

Initiation:

>IF2 g476.t1 (incomplete/incorrect N-terminus ... from ESTs, PGP and inference)

NOT

DETECTED, 741 aa, 78

MIVRVCGIVFCSYASSPRHFIFHILLFRAPLPSPHRFLNAIYGVNIDGSG
ISIHSARQCAVRGRCSPIIIVSFDIFLDSDFNGEQLSIDFLMTQAGGTRR
LYATASEMEKSKMVRKRLAATRKRKLEELKERKAKPKEISIPSRATPKNL
SAVTGLSTIDILKVAIKCGHEPRTVDDVLPPELVDILCEELYFVPRRSDL
NEGTGMKLTTRTIDEADMVPRPPIVAVMGHVNHGKTSLLDALRKTSSVVDVE
EGRITQRLSASMVQLSSGQKITFMDTPGHNAFAAMRQRGAAMTDMVILVV
AADEGVMQQTTEEAIEVTREANVPLLVAINKIEKEGANPSKVQRQLLQHG
ILEEFGGDVQCVELSASTGKNLDELTDAILLQAEMLDLRADPNGPAESV
IESKIDKGRGVVGTVLVRQQLKLNFFVAGGTWGRVRGLTDWLGRSTTK
ADPSTPVEVIGFKTKILPDPGDDLVVVLGEEQAKQILDYRKERLHAKEAL
TDVVQASDPAARAAAQKQEMEKALNVVIKADIGGTLQAVESTISQFPQDE
VKLRRIKSAVGDISTTDIGLAKDTGAVVFGFNVPMMNSVLELARVEKVDI
NNYSIIYQLADDIKRLESMLAPREVEEEVGRGDVLSVFSVTMPNREQHN
VAGLRVVRGALDSRLRVLLRRNKVDNADEEYAALYDGPISLKKFKDDV
TLAKKGDECGLALPKWNLDRPGDIISCYRMKQVPRKFGDPK

>IF3 Contig19975 (and 15548) (complete), 302 aa, 19EB

MKTTTRRLSLVTPRLSHGVGLGSAQPFRRSYSRPASCYGHERACSSLVAQF
NLYRSHQPLVTSSFTAGORRAYAGGYRKTTRVALLVDDAITSDDVQLVSL
EGRNLGEVALADAKLLAKQKGLRLACVVPLANPPVCRLQRIIPVPEVDEL
DDRRDPPEDEIDDFDEDGMPIHRPSSASSSSSSSYNEAAGGGVAKDVPDPN
GNIKRRPKGEKELRFSDTIAEHDVQNKVNQLRRFLDKGLRVRVSVYFKSV
AQFDPDLARALLDNIVTRADDLGRVEGDINIANRFASLLLVPTSPDAATK
DK

Elongation:

>mitochondrial elongation factor G Contig26230 (and 27675,1208) (mostly complete), 777 aa, 1576

MYSASRRASSNPSASGFMRHSAGLMRPSTSSASTLCLNRAPSAMINLPLL
SRFSTDAEGSAPQKELHKIRNIGISAHIDSGKTTLTERILYYTGRIQKIH
EVVKGRDNVGAQMDSMELEREKGITIKSAATYARWGENHINIIDTPGHVD
FTIEVERSLRVLDGAILVMCGVSGVQSQTITVDRQMKRYDVPRITFINKL
DRMGADPFKALRQMKELTHVKSAAQIPVGLDHFQGVVDVITREAYVY
EGGSGEVLSKVAVPENVRAEMEARREELLETTYEVDDVLAEVVIAEGREP
SVEEIKAAIRRATIALKFTPVLMGSAYKNKGVQNLDAVVDYLPNPTEVP
SVGYDLDNNEAPVNLVPEHDKPFVGLAFKLEENPFQQLTYMRMYQGVLLK
GDTIVNMSTTKRTKVPRIIRMHSDMEDIQEVGAGEICALFGIEWLLRHH
LHRRQHPPLHVLHVRPDPVLSLAIWPKAKGQDKNLSKALNRFQREDPTFR
VHTDPESNQIIISGMGELHLEIYMERMRREYNVDLDSPPRVAYRETLTG
KGAFDFTHKKQTGGQGYARVAGYVEAIEEEDLEEHEQKALASGKRVLFQ
NQITIGGSIPPNFIPACEKGFEEAATEGPLIGHPIQGVVTLTDGGWHPVD
SSELAFKIACINAFKQGMKANPQVLEPVMGVEITVPKEFQSTVVSSIGK
RKGVILNSENMTGTDYTRVDAEVPLSNMVGYSTDLRSTTQKGGEFSMEFK
KYAIVPRDSMEKLI AKYKEDKAKEKDD

>elongation factor Tu Contig9759 (complete), 449 aa, F32

MASRSFSRLGFSSQITAPARLTLPLRSRADFSRTLPCAYAGAQSISTYRA
KPHFNICTIGHVDHGKTTLTAAITKVLADTGLAKFRDYQSIDKAPEEIRR
GITINASHVEYETDKRHYGHVDNPGHAEFIKNMITGTSLTDGAILVVDCS
TGPMPQTRHILLARQVGVKNIVVWLNKCDLIPDKELQDMVAMEIREELT
RYEYNGDSTPIIHGSALEAIELKDTYGIQAIRKLLATVDELQPERQTD
KPFLMAIEALYTIISGRGTVATGVVEQGVKIGDEVEVLGMQEDAKKIKGV
VTGIETTFHKQMEEGFAGDSIGLLLRGPNRDDLKRQVVGKPGTLSAHKKF
EANVYVLTKEEGGRHTPFGAGYAPQMFRTANVTGKVMMEGDKVAVPGET
MNVGFETIWPMLSEGLKFSREGGMTVAAGVITKVFPEEEGKKKKGGK

>elongation factor Ts Contig3833 (and 9737,E80POFO01CE59P,E80POFO01DE9EK,E80POFO01EPRIT)
(incomplete - internal gaps), 365 aa, FD

MKSAFACRAAFALAAATTGSGRGAAVFAVRSSSSSLVSLRTPASGGCSNSR
AFADAAAGGGGGMMQIKELRARTGAGVMDCKEALAASAGDPAKAEWL
LDKARSFAKKAERPTTEGTLALALASSEALLLELNSSETDFVGRLEGFQK
LALDAAAAALARAGQVAADGQGPHELLSAWLSALPLGDGTPKTVGDGVV
LFMQVGENMKARRAVLLRTAGSEALGTFIQGTGLPHTGTALVALQAO
PSGGGAAVGEKLVPLANALAKHIAGINPRYLSLEDVPETEAKVGEVKEHV
VLEQEVTYGEETGRVRELLEREGAKLGARVSIHVFRVWVKGDLKPTTD
FAAEVEKELQRSTKH

>elongation factor P Contig26691 (likely complete), 254 aa, 1487

MRRHLQOSTAGSLPSSVQHRRNYKAPISDIKRVVIEHLGKLWEVTETSQ
SRKTAQORRAHINMELRDLAAGTKKSERFRVEDRVETIILDVHKCIFSRSE
GKLLFTNAETGEEVSVKEMVGPAAEAYLKPGTSVARLSVHNGEAVTVKL
PGKAVVTVKEADSTQSATAGYKKAVALDNGRTVVRVPPYLEAGDVIIVSLPD
EVYVKGSDGSALADDGDEEDDEEDDDDDTDTDEDEDEDEDEDEDEDEED
AKKK

Translational GTPases:

>GTP-binding protein TypA/BipA Contig1617 (and 775, 15798), 740 aa, 62C

MLRSALSRSSSSPLAGSASSRSSLVRAFSSSRSTAASSSSSSSSSGN
RLHRCLAAPSTSSSAQSSSTLISSQRPLGASLRRTAPWSALRQVGHGWP
SLASHHRSVGVGRALARRWLSTEAEGAEDLGEGVRNEKLRNIAIIAHVD
HGKTSLVDKLLSQSGTSLRGGERVMSNALEQERGITIMAKQTSIKYKD
YTINIVDTPGHGDFGGEVERVLGMVDGVVMLVDGTEGMAQTKFVLSKAL
GYGLKPIVVLNKMDRDTIRPDEVESEFLDFVSLDASDEQLDYVTLYASA
REGWAVKNRTAPRTDMTELFETIIIEKVPPPLTYPDAPFSMLVTTMEYDMH
LGRILVGRVRSVSTTGDQLHGLSREAKELEKSKVLKVLGRRGLERSPIE
RGECGDIIGIAGFGACSVTDTICAPSVVHALPANPIDPPVLSVVLVSVNDS
PLAGREGTKLTSTLLRQRLYRELESNTLQIGDTGREGALEVKGRGELQL
AVLIENMRREGFEISVSPKVLFKQEEGELLEPEQEEVTVDVPTEFSGVVL
ERFGLRKGELVEMKTDGDKARLIFMCPSRSLIGFRQELNQLCRGTVVLHH
LFHSFIPHKGVIENVRKGVLLSNTNGTTTTYALESLERQGTMFVGPSTTV
YMGMIIGENSKKGDMDVNPVKAKALTNMRTLLKDENVRLTPPRILTLEEA
ITYIADDELVEVTPSALMRKEILDSTRETMMARRAKKSG

>Guf1 g3637.t1 (possibly complete ... N-terminus from Genscan) NOT DETECTED, 606 aa, CE1

MLGRRGLLASRGPAAAVAAEEAAARGAPDLSKFPFSKIRNFCIISHIDHG
KTTMSTRIMEKAGTISLDKEGLYLDKLOVEKERGITVRAHTTSLVYKHS
GESYLLNLIDTPGHVDFTYEVSRLKACQGAVALLDCTQGIQAQTVANYF
LAWEANLKIIPVMNKIDLPTSDPARVIKELANMGFESEVLKASGKTGEG
VEGILKAVIERLPAPSGDPAKPLKALLFENWYDQFRGVVCLVNILDGALK
KGDRIVAASSNKVYELENVGILYPERAPTALYTGQVGYIIGMRSTKEA
RVGDTLYLEGAPVEPLPGFKSAKPMVFAGLYPADGESLDRLTDAFEKLT
NDASVYTKERSDALGMGFRGFLGLLHMDVFLQRLQEQEYGTDVIAAPT
VPYIVTTKEGQEIIVNNPSLFPQHDILTCTEPVAEARI IAPKEYLSPLL
RLCLERRGVQOELS IDEARLHLRYRIPLSELITDFNDSLKALTSGLRHP
VEALSAIAHQSKGVNYGKDLVQKLRKVVKRQLFQVAIQASVDGRIVARET
LQALRKDVTAICYGGDITRKRKLLKQKEGKRMKTIGNVQLSQDAFYSI
LKKGDE

>YchF g6187.t1 (likely complete) NOT DETECTED , 435 aa, 203C

MKVATRRSTTWGSSRSATSTFVGGGRSVLWPPSSSCLTSGSGVLGVRR
QWFAAKAGKQOQTOQAAGGQASALS YFVARTASNGCGIVGMPNVGKSTLF
NALTSQRARAENFPFCTIEPNSGMVWVPDPRDLTLAALANSKRILPCQM
EFVDIAGLVAGASKGEGLGNKFLAHIRNVSMILQVRCFEGADGTEQVTH
VEGSVDPARMEIINTELLADLESITTARAKLEKRTKLDAAEQKRLDLM
HRTIAVLDEGQPARSVLISAEWPTFHAFQLLTSKPVVYCCNVKEEEAAT
GNAMVEQVKQAVLKEEPGVDPNERVLVVS AKLESELANMESVEDRKSFL
LYGLSEADAGLPKVI RATRQLLQHQHFFT VGETEAPRLEHTQTIAFADFV
AAGGEKRAKELGKVRFEGETSYVVQDGDIIILFHHRK

>EngB g15942.t1 (incomplete - poor genomic, poor EST data) NOT DETECTED, 134 aa, 19F9

AFIGRSNVGKSSLINALTAQKVRVSDTPGETQQINWYRVGKHLTLIDL

GYGFAAFAAEKVKAWTELMCEFLTSRKSLKRICVLIDARHGFKPADLDFI
DMLEKAKRKYQIVMTKADLVTPPDLARRYHLVQQ
>EngA g13051.t1/g13050.t1 (incomplete due to retained intron ... N-terminus uncertain) NOT
DETECTED, 675 aa, D48
MPSMSCPIASARGLATSRGAGGSRGGGSGRDRAQQOTTRPHSQKSSSSSS
SSSSATRGAGGKGGGKSNAARGPGAAAATKKRAPSGEASKARPAAEFEEA
LGGVESDTERYTMRRDPVLALVGLPNCGKSTLFNRPMVTMGRLVVRMKNKSL
VTSEPGTTRDRVYAYCDIGGRSVMVVDTGGMVGTGDDFFSPLIHEQALVAI
NEADIILFLFDFREGVTKKDVVARVLRKHKVHDKDIVLVANKCDNPDVLV
ELDERNKAGPTGKPPDYWLLGLGPAIPVSAIHGAGAGELLDKVYDIVQTK
FPAEDQSEGDAEAEAEELARKRISISIVGRPNVGKSSFLNQVLGRERVIVT
NVAGTTHDAVDHSIMWRGKKPRKRRAAKATMGLEEEAAAATTEGKQQD
AEVVHAAEDDEVIDEQEDDLEDEQEDDLDDDEHETKVRAKKANNTKLKE
SAANPDADGVPIRIVDTAGINRRATHVKGLERSVWLWAIKSINRSDIVLQ
LIDATQGITDQDLRIAHEHILNSKATTIVVVNKWDMSSKESKQKWEKYVQET
LKFMKYVPIMFCSAKTGVNVKETIDLAIRITRERAHFIKTSTLMKLLISA
HTRHRPPSKNGRQLKIRYATQAKVKVPSFTFFVNDVELVHFTYQRFLENA
IREFHPTGSPMRLIFKDKEKTIVS

Release/recycling:

>Rf1 g10217.t1 (possibly complete ... from PGP), 370 aa, 1643 NOT DETECTED
MAARQRWVSMQAPLLLFHAGSPFPRLDHMKHQFDDLSATLQTNALSPEE
RGMLTKQLHALDPVMGMVRRIEQQREELRELHQLMEESKQTDKELGALA
EEDYKRILGELMDLEKELENEIMLELLGKDEADEKSAILEVRAAAGGQES
QLFTMELFNMYSAYAEMKDWETLAVSDSEVGGYRESSACITGRGVFGR
LKFETGVHRVQRPETETQGRTHSTVTVAVLPVAQEADIQILPKDIRVD
TFRASGPGGQHVNKTDASAVRVTHNKDRAMKILRSRLYEIERERLASSRAD
QRRKQVGTGARHERIRTYNFPQSRITDHRCLTVHDIEMMQGHLLDTFI
DALVAHHSAAEALNSIDLDSF

>peptidyl-tRNA hydrolase Contig8428 (complete), 216 aa, 6A2
MKRSLGLWKRYPYAGVNHILVGLGNWYYPLSRESVGLYALERYAQRYSLVW
DFIPNICSDALASKTGIALIKPKTYQQKDMGKAVAMATEAMNLTIDDVTI
LHYDANLPCGQVRYRTGALDAPNAVQSIINMFDTERLNRVSIGIKPVSE
DEVFVPTIVQAIDKRYLDNFNDIWRNVLSDTERPLVDKASDKVTDELLH
SATNTTDNTFSRLNTL

>ribosome recycling factor Contig11098 (possibly incomplete at N-terminus), 180 aa, 10F
MAQTKDSLTSQMKRSVDWLTTEEFAKLRVGRANTEILNRIKVEGAPLAKKG
SVYVKDSFTLAIPTPEFEKEQTKKIVEALRDADMDLNPQTDGDNIIVRLPKA
TDEYRQSLKQATKMNEEVKNSIRRARQGALTDLKKHKDAVSKDDMKKLE
NEVQKITDEYNKKTEQLHKAKEQAITGAGN

>EFG2 g6016.t1 (incomplete due to internal gaps ... N-terminus inferred) , 669 aa, 1A01 NOT
DETECTED
MQLRRATLRVGPVAVTIAPRSGGRQWWCQARHSGSSSNSPAAWPPQQGGG
SLVLSSSSSRLIRPSFFLTWVHRRQOHSEAEVVVERVRNIGVVAHVVDAGK
TTTCERMLHYSVTRRIGDVGNTVLDVDFMKLEQERGITIKAAAITFNWE
GHKINLIDTPGHVDFMFEVERSVRVLDGAVAI F DGVAGVQAQSETVWRQA
RKYGVPVIAYINKLDREGASLERAADSMRVRLGARPLLLQLPLPTTLGV
EGVIDVDMRVIRWTDPSGKAMQVVDLTPEEHPGLYAKALQARETLLEQL
ADADEAIMRAVLEEGASAETVAGELLHGALRRVTLAGEGVPVVCSSLRN
RGVQPLLAACRYLPSPLDRPPVVDVQGLMVYLRVYSGELTPATEVYN
STRQVKERSRLLNIQADDMEVGRVAGNIVAALGLKDTCTGDTLLVPA
KGNKKAHKGQHAKGGRLLLEGLDPPPPVFFCSIEPESLSAQKALDDALGL
LRKEDPSFSVSLDPETGQTLLSAMGELHLEILKDRILNHYRVGARVGNVR
VSYRATVGRALSHTLAREYEIGGVKQHVLETLTDIEPTARAHGNEYQASGA
GRGMVRAHVLPVPHRLVEAEAPLKELLGYSTLFRSLTRGSGSFTMEFLRY
GDMGAAESKKLQDELRRGF

tRNA synthetases:

>glutamyl-tRNA synthetase Contig20313 (and13024, 27108) (incomplete due to internal gaps), 555 aa, FF4

MKSSTLVLRSRFVPAGARLGGVLRPLPTTTAGRFYPYTPSSTGRLHSTCSA
ESSSPASGLIDPGRVRVRYAPSPQTGMHLGGLRTALYNFLFARKHGGDY
VLRLEDTDQSRKVEGASANFDRILEWAGIPYDEGSPKGGNYGPYVQSERL
PLYHKHAHDLIEVYLHTFHSFMVSLLLGLTEERLDQLKRSSNIRGIPPLY
DRFCLNLTPOEVQHKLMGVPHTVVRMKVPSGVTSTFDIVRGAVSFNNAFV
NDQILVKSDGFPTYHLASVVDHLMEISHVIRGEEWLASTPKHVMLYNQF
GWDVPRFAHLPLLLNPDKSKMSKRQGDASVDHYIEREYLPESVVNFVAFI
GWAPEDTQEIFTLEQLIEKFSLEKRVHKGGAIVNINKLDWFNGTDDIDWVS
ARVRPVLEQALPSSASFPDAYLHQVIRLNKDRAQNFTDFVEPSRFFFEAA
DLASPEAQKARSTLWKPGQSETLVRALLDRLEKADVPMEHDPLLLALVKEV
CKEHGAGSKVLFHALRYLLTGGKEGPGVVDTMATLGRPRTLHRLRQAFSP
AAPPS

>phenylalanyl-tRNA synthetase Contig21167 (N-terminus incomplete), 457 aa, 215A

TKQIDVTAHRSASTSIHCASRRAGASLTGSSRGVSLQLRPRVLGTPASG
SVLATRCHLLEQAQPLRLSSAAKRFYASSFSFKEHGIEPDEVTNVTDRIL
GKIGTNLHKEDKHPLNTIKKRIEQYFVNKYTTEDNKPLFNIYDSFKPVVS
VKQNFDDLLFPVDHVGRSANDTYLNLKSTLLRTHHTSAHQAEMLRSGERPR
SGERQFLVTGDVYRRDAIDKTHYPVFHQMEGVRIFTPEQLKAQNKTPPEEF
VAADMKDALEGMISAVFGKVQVRWVDAYFPFTHPSWEMEIFFENKWLEVL
GCGIVNPQIVRNCGMPISEDWAFGLGLERLAMVLFDIPDIRLFWSDRRF
LDQFASGENVKFQSYSKFPKYKDIWFVDPDFHENAFFELVGQVAGDLV
ECVEVVDKFTHPKTNRTSLCFRITYRSMDRSLTNEEINELQAKVRDEVPV
KLGVELR

>leucyl-tRNA synthetase Contig9820 (and 12901,4046, 11402) (incomplete N-terminus), 700 aa, 134A

EAVVLQDHRIRGRS GGRILAGLKGWPEQVKLMQOHWIGKSKGAYLEFPIK
RELSASSGAKAEPELRIFTTRLDTLGVTYVVLAPQHPLVQEIANKTEDA
KLRAFVDEFKSKRSLQEDYDGKSKKGMKLPVGTAVHPVTKEVSLPVYIADY
VLMDYEGEGAVMAVPAHDTRDYEFKQFDLPIKTVITPDQHTTEHKEGDPF
CGEGRVVNSGPELDNLTSEEARRKLLRILGEQGVGGEYTNRYLRDNLISR
QRYWGAPIPMVYCEADCGVVPVEKDLPVVLPVDGLEFSGRGGSPLGSLE
HNLHTDCPKCGGRAKRETDTMDTFVDSSWYFLRYPDANNTDAPFDKAVTN
KWMPIDVYIGGIEHAILHLLYSRIFITKFLHAQGHLLNFSEFPNLLTQGMV
QGRTFKDPHTGAFLPKPDTVEKVGDKFIHKPTNQEVASWEEKMSKSKYNGV
DPDRIVDEWGADTARLFLFKAPPHLELEWENAGITGAYRWIGRLWNLVN
TFVQRDPSADTPSPPPSVTERAKEEKDLLALTHEITITSVTKALDAAPYSF
NTAVADLMKLSNKITTLPADSPQYYLSLRSVLVLLHFPAPHVSSEMWOAL
VAHGPAHESAWAGSSAAPELSRQLWPVANEEFMKKDEVVAVQVKGKTRG
TFVMPAAEVGDKAAVERYARESAVGKALWQRDVKKVVIPPNGKIVNFVC

>aspartyl-tRNA synthetase Contig12808 (and 23127,16011) (incomplete N-terminus), 617 aa, 81A

VTAADAGTSVRLCGWLTASRDFGGVFLVVKDHTGPVQVLVDEKRLTPGL
REQVASWRIESVVTVTGKVQLRPASMQNKDMPTGEIEIVCEDIALLNPTS
HTSLPFPSSWSSPLHGDERDALPPEELRLRYRFLDIRRPYIQDNLRLRSQ
SLAARNYLHGQGFSEIETPTLFRSTPEGAREFIVPTRTRGKFYSLPQSPQ
QYKQLLMVGGIDRYFQFARCYRDEGIRFDRQPEFTQIDMEMAFVGD RDVC
NLTEGLVRTMWKTAGHTLPDPFPRMSFRHAMETYGSDKPDTRYDLLLLRDV
TDILQQSRVNVLTAPLTAGASTDAAAHKKGPGRCIKAINVRGMADLSRED
SDGIQKRARDLGGKGVVEIRCGPEGKWRSPIEKHLTDGERRRLGDALEAQ
EGDLLLLCSGPERDDVSLILGGIRSHCAKLMKRRGKLSIXDDQYNFLWVE
EFPLFSFESASPEAKRIVTTHHPFTAPHPDDIDLLMSSDAEHDLLRVRG
LHYDCVVNGVELGGGSIRVHNEAMQRHIFRVLGMSDNVMTRFQHLLDALG
MGCPPHGGLAIGFDRMAILCHAESLREVIAPPKTATGNELMTGAPSEPG
LDELKEYHISVAAAPPS

>valyl-tRNA synthetase E80POFO01A7STM (and 19665, 14725, E80POFO01A4SJK) (incomplete at termini and several internal gaps), 943 aa, 2605

MLQSLRRKKAGGLASIHASGALIPRLEIRSSAVLFRSTFVRSSTTSRRT
LTSASRTKPPTQGPLAAAYDPVRTLCPHQQAPTTLCLVTRHTRHTPARTQ
KAIEGAGWYQWYESQGYFRGKNGVPPGHNFMSVIPPVNTGTLHIGHTLT

VAIQSPQDSIVRWRMMGDVNLVVPDTHAGIATQTVVERRLQKEKKLTR
HDLGREAFIDEVWKKWETHGNHINNQLRRLGTSLDWSREVFTMDPQRSKA
VTEAFVRLHDEGLVYRSTRLVNWCCFLQTVISDIEVEYESLSRRTMIALP
GKGTKKYEFGVVIHFLYRVEGGGELEVATTRPETILGDSALAVHPEDPRY
VDFIGRRAIHPFTGQPIPIVADPILVDRELGTGVVKITPGHDFDDFACGV
RHNLPRLNLLRNDGTLNQHGLHFQGLDRMEARRKVIIEELEQMGLYKDKKD
HESRIALCSRSQDVLLEPLLKPQWYVACQDMGADAARMVRDGTIELIPDFH
KHEWYRWVENVEDWCVSRQLWWGHRVPAYKVVAEAGEERAAANNKDNNDLP
EDWQKERWVIARNQEEALEKAKALYPDIAAPKLEQQOQEDVLDTWFSSSLF
PISALGWPDNTQDLKEFYPLSVMETGADILFFWVARMAMIQVYLHGMVRD
AHGRKMSKSLGNVIDPLHVIEGIPLEQLLQNLNHNLLDEAERKKATAGIK
SDYPAGIPQCGTDALRFTLVNYTQQTRNINLDINKVVANRHFNCNMWNAT
RFVLSYAESTPVAQPEPDDLASKWILSRLSQVVTKCNQGMDSSEFHVATS
SLYDFFLNEFCDVYLEYAKASLLQPRPRQAQIKNVLNTCLESYFRLLHPF
MPYVSEELWQRLPEDCLMHAAYPLAANQVAAWRNEEAYEKPMEEVLRVLH
AVRSLRDGHGATPLKYSVSIHTTASLYDLLSNEASVIRHLAR

>alanyl-tRNA synthetase Contig25588 (and 8930,22115,) (incomplete with internal gaps ..
largely inferred by genscan), 930 aa, 2453

MWRRSAGAGGKQWAVAGGRRVNGGGPSPQHLLQLLEAQRGLSTTSPSSRAS
SSASSSAPGRGAGWVRGSMFDYMSRAGHEGRASAPLVPPRGDGSLLFVN
AGMVYPKDSFLGRVPPAPRVASVQKCVRAGGKHNDLDNVGHTARHHTFF
EMLGNFSFGSYFKEDAIRLAWTYLTRELGLPKERLLVSVHDDREAANIW
HAQEGVPLDRIVYKYAKKGDENFWSMGDGPGPCGCTEIFWDQQQEVVDG
DSFLEIWNLVFMQYQRTESGELQPLARPCVDTGMGLERIASVLQGVRENY
DIDTIRGLVHGTRTILHDKFGGVHQPQAQLSPQESVALKVRASCFLIGDG
VIPSNVSRGYVLRRIIRRAARYANTLAPNRNQGLLADVGKLVIAQMGEAY
PDLFTRQNVILHLIEKEEEAFLATLEQGLAYLQDALRNNPGTDLPEVVI
HLYIRLGFPIIDLTHLIVKENNKTFDMNAVDRMLDEEREKSRHAHAFSLSS
APSSVKLGEGGVPTAVKEWMAEGIAPEFTGYARQVEEETSVALLPDLQR
RTLWLSISPCPFYGMAGGQVGDGKRLIVSGGSGKTLSELRLRVEDSLIPY
EGGLVLRVKVDKGEQGEVSEGELKELADKLIKQVGLRAEVDDRHRRGV
RAHHTATHLLHASLRQVLGTSIVQAGSLVDANRLRFDFTHHSPLTDDQLQ
RIEHNVREVIAAQDTPVATDMREYAKAVESGAMCLFSEKYPVVRVVSVP
GFSTELCSGTHAASTGEIRPFKITGQTSVALGIRRIEAVAAEAADQWYDA
QYQYLSLGRTELEVAVPKIEERVKRLARERELEKEVGVLRKCLASSAAN
SSASQSLAGTYSGHPLAVHVYPEGDDDKVLAKKAEQLREKEPGSVHVVS
GRKVICTLATDQLPALKANKVLQDMLATVG

>Asparaginyl-tRNA synthetase Contig8636 (incomplete), 445 aa, 2304

MPWRVSDILSKATPGQDLVIKGWVRTVRQKQHFVLSGSHQTPLOIV
ATPELVKGASTGCSIEVEGKIVESPAGKQKLEMVASRLNIIGACDPEKYP
LAKKKHSLEFMREIPHLRARTNTIGGVLRVRDTAASAIRDFFHENGFIEL
HTPILTSSDCEGAGEQFTVSALMPASSEQGPREFFDRTVGLTVSGQLQA
EMAACALSRVYTFGPTFRADNSMTRNHAEFWMIEPEIAFCDLNLMRVA
EHMVKAVIEAVLAKCDEDMAFFHKRVDGLMARLHKTLAGPFQEVTYTDA
VKLLEKSGKKFEFPVAWGLDLQKEHERYLVEFEFDNRPFVVTHTYPKDIKP
FYMKLDEDGRTVQAMDLLVPTIGELIGGSVREENLDTLQARMKAMNMVD
DYQCFGTVPHAGFGLGFERLLQYVTGMDNIRDVIPVPRYRGYCRF

>isoleucyl-tRNA synthetase E80POFO01CUGC0 (and 17388, 3605) (mostly from PGP), 1057 aa, 17D1

MLRRVTNKGLSPLHRGAPLLPHRLGGNYNLQSLHFANSSARRLHRGFA
SSPASEANSAAPAAATANSKAFGHTLNLPRTTFFPLYTTEKAQLQLEGLS
LAEVSDNLYAWQVLFATFIPCPRHNNNAKRASSCTMAHPTPTGHCTRVRF
THSQTPIVVPRPLNAGNLLVRTGHVMNKVLKDIVNRYKLLRGHAIKYVPG
WDCHGLPIELKAVDQAKSGSTLSPTEIRAKAHACAEAAIAQOMKGFERSWG
VMGEWNNPYATKDPKYEASQLGLFLDLYKKGYVYRGLKPVWSPSSRTAL
AEAEEVEYSPTHVSPSVYVAFSVKHLANKAGELSRFNNLHALIWTTPWTI
PANMAICVNPNI EYSVVKTTDQHDKHVVIASDRLQAMQELLKQEI EVCAR
LPGSSLADTIYVHPLDGRELKVLPGTHVTTESGTGLVHTAPAHGADDYV
CKAHGIPLRSFVDDNGKFTQDLPEFAGKFFVLGPGNELVIQALTDKGALVH
QHKYTHKYPYDWRTKKPIIMRATEQWFVDLKDVVAPALDEISRVMVPAT
GRTRLESFIRSRQEWICISRQVWGLPIPVFYSRQEGELLLTEESVGHVQKL

VAKHGSDCWWSMPTSELLPPSEKHNADKWEKGRDTMDVWLD SGVSWHSVL
HNRELPFPADMYLEGS DQHRGW FQSS LITSVALTGKAPYRAVLTHGFVLD
EHGRKMSKSLGNTIDPVALVNGDEKKAGCGVDVLRMWVASSDYSRDTLIG
PVVINKMKGSLRKL RNTARFLLGNLADYDRRQAIPYDDL T GIDRYMLHKL
HEFSGVTTDYDDYQFSKVYRGLVNFATVDLSAFYFEVVKDRLYADATDS
LRRRSTQTVLRHTLDALTAALAPIAPFTAQDIHRHDAQAAA VAPNVFHLE
WPRAGDQWKQDGM AQOWDAIRDVRSQTYK VLEAARAHKVI GSSLDARVRL
YTGSDDNQVARWLA EPTSDELAEILVTS AVDLVPEAPAFEVVDDRPPQAD
LTS GPTPSFVGGGLVHAVPVGVEVVPASMHAVKCPRCRWYASAEENTPCP
RCAQAMA

>threonyl-tRNA synthetase Contig6211 (and 15382, 5592) (possibly complete ... mostly from PGP), 797 aa, E37

MRRGAGAASATAASVRRSMGRVPASSFLLTQORTCAQKSGSMRTPAACFS
RSVRVRPPSLAGERPFLRRFASASVVTHRAVPAEARP GKAPSSLPFMQR
RLELWREEWERQQTGKEAQA AAGEGPHPIKITLPDGRIIDTSSSTTPLQV
AASISEGLAREVVVARVNGELWDASRPLEQDCRLELLKFDSP EGAGVFWH
SASHLLGLAIEREYSPATGEHAESSAKVQLCDGPALSDEKGG LGGFFYEF
FLQPGEGATGASTEDFAELEKRVEAFAKEKRQFERMTVSRDFALQMFAYN
DFKREIIEAIPAGEELTLYKCGEFIDLCRGP HIPHTGLVKGFKLVKVSGA
YWKGDSTRPLLQREEA AKRDHRLIGKKQGLFMFHQWSPGNAFFLPPGAKI
YNKLMNFVRDEYRVRGYQEVITPLVFNKELWETS GHWQNYKDDMFAVTGA
SHAHGHDHGHAREGHSCAHHHHS SAGKEEVMGLKPMNCPAHCLIFSGGH
YSYRDLPLRLADFGVLHRNELSGALTGLTRVRRFQODDAHIFCAEDQIES
EIGGCLDFLRKVYSIFGF EFAVQLSTRPEKYL GELALWKAEDALKQSLS
RFGHSWRINEGDGAFYGP KIDIEVTDALKRKHQCATIQLDFQLPLRFGK
YQGLDDAYHTPVMIHRAIFGSVERMMAILLEHTSGKWPFWLSPRQSVILP
VTDDHYDYAKQVHAQLQKQREDKFN EFFVDLDGRTKLTLPKRIKEAQEKQ
YNYILVVG ERERTEGTVSVRTRDGV IHGAKTTADLLTEWRQLLDAFQ

>seryl-tRNA synthetase Contig12892 (and 8346) --> detected in PGPs only, 508 aa, BBE

MKRLSKGFSGLARRTRSAGVVPLCPASWAGLSASRTARFFAGQAAASGAD
ETPMASHHTPOQPEYLF RHLDLKWMKEHADELATSIRARKIEGADIHRTV
ALHDRFVRLDFEIQOMRAQRNRVTDELKQLKKKMNNKSLKGGDGNDAEVE
RLVAQ GKELREQLHAAEKEVKEVEAE LYREAKRIPNVCHPAVPHGSEDQA
RVVCHGGPAKKQHAADF GFEPVDHVTL CQRDLANFEAGSRVAGNNFVFF
RNEAALMELALVQVWVGKAAARGFTPVLPD VVRPVTAEGCGFQPRGTGT
QTYSIEGSDLCLVATSELALAGYYQMCALPPESLPVRMVAFSHCFRAEAG
GTGLRDRGLYRLHQFSKVELFALTAPEQSDDVLESIVQLQOEIFTELGLH
YRVLDMPTEELGAPAYRKYDIEAWMPGRGSYGEVSSASNCTDYQSRLNI
CYPKDDPSGRRRDFVHTVNGTGCAVPRTILAIL ENHQTADGTVKLQHNVG
HFYFHPMQ

>prolyl-tRNA synthetase g100.t1 (probably complete) NOT DETECTED, 622 aa, 197A

MRRGLCVTARRLVASRTNALWHP PQRAPLLRRSLTTPSGATLPAHRVST
LLGAGTGSGAQSSGGGEQDQQLQVASHRLMLQAGIMRQAGSGIYSLLPM
GVRAVEKLTALVDREMGGIGGQKLQMP LLLSAAIWKQTGRWESSGPELFR
LKDRRGADFLAPTHEELITQLFANEAVSYRQLPLLLYQIGLK YRDEV RP
RFGLMRGREFIMKDMYSFDITRDDALRTYQHVV GAYKRILAQLELDYVIA
AADSGNIGGDHSHEFHVMANIGEDTILRCNSCTYA ANTEKARGRLHHHE
HHRRLDHRTLDWPALQAGLADPESLPYSVHVVRVATEAPAASAEGGAARE
WAVVAPKGRQVNELKVKAHLLRHALAPSGEIVDITVR PAAAAADAGARPVV
LVDESLVAEEAVDAAKAVGDFTLTEERDGC AEAGCEGELVGSRGIEVGHV
FYLGTKYSAKLDARVATPSGTNYAEMGCFGLGVTRLLASIVETSHDERGI
VWPVAVAPYKAVVAMTPKDADVQAHARNLYADLQ RSPYFANDVALDDSA
DSPGAKLHRAQLLGF PVMVLV GKAMKNEGRVEFENRKTKEKQFVPYDQMV
AHLEQLARDHARTIGAPLPVGL

>tryptophanyl-tRNA synthetase g3676.t1 (probably complete) NOT DETECTED, 354 aa, 457

MLRQSCGRRGSLALAPYRGLPAEAGRIFSGIQPKGHLHLGN YLGAVVNW
LQLQEQRKGRDRDGVVFCVVMHSYTTDVT PEDLRDSTREMAIALLACGID
PEKCILYAQSEVAEHAELAWILGCRTTMGALNRMTQYKEKKASQ GAMFGL
FAYPVLMAADILLYRASQIPVGD DQLQHLELAREIAEAFNRRY NRTLFPPL
POPILQOATRVMSLRDGTAKMSKSDPNDRSRINL TDSKDEILFKLQKAKT

DPLPGIVYDPENRPELANLLSIFSALTNRSVESLTCHEYADAKMPDFKNAL
APHLVDTVGPIGERIRELRDKPQWVEDVLQOGASRARTIARRNLQEVKQV
IGML

OTHER:

>glutamyl-tRNA(Gln) amidotransferase, A subunit (GatA) Contig7721 (and 18873) (incomplete due to internal gaps), 494 aa, 39

MEATRKGGRAVYRLSRGARRCCFRETSDCGSRRLYSGTSGGSADLVRQSL
ADVGRALAEGRTTSEEVTRACLLQADHTATLNAFVSRHSDEHLLSLAALS
DKRRRDGHQVKGLEGIPVAVKDSFNTHDLPTTCASRMLKDHRPPCDAAVV
SALRKEGAIIMGKTNMDEFSGMSGNTQSYFGPVINPWPSPSTKPEEAFVAG
GSSGGSAAAVASDSCFGALGGDTGGSVRLPGAYCGVVGFKPSYGRISRWG
LVAYGSSLDTPGVLTKTVEDAAIMLGVLGMDARDSTSVDIIEVPDYVKSM
NQPRKLSRSTPSRPTYILAPAEASSNLSRYDGLRYGYRGAGDSITEMYSS
SRSEGFGEVQORRILLGFTLSRRLYDSYRKAQQIRRLVNLDFETAFGQ
GVDVLLHPTAPTPAFALAEKLNVPVDMYINDIMTIPASMAGLPAVSVVPRQ
SAASNLPQGLQLVGRYMDEGTLAAARLLEQAFPRAHALRPPLA

>GatB Contig16382 (and 1895) (complete), 205 aa, 67A

MRRATFVTVSAGGLRASAVPHSSGLLFRSSTRFVLATSARADARVFPLRS
YTTTAAEEFVVKLMADLKEATMAKDKVRLGVIRRLRSEIMNKEKLNVDACL
EFGDCVKVVQMAKQCEDSAKEFDKINQADTAAKEREERLLRITYLPAQL
SEAEVQQLAEEAVKAVGATTIKDMKNVMATLGPVKVQKSDPSLVGEIVRK
LLGGK

>GatC g5738.t1 (possibly complete) NOT DETECTED, 146 aa, 2026

MRRACLTRPFRRGYAAVTPREPSWSVEKFFQSSDTQIDAATLQQLAKR
AQLTIAPEKEESLCREVQOILSCVHIIQEVNTEGVEPLVSPLDARQAQLR
LRADEVTDGDIAEDLMRNAPARDGSFFVVPKVKQSGGEGEGGADA

>translation inhibitor protein g7864.t1 (possibly complete) NOT DETECTED, 203 aa, 1656

MKRTLHVARTSVLPISRGASCGAKMLATRATAPAEKKPRAKRTSASLPK
QAAGHHQVVSTALAPAAIGPYSQAVVATGPFLFVSGCIGLHPQTMDFPGA
DVSTQTEQVMQNMGAILEAGGSSFAEVVKCTILLTDMQHFATVNDIYAKY
FPRDPPARATFATNGLPKGALVEIECIASLAQKTTTRTRKAGTTSGRGKAK
QEP

>ribosome-binding factor A Contig6327.t1 (possibly complete) NOT DETECTED, 849 aa, DE1

MQKTLRGRVARSGHLPPAFPTASRATHFLRFSSHNSLGSAAAAATGIRSR
LSSSSSPLVRSFCFPVAPAATYHTSASRALPRHDRGGGATKAPPSSSAAA
AAAEEKKAPSTSSSASPSSRSSSSSSAKKKGKMLDQLLAEYQDLDLTGDR
PPRAKAGRAQKQDKPAATAVDGDDDDGDEHSASPQAQQRGPRPGDFTLDDL
LAEYDGPAGVGGPVKAQAQAKATTDPLAGREGDFTLDDLLADYDDVSGPA
AEGEDKGDARRLVQGVLAGKQADPRLAQLQGDFTLDDLLSAYDHDPRRR
PRQRRPGGGDEWREDMARFGGAPDEREASLEDLVKTYQPPPAEDQSPAPA
QGASSKARVREELRHFVQSMVADDLGLTSGGEADEREAMEPLRATRARAR
RHPPQATATTQHDDGVRAADVVDVDDDDADYDDAEAEEDVLRHEAVDDVDI
DEQKDDDDDELDDDEEKALDKMMAEAEAEEDQDMELLTRELEAGRTNLPPR
RTREEWERLGGDDVEPAFVGTCIERSESELEGEVETKRFDAVNDNETDEQ
YMERMIQMEEEAEMRRAEGELTGKKQGTVPVRLTKKEKAEAKLATVDPKA
KNARTKLRKERRRQEHEQHMEKVKRHHKEGGVKLDGSMFAHGANVPPE
LMHWFSDPEGLKTKRDAMLAKKCNKLQMAELRKTREKRIDMPSDPTTAE
VEELLGMTRRQKRMASKIQSHLEDVVFVEDLGADSALGQLDININEVMSR
DMRIARVYWKSGNEDAAERLLHARTSMLRGMALQORAGVRFSPPELVFYRE
SAESMYHEVSRMYDQLQKQEGWDEATIKAELKRIKEREAAAAGGRTKT