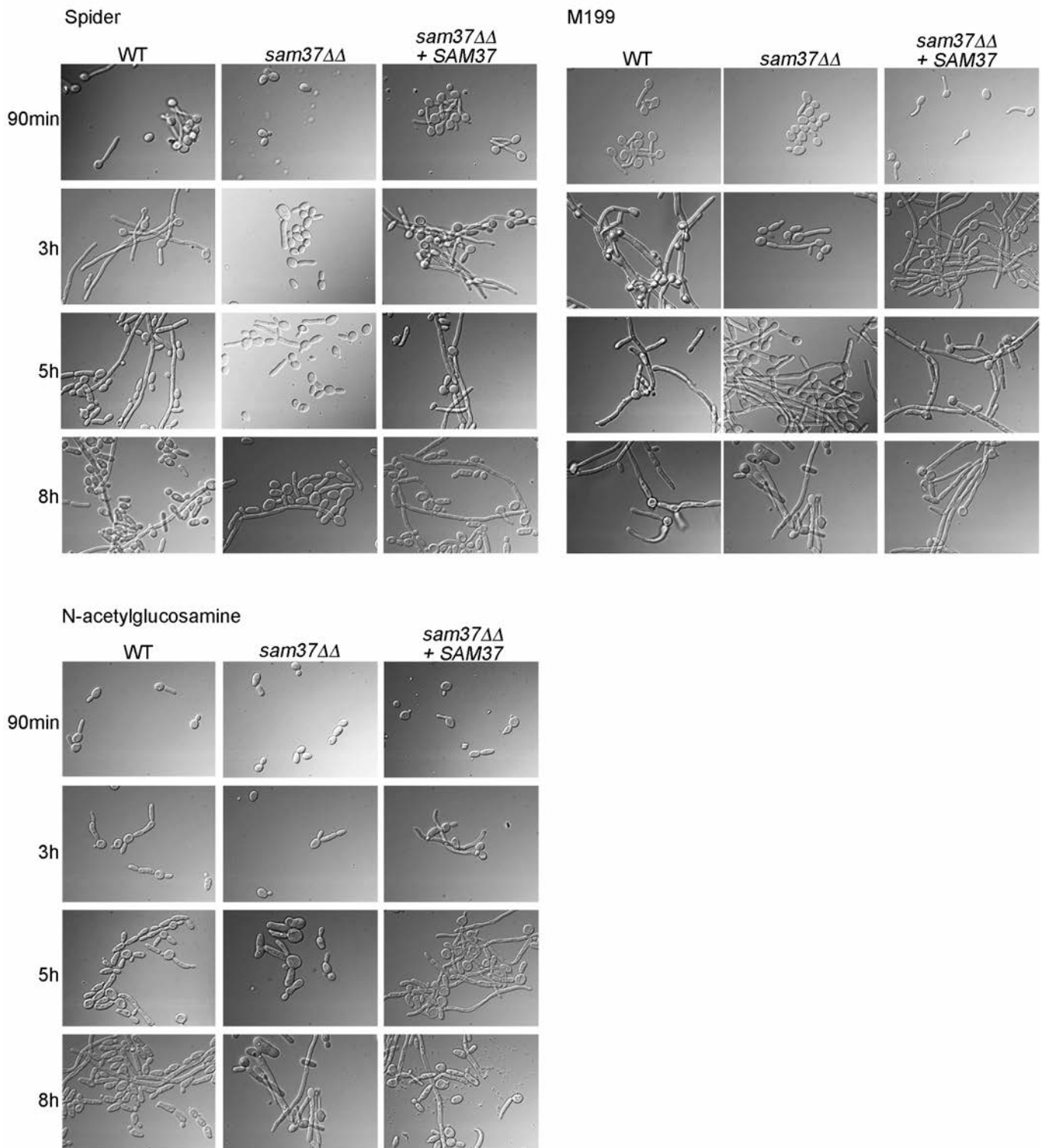


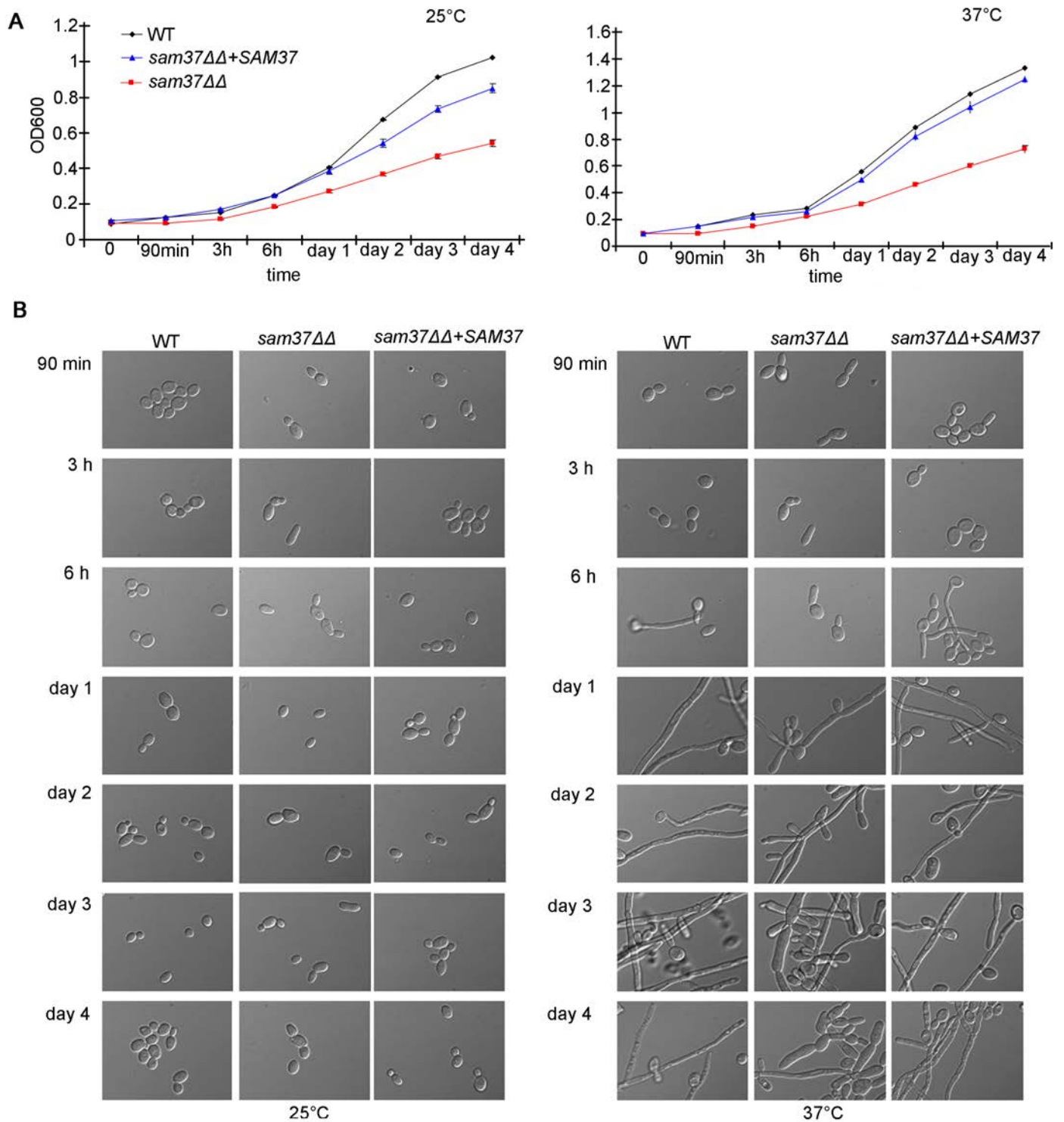
Supplemental Figure 1. Growth and mtDNA stability upon inactivation of *SAM37* in *C. albicans* and *S. cerevisiae*. A) Growth of *C. albicans* and *S. cerevisiae* wild types and isogenic *sam37* deletion mutants was assessed in synthetic complete media. Overnight cultures were diluted to $OD^{600}=0.1$ and growth was monitored by measuring optical density over time. At least two repeats in triplicate were performed. B) Growth of the indicated strains was assessed at 30°C, on YPD or synthetic complete plates.

10 fold serial dilutions starting from $OD^{600}=0.5$ were dropped on the plates, and growth assessed after 3 days at 30°C. The far right panels show that the slow growth of the *C. albicans sam37ΔΔ* mutant is complemented by re-introducing a wild type copy of the *SAM37* gene into the mutant genome. C) Cells derived from wild type *S. cerevisiae* and the *sam37Δ* mutant were stained with DAPI and visualized by fluorescence microscopy. Clear nuclear (bright staining) and mitochondrial (cytoplasmic punctuate) staining is observed in both wild type and mutant cells.



Supplemental Figure 2. Filamentation by the *sam37ΔΔ* mutant in liquid media *in vitro*. *C. albicans* cultures from the wild type (DAY185), the *sam37ΔΔ* mutant and the reconstituted strain were grown overnight in YPD and then diluted into pre-warmed filamentation media at 37°C. Development of filaments was monitored by microscopy over time. Filamentation by the mutant was delayed in M199

(see the 3h time point) but after 5h the mutant was filamentous. In Spider media the filamentation defect of the *sam37ΔΔ* mutant was most pronounced.

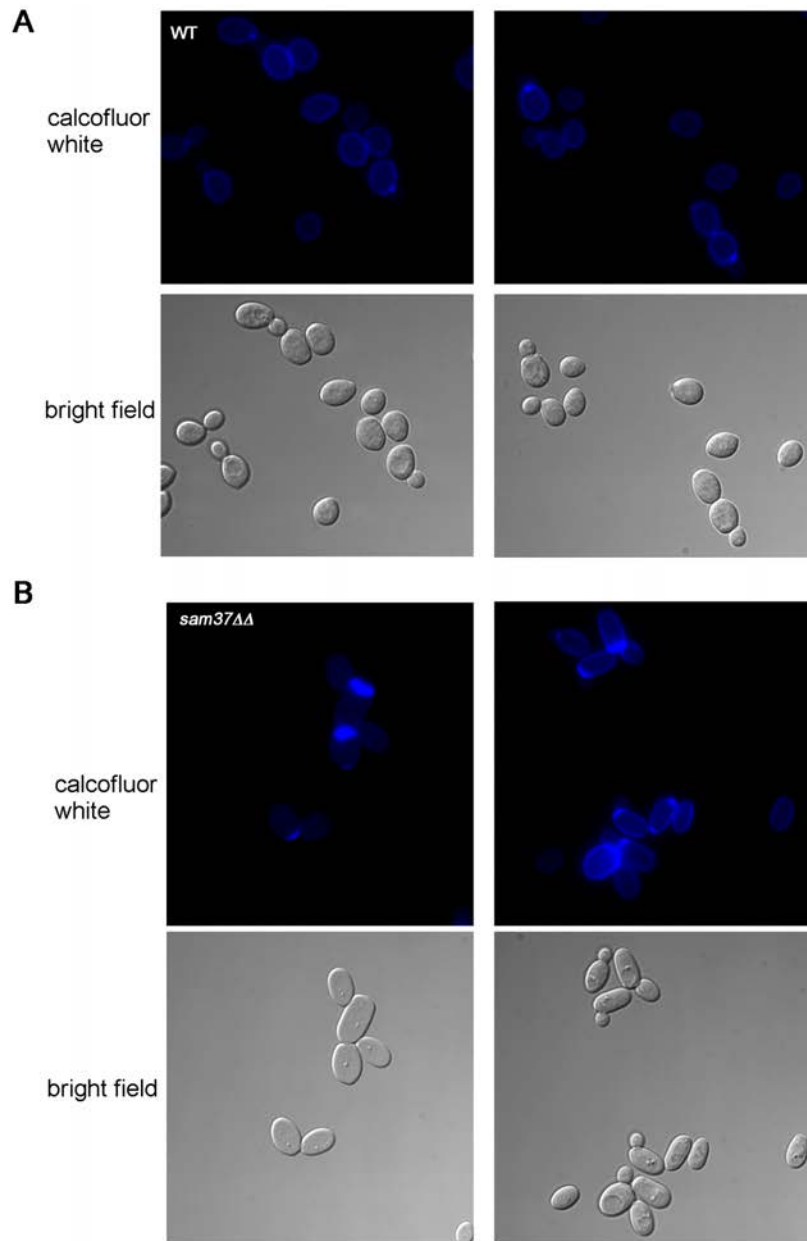


Supplemental Figure 3. *In vitro* growth and filamentation of wild type and *sam37ΔΔ* mutant *C. albicans* under the conditions used in the worm infection assay. A) Growth of the indicated strains was assessed in 20% BHI media in M9 buffer, at 25°C or 37°C, by diluting the overnight cultures to

OD⁶⁰⁰=0.1 and measuring optical density of the cultures over time. Three repeats in triplicate were performed. B) Cellular morphology in 20% BHI media in M9 buffer was assessed in liquid media, at 25°C or 37°C over a 4-6 days time course, which parallels the worm infection assay shown in Figure 3. At 25°C *in vitro* all strains stayed in yeast form. At 37°C, the wild type and the complemented strain filamented at the 6 h time point, while the *sam37ΔΔ* mutant was delayed, but filamentation was observed at day 1.

CaSam37 (Q5ALP4)	1	-----MLQLHWGKDNIEISIIISPCIASAYLLNQVLTPTONIEFEIIPSN	44
ScSam37 (SAM37 YEAST)	1	-----MVGKSVHLWGKDGKAS-----LISVDSIALVWFIKLCTS	34
NcSam37 (Q7SFC4)	1	-----MTLELHWG-----PAFGLPSIDAELCLAV	25
HsMtx1 (MTX1 HUMAN)	1	-----MAAPMELFC-----WSGGWGLPSVDLDSLAVL	27
AtMtx2 (064471)	1	-----MEGDOETNVYTLVAR-----KPSFDLPTACPNCLPAY	32
HsMtx2 (MTX2 HUMAN)	1	-----MSLVAAAFVSIQIAAEEP--WPENATLYQQLKGEQIILLSDNAASLAVQ	45
NcSam35 (Q7S734)	1	MATTSAAAPPRKWWQVPRPLQKVFDTFPLLAYDYNVALPARAQSATSGDLPTLYVVFSTEEEAALLGAPSFNPNCLK	74
ScSam35 (SAM35 YEAST)	1	-----MVSSFSPMPVKRIFDFTPLQTYAAQTDKDE-----AVALEIQRRSFTFERGGGSLELT	55
CaSam35 (Q59ZS4)	1	-----MNVPATIKSLFDVVPLVLYKDERLPHKG-----PNYPFSEETVAVVNVFNCKGM	50
CaSam37 (Q5ALP4)	45	NTNLSIDINQLPVLIDNETKEKYNGYNEIRFIESKYLSTSTKLSLVSYLPS-----DSLK-----TT	101
ScSam37 (SAM37 YEAST)	35	EEAKSMVAGLQIVFSNNTD---LSSDGKLPVLILNDGKIVSGYVNIQVFLHKNICTSKYKGTDYEDDLAIVRK	105
NcSam37 (Q7SFC4)	26	TYFAQTLISAADYLLVQSSP-SAVPSHHPALYNPSTATWISGFDPIVNYLSTLQPPSYHHPDVT-----TLPS	92
HsMtx1 (MTX1 HUMAN)	28	--TYARFTGAPLKVHKISN-PWQSPSGTLPALRTSHGVEISVPHKIITHLRKEKYNADYDL-----SA	87
AtMtx2 (064471)	33	--IYLKLAQLPFELAFNST---FPDSDELPYFESDITYAVYNNEDGGVIEKLLKDGIVNLDL-----QL	90
HsMtx2 (MTX2 HUMAN)	46	--AFLQMCNLPKVVCRANAEMYSPGKVPFIHVGN-QVVELGPIVQFVKAKGHSLSDGL-----EE	105
NcSam35 (Q7S734)	75	WQAFKLKAGVKFQILPSTN--HASPTGALPFILPTRSPPTDAPSPIPSKLHDYALKYGTSNP-----PE	137
ScSam35 (SAM35 YEAST)	56	VEGTLYKGVYVNFLEANTG---AALATDTPWGLFVQLALCQKNGLVLPTHSQEQTPSHTCN-----HE	114
CaSam35 (Q59ZS4)	51	IIPDPIISLIGIVLVAHKNKALPTEQYGRGGIITTSFHASPTNLTPLLIDQTRTRTLDEN-----	112
CaSam37 (Q5ALP4)	102	KEKLINLGLINLLINKFEYINQVLYLNKNYENYTRKLFSSYLFPFMYNOPSKYAAQAEQVKILGLS----	171
ScSam37 (SAM37 YEAST)	106	KDRLLEYSLLNYVDVEISRLTDYQLFLNKNYNEYTKLFSKLLYFPMWYNTPLQLRQARENCEEIIGS----	175
NcSam37 (Q7SFC4)	93	RVYADSQAYKALLTSSAAPLLALSIVSSANSETTRPAYSAILPFPLPWTEPLAVRAAMAARAHLGMS---	163
HsMtx1 (MTX1 HUMAN)	88	ROGADTLAFMSLLEEKLLPVLVHTFVIDTKNYVEVTRKWAAEAMPFLNFFLGRMQRQYMERLQLLTGE---	157
AtMtx2 (064471)	91	QSLSDYLSLKALIVSWLEEALTYEIWVGTEGSS--TSKIYYSDDLWVTSKVLFYKQTLAKNRLGITKEN---	158
HsMtx2 (MTX2 HUMAN)	106	VQKAEMKAYMELVNNMLLTAELYLOWCDEATVGEITHARYGSPYPLNHLILAYOKOMEVKKRMMKAIWGG---	175
NcSam35 (Q7S734)	138	VSALRLDAQALLDVPINAWLQALYRDP-EYTDLLDRFYITPASSYVWRGALRHOLRRAAETIILTKPGGA	210
ScSam35 (SAM35 YEAST)	115	MLVLSRLSNPDEALPTLVEGYKRIIRSVAISEIMRSRILODDAEQLMYTLLDQTLVLYDCWITIQIFCAS---	184
CaSam35 (Q59ZS4)	113	HTVANDLDEPAKLINEIDIKFYDIWVLCILCEDIATTFGVDTLKSLDLLAEVPMNWNFAVRHPNTINIP---	182
CaSam37 (Q5ALP4)	172	-KQKVSFFDFTTGNNEQGSIDVAPTELIN-----	199
ScSam37 (SAM37 YEAST)	176	-LTLFDEEFVESKAMESASQLAQSKTKF-----	203
NcSam37 (Q7SFC4)	164	LDTDAEMERLEREREEREAAGVQVTPKALRKAVGGQNSGVKQLSPENKRIKLEGLAAEVFDVLGEVDFLEEE	237
HsMtx1 (MTX1 HUMAN)	158	-HRPEDEEELEKELYREARECLTLLSQRL-----	185
AtMtx2 (064471)	159	-AEQREK-----QIYKRASEA YEALSTR-----	181
HsMtx2 (MTX2 HUMAN)	176	-KKTLD-----QVLEDVDQCCQALSQRL-----	197
NcSam35 (Q7S734)	211	ASTAVSLLVDEHSVYRAAVQALEALATLL-----	239
ScSam35 (SAM35 YEAST)	185	-DAQFMELYSCQKLSGSIVTPLDVENSL-----	212
CaSam35 (Q59ZS4)	183	-----KLYSQQLVFEFYLDDL-----	199
CaSam37 (Q5ALP4)	200	-----DEDD--EEGDEDEDGANVAISSLHERQLLKKSKSQVLEKSRNSMKCLILITQYIERFKTIFQ----	260
ScSam37 (SAM37 YEAST)	204	-----IAHK--NKIKGQELQVQYVNLQFNRLQSCVSNWLAAR---KLLDDSVILSSDLLFLANLYV-----	261
NcSam37 (Q7SFC4)	238	DGEEEEEEEEEAKEGGARIKVTLTKCLAFAYLALMLLPEVPRPWLKEVLQKQYAGLCKFVLEYRRKTFPDSGK	311
HsMtx1 (MTX1 HUMAN)	186	-----GSDK--FFFG-DAPASLDAFVFSYLALLQAKLPSGKLO---VHLRGLHNLCACTHILSLY---	241
AtMtx2 (064471)	182	-----GEQK--FLFE-DRPSSLDAPLLSHILFIQALPVTSVLR---CKLLEHNSLVRYAEKLFSEFL---	238
HsMtx2 (MTX2 HUMAN)	198	-----GTDP--YFFN-KOPTELDALVFGHLYTILTTQLTNDLS---EKVKYNSNLLAFCCRREEQHY---	253
NcSam35 (Q7S734)	240	-----SESKTGWFFGAETPTIFDASVFAITHMLMKYMS--DAEG---EVEGNMGFILASRKLGTMVR---	296
ScSam35 (SAM35 YEAST)	213	-----KLSAKSLKISLTKRKNKQFRHREIVKSMQGVYVHHNSVNVQEQVNLVLFENSQVLIILGLK---D	274
CaSam35 (Q59ZS4)	200	-----ESYDHPITINLKLAGYIIVINQLLSSTRLGK---IVCTKHALLSRYSYLLNLHT---	249
CaSam37 (Q5ALP4)	261	-HQQRDSDEEFGFIENNQNPSSEILFYAYIFCLTYEKLPRDFIFNYLKLKQDYTLKFITEIMNKNQISKNKFR	333
ScSam37 (SAM37 YEAST)	262	-QLGLPDGNRIRSKLEQTFGSELLNSNKIDDFVHRPSNNLEQRDPQFREQGNVMSLYNLACKYI-----	327
NcSam37 (Q7SFC4)	312	VLPWADRESDPAVSACDSALSIVGRFVRAVIDDIPMLGREWSRWALRQRRVAEENSQVAVVRRSVEGERS	385
HsMtx1 (MTX1 HUMAN)	242	-FPWDGAEVPPQROTPAGPETEEEEYRRRNQILSVLAGLAAMVGYALLSGIVSIQRATPARAPGTRTLGMAEED	314
AtMtx2 (064471)	239	-EASSSSPSPPLHSPSSFPKRSKPKSKPKVEKTEEEKKFKKRARFFLAAQFLAVVIYVSMVGGSSDELEYE	311
HsMtx2 (MTX2 HUMAN)	254	-FEDRGKGRLS-----	263
NcSam35 (Q7S734)	297	-SAGSGELEQHRRLLFELLWLAADSNALLDAKARGNKLLQFQLQA-----	340
ScSam35 (SAM35 YEAST)	275	MLKSDGQPTYLHLKIASYLILCITNVEPKIKLKTFFVENECKELVQFAQDTLKNFVQ-----	329
CaSam35 (Q59ZS4)	250	-----TI-----	251
CaSam37 (Q5ALP4)	334	NPIGNEIPSLTNEVKYWIGSIEY-----	356
ScSam37 (SAM37 YEAST)	386	LLLAGAGLTLAINVAGLGIYWRYRGLLQAPLQWHRPLVGLGSFGAAGAMFAGLA	442
NcSam37 (Q7SFC4)	315	EEE-----	317
HsMtx1 (MTX1 HUMAN)	312	DEDD-----	315
AtMtx2 (064471)	312	DEDD-----	315
HsMtx2 (MTX2 HUMAN)			
NcSam35 (Q7S734)nbsp;			
ScSam35 (SAM35 YEAST)			
CaSam35 (Q59ZS4)			

Supplemental Figure 4. ClustalW alignment of the fungal Sam35 and Sam37 proteins with the animal metaxins. Ca-*Candida albicans*, Sc- *Saccharomyces cerevisiae*, Nc-*Neurospora crassa*, Hs-*Homo sapiens*, At-*Arabidopsis thaliana*



Supplemental Figure 5. Calcofluor white staining of *C. albicans* *sam37ΔΔ* mutants Cells from wild type (A) and mutant cultures (B) were grown over night in YPD and stained with calcofluor white (250μg/ml). Micrographs were taken with the 100X objective. Bright field and calcofluor white stained cells are shown, two fields for each of the wild type and mutant cultures.

>Q6PKY5_XENLA [(score: 6.80e-246, model: Metaxin1) Q6PKY5_XENLA Metaxin 1 (LOC407749 protein).]
MAAPMELYCWKGDWGLPSVDPDCLTVLTYAKFSGAPLKVHKITNPWRSPSGRLPALKTSDDGVLFQPSRIITHLRKQKYN
ADYDLSARQGADTLAFISLLEEKLLPALIHSFWVEGKNYVEHTRKWYAESIPFPLNFFLPNQMHKRNMERLKLIRGESWR
EEDDEMEGRLYTDAHECLSLLSQRLANNNFFFGDSPASLDAVYVFSHLAPILNAKLPNNKLOHLSLPLNLCRYCTSIITV
YFPWEQESGPRVAPKPPSAETQDTEDDPHKRRNQVLSVLAGLLAMVGYAVLSGIVSIQRVAPDHALEQGITMEDNEEEEE
>Q5RKQ2_DANRE [(score: 4.70e-241, model: Metaxin1) Q5RKQ2_DANRE Metaxin 1b.]
MAAPLELFCWKG DYGLPSVDVDC LAVLAYAKFAGAPLKVHKITNPWRSPSGSLPALKTREEEGSISQPSKIIH LRKQKYN
ADYDLSAKEGADTLAFVSLLEEKLLPALVYTLWIDSKNYVDVTRCWYAENIPFPLNFFLPNRMHSQQLEKLR LVRGDPVL
EPGEQLEKELYRDAFECMTLLSQRLG SQKFFFGDSPSSLDAYVFAHLAPLLKIKLPNGKLOHLSLNNLEQFCSNILL
YFPSDQREAPARKIHVQSDSSDFDNEPHMRRNQILSVLFAVGAMLYAVLTGIITIKRERPOLKNSSHEDGDEEDED
>Q4R3I0_MACFA [(score: 5.40e-241, model: Metaxin1) Q4R3I0_MACFA Testis cDNA
clone: QtsA-16827, similar to human metaxin 1 (MTX1), transcript variant 1,.]
MAAPMELFCWGGWGLPSVDLDSLAVLTYARFTGAPLKVHKISNPWRSPSGTLPALRTSHGEVISVPHKIIH LRKQKYN
ADYDLSARQGADTLAFMSLLEEKLLPVLVHTFWIDTKNYVEVTRKWYAEAMPFPLNFFLPGRMQRQYMERLELLSGEHP
EDEEELEKELYREARECLTLLSQRLG SQKFFFGDAPASLDAFVFSYLALLLQAKLPSGKLOAHLRGLHNLCA YCTHILSL
YFPWDGAEVPPRQTPAGPETEEEEPYRRRNQILSVLAGLAAMVGYALLSGIVSIQRATPARAPGTRALGMAEED EEE
>Q1L8P8_DANRE [(score: 1.50e-240, model: Metaxin1) Q1L8P8_DANRE Metaxin 1.]
MAAPLELFCWKG DYGLPSVDVDC LAVLAYAKFAGAPIKVHKITNPWRSPSGSLPALKTREEEGSISQPSKIIH LRKQKYN
ADYDLSAKEGADTLAFVSLLEEKLLPALVYTLWIDSKNYVDVTRCWYAENIPFPLNFFLPNRMHSQQLEKLR LVRGDPVL
EPGEQLEKELYRDAFECMTLLSQRLG SQKFFFGDSPSSLDAYVFAHLAPLLKIKLPNGKLOHLSLNNLEQFCSNILL
YFPSDQREAPARKIHVQSDSSDFDNEPHMRRNQILSVLFAVGAMLYAVLTGIITIKRERPOLKNSSHEDGDEEDED
>Q4VX25_HUMAN [(score: 7.30e-240, model: Metaxin1) Q4VX25_HUMAN Metaxin 1.]
MLLGGPPRSPRSGTSPKGPWSSTGHVQFGKSPQTWPRRTRPRSPEPAAPSGVGRGSTWTRRRDTPRRAGPTALSRYVGH LW
MGRPPSPEARGPVPRSSAASRARRSLASPGISPGPLTATIGGAVAGGGPRQGRAEAHKEVFPGQRV GKMAAPMELFCWS
GGWGLPSVDLDSLAVLTYARFTGAPLKVHKISNPWQSPSGTLPALRTSHGEVISVPHKIIH LRKQKYNADYDLSARQGA
DTLAFMSLLEEKLLPVLVHTFWIDTKNYVEVTRKWYAEAMPFPLNFFLPGRMQRQYMERLQLLTGEHRPEDEEELEKELY
REARECLTLLSQRLG SQKFFFGDAPASLDAFVFSYLALLLQAKLPSGKLOVHLRGLHNLCA YCTHILSLYFPWDGAEVPP
QRQTPAGPETEEEEPYRRRNQILSVLAGLAAMVGYALLSGIVSIQRATPARAPGTRTLGMAEED EEE
>MTX1_HUMAN [(score: 7.30e-240, model: Metaxin1) MTX1_HUMAN Metaxin-1.]
MAAPMELFCWGGWGLPSVDLDSLAVLTYARFTGAPLKVHKISNPWQSPSGTLPALRTSHGEVISVPHKIIH LRKQKYN
ADYDLSARQGADTLAFMSLLEEKLLPVLVHTFWIDTKNYVEVTRKWYAEAMPFPLNFFLPGRMQRQYMERLQLLTGEHRP
EDEEELEKELYREARECLTLLSQRLG SQKFFFGDAPASLDAFVFSYLALLLQAKLPSGKLOVHLRGLHNLCA YCTHILSL
YFPWDGAEVPPQRQTPAGPETEEEEPYRRRNQILSVLAGLAAMVGYALLSGIVSIQRATPARAPGTRTLGMAEED EEE
>Q8R5C0_MOUSE [(score: 2.10e-239, model: Metaxin1) Q8R5C0_MOUSE Metaxin 1 (Lung
RCB-0558 LLC cDNA, RIKEN full-length enriched library, clone:G730021A22
product:metaxin 1, full insert sequence)
MAAPMELFCWGGWGLPSVDLDSLAVLTYTRFTGAPLKIHKTSNPWQSPSGTLPALRTSDGKVIITVPHKIIH LRKQKYN
ADYDLSARQGADTLAFMSLLEEKLLPVLIIHTFWIDAKNYVEVTRKWYAEAMPFPLNFFLPGRMQRQYMERLQLLCGEHKS
ENEELEKELYQEARECLTLLSQRLG SQKFFFGDAPASLDAFVFSHLALLLQAKLPSGKLOAHLRGLHNLCA YCTHILNL
YFPRDGDEVPLPRQTPAAPETEEEEPYRRRTQILSVLAGLAAMVGYALLSGIVSIQRTSPARAPGTRALGLAEDEED
>MTX1_MOUSE [(score: 9.90e-239, model: Metaxin1) MTX1_MOUSE Metaxin-1.]
MAAPMELFCWGGWGLPSVDLDSLAVLTYTRFTGAPLKIHKTSNPWQSPSGTLPALRTSDGKVIITVPHKIIH LRKQKYN
ADYDLSARQGADTLAFMSLLEEKLLPVLIIHTFWIDAKNYVEVTRKWYAEAMPFPLNFFLPGRMQRQYMERLQLLCGEHKS
ENEELEKELYQEARECLTLLSQRLG SQKFFFGDAPASLDAFVFSHLALLLQAKLPSGKLOAHLRGLHNLCA YCTHILNL
YFPRDGDEVPLPRQTPAAPETEEEEPYRRRTQILSVLAGLAAMVGYALLSGIVSIQRTSPARAPGTRALGLAEDEED
>Q4KLN2_RAT [(score: 1.80e-238, model: Metaxin1) Q4KLN2_RAT LOC295241 protein
(Fragment).]
RCSRGHVQFGSKPQRPLSRTRCPSSKPCLSPAVRGYARQRHRESPKRAWTAALLPYGGRLRTSPRRSSEGQCSTSSSAAA
SPAARSHASLDLKL RVATQAETRGCSWREKADAYERVLPQORMCKMAAPMELFCWGGWGLPSVDLDSLAVLTYTRFTC
APLKVHKISNPWQSPSGTLPALRTSSGKVIITEPHKIIH LRKQKYNADYDLSARQGADTLAFISLLEEKLLPMLIHTFWI
DAKNYVEVTRKWYAEAMPFPLNFFLPGRMQRHMERLQLLCGEHRLESEEELEKELYQEARECLTLLSHRLGSRKFFFGD
APASLDAFVFSHLVLLLQAKLPSGKLOAHLRGLQNL CVYCTHILNLYFPRDATDVPPPPCQTPAGPETEEEEPYRRRTQIL
SVLAGLAAMVGYALLSGIVSIQRASPARAPCTQALDLAEDEED
>Q27HK4_PIG [(score: 2.00e-236, model: Metaxin1) Q27HK4_PIG Metaxin 1.]

MAAPMELFCWGGWGLPSVDLDSLAVLTYARFTGAPLKVHKITNPWRSPSGTLPALRTSQGEVIVSVPHKIITHLRKEKYN
ADYDLSARQGADTLAFMSLLEEKLLPVLHTFWVDKKNYVEVTRKWYAEAMPFPLNFFLPGRMQRQYMERLQLLCGEHRP
EEEELEKELYQEARECLTLLSQRLLGAQKFFFGDAPASLDAFVFSYLALLQAKLPSGKLOAHLRGLHNLCAYCTHILSL
YFPWEGAQVPRPQTPASSETEEEEPYRRRNQILSVLAGLAAMAGYALLSGIVSIQRAPPARAPSTRALGMAEEDDEE
>A4QNH5_XENTR [(score: 1.50e-235, model: Metaxin1) A4QNH5_XENTR Metaxin 1.]
MAAPMELYCQKGDWGLPSVDPDCLTVLTYAKFSGAPLKVHKVTNPWRSPSGRLPALKTHDDGVLFQPSKIIITHLRKQKYN
ADYDLSAQGADTLAFISLLEEKLLPALIHSFWVEGKNYVEHTRRWYAESIPFPLNFFLPNQMHKRNLERLQLIRGDSWR
EEDDTERQLYTDAQECSLLSQRLLAKHKFFFGDSPASLDAVYFVSHLAPILSAKLPNNKLQOHLSSLPNLCQYCRAILTI
YFAWEGDSGPRITPKPQSGETPDTEEEPHKRRNQVLSVLVGLLAMVGYAVLSGIVSIQRVGPDPHALEQGIAMEDNEEEEEE
>Q2TBS1_BOVIN [(score: 1.70e-230, model: Metaxin1) Q2TBS1_BOVIN Metaxin 1.]
MAAPMELFCWGGWGLPSVDLDSLAVLTYARFTGAPLKVHKITNPWRSPSGTLPALRTSHGEVIVSVPHKIITHLRKEKYN
ADYDLSARQGADTLAFMSLLEEKLLPVLKHTFWIDAKKNYVEVTRKWYAEAMPFPLNFFLPGRMQRQYMERLQLLCGEHRP
EDEEELEKELYQEAEQECLELLSQRLLGSQKFFFGDAPASLDAFVFSYLALLQAKLPSGKLOAHLRGLHNLCAYCAHILSL
YFPWEGAKAPPRQTPANPETEEEEPYRRRNQILTVLAGLAAMAGYALLSGIVSIQRAPSARAPGTQALGMAEEDDEE
>Q4SW18_TETNG [(score: 1.30e-224, model: Metaxin1) Q4SW18_TETNG Chromosome
undetermined SCAF13694, whole genome shotgun sequence. (Fragment).]
MAAPEELFCWEGDWGLPSVDTDCLVVLAYAKFAGAPLKLQKLSNPWRSPSGCLPALRTSRKETLSRPSDIIHHRKQKFN
ADFDLSAKEGADSLAFISLIEEKLRPALLYAFWAEPKNYVDVTRCWYGEHLFPFPLNFFLPQGMORRQLAKLCLQRGQOSL
EVGEELEKEVSLGGARSPRSLWAGPASASRFLPQLYRDAECMNLSSQRLLGSHKFFFGDSPSSLDAYAFGHLAPILRC
KLPSGRLQOHLKSLDNLSSFCNVLLLYFPRDGPPEGGAARTSSPPDAPDFEQVFNKRRKQLLSALVALGAMLSYALLTGM
LSIQHVQDELQGLGAEEDDEE
>A2THY5_DANRE [(score: 1.30e-202, model: Metaxin1) A2THY5_DANRE Metaxin 1a.]
MAAPCELFCWKAGLGLPSVNTDCLIVLAYARFAGAPLKIHKISNPWRSPGSLPALRTKDEGSCSQPSQIIIIQLRKQKFN
ADYDLSAKEGADTLAFISLLEERLLPALIYALWIDPKNYVEVTRRWYGENMSFPLNFFLPGRMQRQYMERLRLIRGNGLT
EAGEEAEKELYHDALECLNLLSQRLLGSNKFFFGDSPSSLDAYVFGHLAPLKFIRLPNCRLQONLKNLNDLNTFCSNILSL
YFPNESIEGVSRPVSSTQPGSDLDNEPYKRRKQLLSVLVAVAAMLSALFTGIVAIEHVQEEEPVGSHEEEEEV
>Q60UY8_CAEBR [(score: 1.40e-200, model: Metaxin1) Q60UY8_CAEBR Putative
uncharacterized protein CBG19767.]
MELHIWPSDFGLPTIDVSSLQFLACSKMCASPVRVVSARPPWRSPNGELPMVAQIDGNAKPVTDFEKFDILKCKGQDVV
IDADLTTIERAQLDAFSCYLHNNLYPAVLHTFWADDLNYNTVTQYWYASHLHFPYNLYLEKRRKKALRMLGGKNDTEIL
KDAPMALNTLSTKLGDNKFCCGKPTSLDALVFGYLAPELLRVPLPNDRLQVQLSACPNLVRVFVETVSSIYLPLSEDELKR
QQSNRKMWQSRISKAKADKEAAKTTEEAEEAIPDEPPMRDAILFTIGALVLSVAFIHTGLIQVSVVEEIEA
>Q4VX24_HUMAN [(score: 1.80e-197, model: Metaxin1) Q4VX24_HUMAN Metaxin 1.]
MLLGGPPRSPRSGTSPKGPWSSTGHVQFGKSPQTPWPRRTRRSPEPAAPSGVGRGSTWTRRRDTPRRAGPTALSRYVGHLL
MGRRPPSPEARGPVPRSSAASRARRSLASPGISPGLTATIGGAVAGGGPRQGRAEAHKEVFPQORVKGMAAPMELFCWS
GGWGLPSVDLDSLAVLTYARFTGAPLKVHKISNPWQSPSGTLPALRTSHGEVIVSVPHKIITHLRKEVHTFWIDTKNYVEV
TRKWYAEAMPFPLNFFLPGRMQRQYMERLQLLTGEHRPEDEEELEKELYREARECLTLLSQRLLGSQKFFFGDAPASLDAF
VFSYLALLLQAKLPSGKLOVHLRGLHNLCAYCTHILSLYFPWDGAEVPPQROTPAGPETEEEEPYRRRNQILSVLAGLAAM
VGYALLSGIVSIQRATPARAPGTRTLGMAEEDDEE
>Q9BUU3_HUMAN [(score: 1.80e-197, model: Metaxin1) Q9BUU3_HUMAN Metaxin 1.]
MLLGGPPRSPRSGTSPKGPWSSTGHVQFGKSPQTPWPRRTRRSPEPAAPSGVGRGSTWTRRRDSPRRAGPTALSRYVGHLL
MGRRPPSPEARGPVPRSSAASRARRSLASPGISPGLTATIGGAVAGGGPRQGRAEAHKEVFPQORVKGMAAPMELFCWS
GGWGLPSVDLDSLAVLTYARFTGAPLKVHKISNPWQSPSGTLPALRTSHGEVIVSVPHKIITHLRKEVHTFWIDTKNYVEV
TRKWYAEAMPFPLNFFLPGRMQRQYMERLQLLTGEHRPEDEEELEKELYREARECLTLLSQRLLGSQKFFFGDAPASLDAF
VFSYLALLLQAKLPSGKLOVHLRGLHNLCAYCTHILSLYFPWDGAEVPPQROTPAGPETEEEEPYRRRNQILSVLAGLAAM
VGYALLSGIVSIQRATPARAPGTRTLGMAEEDDEE
>MTX1_CAEL [(score: 2.80e-185, model: Metaxin1) MTX1_CAEL Metaxin-1 homolog.
]
MELHIWPSDFGLPTIDVSSLQFLACSKMCASPVRVVIQSTRPWRSPSGELPMVAQTEGEAKPVTDFEKFDILKCKGQDVV
IDADLTTIEKAQLDAFSCYLHNNLYPAVMHTFWTDELNYNTVTQYWYASHLHFPYNLYLEKRRKKALRLLAGKNDTEIL
KEAFMALNTLSTKLGDNKFCCGKPTSLDALVFGYLAPELLRVPLPNDRLQVQLSACPNLVRVFVETVSSIYLPLGEDELKR
QQANRKMWQSRISKAKADKEAAKTTEEAESLPEEPPMRDAILFTLGLTSLVFAIHTGLIQVSVVEEIESE
>Q4VX23_HUMAN [(score: 8.10e-164, model: Metaxin1) Q4VX23_HUMAN Metaxin 1
(Fragment).]

EGGQDGGAHGAVLLVRGLGAAVSGPGQPGRADLCQIYWCSTEGTQDQOPLAEPFRYPVSLGGTLPALRTSHGEVISVPHK
IITHLRKEKYNADYDLSARQGADTLAFMSLLEEKLLPVLVHTFWIDTKNYVEVTRKWYAEAMPFPLNFFLPGRMQRQYME
RLQLLTGEHRPEDEEELEKELYREARECLTLLSQRSGKFFFGDAPASLDAFVFSYLALLLQAKLPSGKLVHLRGLHN
LCAYCTHILSLYFPWDGAEVPPQRQTPAGPETEEEEPYRRRNQILSVLAGLAAMVGYALLSGIVSIQRATPARAPG
>Q5F3K9_CHICK [(score: 1.10e-152, model: Metaxin1) Q5F3K9_CHICK Putative
uncharacterized protein.]
MAAPMELSCWGGDWGLPSLHPESLTVMAYAKFSGAPLTVNTINNSWSTPKDVPVLISETVISQPAKILNFLRKQRYNAD
YELSAKQGADTLAYIALLEEKLLPALLHTFWVEAENYCSVTKPWFASRIPFPLSLYLP GKMSREALNRILLTRGGPPLYS
LTEVEAQIYRDAKECLNLLSKRLGTSQFFFGNTPTTLDADFVFGFLAPVYKVCFPRVQLQEHKQLTNLCRFCDLITCYF
KLTITDG
>Q3KPT9_XENLA [(score: 8.50e-136, model: Metaxin1) Q3KPT9_XENLA LOC407751
protein.]
MELRCWGSWGLPSVHPECLVVLAYARFAGAPLKVTPVDYTWASPKGTVPFLTSAGEDTHQAPANILNFFRKQKYNADYVL
SAKEGSDTLAYIALLEEKLLPAVLHTFWVDTENYCNVTRPWPYASHTPFPLNYYLP GKMSRDALDRILVTRGQPPYLSLSE
VEAQIYKDAKECLNLFNRLGTAQYFFGSTPTSLDAFVFGFLAPLYKAHLHKVNLQOHLKQLSNLCHFCDHILSAYFVSD
DAGTSAAGQEAIDANLQKLTQLVNKESNLIKMDNLRSPQNRPOKLSLTKPVGGAENSHSSDLLSH
>Q6QIT1_XENLA [(score: 3.50e-134, model: Metaxin1) Q6QIT1_XENLA Metaxin 3.]
MMELRCWGSWGLPSVHPECLVVLAYARFAGAPLKVTPVDYTWASPKGTVPFLTSAGEDTHQAPANILNFFRKQKYNADYV
LSAKEGSDTLAYIALLEEKLLPAVLHTFWVDTENYCNVTRPWPYASHTPFPLNYYLP GKMSRDALDRILVTRGQPPYLSL
EVEAQIYKDAKECLNLFNRLGTAQYFFGSTPTSLDAFVFGFLAPLYKAHLHKVNLQOHLKQLSNLCHFCDHILSAYFVS
DDAGTSAAGQEAIDANLQKLTQLVNKESNLIKMDNLRSPQNRPOKLSLTKPVGGAENSHSSDLLSH
>Q4VBW0_DANRE [(score: 3.50e-127, model: Metaxin1) Q4VBW0_DANRE Metaxin 3.]
MAEPIELLCWGGDWDLPSVQTDLSLTVLAYAKFAGAELTVKFVDWTRWRTITASVPOIHYEGTTVTEPTQILNFLRKQRFNA
DFELTAKQGADTMAYIALLEEKLRPALLHTFWVDAENYANLTRPWFSTSHSPFPLNFFVPGRQASLALSRIILLTKAESPLL
NITEVEGKIYSEAKECLNLLSHRLGNFNFFFGDTPSTLDAFVFGHIAPLIKAPLPSGQLQKHLNQLDNLCQFCNTILKNY
FTDATAEKRMDCSPTVAHDFVDANLQKLTQLVNKESNLIKMDNLRSSPQHRPHRHEAKPSAPASDRNSTPA
>Q6Y0L8_DANRE [(score: 7.30e-124, model: Metaxin1) Q6Y0L8_DANRE Metaxin 3.]
MAEPIELLCWGGDWDLPSVQTDLSLTVLAYAKFAGAELTVKFVDWTRWRTITASVPOIHYEGTTVTEPTQILNFLRKQRFNA
DFELTAKQGADTMAYIALLEEKLRPALLHTFWVDAENYANLTRPWFSTSHSLFPLNFFVPGRQASLALSRIILLTKAESPLL
NITEVEGKIYSEAKECLNLLSHRLGNFNFFFGDTPSTLDAFVFGHIAPLIKAPLPSGQLQKHLNQLDNLCQFCNTILKNY
LTDATAEKRMDCSPTVAHDPVDANLQKLTQLVNKESNLIKMDNLRSSPQHRPHRHEAKPSAPASDRNSTPA
>Q7Z380_HUMAN [(score: 3.40e-101, model: Metaxin1) Q7Z380_HUMAN Metaxin-3.]
AQDGGPLGTQLLGRRLGTPIGSQRVPGGDVPIILTTEDDMVSQPAKILNFLRKQKYNADYELSAKQGADTLAYIALLEE
KLLPAVLHTFWVESDNYFTVTKPWFASQIPFPLSLILPGRMSK GALNRILLTRGQPPYHLREVEAQIYRDAKECLNLLS
NRLGTSQFFFGDTPSTLDAYVFGFLAPLYKVRFPKVQLQEHKQLSNLCRFCDLSSYFRLSLGGISPAGQETVDANLQ
KLTQLVNKESNLIKMDNLRQSPQLPPRKLPTLKLTPAEEENNSFQRLSP
>Q17MF9_AEDAE [(score: 5.40e-63, model: Metaxin1) Q17MF9_AEDAE Metaxin.]
MELFLYRGEWGLPTIDYDCARLLAYLKFAEAKITLNFNGNPFSSPTGMLPYLVTEEGKKIGGYNRITRITFLQSRGFDANAQ
LEGQNYIVINGCIQYVFENLFPYFMYSLWGDPKNLDTRALYAKRIPFNFYCPKRYVLKTNELTVSLAGFALEDSIEL
HDVKDLQLNAKKCINWISEKLGENRFFFGDTPSEIDAILYGYLSVLLKLTLPNNVLQNHVKQCSNLVKFVERITTIYFAR
EGFTSASSNSSSSSSSSNDSSKEKPEQEQKFYDGTQKSDSDTPYERRKRYVVSIGIFATIAMVSYALLSGILSISQHDHGGG
GFISYDEPEYDDEE
>Q4RUS1_TETNG [(score: 1.30e-52, model: Metaxin1) Q4RUS1_TETNG Chromosome 12
SCAF14993, whole genome shotgun sequence.]
MCSFKAYAKFSGAKVTVSPIDWTWRTLTGEPARHASTHTDHCWRSSSTRFNTGSKNNTDLLNTVNLOQQSRSCLVRFNAD
YELSAREGADTMAYIALIDEKLRPALLHTFWVDAENYVNLTRPWFASRSPFPLNLVVPGRQANAAF SRILLTKGEAPLQR
ITEVEAKIYSEAKECLNLLSYRLGSA DFFFGKSALPSSPLQRHLTQLENITRFCD SILALYFSPDRPGSPQVPDTKDAN
LQKLTQLVNKESNLIKVLLLRYSHTCNSNRFCVLLSVFQMDNLRSSPQHKSHRADLRASLAAGKSSSTPA
>MTX1_DROME [(score: 2.30e-41, model: Metaxin1) MTX1_DROME Metaxin-1 homolog.]
MEMQLGAMLYVYKGEYGLPSIDFECLRALCLLRFTRCPMDVQTSNPLRSAGKLPYLQIGNQKFAGYRQIKRVL DLEGY
PIDAHLSTKQKHLSTAYANWVFTNLHAYYHYFLFGEPHNFDTTTRGLYAKRTPFPFNFYYPSSYQREACDVQVMAGFDV
NDKLDKHEGDYLVNNAKVVNLLSRKLGKRVWFFGDYSEFDAIVYSYLAIIFKIALPNNPLQNHKGCQNLVNF INRIT
KDIFRIEGYSSVKLTKTPSGTEASLTASERKFLDSELNTKIVAGVGAVLAMGAFAAWRGIYNQLTTRSSSTDYDGDYEDD
EMEEGLD

>Q295J4_DROPS [(score: 7.50e-35, model: Metaxin1) Q295J4_DROPS GA21755-PA (Fragment).]
MDIQLGAMLHVYKGEWGLPTIDFECLRALCLLRFTTRCPMDVETNANPLRSGAGKLPYLQIGNDKFVGYEQIKRVLBLEGY
PIDAHLNTRKQKHLSATYANWVFTNLHAYYHYFLYGEFPNFDKTTTRGLYAKRTPFPFNFYYPSTYQREACDVVQVMASFDV
NDKLDKHESDYLVLNAKCKVNLRSRKLGRKVVFFGDTYSEFDAIVYSYLAIFKITLPLNPLQNHKIGSQNLVNFINRIT
KDIFRNEGFSSIKPTKTANGTVDVNVTHSEHKFLESECSTKI IAGVGALLAMGAFAAWRGIYNQLTTRSSSTDYDGDIDYDD
DAEEGLE

>Q5HYI7_HUMAN [(score: 1.10e-32, model: Metaxin1) Q5HYI7_HUMAN Putative uncharacterized protein DKFZp313L052.]
MAAPLELSCWGGGGLPSVHSESLVVMAYAKFSGAPLKVNVIDNTWRGSKGDVPILTTEDDMVSQPAKILNFLRKQKYNA
DYELSAKQGADTLAYIALLEEKLLPAVLHTFWVESDNFYFTVTKPWFAEQIPFPLSLILPGRMSQQILSSRAGTHMLRK

>Q7Q284_ANOGA [(score: 2.70e-15, model: Metaxin1) Q7Q284_ANOGA ENSANGP00000014380 (Fragment).]
EMEIFVYRGEWGLPSIDYECRLLAYLKFSGAKVTNVFNNGNPFSSPNGMLPYMIADGKKIAGYGRIVEHLVAAGIGPPTA
TDRAENINGYMQYVQENLHPYFMYMLWGDPKNVDTTRTVYAKRIPIPFNFYCPKRYVLRNTDITQSLVGFSLSDSIEFHD
VAEFQHNAKTCLNVAARLEESRWFTGDRPTEVDALLYGYLSVLLKLTLPNNVLQNHIRQCPKLMQFVDRTTATYFAKEG
FNS

>A1CES6_ASPCL [(score: 4.80e-13, model: Metaxin1) A1CES6_ASPCL Mitochondrial import receptor subunit (Tom37), putative.]
MVLELHVWGPAPGLPSIDPQCLATIAFYSLVLPKDAWVLIASSDPSVSPTELPAKNGKAWVSRFRNIVDYLRQYSNGE
WDLDEVLSGTDRADNIAFSSFIESRGQPLIDLISLYITSQNYDKTSPAYGAILQWPNQWIIPRLHSAKKRTEPLGLSS
LDLQAMEDQRKREHSAVAAGQIPENLIQRPRDTSVGLLGKTAQQRNRFKLEALTAELFDPLEEMLGQKSYFFPGDKPATA
DCLALGYLSLALVPDLPYPWLRDAMKIKAPNLSRYTERLRQHCHYGAVALVDVSHAFDGPSPATDAASPLPWLAPARATAV
TVGSTLLNTLADATPILKNIRAHERLRQAAQSPDSGLSRVESHALSAYATGQKKDVLVSVAAVVGGVAALLGYMAHVGLL
QISYGSDEEEWEEEEEEEEEEQOEGGIAGIPESLSATEFLNF

>Q6GPN0_XENLA [(score: 1.40e-12, model: Metaxin1) Q6GPN0_XENLA LOC407750 protein.]
MSLVTDAFVSQIAAVEPWPENAAALYQPMKSEQVLLSDNASCLAVQAFKMCNLPVQVVCRAEAEMSPSGKVPFIHVGNO
VISELGPVIVQFVKAKGHSLSDGLDEVQRAEMKAYMELVNNMLLTAELYIQWCDEATLEEITQPRYSYPYSWPLNYFLVFQ
RKWEIKRKMKAIGWATKTLEQVFEDVDQCCQALSQRLGTQSYFFNKQPTELDALVFGHLFTILTTLTQNTDELQEKVKNS
NLIAFCRRIEQHYPEDHDGSISSSMKLSKGPTLP

>Q6Q8B0_XENLA [(score: 1.70e-12, model: Metaxin1) Q6Q8B0_XENLA Metaxin 2.]
MSLVTDAFVSQIAAVEPWPENAAALYQPMKSEQVLLSDNASCLAVQAFKMCNLPVQVVCRAEAEMSPSGKVPFIHVGNO
VISELGPVIVQFVKAKGHSLSDGLDEVQRAEMKAYMELVNNMLLTAELYIQWCDEATLEEITQPRYSYPYSWPLNYFLVFQ
RKWEIKRKMKAIGWATKTLEQVFEDVDQCCQALSQRLGTQSYFFNKQPTELDALVFGHLFTILTTLTQNTDELQEKVKNS
NLIAFCRRIEQHYPEDHDGSISSSIKLSKGPTLP

>Q9UUA5_SCHPO [(score: 2.00e-12, model: Metaxin1) Q9UUA5_SCHPO Metaxin; 1 predicted transmembrane helix; similar to S. cerevisiae YMR060C.]
MLQLFIYSPGLGQPTMDPGCLAALIYCALAVPKDEIEILRTANSGMSPHKLPLWDGHVWIGSLKNILYIKQKGYNLD
NFDKQLANVMAFTSLLEGSVNDLWLEAFVNEENFVEAIRPAWSKALKFPHNYLTPNALQRQAKERLAQTLGIRDEEVS
YEASRMPISHKWTNATRHRQALLRTQARRIRISSLARQVYGSLESLSISDSKFIKFKPTSLDCLFYAYLSFHAFHTNELPQ
ATLRPCLQFNSPKLYAYLKSRETWFSDSNILSPLSIKQVOPENLLTIARLAWNNVTAKANDTRKSITKFSVPPERKLLW
ARNGFFIFASAFSFWVVISNGIVVIETEDDEASFEVDDAKESIQEKEIDETTESKATHDSSETSSSKELPKEEEKESS
SFDLQPLSAQDLLFSGFAEDEIMDEEFGYDDDDDEEFDLDDLDLEEEIV

>Q6GUH5_XENTR [(score: 3.00e-12, model: Metaxin1) Q6GUH5_XENTR Metaxin 2.]
MSLVTDAFVSQIAAVEPWPENAAALYQPLKSEQVLLSDNASCLAVQAFKMCNLPVQVVCRAEAEMSPSGKVPFIHVGNO
VISELGPVIVQFVKAKGHSLSDGLDEVQRAEMKAYMELVNNMLLTAELYIQWCDEATLEEITQPRYSFPYSWPLNYFLVFQ
RKWEIKRKMKAIGWATKTLEQVFEDVDQCCQALSQRLGTQPYFFNKQPTELDALVFGHLFTILTTLTQNTDELQEKVKNS
NLIAFCRRIEQHYPEDHDSSISSTKLSKGPTLP

>Q6WFZ4_DANRE [(score: 6.10e-12, model: Metaxin1) Q6WFZ4_DANRE Metaxin 2.]
MSLAAEAFVSQIAAAEPWPENAAALYQPLKEDQILLSDSASSLAVQTFLRMCGLPVQVSCRANAEMSPSGKVPFIQVGNQ
VVSELGPVIVQFTKAKGHSLSDGLDDVQRAEMKAYMELVNNMLLTAELYIQWCDDFTATEISRPRYSSPYSWPLNHILAYQ
KQWEVRRKMNAIGWSGKSLEQVYEDVSQCCQALSQRLGTQPYFFNKQPTELDALVFGHLFTILTTLTQNTDELVEKVKSYS
NLLSFCHRIEQAYFKEQEREGQSGSSRHSKGSPLP

>Q5B6M7_EMENI [(score: 2.40e-11, model: Metaxin1) Q5B6M7_EMENI Putative uncharacterized protein.]
MVLELHIWGPGLPSIDAQCLATIAFYSLAVPKDSWVLVASSDPTVSPTHELPALKNGSTWVSRFRNIVDYLRQYSNGA
WDLDRDLSALEKADSVAFSSVFVESHQAQLLDLSLYVTSQNYYNSTSPAYGAILQWPNQWILPPQLHATAKARTEPLGLSS
LDLEATEEQQRKRDHSAAVAAGRIPQNLISRPRETVTNLLGKTPQOQHFRLEALTGELFVPLEELDDKTHLLGTTSSLD
CLSVGYLSLALVPDLPLPWRDAMQRKAPRLSQYIERLRLELFGTVNVADAFNSGANSLLPWQAPERASFARVGTSLTSS
LADSTPILKEIRMNNKLRETAECSSAGLSEVESKSLSEYARAQKDTLLSIATVIGGVAALIGYMAHIGVFSAPQEEKE
EPEEYQVELPKSISANDFLGI
>Q4WHX7_ASPFU [(score: 3.80e-11, model: Metaxin1) Q4WHX7_ASPFU Mitochondrial import receptor subunit (Tom37), putative.]
MVLELHVWGPFAFSLPSIEAQCLAAIAYFSLAVPKDAWVLIASSDPSVSPTNELPALKNGTTWVSRFRNIVDYLRQYSNGA
WDLDRDLSGIDRADNIAFSSVFVESRQPLLDLSLYVSSSENYNRTSPAYGAILQWPNQWIVPPRLRSAAKSRTEHLGLSS
LDLEAAEDQRKREHSAAVAAGQIPKTLAQRPRDTSVSSLLGKSPQOQFKLEALTAELFEPLEEILGQKTYLVSDGDATSV
DCLALGYLALILVDPDLPYSFLRNAMRTKAPRISAYTERLRQRCYGTGVGEVAHAFDETRRSVTDATPLPWQPAQRANLTT
VCSTLLNTLADATPILKDIRSSERLRQAQSPDSGLSGIESRALSEYATGQKIDILVSIAAVAGGVAALVGYMVHVGFIE
ISFGGEEGHWEEEGHAGEEEGGSEFALPELPTSVSATEFLGI
>A1DFG3_NEOFI [(score: 4.80e-11, model: Metaxin1) A1DFG3_NEOFI Mitochondrial import receptor subunit (Tom37), putative.]
MVLELHVWGPFAFSLPSIEAQCLAAIAYFSLAVPKDAWVLIASSDPSVSPTNELPAVKNGTWVSRFRNIVDYLRQYSNGA
WDLDRDLSGIDRADNIAFSSVFVESRQPLLDLSLYVSSSENYNRTSPAYGAILQWPNQWIIIPRLRSAAKSRTEHLGLSS
LDLQAEDQRKREHSAAVAAGQIPKNLVQRPRDTSVSSLLGKTPQOQFKLEALTAELFEPLEEILGQKTYLVSDGDATSV
DCLALGYLALILVDPDLPYSFLRNAMQTKAPRISTYTERLRQRCYGTGVGEVAHAFDEARRSVTDATPLPWQPAQRANLAT
VCSTLLNTLADATPILKDIRSSERLRQAQSPDSGLSGIESRALSEYASGQKIDMLVSIAAVAGGVAALIGYMVHVGFIE
ISFGGEEGWEEEGQEGEEGGSEFALPELPTSVSATEFLGI
>O64471_ARATH [(score: 8.50e-11, model: Metaxin1) O64471_ARATH Expressed protein (At2g19080/T20K24.9) (Putative uncharacterized protein).]
MEGDQETNVYTLVARKPSFDLPTACPNCLPAYIYLKLAQLPFELAFNSTFPDSELPYFESDITYVAYNNEGGVIEKLLK
DGIVNLDSQLQSLSDYLSLKALIVSWLEEALTYEIVWGTEGISTSKIYYSDLPWVISKVLFYKQTYLAKNRLGITKENAE
QREKQIYKRASEAYEALSTRLGEQKFLFEDRPSLDAFLLSHILFIIQALPVTSLRCKLLEHSNLVRYAEKLFSEFLEA
SSSSPSPPLHSFSSFPKSSKPKSKPKVEKTEEEKKFKKRARFFLAAQFLAVVIYVSVMMGGSSDELEYEDDD
>Q5C360_SCHJA [(score: 9.30e-11, model: Metaxin1) Q5C360_SCHJA SJCHGC05855 protein (Fragment).]
ILSAPDELLPCDPNCLLILCYIRLKEARINIKVCLPDHSSVGEFPVLNHDSDYHGIPVILTYLRKENYGLYDLSDETEG
VQLCALISTIDRRLAPAVNWFLWADDSVYTKFTRKMYFGSLRFFQQLYIPHIWRNRQINKAKSSQLITCLKNMSESEVGE
HLYSLAKLCITSLSYILGENTFFVGDRTAVDAYVFAFMWPLLMYESQHGSDSNWWDVDYKSSSTNYVQSGSH
>Q1KKR5_FUGRU [(score: 1.30e-10, model: Metaxin1) Q1KKR5_FUGRU Metaxin 2.]
MSLAAEAFVSQIAAAEPWPESATLYQPLKEDQVLLSDCASSLAVQTYLRMCLPVEVMYRANAEMYSPSGKIPFIHVGNQ
VVSELGPIVQFTKAKGHSLSGDLDDVQRAEMKAYMELVNMLLTAELYIQWCDDATATGITRPRYSSPYSWPLSSFLAYQ
KQWEVRRKMNAIGWGGKTLQVYEDVNQCCQALSQRLGTQPPFFNKQPTELDALVFGHLFTILTTRLTSTELAERIKSHS
NLLSFCRRIEQTYFEDKSS
>Q1T1H8_MEDTR [(score: 2.00e-10, model: Metaxin1) Q1T1H8_MEDTR Glutathione S-transferase, C-terminal-like.]
MAEVYTLVVRKPCFGLPTGCPQCLSSLIYLNFSQIPFQDFHVNHPHSDKIPYIEVGDDYVAYNNEIEGIIIECLKKDVGV
VDLDSEVSSLPDWISIKAILTTWLHDALTYELWVSGDSSANSIYYSDLPWPLGKILYSHKVRWVKLKHGITDDNAVVK
EEIYERANSAYGALSPLLGEKNYLFDESRLSDAIFLAHGLVALQALPESSTLRKFSEHDNLVRYVHKCKTELKDGAGT
SPPSAPSGRSQSTQRPKSKSIPKREKTKEEKTLLKRKGKYFVAAQLVAVVVFLTMLVTFDITEGEVEDVDAGEY
>Q2UPU0_ASPOR [(score: 2.20e-10, model: Metaxin1) Q2UPU0_ASPOR Translocase of outer mitochondrial membrane complex.]
MVLELHVWGPFAFSLPSIEAQCLATIAFYSLAVPKDAWVLIASSDPSVSPTCELPALRNGSTWVSRFRNIVDYLRQYSNGE
WDLDAGLSGLRADNIGFSSVFVESRAHALVDLSLYVTSQNYYNQTSPAYGSILQWPNQWILPPKIHAAKARTDHLGLSS
LDLQAIEDQRQREHSAAVAAGQIPPNFIRRPRDTSVSSLLGKTSQOQFKRLDALTGELFEPLEEILGDKVYLLTGENEGPS
SLDCLAVGYLSLALVPELSFSLRDAMKSKAPRLTVYTERMRQOCYGLGAEVSHAYTPTNSGSSLPWRAPERARLTTLG
NTLNFVNLADNTPILKDIRAQDRLRVAAESPDGSLSEPDSRKLALAKGQKIDILVNIAYAVGGIAALIGYMTYEGFFSAE
IGDEYEEDDEFEPMPDIEPDSLQVQNMLAGL
>MTX2_PIG [(score: 2.50e-10, model: Metaxin1) MTX2_PIG Metaxin-2.]

MSLVAAEFVVSQIAAAEPWPENATLYQQLKGEQILLSDNAASLAVQAFLOMCNLPKVVCRANAEMYSPSGKVPFIHVGNO
VVSELGPIVQFVKAKGHSLSDGLDEVQKAEMKAYMELVNNMLLTAELYLQWCDEATVGEITHARYGSPYPWPLNHILAYQ
KQWEVKRKMKAIGWGNKTLDOVLEDVDQCCQALSQRLGTQPYFFNKQPTELDALVFGHLYTILTTQLTNDELSEKVKVNS
NLLAFCRRIEQHYFEDHSGSSSVRLS

>Q7SFC4_NEUCR [(score: 4.80e-10, model: Metaxin1) Q7SFC4_NEUCR Predicted protein (Putative uncharacterized protein G17B7.090).]

MTLELHVWGPFAFGLPSIDAELATVYFAQTLAADYLLVQSSPSAVPSHHPALYNPSTATWISGFDPVNYLSTLQPP
SYHHPDVTTLPSRVYADSQAYKALLTSSAAPLLALSIVSSANYSETTRPAYSAILPFPLPWTEPLAVRAAMAARAHLG
MSSLDTDAEMERLEREEREREAAAGVWQIPKALRKAVGGQNSGVKQQLSPEMKRRIKLEGLAAEVFVLDVGEVDFLEEDGE
EEEEEEEEAKEGGARIKVTLETCKLAFAYLALMLLPEVPRPWLKEVLQKKYAGLCKFVLEYRRTFPDSDGKVLWADRES
DPAVSACDSALSIVGRFVRAVIDDIPMLGREWSRWALRQRVAEENSAETQLVVRRSVGESERSLLL LAGAGLTLAINV
AGLGIYWYRGRLLGAPLQWHRPLVGLGSFGAAGAMFAGLA

>MTX2_HUMAN [(score: 6.70e-10, model: Metaxin1) MTX2_HUMAN Metaxin-2.]

MSLVAAEFVVSQIAAAEPWPENATLYQQLKGEQILLSDNAASLAVQAFLOMCNLPKVVCRANAEMYSPSGKVPFIHVGNO
VVSELGPIVQFVKAKGHSLSDGLEEVQKAEMKAYMELVNNMLLTAELYLQWCDEATVGEITHARYGSPYPWPLNHILAYQ
KQWEVKRKMKAIGWKKTLDOVLEDVDQCCQALSQRLGTQPYFFNKQPTELDALVFGHLYTILTTQLTNDELSEKVKVNS
NLLAFCRRIEQHYFEDRGGKGRLS

>Q8IZ68_HUMAN [(score: 6.70e-10, model: Metaxin1) Q8IZ68_HUMAN Metaxin 2.]

MYIAAEPWPENATLYQQLKGEQILLSDNAASLAVQAFLOMCNLPKVVCRANAEMYSPSGKVPFIHVGNOVVSELGPIVQ
FVKAKGHSLSDGLEEVQKAEMKAYMELVNNMLLTAELYLQWCDEATVGEITHARYGSPYPWPLNHILAYQKQWEVKRKMKA
AIGWKKTLDOVLEDVDQCCQALSQRLGTQPYFFNKQPTELDALVFGHLYTILTTQLTNDELSEKVKVNSNLLAFCRRIE
QHYFEDRGGKGRLS

>Q5VRG1_ORYSJ [(score: 7.90e-10, model: Metaxin1) Q5VRG1_ORYSJ Putative uncharacterized protein OSJNBa0033B09.11 (Putative uncharacterized protein P0680A03.32).]

MWAGIGFPVYVMGFIDAAGRGEQTHKPSAFFSSRSSKESPLPAMASAAAAAAAEWEEAERKVLVARKAAAFGLPTACPT
CLPVLLYLRLMCNVPFDIHVDSSFPDADHIPYVEFGECVAFNNEKGGVIEYLKEEKIVDLNSKHPSVSYSDVLSKAMVMT
WLSDALQYELWLASDGSIPHDIFYSDLSWPIGKILYWKKTREVKQQLGITKLNAAEKEEEIYQKANAAYDALSTRLDQI
FLFDNSPTDQVLDALFLGHALFVLNVLDPDTSVLRSCLOKYDNLVNFTKHLKVQLLEADSDSSATGLGSTDPSSSSTPRKRAS
SGRSYKPKPRAKKERTEEEKFRKAKYFLATQLVAVLLFSLMGGADSSSELDDDEDGVDYED

>Q0DE86_ORYSJ [(score: 7.90e-10, model: Metaxin1) Q0DE86_ORYSJ Os06g0168000 protein.]

MASAAAAAAAEWEEAERKVLVARKAAAFGLPTACPTCLPVLLYLRLMCNVPFDIHVDSSFPDADHIPYVEFGECVAFNNEK
GVIEYLKEEKIVDLNSKHPSVSYSDVLSKAMVMTWLSDALQYELWLASDGSIPHDIFYSDLSWPIGKILYWKKTREVKQ
QLGITKLNAAEKEEEIYQKANAAYDALSTRLDQIFLFDNSPTDQVLDALFLGHALFVLNVLDPDTSVLRSCLOKYDNLVNFT
KHLKVQLLEADSDSSATGLGSTDPSSSSTPRKRASSGRSYKPKPRAKKERTEEEKFRKAKYFLATQLVAVLLFSLMGG
GADSSSELDDDEDGVDYED

>Q5U1Z9_RAT [(score: 9.10e-10, model: Metaxin1) Q5U1Z9_RAT Metaxin 2.]

MSLVAAEFVVSQIAATEPWPENATLYQQLRGEQILLSDNAASLAVQAFLOMCNLPKVVCRANAEMYSPSGKVPFIHVGNO
VVSELGPIVQFVKAKGHSLSDGLDEVQKAEMKAYMELVNNMLLTAELYLQWCDEATVGEITLARYGSPYPWPLNLILTYQ
KQCEVKRKMKAIGWGNKTLDOVLEDVDRCQALSQRLGTQPYFFDKQPTELDALVFGHLYTILTTQLTSDDELCEKVKVNS
NLLAFCRRIEQDYFEDRGGKGRLS

>Q8C454_MOUSE [(score: 9.50e-10, model: Metaxin1) Q8C454_MOUSE 12 days embryo spinal cord cDNA, RIKEN full-length enriched library, clone:C530040G04 product:METAXIN 2 homolog.]

MSLVAAEFVVSQIAATEPWPENATLYQQLRGEQILLSDNAASLAVQAFLOMCNLPKVVCRANAEMYSPSGKVPFIHVGNO
VVSELGPIVQFVKAKGHSLSDGLDEVQKAEMKAYMELVNNMLLTAELYLQWCDEATVGEITLARYGSPYPWPLNHILAYQ
KQWEVKRKMKAIGWGNKTLDOVLEDVDQCCQALSQRLGTQPYFFNKQPTELDALVFGHLYTILTTQLTSDDELSEKVKVNS
NLLAFCRRIEQHYFEDRGGKGRLS

>Q2M4G1_MOUSE [(score: 1.20e-09, model: Metaxin1) Q2M4G1_MOUSE Metaxin 2.]

MSLVAAEFVVSQIAATEPWPENATLYQQLRGEQILLSDNAASLAVQAFLOMCNLPKVVCRANAEMYSPSGKVPFIHVGNO
VVSELGPIVQFVKAKGHSLSDGLDEVQKAEMKAYMELVNNMLLTAELYLQWCDEATVGEITLARYGSPYPWPLNHILAYQ
KQWEVKRKMKAIGWGNKTLDOVLEDVDQCCQALSQRLGTQPYFFNKQPTELDALVFGHLYTILTTQLTSDDELSEKVKVNS
NLLAFCRRIEQHYFEDRGGKGRLS

>Q3TI19_MOUSE [(score: 1.30e-09, model: Metaxin1) Q3TI19_MOUSE TIB-55 BB88
cdNA, RIKEN full-length enriched library, clone:I730049A07 product:metaxin 2,
full insert sequence.]
MSLVAAEFVVSQIAATEPWPENATLYQQLRGEQILLSDNAASLAVQAFLOMCNLPVKVVCRAEYMSPSGKVPFIHVGNQ
VVSELGPIVQFVKAKGHSLSDGLDEVQKAEMKAYMELVNNMLLTAELYLQWCDEATVGEITTIARYGSPYPWPLNHILAYQ
KQWEVKRKMKAIGWGNKTLDOVLEDVDQCCQALSQRLGTQPYFFNKQPTELDALVFGHLYAILTTQLTSEDELSEKVKVNS
NLLAFCCRRIEQHYFEDWGKGRLS

>A2AT31_MOUSE [(score: 1.40e-09, model: Metaxin1) A2AT31_MOUSE Metaxin 2.]
MSLVAAEFVVSQIAATEPWPENATLYQQLRGEQILLSDNAASLAVQAFLOMCNLPVKVVCRAEYMSPSGKVPFIHVGNQ
VVSELGPIVQFVKAKGHSLSDGLDEVQKAEMKAYMELVNNMLLTAELYLQWCDEATVGEITTIARYGSPYPWPLNHILAYQ
KQWEVKRKMKAIGWGNKTLDOVLEDVDQCCQALSQRLGTQPYFFNKQPTELDALVFGHLYTILTTQLTSEDELSEKVKVNS
NLLAFCCRRIEQHYFEDWGKGRLS

>Q3TI40_MOUSE [(score: 1.50e-09, model: Metaxin1) Q3TI40_MOUSE TIB-55 BB88
cdNA, RIKEN full-length enriched library, clone:I730047J24 product:metaxin 2,
full insert sequence.]
MSLVAAEFVVSQIAATEPWPENATLYQQLRGEQILLSDNAASLAVQAFLOMCNLPVKVVCRAEYMSPSGKVPFIHVGNQ
VVSELGPIVQFVKAKGHSLSDGLDEVQKAEMKAYMELVNNMLLTAELYLRWCDEATVGEITTIARYGSPYPWPLNHILAYQ
KQWEVKRKMKAIGWGNKTLDOVLEDVDQCCQALSQRLGTQPYFFNKQPTELDALVFGHLYTILTTQLTSEDELSEKVKVNS
NLLAFCCRRIEQHYFEDWGKGRLS

>Q1DNN1_COCIM [(score: 1.60e-09, model: Metaxin1) Q1DNN1_COCIM Putative
uncharacterized protein.]
MVLELHTWGPAGLPSIDAQCLATIAYFALALPTNGSPEWVLPVSDPKIVPTNELPAVWTGSRWISGFRNIVAFKQYS
DGEWDLDRWMPGGEQADCVAFSSFLELHGQSLIDLISLVSSDNYTSVTSPAYGTLLOWPNQWIIPPQVRSQAKARTEHLG
LSSLDLDAVEEERQQRDINSVAAGQIPRSLATRPRQTVSGLLGKPSQKSRIRLEGLTASFVEPLQEMLEKKGYLLSDNI
PSSLDCLALGYLSLAMVPELPPFWLKDDIQAQAPRLGAYVKKLGARCFGGSVDAAVLSGIQAGTGSRLPWQIPERISLG
GIGLRIFEGIADSIPVVKDIRLSRRLKQMGQDRSLESEVLAALADGYKREALTSAATVALGLGMFMFYLFYTAGPLQVSFA
TEDDHSSSSAENEEAGDDSEEKGEKGSSEKPFDLGEVGSMLGL

>A5B6D4_VITVI [(score: 3.50e-09, model: Metaxin1) A5B6D4_VITVI Putative
uncharacterized protein.]
MDELDNQKLTLVARKPCFGLPTACPSCLPVYIYLRFAQVPPFDLSFNLIHPDSDQIPYIESGAYVAYNNEKGGVLESKED
GIIDLSQLHAIPWLSMKVMISTWLEEAIMYELWVCSGDTSAKKIYSDLPWPIGKILYFKQIHAVKQLLGITKDNAER
REEEIHRRTIAYGALSTRLGEQTFFFENRPSGVDALFLGHALFTLQALPDTSVLRSKLEHSNLVQYAEKLEKTEFMEAG
SSSSSVPRFPAEPSSSTSRRGPSNWSKAKSKPKREKTEEEKTFRRRAKYFLVTQLVAVLVFLSLLGVSGGDNEVDLDE
DDDNY

>Q7Q415_ANOGA [(score: 6.30e-09, model: Metaxin1) Q7Q415_ANOGA
ENSANGP00000010484.]
MKDWPRDAVLYQPYEEEQILLAENASCLAVRTYLKMLNLPVALEQRANAEMSPGGKRTKLPVLRVENFIYA EFDHIVTF
LEKNFNKSL SAPLTPEEKQMRSTNCLVEHLFTTAEQYVSWIDPEVRNTVTKKRNGCVFPFPLNHVQNRKESAVRRQLR
MADYLHEGIDTIMGEVDHLCQDLSSRLGDKRYFFGDSPTELDALVFGHLYSIFTMMLPNNVLALTIHKYSNLNQFCKNID
ETYFSVKGK

>Q17FN8_AEDAE [(score: 1.30e-08, model: Metaxin1) Q17FN8_AEDAE Metaxin.]
MSAITSEYLKNETIASQPWPOQAHLYQPYEEEQILLAENASCLAVRTYLTMLNLPFVVDQRANAEMSPGGKRTKLPVLR
VENYTYAEFEHILSFVELKGLSLTKQLTPDQKDDMRAHLCLVEQIFTNAEQYISWVDPEVLHKVTRQRNGCVYFPPLNHI
QNWRKQMAVRRQLGVADFLNITLDEVVEKVEKLCSTLSMQLGDKKYFYGDEPTELDALVFGHLFSIFTMTLPNNVLAVTI
NQFKNLTKFCKNIEEKYFKKVAGGR

>Q629F8_CAEBR [(score: 1.60e-08, model: Metaxin1) Q629F8_CAEBR Putative
uncharacterized protein CBG00033.]
MNAAQDWEDVSLFTPYLNDQALMYDFADCLAVQTFRLRMTSLPFNVRQRPNVDFISP DGVVPLLKINKTLITGFNAIVDFV
HKKGVTLTSHLSETQVADMRANISMI EHLTTVEKFVLWKHDETYDKVTRLRYGSVYHWPLSTVLPFLKRRSVLEELADK
DWDAKTMDEVEGEQADKVFRLSAQLGTQKYLTDGLPTEADALLFGHMYTLITVRLPLTNITNILKKYTNLIEFTKRVEQQ
YFKQ

>Q55NT1_CRYNE [(score: 6.70e-08, model: Metaxin1) Q55NT1_CRYNE Putative
uncharacterized protein.]
MSRPSIILHATPPLHPLPASDAESLYYAALLQLAAPDGWALTRGDWGDNGGKLPFITHLAHPVPPAHLSSLSPSFSDPDEE
LEDGEKLDAA CWKAYIEGNVVDIVNHTYYSLPPNYPSTVAKSQFAGLPFPMNQYIPQRIRSIKSRLEFVGLWGLGGLNV

GDAEDEDKRKQEEQFIIGPGGTTAPRAWTGWRSGQETDKRRRKWGEQOLEQKIKAI FDSLARRLGKKAYFFGERPTTVDL
ALFAQLAFVLTPTLPNLLPNILRSSYPSLVGHHDRLLERLFSWSTVPMASVQTPARTTWGETFASWLPGPSRSRTQPS
SSSSTDSKENS KGGSPSKPKTDKQKAFERGRWLWFAGAAVSMVTYLFVSGVIAFEFGDEEDEDWVAYEEDGEGEVGETT
VLDYEEEE

>Q2HCV5_CHAGB [(score: 7.40e-08, model: Metaxin1) Q2HCV5_CHAGB Putative uncharacterized protein.]

MDAGSLHQTNRLEIRICRADLSQSGSVTQLTQLLQFAMVLQLHVWGPAGLPSIDAECIAVIAYLAQTASPADYQLVQSS
PSAVPTQHLPALHDPSTSTWTSQFSSITTYLAAHPRSSQPITPTPPKQPQPTPTSTPTTTANATAYTAFLLTHAAPLLS
LTLYVSSANYAATTRPAYSAVLFPPLPWTEPPAVRAAHARRAAPLGLSGLD TDAVRARERAERERAVAEGWVTVPEGLGK
GVGGGGGGKGVAAALSPEQKMRIRLEGVASEVLDVLEGEVEWEGQEVGVRCLAFGYLALMLVPEVPRPWLEVMESRYPEL
CKFVRGFRGDVFPKERALPWAEQQSASAVAVGMRVFRGVLGEVPLVGERWSQWWTARKRREVLASKGVKSEPSGDLMLF
LGAGLGLTAMGAGVFFYRGLPPFAGAAVQVWRKPMVSLSSFGAAGAMFSGALYCID

>Q5KC66_CRYNE [(score: 7.70e-08, model: Metaxin1) Q5KC66_CRYNE Expressed protein.]

MSRPSIILHATPPLHPLPASDAESLYYAALLQLAAPDGWALTRGDWGDNGGKLPFITHLAHPVPPAHLSSLPSFSDPDEE
LEDGEKLDAAWKAYIEGNVVDIVNHTYYSLPNYPSTVAKSQFAGLPFFMNQYIPQIRISIVKSRLEFVGLWGLGGLNV
GDAEDEDKRKQEEQFIIGPGGTTAPRAWTGWRSGQETDKRRRKWGEQOLEQKIKAI FDFLARRLGKKAYFFGERPTTVDL
ALFAQLAFVLTPTLPNLLPNILRSSYPSLVGHHDRLLERLFSWSTVPMASVQTPARTTWGETFASWLPGPSRSRTQPS
SSSSTDSKENS KGGSPSKPKTDKQKAFERGRWLWFAGAAVSMVTYLFVSGVIAFEFGDEEDEDWVAYEEDGEGEVGETT
VLDYEEEE

>A2Y9S6_ORYSI [(score: 1.20e-07, model: Metaxin1) A2Y9S6_ORYSI Putative uncharacterized protein.]

MASAAAAAAEWEEAERKVLVARKAAFGGLPTACPTCLPVLLYLRCMNVPFDIHVDSSFPDADHIPYVEFGECVAFNNEKGG
VIEYLKEEKIVDLNSKHPSVSYSDVLSKAMVMTWLS DALQYELWLASDGSIPHDYFSDLSWPIGKILYWKKTREVKQQ
LGITKLNAAEKEEEIYQKANAAYDALSTR LGDQIFLFDNSPTDVDALFLGHALFVLNVLPDTSVLRSC LQKYDNLVNF TK
HLKVQLLEADSDSSATGLGSTDPSSSSTPRKRASSGRRFSWA

>A3B8S3_ORYSJ [(score: 1.20e-07, model: Metaxin1) A3B8S3_ORYSJ Putative uncharacterized protein.]

MASAAAAAAEWEEAERKVLVARKAAFGGLPTACPTCLPVLLYLRCMNVPFDIHVDSSFPDADHIPYVEFGECVAFNNEKGG
GVIEYLKEEKIVDLNSKHPSVSYSDVLSKAMVMTWLS DALQYELWLASDGSIPHDYFSDLSWPIGKILYWKKTREVKQQ
QLGITKLNAAEKEEEIYQKANAAYDALSTR LGDQIFLFDNSPTDVDALFLGHALFVLNVLPDTSVLRSC LQKYDNLVNF TK
KHLKVQLLEADSDSSATGLGSTDPSSSSTPRKRASSGRRFSWA

>A4RLK1_MAGGR [(score: 2.90e-07, model: Metaxin1) A4RLK1_MAGGR Putative uncharacterized protein.]

MGLLRLYVWGPAGLPSLDAECLAVIAYFQQNVRPGDYEIVASSPSAVPTTSYQGILDMLTSHPSSKTQNSSPDPSAAAR
IAHLTAQASPLLALS LYVSSANYAATTRPALSSVLPFLGWTEAPARRRMLARRADHLGLSDLD TADPDDPQNLSVADS
TRKSFIPARLQPRATKTISSALTPEAKARFRLDAAA AVLDVVA AAPPTAASPPSAYDCLAFGYLALMTVPDLPRPFLEE
FVNARHPALRDFVTDARIAWFSSPSSLPWSSDRTLTADSPLCVASRLAAGCVAALPGMGMTAWSAWAHGRRSGRLAGR
TTGRRGSMEHGEVWWTGLGLVLSASVVATAVMLLQDVVTTTHRFGAPLQVFERVRRVGGGLWAVGSAGAVLGGAGRQLGAGO
FAR

>Q4PHX6_USTMA [(score: 1.30e-06, model: Metaxin1) Q4PHX6_USTMA Putative uncharacterized protein.]

MSTYASTSSGSAPDGPRTLRLHVWGTSPPTLPTLDPASLYAASLLRATFAHKGDVQLQLASASTSLARVPLLQVLEGNNET
VELIDSVEAIKSFCTAVGLDSALVSDEELEAKHTALHAFVDDHLLDLILHSLFSLPANFRTVTASAYSSVGGIEAPASSL
AKLASLPLRFQPSIPSR LRNVVETRLTAVGLWGLGKKEALAQSGEADDLAARAGIIPARKOGLGQSAKQAVHDEFERSKL
VSKWREVLVDIDAALGGGMYLFGGSKVSSLD AHVFGYLAPLLFASP KMPVDILPRLVKTSYPRLAHYLT KMNQQLFP GPD
ELSLWATHTEVLSSPPTVPTSSSTPLSGLLSYIWPFSAPTTSNKASSPSTTDSTPAAAAADSIPRTTPTATRQQOQRQSR
PSASPEDRRRLRGRALWVCSALIGLVGYTFASGIVSVRFVDSDELMEEEEEEEEEEDGWQVQSEDVLDDELDEME LSDQD
DDDIKPLVRRVNLILVLSFVNGVAGCERGPCADIDV FASSTHTSFAVCHCNVIQPTTNLTQHDPSTSCGIATSSNPF CV
RSCLTTSDDTCAQNYHIVTGTFNRSRSLFVLT YDVLNSKLSILHSIRAE GPHQYLALGVSSRQQQTVYATTWGTSPSALS AW
HVSPTDYSLSFGNREITATGSYVHVQPPPYLTRSAPGFGSLPGVARWLGSAGGPTGELHTLDPETGRIETRVKEMIFLA
GGEKQLATADKTRKALRYGAHSFDCSASSSSGQGVAYVADLGANAIQAYRFASLDHLYTIVSKREEDGPRHVIPHPEWP
LVFTVTEHSNYVDAYQVPPYDSDIKEGARHVAEADLLTPQQAASGRSNWRGDTLRFSSDLRYIYATTRGK TMSNKGLLVA
LRLTITPSSSGIHVDLREVARFHTRTSGGKANAIELAPTRIMDGLDHMVLTDDEQGWIDVVAFDLNEPSFHVKASTQLPP
IQHHHQPPQGASHAIWLL

>Q9HE00_SCHPO [(score: 2.40e-06, model: Metaxin1) Q9HE00_SCHPO SPAC589.04 protein.]
MGGLTKFSSYFHSIFSRFPLITFSNPYPGENEDYKTKTVMYLTMWNSDLNSEALDVNSLQWQWAKLNDPSIVFLNVSNH
ASPDEKVPFIQIESRKLVLNPSLLQYFLKDESTLQOISPWMSLLINQVETAILLTMYLNDNENFSEIQKKWLPNMSWPLNI
IKSIGLPSQIKRKICLQLNESTLDFDAILEDASKAFSALSSELLGSDKWFFNNESSPSFLDVSLFAHAEIINHLPLKNDQLK
VVLGTHKNLTDLTTTRVRTLAGYTSAGPIALR
>Q0C9X8_ASPTN [(score: 2.80e-06, model: Metaxin1) Q0C9X8_ASPTN Putative uncharacterized protein.]
MVLELHIWGPFAFSLPSIDAQCLATIAYFSLVVPKDAWVLVASSDPTVSPTSASFSTSYATPSLTTTPDELPAKNGSTWVS
RFRNIVDYLRQYSHGEWLDLHKPTSTGDSQRRADSIASFLESRAQPLLDLSLYVTSQNYAQATAPALAALLHWPQW
LVPPRLHAAAKHRTAPLGLSALDLAAMDEQRTDLSAAVAAGHLPEAFHLNRALTAARDASAASAALARSQFRLDALTAD
LFAPLEALLAGGAYLLTDEPDGPTTLDCLATGYLALALVPDAAGATSRRERYENEKDGITPIV
>Q0V5D9_PHANO [(score: 3.90e-06, model: Metaxin1) Q0V5D9_PHANO Putative uncharacterized protein.]
MLELHTWGPFAFGLPSIDPECIATIAYCRRVIPNGFWSLVADYDTTVGATGTPKYPALSIFIAFLQSTAAPLIDLLLYVSA
ENYNTTSSAYTALLPWFANYTIPPKRRDIARSRTGHMGLSSLDVDTTGEAFAPGRGTASSDYEAAKRAAGIPTGGQPS
ALRMGRGKIGGFLGTPAYAARFRDLSNELDPVADLLGKTDFLLTEDRISLDCLAFLGYLSLLFYPAVPQAWVKETI
QTKFPRIASYIRRLRKDIFCDEDIKPADVWTISSGPPQASSGMLLPWQPRSQGMSSALDGAIEAGNLPLVSWFTQGTS
VVHMDYPLSSKNMRSSMPSVPVINTLLGATAAATIGFASLAIHRRSPREGALIFWALRPSTGFGEAGDILSIFANQMP
GAYSQF
>Q8T4F2_DROME [(score: 6.00e-06, model: Metaxin1) Q8T4F2_DROME AT01806p (CG5662-PA).]
MELEQNLTAAALMQSSAEEGKSEEAWPADAHLHQPAAEQLLLPERSSSCLAVKTFLRMCNLPFTEHISDNAEFMSPGGRLT
HLPLLRGVPKTFAEFEPIVAQVEAVQGGNCLDSWMSQDQDNIRCLVSYVENVFTLAEIHMSFVDEVNYQLYTATRCAA
AHPWPLSTIRRFKQKDAQKILKVYRWQDLNDQVIEVSI CADALIAELEEDQAKSYFGGSRPCKLDALVFGHVVAIMT
TKLPNMELAAVLATYPRLLAHCRRIDQSLFDGKLLTSAVEEQEDEMELEKIE
>Q9VW58_DROME [(score: 9.90e-06, model: Metaxin1) Q9VW58_DROME CG8004-PA (LD33138p).]
MTSQYLSQLITADKLSAEPWPEDATLYQPYEAEQILLPENASCLAVKAYLKM CNLPFLIRSCANAHEMSPGGRM TKLPFI
RAGAFIFAEFEPIVNFVEQKELAIQSWQDEDEKADMRTYVSLVENIFTMAELYISFKNERVYKEVTAPRNGVVPWPLNH
MONEYKRRNALRLLKVYQWDDLIDSDVIDKVAKCETLEYKLEKESPETPFYGDQPCELDAIAFGHLFSILTTTLPNMAL
AQTQVKFQHLVEFCRFVDEKYFQTRCLPN
>Q6CII7_KLULA [(score: 1.10e-05, model: Metaxin1) Q6CII7_KLULA Kluveromyces lactis strain NRRL Y-1140 chromosome F of strain NRRL Y-1140 of Kluveromyces lactis.]
MSGSKVLHLWGLNGEPSLVSPECIALCWLLKGGYVASGTVQVVYSNNTDLSPTGELPILIDTSAKITVGLYSIIIEHLVHD
NDVKLLSSALLQFISEELKTCTMYQLYLNPVNYEYTSKIYSYLLHWPFWYNTPLSARSRARELCR DIMVTIPEDEENES
TSNHQDELSEKATELAQSKVFKITRDSKRQQTKKLQELKNNSRFTTKLDNVL TNWESARQSLASAVLPADLV LVAHLKVQ
MALPQGDLLRSHLRNQYPSLYDKVNELEKYDNVSPVNRDPTFSESGNVVTSTCYFLRTFV
>MTX2_CAEEEL [(score: 3.60e-05, model: Metaxin1) MTX2_CAEEEL Metaxin-2 homolog.]
MSSSGVITQLVTDALSMNAAQDWEDVSLFTPYLNDQALMYDFADCLAVQTFLRMTSLPFNVRQRPNVDFISPDGVPPLK
INKTLITGFNAIVDFVHKKGVTLTSHLSETQVADMRIANISMIEHLLTTVEKFVLWNHDETYDKVTKLRYGVSVYHWPLSSV
LPFVKRRKILEELSDKDWDTKTMDVEGQADKVFRAQSAQLGSQKYLTDLPTEADALLFGHMYTLITVR
>Q1ZZ46_ASPNG [(score: 3.70e-05, model: Metaxin1) Q1ZZ46_ASPNG Putative uncharacterized protein.]
MVLELHIWGPFAFSLPSIDAQCLAAITYLSLTVPKDAWVLVASSDPSVSPTELPALRNGSTWVSRFRNIVDYLRQYSNGD
WLDLQGLSGIEKADNTAFSAFLESRAQSLLDLSLYVTSQNYNCTSPSYGAILQWPNQWILPPKLHSAAKTRTEHLGLSS
LDIQAIEDQRKRHSAVAAGQIPKNLIPQPRDTSVSSLLGKTAQQG
>Q6C8L9_YARLI [(score: 4.50e-05, model: Metaxin1) Q6C8L9_YARLI Yarrowia lipolytica chromosome D of strain CLIB122 of Yarrowia lipolytica.]
MFRLHVWGPVSTSLTFSAPCLATIYWMQLCDIDFTVVQSSNEGLAGELPCLTSEKKIGGAESIIRYLKSLGHNLADALT
SDEQIKNTALLAYMSSLQITITEYCLFVDEEAYQKVTRPMFNEFMPFLMQYNVSVRLREQAKDRCCAAGIDTATPSWAVSA
TKMASESLTNPKPSMGKLYDQSVEREKQKDAKAVSKTVFRLLNSATEIYTDMMDTATANVAKGSLFSTVSTSDVFLCAH
LQLQMLPALPDCAVAGLLKSKFPALLQYEDVFVEKIGNKDLKVEGPLGKDAPLWIYHLKQILGWY

>SAM37_YEAST [(score: 3.70e-04, model: Metaxin1) SAM37_YEAST Sorting assembly machinery 37 kDa subunit (Mitochondrial 37 kDa outer membrane protein) (MAS37 protein).]
MVKGSVHLWKGDKGKASLISVDSIALVWFIKLCCTSEEAKSMVAGLQIVFSNNTDLSSDGKLPVLILDNGTKVSGYVNIQVQF
LHKNICTSKYEKGTDYEDDLAIVRKKDRLLLEYSLLNYVDVEISRLTDYQLFLNFKNYNEYTKKLFKSKLLYFPMWYNTPLQ
LRSQARENCEEIIIGSLTLEDDEEFVESKAMESASQLAQSKTFKIAHKNKIKGKQELQOVKYNLQFDNRLQSCVSNWLAAR
KKLDDSVILSSDLLFLANLYVQLGLPDGNRIRSKLEQTFGSELLNSMSNKIDDFVHRPSNNLEQRDPQFREQGNVMSLY
NLACKYI
>A2QRI9_ASPNG [(score: 4.40e-04, model: Metaxin1) A2QRI9_ASPNG Function: human Metaxin participates in preprotein import into mitochondria.]
MSVQMALPRPQVGLIVPRPQAGFGNGCASLLRQVLPLEAKVDQDAHHEWNDERLERVGPATDSNERKVSRRWDGFORRG
RDEGQPGVAEGLLGTTRMLQOVITNPQEINWARTDLFLCSSNTNKPSTSRLLAGPVANSPALSNWPRLPPCLLNPLR
SPLHPSINPMTPEYRDDPGQTPDNVSTVSRARDFFSVPTPIKRIFDRFPLVTYPSNDLPHSAWSDKRGNRLYVFTDAASA
RHGRPSFNPQCLKWQAYLRFVGDVDPVIPSNNHASPSGALPFLIPAHPINNNAPIPSSKLOKWAIEQVHCEEEQQLDLRF
EVYASLLDHRIRNAWLYTLYLDPEEFEAVARPLYVNPSSSTNSAVRTALALQLOQAARTEILKTSSYIDVGALEAEANDAF
EALSTLLGDNQHFDRPNPGLFDASVFAYTHLILEEKLGRNRRLGQLLRQHENLVQHRDRLLKFF
>A3LTE5_PICST [(score: 5.90e-04, model: Metaxin1) A3LTE5_PICST Predicted protein.]
MIQLHVWGCSTEISVISPECLAASWLLTDSLNTSEEYIEVTSSTNVSDIGKLPVLTTAERKLGQFEEISKYILETYGD
TNFVSKELSTHNQVLNKALIAKLQYKVEYIHQYNMFVNSRNYEKYTTKLFQKYLFPMMYNQPLKLHQNAQEQQVQLLGLN
KNKTGFFDFSGSVNNSEIAETEYINDENEEQDEVALSALHERQLVAKSKEKSLRESKNSLKCLHLLNDYLDYFSKLYEK
LNGNKNSYGFIFDQKRASSCEILLCAVYVSLTYEDLPDRFIYNYLKIKRPDFTEFIATCTQRWNTQLQIEDAVRGPENEE
TPSLWNEVKYQTGIVHY
>Q0D0L7_ASPTN [(score: 6.20e-04, model: Metaxin1) Q0D0L7_ASPTN Putative uncharacterized protein.]
MTTDSRDPSGQAPANGTVSRARDYFVSPAPIKRFFDHFPVTPPNDLPQRALSSRRGNRLFVFTDAAGARHGSPSFNPQ
CLKWQAYLRFVGIQFVDPVPSNNHASPTGSLPFLHPALPIGTNAPIPSHKLQKWAIEQVHCEEEQQLNLRFEVYASLLDHR
IRNAWLYALYLDNENFGAVARRLYVDATTTNPLVRAALAFELRQAAQTELKTSQYVDASALEAEAGEAFEALSTLLGDD
QHFFARPNGPLFDASVFAYTHLILDDKMGWKQNRGLGQLLKQHTNLVQHRERLLSFF
>A5DUS1_LODEL [(score: 6.40e-04, model: Metaxin1) A5DUS1_LODEL Putative uncharacterized protein.]
MIQLHVWGLQDKVSIISPQCVASVWLACLVLDSKAFEVVTSNNTNLSTSGEFPILLLENGQCISGYLAIALYLLSNYTSL
ETLQVLNRRQQLINVGLVSQLTETLEIINQYNLFINTTNYEKYTRKLLSNFYFPMMYNLSLSFYNTAQKVKLLGLDKS
KTSLSFNFSNNADVVAETETVNSEQSDSEVGEETNGKISGLHERYLLQKSKTKEVLKESKASMRCLMKVEKYVNEIE
SLKESENGKEEKRDEEKEKEKEKDDNQKNNRENSYIFGNLPSSGDILFLACIYCLTSKEIPDRFIQDYLLSSQKASFSET
AKLKIDELQKNTITNCTIRPPKGREIPSLYNEVMYWTGYVKY
>A5DPS2_PICGU [(score: 8.10e-04, model: Metaxin1) A5DPS2_PICGU Putative uncharacterized protein.]
MVDYELHVWGCCKSISVVFPECLAAAWLVTTTCIPHEKINIVTSLNTNLSTGVLPLVLLTKDVSYEGFGPISSFILSEFSG
KNVIETKDLAQSAVILLIENKLVRVHQFNLYSNLKNYEGYTRKQFKKYLFPMMYNQPLKLYNVAQDQVRMAGLLPSPPG
LFGVFSGSSGPHDEVEETSEVALSALHERQMTAKSNKRELLRQSKNSLKCLNYLGEILDDIVKLNHQLNPHRPDDTFAL
IFNESKISVAELLLFAYIHSPTYDGLPDHAIHDYIRLKYLSFADFSQTKINELNQLLDDSAIQPPNSSQVPNLINEVRYR
LGY
>Q7S734_NEUCR [(score: 8.40e-04, model: Metaxin1) Q7S734_NEUCR Predicted protein (Putative uncharacterized protein G11A3.010).]
MATTSAAPPRKWWQVPRPLOKVFDTFPLLAYDVNALPARAQSATSGDLPTLYVFSTEEALLGAPSFNPNCLKWQAFKL
LAGVKFQILPSTNHASPTGALPFILPTRSSPTDAPSPIPSSKLHDYALKYGTSNPPEVSALRLDAYQALLDVPVIRNAWLO
ALYRDPEYTDLLDRFYITPASSYVWRGALRHQLRRAAETEILKTGPGGAASTAVSLLVDEHSVYRAAVQALEALATLLS
ESKTGWFFGAETPTIFDASVFAYTHLMLKYMSDAEGEVEGNMGFILASRKLGTMVRSAGSGELEQHRRRLFELLWLADSN
AELLDAKARGNKLLQFQLQA
>A1D2A2_NEOFI [(score: 1.50e-03, model: Metaxin1) A1D2A2_NEOFI Mitochondrial outer membrane protein (Sam35), putative.]
MTPDNRTSGQAPEDTPSSRARDFFSVAPAPIKRIFDRFPLVTYPSNDLPHHSGIARRGNRLFVFTDPASARRGRPSFNPQ
CLKWQAYLRFVGIIDLEIVPSNNHASPTGALPFLPALPAATTGPIPSNKLQKWAIEQVHCEEEQQLDVRFEVYASLLDHR

IRNAWLYMLYLDKDNFEAVARRLYVDPSTSNCAVRAALAMQLOHAARDELLRTSAYVDVIALEADAADAFAEALSTLLGDN
EHFFNRPNPGLFDASVFAYTHLILDEEMGWKQNRGELLRQHENLVQHRDRLLRFF
>Q6BJD7_DEBHA [(score: 2.40e-03, model: Metaxin1) Q6BJD7_DEBHA *Debaryomyces
hansenii* chromosome G of strain CBS767 of *Debaryomyces hansenii*.]
MIELHVWGHSTISVISPECLASSWLLNLHLKPQNIPIFKIVTSSNTNLSETDKLPLLLVSNEECASERYEGFHNISQYIS
SNFDTEHSTGNDIKYVPNHNLSSEQKLINSSLTSEFIENKIHNISQYNYLYINTKNEYKYTRKLFQKFFPFPMYNOPLKF
YHSAQRQVQVIGLNSNPGFFSISGSEAVAQTEYFNDEDDDDAEADPVAISSLHEKQLLAKSKRKDLLKESRNSLKCLN
LVNEYIDYVVLVLYQELNSFNKPDEFSYLFSDKASNAISSSELLFFAYIHSLCLPELPDKFIVNYLTLKYPKFLTFIYDFT
SKLNESLYKEKSIIFREPEGIEVPNLWNELIYSTGYVKY
>Q5BFM3_EMENI [(score: 2.60e-03, model: Metaxin1) Q5BFM3_EMENI Putative
uncharacterized protein.]
MTSNYDDHDLPPQQRPSRRAPRRVRDFFSVPAVVKRVFDRFPLLTYPANDLPHHAGSGRSGNQLFVVIDAAGARRGRPSF
NPQCLKWQAYLRFMGIDFELVPSNNHASPSGFLPFLPALPVGTDAPIPSNKLQNWAIIEEVHCEEEQQLNVRFEVYSSLL
DTRIRNAWLYHLYLNHENFEAVARRLYVDPSTTNTAVRFALAAQLOQAARDELLKSSPYIDAGALEAEAAEAFEALSTVL
GDKDYFFERPMPGLFDASVFAYTHLILDQKMGWKYNRLOQLLSQYKNLVQHRARLLEFF
>Q6FU46_CANGA [(score: 2.80e-03, model: Metaxin1) Q6FU46_CANGA Similar to
sp|P50110 *Saccharomyces cerevisiae* YMR060c TOM37.]
MTGSVLYLWKGDRASGISGESIALEWYLKSKALREVEIVFANNTDISPLGRPLVVKVCSNGDYIHGFLNIVDYLEPKRKD
EFTDMEKLMELMSAMSQDLSNLKTLNEYQLYLDKNNYITFTRKELSQLLYFPFNFAAYEYRNRAKEQCVDLEYLPVEEKE
DEDEDGPDAMELAKSQTALRGLRKRQRAEELKSVRLNRNYMHKLEFLDQWDSITDDLPKTSPVPIILFYSYMIIQLVI
LPNNNEICKYLKEMKSNGYVDTLKETFTKYNALDFNLNVREPVFREGRGLISTLLNKISV
>Q4WSD2_ASPFU [(score: 2.90e-03, model: Metaxin1) Q4WSD2_ASPFU Mitochondrial
outer membrane protein (Sam35), putative.]
MSPDNHGASVQATEDTPSSRRARDFFSVPAPVKRIFDRFPLVITYPSNDLPHHSGIARRGNRLFVFTDPASARRGRPSFNPO
CLKWQAYLKFVGDLELVPSNNHASPTGALPFLPALPAATTGPIPSNKLQKWAIEQVHCEEEQQLDVRFEVYASLLDHR
IRNAWLYMLYLDKDNFEAVARRLYVDPSTSNCAVRAALAMQLOQAARDELLKTSAYVDVVALEADAADAFAEALSTLLGEN
DHFFNRPNPGLFDASVFAYTHLILDEMGWKQNRGELLRQHKNLVQHRNRLLRFF
>Q0UDF6_PHANO [(score: 3.50e-03, model: Metaxin1) Q0UDF6_PHANO Putative
uncharacterized protein.]
MSHTEEDKEPTPQSHNAPAQRSSRSLAVPTPIKQLFDIFPLLTYPVNDLPQRAPQDRNKHVLYIFTSEDGALKGLPSYN
PACLKWQAYLKFISKIDFRIASANNHASPSGALPFIIPASPEPYKHIQVPVSGKLQWAMNNSKKAWEPEGDLRYEAYLSL
LDHRIRRAWLYCIYLSHNSTIAEPLYILPSSGNPFVRLTIARELRTAAEKELKFSVINASTLYSQAEFAALETLL
DKDDWFFGAPGGLFDASVFAYTHLLLDGLGKGLDTRLRDLALMSRKRLTSHRNRIILSTYFPGQS
>Q759Y7_ASHGO [(score: 3.80e-03, model: Metaxin1) Q759Y7_ASHGO ADR136Cp.]
MATIHLWGVGDGAPALISPECIALFWLVNTCEVECTVVFSSNAHLSPREELPLYVGEDGSAAYEYPEIVEQLLGLRELGLEE
RSLVCWAAERCGALSDYQLYLNRKNYEQYTRRVFSQLLPWPLWYNTPVQRRERARAQRGGTPAPAHDAEKELAQHSKTLQ
ATRELREGERKALADAAAEYAAALDRALQPWIAVRGAAATLGAPELLFAAHLVYVQQQLPDGARVTAHLRAHYPALCDG
LLRACELHACAPRAAAVAVRAPTAAETPSVPRELYRYVTSYWTI
>A1CPE3_ASPCL [(score: 4.50e-03, model: Metaxin1) A1CPE3_ASPCL Mitochondrial
outer membrane protein (Sam35), putative.]
MAPDNRGPSDQASDHTTASRRARDFFSVPTPIKRIFDQFPLVITYGPNDLPYRSGLERGNRLFVFTDPARARRGRPSFNPO
CLKWQAYLRFVGDVETVPSNNHASPTGALPFLPALPAGTSSPISSKLQKWAIEQVHCEEEQQLNLRFEVYGSLLDHR
IRNAWLYTLYLDQENFTAVARRLYVDPSTSNFAVRAALSMQLOQAARDELLKTSAYVDAAALEADAADAFAEALSALLGDN
LHFFDRPNPGLFDASVFAYTHLILDEMGWKQNRGELLRQHENLVQHRERLLKFF
>Q2HGR1_CHAGB [(score: 5.60e-03, model: Metaxin1) Q2HGR1_CHAGB Putative
uncharacterized protein.]
MRTLVVQATVFPVSYLPAMVLDEAAALFPFTLIDFVAPGPGSLSVEQQLASLGPPLHCAESFWLNSAQRSGPLKYCRVT
PGESEVVGSGTLPWALLDPHVGGDAVFYQGRASHGISGALYLARGKSILLPTGFFAYSSDAADENNAACRALDEGPHLP
WRSIVTRSAAQDICEFPHYLEGCSAIDMAKARAAEPQLASAGRWRGVEGPGFSAPSSAPGEKNSGHLTIPIGKTPKL
LLAFGLSGPEFGRENVTKKGKSARSSSGTFRDLRRNLYAQAGEKPHPGRCVLSARSCGSRFAPYGEETEENPRIGTFT
FTTTLRRAYLQFAERNRTARPLSSKSPFTGMSSITSPASSWRKMQIPRPLQQLFDHFLPQTYEPNHLPEQSHLTSSDLP
TLYIFSTDADARLGLPSFNPGCLKWQTLRLAKLDFRTLPTSNHASPTGSLPFLPPRTSPTTAPLPIPASNLLAYAQRS
QPPTGDLDPDLPPRSQAYLSLNLRSALWLYALYLDPSHAALLRQLYIRPASSRQVQAALLYQLRRAAAEQIATTSAG
GGKIVSLAPVASVEGIDEEAVYRSAREALEALASLLSQSETGWFFGRERPGVFDAAALFSYTHLMMEYMPEEGGSAGEGTG
VALGRMVLGAGDGELARHRERMLQTAWPGWDGYRK

>Q4SGB1_TETNG [(score: 8.20e-03, model: Metaxin1) Q4SGB1_TETNG Chromosome 17 SCAF14597, whole genome shotgun sequence.]
MSLAEEAFVSQIAAAEPWPESATLYQPLKEDQILLSDCASSLAVQAYLRMCGLPVEVVCKANA EYMSPSGKIPFIHVGNQ
VVSELGPVQFTKAKGHSLSLSDGLDDVQRAEMKAYMELVNNMLLTAELYIQWCDDATAAEVCLDYLLKKREKSVFIILTSL
IKVFFQITRPRYSSPYSWPLSLLAYLSAAKLSPKDWEHNHSSLINSRFLFPYILVHMFISTEINTKCMYVTGRQNWML
WCSATSSPSSPPDSRAQSWQGRSRATATCCPSAGASNRLTLKTRAPEGWK
>A4RI50_MAGGR [(score: 8.60e-03, model: Metaxin1) A4RI50_MAGGR Putative uncharacterized protein.]
MSSYNVATYLWMYGKKA AAIKLNITLAEMSFFHPNLVKKHVHLATQLLVGNAQMAEQLOQPAQGTTPPKTSAASASSA
ATPGYTIFPGRIAPLQKLFARFPLYTYPANDLPARCPRPRESSSSNNSLPTLFVVISDDDAAKGRPSFNPTCLKWQTF
RIAGVEVQILPSTNHASPTGALPFLPSSSPTPI PANKLOAYAAAATKANNNSSQQQPEPTTILAKESEALYTSLVDPHPIR
RAWLHTLYLDPANTQLLTSYLSPASRSPLAQRALHAQLRAAAHAELAASHNGVDCPAPETLRADAARAFASLGAELLAG
SGREWFTGAAGPGLLDAAVFAYTHLLALPWGDRSLAEALAAEAPALVDHRDRMLERLWGGGGGAEDCGASVEWEKI
>Q6CMW8_KLULA [(score: 1.40e-178, model: Sam35) Q6CMW8_KLULA Similar to sp|P14693 Saccharomyces cerevisiae YHR083w hypothetical protein singleton.]
MVSILAVPGPLKTFDFKFLKTFEYVNDKAMDYQISQRSAYFEGPDAVQSSKDDVDFQLGVYQIVRDSSETGVLLASDPW
GLFAELSLSKNNLKL PSEGFNANGTNAPTKRRLQHSMCVLSPRASVTKSLPILVEGFTRKRHVRSTESINEILYSRIATG
EHTMYLKLINTIVDGYIVDLLCNVPSNKFCELYAHINERETSITNWVTIQDTKTITILERNGFQIRHEVLSKYLVELKYP
IRTPRVTLAELSENIILETINCLERLQTHWKSSKSEPDSTTNLNKYQYIDLALVSYILAIQAQLGSESVLNQWLQTNQO
YLLQYSYQLLKKCS
>SAM35_YEAST [(score: 1.60e-178, model: Sam35) SAM35_YEAST Sorting assembly machinery 35 kDa subunit (TOB complex 38 kDa subunit) (Mitochondrial 38 kDa outer membrane protein).]
MVSSFSVPMPVKRIFDTFPLQTYAAQTDKDEAVALEIQRRSYTFTERRGGSSSELTVEGTYKLGVYNVFLEANTGAALATD
PWCLFVQALALCQKNGLVLPHTSQEQTPSHTCNHEMLVLSRLSNPDEALPILVEGYKKRIIRSTVAISEIMRSRILDDAEQ
LMYYTLLDFTVLYDCWITQIIFCASDAQFMELYSQKLSGSIVTPLDVENSLQKLSAKSLKISLTKRNKFQFRHREIVKS
MOGVYHNHNSVNVQEQVLNVLFENSKQVLLGLKDMKSDGQPTYLHLKIASYILCITNVKEPIKLTFFVENECKELVQFA
QDTLKNFVQ
>Q6BK36_DEBHA [(score: 9.10e-172, model: Sam35) Q6BK36_DEBHA Debaryomyces hansenii chromosome F of strain CBS767 of Debaryomyces hansenii.]
MFEVPKPIKKVFDTFPLYTYDPIPNNTPSNFQSIENKFYFTSSNDQAKDNACFTLGVHNIYLVNTANGEKKIPSDPISF
GHALILCHKNDLKL PSSGDNVGSKSKHSIMKLSYHASPNDQLPILIEDDLKSQTRNIRSSLSMNQSVKVNNSNFSENALAR
IINELVDTELADLWILCLLSDLPSSNPLVFNKLFKLD EETKSTFTNKITIMSILNEIPRWGSFHLRYSYLFDHRSRTKSF
INMPLRLLSEDI LEVFANTNNESIRKAYNDKLKEFEINLELLIDYIKESDSNEQKKI IELKLVGFIIIMDSLNTKLHEV
LSKEKFFSSFVKLCYEIIALFPNLYKAFI
>Q6FSA5_CANGA [(score: 4.30e-168, model: Sam35) Q6FSA5_CANGA Similar to sp|P14693 Saccharomyces cerevisiae YHR083w.]
MSSTTMKVPTPVKWFDRFPVQYQTI PQSKAIAYS DTVNRCFEFRDVKSSMHNPEYDGGNSKNDNSGNDNFQLGVS
VHGFEIGGTDVMLARDPLCLYAQLSLCKKNNLRLPTKFEEGNNEKKNQPKLDAESTLDSHFTTDVAGIRKPGNKVVILSEKA
HKDERLPILIEFTMNGQSKNIKRYVRSMDSIMIILDSKLESAELAIGNLLDFTVYDAFLLCTIHNHLVYETYGCSPDTLH
TLSKRNRFFTRHPQISSLSLQIYTPSPSDLEKQLAMAKDILLLLQSTHDKFSDYLRLKVASYVLALLHLPSFGEFLRAE
CSKLLDDSTTIVKDFV
>Q759H5_ASHGO [(score: 3.00e-148, model: Sam35) Q759H5_ASHGO ADR303Wp.]
MHTLTQVPAPIKQLFDALPLSQYGPVPATDDATLNDHAVRSYFPRGGPTDNQPTFRLGVYAVVEHESGAFLAPDPWCLLA
QLAVCKRNGLLLP TSTSAPSKGSCVLLLSRYAAADRQLPLL VETSSRAQRGAGAVHDAVAARITDPHAALLATLLNSTVY
DAYMATLLFELPDSELLRLYGVSAEPPLRVFAARTLRLALAFRNSFQVRNARLVSHAGAFPTPATAPARPLLDVLQARG
SRTLLOQLLHDGQFFPAPSDCGPGYLDLAVASYVFAISLLRSSALHQYLAKHCQPLCRHAAARVISCYT
>Q6C5Q4_YARLI [(score: 7.80e-141, model: Sam35) Q6C5Q4_YARLI Similarity.]
MLKVPAPIKTFDFAPLEKLPPELVSETDSNACQVVGGSSTQSPDFYLYTYGHKNGVGTTLSTEPTSLAVQLLSHFHPK
KSTQLATVSHLANMDGKLP LLVQPSNRFTLTFNSIYKNLVPLTPQINVLSL VFNHLYHAWIVTILDPAYSROFENTFL
SVKLESNTSEARFVEPLKIRFMQDLITDHKNLATAMEQSTRLPTRLVMSMESVYDSHPEIEEIEY CRAHDALTAFSKLLAE
SPSQFFNAKDKGFEQSEIGSLDCVVAAFIYSLRPESPFQTRLGHRMVQDFPDLSSHAVSVIEEVYKKN
>Q59ZS4_CANAL [(score: 2.90e-105, model: Sam35) Q59ZS4_CANAL Possible mitochondrial protein.]

MNVPATIKSLFDVVPLVITYKDERLPHKGPNYPFSEEFVAVHNVFNCKGMIIPDPIISLGIVLVLAHKNKLALPTEQGYG
RGGIITTSFHASPTNTLPLLIDQTTTRLDEINHTVANDLDEPAKLINEIIDTKFYDIWVLCILCEDIATTIFGVDTL SKL
DLLAEVFNWNNFAVRHPNTNIPKLYSQQLVEFEEYLDLLESYDHPIINLKLAGYIIVINQLLSSTRLGKIVCTKHALLSR
SYSLLNLHTTI

>A5DCQ6_PICGU [(score: 1.10e-35, model: Sam35) A5DCQ6_PICGU Putative
uncharacterized protein.]

MSRLQVPQWVKSVDTFPLSTYEATPLGDHSDIEKSRFYFISDDPEKAPDHNFILGVDGVIGVNLKIIPSTPVALAHSLI
LCYKNGLKLPRENSKSKTSPHSILSLSYLAASNNELPIIIETNERTQVRNTIPKKGLLASIVTNNNFESDPKAKLINSMV
DSCIQDLWILTLICDPQGKNKYERIFNWNAGAKKSGNMTFLQTLAVQEEIPEWNDIRTRNPNLFPGKIWNALDQEALQIV
YQDKLKQFEQELPLLEIYATGHDPLTKIISFKLVALAILANEILPETGLANLVQQHQNFVTCYNIIDEY

>A3LWP5_PICST [(score: 1.40e-24, model: Sam35) A3LWP5_PICST Predicted protein.
]

MFDIPESVKKLFDTFPLTTYPAIPKTTSGNDEFIEKKFYFENEKQSQISTNASFSLGVHNVVEFKGQDGKRKYIPSDPV
SLGQALILCHKNKLKLPSTTSSTNRSCNSIMKVSFHASPKQLPILIEDDKQSRRTIRTISSIIETVAKSNFQKHPYLD AEL
LVLNDFIDLKFLDLWILCLLNENIDRFDEIFDIDSKLDLSFVAKSLVINNIYSEVEHWRAFTRNPNLFDYMELLLSTN

>A5E230_LODEL [(score: 2.50e-23, model: Sam35) A5E230_LODEL Putative
uncharacterized protein.]

MFSVPSPIKRVFDSVPLQVYKNGGETVQPHNLYSFSKVSELGSGPTFVVGVYNTFEYRISTSSQDSVILPTDPI SLATIL
ILARKNGCGLPSSGAKGPSGIVRIPFRGSPFNLSLPILISGDETRSIESAETIKSTITKNNIKNLDLKFISDYVDKSLYDL
WILCLLAEELDISVYSKIFSINDQLELHDLKTEMVKWNNLSLRHPSLFFERQQKHKNLYNFYISELDQFDTNMNWFSEILE
KPEGDNWIIYYKIASFVIIVNQFLQSTKLGAVVVGKPDLVAKCYKVLESI

>Q5ALP4_CANAL [(score: 3.70e-145, model: Sam37) Q5ALP4_CANAL Putative
uncharacterized protein TOM37.]

MLQLHVWGKDNEISIIISPSCIASAYLLNQVLTPQNI EF EII PSNNTNLS DINQLPVLIDNETKEKYNGYNEIIRFIESKY
LSTSTKLSLVSYLPSDSLKTTKEKLINKGLINLLINKFEYINQYNLYLNNKNYENYTRKLFSSYLPFPMMYNQPSKYAQ
AQEQVKILGLSKQKVSFFDFTTGNNEQGSIDVAPTELINDEDDEEGDEDEDGANVAISSLHERQLLKSKSKQVLKESRN
SMKCLILITQYIERFKTIFQHQRDSDEEFGFIFNNQNPSSSEILFYAYIFCLTYEKL PDRFIFNYLKLKQDYTLKFITE
IMNKNQISKKNFRNPIGNEIPSLTNEVKYWIGSIEY