

TOM complex:

>Tom40 Contig13048 (complete), 361 aa, 1B8C

MDKLPTPPAAAPSALPSVPMPLPPLAGAGSPSEPIAPAETHKEAPPSF
WRRVLDHGPLPYPGKFDLDSKESKILDSRENFDGFNFVSRITITANFDM
THAIHFGSQTEPPSYNFMTRYFSPTGMFLDGKLSPPGMLLNGTVQGRIAF
PLKTWYRTTPGGRSKPVSKLSLRLTGVVGKPSAKPIPPQFNMELDMKGS
YQAQFKWHNPGMYELSYAQSHPNVALGLHGLFDSRMGRTELTAAGRVAW
NGRKCIATASMASYGHLTSSYTQVMEDGRKSWSTDMQLIHLEDHGVEAV
YSAGYAYNLLQSRVRGRVDSNWCCSAILEEKVLDVTLLICGDMNYAKDV
YKVGFGFSFHL

>hypothetical protein (likely Tom22) Contig16787 (complete), 120 aa, F89

MVRLNIEELKQPQKKGFFSGISGLPEPVRVANTWSNGLYAASMYAQOGLG
YVSSFAWIFATAAVVIYLP LLRAMSDRETIRAIRAEMVQKTAGMVPGAA
PRGPD LGNLDISGLDFKIQ

>TOM7 Contig18214 NOT DETECTED, 64 aa, E0

MTLGGLDLEVM SAKAARLYDKAVVVARVGFHWGFIPFIIIFLGVRSMRREQ
SWLSLLVPTPYLQA

SAM complex:

>Sam50 Contig10559 (complete), 446 aa, 2628

MSYTDDEPIDLGVGEDAWRVRRVWVKGNRRTRPDVVAACVKPVLKART
FDEVLARVAEAAAGELKGLGIFKSVNLVLDLDDLVAAADPSACDLRVELV
EHKLTRIEVKTSTTVGENEPDVQATVGLCNAFGRAETVSVAQV GASNR
EHWSSAFSLAFKRPVVGQGPGRHIEADATRASHRLPWCALQTTHGLAL
RYSLSHQVSYEASARHVIPESSAPLALRSHAGHSLKSAVKYVYAHDRD
DPLTPTTGHAFTSSTELAGLGGDVRVFKQEMAAQLNPLGKTRCSFNVLA
KAGYLHALDSGSRIVDRFFLGGPGSIRGFQYNAVGPSHQQRALGGGAYWA
GSLHLSFPLPLRDVPDFVSGHLFANAGNLRQPTPGRSVAANVQDLFSADD
VRAAVGAGLVLRMTMFRVNLNLSHPIRKAATDLVQPFQVGLSVRFL

>metaxin-like protein Contig19964 (complete), 292 aa, 1111

MHLSLLEEGSLPCLALLFILGAIGARAVFRFLREEPEPKTSDVIDRGDSS
VTHIKLHTFKQPASAQTACSLSPFCEKLELFLRMAALDFKAIDGNVVTAP
KAKLPMIEHGENLVPDSELAIRYLINTFGENKTHLGRIRIKLTPEEQARS
VLLTNVTNDSLYQLLLHARVWDLVWVNVKGLYFGDLPLPFRLIIVPSIR
RNMVGWLWGHGYSRYSQKDRVWLARREIDALATILGDHPYFNGDEPTPVD
AAVFGILDNCIYGIGSVYGIRDHVQTKKNLVAFVEGIRQEFF

>metaxin 1 Contig18718 (and 15904, 11378) (complete), 295 aa, 19E7

MASSSSAAPAVLKLHQYGARWELPSFDPFCLSAQAYMRLAGVTFEEVPSN
NPDVSPTSNLPLVQLGDDYVAGTNAIFTYVGNKTGKSLDSALNAEQKATA
AAFIIHLIETKLHPTLLYNWAAEKQNMGTLLVLPHFNSMVFP LGYVLPRLK
QRNVQSYLYTLNLQDEKVVNDAAECCYAALADFLGDKHFFF GDS PSSLDA
VAFGHLAIHLVAPQSHKLRSLLOHKNLEAFCKRVMTLYLGQDFPAIPAP
PPATEDKDQKQEMSOHKKTGMYYLLTGAGLLILLHYLTKQHQA AHQ

>mitochondrial distribution and morphology 10 (MDM10) Contig673 (and 7019) (likely complete), 375 aa, 23FF

MDFEEAPEELPNNPGDYEGVDGRSTGIIDFDAMPFGFRWGSQISSRFER
SIRLMILPPFP TIGFSYSSRPMSMHQAMEEAMAREMEALHDEEDAGEGQ
AEGEAESAEEAKPLLRPLDVAVLSKAGAEVTERPDNDNTTSEDEEEEEE
EEAEQKESGGHFMLS AEATFDGMVQGMQRFNKNWSTRHMILTSMEPGR
SMLMSSLSYSGGSFTSKLSWSSERDRACFSHQAITQRLSVGGEVGYAMK
DKQPVGWSVGGRYVIRKEEGKFAATHITATYNHLGRVKTYYTLPFSETV
FASARYTVNAF SFKSNMAVGVESWPSATMPLMTKAKWDTDKGFGVSLGAH
LGLAALMFSASYGKDGPMVGLHFEL

>Mdm12 Contig7451 (and 3688) NOT DETECTED, 255 aa, 134F

MSFKIYWRMGEEQAAMKDYLN AFFSSAPKPEFIGDIAITALTGDKAP
EVRLIDVSDPPAHFSSLPMNDAPSSLDSPATTARTTSCRQFDGSDRHIVI
IASSSSSSSSSSTTTEPEVKATDMDMMIKVFLEYSGTAKLTMRCLISL

VNWPRPRTVCLPVTFTLSDFHFEGVVCAIHHANKVHFCDKREGDDVGPL
KSLKIEAQIGDSTQQVLKNLEKVENFIVGMLKLIKDRILIFPNFITVLDQ
TNKAH

>maintenance of mitochondrial morphology 1 homolog Contig7284 (uncertain of completeness), 327
aa, 1C78

MELLSIVIGFLLGLVAAGAGVAYTLFVLLFRRRTDAPLPLAPAPSFAPQL
ASALLADAAVSEDLELFKAEWLNLFAGRIFAEVSTPAFQEHTRWLLTEK
LNAVDPKPNLIGPIVIEDFSFGTGVPRIEGVA SFKTGKELELVLDVSYDGG
ALFAVQTELWLNLP TLERLASLPVMSVSLAHFRGRVSLTVPLESDPECT
LAFAEEPQLDFRIGSLIGYDYQLRDVPKISNFIINKIRSVIREEAVLPKA
FSFHLPLSGRPLDLKQVLRPPRELRRNTVEELKEAAVSASKAKLRERVKR
EKDSRKGRDAEENAVVVLNTRSALVRT

>mitochondrial distribution and morphology 34 MDM34 Contig6411 (complete), 245 aa, 8EA

MSFQIEWPTLDEITLEKIKAQITEVMNKGELPDAICDVMRVTDLDLGNIA
PTLQFMDIPDVSEDFEGHFKVAYAGNGSITLQTKVQVNPFAAKTVPSKR
ALRHLGGLIAHEPMVPLRITISQVRIDGDLV LNIKKRAKAHDPRSDGSL
ILENTNTAVSAPAA DSELSIPHIAAQFKVDPLQSVNISSSFDDFGSVKDY
LQEQVEGSLRKL FVEDFPQIVSGINKQLETA AHAKHNTVVVLAPK

Tiny Tims:

>Tim9 Contig18985 (complete), 106 aa, 20D7

MDIAPDAKKSEAAARNMVQLMNMOMKSVLGMFNMSERCFRLCMKNVDD
DAPITTKEDSCIKNCTEKWQRYSORVQLIFAEENTRANTKADLMQDRPSS
NLEGQD

>Tim9a Contig4832 NOT DETECTED, 88 aa, A34

MQRGRMSKDDEASISQMMERMOMEDIITHYNRLADTCFTQCVGDFKSNAL
LQNEEVCVRRRCVEKFTQFSTRFQRFVVDHQTAAANKQRO

>Tim9b Contig26620 NOT DETECTED, 127 aa, 2699

MGNRQFGMGYGMGAGQSRAGSASDEERMMQVMMSMOMQDYLTMYNSTTE
KCFKKCVFNLRTPQLVEKEEVCLNRCIEKMSHYNLRFOQKVGAEASAALRE
QQQKEAEQKQPPTEAAQADKEAPSSK

>Tim8 Contig15686 (and 20235) (complete), 84 aa, E76

MDDTTLRQRAAALQAEVMIQVSVLATTDDCWKVCMKGKTSFGTTLNKNEK
ECFHNCTMATVQSENFLTKRTAQHIEQQARQSGH

>Tim8 Contig5911 (complete), 83 aa, CCA

MDHTTLARNLQAIQVAVESQKQLMETTDFCWPICMRNARIGTELDRSQKV
CFSNCVVRSIDAERMIAQRVLVAMKQSSTGEAE

>Tim13 Contig20011 (complete), 91 aa, 45A

MAQITDQORADFYRKQEE SVGQQLFQOMVQTTKNRCFKTCVTRPGAALSK
DEQKCLINCVDRFFEARAIVMHSYNKVYQSMQOQEGGSDEF

>Tim10a Contig2235 NOT DETECTED, 106 aa, 2360

MNGQPMPSGMSEQEREDVLAASEFITIQMDLYNRVLRGRCWDKICIAHYWDK
DLTVGEGSCVDRCVVKYMTVQRTVAKRVLGIRAWTKREEERQKVIQKLRD
NHFFGV

>Tim10b Contig8351 NOT DETECTED, 84 aa, 14D6

MSNEQYMTREQMLASAOQELVAFQDMYNRMQHQCWKKCVLRLGESELSVS
EGLCADRCVKKYM EVHNRVGVKVLQGLQQQQPQPQ

>possible Tim15/Zim17 protein Contig327 (uncertain of N-term.), 227 aa, 1B18

ATVAKGELALLARSVPSSALLGIRQSTLASRV SASPLHGAATRPRPSPS
CFLRISARSLHASSTLQSAKSSMVEATSADAPTDSAEAKETSAESAATP
TTTTTLNIGRIQPKLELHYTCGVCEL RSTKQFSRVAYEKGVV IIRCGGCE
SLHLISDNLGWFGEKDNIEEIMRKRGEAVERGRRDAGGNILLDNNNTNTA
GDDTITTDLEHDGTQTVVEESED CILI

Tim22 complex:

>Tim22 homolog (probable true identity is CI B14.7 subunits) Contig22734 (complete), 196 aa,

F9D

MAHEHDHHTAKDSKKDVEIPDLFGIDALDIHGGEPCLVQAKMAATSFIA
GSFFGGVLYVYWKDVGVVQKRGRFAALQGTLSIGSYGAFFALVGATYGT
FCALQHSRTKNDPNTVFLASCAAGGVI GARVNGTVFVGSVLGCAVTGGLAA
MGEFFDWTLS PNSAKLFALREQKHQRLLRTSPGVGSDAASSDSDAQ
>Tim22 Contig19250 NOT DETECTED, 189 aa, 182D
MEGRDAASQGE PETARRQESQSPFPQAPPGTWQQKLD AFVEPFVIKYLWD
PRFAENCAFRGVQTFVVGAMGFVMGIFFSSLGGPSSMGMPDVEMKGGWK
KQTAEHFKHMGRSGVSMMAKAFAYVGALYATTECVVEKYRGKSDLMNPLIA
GCISGGLLASRAGFTATAMGCGGFAAFVSVGIDWLMMENH

Tim23 complex:

>Tim23 Contig27058 (complete), 201 aa, 253F
MGDSSYADSSSMPDFDAFPEPKLDNIGIDVDSISYTNPMYGLSGPKGAEY
IFADDNQARKMSWADRSTWLWGGAWLTGGVIGTTWGGGLKGLRDAERGLPW
KLRLNACLNGAGRKGGRMANGLGVLVLLYSGVETATAAARQKQDGLNIVA
GTTMAPLIYWSGAGLIRSMAGALGGVVGFGVLVGHKYNVMGLRKILPAD
E
>Tim17 Contig25569 (complete), 212 aa, 1F
MDAYRDPSPRIVTD CGSAFAMGAIGGSLWHGVIMGWPQAPRGMRSSAI
TALKTKAPSLGGSFAVWGGLYSSFDCTFAYLRGKEDFKNSIMSGAATGAV
LAARTGWKGLKSGVVGGLLALIEGIVFVISRQSPAQQDFGYAPPPPP
LEDVLDVEEKGGFFSSLTNLFSKKEESKPFEMEEETTMDDFGQETKEDDF
GDLFQPPPATSW
>putative Tim50 Contig18694 (complete), 369 aa, 1C71
MRRIASGTPRSYAAMSGVWTS GAAAAASFSSQSLFKCATSSAAPLFTRSA
SLATPSTARLFARTTKPLGLAGRPLQORFASTTAEGVQASGSGRARITAI
GVLIAAVGGVTGVVYAAEGGNQEGEAGLFANLKKKFTAQTNKLLNIDENK
KILPDAHPPPYGKPI TVVISDDVLLVQEQPLSGGMLTKKRPVGEFFLAQ
LSQDYELVIWSLQOVMSFGPVIEKLDPNHHAHRVYVDATVVNAEGMNVK
DLKFLNRPLDKTIVLDISPDHVQKENLIVAPKYDGRLEDVYLLEMLNFF
RLLAASSKSQSGVPDVRNWVAAMNKKGPQYFKELYADAVKKAKDRAEEER
KKREEQLQMRDVGNTGRKW
>Pam16 Contig10914 (complete), 111 aa, 17C1
MVRLLLLNILGVGSQVFGKAFLDAWRQAGLKAKQTGAGLSLAEAQKILGL
RPPYELKEVTKRYEQLFKSNPDANGGSFYLQSKVYRERERLEQEFKTNAE
WQAKGGGTNAE
>Pam18 Contig13309 NOT DETECTED, 143 aa, 24A0
MQRTTAQAAKTSQPKMGPGTIFLALGVGGAGLALAPRLVSSAAKHFSKGG
SSGKGFATMGSMWKRSGGGASTGFKNFYKGGFESEMTRAEALILGIRQS
APKEKIRLAHRRIMLLNHPDNGGSDYMASKINEAKDVLVKDLN
>Tim44 Contig12315 (and 15550) (likely complete), 392 aa, 12E5
MSFWSEFVKSFKQAENSKELNESMAELKKLQESLKKTKESVEKLDK
SAEGLAQLKNLSEKAAATGGRVTARVSDSVTSTLGDITQRVGMDEKLEKT
KEGFEKVADSLNKARENIEKVENIKTSAEESSELVKKVKEKVPFGLLDGS
DAAAGEGSGGEGAVAGARSQLVVKTQEVQTAIEKRLQDARDRLRATGAFK
KALALREKIVESDNPLIQRVLDLGDGITRRTSKLFSENDHAKTIKLIHEL
DPTFSPEKFKQKMASSFPVTLRSALLRGDPAPISALMSKRLAEHELEAYK
EWDAGHYRSHSKLLNLDTVEILNAHTRDDGRPTLLIHVFSQENHCIRDSS
GAVVEGAPDNIQDVEQTWAMQINSQGEWEVIEYMMVVASRPSW
>Hsp70 Contig3529 (and 25050) (complete), 669 aa, EC4
MLRRVAATTRRAPVSAASFLRSSWNAPAAARLYSAKSGDHIIGIDLGTTNS
CVAIMEGSTPRVIENSEGERTTPSVVAFVKDDHGTNRLVGATAKRQAVTN
PTNTFFAVKRLIGRDFNDPMTQKDLKMVPYKIVRHSNGDAWLED SWGKKY
SPSEISAFTLTKMKETAEGYLGTQVKKAVITVPAYFNDSQRQATKDAGKI
AGLQVERIINEPTAAALAYGLTNKGGETVAVYDLGGGTFDISILEISKEG
VFEVKATNGDFTFLGGEDFDNTLMQHLVGEFKAEGIDLSKDKLALQRLKE
AAEKAKCELSSTVSTEINLPPFITATAEGPKHLHIKLTARQFESLVDPLVQ

RTIDPCKSCLKDAGLDKSDINNVLLVGGMTRMPKVQEVVKQFYGKQPSKG
VNPDEAVAVGAAIQAGVLKGDVKQLLLLDVTPLSLGIETLGGVCTKLITR
NTTIPTKKSQVFSSTAADGQTEVEIKVLQGERHMANDNKTLGSGFILSGIPP
APKGVPPQVEVTFDIDANGIVNVSARDKATGKEQAIRIQSSGGLSESEIDR
MVKDAETHEEEDRKRKQTEARNHAESVIYDIEKNLNEFKHEVDQTEAER
LREQITELRKTLESADDDHQAIKSGADSLQRESLKAFESAYKQKASSNSDSG
SSSSTENKEDDTPDADIKK

>Hsp70 Contig14215 (complete), 683 aa, 16FF

MRATGRLNPMQGMFAFASLGGCRATAAASSASALFNRSAAAMRSTFAGPVF
SRRYTSTSDPLVMGIDLGTNSCVAVIENGKPRVIDNVDVTGYNTTTPSMVA
FTKDKATGQQTMLVGDPAKRQCVLNPRGTVYGVKRLIGRRFDSEEVAKIK
KHVPYEIVKAAANTGDAAVSVGGKSYSPSQIGAFILQKCKESAETHVQGT
ISKAVITVPAYFNDSQRQATKDAGAIAGLDVLRINEPTAASLAYGFSEE
NSKERQRLAVFDLGGGTFDISILEIGDGMQVSTNGDTFLGGEDFDETV
LQYLMNEFKKKEGVDLSKDVFAIQRLREGAEKAKKALDHMPNYEINLPFI
TRDKNFSYSLTKEKFNELIKPLVDRTIKPCQSALKDAGLDKVDNVILVGG
MTRTPAVIEKVKEVFGLNPSKGVNPDVAMGAAIQGGVLSGKVNLSLILL
DVTPLSLGVSVKGDLFSRIIKRNSSIPCSNTQTYTTAADGQRQVFDLLQ
GEREIASANHLLGQVTLVMPAPKGIKIDVTFNIDVNGIVHVTAKDPVL
NKVATVQIQANSGLSQRDIDRMLKEAELQKERDQOIKELAEVKNEAETLI
RSAETDYLHNDVVPEEDKETIRQAVSQLOTAMDGNSDELKTIYASLKDTI
LNVGAKLYQQGGASSSSNDGHNHDNNNQETKQ

>Tim21 Contig1844 (complete), 235 aa, 107B

MQRSAVCTSGRALLGGRVSLATACTRPVGI VGRRGVWEGALYSRPPQOQO
SLGRRRFATDSNGGQKEPPSGTKGGLQAAKPSGQGTAVTVAQKVVEGGKD
AGYGLVILGGVVLLGAAAYQLFSAGFAPSSPQHVYSKASDLLRRDPEVQK
LLGPNIKTYGEETSRRRRRLQSTKYFNAATQRDHVRVLFSAEGDVNAADV
IADVTASGQFYLLTVEVPVTGEKLVYTTNTGKFERR

Oxa complex:

>oxal Contig3549 (complete), 416 aa, 1BCE

MLARRGVNPRVLVLEGRAGSVSRYGIASSPAARHLAFPTRTFATTTTRSSS
SSSSSAPSLARRRLPSIISRGSVFSSTSSSSSISSSVSAAMLIRHERRCY
ATETVEEGATAAAEAATQTGAVERGSDAMASFIAADPVTSITPAALEVV
ERTTSSFPPIINWLDAMTFVHYTVPLSWAATAVCFTLAFRTMILPAVALT
MONSAMRAVQPELEKIKAKYGPVNGKDVNVAMQYREEVRKMMQAQSGVSM
WKTMPVFLVQTPFLVSVFFFTTRKLAEEEPGLRDASFLFFNDLSAADPYII
MPILTSLTMLATIELGSDGVGGQSNPALKNFLRLFSVLAIPATSSLPIFT
HIYWFSSNLFSLCQLGLFKVPFIKKALGLPDYQGVSPMLGSSDPQPAKPE
VTFQOKPRIIRTKNQK

>calcium-binding EF hand family protein (Mdm38) Contig14024 (and 8425, 8848, 4882 .. also Genscan) (incomplete), 697 aa, 174C

MQRIRAATKGPVVGRAFAGPSGSLGAPGAFGSFSTALVRRSTTGCTAS
SSSSLRLRRLHSPILPTALPSPPLVHLRHGGPCNYSLVSSPSSLSRLRCG
ELQPPGNVRSYTTPTTTTTPTIGSSSPAVAAADTAPPSTPTATTATPQKV
GLGQKVMMDTLRHFVWAGSRLAANVKAASMLLRKKIAGQNLTRRERRLLTQ
TTVDLFRLLVPLAIVVIPAELLPLVLLAVFPNMLPSTFEDKIKKEEARR
KAVQLKLEMAKFLEDALYLRSLQISHDTPSAATFAEAMKKVKEGQSLETK
EILGLSKLFEDKFTLEMLDRQOVVAMCKYMGLSRFGTTHYLRNQLRSLKH
DIREDDDLIAQEAALDKFTEAEMKQATQVRGMDYKDFNTAKAQMEQWLLL
SAQHVPSSLLILSRAFALTSAYSSLKPLEGQOVVTKKAETGEIALPKAME
EALHKTISALPDQLVADTKLTSATKTTQDMVSKLEVLQEQIQAIKTEEKE
KKEKEREKAKAPATEAEAKQATKKDAAGAYSAEQMKVVSEAVSLLFASA
PSKIKREREALEQLKERKEERKEEREELSAAASASTDQPOHQPOPPQDK
VVHTLETKLEKMIAKLDKEMDKIDQRAHTLMSIIDTNQDQGISFEEFQEA
VSHLKAKYSPEDITTMRKLDTNNDGQVSLEQLEQLYSAGADEHHER

>Mdm38/LetM homolog Contig17709 (and 2982, 21306, 7920) (incomplete ... with mistakes), 387 aa, 49B

MAARSRYLATTYMATPSATIVGTPFVVRMSQTSMLRRLGATSRGISSSAVA
LALPRGTSAGSFAFLGPHAAASWRRSGRSSATVLQWPGAGSSAAAGRLRV
SEAACARYYATGGSLPDSNQSPKAVSAEDDKEAVPKKTLVGRAVHSTKKV
VTFIKEGIHYYWLGSKLLALNVRTAFNIAVRLKNGHTLTRRERQHMIRTT
ADLFRLVFPFAVFIIVPFMEFLLPALKIFPNMLPSTFQDTMKKEEDMRKQ
LLLKLKMASFLQDTLQEMAETGETHADIPKEEFLDFMKRVRGGGEVSGEE
VLKFAKLFKDDFTIMNLSRAQLSSICKFLNLRPYGTDAFMRWQISRRVSK
LREDDTMIAQEGVKSLTFEELQOACIARGMPATGLSK

>Mdm38/LetM homolog Contig3961 (and 13276, 19860) NOT DETECTED, 339 aa, 1BA

MRRLTRTTTAAAAVDGVMRHSWAERAKAGAKAMWAQYWGGRQLWVDA
GAARALRRRVRESVASGGVAADGVALSRRETRFVRRVADDVRALVPFLA
FFMLPFSAYALPVIVRFFPGFLPSTYHSSSYRVAQMQRQKVKVEAARQL
RDALSERLLATEGPSARERDLLLDFIHRAAAGEAIPLTQLRPLDRYFATH
LKLDDLEPRSSGASLGSWLGSTLWLCPAELRALCTFYGLSALPLPTFDH
CANQLILHASRIQHDDKLLVQEGDRWPTTELDEELLEACDERGLPTDVTE
RDRLVAQINQWLAFRPPPPVSAELTLFAPALATNTRAK

>Mdm38 (Contig17895) NOT DETECTED, 386 aa, 9AC

MRKCPTTTTTTALGLRFARRSPSSGLLTARRLFPSSGAYRSQLRPAAVAG
WRGMSTTGHGPAAPDTKDEQOPLGATTTPPPAIAPEAEAAAPAAVAAAPKW
QTLMAKAKELARGIKDGTVELYRNVKHTRRLRAVVRERGIIDALTRREIRL
MNRTRDLKALVPFLILEIVLPEATPFVVMLFPGILPSYQRLIPQQRK
ERERKRTVEALEQMRSELHALGGQRPINF'TDSSLDDLVASLQDESGLRE
KLEVASLPDGMVEAMTRYTSVWSRFRTQNGLRSSLQKLDALRKDDELIA
KEGGIDSLSEEEKEEAYYERRIGLAATSPASPAATVEPSSAVGPTDPDRE
RHLREWLHLSSAAIRDCREQHRATVPDTSLLLLLALRH

Inner membrane protease:

>Imp1 (Contig19247 and 2953) NOT DETECTED, 241 aa, 12FE

WRSGGGSRLGAVLRTTIMVGAYYGVAITFCNTVLKPSTTAGPSMHPTFNA
AGDSVWVYRRIDPATDLRVGDIVHARTPTYCRLEGGKQPGVLKRIKGLPGD
TIKVTFYSPSKVTIKVPAGHVWVEGDNPGQSTDSRMWGPLPLALIEGKVV
SRLNPFSLQTLDAPGHIKRWERQARDIADSRATGKRSGEALRAIDRLI
KSGSEASDNTLLVSDRHDADVNDTALAPPQDTVQGERVVA

>Imp2 (Contig6343, 15292) NOT DETECTED, 169 aa, 1090

DGKQAKQITQTGGAVRTRRGCGVLLWLHARRHLPIWGHTAVEGESMYPTL
EKNDWVLTSSRRNGLHRGDVVVLRVSVKEPKERMIKRVTGLPDDLIHTDDA
KLVRVPRGYCWIEGDNASVSLDSNVFGAVPVGLVESRALYRLDRGWRLHK
LESVPRERLQRTKKEREVR

Matrix protease:

>Matrix processing peptidase alpha subunit/Complex III Qcr2 Contig18841 (and 14090)
(complete), 502 aa, 1183

MKPQHAARLSLAKGVTRASSPSASVLGSKSYSSWTATSSSLKQAHSSVPQT
WEATPQTLDNVQTTTLDLGLKVTTVSSELPLAAVGLHVKAGARFETGESR
GAAHFLRHAFSRTSSRSPLTVTREMIVATAAFDVSASRENISYSGQLMP
DYLEDYVWMLRDLMHPLAWYIIVRDAAPQVAAEVHEAETNPATALVEAIH
REAYRDEGLGNSIYCPNYRVGAVTREAIIRYHHERYQASNVALVGYGIKH
EQLVAQANKYFPADAFEDKAPWTTLEAADRKPGAVYTAASSYTGGELRL
PGPGNSRVALAFEGASLADPDVFAVRTLSLLGGAARFTRDGPVGLRSR
LARNVLAKGDYVVLASSALNASYSDSGLFGVFVEALPGHGADAARLLSAEL
NSLAGSFSVDDAELTRAKNQAKASFFREVESRTGLVDYLARHTLAGTAPL
APAQYAARFDAVTRDDLARVARRVFSPLTLVSTGDIHGVPKEELRPKL
KA

>Matrix processing peptidase beta subunit/Complex III Qcr1 Contig18201 (complete), 491 aa,
1F42

MSSIRSAPSMLLPKLTSGRLGAAARRLSSGQPQAARDVEKRLRLPEY
LLNVPPTQVTALPNKFRVASEHKHGETATVGWIDAGSVWETAENNGVAH

FLEHLAFKGTKNRTKEQIEVEIENMGGQLNAYTSREQTVYHAHVFKKDVP
KAVEIISDIIQNSNLKEDDVERERGVILREMEEVESQTEEVIFDHLHSIA
FQNTSLGYTILGPEKNIKKIKREDLVSIVGKHYTAPRMVLSAAGAVDHDE
LVKLAEKHFSGLSSETNVDYSNREKLFDFGTGSMVQVRDTSIPLVHTTVAA
KSVGWSDPDYFTFLVLQQLVGSWDRSLGGAKNLSSNLAETFATEELAHSL
MSFNICYHETGLFGAYFVGEMERTSDAIFEVLREWVRIGSGVSEVEVERA
KNKCLKSTYLMQLDGTQAVAEDIGRQLLTLGRRMPAAEAFMRIDAIDAKKV
REVAYTYLNDVDVAVAAVGSVDSGLFPDYNVLRGWTYWNRL

>similar to MPP beta subunit Contig27020 (and 7554, 25735, 23118) (incomplete due to internal gaps), 460 aa, E4D

MKASLHNVRPVRLPRFVGLSANHLRRLNFSGSALLLASAQRRWATTAA
TDVRPLKPKLERGSPMKSPLLDMPTPLAHVSQKTPSTRITTLRNGVRVA
TEETYQATAMGVFIDAGSRNETFETNGTTHVLQRMGFKATTNRTSAEIV
QKLESLGVNAISSSSREAMVYTAEVVRGDVEEVVEVLADSVTNPLLLLEED
LQEQKIAVGRELEDMVHDPSPWLPEILHELAYGPEGLGLSHLCPPSNLEH
HIGREQLHNFVKTYVYVGRVVVAAAGVEHDSFVKLCAKHFDSLPAEAGGK
PLHVPSVYKGGAHVEFMSPENKRLQELQAESDKPPPSHVALVFEGSGLN
DPDLYATCVLQSLGSGSSGRQRAVLCDDIGRQVLSYGERKSAQELSDLI
EKVTIEDVMRVARRILSTKPTLVVYTPKEYATLVPSHERLCAWFDAINDK
LNGKESSESK

Disulfide relay system:

>Erv1 Contig2125 (N-terminus inferred from genome) (possibly complete), 215 aa, 21B7

MEQFKKIKEKLQKEGDQLVVGGADEEDCGACKPRAGGLYGSDMRRRFRSQ
QQAREQRS AQEQDGGTTSTDATATSAGTEEDASNENTTECYDSEGYWEKQ
DAPDVIELGQAGWTLHLSMAAYPPKPSRQHQERMRSFLSLFPHLYPCKV
CAKDFEETMDEIPPELESHDALSDWMCRAHNRVNQQLGKPLFPCERVRR
WGPSNAFHTKEQDDSD