ref|NP_014345.1| Tyrosine protein phosphatase involved in adaptation response to pheromone; Msg5p [Saccharomyces cerevisiae]
MQFHSDKQHLDSKTDIDFKPNSPRSLQNRNTKNLSLDIAALHPLMEFSSPSQDVPGSVKFPSPPTPLNLFM
KPKPIVLEKCPPKVS PRPTPPSLSMRSEAS IYTLPTSLKNRTVSPSVYTKSSTVSSISKLSSSSPLSSF
SEKPHLN RVHSLSVKTKDLKLGIRGRSQTISGLETSPTI SSTREGTLDSTDVNRFSNQKNMQTTLIFPE
EDSDLNIDMVHAEIYQRTVYLDGPLLVLPPNLYLYSEPKLEDILSFDLVINVAKEIPNLEFLIPPEMAHK
IKYYHIEWTHTSKIVKDL SRLTRI IHTAHSQGGKILVHCQCGVSR SASLIVAYIMRYYG LSLNDAYNKLK
GVAKDISPNMGLIFQLMEWG TMLSKNSPGEGETVHMPEEDDIGNNEVSSTTKSYSSASFRSFPMTNLS
SSPNDSSVNSSEVTPRTPATLTGARTALATERGEDDEHCKSLSQPADSLEASVDNESISTAPEQMMFLP

Modeled residue range: 229 to 374 based on template [2ji6B](#) (2.70 Å) Sequence Identity [%]: 53 Evaluate: 8.35e-39

>gi|6324374|ref|NP_014444.1| Protein required for cell viability; Ynr046wp [Saccharomyces cerevisiae]
MKFLTTNFKCSVKACDTSNDNFPLQYD GSKCQLVQDESIEFNPEFLLNIVDRVDWPAVLTVA AELGNNA
LPPTKPSFPSSIQELTDDDMAI LNDLHTLLQLTSIAEGEMKCRNCGHIYYIKNGIPNLLLPPHLV

Modeled residue range: 1 to 135 based on template [2i6aA](#) (1.70 Å) Sequence Identity [%]: 100 Evaluate: 9.97e-73

>gi|6324648|ref|NP_014717.1| cell division cycle blocked at 36 degree C; Cdc21p [Saccharomyces cerevisiae]
MTMDGKNKEEQYLDLCKRI IDEGEFRPDRITGDANLLSEQGVKIWDGNGSREYLDKMGFKDRKVGDLGP
VYGFQWRHF GAKYKTCDDDYTGQ GIDQLKQVIHKLKTNPYDRRI IMSAWN PADFDK MALPPCHIFSQFYV
SFPKEGEGSGK PRLSCLLYQRSCDMGLGVFPNIAS YALLTRMIAKVVDMEPGEF IHTLGD AHVYKDHIDA
LKEQITRNPRFPFKLKI KRVDKIDDFKLTDFEIEDYNPHPRIQMKMSV

Modeled residue range: 7 to 259 based on template [1f28A](#) (1.90 Å) Sequence Identity [%]: 54 Evaluate: 1.01e-95

>gi|6324764|ref|NP_014833.1| Sporulation regulated genes; Spr1p [Saccharomyces cerevisiae]
MVSFRGLTTLTLLFTKLVN CNPVSTKNRDSIQFIYKEKDSIYSAINNQAIN EKIHG VNLGGWLVLEPYIT
PSLFETFRTPNPYNDGIPVDEYHFCEKLG YEKAKERLYSHWSTFYKEEDFAKIASQGFNLVRIPIGYWAF
TTL SHDPYVTAEQEYFLDRAIDWARKYGLKVWIDLHGAAGSQNGFDNSGLRDSYKFL EDENLSATMKALT
YILSKYSTDVYLDTVIGIELLNEPLGPVIDMERLKNLLLPAYDYLRNKINSNQI IVIHDAFQPYHYWDG
FLNDEKNEYGVIIDHHHYQVFSQVELTRKMNERIKIACQWGKDAVSEKHWSVAGEFSAALTDCTKWLNGV
GLGARYDGSWTKDNEKSHYINTCANNENIALWPEERKQNRKFI EAQLDAFEMTGGWIMWCYKTENSIEW
DVEKLIQLNIFPQP INDRKYPNQCH

Modeled residue range: 42 to 444 based on template [1h4pA](#) (1.75 Å) Sequence Identity [%]: 67 Evaluate: 1.57e-168

>gi|6324818|ref|NP_014887.1| contains amino-terminal chromodomains; Essential SAS family Acetyltransferase sharing homology with acetyltransferases from many different organisms; Esalp [Saccharomyces cerevisiae]
MSHDGKEEPGIAKKINSVDDII IKQCWVQKNDEERLAEILSINTRKAPPKFFVHYVNYNKRLEDEWITTD
RINLDKEVLYPKLKATDEDNKKQKKKKATNTSETPQDSLQDGVDFGFSRENTDVMDLNLDNLNVQGIKDENIS
HEDEIKKLRTSGSMTQNPHEVARVRNLNRIIMGKYEIEPWYFSPYPIELTDEDFIYIDDFTLQYFGSKKQ
YERYRKKCTLRHPPGNEIYRDDYVSFFEIDGRKQRTWCRNLCLLSKFLDHTLYYDVPFLFYCMTRRD
ELGHHLVGYFSKEKESADGYNVACILTLPOYQRMGYGKLLIEFSYELSKKENKVGSPKPLSDLGLLSYR
AYWSDTLITLLVEHQKEITIDEISSMTSMTTDILHTAKTLNLRYYKGQHIIFLNEDILDYRNRLKAKK
RRTIDPNRLIWKPPVFTASQLRFAW

Modeled residue range: 162 to 434 based on template [1fy7A](#) (2.00 Å) Sequence Identity [%]: 100 Evaluate: 3.29e-158

>gi|6324899|ref|NP_014968.1| gamma-glutamyl phosphate reductase; Pro2p [Saccharomyces cerevisiae]
MSSSQI AKNARKAGNILKTI SNEGRSDILYKI HDALKANAHAI EEEANKIDLAVAKETGLADSLKRLDL
FKGDKFEVMLQGIKDVAELEDPVGVKVMARELDDGLTLYQVTAPVGVLLVIFESRPEVIANITALSIKSG
NAAILKGGKESVNTFREMAKIVNDTIAQFQSETGVPVGSVQLIETRQDVSDLLDQDEYIDLVVPRGSNAL
VRKIKDTTKIPVLGHADGICSIYLDDEDADLIKAKRISLDAKTNYPAGCNAMETLLINPKFSKWWEVLENL
TLEGGVTIHATKDLKTAYFDKLNELGKLTEAIQCKTVDADEEQDFDKEFLSLDLAAKFVTSTESAIQHIN
THSSRHTDAIVTENKANAEEKFMKGVDSGIVYWNASTRFADGFRYGFGEVGI STSKI HARGPVGLDGLVS
YQYQIRGDGQVASYDLGAGGNKAFVHKDLDIKTVTL

Modeled residue range: 1 to 435 based on template [1vluA](#) (2.29 Å) Sequence Identity [%]: 91 Evaluate: 0.00e-1

>gi|6324950|ref|NP_015019.1| Glucose repressed. Utilizes NADP+ or NAD+ as a coenzyme equally well. Ald4p [Saccharomyces cerevisiae]
MFSRSTLCLKTSASSIGRLQLRYF'SHLPMTVPIKLPNGLEYEQPTGLFINNKFVPSKQNKTFEVINPSTE
EEICHIYEGREDDVEEAVQAADRAFSNGSWGIDPIDRGKALYRLAELIEQDKDVIASIEITLDNGKAISS
SRGDVDLVINYLKSSAGFADKIDGRMIDTGRTHFSYTKRQPLGVCGQIIPWNFPLLMWAWKIAPALVTGN
TVVLKTAESTPLSALYVSKYIPQAGIPPGVINIVSGFGKIVGEAITNHPKIKKVAFTGSTATGRHIYQSA
AAGLKKVTLELGKSPNIVFADAELKKAQNIILGIYNSGEVCCAGSRVVEESIYDKFIEEFKAASES
IKVGDPPDESTFQGAQTSQMQLNKILKYVDIGKNEGATLITGGERLGSKGYFIKPTVFGDVKEDMRIVKE
EIFGPVVTVTKFSADEVINMANDSEYGLAAGIHTSNINTALKVADRVNAGTVWINTYNDFFHHA VPFGGF
NASGLGREMSVDALQNYLQVKAVRAKLDE

Modeled residue range: 47 to 519 based on template [1o04G](#) (1.42 Å) Sequence Identity [%]: 51 Evaluate: 2.21e-138

>gi|6325196|ref|NP_015264.1| Utilizes NADP+ as the preferred coenzyme. Activated by Mg2+; Ald6p [Saccharomyces cerevisiae]
MTKLHFDTAEPVKITLPLNGLTYEQPTGLFINNKFMKAQDGKTYPVEDPSTENTVCEVSSATTEDVEYAIE
CADRAFHDTEWATQDPRERGRLLSKLADELESQIDLVSSEI EALDNGKTLALARGDVTIAINCLRDAAAAYA
DKVNGRTINTGDGYMNF'TLEPIGVCGQIIPWNFPIIMMLAWKIAPALAMGNVCILKPAAVTPLNALYFAS
LCKKVGIPAGVVNIVPGPGRIVGAALNDPRIRKLAFTGSTEVGKSVAVDSSESNLKKITLELGKSAHL
VFDDANIKKTLPNLVNGIFKNAGQICSSGSRIVYQEGIYDELLAAFKAYLETEIKVGNPFDKANFQGAIT
NRQQFDTIMNYIDIGKKEGAKILTGGEKVGDKGYFIRPTVFDVNDMRIVKEEIFGPVVTVAKFKTLEE
GVEMANSSEFFGLGSGIETESLSTGLKVAKMLKAGTVWINTYNDFFDSRVPFGGVKQSGYGREMGEVYHAY
TEVKAVRIKL

Modeled residue range: 28 to 500 based on template [1o04G](#) (1.42 Å) Sequence Identity [%]: 47 Evaluate: 7.03e-125

>gi|6325237|ref|NP_015305.1| Ubl (ubiquitin-like protein) - specific protease 1; Ulp1p [Saccharomyces cerevisiae]

MSVEVDKHRNTLQYHKKNPYSPLFSPISTYRCYPRVLNPNPSESRRSASFSGIYKRTNTSRFNYLNDRRV
LSMEESMKDGS DRASKAGFIGGIRETLWNSGKYLWHTFVKNEPRNF'DGSEVEASGNSDVE SRSSGSRSSD
VPYGLRENYSSDTRKHKFDTSTWALPNKRRRIESEGVGTPSTSPISL LASQKSNCDSDNSITFSRDPFGW
NKWKTSAIGSNSENNTSDQKNSYDRRQYGTAFIRKKKVAKQINNTKLVSR AQSEEVTYLRQIFNGEYKV
PKILKEERERQLKLMMDMKEKDTGLKKSIIIDLTEKIKTIL IENKNRLQTRNENDDDLV FVKEKKISSLE
RKHKDYLNQKLFDRSILEFEKDFKRYNEILNERKKIQEDLKKKKEQLAKKKLVPELNEKDDDQVQKALA
SRENTQLMNRDNIEITVRDFKTLAPRRWLNDTIEFFMKYIEKSTPNTVAFNSFFYTNL SERGYQGVRW
MKRKKQTQIDKLDKIFTPINLNQSHWALGIIDLKKTIGYVDSL SNGPNAMSFALITDLQKYVMEEKHTI
GEDFDLIHLDCPQQPNGYDCGIYVCMNTLYGSADAPLDFDYKDAIRMRRFIAHLILTDALK

Modeled residue range: 403 to 621 based on template [1euvA](#) (1.60 Å) Sequence Identity [%]: 100 Evaluate: 1.68e-124

>gi|6226540|ref|NP_009326.1| subunit II of cytochrome c oxidase; Cox2p [Saccharomyces cerevisiae]

MLDLLRLQLTTFIMNDVPTPYACYFQDSATPNQEGILELHDNIMFYLLVILGLVSWMLYTI VMTYSKNPI
AYKYIKHGQTIIEVIWTFPAVILLIIAFPSFILLYLCEDEVISPAMTIKAI GYQWYWKYEYSDFINDSGET
VEFESYVIPDELLEEGQLRLLDTDTSMVVPVDTHIRFVVTAADV IHDFAI PSLGIKVDATPGRLNQVSAL
IQREGVIFYGACSELCTGHANMFIKIEAVSLPKFLEWLNEQ

Modeled residue range: 20 to 247 based on template [1v54O](#) (1.80 Å) Sequence Identity [%]: 42 Evaluate: 5.21e-45

>gi|6319488|ref|NP_009570.1| Hypothetical ORF; Ybr014cp [Saccharomyces cerevisiae]

MAIVINKRNVRLVITNLLLIVVFFVLRNSNASVNESITTHHPDSLVTFDNSGNAPGTHQSVHDTVNTQD
KEAEVVDKNSGDAEFDAAAEYNKIMEQSPMIVFSKTCGPYSKKLKALLTNSYTFSPSYVVELDRHEHTK
ELQDQIEKVTGRRTVFNVIIGGTSRGGYTEIAELHKNDEL LLSFKKWS DGAF TVKANSQSESA

Modeled residue range: 84 to 199 based on template [2e7pC](#) (2.10 Å) Sequence Identity [%]: 43 Evaluate: 5.31e-15

>gi|6324975|ref|NP_015043.1| Hypothetical ORF; Ypl280wp [Saccharomyces cerevisiae]

MTPKRALISLTSYHGPFYKDGAKTGVFVVEILRSFDTFEKHGFEVDFVSETGGFGWDEHYLPKSF IGGED
KMN FETKNSAFNKALARIKTANEVNASDYKIFFASAGHGALFDY PKAKNLQDIASKIYANGGVIAAICHG
PLLF DGLIDIKTTRPLIEGKAITGFPLEGEIALGVDDILRSRKLTTVERVANKNGAKYLAPIHPWDDYSI
TDGKLVTGVNANSSYSTTIRAINALYS

Modeled residue range: 3 to 235 based on template [1rw7A](#) (1.80 Å) Sequence Identity [%]: 70 Evaluate: 3.36e-90

>gi|6320193|ref|NP_010274.1| Hypothetical ORF; Ydl010wp [Saccharomyces cerevisiae]

MIPSNKRNRARILSITTL LLLL VFFVAQANANFLTVEIKEETS KAFSTNMDNMAGGSSREYAAMPTSTTNKG
SSEVDEEINEIKQKVLGQQPIASVDDSLSAIKNDKGSRI TKAFNVQKEYSLILDLSPII IFSKSTCSYSK
GMKELLENEYQFIPNYYI IELDKHGHGEELQEYIKLVTGRGTVPNLLVNGVSRGGNEEIKKLHTQ GK LLE
SLQVWSDGKFSVEQREKPSNN

Modeled residue range: 126 to 213 based on template [2e7pD](#) (2.10 Å) Sequence Identity [%]: 38 Evaluate: 2.28e-11

>gi|6320661|ref|NP_010741.1| Hypothetical ORF; Ydr453cp [Saccharomyces cerevisiae]

MVAEVQKQAPPFKKTAVVDGIFEEISLEKYKGYVVLAFVPLAFS FVCPTEIVAFSDAAKKFEDQGAQVL
FASTDSEYSLLAWTNLPRKDGG LGPVKVP LLADKNHSLSRDYGV LIEKEGIALRGLFIIDPKGIIRHITI
NDLSVGRNVNEALRLVEGFQWTDKNGTVLPCNWTPGAATIKPDVKDSKEYFKNANN

Modeled residue range: 3 to 195 based on template [1qmvH](#) (1.70 Å) Sequence Identity [%]: 62 Evaluate: 1.33e-64

>gi|6320742|ref|NP_010822.1| Hypothetical ORF; Ydr533cp [Saccharomyces cerevisiae]
MAPKKVLLALTSYNDVFYSDGAKTGVFVVEALHPFNTRKEGFEVDFVSETGKFGWDEHSLAKDFLNGQD
ETDFKNKDSDFNKTAKIKTPKEVNADDYQIFFASAGHGTLDYDPKAKDLQDIASEIYANGGVVAACHG
PAIFDGLTDKKTGRPLIEGKSITGFTDVGETILGVDSSILKAKNLATVEDVAKKYGAKYLAPVGPWDDYSI
TDGRLVTGVNPASAHSTAVRSIDALKN

Modeled residue range: 2 to 236 based on template [1rw7A](#) (1.80 Å) Sequence Identity [%]: 100 Evalue: 5.92e-126

>gi|14318475|ref|NP_116610.1| Hypothetical ORF; Yf1044cp [Saccharomyces cerevisiae]
MKLKVTGAGINQVVTLKQDATLNDLIEHINVDVKTMRFYPPQRINLQGEDASLGQTQLDELGINSGEKI
TIESSDSNESFSLPPPQPKPKRVLKSTEMSIGGSGENVLSVHPVLDDNSCLFHAIAYGIFKQDSVRDLRE
MVSKEVLNNPVKFNDAILDKNPKDYAQWILKMESWGGAIEIGIISDALAVAIYVVDIDAVKIEKFNEDKF
DNYILILFNGIHYSLTMNEFKTVFNKNQPESSDVLTAALQLASNLKQTGYSFNTHKAQIKCNTCQMTFV
GEREVARHAESTGHVDFGQNR

Modeled residue range: 91 to 301 based on template [3by4](#) (1.55 Å) Sequence Identity [%]: 100 Evalue: 1 e-124

>gi|14318532|ref|NP_116665.1| deubiquitinating enzyme (putative); Ubp6p [Saccharomyces cerevisiae]
MSGTEFEFNIRHSGKVYPITLSTDATSADLKSKAEEELTQVPSARQKYMVKGGLSGEESIKIYPLIKPGST
VMLLGTDPANLISKPAKKNFIEDLAPEQQVQQAQLPVGFKNMGNTCYLNATLQALYRVNDRDMILNY
NPSQGVSNSSGAQDEEIHKQIVIEMKRCFENLQNKSFKSVLPVLLNLTLRKCYQFAERDSQGGFYKQODA
EELFTQLFHSMSIVFGDKFSEDFRIQFKTTIKDTANDNDITVKENESDSKLQCHISGTTNFMRNGLLEGL
NEKIEKRSDLTGANSIYSVEKKISRLPKFLTQYVRFVWKRSTNKKSKILRKVVFPFQLDVADMLTPEYA
AEKVKVRDELRRKVEKEKEREIKRRKFDPSSENVMTPREQYETQVALNESEKQWLEEYKHHFPPNL
EKGENPSCVYNLIGVITHQGANSESGHYQAFIRDELLENKWKYFNDDKVSVEKEKIESLAGGSESLSAL
ILMYKGFGL

Modeled residue range: 103 to 499 based on template [1vjvA](#) (1.74 Å) Sequence Identity [%]: 92 Evalue: 0.00e-1

>gi|6323984|ref|NP_014055.1| Hypothetical ORF; Ymr322cp [Saccharomyces cerevisiae]
MTPKRALISLTSYHGPFYKDGAKTGVFVVEILRSFDTFEKHGFEVDFVSETGGFGWDEHYLPKSFIGGED
KMNFEKNSAFNKALARIKTANEVNASDYKIFFASAGHGALFDYDPKAKNLQDIASKIYANGGVIAAICHG
PLLFDFGLIDIKTRPLIEGKAITGFPLEGEIALGVDDILRSRKLTTVERVANKNRAKYLAPIHVWDDYSI
TDGKLVTVGNANSSYSTTIRAINALYS

Modeled residue range: 3 to 235 based on template [1rw7A](#) (1.80 Å) Sequence Identity [%]: 70 Evalue: 6.61e-90

>gi|6323396|ref|NP_013468.1| Hypothetical ORF; Ylr364wp [Saccharomyces cerevisiae]
MSAFVTKAEEMIKSHPYFQLSASWCPDCVYANSIWNKLNVDKVFVFDIGSLPRNEQEKWRIAFQKVVGS
RNLPTIVVNGKFWGTESQLHRFEAKGTLEEELTKIGLLP

modelled with HOMER.

residue range: 103 to 499 based on template [2ht9](#) (1.9 Å) Sequence Identity [%]: 30 pdb Blast Evalue: 2.0e-7

>gi|6323730|ref|NP_013801.1| Hypothetical ORF; Ymr084wp [Saccharomyces cerevisiae]
MCGIFGYCNFLIEKTRGEIIDTLIEGLQALEYKEYDSSGISIQGDELESLSNIYKQTKISSLKEEIDLIN
LNKNLPPFISHCGIAHTRRATHGGLRRANCHPHNSDPSNEFVVVHNGVITNFANLKALLMAKGVYFKSDTD
TECIPKLYKHIYDTSIELGYNLDFHVLTLNLVLEKELEGSYLLCTSSHFPDEVVAARKGSPLVIGVKGKTD
MDVNFVEVEYLDQEEDYLKLNLTQTKSSGNVLAAPVKYNTCLRKSPPFVHNT

Modeled residue range: 1 to 221 based on template [1xffa](#) (1.80 Å) Sequence Identity [%]: 37 Evaluate: 1.39e-28

```
>gi|6323761|ref|NP_013832.1| Hypothetical ORF; Ymr114cp [Saccharomyces cerevisiae]
MCGRFALAYDSGDLPLQLLRDWNLPVNTPKDASSNSQHPHDEEDTKDQPTVSKDIFKASYNISPTNYSVAVY
RPDTKAIQFMRWGLVPFWTKDVSQFKTYRTFNARLENLQESKMWMRPCEKKRCAVLMMSGYFEWKTVGKKK
TPYFISRRDGRMLMFVAGMYDYVEKDDLYTFTIITAQGPRELEWLHERMPCVLEPGTESWDAWMDVDKTTW
STEELVKLLKPDYDESKLQFYQVTDDVGKTTNTGERLIKPLLKEDSDMFSVKREKEEALLENDNEQGIDN
RGVKGDKSLKGEDVFNQKSLKRNSYDGLKKNEEQEETTLPEEGSIGDRVKREEANLSPKREGNREKRNI
VNMLGNQKDSRGKKKIKK
```

Modeled residue range: 77 to 253 based on template [2f20A](#) (2.10 Å) Sequence Identity [%]: 32 Evaluate: 1.85e-17

```
>gi|6324967|ref|NP_015036.1| Hypothetical ORF; Yor391cp [Saccharomyces cerevisiae]
MTPKRALISLTSYHGPFYKDGAKTGVFVVEILRSFDTFEKHGFVDFVSETGGFGWDEHYLPKSFIGGED
KMNFEKNSAFNKALARIKTANEVNASDYKVFASAGHGALFDYPAKAKNLQDIASKIYANGGVIAAICHG
PLLFDFGLIDIKTRPLIEGKAITGFPLEGEIALGVDDILRSRKLTTVERVANKNGAKYLAPIHPWDDYSI
TDGKLVTVGNANSSYSTTIRAINALYS
```

Modeled residue range: 3 to 235 based on template [1rw7A](#) (1.80 Å) Sequence Identity [%]: 70 Evaluate: 3.36e-90

```
>gi|6319407|ref|NP_009489.1| Hypothetical ORF; Ybl064cp [Saccharomyces cerevisiae]
MFSRICAQKRTAWTLPKQAHLQSQTIKTFATAPILCKQFKQSDQPRLRINSDAPNFDADTTVGKINFY
DYLGDSWGVLFSHPADFTPVCTTEVSFAFLKPEFDKRNVKLIGLSVEDVESHEKWIQDIKEIAKVKNVG
FPIIGDTRFNVAFLYDMVDAEGFKNINDGSLKTVRSVVIDPKKKIRLIFTYPSTVGRNTSEVLRVIDAL
QLTDKEGVVTPINWQPADDVIIPPSVSNDEAKAKFGQFNEIKPYLRFTKSK
```

Modeled residue range: 55 to 258 based on template [1prxA](#) (2.00 Å) Sequence Identity [%]: 49 Evaluate: 4.25e-47

```
>gi|6320492|ref|NP_010572.1| Hypothetical ORF; Ydr286cp [Saccharomyces cerevisiae]
MLRAFRCSIHTSRVLLHDAGVKLTFFSKPNCLCDQAKEVIDDVFERKEFHAKAVSLEIVNITDRRNAKW
WKEYCFDIPVLHIEKVGDPKSC TKILHFLEEDDISDKIRRMQSR
```

Modeled residue range: 23 to 83 based on template [1wjka](#) (99.9 Å) Sequence Identity [%]: 43 Evaluate: 2.53e-7

```
>gi|6320714|ref|NP_010794.1| Hypothetical ORF; Ydr506cp [Saccharomyces cerevisiae]
MKVILLKPVQLPMLLLILLKFIMAAKEGKIHVLEFNASSEYTLDKRRVISINGYSATFGPEIRVKSGDTL
NLKLTNWCSEEEASKDSVDVWVDYCYSTALHFHGVVPLANEFDGIPGLTQPTIGYGESYWNFTIDQSTCG
TFWYHSHSSVQYGDGMRGVLIVECDDYDNHVANTINSVRDIETLDDGVVTMCKDKHTKELTDYEVQERII
TSLSDWYTNWNLIDILNDKVLSSSTGGTDPKFDGSLINGKSSDGETIKIGFNTEYLLLRIVNSGMSGTQVFHL
DGFQLIVLEADGIMIKPFIVQTNLAVGQRYTILVKLKSDFIRMINGCNKMMGYITKQWWFYKEGAHL
DLPKNPNDVSIHPLPGFTKAELYRDIEPTQEENKLRKADPVAVFEFDYAYYKDESTKQKYGTGMYKVN
ERTFSEYVKDPVRFVGFNETYDIVINSLDHRHPWHMHGHFFQIISLGNKGDGPFHKDVQEGKAWSRYQND
LRHLARTGKAPMVRDSINIAGNSYAVLRINTEMPGKWLHCHVEWHMMKGLGIVFEVPTTTEDSTKQATT
AVLSYPTKEPDPNTVVHTAALEQNKSKVIAVYILIMCAVDAIFYWLLM
```

Modeled with HOMER

Modeled residue range: 25 to 546 based on template [1v10A](#) (1.70 Å) Sequence Identity [%]: 24 Pdb Blast Evaluate: 9.0e-30

```
>gi|6321388|ref|NP_011465.1| Hypothetical ORF; Yg1050wp [Saccharomyces cerevisiae]
MAAQNAFEQKKRAILNEIDSTQPDLSPKGTIDELCLPIIDLINASADMVTTSSCSGRVSVFLEGTKSYNG
```

EVKIGGKGQGGKWLIVTHDREKVIWGLDELKSKSEFSFELSGKEIPTEKVTGSI RYI LYKYEPFILHVKC
RDFQAASKLYNTAMSCGFRESGIGSNNLVAIRINIKLDVPLGYLDETSGLTKFFVTPEYVSVLDSL SLSK
FDENTRKMQUALYDRIEKELINCAPDVNSKVNITPIETKEERRERKKREGMERQRQLKSPQNVL

Modeled residue range: 28 to 220 based on template [2it2A](#) (1.50 Å) Sequence Identity [%]: 28 Evaluate: 2.22e-9

>gi|6322078|ref|NP_012153.1| Hypothetical ORF; Yil113wp [Saccharomyces cerevisiae]
MNIYTSPTTRPNIAPKSGQRPSLPMLATDERSTDKESPNE DREFVPCSSLDVRR IYPKGPLLVLPEKIYL
YSEPTVKELLPFDVVINVAEEANDLRMQVPAVEYHHYRWEHDSQIALDLPSLTSIIHAATTKREKIL IHC
QCGLSRSATLI IAYIMKYHNLSLRHSYDLLKSRADKINPSIGLIFQLMEWEVALNAKTNVQANSYRKVP

Modeled residue range: 54 to 196 based on template [2i16B](#) (2.70 Å) Sequence Identity [%]: 100 Evaluate: 1.44e-76

>gi|6322467|ref|NP_012541.1| Hypothetical ORF; Yjr008wp [Saccharomyces cerevisiae]
MSIRPATHAGSWYSNRAQELSQQ LHTYLIKSTLKGPIHNARI IICPHAGYRYCGPTMAYSYASLDLNRNV
KRIFILGSPSHHIYFKNQILVSAFSELETPLGNLKVDTDLCKTLIQKEYPENGGKLFKPM DHDMDMAEHSL
EMQLPMLVETLKWREISLDTVKVFPMVSHNSVDVDR CIGNILSEYIKDPNNLFI VSSDFCHWGRRFQYT
GYVGSKEELNDAIQEETEVEMLTARSKLSHHQVPIWQSIEIMDRYAMKTLSDTPNGERYDAWKQYLEITG
NTICGKPI SVILSALS KIRDAGPSGIKFWPNYSQSSHVTSIDSSVSYASGYVTIG

Modeled residue range: 4 to 337 based on template [3bczA](#) (2.10 Å) Sequence Identity [%]: 37 Evaluate: 1.43e-49

>gi|6322557|ref|NP_012631.1| Hypothetical ORF; Yjr097wp [Saccharomyces cerevisiae]
MSLVNSLTHYEILRIPSDATQDEIKKAYRNRLNTHPDKLSKSIHDTVSNVTINKIQDAYKILSNIKTRR
EYDRLILENYKRQGFHNCGDGLDEFSLDDFSFDEDKLEFMMNCPRCQFVGGGFHFSESL LDECIDNVDAME
RSHSGYQLLTQCSACSLWLKVNFDIEEEEQEGQ

Modeled with HOMER

Modeled residue range: 93 to 172 based on template [2ej7IA](#) (99.9 Å) Sequence Identity [%]: 38
PDB Blast Evaluate: 0.036

>gi|6322764|ref|NP_012837.1| Hypothetical ORF; Ykl086wp [Saccharomyces cerevisiae]
MSLQNSNVKPT EIP LSEIRRPLAPVLD P QKIDAMVATMKG IPTASKTCSLEQAEAAA SAGELPPVDVLGV
RVKGGTLYYAFGGCHRLQAYDRRARETQNAAFPVRCRVLPATPRQIRMYLGSSLDIE

Modeled residue range: 1 to 123 based on template [1xw3A](#) (1.65 Å) Sequence Identity [%]: 33 Evaluate: 3.16e-11

>gi|6323109|ref|NP_013181.1| Hypothetical ORF; Ylr080wp [Saccharomyces cerevisiae]
MTTRKTASSLQLLGKITGT KAGTKQKKMNFINGLIWLYMVCVMMVHGKVTQKDELKWNKGYS LPNLLEVTD
QQKELSQWTLGDKVKLEEGRFVLT PGKNTKGS LWLKPEYSIKDAMT IEWTFRSFGFRG STKGGLAFWLKQ
GNEG DSTELFGGSSKFNGLMILLRLDDKLGESVTAYLNDG TKDLDI ESSPYFASCLFQYQDS MVPSTLR
LTYNPLDNHLLKLQMDNRVCFQTRKVKFMGSSPFRIGTSAINDASKESFEILKMKLYDGVIEDSLIPNVN
PMGQPRVVTKVINSQTGEESFREKMPFS DKEESITSNELFEKMNKLE GKIMANDIDPLLRKMNKIVENER
ELIQRLRPLLDLKKTAISDDSFQDFLSMNNANLDR LIKEQE KIRQDAKLYGKQTKGHDEIFSKISVWLALL
IFIMITLAYMFRINQDIKKVKLL

Modeled residue range: 55 to 272 based on template [2a6vA](#) (1.52 Å) Sequence Identity [%]: 100 Evaluate: 5.20e-122 (this is a crystal!!)

>gi|6323757|ref|NP_013828.1| Hypothetical ORF; Ymr110cp [Saccharomyces cerevisiae]
MSNDGSKILNYTPVSKIDEIVEISRNF FFEKQLKLSHENNPRKKDLEFRQLQLK KLYYAVKDHEEELIDA
MYKDFHRNKIESVLNETTKLMNDILHLIEILPKLIKPRRVSDSSPPFMFGKTIVEKISRGSVLI IAPFNF

PLLLAFAPLAAAALAGNTIVLKPSELTPHTAVVMENLLTTAGFPDGLIQVVQGAIDETTRLLDCGKFDLI
FYTGSPRVGSIVA EKAASLTPCVLELGGKSPFTITENFKASNIAKRIFFGAFGNSGQICVSPDYLL
VHKS IYPKVIKECESVLNEFYPSFDEQTDFTMRIHEPAYKKAVASINSTNGSKIVPSKISINSDTEDLCL
VPPTIVYNIWDDPLMKQENFAPVLP IIEYEDLDETINKIIEEHDTPLVQYIFSDSQTEINRILTRLRSG
DCVVGDTVIHVGITDAPFGGIGTSGYGNYYGGYGFNTF'SHERTIFKQPYWNDFTL'FMRYPPNSAQKEKLV
RFAMERKPFDRNGNKNWGLRQYFSLSAAVILISTIYAHCSS

Modeled residue range: 39 to 484 based on template [1ad3B](#) (2.60 Å) Sequence Identity [%]: 33 Evaluate: 5.48e-66

>gi|6323962|ref|NP_014033.1| putative deubiquitinating enzyme; Ubp15p [Saccharomyces cerevisiae]
MSEDELGSIGTVFPGSPIDKSIGSILPQFDEEVETLLEDSTWNIIPDWNELTNPKYNSPRFRIGDFEWD
ILLFPQGNHNKGVAVYLEPHPEEKLEDETTGEMVVPDPDWYCCAQFAIGISRPGNGDTINLINKSHHRFNA
LDTDWGFANLIDLNNLKHPSKGRPLSFLNEGTLNITAYVRILKDPTGVLWHN'FLNYDSKKVTGYVGF'RNQ
GATCYLNSLLQSYFFTKYFRKLVYEIPTEHESPNNSVPLALQRAFYLQVSDIPLDTELEL'TRSFGWDTAE
SFTQHDVQELNRI LMDRLENMKGTPVEGKLEIFVGMKMSYIKCINVDYESARVEDFWDLQLNVKNFKN
LQESFDNYIEMELMNGENQYAAQDYGLQDAQKGVIFESFPPVLHLQLKRF'EYDFNYDQMVKVNDKYEFPE
TIDLSPFVVDKDVLLKKTLDSENKDKNPVYNLHGLVHVHSGDISTGHYYTLIKPGVEDQWYRF'DDERVWRVT
KKQVFQENFGCDRLPDEKVRTMTRGEYQNYI IQRHTSAYMLVYIRQEQEEDLLRPVLES'DVPKHVITRVR
EEIKERETKEKEIREAHLYVTLRLHSIKEFIHYEGFDYFAHDGFR'LF'AEELNDSGLQQINLKVLR'TTKLS
DIFASIKETMNIPIQERDVKYWKMDYRRNSTLRLTQPI'NFESVNIITLQ'EALKKEKKRTMQTYGEEGVAST
EEDDKALLETVSFLDLFIEEPYLELQFLNKLKEASLISKAQLDDELISTIRTNLPELTKGGIEPVFATDN
KSNLLFVKSYDPHTQKLLGFGHF'AVNQLQQLSDISAI IEDSISSENEKLT'FYEEVQPGTINEIYMKETIYD
ADIDTGDIVSFEVPGAVLPDTPFPVYATIKDFYSYLRYR'VKLKF'SKFDGSSEYGVSN'EIPESFEFWISAY
APYDDLARMVSKYAHVKPEY'LYKIALYSNGRFVLKSTSL'LN'DYLLKDFNCDQIPPF'AFEVLSVPLKELER
LRPIKLYWLKNSYIHYQCFE'FEVANDYTESQFLEK'VQHKIGFTDEEKENILLWTNTNFQFQGLLSDQNTF
KDVSKHSL'LFGRILPEESKLFKELNRL'ENVQ'TSSLEDFMDDENATDRPM'DDEQDLGMAIEHSEDMKGRIV
VVQQYFKDLENRHGISFL'FNLPDETFPKTKDRLHAKFGLGQKEF'SKIKLSIGYSTEEGTVFRSLQGFSD
EELDKVILYDIMS'NL'DYIYMDHPDRLRSHSSYDRPMI IKN

Modeled with HOMER

Modeled residue range: 39 to 575 based on template [2f1z](#) (3.20 Å) Sequence Identity [%]: 40% PDBBlast Evaluate: 2e-111

>gi|6324230|ref|NP_014300.1| Hypothetical ORF; Ynl099cp [Saccharomyces cerevisiae]
MTSKVGEYEDVPEDESRLTEENVSVPEEEVEDEDEEEDDDDDHIYINEETESG'GREKVLVSHAPQERIVPP
LNF'CPVERYLYRSGQPSVNF'PFLNLKLTIIWLSNEEPQD'TLLEFC'DTHRINLQFAAINPDAGEDDNP
WDGLTEHSIINVLQTI'VTQENYPLL'VCCGMGRHRTGT'VIGCLRRIMGWNLASVSE'EYRRFTGSRGGRILV
ELLIEAFD'TNLVKIDKNKAPSWLLTALE

Modeled residue range: 67 to 220 based on template [1xriA](#) (3.30 Å) Sequence Identity [%]: 35 Evaluate: 2.92e-24

>gi|6324356|ref|NP_014426.1| Hypothetical ORF; Ynr029cp [Saccharomyces cerevisiae]
MSALRNIFNEEEDGELPCLVTGEENNLQEI'LENVSYDGGNIVSDAKVERV'NKQVENTSAGATDVHEKKR
IPVSIITGYL'GSGKSTLLEKIALKGADK'KIAVILNEFGDSSEIEKAMTIKNGS'NSYQEWL'DL'GNGCLCCS
LKNIGVKAIEDMVERSPGKIDYILLETSGIADPAP'IAKMF'WQDEGLNSSVYIDGIITVLDCEHILKCLDD
ISIDAHWHGDKVGL'EGNLTIAHFQLAMADRIIMNKYDTIEHSP'EMVKQLKERVREINSIAPMFF'TKYSDT
PIQNL'LDIHAYDSVRISDILDSGSGNGT'IHDDRMGTIML'TFRPLKNEE'EYNNKFIKQFLQ'PLLWKNFGAM
TVLGGRRR'RDGRDWEVQRTKGLILIEGENPIARV'IQGVRD'TYDVFP'GKYDGSNKECKIVLIGKYLEKESI
EELLRKTLE

Modeled residue range: 71 to 291 based on template [1niiA](#) (2.00 Å) Sequence Identity [%]: 29 Evaluate: 4.23e-20

>gi|6324401|ref|NP_014471.1| Hypothetical ORF; Ynr073cp [Saccharomyces cerevisiae]

MTKSDETTATSLNAKTLKSFESTLPIPTYPREGVKQGIIVHLGVGAFHRSHLAVFMHRLMQEHHLKDWSIC
GVGLMKADALMRDAMKAQDCLYTLVERGIKDTNAYIVGSI TAYMYAPDDPRAVIEKMANPDTHTIVSLTVT
ENGYHSEATNSLMTDAPEIINDLNHPEKPD TLYGYLYEALLRKYRGLTPFTIMSCDNMPQNGVTVKTM
LVAFALKKDEKFAAWIEDKVTSPNSMVD RVTPCRCTDKERKYVADTWGIKDQCPVVAEPFIQWVLEDNFS
DGRPPWELVGVQVVKDVDSYELMKLRLLNNGGHSAMGYLGYLAGYTYIHEVVNDPTINKYIRVLMREEVIP
LLPKVPGVDFE EYTASVLERFSNP AIQDTVARICLMGSGKMPKYVLP SIYEQLRKPDPGKYKLLAVCVAGW
FRYLTGVDMNGKPF EIEDPMAPTLKAAAVKGGKDPHELLNIEVLF SPEIRDNKEFVAQLTHSLETVYDKG
PIAAIKEILDQV

Modeled residue range: 12 to 501 based on template [1lj8A](#) (1.70 Å) Sequence Identity [%]: 42 Evaluate: 1.72e-109

>gi|6324825|ref|NP_014894.1| Hypothetical ORF; Yor251cp [Saccharomyces cerevisiae]
MPLFDLISPKAFVKLVASEKVHRIVPVDATWYLP SWKLDNKVDFLTKPRIPNSIFFDIDAI SDKKSPYPH
MFPTKKVFD DAMS NLGVQKDDILVVYDRVGNFSSPRCAWTLGVMGHPKVYLLN NFNQYREFKYPLDSSKV
AAFSPYPKSHYESS ESFQDKEIVDYEEMFQLVKSGELAKKFNAF DARS LGRFEGTEPEPRSDIPSGHIPG
TQPLPYGSLLD PETKTTYPEAGEAIHATLEKALKDFHCTLDPSKPTICSCGTGVS GVI IKTALELAGV PNV
RLYDGSWTEWVLKSGPEWIAENRD

Modeled with HOMER

Modeled residue range: 6 to 303 based on template [1ORBIA](#) (2.0 Å) Sequence Identity [%]: 31 Evaluate: 4.00 e-34

>gi|6325169|ref|NP_015237.1| Hypothetical ORF; Yp1088wp [Saccharomyces cerevisiae]
MVLVKQVRLGNSGLKISPIVIGCMSYGSKKWADWVIEDKTQIFKIMKHCYDKGLRFTDADFYSNGLSER
IIKEFLEYYSIKRETVMIMTKIYFPVDETLDLHNNFTLNEFEELDLSNQ RGLSRKHI IAGVENS VKRLGT
YIDLQIHRLDHETPMKEIMKALNDVVEAGHVRYIGASSMLATEFAELQFTADKYGWFQF ISSQSYYNLL
YREDERELIPFAKRHNIGLLPWPSPNARGMLTRPLNQSTDRIKSDPTFKSLHLDNLEEEQKEI INRVEKVS
KDKKVSMAMLSIAWV LHKGCHPIVGLN TTARVDEAIAALQVTLTEEEIKYLEEPYKPKQRQRC

Modeled with Homer

Modeled residue range: 6 to 303 based on template [1PFYIA](#) (1.93 Å) Sequence Identity [%]: 29 PDB Blast Evaluate: 3.0 e-27

>gi|6319721|ref|NP_009803.1| Glutathione peroxidase paralogue; Gpx2p [Saccharomyces cerevisiae]
MTTSFYDLECKDKKGESFKFDQLKGVVLI VNVASKCGFTPQYKELEELYKKYQDKGFVILGFP CNQFGK
QEPGSDEQITEFCQLNYGVTFFPIMKKIDVNGSNADSVYNYLKSQKAGLLGFKG IKNWF EKFLVDSNGKVV
QRFSSLT KPSSLDQEIQSLLSK

Modeled residue range: 4 to 160 based on template [2p5qD](#) (2.00 Å) Sequence Identity [%]: 51 Evaluate: 6.10e-38

>gi|6319814|ref|NP_009895.1| Glutaredoxin; Grx1p [Saccharomyces cerevisiae]
MVSQETIKHVKDLIAENEIFVASKTYCPYCHAALNTLFEKLLKVP RSKVLVLQLNDMKEGADIQAALYEIN
GQRTVPNIYINGKHIGNDDLQELRETGELEELLEPI LAN

Modeled residue range: 1 to 92 based on template [2jacA](#) (2.02 Å) Sequence Identity [%]: 99 Evaluate: 4.15e-46

>gi|6320001|ref|NP_010081.1| 6-O-methylguanine-DNA methylase; Mgt1p [Saccharomyces cerevisiae]
MHKKKIENGRIFDLNGPTMKELLYYTFIETEVTGAF LVFREKTQNLVVFASLGNDKLFLLGKVEGF LKKHE
KQD TMYDLQELKEAETYKKS IENY TICLENKMPLPSGAIPFEFLFGTDFQRKVWNE LLNVEHGHVV TYGD
IAKRIGKPTAARSVGRACGSNNLALLVPCHRIVG SNRKL TGYKWSCKLKEQLLNNEKENSLSLSRL

Modeled residue range: 116 to 199 based on template [1sfeA](#) (2.10 Å) Sequence Identity [%]: 46 Evaluate: 2.35e-19

>gi|6324862|ref|NP_014931.1| Disulfide isomerase related protein; Mpd1p [Saccharomyces cerevisiae]
MLFLNI IKLLGLFIMNEVKAQNFYDSDPHISELTPKSFDKAIHNTNYTSLVEFYAPWCGHCKKLSSTFR
KAAKRLDGVVQVAAVNCDLNKNKALCAKYDVNGFPPTLMVFRPPKIDLSKPIDNAKKSFS'AHANEVYSGAR
TLAPIVDFSLSRIRSYVKKFVRIDTLGSLLRKSPKLSVVLFSKQDKISPVYKSIALDWLGKFDYFYSISNK
KLKQLTDMNPTYEKTPEIFKYLQKVIPEQRQSDKSKLVVFDADKDKFWEYEGNSINKNDISKFLRDTF'SI
TPNEGPF'SRRSEYIAYLKTGKKPIKKNHSSSGNKHDEL

Modeled residue range: 24 to 155 based on template [2dmlA](#) (99.9 Å) Sequence Identity [%]: 42 Evalue: 1.81e-21

>gi|6319806|ref|NP_009887.1| Catalyzes the formation and isomerization of disulfide bonds durin
MKFSAGAVLSWSSLLASSVFAQQEAVAPEDSAVVKLATDSFNEYIQSHDLVLAEFFAPWCGHCKNMAPEYVCAAETLVEKNITLAQIDCTENQDLC
MEHNIPGFP'SLKI'FKNSDVNNSIDYEGPRTAEAI'VQFMIKQSQPAVAVVADLPAYLANET'FVTPVIVQSGKIDADFNAT'FYSMANKHFNDYDFVSAE
NADDDFKLSIYLPSAMDEPVVYNGKKADIADADVFEKWLQVEALPYFGEIDG'SVFAQYVESGLPLG'LYFNDEEELEEYKPLFTELAKNRGLMNFV
SIDARKFGRHAGNLMKEQ'FPLFAIHDMTEDLKYGLPQLSEEA'FDELSDKIVLESKAI'ESLVKDFLKGDA'SPIVKSQEIFENQDSSV'FQLVGKNHDE
IVNDPKKDVLVLYYAPWCGHCKRLAPTYQELADTYANATSDVLI'AKLDHTENDVRGVVIEGYPTIVLYP'GGKKSESVVYQGSRLSDSLFDFIKENGH
FDVDGKALYEEAQEKAAEEADADAELADEEDA'IHDEL

Modeled residue range: 23 to 494 based on template [2b5eA](#) (2.40 Å) Sequence Identity [%]: 100 Evalue: 0.00e-1)

>gi|6319816|ref|NP_009897.1| Hypothetical ORF; Ycl033cp [Saccharomyces cerevisiae] (Putative protein-methionine-R-oxide reductase)
MNKWSRLYVITVRRTFP'GRRNIVLTQYWNKSKKMSDESNDVKW'NDALTPQLQMLVLRDKATERPNTGAYLHTNESGVYHCANCDRPLYSSKAKFDARC
GWPAFYEEVSPGAI'ITYHRD'NSLMPARVEICCARCGH'LGHVFE'GEGWKQLLNL'PKDTRHC'VNSASLNLK'KD

Modeled residue range: 39 to 166 based on template [3cezA](#) (2.10 Å) Sequence Identity [%]: 39 Evalue: 1.49e-22

>gi|6320560|ref|NP_010640.1| Thioredoxin reductase; Trrlp [Saccharomyces cerevisiae]
MVHNKVTIIGSGPAAHTAAIYLARAEIKPILYEGMMANGIAAGGQLTTTTEIENFP'GFPDGLTGSELMDRMREQSTKFGTEIITETVSKVDLSSKPF
KLWTEFNEDAEPVTTDAIILATGASAKRMHLPGEETYWQKGISACAVCDGAVPIFRNKPLAVIGGGDSACEEAQFLTKYGSKVFMLVRKDHLRASTI
MQKRAEKNEKIEILYNTVALEAKGDGKLLNALRIKNTKKNEETDLPVSGLFYAIGHTPATKIVAGQVDTDEAGYIKTVPGSSLTSVP'GFFAAGDVQD
SKYRQAITSAGSGCMAALDAEKYLT'SLE

Modeled with HOMER

Modeled residue range: 3 to 318 based on template [1VDCIA](#) (2.50 Å) Sequence Identity [%]:62 PDB Blast Evalue: 6.0 e-111

>gi|6320598|ref|NP_010678.1| Protein with homology to mammalian ubiquitin activating (E1) enzym
MPRETSLVTIIGEDSYKKLRSSRCLLVGAGGIGSELLKDIILMEFGEIHIVDLDTIDLSNLNRQFLFRQDKIQPKSTTAVKAVQHFNNSKLV'PYQG
NVMDISTFPLHWFQFDIIFNALDNLAA'RRYV'NKISQFLSLPLIESGTAGFDGYMQPIIPGKTECFE'CTKKE'PKTFPVCTIRSTPSQPIHCIVWAK
NFLFNQLFAS'ETSGNEDDNNQD'WGTDDAEI'KRIKQETNELYELQKIIISRDASRIPEILNKLFIQDINKLLAIENLWKTRTKPVPLSDSQINTPTK
TAQSASNSVGTIQEQISNFINITQKLM'DRYPKEQNHIEF'DKDDADTLEFVATAANIRSHIFNIPMKS'VFDIKQIAGNIIPAIAT'NAIVAGASSLIS
LRVLNLLKYAPT'TKYTDLNM'AF'TAKASNLSQNRYLSNPKLAPPNKNCPVCSKVC'RGVIKLSSDCLNKMKLSDFVVLIREKYSYPQDISLLDASNQRL
LFDYDFEDLNDRTLSEINLNGSII'LFSD'EEGDTMIRKAI'ELFLD'VDELPCNTCSL'PDVEVPLIKANN'SPSKNEEEEEKNEKGADVVATTNSHGKDG
IVILDDDEGEITIDAEPINGSKKRPVDTEISEAPSNKRTKLVNEPTNSD'IVELD

Modeled residue range: 23 to 508 based on template [1y8qD](#) (2.25 Å) Sequence Identity [%]: 38 Evalue: 4.02e-80

>gi|6320661|ref|NP_010741.1| thioredoxin peroxidase; Tsa2p [Saccharomyces cerevisiae]
MVAEVQKQAPPFKKTAVVDGIFEEISLEKYKGYVVLAFVPLAFS'FVCPTEIVAFSDAAKKFEDQGAQVLF'ASTDSEYSL'LAWTNLPRKDGGLGPVK

VPLLADKNHSLSRDYGVLIEKEGIALRGLFIIDPKGIIRHITINDLSVGRNVNEALRLVEGFQWTDKNGTVLPCNWTPGAATIKPDVKDSKEYFKNANN

Modeled residue range: 3 to 195 based on template [lqmvH](#) (1.70 Å) Sequence Identity [%]: 62 Evaluate: 1.40e-64

>gi|6322186|ref|NP_012261.1| Eps1p [Saccharomyces cerevisiae]
R protein with chaperone and co-chaperone activity, involved in retention of resident ER proteins; has a role in recognizing proteins targeted for ER-associated degradation (ERAD), member of the protein disulfide isomerase family
MKMNLKRLVVTFFSCITFLKFTIAAAEPPEGFPEPLNPTNFKEELSKGLHIIDFYSPYCPHCKHLAPVWMTWEEFKKEESKTLNITFSQVNCIESA
DLCGDENIEYFPEIRLYNPSGYIKSFTETPRTKESLIAFARRESMDPNNLDTDLDSAKSESQYLEGFDFLELIAGKATRPHLVSFWPTKDMKNSDDS
LEFKNCDKCHEFQRTWKIISRQLAVDDINTGHVNCESNPTICEELGFGLVKITNHRADREPVALVLPNKTSNNLFDYPNGYSAKSDGYVDFARRT
FTNSKFPNITEGELEKKANRDIDFLQERGRVTNNDIHLVFSYDPETVVIEDFDILEYLIIEPLSKIPNIYLVHQLDKNLINLSRNLFGRMYEKINYDAS
QTQKVFNKEYFTMNTVTQLPTFFMFKDGDPI SYVFPGYSTTEMRNIDAIMDWVKYSNPLVTEVDSSNLKLLISFQTKSYSDLAIQQLISSTDHKKHIK
GSNKLKLNLLASWEYEHIRMENNFEEINERRARKADGIKKIKEKKAPANKIVDKMREEIPHMDQKKLLLGYLDSKEKNFFRKYGITGEYKIGDVI
IIDKSNYYYNKDNFNSLTSNNPQLLREAFVSLNIPSKALYSSKLGRLINSPFHNVLSDLIIHGNGMPGYLIVIVLFIAILKGPSYRRYKVRK
HYRAKRNAVGI LGNMEKKKNQD

Modeled residue range: 26 to 151 based on template [2b5eA](#) (2.40 Å) Sequence Identity [%]: 32 Evaluate: 2.59e-12

>gi|6322228|ref|NP_012303.1| Hydroperoxide resistance conferring gene; Hyr1p [Saccharomyces cer
MSEFYKLAPVDKKGQFPFDQLKGVVLI VNVASKCGFTPQYKELEALYKRYKDEGFTIIGFPCNQFGHQEPGSDEEIAQFCQLNYGVTFPIMKKID
VNGGNEDPVYKFLKSQKSGMLGLRGIKWNFEKFLVDKKGKVVYERYSSLTKPSSSLSETIEELLKEVE

Modeled residue range: 11 to 160 based on template [2p5qA](#) (2.00 Å) Sequence Identity [%]: 50 Evaluate: 4.45e-36

>gi|14318501|ref|NP_116635.1| an FAD flavoprotein which contains a pair of redox-active cysteines
MLRIRSLNKNKRAFSSVTRTLTINKSHDVV IIGGGPAGYVAAIKAAQLGFNTACVEKRGKLGGTCLNVGCIPSKALLNNSHLFHMHTEAQKRGIDV
NGDIKINVANFQKAKDDAVKQLTGGIELLFKKNKVITYYKNGSFEDETKIRVTPVDGLEGTVKEDHILDVKNII VAVTGSEVTPFPGIEIDEKIVSS
TGALSLKEIPKRLTIIGGGIIGLEMGSVYSRLGSKVTVVEFQPIGASMDGEVAKATQKFLKQGLDFKLSTKVISAKRNDKKNVVEIVVEDTKTNK
QENLEAEVLLVAVGRRPYIAGLGAEKIGLEVDKRGRLVIDDQFNSKFPHIKVVGDVTFGPMLAHKAE EEGIAAVEMLKTGHGHVNYNNIPSVMYSHP
EVAWVGKTEEQLKEAGIDYKIGKFPFAANSRAKTNQDTEGFVKILIDSKTERILGAHIIGPNAGEMIAEAGLALLEYGASAEDVARVCHAHP TLSEAF
KEANMAAYDKAIHC

Modeled residue range: 22 to 499 based on template [1v59B](#) (2.20 Å) Sequence Identity [%]: 100 Evaluate: 0.00e-1

>gi|6321898|ref|NP_011974.1| mitochondrial thioredoxin reductase; Trr2p [Saccharomyces
cerevisiae]
MIKHIVSPFRTNFVIGISKSVLSRMIHHKVTIIGSGPAAHTAAIYLARAEMKPTLYEGMMANGIAAGGQLTTTTDIENFPGFPELSGSELMERMRKQ
SAKFGTNIITETVSKVDLSSKPFRLWTEFNEDAEPVTTDAIILATGASAKRMHLPGEETYWQQGISACAVCDGAVPIFRNKPLAVIGGGDSACEEAE
FLTKYASKVYILVRKDHFRASVIMQRRIEKNPNIIVLFNTVALEAKGDGKLLNMLRIKNTKSNVENDLEVNGLFYAI GHSPATDIVKGQVDEEETGY
IKTVPGSSLTSPVGFFAAGDVQDSRYRQAVTSAGSGCIAALDAERYLSAQE

Modeled residue range: 126 to 330 based on template [1tdeA](#) (2.10 Å) Sequence Identity [%]: 51 Evaluate: 4.03e-49

>gi|6321903|ref|NP_011979.1| Ubiquitin activating enzyme; Uba4p [Saccharomyces cerevisiae]
MNDYHLEDTTSELEALRLENAQLREQLAKREDSSRDYPLSLEEYQRYGRQMIVEETGGVAGQVKLNKTKVLVVGAGGLGCPALPYLAGAGVGGQIGIV
DNDVVETS NLHRQVLHDSSRVGMLKCESARQYITKLNPHINVVTYPVRLNSSNAFDIFKGYNYILDCTDSPLTRYLVSDVAVNLGITVVSASGLGTE
GQLTILNFNNIGPCYRCFYPTPPPPNAVTSQEGGVIGPCIGLVGTMMAVETLKLILGIYTNENFSPFLMLYSGFPPQQLRFTKMRGRQEKCLCCGK
NRTITKEAIEKGEINYELFCGARNYNVCEPDERISVDADFQRIYKDEFLAKHIFLDVRPSHHYEISHFPEAVNIPIKNLRDMNGDLKLLQEKLP SVE
KDSNIVILCRYGNSQLATRLLKDKFGFSNVRDVRGGYFKYIDIDQTI PKY

Modeled residue range: 39 to 290 based on template [1jw9B](#) (1.70 Å) Sequence Identity [%]: 35 Evaluate: 1.05e-36

>gi|6322639|ref|NP_012712.1| similar to Uba2p; Ubalp [Saccharomyces cerevisiae] (Ubiquitin activating enzyme E1)
MSSNNSGLSAAGEIDESLYSRQLYVLGKEAMLKMQTSNVLIILGLKGLGVEIAKNVVLAVGKSMVTFDPEPVQLADLSTQFFLTKEDIGQKRGDVTRA
KLAELNAYVPVNVLDLSDDDVTQLSQFQVVVATDVTSLQEDKVKINEFCHSSGIRFISSETRGLFGNTFVDLGDFTVLDPTGEEPRTGMVSDIEPDGT
VTMLDDNRHGLEDGNFVRFSEVEGLDKLNDGTLFKVEVLGPFVAFRIGSVKEYGEYKGGIFTEVKVPRKISFKSLKQQLSNPEFVFSDFAKFDRAAQ
LHLGFQALHQFAVRHNGELPRTMDEDEDANELIKLVTDLSVQQPEVLGEGVDVNEDELIKELSYQARGDIPGVVAFFGGLVAQEVLKACSGKFTPLKQF
MYFDSLESPLDPKFNPRNEKTTPVNSRYDNQIAVFGGLDFQKKIANSKVFLVVGSGAIGCEMLKNWALLGLGSGSDGYIVVTDNDSIEKSNLNRQFLF
RPKDVGKKNSEVAEAVCAMNPDLKGINAKIDKVGPETEEIFNDSFWESLDFVTNALDNVDARTYVDRRCVFRYRKLPLESGTLGKGTQVIIPRL
TESYSSSRDPPEKSIPLCTLRSFNPKIDHTIAWAKSLFQGYFTDAENVMNYLTPNFVEQTLKQSGDVKGVLESISDLSLSSKPHNFEDCIKWARLE
FEKKFNHDIKQLLFNFKDAKTSNGEPFWSGAKRAPTPLEFDIYNNDHFHFVAVAGASLRAYNYGIKSDSNSKPNVDEYKSVIDHMIPEFTPNANL
KIQVNDDDPDPNANAANGSDEIDQLVSSLPDPSTLAGFKLEPVDFEKDDDTNHHIEFITACSNCRQNYFIETADRQKTKFIAGRIIPAIATTTSLV
TGLVNLLEYKLIIDNKTDIEQYKNGFVNLALPFFGFSEPIASPKGEYNNKKYDKIWRDRFDIKGDIKLSDLIEHFEEKDEGLEITMLSYGVSLLYASFFP
PKKLERLNLPIITQLVKLVTKKIPAHVSTMILEICADDKEGEDVEVPFITIHL

C-term Modeled residue range: 597 to 861 based on template [1z7IC](#) (2.80 Å) Sequence Identity [%]: 44 Evaluate: 1.81e-62 C

>gi|6322826|ref|NP_012899.1| Glutathione peroxidase paralogue; Gpx1p [Saccharomyces cerevisiae]
MQEFYSFSPIDENGNPFPFNSLRNKVVLIVNVASHCAFTPOYKELEYLYEKYKSHGLVIVAFPCGQFGNQEFEKDKEINKFCQDKYGVTFPILHKIR
CNGQKQDPVYKFLKNSVSGKSGIKMIKWNFEKVVDRNGKVVKRFSCMTRPLELCPITIEELLNQPPPEEQI

Modeled residue range: 2 to 159 based on template [2p5qA](#) (2.00 Å) Sequence Identity [%]: 43 Evaluate: 1.46e-27

>gi|6323001|ref|NP_013073.1| Iron Sulfur Assembly -- IscA/NifA homolog; Isalp [Saccharomyces ce
MINTGRSRNSVLLAHRFLSTGGFWRGGTNGTMSRTINNVNPFKLFIPKTVPAAADSVSPDSQRPGKPKFKFIVSNQSKSSKASKSPKWSSYAFPSR
ETIKSHEEAIAIKKQNKAIIDEQIAAAVSKNDCSCTEPPKRRKRLRPRKALITLSPKAIKHLRALLAQPEPKLIRVSARNRGCGLTYDLQYITEPGKF
DEVVEQDGVKIVIDSKALFSIIGSEMDWIDDKLASKFVFKNPNSKGTGCGGESFMV
(Cys178)

Modeled residue range: 147 to 239 based on template [1r94B](#) (2.30 Å) Sequence Identity [%]: 38 Evaluate: 4.70e-12

>gi|6323505|ref|NP_013576.1| essential, FAD-dependent oxidase of protein disulfide isomerase; E
(This is a Erol-p)
MRLRTAIATLCLTAFTSATSNNYSIATDQTQNAFNDTHFCVKVDRNDHVSPSCNVTFNELNAINENIRDDLSALLKSDFFKYFRDLDYKQCSFWDAND
GLCLNRACSVDDVEDWDTLPEYWQPEILGSEFNNDTMKEADDSDECKFLDQLCQTSKPPVDIEDTINYCDVNDNFNGKNAVLIDLTAANPERFTGYGGK
QAGQIWSITYQDNCFTIGETGESLAKDAFYRLVSGFHASIGTHLSKEYLNTKTKGWEPNLDLFMARIGNFPDRVTNMYFNAYAVAKALWKIQPYLPE
FSFCDLVNKEIKNKMDNVI SQLDTKIFNEDLVFANDLSLTLKDEFRSRFKNVTKIMDCVQCDCRCLWGKIQTGTGATALKILFEINDADEFTKQHIV
GKLTKEYELIALLQTFGRLESIESVNMFEKMYGKRLNGSENRLSSFFQNNFFNIIKEAGKSIRYTIENINSTKEGKKKTNNSQSHVFDLDMKPKAEI
VPRPSNGTVNKWKKAWNTEVNNVLEAFRFIYRSYLDLPRNIWELSLMKVYKFWNKFIGVADYVSEETREPI SYKLDIQ

Modeled residue range: 55 to 424 based on template [1rp4A](#) (2.20 Å) Sequence Identity [%]: 100 Evaluate: 0.00e-1

>gi|6324484|ref|NP_014553.1| protein disulfide isomerase related protein; Mpd2p [Saccharomyces
MKLHGFLFVSLSTCVVILPALAYSEAVTMVKSIEQYFDICNRNDSYTMIKYYTSWCQHCKTLAPVYEEELGELYAKKANKDDTPINFLEVNCEFFGPT
LCTDLPGFPPIIELVKPRTKPLVLPKLDWSSMKFHERLWQRIRKTFWNNPKYQLDTSRVVRFEGSRNLKLSLNFIDTVRSKDTEERFIEHIFDSSRNCN
EELRSQQLLCKAGKEYYSDTLSKLYGDVNGLEKERRRLEALIKQNGDDLSKEVKEKLLKIRLQSLLSLHIEDQLEDTSSHDEL

Modeled residue range: 24 to 110 based on template [2dja](#) (99.9 Å) Sequence Identity [%]: 37 Evaluate: 4.92e-9

>gi|6325166|ref|NP_015234.1| converts oxidized glutathione and NADPH into two glutathiones and N (GR)

MLSATKQTFRSLQIRTMSTNTKHYDYLVIIGGGSGGVASARRAASYGAKTLLVEAKALGGTCVNVGCVPKKVMWYASDLATRVSHANEYGLYQNLPLD
KEHLTFNWPEFKQKRDAYVHRLNGIYQKNLEKEKVDVVFQWARFNKDGNEVQKRDNTTEVYSANHILVATGGKAIFFPENIPGFELGTDSDGFFRLE
EQPKKVVVVGAGYIGIELAGVFHGLGSETHLVIRGETVLRKFDECIQNTITDHYVKEGINVHKLKIVKVEKNVETDKLKIHMNDSKSIDDVDELIW
TIGRKSHLGMGSENVGIKLNSHDQIIADEYQNTNVPNIYSLGDVVGVKVELTPVAIAAGRKLSNRLFQPEKFRNDKLDYENVPSVIFSHPEAGSIGIS
EKEAIEKYGKENIKVYNSKFTAMYAMLSEKSPTRYKIVCAGPNEKVVGLHIVGDSSAEILQGFGVAIKMGATKADFNCVAIHPTSAEELVTMR

Modeled residue range: 22 to 483 based on template [2hqmB](#) (2.40 Å) Sequence Identity [%]: 100 Evalue: 0.00e-1

>gi|6325323|ref|NP_015391.1| Required for activation of RUB1 (ubiquitin-like protein) together
MDCKILVLGAGGLGCEILKNLTMLSFVKQVHIVDIDTIELTNLNRQFLFCDKDIGKPKAQVAAQYVNTFRFPQLEVVVAHVQDLTTLPPSFYKDFQFII
SGLDAIEPRRFINETLVKLTLESNYEICIPFIDGGTEGLKGHVKTIIIPGITACWECSIDTLPQQDTVPMCTIANNPRCIEHVVEYVSTIQYFDLNI
ESTADMEFLLEKCCERAAQFSISTEKLSTSFILGIIKSIIPSVSTTNAMVAATCCTQMVKIYNDLIDLLENGNFTLINCSEGCFMYSFKFERLPDCT
VCSNSNSN

Modeled residue range: 3 to 299 based on template [2nvuB](#) (2.80 Å) Sequence Identity [%]: 43 Evalue: 5.36e-72