

>Hsp60 Contig14920 (complete), 575 aa, 1008
MLRTAAPPHARVAVRGSSRSASSLRLYASVAGKEIKFGSEARSLMLRGVDS
LTDAVQTTTLGPKGRNVVLEQSFQAPKITKDGVTVAKHIEFKDKYMMNGAQ
LVRGVASKANDVAGDGTATVTLARAIIFSEGTKVVAAGMNPMDVVRGVDQ
AVSIVVGELKKLAKKVTTEEIRQVATLSANSDDSIGSLIATAMEKVGSO
GVITVTDGKTLNEVEVIEGMKFDQGYISRYFVTDPKTQKCEYEDALFLL
TDGKISSIHSLLPCLEEVSRHKKLVIIISDNVEGEALATLIINKMRGLPV
VAVKAPGFGDNRKNNLQDIAVLTGATVVSEEMGLKLENFERSWLGSCKV
IISDDTIIMDGGGENSENIKERCEQITEALQRTTSSYEQEKLRERLAKLS
SGVAVLVKVGATEVEVSEKDRITDALSATRAAVEEGIVPGGGVALLHAS
KALEGVTGANADQTSIGIQLVARAIRIPARTIATNAGKEGGVIVEKILQST
DAHGWYNAQTDEYGMFKAGIIPVKVVRTAIDAAASVSSLMTTTEAIVV
ELPKESSMPAAPGMGGMGGMGGDMF

>Hsp10 Contig24909 (complete), 97 aa, 15B5
MSKRLFPLSDRVLIRKAKPVERIGGIVLPESAQKRLNHGTVLAVGPGARN
REGALIPPTTLKEGDNVVLSEYGGTEVEIDGEEHLHFRREDDILGILKK

>Grpe co-chaperone Contig881 (complete), 247 aa, 10A5
MRAAVRRLPNVASHSAASRGIFALNVPLRSRTLAIRPFSTEQNGEQKVE
GEHPPAQOQAEGENKEQOQEQODPQAAKIDELQNKVKDLEEONKELNGNY
LRSLADLDNMRIGKTNVENAKLYSIKFAEGMLEIADNLSRALESLEPEE
KRGLPDVKVLFEGVAMTERVLQOVFARYGIKKFNPLNEKFDPTKSSALFE
IQDPTKAPGTVAVFQAPGYTLHDRLLRAAQVGVVAQPPDEPSSSDQA

>Hsp70 Contig3529 (and 25050?) (complete), 669 aa, EC4
MLRRVAATTRRAPVSAASFLRSSWNAAPAAARLYSAKSGDHIIGIDLGTNS
CVAIMEGSTPRVIENSEGERTTPSVVAFVKDDHGTNRLVGATAKRQAVTN
PTNTFFFAVKRLIGRDFNDPMTQKDLKMPYKIVRHSNGDAWLEDSWGKKY
SPSEISAFITLTKMKETAEGYLGTOVKKAVITVPAYFNDSQRQATKDAGKI
AGLQVERIINEPTAAALAYGLTNKGGETVAVYDLGGGTFDISILEISKEG
VFEVKATNGDFTFLGGEDFDNTLMQHLVGEFKAEGIDLSKDKLALQRLKE
AAEKAKCELSSTVSTEINLPIITATAEGPKHLHIKLTARQFESLVDPLVQ
RTIDPCKSCLKDAGLDKSDINNVLLVGGMTRMPKVQEVVKQFYGKQPSKG
VNPDEAVAVGAAIQAGVLKGDVKQLLLLDVTPLSLGIETLGGVCTKLITR
NTTIPTKKSQVFSTAADGQTEVEIKVLQGERHMANDNKTLGSFILSGIPP
APKGVPPQVEVTFDIDANGIVNVSARDKATGKEQAIRIQSSGGLSESEIDR
MVKDAETHEEEDRKRKQTEARNHAESVIYDIEKNLNEFKHEVDQTEAER
LREQITELRKTLESADHDQAIKSGADSLQRESLKAFESAYKQKASSNDSG
SSSSTENKEDDTPDADIKK

>Hsp70 Contig14215 (complete), 683 aa, 16FF
MRATGRLNPMQGMFAFASLGGCRATAASSASALFNRSAMRSTFAGPVF
SRRYTSTSDPLVMGIDLGTNSCVAVIENGKPRVIDNVDTGYNTPSMVA
FTKDKATGQOTMLVGDPAKRQCVLNPRGTVYGVKRLIGRRFDSEEVAKIK
KHVPYEVKAANNTGDAAVSVGGKSYSPSQQIGAFILQCKKESAEKHVQGT
ISKAVITVPAYFNDSQRQATKDAGAIAGLDVLRINEPTAASLAYGFSEE
NSKERQRLAVFDLGGGTFDISILEIGDGMQVSTNGDFTFLGGEDFDETV
LQYLMNEFKKKEGVLDLSDVFAIQRLEGAEKAKKALDHMPNYEINLPII
TRDKNFSYSLTKEKFNELIKPLVDRTIKPCQSALKDAGLDKVDNVILVGG
MTRTPAVIEKVKEVFGNPSKGVNPDEVVAMGAAIQGGVLSGKVNLSILL
DVTPLSLGVSVKGDLFSRIIKRNSSIPCSNTQTYTTAADGQRQVFDLLQ
GEREIASANHLLGQVTLVMPAPKGIKIDVTFNIDVNGIVHVTAKDPVL
NKVATVQIQANGLSQRDIRMLKEAELQKERDQOIKELAEVKNEAETLI
RSAETDYLHNDVVPEEDKETIRQAVSOLQOTAMDGNSDELKTIYASLKDTI
LNVGAKLYQQGGASSSSNDGHNHNNNQETKQ

>Hsp90 E80POFO01D2V4R (and 16204, 12961, E9BS9UA01DIVA4, 9423) (likely complete), 767 aa, 60
MRSAAVKNSSRPHRAVLRAPAPAHVVPARPLAEVAGTHNKVVVVGRRSRS
CVPSALQVNHTAGAKRAYRSTAIGMRAAGAREPEEAELVRTAEAAAATPES
ARAGGAVSEAEEGKETLIEETETVSGQAETLPPQSETAKLLRIVAHSLYT
DKEVFFVRELISNASDASEKLRHLVDVTGKEYDDKYLPLEIHIATDDKNKTI
TIQDFGIGMKKEELIKNLGTIAHSGTQEYLRQLEKGDASNIIGQFVGVFY
SAFMVGNRVKVVYSRAAPGSKGYCWTSDGTGAYTIAEAEGVSRGTKIIIQ
LLEGQEHFAKKQTIDSIIKKYSNFVGFPIKLN GERVNTVRPLWTLPKQSI

SEEDHKQFYQFLAHSYDLPIYRLHFTSDAPFSIQSLFYVPEQHQEKEYGMG
RMDPGVSLFSRKVLVVKPKMKALVPDWLRFMKGVVDCEDVSLHLSREHFQD
SDLIKRLGNVVTGRLLKLFQDEAASDPDKYNAKFWKEYGSFIKEGICTDA
KWKDELGGLLRCESSATGEGDVTSL EAYAKRMQDQQTAIYYL CVPSRTFA
ESSPYEAFKQRGVEVLFlyTSMDDFVMQNLAEYAGKRILSIESAQLPAE
LARPASTTTGNNNNDASSPQAHAGELSLDPQVEEELAKWMKTTLLDRV
SSVKETKRLVSSPAIIVDHESASFRRMMKFVDP SRAPKLPKQRL E INAAH
PIITRLNSLRRREPSFAKAVAEQVFDNALIAAGLMDDPRSMLARLNSILE
AAARNSDTTSTTSTSTA

>prohibitin-1 Contig2302 (complete), 281 aa, 148F
MMQKLQALGPALNKVAIGAVSVGAVGYALNESMYTVDGGERAIIFDRLRN
GTRDFIVKPGTHFLIPFLQFPPIIYDTRTTPFNIKTETGSKDLQRVNITLR
VLYRPDKKKLPYIYQRLGVDYSANVFNSVGNV LKAVVAQYDATELISRR
ETISNQIRQRLVKRAGTFGLKLEDVSI THLTFSP EYVRAIEHKQVAQQLA
EQAKFVVAKNEQEKLAKIIVAEGEAEAAALISKAMSGPGYIALRRIEASR
DIAEELSRSRNIVYLP SGTNVLMNLPQVGQQ

>prohibitin 2 Contig2720 (complete), 312 aa, 888
MSKSPFQGLVKANLPGMGGKGLKTAMSLAVVGVGASAVAYNSLFTVEGGQ
KAIIFSRFSGVLPKVYNEGLHFRMPWLHIPHVFNVTRPTSIPSLTGSKD
LQMVNITLRVLT KPKWEKLP E IYKKGTDYDQ RVLPSIVNEVLKGVVARF
NAAQLITQRELVS GMIQDR LRERAADFFIDLDDVSI THLSFGREYTA AIE
AKQVAQQAERAKFIVEKALQDKRSIVIRAEGDAESARMISEAVQSNPYY
LELKTIEAARDIAGSLANSQNKVYLS S DMLMFNLLSSISGSNTASSLVGS
VLSAKDATIARQ

>ATP-dependent metalloprotease FtsH (Yme1) Contig65 (and 1863, 1932) (largely complete), 692 aa, F06

MSATPSATPNLTSL LKLRSTGGRIGGQYWNVHRKLP LSLYRTITSSSQRS
GSPLFSSPHARLPLAAETPHSVERFPALNGRR TFFSGAGSKRLEGLERQV
ESGRASGTI WASYFRELNKMDSPKEVIRQFERLEESA KTQEVVKEYL KAL
VLTGRLEGANLGHLLSRGASGGAGGNAGRLTLVADSP IPIITVTGGSLTGS
AGGSTFSKIANVTGFMVSLAILYLF T AMFKGGDSIMGVNTKVKFAQKSN
ITFEDVLGVDEAKSELQEVVQYLKDPQKYTKLGAKLPKGILLVGP PGTK
TLLAKAIAAGEAGVPFLYCSGSEFDEVFVGVGPRRVRKLFEEAKKNAPAI I
FIDELDSVGGSRNRDHHQVYTH TINQLLTEM DGFQENQGVIVLAATNFPD
VLDPALTRPGRFDKQVEVPRPDVRGRKMILEHYLKKI VVAPDVNVDMIAR
GTPGFTGAELANLVNIAATKAATKGMEAVTTACMDEARDDVMMGVQRKSM
IMSDDEKKLTAYHEGGHALVAIYTEGAKPLHKATILPRGRALGVTHFLPE
SDQLSLSRMQIMADVAVAMGGRAAEVIFGPKMITTGASSDFKHATRLAN
AMVAQMGMSDKVGPIYRDERDLERASSETRQKIESEVEALLQGOYAVAKR
ILTDHQDELHRLAQALLEHETL NKEEIMAVIKGKKTNLNLFYQ

>Lon protease (Pim1 homolog) Contig2814 (and 24099) (possibly complete), 1043 aa, 681

MKTCLGRLTPRPAQAQSHRYASSMLRGNASRLVGLRASAGARRPPLSTSS
PLICGSHHGPA YRFVGVRAVHDQAGGNRKN GGGGTNNRGGVAAATDKKP
SLVLSQADTGAMLRNMATMPTPQT VYILPLTLNPVFGGTSYYALVDRRTL
ERMQDLQAKGDLFLGLFLQKDPNPNVKVADVSQLYQVQQLGCAIGAVQYT
SNPDVHLLQITPLSRRIRIKAPVPGAERENDATLLAVEIEELIEGEYNRK
DPVIRTNHEAIVSAIQQLHEHDPSSHYQKLLDEMPDNPAEFVDLAAAVM
TSEPQMQQAVLETTDVKQRQLKCLELLHKKLEMFKKQKDVRTENMEQEA K
LEAAQKKLYLERKKKAI EKELKLDVEDSDKLIEDFKKKLETLOVPEEAMH
VINEEMNKLTSLERSSEYNI TRTYLNWLT TLPWGLH SKENLNL SHAISV
LNEDHFGLKDIKERILEFIAVGNLKG SVQ GKILCFVGP PGV GKTSIGQSI
ARALDREFFRFSVGGMSDVSEIKGHRRTYVGAMP GKIVQSMKNLKSANPV
ILIDEIDKMGNSRQGD PASALLEVLDP EQNKTFLDH YLDVPPDLSKVL FV
CTANVSDTIPGPLDRMEVIQLSGYILEEKMNIAKKYLVPQIMKDSGLQP
GQIAVND S ALHALIQSYAREAGVRELYKHIEKIFRKVAYKVAKERKLATD
ATDATPAGGDGA EKT KKR SRKTKKPSKADEEEGKETKSEGESGDGQTQP V
VITASNLTEFVGP KFTSDRFYDVTPPGVVMGLAWTAMGGATLYIETVND
RPLYSALKRSQPAELEHAKEGDAEGDKDRGVKTFGGAGGAMRLTTGQMG
SVMQESTSIAFTFARNFLEDVSPRNEFFDRAALHMHIPEGATPKDGPSAG
CTMVTSLLSLATGRPVPPDIAMTGEITLTGKILTIGGVKEKTIAARRSGV

KRLFFPDGNRKDWHEELPDYIREGLEARFVKDYRQIYDVIFADPDPAASST
STTTTSTTAIDGETTSTTTKSPGPPAGGSRQTRKRSCDDSAH
>lon protease (Pim1 homolog) Contig10152 (and 3185, 21213,14877,1398,5437) (incomplete, with
many internal gaps .. large part gen, 1052 aa, 1B0B
MLRSRSLKHSATPSLLRTGGRGWAPQCRSGLSVAGALPSPRGANLPFST
TPLPALRCSRGTGTSGSSLSVQTWDRQRNAAAAAPNGARRGFRTTAP
AAAAAGDDNDDNENKKKDEPEYRESDDDDDDDDFSDGEQDGEDVMPPR
DMPLQVMVKTVTTPEQVLVVPVIKTSIMPGMTGRATVRDPEFLKELQELR
QKHPSPIYIGLFIVKDAEEAKQKGVQITTLDQLHQTVGLGVLTNVPMRPS
QQKDGVVGVIOFLSVHKRIKIDETVSGTKRLVAKVSELQDKPYDPKDPQI
RGFQAELEAIVHRIGAKGDFVARDNAAQLLLNFWTFHNPLNAAESADFVA
GIITHIALDDAAMQAQOAVIEELDVSERLKKTLALTKRELSLSDLTQKIK
EDINAKMEERHRQMTLRDELKAIRTELGLEQPQTETLMAKFKERIKDKQV
PEHAAKVINEEMEKFOHLSPSSTEYNVVRTYLDWLTTLPWDTLTKDNLDM
HHAEKVLEDEHYGLKDVKERILEFIAVGALKGEVGTGHRRTYVVGAMPGKLL
QALKRVKTSNPVLLDEVKVGTSYKGDPSALLEVLDPSONTKFLDHY
LDVSYDLSKVLFICTANVLHTIPRPLLDREMEVIRLSGYVEEEKVAIAERY
LVPKAVSEAGLSEIKVNFEREALHKLHISYAREAGVRNLQQQIDKIMRKV
AHQVVVEQEKROEGAVEGSDGKKGAKGGVRKGRGKKKSTQERADESAQPG
SSEALTLEKQHGAIVIKPAGLGQFLGKPPFSNDRYYDTTPPGVVMGLAW
TSMGGSTPYIETVVDKHQLLVRKEEKRRREAKEKLEKNKKTNDVASSE
SPATASSEDAAEEEGSGSRLITTTGQMGEVMQESCSIAYTCAKIFWNKL
GAKRARSPOGATQGEDEGFDEGFFRDVTLHMHLPEGATPKDGPSAGIGMV
SLLSLGLGTALRQDVAMTGEITLTGKVLVPGGIKEK VIAARRAGVKTLV
FPEGNRKDWDELEPFLREGLDAHFDVYGDVVFQVFPDAPKEYHQALRRT
SA

>Yta12 protease Contig24281 (and 20121, 1341) (incomplete due to internal gaps), 698 aa, 1D09
MMRMGTAAHSGSYAMPRTLSLLGRTSYSPSALSRLPRHPLLSSTSTQTT
LYPPRVLGVRRLTTPAGGPPPGNLPYGWERWRNVAPNGQOTPKQSASG
TGGSRPWGVIALPLLLAGLGAPTPTGSEISFQQLTNELLPEDKIAKLEVV
NGNRVRVYLKDDATRDPRTGELQHTKAAAYTITIGSVETFEKQLEEVQRLL
EIDPHQFIPVYTTLPDWGMLANWLPPLLLVGFLVWMTRSSLKAAGGPL
KGMFDAASNPAKLYNKETGVKLSFSDVAGLEEAKEEIMEFVSFLKFPEQY
RALGAKIPKGALLVGGPTGKTLAKATAGEASVPFYSVSGSDFIEMYVG
VGPVRVRLFEEARKNAPCIVFIDEIIDAAGRARGKGFKGGGNDERENT
LNQLLVEMDGADIANVCNEAALIAARHNKLAVDEQDFEAAIDRVIGGLEK
KNKVLNPEEKRTVAYHEAGHAVAAWFLRHCDPLLKVSIVPRGQAALGYAQ
YLPKDTYLVTOEELFDRMCMLGGRIAEQLEFQKMSTGASDDLKDVTRMA
YSQVIGYGMNERVGP IAFNPNEESSGRPYSENLAEIVDEEVREMVKKAYA
TTRALLQDKYEGLKQVAELLLQKEKIRGEDLEAVLGRPPFKDTALEDIRH
LLPAGYDEMEKAREKLFHDERERIQOREQELREAGGSSTPPSATQPOP

>AGF3 protein 2 Contig9344 (and 1852, 15971) (incomplete due to internal gaps), 664 aa, 2003
MLRLRSGWSVAGRASCAGQLGGSRLLLSRNAALHSSYISTSAPQLASK
SSAWRWSCVQORINTLGGRNNEIDFNTFRTEYLENGKVREIVIVNGERAR
ITLENEVRPTLYFNIGDLHNFERKLEEAQRNMGLDPDFVSVRHRVREENL
AGDLLAVALPTLLLIIGTLIIVWSRKTASSMGGGLFSVGKHKATLFTKDMKV
GTTFNDVAGCDEAKQEIIMEFVAFLKNPDKYRQLGAKIPKGALLVGGPTG
KTLARATAGEAGVPPFSSISGSDFIEMFVGVGSPSRVRDLLFAAARKNAPC
IIFIDEIDAAGRARSKSGYNDERENTLNQLLVEMDGFNPTLNIVVLAGTN
RPDILDDALLRPRGFRQVSVDLDPVKGRQAI FNVHLKPLKLAEEVLGVTI
GDKLAVLTPGFSGADIANVCNEAALVAARHRKPAVELIDFEKAIERIIGG
LEKKSRIISREERTRVAYHEAGHAICGWFLHETDPLLKVSIVPRGVAALG
YAQYLPKEQNIYTKEQLLDRMCMLGGRAAESLIFGKITTTGAQDDLQKVT
KLAYSQVSRYGMSEEVGTISFAFAEGDGERPQVDKPYQATARLIDDEVR
SVIMNAYKRTEQLLREKQSQLESVAKLLLTKEVLSADDMISLLGQRPYGL
PRKVDNPEFKVEL

>putative degp2 serine endopeptidase Contig16074 (and 16936, 3997, 4088) (incomplete), 632 aa,
1134
MRQGFISTLARGWAEQGGHLRSSRTVKALGQSYGPLTRRDYSAAASSKMK
INNNPAVSSSVRTKEVTKRAPRGLGKRKAEEVLAAPQLIGSEMAGDKTT

AASAPVPVATVGQNEALRSVVRLEVAAAEPDYSLPWQKGDOPYTSGSACV
IESPPGKLRILTAAHVVANNTFVRAQRQDTARFFSATVVAINQDCDLALL
EVSNPKFFDGLKPLQFVDTPSLQNTVVVFGYPEGGESLCATRGVVSRLLEL
QQYQIVRSFKDEGLKLLTLQIDAAINPGNSGGPVLDQENKIVGVVVFQKMG
GMWTESVGYVIPTEIIRHFLTVDENGRSPQFCSAGFEYQKTDNDSLKWA
KLKKGQTVGMVTKVDELSSAKSVIQPGDVIITRVEGVEIGNDGTVLSSEK
DKENLRLSFEYFVTKKFVGEKLSLTLVRNGEEHSVKVTAEPKYLIPPHE
EQHGVAVPNYFIHAGLVFIGLNENYVGHVDAEPIVGRYYYYQNTKRFEDQ
VVVMTKILQDQVNAGFSQEHQHQLLSLNGCDIRNLRHLIDEVERCAEPFL
EFRFDSGERIVLATQPARATERILRKYGIRSAKSSNFLPVKAKATTKKK
TATKAQTSSPRMCKKKEKKNDSSTEKKEEELS

>neurolysin metallopeptidase M3 family E80POFO01AOL9H (incomplete - ** this gene prediction
has lots of mistakes ... I am not eve, 717 aa, 8AA

MKRIQRYTTRRNHPRLPTHATNIRVGVAATASAPHVLSTTSPASATASRA
VVVESLFAANPSSSSSLSTTIASRRASTTLTASTPAIHRLPPPQVLLPAV
VALRHSPFASRIHLDMLHADEHLWNLLRLHSMQGSRQERGTDALARQIFY
QLQRAASNAQSARSRRSDAMAGLLPSVMERGREVHIANRASISTDRKS
IHKFSRDPKMLRALRAGLALACGCASSHGRHLGGVCSLLTARDSQMXL
RFDLSAAEIAKTSHEVMESYKKVSGRFTEYNNHTMPQETLTPVQRRRTAH
RPLFTTFFHFRLLIYGSDALIEKTMHDFKKNGLMLSPEKREQLKAMRKMSD
NAITFQKNLNEDSGRRRRRGEQGPQVRVGRDRHAVCRTSHLLSDVLSHTTC
APRVIGRTSLKRSRSTTTIRCRRRHSLPCSDGVLRTALYSLHSTTTAFYF
SREELDGLPQDFLDGLEKVDGQEGGATKYKVSRLYPELLPVMRYANNAET
RRKLDTANAARSMRENTPLLEETLALRHEAALLLGYEDHASVLEDRMAK
NPAHVLDFINELSVKVEPLARREWEKMIALKKATVGGSDNVTIDSHDFTF
YNQRILERDYQVDENLIKDYFPFETVTEGMLGVYQDILGLRFEELNDAHT
WHRDVRMYAVYDRSTNAFMGQFYLDLWPREGKYPHAAVFPLVPSHHFSPG
SSSDIPASFLAHLHPVT

>ATP23 Mitochondrial inner membrane protease Contig3855 (uncertain of N-terminus), 180 aa,
1A68

MRERQHSQCETTIRDILIKDRVMQHLMAGMEDRGCVRVYKNNFFHCKQCTG
SDHGGYWDPEDEGVVICENNLEQKEMVRDMLHEGVHAFDDCRANVDWSNC
VHHACSEIRAANLSGDCSFRAEVARGHFNVRAQQKECVRRRRATLSVIKNP
NCPGADADWAVNKAWERCYSDFEPFGQVFN

>degP10 protease relative E9BS9UA01B3LRE (and 22468,21474,3995) (incomplete), 544 aa, 701

MAHMLDTLVKNDELATARVVVMGDMNVDTGHKALQAFSDSQTWGLVLDNA
LDVSPVAKRSSGFTTGWSKRSVGITIDHIFVRRHGGDPGARHSIMDVVRY
EVGTNIDPKIEGVLALARKRTSLFHTSSVVEARKASPALPLVPDDVQEV
PIEEANWEESTNMLPLEPVIKVYSHVTSPTYVMPWQMKATSEKVGSAFAL
SGRRILTNAHVADHTYIAVKKFSGTQKYPKAVLSVAHDCDLALLTVTED
DFWTDITPLELGDVPHLQDTPAVVGYPTGGDTISVTRGVVSRIEPQRYAH
ASGHLLAVQIDAAINPGNSGGPVLDKDDKVVGVAFQSLVNAENMGFIIPVP
IIKHFLKDIELHGKYTGFGAMGIQCQPMQPLRHFHKMARDITGVLVNH
VEAVSKAKGVLQKDDVLLSIDGNRIANDGTVAFRKRERIFFDYVTSMKQV
GEYCRLEILRNGEKQEVSVQLSPVQPLIKNLKQLAKLVAANKQPYLRFDF
DEHVVIILEADAACKAAEEAILTRHRIPSPHSPDLFDKKEETDVV

>ATP-dependent Hsl protease Contig14467 (complete), 531 aa, 43C

MLKRAARLNAAVVGASSSIPIMQRAAAARALRSSMREEALCLSSTSVHG
NGRTEADRLRFYSSENDTTTATVKSEEAAPPPVEEGKDEEQEVAAPATP
AEVERALLPSEIVNELDKFIIQAEAKKAVAIALRNRWRRRQLSPELATE
IIPKNILMIGPTGVGKTEIARRLAKLAQAPFIKVEATKFTVEVGFHGRDVD
MIIRDLDVAVVHDFMTKAREQEKQORVKQEVVEERLLDILAGAQAQERTKTM
FRKMLQNGELEGRVDFEVPQSTPATQMPFGSEMGAQGVFVQLDKIFGGA
KKQKRKMTIAECRPLYEEQEAELINKDAIVKNALEAVQSNQIVFIDEID
KICKDKNSYGADASSEGVQDRLPLIEGTTISTKYGNVDTSKILFVASGA
FHSCKPSDLLAELQGRLPPIRVQLKPLKKGDYRILTETKFNQIDQAKALL
LTEGVELDFTDDAIHEITKLTAEVNETVENIGARRLHTVMERILEEVSYE
CTPGKVTIDVAEVRKHLSELLLKTDLSTRYVL

>Heat shock protein HslV Contig17806 (and 5657) (likely complete), 267 aa, 1F79
MKSFARRGAIITAGLGARSSIATTGNGSRPLLPMTNGIITSSAAAAASY

HSEGGSGRHPGFWGPDPNPAYATTILCVRKGNSSVVMVGDGQVTLGSTVVVKP
NARKVVRQIRPGIVAGFAGATADAFTLFERLEEKIEEHQGLLRSCVDLAK
QWRTDKYLRRLEALMVVADKNISLTLTGTGDVIEPNDGIIAIGSGGTAL
ACARGLIDLDPIDAETIALKSMKVAADLCIYTNHNFVVERISIDADEAKE
KGGSNILSAPDQHKEEP

>pitriylisin presequence protease Contig2181

(23044,16875,23840,23534,18838,2992,E80POFO01EPXMF) (incomplete, with many gaps .. mo, 1163
aa, F27

MKRLLLATTARGRSL SARAAAAASAGIVDASRHALPTGAAATRLLRSRLSGS
SGATRPPORRGWATQAAAPSTTSQSTSIDFTGLKRGEERERPALAAGDKLH
GFRVLKVVPIPERNFMTYQLVHEKTGARLFHVDCSDTNNVFCVTFKTVPT
DSTGVVAHILEHTTLCGSEKYPVRDPFFNMLKRSLNTYMNAYTAPDHTSYP
FSTQNVKDYNNLLSVYLDATFFPKLEPFDFMQEGHRLEFEKIDGTPIANR
GMCQSPLTHTLSIGDSHQLDPSSALKFKGVVYNEMKGMVRSVCVTIFTG
PDLRPADRVPSKPLPPVQRLVRIAPAFLCFLNDSLLAVLPITDHTILWNI
RFYTYGDL SLEHRLQOINENVLSRFSQIDPGTDLPEVRLTQPKRVEAVY
PPVAGSDPKRQEKFTVAWLTKNTTDPFENMSMNL SRRLLLNPNAPMYKV
LIDTNI GLDYAPSTGYDSGAREAPFAIGLSGMNEKDVPKVEEGIMSTLKQ
VAAEGFPEERI QSVLHQIELS QKHVTTDFGMSVGHAINYTWIHGADPAEV
LSVNKKIERL KQELEAGPYFQHKVKQYFLDNPHMVSLLMKPDEKYLEKLD
KEEQARLEKIRASLSQAEIDDI IAKAKFLKERQEQQSALSFWEAHFTNL
KRPRLTRNAPS VRLQMCRFCLRFTRMCPGKRPTRTPGSNERRFLWRTRP
TRYPTRL CGAAAWNVGQGLTHRTDRVCHVLP LQIPLLSVPQPTNGLTYFR
GMASLNSLPSELEVPLFCSAMASMGAGSMDYRQLAQKIESHTGGIEFSPV
CSTHHS DLSKFRAGIYVSSFCLDRNLDHMFELLHTVLSAPRFEDVERLKS
IIYGNTSDMQESL VESGHSYARSLAASVFSRASALHETWSGISQVTLMOQ
LAQSEDVSTV IPHLKAIAEHVLDASLMRCSIVGEEGSLPQAEQKLT HLLG
GLKSSSSAQPTAAADYRESEYAPLSRPHRLFVPIPAQVNFVSQILPTVPF
THPDFPKLKALSSLVSSYLHPEIREKGGAYGSGAMSGEGLWSFYFRDP
NTTKYVVVVSTHAHTHTHSTHARAI SVVIDNAHLFVVFVIAGRQNVGRV
FVVAGMDEEGRRLSGQGHRRGQAPAVLLHRPPRRPVPTRLTTMNYEKKKK
KKKLTNRCEYVCV

>X-prolyl aminopeptidase Contig7161 (and 25246, E9BS9UA01B4HZO) (likely complete ... some from
PGP), 520 aa, 146A

MQRGRSVAARAFAGRARGAASSSAPSSCLSFSSAVGRRRCLVSAATPGGE
RRPFSSSSSRMGLSDSLAGKRPRPMNYGQPHSTHPLVKEGEITPGIT
AKEYAQRRENLMARVPVGTVMIVPSHPMMMSYDIPYSFRQQTDFYYLSG
YQEPDALLVLAKRSDSEPIHF'TMFLRPRDPAREIWDGPRSGVEGAVSFFG
ADEAHPIDRLAEKLDLTDGVKNILYSPDVHLEFTHQIFALIPPEKIACP
RNLLQTMRLIKSPAEIDVMRRSTEISGQAFREIMRATQPGITEGQLAALY
EYECRKRGSORLAYPPVFASGIHANTLHYVANDDIMQDGMVLVDAGGEY
NMFSSDITRTWPVNGKFTPAQLDLYNTVLDVQKKEIELCVSDGRMSPSAL
HQMSTQFITEGLKNLGLIKPGQTSGVSRFYPHSIGHWLGMDVHDVHDVST
RVPFKPGMMATVEPGIYVDPDPDIPAE LRGMGVRIEDDVLITTGAP EILT
AGAPKEAHDIEAVMRDRKPL

>aminopeptidase N Contig3296 (and 19646, 2341, 22716, E9BS9UA01DOPF5) (incomplete and internal
gaps), 813 aa, 1AA5

MLRRRCTTATAPAEQQAELGLTWLADYRPPLYTVDDVHLTFGIEDAHTT
VSSILHCRHNPKAGEMAPIVLDGGPPSDMKLLSVTLDRVPLQAGSDYKVP
PGSNKADRVAQCPQVCVLTQVQVDEASGRLHISKRPAQPAFTLEIATAIE
PKKNTALEGFRRITYFFDRPDVLAKYTTTIVADKVYPVLLSNGNLVAEG
QTEGGKHWAkWEDPYPKPAYLFALVAGQLHYLEETYTTAASKRKVTLRIY
TEEENVYKVGHAMASLRRAMKWDEDKYGLEYDLANMNIVAVNDFNMGAME
NKGTRPFPSVHIRYKSLLVYFHNITGNRVTLRDWFQLSLKEGLTVFRENQ
FMADHHS PAVQRINEVTTLRNSQFREDSGPMAHSVRPAS YIDISNFYTTT
IYEKGAEVVGM LHTLLGDDTFTRGVQTYLRENDGKAATVEDFVRAMETVS
GRTLSQFYRWFGLHSRALS VRYDQAGTPEVKVAKESFDERARQYKLT LAQ
SPASTPGQPAESKRPFLLIPVTVGLLGRYPLRHIWARPEARLTNRGVMCVD
DRDGQPIHSQ LSDSDPELASHTLELSDVEQS FVFNNVASKPVLSVLRHFS
APVKLVHQQT KEDRLLLLRHDTDAFNRWESCQHLALDAALALVEQQATSP

PVRAPILVGGFIAADLLFAFSAPESSISHAGHLGGALYGLLYALYLRRRF

GRR

>Oma1 incomplete, with gaps ----- NOT DETECTED -----, 302 aa, 594

TLPSALIQRHKSQYFHKFHHKMRTFWSQVQKEGKRPKRLAFAVGLLL

AIPLGGYGYWQYYQDIVPHSGRRRMDVSREEEQRMGLASFHLLKQYKD

QILPENHELVLAVKRIGRIIEQTDLQGLHWEFLVIQSDEMNAFVLPGGK

VCVFTGILSVTQDEYGLATVLGHEVGHVVARHGAENGWERALGWLTAILI

AREEPGWLINQFLTLFLALPFSRKFEHEADFIGLMLMAEAGYDPTNAVDL

WIRFSAASPSMLKYLSTHPPNADRIVLLKRWMPQALDQYHKHTRPQATAV

IV