TMHMM2.0 predictions of 25 possible anchor proteins and their genetic information

1

# WP\_011013739.1 Length: 414

# WP\_011013739.1 Number of predicted TMHs: 1

# WP\_011013739.1 Exp number of AAs in TMHs: 21.08393

# WP\_011013739.1 Exp number, first 60 AAs: 0.34162

# WP\_011013739.1 Total prob of N-in: 0.03842

WP\_011013739.1 TMHMM2.0 outside 1 376

WP\_011013739.1 TMHMM2.0 TMhelix 377 396

WP\_011013739.1 TMHMM2.0 inside 397 414



# [plot](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_011013739.1.eps) in postscript, [script](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_011013739.1.gnuplot) for making the plot in gnuplot, [data](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_011013739.1.plp) for plot

gene complement(586396..587640)

 /gene="mycP"

 /locus\_tag="CGL\_RS02890"

 /old\_locus\_tag="NCgl0550"

 CDS complement(586396..587640)

 /gene="mycP"

 /locus\_tag="CGL\_RS02890"

 /old\_locus\_tag="NCgl0550"

 /inference="COORDINATES: similar to AA

 sequence:RefSeq:WP\_003854454.1"

 /note="Derived by automated computational analysis using

 gene prediction method: Protein Homology."

 /codon\_start=1

 /transl\_table=11

 /product="type VII secretion-associated serine protease

 mycosin"

 /protein\_id="WP\_011013739.1"

 /translation="MRRLIAVSLAALFMLASTPATRAQEVEALACPEVAIADPSSAVLDEHLSQSLSQAHQLATGAGVMVAVIDTGVSLHPRLPHLIPGGDFVGAHQSPDVPGELIDCDGHGTIVAGIIASQGNPGTGWPYDGSSDPYIGVAPDSGIISIKQTSSYVRTREDSNVGTLSTLAESIHRALDSGAHVINISVVSCLPQSPDEAASFQPLTDALNRAELQGVIVVAAAGNLGQDCPVGSTVYPAHSDTVLSVSARFDSHTLAEYSMPGNQQILSAPSHIQAGLSPRGDGFASHMITTAGESPFEGTSFAAPVVSATAALLRQHFPFATPYEIRARIFNSIDPARGAIDPYLALTQEIYPTTPLVHEIALSVPTPPDDSPRERGILVTAIIVGLLAVLAVLMGLRRIHHHSAFQKASSSVIT"

2

# WP\_011013799.1 Length: 234

# WP\_011013799.1 Number of predicted TMHs: 1

# WP\_011013799.1 Exp number of AAs in TMHs: 25.20672

# WP\_011013799.1 Exp number, first 60 AAs: 3.518

# WP\_011013799.1 Total prob of N-in: 0.18043

WP\_011013799.1 TMHMM2.0 outside 1 200

WP\_011013799.1 TMHMM2.0 TMhelix 201 223

WP\_011013799.1 TMHMM2.0 inside 224 234



# [plot](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_011013799.1.eps) in postscript, [script](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_011013799.1.gnuplot) for making the plot in gnuplot, [data](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_011013799.1.plp) for plot

gene complement(677044..677748)

 /locus\_tag="CGL\_RS03310"

 /old\_locus\_tag="NCgl0633"

 CDS complement(677044..677748)

 /locus\_tag="CGL\_RS03310"

 /old\_locus\_tag="NCgl0633"

 /inference="COORDINATES: similar to AA

 sequence:RefSeq:**WP\_011013799.1**"

 /note="Derived by automated computational analysis using

 gene prediction method: Protein Homology."

 /codon\_start=1

 /transl\_table=11

 /product="hypothetical protein"

 /protein\_id="WP\_011013799.1"

 /translation="MRFSRVLPALLITTAVSIPTASAATLTADTDKELCIASNTDDSAVVTFWNSIEDSVREQRLDELDAQDPGIKAAIESYIAQDDNAPTAAELQVRLDAIESGEGLAMLLPDDPTLADPNAEESFKTEYTYDEAKDIISGFSSDPASDVLSQLQQAATTGTRTAEIRAEVFADRTDDYNESQTALKEDFQNCIDAIDDARPIPLQYILIGGAIALAVIVLGIRAWTNSRKQSKHSQ"

NCgl0633 WP\_011013799.1

gene complement(586396..587640)

 /gene="mycP"

 /locus\_tag="CGL\_RS02890"

 /old\_locus\_tag="NCgl0550"

 CDS complement(586396..587640)

 /gene="mycP"

 /locus\_tag="CGL\_RS02890"

 /old\_locus\_tag="NCgl0550"

 /inference="COORDINATES: similar to AA

 sequence:RefSeq:WP\_003854454.1"

 /note="Derived by automated computational analysis using

 gene prediction method: Protein Homology."

 /codon\_start=1

 /transl\_table=11

 /product="type VII secretion-associated serine protease

 mycosin"

 /protein\_id="**WP\_011013739.1**"

 /translation="MRRLIAVSLAALFMLASTPATRAQEVEALACPEVAIADPSSAVL

DEHLSQSLSQAHQLATGAGVMVAVIDTGVSLHPRLPHLIPGGDFVGAHQSPDVPGELI

DCDGHGTIVAGIIASQGNPGTGWPYDGSSDPYIGVAPDSGIISIKQTSSYVRTREDSN

VGTLSTLAESIHRALDSGAHVINISVVSCLPQSPDEAASFQPLTDALNRAELQGVIVV

AAAGNLGQDCPVGSTVYPAHSDTVLSVSARFDSHTLAEYSMPGNQQILSAPSHIQAGL

SPRGDGFASHMITTAGESPFEGTSFAAPVVSATAALLRQHFPFATPYEIRARIFNSID

PARGAIDPYLALTQEIYPTTPLVHEIALSVPTPPDDSPRERGILVTAIIVGLLAVLAVLMGLRRIHHHSAFQKASSSVIT"

3 **WP\_003859654.1 @Multi-transmembrane (Lipid modified N-termini)**

gene complement(2326919..2327998)

 /locus\_tag="CGL\_RS10895"

 /old\_locus\_tag="NCgl2115"

 CDS complement(2326919..2327998)

 /locus\_tag="CGL\_RS10895"

 /old\_locus\_tag="NCgl2115"

 /inference="COORDINATES: similar to AA

 sequence:RefSeq:**WP\_003859654.1**"

 /note="Derived by automated computational analysis using

 gene prediction method: Protein Homology."

 /codon\_start=1

 /transl\_table=11

 /product="cytochrome c oxidase subunit II"

 /protein\_id="**WP\_011014951.1**"

 /translation="MEQQNKRGLKRKALLGGVLGLGGLAMAGCEVAPPGGVLGDFLRMGWPDGITPEAVAMGNFWSWVWVAAWIIGIIMWGLFLTAIFAWGAKRAEKRGEGEFPKQLQYNVPLELVLTIVPIIIVMVLFFFTVQTQDKVTALDKNPEVTVDVTAYQWNWKFGYSEIDGSLAPGGQDYQGSDPERQAAAEASKKDPSGDNPIHGNSKSDVSYLEFNRIETLGTTDEIPVMVLPVNTPIEFNLASADVAHSFWVPEFLFKRDAYAHPEANKSQRVFQIEEITEEGAFVGRCAEMCGTYHAMMNFELRVVDRDSFAEYISFRDSNPDATNAQALEHIGQAP

 YATSTSPFVSDRTATRDGENTQSNA"

# WP\_011014951.1 Length: 359

# WP\_011014951.1 Number of predicted TMHs: 3

# WP\_011014951.1 Exp number of AAs in TMHs: 68.0102800000000001

# WP\_011014951.1 Exp number, first 60 AAs: 22.54847

# WP\_011014951.1 Total prob of N-in: 0.99961

# WP\_011014951.1 POSSIBLE N-term signal sequence

WP\_011014951.1 TMHMM2.0 inside 1 12

WP\_011014951.1 TMHMM2.0 TMhelix 13 35

WP\_011014951.1 TMHMM2.0 outside 36 64

WP\_011014951.1 TMHMM2.0 TMhelix 65 87

WP\_011014951.1 TMHMM2.0 inside 88 106

WP\_011014951.1 TMHMM2.0 TMhelix 107 129

WP\_011014951.1 TMHMM2.0 outside 130 359



# [plot](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_011014951.1.eps) in postscript, [script](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_011014951.1.gnuplot) for making the plot in gnuplot, [data](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_011014951.1.plp) for plot

4

>WP\_011265759.1

# WP\_011265759.1 Length: 341

# WP\_011265759.1 Number of predicted TMHs: 1

# WP\_011265759.1 Exp number of AAs in TMHs: 19.85003

# WP\_011265759.1 Exp number, first 60 AAs: 19.82027

# WP\_011265759.1 Total prob of N-in: 0.89183

# WP\_011265759.1 POSSIBLE N-term signal sequence

WP\_011265759.1 TMHMM2.0 inside 1 11

WP\_011265759.1 TMHMM2.0 TMhelix 12 34

WP\_011265759.1 TMHMM2.0 outside 35 341



# [plot](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_18373/WP_011265759.1.eps) in postscript, [script](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_18373/WP_011265759.1.gnuplot) for making the plot in gnuplot, [data](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_18373/WP_011265759.1.plp) for plot

5

WP\_011014306.1 @Lipid anchored

# WP\_011014306.1 Length: 366

# WP\_011014306.1 Number of predicted TMHs: 0

# WP\_011014306.1 Exp number of AAs in TMHs: 17.80803

# WP\_011014306.1 Exp number, first 60 AAs: 17.79535

# WP\_011014306.1 Total prob of N-in: 0.73297

# WP\_011014306.1 POSSIBLE N-term signal sequence

WP\_011014306.1 TMHMM2.0 outside 1 366



# [plot](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_011014306.1.eps) in postscript, [script](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_011014306.1.gnuplot) for making the plot in gnuplot, [data](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_011014306.1.plp) for plot

gene 1426257..1427357

 /locus\_tag="CGL\_RS06795"

 /old\_locus\_tag="NCgl1307"

 CDS 1426257..1427357

 /locus\_tag="CGL\_RS06795"

 /old\_locus\_tag="NCgl1307"

 /inference="COORDINATES: similar to AA

 sequence:RefSeq:WP\_011897187.1"

 /note="Derived by automated computational analysis using

 gene prediction method: Protein Homology."

 /codon\_start=1

 /transl\_table=11

 /product="hypothetical protein"

 /protein\_id="WP\_011014306.1"

 /translation="MKDYAVHTRGLVSLLSLIFLFVLSGCGGNATTADEAAESDVVTS

SSAPPSKRALDVGEAVEIPGVVLTVNSVTQSDQLMLYSEGSARGSEPREQRNAASGEK

FVSVDTTVKNSSSDPWDLSCGHVLQTWLLEDELDDQQGDQEKKFSPIDNLDQISGNPE

CGVLLEVGTEIEMTWSFTIPDDIEITHFGFSLSDSTSNDLAIISLGGAIETSSAITTT

EVIAPENDTETLLEITPVDCQVGLGPIVTSWSDGTVGGWSQHCQDVHDEVLAGEVAAN

TPVCDGVVCTYPSGATMPDPNAPQIPSDTSGAVCDENQCVYPNGYIARIGDPNVPNYL

KPGNSPWVQGQIDFQNCLDSGKTIEQCREELN"

6

# WP\_011014779.1 Length: 295

# WP\_011014779.1 Number of predicted TMHs: 0

# WP\_011014779.1 Exp number of AAs in TMHs: 11.02134

# WP\_011014779.1 Exp number, first 60 AAs: 11.02018

# WP\_011014779.1 Total prob of N-in: 0.58364

# WP\_011014779.1 POSSIBLE N-term signal sequence

WP\_011014779.1 TMHMM2.0 outside 1 295



# [plot](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_011014779.1.eps) in postscript, [script](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_011014779.1.gnuplot) for making the plot in gnuplot, [data](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_011014779.1.plp) for plot

gene 2060620..2061507

 /locus\_tag="CGL\_RS09710"

 /old\_locus\_tag="NCgl1876"

 CDS 2060620..2061507

 /locus\_tag="CGL\_RS09710"

 /old\_locus\_tag="NCgl1876"

 /inference="COORDINATES: similar to AA

 sequence:RefSeq:WP\_003861643.1"

 /note="Derived by automated computational analysis using

 gene prediction method: Protein Homology."

 /codon\_start=1

 /transl\_table=11

 /product="glutamate ABC transporter substrate-binding

 protein"

 /protein\_id="WP\_011014779.1"

/translation="MSAKRTFTRIGAILGATALAGVTLTACGDSSGGDGFLAAIENGS

VNVGTKYDQPGLGLRNPDNSMSGLDVDVAEYVVNSIADDKGWDHPTIEWRESPSAQRE

TLIQNGEVDMIAATYSINAGRSESVNFGGPYLLTHQALLVRQDDDRIETLEDLDNGLI

LCSVSGSTPAQKVKDVLPGVQLQEYDTYSSCVEALSQGNVDALTTDATILFGYSQQYE

GDFRVVEMEKDGEPFTDEYYGIGLKKDDQEGTDAINAALERMYADGTFQRLLTENLGE

 DSVVVEEGTPGDLSFLDAS"

7

# WP\_011265985.1 Length: 536

# WP\_011265985.1 Number of predicted TMHs: 0

# WP\_011265985.1 Exp number of AAs in TMHs: 14.57839

# WP\_011265985.1 Exp number, first 60 AAs: 14.57396

# WP\_011265985.1 Total prob of N-in: 0.69370

# WP\_011265985.1 POSSIBLE N-term signal sequence

WP\_011265985.1 TMHMM2.0 outside 1 536



# [plot](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_011265985.1.eps) in postscript, [script](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_011265985.1.gnuplot) for making the plot in gnuplot, [data](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_011265985.1.plp) for plot

gene 2820585..2822195

 /locus\_tag="CGL\_RS13230"

 /old\_locus\_tag="NCgl2562"

 CDS 2820585..2822195

 /locus\_tag="CGL\_RS13230"

 /old\_locus\_tag="NCgl2562"

 /inference="COORDINATES: similar to AA

 sequence:RefSeq:WP\_011265985.1"

 /note="Derived by automated computational analysis using

 gene prediction method: Protein Homology."

 /codon\_start=1

 /transl\_table=11

 /product="twin-arginine translocation signal

 domain-containing protein"

 /protein\_id="WP\_011265985.1"

 /translation="MSTTITRRNFLRATGILGVAAGIGATLAACAPDNTGTSGSTSTA

 AGTGTANEEGTITAAISYELGTNGYDPMTTTSALTVAANWHTLEGLTEIDPATGEVYA

 ALASALPSADATSLDIKLRDGATFHNGDAVTADDVVFSFERVLDPANNSLYASFIPFI

 KSVTKKDDTTVTIDLDYATGIISERLAVVKIVPKSVVEADASGFDANPIGSGPYKMTD

 NGASKVVKFERNDDYNGPRPARAAKMEWQIIPDASTRTNSLQSGSTMAIDSVPYLSIP

 QLEATSTVESVQGFGLLFAMFNCSEGNPFNDVRNRQAFLYALDMDKIVKTGMSDQATP

 ATSFVQKEHPNYNQASTVYSLDADKAKALFAETGLTSLNLLCTDHDWVKNCTPLIQES

 LAALGINVSFTERKSADVYNTIDGKPEAYDVVIAPGDPSVFGNDPDLLMRWWYAGDVW

 TDSRMHWKGSESYDQVQNLLEEGIRATDKAEQQDIWNRTFDVISDNVPLYPLFHRKVP

 TAWNSNALVDFKPISLTGLNFSGVATTE"

8

# WP\_011013364.1 Length: 551

# WP\_011013364.1 Number of predicted TMHs: 2

# WP\_011013364.1 Exp number of AAs in TMHs: 45.52837

# WP\_011013364.1 Exp number, first 60 AAs: 22.88811

# WP\_011013364.1 Total prob of N-in: 0.02712

# WP\_011013364.1 POSSIBLE N-term signal sequence

WP\_011013364.1 TMHMM2.0 outside 1 22

WP\_011013364.1 TMHMM2.0 TMhelix 23 45

WP\_011013364.1 TMHMM2.0 inside 46 191

WP\_011013364.1 TMHMM2.0 TMhelix 192 214

WP\_011013364.1 TMHMM2.0 outside 215 551



# [plot](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_011013364.1.eps) in postscript, [script](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_011013364.1.gnuplot) for making the plot in gnuplot, [data](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_011013364.1.plp) for plot

gene 70506..72161

 /locus\_tag="CGL\_RS00375"

 /old\_locus\_tag="NCgl0067"

 CDS 70506..72161

 /locus\_tag="CGL\_RS00375"

 /old\_locus\_tag="NCgl0067"

 /inference="COORDINATES: similar to AA

 sequence:RefSeq:WP\_011013364.1"

 /note="Derived by automated computational analysis using

 gene prediction method: Protein Homology."

 /codon\_start=1

 /transl\_table=11

 /product="sensor histidine kinase"

 /protein\_id="WP\_011013364.1"

 /translation="MSVGGSDWKNFKEVDIIRFATRILVIQVATVALVVAICTGIFAV

 LMMDQMKTEAEHTALSIGRSVASNPQIREEVALDTQTGANPSAEELADGDIQAVAQAA

 NERTGALFVVITDGLGIRLSHPDEERLGEQVSTSFEAAMRGEETMAWETGTLGASARA

 KVPIFAPDSSVPVGEVSVGFERDSVYSRLPMFLAALALISVLGILIGVGVAMGMRRRW

 ERVTLGLQPEELVTLVQNQTAVIDGIDEGVLALSPNGTIGVHNEQAQSMIGAGPMSGR

 TLKELGLDLGLDGVVLHGQHPETVAHNGRILYLDFHPVRRGDQDLGYVVTIRDRTDII

 ELSERLDSVRTMTHALRAQRHEFANRIHTATGLIDAGRVHDAAEFLGDISRNGGQSHP

 LIGSAHLNEAFLSSFLSTASISASEKGVSLRINSDTLILGTVKDPEDVATILGNLINN

 AIDAAVAGEAPRWIELTLMDDADTLVISVADSGPGIPEGVDVFATATQIGDSEDNERT

 HGHGIGLKLCRALARSHGGDVWVIDRGTEDGAVFGVKLPGVME"

9

# WP\_004567665.1 Length: 141

# WP\_004567665.1 Number of predicted TMHs: 3

# WP\_004567665.1 Exp number of AAs in TMHs: 71.31589

# WP\_004567665.1 Exp number, first 60 AAs: 24.46692

# WP\_004567665.1 Total prob of N-in: 0.20597

# WP\_004567665.1 POSSIBLE N-term signal sequence

WP\_004567665.1 TMHMM2.0 outside 1 26

WP\_004567665.1 TMHMM2.0 TMhelix 27 49

WP\_004567665.1 TMHMM2.0 inside 50 61

WP\_004567665.1 TMHMM2.0 TMhelix 62 84

WP\_004567665.1 TMHMM2.0 outside 85 98

WP\_004567665.1 TMHMM2.0 TMhelix 99 121

WP\_004567665.1 TMHMM2.0 inside 122 141



# [plot](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_004567665.1.eps) in postscript, [script](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_004567665.1.gnuplot) for making the plot in gnuplot, [data](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_004567665.1.plp) for plot

gene complement(2513690..2514115)

 /locus\_tag="CGL\_RS11770"

 /old\_locus\_tag="NCgl2291"

 CDS complement(2513690..2514115)

 /locus\_tag="CGL\_RS11770"

 /old\_locus\_tag="NCgl2291"

 /inference="COORDINATES: similar to AA

 sequence:RefSeq:WP\_003859287.1"

 /note="Derived by automated computational analysis using

 gene prediction method: Protein Homology."

 /codon\_start=1

 /transl\_table=11

 /product="DUF4233 domain-containing protein"

 /protein\_id="WP\_004567665.1"

 /translation="MSKREESIEYGPLGKGHDPLKDPMKGIRGVMAGTLVMEAITLGL

 VLTVILRVDDGIYWTTFNWVYVSAVAIAHFVAAFLQRFSWSIPMNIVLQVLALAGFFV

 HPAMGFAAIIFIIAWAYLFYLRSNLIDRMKRGLLTTQHS"

10

# WP\_011014192.1 Length: 467

# WP\_011014192.1 Number of predicted TMHs: 4

# WP\_011014192.1 Exp number of AAs in TMHs: 90.04242

# WP\_011014192.1 Exp number, first 60 AAs: 22.89888

# WP\_011014192.1 Total prob of N-in: 0.03175

# WP\_011014192.1 POSSIBLE N-term signal sequence

WP\_011014192.1 TMHMM2.0 outside 1 3

WP\_011014192.1 TMHMM2.0 TMhelix 4 26

WP\_011014192.1 TMHMM2.0 inside 27 60

WP\_011014192.1 TMHMM2.0 TMhelix 61 83

WP\_011014192.1 TMHMM2.0 outside 84 97

WP\_011014192.1 TMHMM2.0 TMhelix 98 120

WP\_011014192.1 TMHMM2.0 inside 121 139

WP\_011014192.1 TMHMM2.0 TMhelix 140 162

WP\_011014192.1 TMHMM2.0 outside 163 467



# [plot](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_011014192.1.eps) in postscript, [script](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_011014192.1.gnuplot) for making the plot in gnuplot, [data](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_011014192.1.plp) for plot

gene complement(1257862..1259265)

 /locus\_tag="CGL\_RS05950"

 /old\_locus\_tag="NCgl1147"

 CDS complement(1257862..1259265)

 /locus\_tag="CGL\_RS05950"

 /old\_locus\_tag="NCgl1147"

 /inference="COORDINATES: similar to AA

 sequence:RefSeq:WP\_011897093.1"

 /note="Derived by automated computational analysis using

 gene prediction method: Protein Homology."

 /codon\_start=1

 /transl\_table=11

 /product="HlyC/CorC family transporter"

 /protein\_id="WP\_011014192.1"

 /translation="MLTAVLSLIAGLVVIGVIIVLNGYFVAQEFAYMSVDRNELRALA

 DSGDKKARRALSITKRTSFMLSGAQLGITVTGLLVGFVAEPLVGNALGVLLGGVGVPA

 AVSISVGTVLALAISTVVQMIFGELFPKNYTLATPLKSALALAPSTTWYLKLAGWLIT

 FFDFASNALLRLFRIEPVEDVDSSATAQDLPHIVASSRDSGVLNNSMSLSLDRLLDFP

 SHDVGHAMIPRSRVGVVDPETTIAEVKALMRKAHTRYPIIDDNHVPIGVINLIDILGT

 DIHGAEISDSAKVTEFMHQPVIVPEFMSLPDVVTELHNREDRLACVIDEYGGFIGIVT

 LEDLAEEVLGDINDEHDVFSSEDITETSPDKWLIDGDTPLDEVERAIGYELPEGDYET

 ISGLLFDHANALLKTGDVIEIPLDFEPEDYLNNTSPTQRILRITVLEVERNVPVKLAL

 ALLEDHPDNHPAPKENR"

11

# WP\_011014865.1 Length: 510

# WP\_011014865.1 Number of predicted TMHs: 5

# WP\_011014865.1 Exp number of AAs in TMHs: 111.87541

# WP\_011014865.1 Exp number, first 60 AAs: 35.84029

# WP\_011014865.1 Total prob of N-in: 0.98452

# WP\_011014865.1 POSSIBLE N-term signal sequence

WP\_011014865.1 TMHMM2.0 inside 1 19

WP\_011014865.1 TMHMM2.0 TMhelix 20 42

WP\_011014865.1 TMHMM2.0 outside 43 46

WP\_011014865.1 TMHMM2.0 TMhelix 47 69

WP\_011014865.1 TMHMM2.0 inside 70 120

WP\_011014865.1 TMHMM2.0 TMhelix 121 143

WP\_011014865.1 TMHMM2.0 outside 144 146

WP\_011014865.1 TMHMM2.0 TMhelix 147 169

WP\_011014865.1 TMHMM2.0 inside 170 239

WP\_011014865.1 TMHMM2.0 TMhelix 240 262

WP\_011014865.1 TMHMM2.0 outside 263 510



# [plot](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_011014865.1.eps) in postscript, [script](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_011014865.1.gnuplot) for making the plot in gnuplot, [data](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_011014865.1.plp) for plot

gene 2193165..2194697

 /locus\_tag="CGL\_RS10315"

 /old\_locus\_tag="NCgl1998"

 CDS 2193165..2194697

 /locus\_tag="CGL\_RS10315"

 /old\_locus\_tag="NCgl1998"

 /inference="COORDINATES: similar to AA

 sequence:RefSeq:WP\_003856383.1"

 /note="Derived by automated computational analysis using

 gene prediction method: Protein Homology."

 /codon\_start=1

 /transl\_table=11

 /product="ABC transporter ATP-binding protein"

 /protein\_id="WP\_011014865.1"

 /translation="MISRLLQLAKKVWPELGASTLLRLLNQLLTAALIVFPAWVLSRK

 PDISLLAVAIIMALIALTAAVCRWGEQVCGHRAAFGLLAHMRVMLYDALVHKGSPSPI

 HGSGSIMSVATRDINSIEVFFAHTIGPTVTAVLLSAGGVITLATLDPVAGLIGLLGVL

 IAWLIPLIGKQSSSSEATSRGHIAQHLTEDAAGRLEINSHGAQATRLNALEVKEQQLE

 QVVTRQGLIVGIRQGAALLWPWISAVLLVALVPHVGIVAAAIILGISPALDAVEGFAR

 TMPTALNSAQRYFQIIDAPVAIAEPDEPKPLPKGPLKLRISRVPVSAKGTVSLEVAAG

 EHIGIIGSSGSGKSTLAKLILKLAQLRSGTITIGGVDIAEVSSAELRKSVTLVEQKSV

 LFRASVLENLRMGNPELSEDEAREALRLASISELPLDADALRLSGGQQQRLCLARALA

 RTPQVLIVDEATSHQDALNQADLSQTLATLKDTTVIIIAHRTAALTHVDRIIDLEEIK

 NP"

12

# WP\_003859459.1 Length: 440

# WP\_003859459.1 Number of predicted TMHs: 4

# WP\_003859459.1 Exp number of AAs in TMHs: 88.9375700000000001

# WP\_003859459.1 Exp number, first 60 AAs: 22.39455

# WP\_003859459.1 Total prob of N-in: 0.02419

# WP\_003859459.1 POSSIBLE N-term signal sequence

WP\_003859459.1 TMHMM2.0 outside 1 9

WP\_003859459.1 TMHMM2.0 TMhelix 10 32

WP\_003859459.1 TMHMM2.0 inside 33 64

WP\_003859459.1 TMHMM2.0 TMhelix 65 87

WP\_003859459.1 TMHMM2.0 outside 88 91

WP\_003859459.1 TMHMM2.0 TMhelix 92 114

WP\_003859459.1 TMHMM2.0 inside 115 126

WP\_003859459.1 TMHMM2.0 TMhelix 127 149

WP\_003859459.1 TMHMM2.0 outside 150 440



# [plot](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_003859459.1.eps) in postscript, [script](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_003859459.1.gnuplot) for making the plot in gnuplot, [data](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_003859459.1.plp) for plot

 gene complement(2418988..2420310)

 /locus\_tag="CGL\_RS11335"

 /old\_locus\_tag="NCgl2206"

 CDS complement(2418988..2420310)

 /locus\_tag="CGL\_RS11335"

 /old\_locus\_tag="NCgl2206"

 /inference="COORDINATES: similar to AA

 sequence:RefSeq:WP\_003859459.1"

 /note="Derived by automated computational analysis using

 gene prediction method: Protein Homology."

 /codon\_start=1

 /transl\_table=11

 /product="HlyC/CorC family transporter"

 /protein\_id="WP\_003859459.1"

 /translation="MESSVIWLSIATVVALLFSGLLGAVESALSSVSRARVEQMLKDE

 ASGSASLLRVIDERALHINMLIMLRTLLDASAAVFAGAIAVNVMDSWAWGIVLAIVVV

 SLLTFAVVGVFGRTVGRKNPYSVMLRSAVVLSGLAKILGPIARGLIWIGNIIAPGPGF

 RNGPYATEVELREMVDIAQEHGIVEIEERRMIQSVFDLASTTVRQVMVPRPEMIWIES

 GKTAGQATALCVRSGHSRIPVIGENVDDIIGIVYLKDLVQKTYYATDGGKSVLVDEVM

 REATFVPDSKSLDALLQEMQEDHKHIAILVDEYGGVAGLISIEDILEEIVGEIADEYD

 AREVAPIEKIGDRTYRVVSRLSLEDLKDHIEEELDLEIEFGDEIEDQVDTVGGLIAFE

 LGRVPLPGATVETCGLKLTAEGAKNRRGRLRMHSAVVEVGEPSEDNEG"

13

# WP\_003863539.1 Length: 353

# WP\_003863539.1 Number of predicted TMHs: 3

# WP\_003863539.1 Exp number of AAs in TMHs: 62.6236199999999999

# WP\_003863539.1 Exp number, first 60 AAs: 22.60486

# WP\_003863539.1 Total prob of N-in: 0.95718

# WP\_003863539.1 POSSIBLE N-term signal sequence

WP\_003863539.1 TMHMM2.0 inside 1 32

WP\_003863539.1 TMHMM2.0 TMhelix 33 55

WP\_003863539.1 TMHMM2.0 outside 56 64

WP\_003863539.1 TMHMM2.0 TMhelix 65 84

WP\_003863539.1 TMHMM2.0 inside 85 96

WP\_003863539.1 TMHMM2.0 TMhelix 97 119

WP\_003863539.1 TMHMM2.0 outside 120 353



# [plot](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_003863539.1.eps) in postscript, [script](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_003863539.1.gnuplot) for making the plot in gnuplot, [data](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_003863539.1.plp) for plot

gene 817465..818526

 /locus\_tag="CGL\_RS03875"

 /old\_locus\_tag="NCgl0743"

 CDS 817465..818526

 /locus\_tag="CGL\_RS03875"

 /old\_locus\_tag="NCgl0743"

 /inference="COORDINATES: similar to AA

 sequence:RefSeq:WP\_003863539.1"

 /note="Derived by automated computational analysis using

 gene prediction method: Protein Homology."

 /codon\_start=1

 /transl\_table=11

 /product="potassium channel family protein"

 /protein\_id="WP\_003863539.1"

 /translation="MGRMKNDGELADLPDHALLSIIRIPQAAKRSPWALILTRIGYAM

 VLLVIVTMVVYFDRNGYSEDLTFIDALYYSTVSLTTVGYGDITPVTQSARLINIIVLT

 PARIGFLILLVGTTLSVLTEESRRALQIQRWRKRMRNHTVVVGYGTKGRSAVAALLAD

 GVPANQIVVIDTDQVSLDAANNSGLVTVKGSATKADVLRLAGVSRARAVVVAPNLDDT

 AVLVTLSVREIAPQAMIVASVRESENQHLLEQSGADSVVISSETAGRMLGLATVTPSV

 VEMMEDLLSPDEGFSVAERLVGEDEIGSNPRHLADIVLGVVRSGELYRIDSPEAETVE

 PGDRLLYVRRVFSEEVNDK"

14

# WP\_003856281.1 Length: 554

# WP\_003856281.1 Number of predicted TMHs: 1

# WP\_003856281.1 Exp number of AAs in TMHs: 18.32236

# WP\_003856281.1 Exp number, first 60 AAs: 18.31511

# WP\_003856281.1 Total prob of N-in: 0.81366

# WP\_003856281.1 POSSIBLE N-term signal sequence

WP\_003856281.1 TMHMM2.0 inside 1 12

WP\_003856281.1 TMHMM2.0 TMhelix 13 35

WP\_003856281.1 TMHMM2.0 outside 36 554



# [plot](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_003856281.1.eps) in postscript, [script](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_003856281.1.gnuplot) for making the plot in gnuplot, [data](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_003856281.1.plp) for plot

gene 1493513..1495177

 /locus\_tag="CGL\_RS07090"

 /old\_locus\_tag="NCgl1362"

 CDS 1493513..1495177

 /locus\_tag="CGL\_RS07090"

 /old\_locus\_tag="NCgl1362"

 /EC\_number="6.3.4.2"

 /inference="COORDINATES: similar to AA

 sequence:RefSeq:WP\_003856281.1"

 /note="Derived by automated computational analysis using

 gene prediction method: Protein Homology."

 /codon\_start=1

 /transl\_table=11

 /product="CTP synthase"

 /protein\_id="WP\_003856281.1"

 /translation="MTSSRKVRPTKHIFVTGGVVSSLGKGLTAASLGQLLIARGLSVT

 MQKLDPYLNVDPGTMNPFEHGEVFVTEDGAETDLDLGHYERFLDRNLGLNANVTTGKV

 YSTVIAKERRGEYLGKTVQVIPHITDEIKARILSMGEPDAHGNAPDVVISEVGGTVGD

 IESQPFLEAARQVRHEIGRENCFFIHCSLVPYLATSGELKTKPTQHSVAELRGIGILP

 DALVLRCDREVPQGLKDKIAMMCDVDYEGVVSCPDSSSIYNIPDVLYREHLDTFIIRR

 LGLPFRDVDWSTWHDLLERVNNPRHELTVGIVGKYIDLPDAYLSVVEAVRAAGYANWT

 RTNIKWITSDDCETPSGAMKALSGLDAIVVPGGFGIRGIEGKIGAITFAREHKIPLLG

 LCLGLQCTVIEAARQAGLEQASSTEFDPAATQPVIATMEEQKAAVSGEADLGGTMRLG

 AYPATLEEGSLVAELYGTTEVSERHRHRYEVNNAYRAQIAEGSDLVFSGTSPDGHLVE

 FVEYPKEVHPYLVATQAHPEYKSRPTHAHPLFYGLVKTALELRVHP"

14

# WP\_011013342.1 Length: 474

# WP\_011013342.1 Number of predicted TMHs: 1

# WP\_011013342.1 Exp number of AAs in TMHs: 22.48962

# WP\_011013342.1 Exp number, first 60 AAs: 22.4317

# WP\_011013342.1 Total prob of N-in: 0.99873

# WP\_011013342.1 POSSIBLE N-term signal sequence

WP\_011013342.1 TMHMM2.0 inside 1 6

WP\_011013342.1 TMHMM2.0 TMhelix 7 29

WP\_011013342.1 TMHMM2.0 outside 30 474



# [plot](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_011013342.1.eps) in postscript, [script](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_011013342.1.gnuplot) for making the plot in gnuplot, [data](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_011013342.1.plp) for plot

gene complement(43923..45347)

 /locus\_tag="CGL\_RS00245"

 /old\_locus\_tag="NCgl0042"

 CDS complement(43923..45347)

 /locus\_tag="CGL\_RS00245"

 /old\_locus\_tag="NCgl0042"

 /inference="COORDINATES: similar to AA

 sequence:RefSeq:WP\_015439388.1"

 /note="Derived by automated computational analysis using

 gene prediction method: Protein Homology."

 /codon\_start=1

 /transl\_table=11

 /product="penicillin-binding protein 2"

 /protein\_id="WP\_011013342.1"

 /translation="MNRSIRITSLFSLLLILVLVANLTWIQAFRDDDLAQNPLNARGF

 LEAKSTPRGQISTGGQVLAESSQDDQGFYQRSYITNPTAYAPVVGYLSDVYGAAGLEL

 GYNSILNGSDSSLFTSQWLDVISGSPTHGANIELTLDPNAQQTAYEQLSQSGYEGAVV

 ALRPSTGEVLAMASSPSYDPNQIVDPATAEDAWAEYTSTEGAPLLNHATQESLPPGSI

 FKIITTAAALENGYSADSTVTAEAAVTLPGTNTTLTNYGGQTCAGGGTTTLLTAFQLS

 CNTAFVETGIDVGADALRASAEDFGVGQTYSLGLDNVPGGLGEIPDDAALGQSSIGQR

 DVQMNVLQAAVMAGTVSNGGVRMEPYLVSRVTGQDLSELSTHKPKSVGGVEPEIAEQL

 KTLMEASERNTSGYTGIQIASKTGTAEHGDENTPPHTWYVAFNNDIAVAVLVKDGGGF

 GTSATGGQVAAPIGRAVLQAAGGF"

15

# WP\_011013540.1 Length: 186

# WP\_011013540.1 Number of predicted TMHs: 1

# WP\_011013540.1 Exp number of AAs in TMHs: 23.50677

# WP\_011013540.1 Exp number, first 60 AAs: 21.93674

# WP\_011013540.1 Total prob of N-in: 0.98569

# WP\_011013540.1 POSSIBLE N-term signal sequence

WP\_011013540.1 TMHMM2.0 inside 1 6

WP\_011013540.1 TMHMM2.0 TMhelix 7 29

WP\_011013540.1 TMHMM2.0 outside 30 186



# [plot](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_011013540.1.eps) in postscript, [script](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_011013540.1.gnuplot) for making the plot in gnuplot, [data](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_011013540.1.plp) for plot

gene 308745..309305

 /locus\_tag="CGL\_RS01540"

 /old\_locus\_tag="NCgl0289"

 CDS 308745..309305

 /locus\_tag="CGL\_RS01540"

 /old\_locus\_tag="NCgl0289"

 /inference="COORDINATES: similar to AA

 sequence:RefSeq:WP\_003863302.1"

 /note="Derived by automated computational analysis using

 gene prediction method: Protein Homology."

 /codon\_start=1

 /transl\_table=11

 /product="TlpA family protein disulfide reductase"

 /protein\_id="WP\_011013540.1"

 /translation="MTSSAKWSIVGVVAILAVIVALIPQLVGGESAEEAQGETSTSKI

 TTRPDCVASGAAGVDLPCLGGANGVGNELATVVNLWAWWCEPCRAELPIFDEFATTHP

 ELNVIGVHADQNAANGAALLEDLGVNLASYQDDSNLFAGTLGLPGVVPITIVVSPDGN

 VVDTFPQPFETIDDLETAVAGALQNA"

16

# WP\_011014270.1 Length: 60

# WP\_011014270.1 Number of predicted TMHs: 1

# WP\_011014270.1 Exp number of AAs in TMHs: 21.67789

# WP\_011014270.1 Exp number, first 60 AAs: 21.67789

# WP\_011014270.1 Total prob of N-in: 0.96355

# WP\_011014270.1 POSSIBLE N-term signal sequence

WP\_011014270.1 TMHMM2.0 inside 1 8

WP\_011014270.1 TMHMM2.0 TMhelix 9 31

WP\_011014270.1 TMHMM2.0 outside 32 60



# [plot](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_011014270.1.eps) in postscript, [script](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_011014270.1.gnuplot) for making the plot in gnuplot, [data](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_011014270.1.plp) for plot

gene complement(1365214..1365396)

 /locus\_tag="CGL\_RS06465"

 /old\_locus\_tag="NCgl1250"

 CDS complement(1365214..1365396)

 /locus\_tag="CGL\_RS06465"

 /old\_locus\_tag="NCgl1250"

 /inference="COORDINATES: similar to AA

 sequence:RefSeq:WP\_011897149.1"

 /note="Derived by automated computational analysis using

 gene prediction method: Protein Homology."

 /codon\_start=1

 /transl\_table=11

 /product="SRPBCC family protein"

 /protein\_id="WP\_011014270.1"

 /translation="MKTKKQSRILFIALGLVIALPALSFGLSQLLPATTTREITIDAQ

 PDQVWEVLSDLEPFPQ"

17

# WP\_011015453.1 Length: 309

# WP\_011015453.1 Number of predicted TMHs: 1

# WP\_011015453.1 Exp number of AAs in TMHs: 20.74758

# WP\_011015453.1 Exp number, first 60 AAs: 20.73199

# WP\_011015453.1 Total prob of N-in: 0.97932

# WP\_011015453.1 POSSIBLE N-term signal sequence

WP\_011015453.1 TMHMM2.0 inside 1 4

WP\_011015453.1 TMHMM2.0 TMhelix 5 27

WP\_011015453.1 TMHMM2.0 outside 28 309



# [plot](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_011015453.1.eps) in postscript, [script](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_011015453.1.gnuplot) for making the plot in gnuplot, [data](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_011015453.1.plp) for plot

gene complement(3070212..3071141)

 /locus\_tag="CGL\_RS14315"

 /old\_locus\_tag="NCgl2775"

 CDS complement(3070212..3071141)

 /locus\_tag="CGL\_RS14315"

 /old\_locus\_tag="NCgl2775"

 /inference="COORDINATES: similar to AA

 sequence:RefSeq:WP\_011898015.1"

 /note="Derived by automated computational analysis using

 gene prediction method: Protein Homology."

 /codon\_start=1

 /transl\_table=11

 /product="cutinase family protein"

 /protein\_id="WP\_011015453.1"

 /translation="MRKTITVIAVLIVLALIGVGIVQYVNTSDDSDFIGQPGEPTGTE

 TTEPPVQPDWCPAVEVIAAPGTWESAANDDPINPTANPLSFMLSITQPLQERYSADDV

 KVWTLPYTAQFRNINSQNEMSYDDSRNEGTAKMNEELINTHNECPATEFIIVGFSQGA

 VIAGDVAAQIGSEQGVIPADSVRGVALIADGRREPGVGQFPGTFVDGIGAEVTLQPLN

 LLVQPIVPGATMRGGRAGGFGVLNDRVQDICAPNDAICDAPVNVGNALDRALAMVSAN

 GVHALYATNPDVFPGTTTNAWVVDWATNLIDNG"

18

# WP\_003853779.1 Length: 137

# WP\_003853779.1 Number of predicted TMHs: 1

# WP\_003853779.1 Exp number of AAs in TMHs: 21.1903

# WP\_003853779.1 Exp number, first 60 AAs: 21.14386

# WP\_003853779.1 Total prob of N-in: 0.91031

# WP\_003853779.1 POSSIBLE N-term signal sequence

WP\_003853779.1 TMHMM2.0 inside 1 4

WP\_003853779.1 TMHMM2.0 TMhelix 5 27

WP\_003853779.1 TMHMM2.0 outside 28 137



# [plot](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_003853779.1.eps) in postscript, [script](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_003853779.1.gnuplot) for making the plot in gnuplot, [data](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_003853779.1.plp) for plot

gene complement(2875868..2876281)

 /locus\_tag="CGL\_RS13475"

 /old\_locus\_tag="NCgl2610"

 CDS complement(2875868..2876281)

 /locus\_tag="CGL\_RS13475"

 /old\_locus\_tag="NCgl2610"

 /inference="COORDINATES: similar to AA

 sequence:RefSeq:WP\_011897913.1"

 /note="Derived by automated computational analysis using

 gene prediction method: Protein Homology."

 /codon\_start=1

 /transl\_table=11

 /product="DUF4247 domain-containing protein"

 /protein\_id="WP\_003853779.1"

 /translation="MSSRNYRSIGFILLFLAVLCLFAAVFAKPAVGSQVSDRWPGNNG

 TYSCAGESGVVDEIVNMSTPTDRATDPATGDTYLRYSKNLIIISGEGTPECTITVEGL

 DRVNSGAFIWLGGGFGPSSPSSSSGGSSGSGGGVK"

@Secretory (released) (with CS)

19

# WP\_011013420.1 Length: 163

# WP\_011013420.1 Number of predicted TMHs: 1

# WP\_011013420.1 Exp number of AAs in TMHs: 22.57328

# WP\_011013420.1 Exp number, first 60 AAs: 22.17864

# WP\_011013420.1 Total prob of N-in: 0.97599

# WP\_011013420.1 POSSIBLE N-term signal sequence

WP\_011013420.1 TMHMM2.0 inside 1 6

WP\_011013420.1 TMHMM2.0 TMhelix 7 29

WP\_011013420.1 TMHMM2.0 outside 30 163



# [plot](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_011013420.1.eps) in postscript, [script](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_011013420.1.gnuplot) for making the plot in gnuplot, [data](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_011013420.1.plp) for plot

gene complement(150963..151454)

 /locus\_tag="CGL\_RS00735"

 /old\_locus\_tag="NCgl0136"

 CDS complement(150963..151454)

 /locus\_tag="CGL\_RS00735"

 /old\_locus\_tag="NCgl0136"

 /inference="COORDINATES: similar to AA

 sequence:RefSeq:WP\_003857177.1"

 /note="Derived by automated computational analysis using

 gene prediction method: Protein Homology."

 /codon\_start=1

 /transl\_table=11

 /product="hypothetical protein"

 /protein\_id="WP\_011013420.1"

 /translation="MRNQTIAAVAALVLLTAATPAIAATPATAGNGLYSIDMGDEQKL

 TCVLFDEPSTEAHVVASCAATFPVTWKLLDGAHEQAAKLEITQAQDGELSVTASKQPL

 ITTMIAPTSITKPITVNRLVVVPGENEVRFYATDPDVLPVLITPDSYEVLTDSAAKVK

 ATL"

20

# WP\_011013818.1 Length: 162

# WP\_011013818.1 Number of predicted TMHs: 1

# WP\_011013818.1 Exp number of AAs in TMHs: 21.26988

# WP\_011013818.1 Exp number, first 60 AAs: 21.25332

# WP\_011013818.1 Total prob of N-in: 0.95903

# WP\_011013818.1 POSSIBLE N-term signal sequence

WP\_011013818.1 TMHMM2.0 inside 1 6

WP\_011013818.1 TMHMM2.0 TMhelix 7 29

WP\_011013818.1 TMHMM2.0 outside 30 162



# [plot](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_011013818.1.eps) in postscript, [script](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_011013818.1.gnuplot) for making the plot in gnuplot, [data](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_011013818.1.plp) for plot

gene 709793..710281

 /locus\_tag="CGL\_RS03450"

 /old\_locus\_tag="NCgl0661"

 CDS 709793..710281

 /locus\_tag="CGL\_RS03450"

 /old\_locus\_tag="NCgl0661"

 /inference="COORDINATES: similar to AA

 sequence:RefSeq:WP\_003858282.1"

 /note="Derived by automated computational analysis using

 gene prediction method: Protein Homology."

 /codon\_start=1

 /transl\_table=11

 /product="CAP domain-containing protein"

 /protein\_id="WP\_011013818.1"

 /translation="MKKAMRAAIGLAVSTAMTFGIAPSAHAFTALSSNIFAPPARNTE

 NANGDVSQVELEVFALVNQHRIAHGVAPLAMNESLNSGSKSWSYTMSRTGNFVHSSGG

 NYGENIYWASNIRPASLIFESWKNSPGHNRNMLDTRYSQIGVGVVYDSSGQTWATTQF

 YF"

21

# WP\_011013866.1 Length: 261

# WP\_011013866.1 Number of predicted TMHs: 1

# WP\_011013866.1 Exp number of AAs in TMHs: 21.8299

# WP\_011013866.1 Exp number, first 60 AAs: 21.8299

# WP\_011013866.1 Total prob of N-in: 0.99769

# WP\_011013866.1 POSSIBLE N-term signal sequence

WP\_011013866.1 TMHMM2.0 inside 1 6

WP\_011013866.1 TMHMM2.0 TMhelix 7 29

WP\_011013866.1 TMHMM2.0 outside 30 261



# [plot](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_011013866.1.eps) in postscript, [script](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_011013866.1.gnuplot) for making the plot in gnuplot, [data](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_011013866.1.plp) for plot

gene complement(787167..787952)

 /locus\_tag="CGL\_RS03735"

 /old\_locus\_tag="NCgl0717"

 CDS complement(787167..787952)

 /locus\_tag="CGL\_RS03735"

 /old\_locus\_tag="NCgl0717"

 /inference="COORDINATES: similar to AA

 sequence:RefSeq:WP\_011013866.1"

 /note="Derived by automated computational analysis using

 gene prediction method: Protein Homology."

 /codon\_start=1

 /transl\_table=11

 /product="hypothetical protein"

 /protein\_id="WP\_011013866.1"

 /translation="MKTETRRALVFIVAGCLAATALGFMVWQMSSPSRPTSDIATSTT

 TSTTQTQARYDSPGNTETKEAEPDLENQTLAPINTEDPYLPPNAFVRPDNGRSSGLTP

 SGSSPTTTSRVSSPSSAGSASPTQITSRSNEPSEPGDESTAATQPSSPDRPTEPTNPV

 DPTGPSEPTEPTDPIETTDPIETTDPVAPSTPPTSDDSTSTPQPDESDTPPTDFVEEP

 TAPLNPDQPAGSTTDATPNATPSAPADTTSNSVANSVEPTATS"

22

# WP\_011014348.1 Length: 321

# WP\_011014348.1 Number of predicted TMHs: 1

# WP\_011014348.1 Exp number of AAs in TMHs: 21.3604

# WP\_011014348.1 Exp number, first 60 AAs: 21.35867

# WP\_011014348.1 Total prob of N-in: 0.99411

# WP\_011014348.1 POSSIBLE N-term signal sequence

WP\_011014348.1 TMHMM2.0 inside 1 8

WP\_011014348.1 TMHMM2.0 TMhelix 9 31

WP\_011014348.1 TMHMM2.0 outside 32 321



# [plot](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_011014348.1.eps) in postscript, [script](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_011014348.1.gnuplot) for making the plot in gnuplot, [data](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_011014348.1.plp) for plot

gene 1492147..1493112

 /locus\_tag="CGL\_RS07085"

 /old\_locus\_tag="NCgl1361"

 CDS 1492147..1493112

 /locus\_tag="CGL\_RS07085"

 /old\_locus\_tag="NCgl1361"

 /inference="COORDINATES: similar to AA

 sequence:RefSeq:WP\_003856283.1"

 /note="Derived by automated computational analysis using

 gene prediction method: Protein Homology."

 /codon\_start=1

 /transl\_table=11

 /product="copper transporter"

 /protein\_id="WP\_011014348.1"

 /translation="MAKRRGRGAATFAALGFGAAAGIAFGTYVLAPNLPENIDPNAPT

 SAELVEAETLAEVNAVQADQADSIIDHIVEDVVAGTLTDRPVLVMRTADAEESDVADV

 SWLLQQAGAINAGSITLEENFFSQDGADQLKSIVANTLPAGAQLSETQLDPGTHAGEA

 LGAALLLNPETGEPLASTAERGLLLNVLRDNGYISYEDGTILPGQVIVMITGDSDGSG

 DGAFAAETQSLFARALDAQGSGVVVAGRIHTAADTGVIGRLRANPDAAENVSTIDSVN

 RTWGKMATVLSVREELAGRSGAFGSAASADAASPSLDGTAAAPAQ"

23

# WP\_011014599.1 Length: 192

# WP\_011014599.1 Number of predicted TMHs: 1

# WP\_011014599.1 Exp number of AAs in TMHs: 22.31558

# WP\_011014599.1 Exp number, first 60 AAs: 22.31433

# WP\_011014599.1 Total prob of N-in: 0.92643

# WP\_011014599.1 POSSIBLE N-term signal sequence

WP\_011014599.1 TMHMM2.0 inside 1 11

WP\_011014599.1 TMHMM2.0 TMhelix 12 34

WP\_011014599.1 TMHMM2.0 outside 35 192



# [plot](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_011014599.1.eps) in postscript, [script](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_011014599.1.gnuplot) for making the plot in gnuplot, [data](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_011014599.1.plp) for plot

gene complement(1850471..1851049)

 /locus\_tag="CGL\_RS08765"

 /old\_locus\_tag="NCgl1682"

 CDS complement(1850471..1851049)

 /locus\_tag="CGL\_RS08765"

 /old\_locus\_tag="NCgl1682"

 /inference="COORDINATES: similar to AA

 sequence:RefSeq:WP\_011014599.1"

 /note="Derived by automated computational analysis using

 gene prediction method: Protein Homology."

 /codon\_start=1

 /transl\_table=11

 /product="LysM peptidoglycan-binding domain-containing

 protein"

 /protein\_id="WP\_011014599.1"

 /translation="MAIKGAMPKNRVPGVAAGAFIAAAVIAGGSGVTFLAQGGGDVNT

 VAVVEPQDEVKNQVVTETEIVTKVHDPSSSDASDADSNTGTAEGADSDHKEPREHDSA

 QEPTAPTDPTLTITGNGDTPVSALDAVAGPARPGTVHVIENGETLSSISQDSGVPVGL

 IIDRNKLVDPDLIYAGTPLAIPTEQELAAAIQ"

24

# WP\_042383306.1 Length: 211

# WP\_042383306.1 Number of predicted TMHs: 1

# WP\_042383306.1 Exp number of AAs in TMHs: 19.55342

# WP\_042383306.1 Exp number, first 60 AAs: 19.54804

# WP\_042383306.1 Total prob of N-in: 0.92827

# WP\_042383306.1 POSSIBLE N-term signal sequence

WP\_042383306.1 TMHMM2.0 inside 1 1

WP\_042383306.1 TMHMM2.0 TMhelix 2 21

WP\_042383306.1 TMHMM2.0 outside 22 211



# [plot](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_042383306.1.eps) in postscript, [script](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_042383306.1.gnuplot) for making the plot in gnuplot, [data](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_042383306.1.plp) for plot

gene complement(2835281..2835916)

 /locus\_tag="CGL\_RS13305"

 /old\_locus\_tag="NCgl2577"

 CDS complement(2835281..2835916)

 /locus\_tag="CGL\_RS13305"

 /old\_locus\_tag="NCgl2577"

 /inference="COORDINATES: similar to AA

 sequence:RefSeq:WP\_006285906.1"

 /note="Derived by automated computational analysis using

 gene prediction method: Protein Homology."

 /codon\_start=1

 /transl\_table=11

 /product="hypothetical protein"

 /protein\_id="WP\_042383306.1"

 /translation="MAALLVLLVVIALIIWAVVALRGGSSEPEEEQPNNAVVTSSMES

STTSSSSSKESTTEATTEEETSSAEPTATSTVAADAKKTCELSDLVISASTNQPTFSG

SAQPELFMAVHNPTAVDCEIDLEENKLRFEVYNLATNARIWSDVDCNPAVEDGTSVFP

AGEDRYFQATWSRTTSAPNQCNNRTDVPAGGYYLHTVVGNNPSPAVTFNLT"

25

# WP\_003858490.1 Length: 374

# WP\_003858490.1 Number of predicted TMHs: 1

# WP\_003858490.1 Exp number of AAs in TMHs: 20.20109

# WP\_003858490.1 Exp number, first 60 AAs: 20.19552

# WP\_003858490.1 Total prob of N-in: 0.93408

# WP\_003858490.1 POSSIBLE N-term signal sequence

WP\_003858490.1 TMHMM2.0 inside 1 16

WP\_003858490.1 TMHMM2.0 TMhelix 17 39

WP\_003858490.1 TMHMM2.0 outside 40 374



# [plot](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_003858490.1.eps) in postscript, [script](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_003858490.1.gnuplot) for making the plot in gnuplot, [data](http://www.cbs.dtu.dk/services/TMHMM-2.0/tmp/TMHMM_7933/WP_003858490.1.plp) for plot

gene 963813..964937

 /locus\_tag="CGL\_RS04555"

 /old\_locus\_tag="NCgl0872"

 CDS 963813..964937

 /locus\_tag="CGL\_RS04555"

 /old\_locus\_tag="NCgl0872"

 /inference="COORDINATES: similar to AA

 sequence:RefSeq:WP\_003858490.1"

 /note="Derived by automated computational analysis using

 gene prediction method: Protein Homology."

 /codon\_start=1

 /transl\_table=11

 /product="resuscitation-promoting factor"

 /protein\_id="WP\_003858490.1"

 /translation="MAPHQKSRINRINSTRSVPLRLATGGVLATLLIGGVTAAATKKD

 IIVDVNGEQMSLVTMSGTVEGVLAQAGVELGDQDIVSPSLDSSISDEDTVTVRTAKQV

 ALVVEGQIQNVTTTAVSVEDLLQEVGGITGADAVDADLSETIPESGLKVSVTKPKIIS

 INDGGKVTYVSLAAQNVQEALELRDIELGAQDRINVPLDQQLKNNAAIQIDRVDNTEI

 TETVSFDAEPTYVDDPEAPAGDETVVEEGAPGTKEVTRTVTTVNGQEESSTVINEVEI

 TAAKPATISRGTKTVAANSVWDQLAQCESGGNWAINTGNGFSGGLQFHPQTWLAYGGG

 AFSGDASGASREQQISIAEKVQAAQGWGAWPACTASLGIR"