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SEQUENCE LISTING

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 <150> EP07110472.3
 <151> 2007-06-18
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aaagact ct a t agt t t t agg aat t t ct cga aact t gaat c aagacgt t ca t at t t ct aga 180
gcacaagcag accat at t cc t at cat acgc cgct at agt g gagggggggac ggt at t cat a 240
gat t ccaat a cct t gat ggt at ct t ggat t at gaacagt t cagaagct t c t gccaacct 300
caggaat t at t agcat ggac t t at ggcat c t at agt ccac t act t cct aa t acct t t t ct 360
at t cgagaaa acgact at gt t ct t ggt cat aagaaaat ag gaggt aat gc acaat at at t 420
caaagacat c gct ggt aca t cacacgaca t t t ct gt ggg at at cgacct agat aagt t g 480
t cct act acc t gccaat t cc t caacaacia cct acct acc gt aat caacg ct ct cacgaa 540
gaat t t t t ga ct acgt t acg t cct t ggt t c ccct ct cgcg at gact t ct t ggaaaggat c 600
aaggcat ct g gt agt t t gt t gt t t acct gg gaagaat t t c t t gat aat ga gct agaagaa 660
at t ct t gct c aacct cat cg t aaagcaact acagt act aa ac 702

<210> 9
<211> 2373
<212> DNA
<213> Chl amydi a pneumni ae

<400> 9

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t t agaagcct gt gat cat at t ggcat agaa gccgagat t g aaaat act ac cct at act ct	120
t t cgct t ct g t gat t acagc aaaaa t t t a cat acgat t c cccat cct aa t gcggat aaa	180
ct ccgggt ag ct accct gac cgacggggaa aaagagcacc aagt ggt t t g cggagcccc	240
aaact gcgaag caggat t gat t gt agct ct t gct ct acct g gagccaaat t at t t gat agc	300
gaaggacaag cct acacaat caaaaaat ct aaact t cgt g gt gt agaat c t caagggat g	360
t gct gcggag ccgacgagt t gggcct t gat gaact ccaaa t t caggagag agct ct t t t a	420
gagct cccag aagccacccc t t t aggt gaa gat ct cgcaa cagt t t t agg gaat act t ct	480
t t agagat ct ct ct aacacc gaat t t aggc cact gcgcct cct t cct agg at t ggcccga	540
gaaat ct gcc acgt cact ca ggcaaacct c gt cat ccct a aggaat t ct c gt t cgaaaat	600
ct cccgact a cagccct aga cat gggcaat gat cct gaca t t t gccct t ct t t t ct t at	660
gt cgt cat t a cgggaat ct c t gcgcaacct t caccaat ca agct t cagga at ct ct acaa	720
gccct caaac aaaagcccat aaat gct at t gt cgat at t a caaat t acat cat gct t t ct	780
ct agggcaac ct ct gcacgc t t acgat gcg agt cacgt cg ct t t agact c t ct gcgagt a	840
gaaaagct ct ccaccccaga at ct ct cacc ct at t gaacg gagaaaccgt cct ct t gccc	900
t caggagt gc ct gt agt ccg cgat gat cat agt ct ct t gg gt ct t ggagg t gt t at ggga	960
gcgaaagcac cct cat t t ca agaaaccaca accact acag t cat caaagc t gcct at t t c	1020
ct ccccgaag ct ct ccgt gc ct ct caaaaa ct t ct cccga t t ccat cgga at ct gcct at	1080
agat t cacc cgggggat cga t ccacaaaat gt t gt accag cact acaagc t gcaat t cac	1140
t at at t t t ag agat ct t ccc cgaagct aca at ct cccca t ct at agt t c t ggagaaat t	1200
t gt cgt gaat t aaaagaggt cgct ct acgc cct aaaacc t acagagaat t ct agggaaa	1260
t ct t t ct caa t agagat cct ct ct caaaag t t acagagct t aggggt t ct c t acgact cca	1320
caagaaaact t cct t act t gt aaaagt ccct t cct accgcc at gacat caa t gaagaaat a	1380
gat ct agt ag aagagat ct g t aggacagaa t ct t ggaat a t agaaact ca aaat ccagt a	1440
t cct gct aca ct ccaat ct a caaact aaaa cgt gaaact g ct ggggt t cct agcaaacgca	1500
ggact t caag aat t ct t cac t cct gacct g ct agat cccg aaacagt ggc t ct aacaaga	1560
aaagaaaaag aagaaat ct c t ct t cagggc t ccaaacat a ccact gt at t gagat cct ca	1620
ct gct t ccag gat t at t aaa aagt gct gcg acaaacct aa at cgccaggc accct ct gt t	1680
caagct t t t g agat cggcac t gt ct at gca aaacat ggag agcagt gt ca agaaact caa	1740
act ct ggca t cct gct cac t gaagat ggc gaat ccaggt cct ggct ccc caaacct ct	1800
ct t t ct t t t at t ct t t aaa ggggt ggg a gagaggct gc t ct at cacca ccat ct t t ct	1860
at agat gct t t gacct t aga gt ccagcgcg ct ct gcgaat t t caccct a ccaacagga	1920
gt gt t gcgca t ccacaaaca gagt t t t gct act t t aggt c aggt acat cc t gagt t agca	1980
aaaaaagcac agat aaaaca ccct gt gt t c t t t gcagaac t caact t aga cct t ct at gc	2040
aagat gct aa aaaaaacaac gaagct t t at aaacct t acg ccat at at cc t t cat ct t t t	2100

eol f - seq | . app

cgt gat ct ca cct t gacagt acct gaagac at ccct gcaa at t t act gag acaaaaact t 2160
 t t acacgaag gt t ct aaat g gct t gaaagt gt aaccat t a t cagt at at a t caagat aaa 2220
 agct t ggaaa cacgaaat aa aaat gt t t ct ct acgcct cg t at t ccaaga t t at gagcga 2280
 acat t at ct a accaagacat t gaagaagaa t act gt cgt t t ggt agct t t act t aacgaa 2340
 t t gct aacag aact aaagg gact at caat t ca 2373

<210> 10
 <211> 753
 <212> DNA
 <213> Chl amydi a pneumni ae

<400> 10
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 accact t t at t t acccct ga aggact ct t t acct t t t t g caaagcaagg acaaaccct c 120
 caat gt gat t at cgagaaac cct t gt cccc at at ct t t gg ggaagt at ac gt t acat cgt 180
 aat ggct cac gcct t cct aa act gaccac ggggat at cc t caat gcct t cgaagcaat c 240
 aaacaaacct acgct ct cct agaagct agt ggaaaaat ga t t caagct ct t ct ggct t ct 300
 cagt ggaaag aaaagcct t c gcat aagct c t t ct ct t t at t ct t gaat t t cct ccaccgt 360
 at t cct gaaa gcagcaat cc agaat t t t t t gcagccat ct t t gt act t aa act t ct ccaa 420
 t acgaaggaa t cct agacct gact ccagca t gt t cgct at gcaaagcat c t ct accct at 480
 gcct gct at c gct accaagg ccat aaact a t gt aagaac at cagcat aa acaagccat c 540
 t ccat cgaga aagaagaaga acaaat ct t a caggct at ca t t cat gcgaa gcagt t t t ct 600
 gaact t ct ag ct at t gcaga at t cccgat t gct at agct g aaaaaat t t t t t at t t gt t t 660
 gact cgct ac aagaggaaaa aaaat cagaa agaaat t ct t cggaagat cc at at cat gaa 720
 at cct aagac t t t ct aaagt agt ccat ccc t ac 753

<210> 11
 <211> 714
 <212> DNA
 <213> Chl amydi a pneumni ae

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 t ct gt ct at g at ggcgact t t at aggaat c at aggaccaa acggaggggg gaaaagcacc 120
 t t aacgat gt t aat t t t ggg ct t gct t act cct acat t cg gat cct t gaa gact t t ccct 180
 t cgcat t ccg cggggaaca aacccat t cc at gat cgggt t ggggt t ccca acat t t ct ct 240
 t at gat cct t gt t t t cct at ct cagt aaaa gat gt t gt cc t ct caggaag at t gt ct caa 300
 ct ct cct ggc at ggaaaaat a t aaaaagaaa gat t t t gaag ct gt agat ca cgct t t ggat 360
 ct t gt t ggac t t t ct gacca ccaccaccac t gct t cgccc at ct ct cagg aggacaaat c 420
 cagcgt gt ac t t ct ggcaag agcct t agcc t cct accct g aaat t t t aat t ct t gat gag 480
 ccgacgacaa acat t gat cc t gacaat caa caaagaat t t t aagt at cct aaaaaagct c 540

eol f - seq | . app

aaccgt acgt gcacat t ct t at ggt aact cacgat ct t c accat acgac gaat t act t t	600
aat aaagt t t t t at at gaa caaaact t t g act t cat t gg cagacact t c gacct t aaca	660
gaccaat t t t gt t gt cat cc ct at aaaaat caggaat t t t cat gct ct cc t cac	714

<210> 12
 <211> 1176
 <212> DNA
 <213> Chl amydi a pneumni ae

<400> 12 at at t t g agt t ccgat t ccc t aaaat agga gagacgagt t ccggaggat c t at agt ccgt	60
t ggt t aaaaa at t t g ggt ga t cat gt agct agagat gaggc ct ct gat t ga agt at ct acg	120
gat aaaa t t g ct acagaat t accct ct cct aaagcaggcc gact ggt gcg t t t ct gcgt c	180
aat gagggag acgaggt t gc t t ct ggggat gt t t t aggat t gat agagct t gaggagat t	240
t ccgaagct g at gat gagag cacct cat gt cct ct gact t ct t gt gaaac aaagt cggag	300
gcgggt t cca gcagt t ct t c ggt at ggt t t t ct cct gccg t gct gagt t t agct caacgt	360
gaaggcat t g gt ct t gat aa cct caaaaag at t gccggca cggggaaagg gggacgagt g	420
act cgt cagg at t t agaagc gt at at t t ca gaat cgcaac aagt t t ct at t cccgaaat a	480
t t t caaggag aagt gaat cg cat t cct at g t ct ccgct ac gt cgggcaat agct t ct t ct	540
ct ct ccaagt ct t cagat ga ggt t cct cac gcat ct t t gg t t gt t gat gt cgat gt caca	600
gat ct t at ga at ct gat t t c t ggt gaacgc caacgct t ct t agat acgca t ggggt gaag	660
ct aacgat t a caagt t t cat t gt acagt gt t t agct caga ct t t aaggca gt t t cct t t a	720
t t gaat ggt t cct t agat gg gact accat t gt t at gaaga aat ct gt gaa t gt aggcgt t	780
gccgt gaacc t caat aagga aggggt t gt t gt t cct gt ca t ccacaat t g t caagat cgc	840
ggt t t agt aa gt at t gcaaa ggcct t ggcg gat ct at ct t caagggct cg gt t aaat aaa	900
t t ggat cct a gt gaagt gca agat ggcagc gt t act gt ca cgaat t t t gg aat gacggga	960
gct t t gat t g ggat gccat cat acgt t at cct gaagt t g ct at t t t agg aat t ggcaca	1020
at acaaaaac gt gt t gt cgt ccgt gat gac gat t ct t t ag ccat t cgcaa aat ggt ct at	1080
gt gacact t a cct t t gacca t agagt at t g gat ggt at t t acggcagt ga gt t t t t aacc	1140
t cat t gaaaa at cgt t t gga gt ct gt t acg at gggc	1176

<210> 13
 <211> 708
 <212> DNA
 <213> Chl amydi a pneumni ae

<400> 13 aaaaat t ccg ggaat at t at ggaaccct ct accaacaagc ccgact gt aa aaagat ct t c	60
gat t ccat ag cgagt aagt a t gat cgcaca aat acaat ac t ct ct t t agg aat gcacat	120
t t ct ggaat c gct ct t t gat ccagat cct a gggg cgggat act ct ct cct ggat ct ct gc	180
gcaggaacag gaaaagt cgc gaagcgt t at at t gccgcac accct caagc at cagt aact	240
ct cgt cgact t t t cct cagc aat gct cgac at t gcaaaac aacacct t cc ccagggct ct	300

eol f - seq | . app

t gct ct t t t a t t cat agcga t at t aat caa ct gccct t gg agaat cat t c t t at ccct a 360
 gcagcgat gg cct at ggct caggaacct c t cggat ccac at aaagccct acaagaaat c 420
 t cccgagt gc t t at gcct t c t ggaaaact g ggcat t ct ag agct cacacc t ccaaaaaaa 480
 acacaccct a cct at agt gc ccat aagct c t at t t gcgt g ct gt cgt ccc ct ggat t gga 540
 aagt ct gt t t ct aaagat cc cgacgcct at agct at ct ca gcaaaagt at ccagcaact t 600
 ccaaaggacc acgat ct t ga agacct at t c t ct aat cag gat t t t at at t gcgaaaaag 660
 aaaaaat t gt t cct aggagc ggct acgat t t ggct act ag agaaacaa 708

<210> 14
 <211> 1815
 <212> DNA
 <213> Chl amydi a pneumni ae

<400> 14
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 aat gt aat t t gact t agc aggaagt ggg aaaccacag at t gggaagc ccccgcgaca 120
 gat ct ct ccc aaact agaaa cgt aat ct ac gcagaaat gc cagaaggcga aat cat cgaa 180
 gcaaccgcca t t cct gt aaa agacaat ccc gt t ccacaat t cgagt t t ac t ct ccct ac 240
 gaact t caag t aggagaaac cct cact at t gt cat gggag cct ct ccaaa ccat cct caa 300
 gt cgat gat g ct gggaacgg agcccaact t t t cgcacaac gt cgcaaacc ct t t t acct c 360
 t acat cgat c ct acaggaga aggaaact at gat gaaccg at gt ct t ct c t at ggat at c 420
 cgcggaacg t cct aaaaaa aat agagat c t t t act ccct cct at gt cgt t aaaaacaaa 480
 cgct t cgat a t caccgt gcg at t t gaagac gaat t cggga acct caccaa ct t ct ct cct 540
 gaagagacc gaat cgagct t t cct acgag cat ct t agag aaaat t t aaa t t ggcagct c 600
 t t cat cccag aaacaggct t t gt t at t ct t cct aat ct ct at t t caat ga gcct ggaat t 660
 t at cgcat cc aat t gaaaaa cct ct ct aca caagaaat t t t cat ct ct gc ccct at caaa 720
 t gt t t cgct g act cgcgcc gaat ct t at g t ggggt ct cc t ccacggcga at ccgaacgc 780
 gt cgact ct g aagaaaat at t gaaact t gt at gcgt t at t t ccgagat ga ccgct ct g 840
 aat t t ct at g ct t ct t cat c at t cgaaaat caagagaacc t ct ct ccaga t at t t ggaag 900
 ct cat caat c aaact gt ct c cgact t t aat gaagaagat c gct t cat cac act at ccgga 960
 t t ccaat at a gcggagaacc t cat ct cgag ggagt gcgt c acat cct t ca t accaaggaa 1020
 acaaagt ccc act cgaacaa caaagaat ac aaacat at t c ccct cgccaa gct ct at aaa 1080
 agcact gt ca accacgacat gat t t ct at t cct t cgt t ca cagct t ct aa agaacat ggt 1140
 t t t gact t t g agaat t t ct a ccccgagt t c gaaagagt t g t agaaat t t a t aat gcct gg 1200
 ggat ct t cag aaaccacagc cgct ct aac aaccct t cc ct at ccaagg t aaagat agc 1260
 gaagat cct c gaggt acagt aat t gaagga t t aaagaaga at ct ccgct t cggat t t gt t 1320
 gct gggggc t cgacgat cg aggaat t t at aaagact act t t gact ct cc gcaagt gcaa 1380
 t at t cccag ggt t gacggc t at cat t t gt aat aat at a cccgagagt c t ct t gt t gaa 1440

eol f - seq | . app

gct t t at t cg cacgt cat t g ct acgct aca acaggacct a ggat cgt ct t aagct t caac 1500
at cact t cag cccct at ggg ct ccgaact c t ccacagggt cgaaacct gg act caacgt c 1560
aaccgt caca t ct ct ggt ca t gt ggcaggc act gccct ac t caagact gt agaaat cat c 1620
cgcaat ggcg aagt t ct cca t acct t ct t c cccgat agca at aacct gga ct at gaat ac 1680
gat gat at gg t acccct aag t t cagt gacc ct aaaagat c caaacggg aa agcacct t t t 1740
gt at t ct act at ct cagggt cact caggca gacaat gct a t ggcct ggag t t cccaat c 1800
t gggg ggat t t aaat 1815

<210> 15
<211> 513
<212> DNA
<213> Chl amydi a pneumni ae

<400> 15
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aaagct at t a aaagagt ct g cggaaacaaa gaaaacgat t t at gt cgct a t ct t ccaggc 120
cct agcggcg gt t at at gca t cat t t cact ct aaaaaaga t gaaaagcgc t gct cccgaa 180
caact t t t aa aaat gt t aaa aacat t t at t t t agaat cgg aaaccccacg cacaat t aat 240
cct aagcct a gagct cct ag aggct ct aaa aaacgt cgt g act t t at t aa ct t t act aaa 300
acagat at t g aacgcgt t t t agaact ggca agacaagt t g gagacaaaga cct cct cgct 360
cgct t t agcc ct aaaaaacc gt t aact t ct t t aaaaaggg agt t aat t cg t t cgat t cgc 420
aacggg at cg t gagcgt aga gct at ggaat gcct acgt cg aagct gt gaa ggct gt aagc 480
t ct cccaacc t t gaagt t ac ct ct cct t t c gt t 513

<210> 16
<211> 858
<212> DNA
<213> Chl amydi a pneumni ae

<400> 16
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gaaaat act g gaat aaaaga t cagaact t a t t t ct t gat c aagcgact ct t aat gt ggat 120
ggcaat gt cg at at agaaaa ct t t t agag act cgagat t t aaaagt t gc agat acaat c 180
act t ct ccat gt gaat t t ac t gt cgggggc ggat t at cag cagaaagt t c t caat t t aaa 240
gcgacaacac t t t ct aaagg t t t ggagat c act t ct gaag at caggat gg ccgagt t cct 300
aagt t t acaa at gt t agcga t cccaat ct ccaagagat g ct t t aacat a t aact at t at 360
aggaacact g gat gccaggc cct t aat ct g t at acct act at agt t cat c t cagcct act 420
act gt aggt a aaccaat cga aacggg gt gt caaaaccga at ccagagac gt at cgcat t 480
agcgc t t cag ct aaaa t t a t gat gct gt a acgagat t cc cct at at t ca gt t caaggca 540
cct ggaat ct at caagt cac aat acaaat a cgt cgcgaga gcgggcaaca t agt ggact t 600
gat aat cct a at t t at at ct gaact t aat g at t gggaat a at aagacgct gct t t gt gct 660

t cagat acga gaggt t act c aggaggacat aggact agt a t t gct gt aac aggcacgt t t 720
 act t t aacag aaat t gt t gc t accccccct cat gat t acc ct t ggt t at t ct t agaaact 780
 act at t ggt t t agat at t aa at ccat gt ca acat gt gt t a t t t ggt t t cc at t t caagct 840
 aat t t t gcgg aggt agat 858

<210> 17
 <211> 615
 <212> DNA
 <213> Chl amydi a pneumni ae

<400> 17
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 caggaagagg ct agaat t t t accagt t aaa gacagt ct t t cat ggaaacg ct at gact at 120
 acat caagt t ct ggg t t t t c t gt ggaat t t cct ggggagc ct gat cat t c ggggcaaat t 180
 gt agaagt cc ct caat caga gat t accat a cgt t at gat a cct at gt aac agagact cat 240
 ccagacaaca ct gt gt at gt agt ct ct gt t t gggagt at c ct gaaaaagt agat at aagt 300
 cgt ccagagc t caat ct gca agaggggt t t t caggcat ga t gcaggct ct ccct gaat cc 360
 caggt t ct t t t cat gcaagc aaggcagat t caaggccat a aggct t t gga at t t t ggat t 420
 gt t t gcgaag at gt t t at t t cagagggat g t t gat t t ccg t aaat cacac t ct t t at caa 480
 gt ct t t at gg t t t at aagaa t aagaat cct caggcct t gg at aaagaat a cgaggcgt t t 540
 t ct cagt ct t t t aaaat t ac t aaaat acga gaaccaagaa cgat t cct t c t t cagt gaaa 600
 aagaaagt ga gt ct g 615

<210> 18
 <211> 1647
 <212> DNA
 <213> Chl amydi a pneumni ae

<400> 18
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 gaat t t caag aagcagcct c t t t aat t gct gt t ccagat a ct t cacat t c t aagcct gt c 120
 gt t ccaggag t gaaaaccct ct t t ccacaa acct accacc t t ccct at ct aaagt t t gt c 180
 caaggagaaa at gt cgt t ca cact cct ct a aaagt aggcg t aat gt t ct c aggaggacct 240
 gct ccaggag gacat aat gt cat ccaagga ct ct t caat a gt ct aaaaga t t t ccat ccc 300
 gat t cct ccc t cgt ggggt t cgt aaat aat ggagacggc t t acaaaca t aaaagcat a 360
 gacat t act g aagagt t t ct ct ccaa t t c cgaaat t ccg gaggct t caa ct gt at agga 420
 acaggaagga aaaaaat t gt aact ccagaa gct aaagagg ct t gt ct aaa gaccgcagag 480
 gct ct ggat c t cgacggact agt cat t at t ggccgt gat g gct ccaat ac agcaaccgct 540
 at t ct t gcag agt at t t t gc aaaacgacgc ccaaaaacct ct at t gt cgg agt t cct aaa 600
 act at agat g gggat ct aca acacacct t c t t ggat ct ga cct t cggat t t gat act gca 660
 acaaaaat t ct act ct t caat cat t agcaat at t t caagag at gct ct t t c ct gt aaagct 720
 cat t accact t cat t aaact t at gggacgc t cagcat ccc at at t gct t t ggaat gt gct 780

eol f - seq | . app

ct ccaaact c at ccaa at t gccct t at c ggcgaagaaa t t gccgaaaa aaat ct acca 840
ct aaaaacca t cat ccat aa aat ct gct cc gt aat t gcag at agagccgc t at ggaaaa 900
t act at ggcg t cat cct cat cccagaaggc at t at cgagt t cat cccaga aat cat caac 960
t t aat t acag aaat cgaaag cct at cagaa t acgaagat a aaat ct ccag gct ct ct cca 1020
gaat cccaac gcct act gaa aagct t ccca gcacct at ca t cgagcaaat cct caat gac 1080
cgcgat gct c acgg t aat gt ct at gt t t ct aaaat t agt g t cgat aaact act cat ccac 1140
ct ggt cagca at cat ct cca acaat at t t c cct aacgt cc ct t t caat gc gat ct cacat 1200
t t t ct aggat at gaaggacg ct cgggat t g cct acaaaat t cgat aat ac ct acggct at 1260
agcct cggat acggcgccgg t at t ct cgt c cgcaat cact gcaacggct a t ct ct ct act 1320
at agaat ccc t agcat gcc t t t cat gaaa t ggaaat t ac gggcaat t cc cgt agt gaaa 1380
at gt t cacag t aaaacaaca ggcagat gga act ct acaac ct aaaat t aa aaaat acct c 1440
gt agat at ag gaagcacggc at t t cgt aaa t t t aagct ct at aggaaaat t t gggcct c 1500
gaagact cct accgat t cct agggcct ct a caaat agaaa ct cct ccaga aat gcaact ct 1560
gat aat t t cc ct cct ct t ac cct t t t gct t aat cat aact t t t ggcaacg t caccagggt 1620
t gcat agaaa t ccct gat ac t acgt at 1647

<210> 19
<211> 1929
<212> DNA
<213> Chl amydi a pneumni ae

<400> 19
act t cgt ct t ct t gccccct t t t agacct g at at t gt ct c ct gcagat t t aaagaaact c 60
t ct at t t ct c agct t cct gg t t t agct gaa gaaat ccgt t at cgcat cat ct ct gt at t a 120
t cacaacag gaggccact t at ct t caaat ct t ggaat cg t agagct t ac t at agcct t a 180
cat t acgt gt t ct ct t cccc aaaagat aaa t t t at t t t g at gt aggaca t cagacct at 240
cct cat aaac t act gacagg aagaaat aat gaaggat t t g accat at acg caat gacaac 300
ggcct cagt g gt t t t accaa ccct acggag agt gaccacg at t t at t t t t ct ct ggacat 360
gcagggacgg cat t gt ct t t agct ct agga at ggct caaa caaccct t t agaat cacgc 420
acacacgt ca t t cccat cct t ggagat gct gcat t ct ct t gt ggt ct t ac ct t agaagcg 480
t t gaacaat a t t t caacaga t t t at cgaag t t t gt t gt t a t t t t gaat ga caacaat at g 540
t cgat ct ct a aaaacgt agg agccat gt ct cgaat ct t t t cccgat ggct acaccacct 600
gcaaccaat a aact cact aa gcaagt ggaa aaat ggct cg ct aaaat t cc acgct at ggg 660
gat agct t ag caaagcacag t cggagact t t cacaat gt g t t aaaaat ct ct t ct gt ccc 720
act cct t t at t t gaacaat t cggat t agcg t at gt cggcc ct at agacgg t cat aat gt t 780
aaaaaact ga t ccccat cct t cagt ccgt t cgt aacct cc ct t t t cct at t ct t gt ccac 840
gt ct gt acaa ct aaggggaa gggcct agac caagcccaaa at aaccct gc aaagt at cac 900
ggagt cagag caaact t caa t aagcgagaa t ccgcaaaac at ct t ccygc gat t aagcct 960

eol f - seq | . app

aagcct t ct t t ccct gat at at t t ggccaa acgct at gt g aact t ggaga ggt t t cct ca 1020
 cgt ct ccat g t ggt gact cc t gcaat gt ct at aggat ct c gt t t ggaagg t t t caaacag 1080
 aagt t cccag aacgct t ct t t gat gt aggg at t gct gaag gccat gcagt gact t t cagt 1140
 gcaggcat t g caaaagccgg caat cct gt g at ct gt t ct a t at at t ct ac at t t t t acac 1200
 cgt gct ct cg at aat gt t t t ccacgat gt t t gcat gcaag at ct t cccgt gat t t t t gct 1260
 at agat cgt g caggact t gc ct at ggt gat ggacgt agt c at cacggcat ct at gat at g 1320
 agt t t cct ac gt gcgat gcc ccagat gat t at ct gt cagc cacgt agcca ggt ggt at t c 1380
 caacagct ac t gt at t ct t c t ct acact gg t cct ct cct t ct gct at ccg ct accccaat 1440
 at cccagct c ct cat ggaga cccact cact ggagat ccaa at t t cct aag at ccccaggc 1500
 aat gct gaga ccct ct caca aggt gaggac gt t ct cat ca t agct ct t gg aaccct ct gc 1560
 t t cacggccc t at ct at aaa acat cagt t g ct t gct t at g gcat ct ccgc aact gt t gt a 1620
 gaccgat ct t t at aaaacc t t t t gat aac gat ct t t t ca gt ct t t t act gat gagt cac 1680
 t ct aaggt ga t t accat aga agagcact cc at t cgaggag gat t agcgt c cgagt t t aat 1740
 aat t t t gt ag ct acgt t caa t t t t aaggt c gat at ct t aa at t t t gcaat ccccgat aca 1800
 t t cct at ccc at gggagt aa ggaagccct c acaaaat ct a t aggcct t ga t gagagt agt 1860
 at gaccaacc gcat t ct cac t cat t t caac t t cagat caa aaaagcagac t gt t ggagac 1920
 gt cagagt t 1929

<210> 20
 <211> 1026
 <212> DNA
 <213> Chl amydi a pneumoni ae

<400> 20
 gaagt t t at a gt t t t t cccc t t cagt aaga act t cgt t t c agcaccgt gt aat ggcggca 60
 ct agat aat t ggt t t t t t ct aggagggcgc cgt t t aaaag t agt t t ct ct agat agt t gt 120
 aact cagggc aggct t gt ga agaat acgt g cct at t t caa cgacagaaaa ggt ct t aaag 180
 at act ct ct t acct act cat accgat t gt c at aat agct c t gt t aat t cg t t at ct t t t g 240
 cat agcaat t t t acggcaaa ggt at cacag aaacct t ggt t aaagaccct gcagt t agga 300
 at t gat at aa aaagct t cat act t cccggt t ct cat gt aa acacgat gga t t cagct act 360
 t t gt t t aaag caat t cgt t t ggaaggggaag cgt gt t gat g t agaat at ca t aggct acat 420
 agcagcgat a aggt ggt t t t t t at at ccct gct cagaaac t t ccagat ga t ct gcgt t t g 480
 act cat t ggc t t ccagaaaa agaaacaaga aagact gagt at gt gagaca t at gct ggcc 540
 cat gt cat gg gt t at ct aac at cacagggt aaggaacggc t t caacaggt agt gcaagac 600
 t ct cgaagca gt act t cct t gggggct gaa aaagt cct t c aat acagat t cat t gat cat 660
 ccacagagt c aaggagaat t t caacgt ct g ct t aat gaaa at at aacgac caaaggt t cc 720
 gaggat aagg aagt t gt aca gagt gat t t a t t t gacat gg ct t t t cagt g t t ggt ggcca 780
 cagt t t at t t cagt t at aca at ct ccgacc t t cagt gaag aat t agt aca cgaaat gagt 840

eol f - seq| . app

cagaaact t g at t t agat t g t at at accca gaagat gat g aat t t gagca gaagt t cct t 900
aat accct t c t gaaagcagt ct t gcaccac ggt t t t gaag gaat cagt gt t gcgagt at g 960
ggt gt t at ct t cct gat t t g t ccggact ct ct t gcatt ac agat t ccct t ct t aaggaat 1020
caaaaa 1026

<210> 21
<211> 1098
<212> DNA
<213> Chl amydi a pneumni ae

<400> 21
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cagt t aagt g act t t agt aa gaagcaccac at act cacca aaat t gt t ac gat cat t gt t 120
aaaat t t t ca aact ct t aat cgggt ct gat t at t ccgcccc t gggaaat t t a t t ggt t at gt 180
caat t agt at gt t cct t ggc t ct t t t cccc cgt t ct t cga t gct t t acag cgt ct t gaaa 240
acct gct t t a aaaagt at cg t t t ggaacag gaaat acaag at t at t t t gt aaagaat ct a 300
gat ccct ct t t caaagacc agcagt ct cg gaaagt aaaa gaat cacgat ccaacaagac 360
cat ct t acca t t gat act t t agcaat acat t t cagt acgg caaggcct aa acgt t ggct g 420
ct gat t t ct c t aggaagt gg agat t t cct c gaagacat ga t aggcct gaa agat t cct t g 480
t t t ct ct cct ggaagagt t agct aaact g ct aggcgct a at at cct aat t t acaact at 540
cct ggggt t a agt cgagcac aggaaaat t g aact t agaga acct agcgac agct cat aat 600
ct at gt gcaa agt acct aca agat aaaat t cagggccct g gggct aacga aat cat cacc 660
t acggat at t cct t aggagg ggt agt ccag t ct gcagct t t gcaaaaaaa t cct t t t aca 720
aat agcgaga ct t ct t ggggt agcagt caaa gaccgt gct c cccact ct t t acccgagct 780
gct aat agt t t ct t cgggcc aat aggaaaa ct cat cgcag t cct cgct cg at ggaaaat g 840
gat gcggaaa aaaacagccg agagct t cct t gccagaaa t t ct t gt t t a t t ct gcggat 900
cgat t t cgcc ct t cagaagt t ggt gat gat accgcat t gc t cccggagt t t act ct t gct 960
cat gcaat aa aacgaacccc at t t gccagg agt aaaaaat t t at aggaga ggt aat ct a 1020
ct ccaact caa gccct ct gaa acaccct aca at acaaaagc t t gct gaagc aat cct t gag 1080
agt ct ct ct a gaaaaaat 1098

<210> 22
<211> 972
<212> DNA
<213> Chl amydi a pneumni ae

<400> 22
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caact act aa act at cgaag cgagcaccgt t t ggt t cct t t t t gggaaaa at ccgat ggt 120
t ct t t t at ca ccgct gct ga t t acggcagt caat at t at c t aaaacaaca gct t gcaaaa 180
gcct t t ccca at at t cct t t t at t ggagaa gaaact ct at at cct gat ca agacaacgaa 240

aaaat ccct g aaat ct t aaa at t t acacgc ct gt t aact t ct t cagt ct c aagagat gac 300
 t t aat t t ct a ccct ggt ccc t cct ccat ct ccgact t ct t t at t t t ggct t gt cgaccct 360
 at t gat ggt a ct gcaggt t t t at cagacat cgt gct t t t g ccgt t gct at at cact aat t 420
 t at gagt at c gaccgat t t t gt cggc cat g gcat gccct g cct at aat ca gacat t t aaa 480
 ct at at t cag cagct aaagg t cat ggt ct t t ct at t gt t c at t ct caaaa t ct agat aga 540
 cgct t t gt t t at gct gat ag aaaacaaca aaacaat t ct gt gaggct t c gt t agct gca 600
 t t gaat caac agcat cat gc aacacgt aag ct aagcct gg gt ct ccccaa cact ccgagt 660
 cct cgt cgt g t agaaagcca at at aagt at gct t t agt t g ct gaaggcgc cgt agat t t t 720
 t t cat t cgct accct t t t at t gat t ct ccc gct cgt gct t gggat cacgt acct ggagcc 780
 t t cct cgt t g aagaagct gg gggc agagt c acggat gct t t aggagcccc t t t agaat at 840
 agaaaagaaa gt t t ggt ct t aaat aat cac gcagt gat t c t t gct t ct gg agaccaggaa 900
 acccat gaga caacat t agc agcgt t acaa aaccaact ca at gt t gt ccc cacggat aag 960
 ct t at t gct c t a 972

<210> 23
 <211> 1371
 <212> DNA
 <213> Chl amydi a pneumni ae

<400> 23
 t t caacgt ca act t t aaat t ct t agaagga ct t cat caac ccgcgcccag at acacaagc 60
 t accct acag ct t t agaat g ggaacct t cc gat gcggt c cagct ct t ct agcgt t ccaa 120
 agaat t agag aaaat cct ca gcct ct ct ct ct t t at t t t c at at cccct t ct gccaat cc 180
 at gt gt t t gt at t gcggt t g t t ct gt t gt t t t gaat cgt c gt gaagat at t gt agaagct 240
 t at at caaca ccct aat cca agagat gaaa ct t gt cgt t g agaccat agg at t ccggcct 300
 caggt at cca ggat t cat t t t ggaggaggc acccct agca gact ct ccag ggagt t gt t t 360
 accct gct t t t t gaccacat ccat aagct t t t t gat ct t t cacat gct ga agaaat t gct 420
 at t gaagt gg at cct cgt t c t t t aagaaac gacat ggaaa aagcagat t t ct t t cagaac 480
 gt aggt t t t a at aggt t ag ct t aggcgt t caagat accc aagct gat gt t caagaagct 540
 gt acgacgac gccaat cgca t gaggaat ct t t aaaggcat acgaaaaat t t aaggaact c 600
 gcct t ccaaa gt at caat at agact t aat t t at ggt ct t c ccaaacaac caaggagt cc 660
 t t t t ct aaaa caat t caaga t at ct t agcg at gt at ccag at cgt ct t gc t t t at t t t ct 720
 t t t gcct cag t t ccat ggat caagccgcac caaaaagcca t gaaagct t c ggat at gcct 780
 t ct at ggaag agaaat t cgc gat t t at t ct caat cccggc at t t act t ac aaaagcagga 840
 t at caggcca t cggc at gga t cat t t ct ct ct t ccccat g at cct ct t ac cct cgct t t c 900
 aaaaacaaaa ct ct aat ccg caact t t cag gggc at t ct c t acccccaga agaagat ct g 960
 ct cgggt t ag gaat gact t c t acaagct t c at t cgt ggaa t t t at ct aca aaat gcaaaa 1020
 accct t gagg aat at cacia t acggt gct t cgaggaacat t t gccact gt gaaaagt aaa 1080

at t ct t accg aggat gat cg gat t agaaaa t gggcaat cc at aagct gat gt gcacgt t t 1140
 acgat caat a aggaagagt t t t t caacct t t t t ggat at g agt t t gat ac t t at t t t at a 1200
 gaaagt cgt g at cgct t gat aagt at ggaa act acaggt c t cat ccat aa cagt cct ggc 1260
 t ct t t gaaag t aact cct ct t ggagaat t g t t t gt cagag t cat t gccac agct t t cgat 1320
 cact at t t t c t caat aaggt at ct aaaaaa gaat gt t t ct cagct t ct at a 1371

<210> 24
 <211> 1047
 <212> DNA
 <213> Chl amydi a pneumni ae

<400> 24
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 at cat gcagc t caggcat t t cgct ct agga t gggg cgt t t t t t t at ct g t gcct act t c 120
 gat t at cact t at t t aaacg at gggcat gg gt act ct act t t t t cat gat t t gt gct ct c 180
 gt gggcct t t t t t t gt t cc gt cagt ccaa aat gt ccat a gat ggt accg t at t cct t t c 240
 at ccat at ga gcgt acagcc ct cagaat at ggaaagct t g t gat cgt gat aat gct cagt 300
 t at at ct t gg aat cccgaaa agcagat at t acat cgaaaa caacagcat t cct t gct t gc 360
 t t agt t gt cg cact t ccgt t ct t t ct aat t t t aaaagagc ct gat t t agg aaccgcat t a 420
 gt ct t at gt c ct gt gacat t gacgat t t t c t at t t aagt a at gt ccat t c t t t act agt a 480
 aaat t t t gt a cagt ggt cgc t accat cggg at t at aggct cgt t at t gat t t t t cagga 540
 at cgt ct cac at cagaaagt gaaaccct at gct ct gaaag t cat caagga at at caat ac 600
 gagcgact ca gcccgt caaa t cat caccaa cgcgct ct c t cat t t ct at agggct ggga 660
 ggaat t cgag gt cgt ggat g gaaaact ggg gagt t t gcag gt cgt ggat g gct accct ac 720
 ggct acacag act ct gt at t ct cggcat t a ggagaggaat t cgggt t gct ggggct act c 780
 t t t act ct ag ggct at t t t a t t gt ct t at c t gt t t t ggt t gt cgaact gt t gcagt cgcc 840
 act gat gact t t ggaaaact cct cgct gct ggcat t accg t at acct agc gat gcacgt c 900
 t t aat caat a t t agcat gat gt gcgggct g ct acct at ca caggagt ccc t ct gat t ct a 960
 at t t cct at g ggggct ct t c ggt aat ct ct acaat ggcat ccct t ggt gt at t gcaaagt 1020
 at ct at agcc at cgct t t gc t aagt ac 1047

<210> 25
 <211> 2619
 <212> DNA
 <213> Chl amydi a pneumni ae

<400> 25
 at gt ct acct t t t ct at cca aaat cgact a agaaccat t t cagggt gaaag t act cgaat c 60
 at caagct gg accat aagt a ct ct ggt t t t gat cccagat cagt gcct gc gat aaat t t a 120
 gaagagt t aa at t cagggat t t at gct ct a aggcatt t aa t gaacgccct gcaat cagaa 180
 aat accaat g t t gct gct t t at t aaacca aacaat acga t ct t cccac aacat ct t gg 240
 acagat t aca agcat t cgcg t ccgcaagct agct ct ccaa gagcaccct c at cacaaact 300

eol f - seq | . app

cccacagat a t cgt at cagc agcagct ct t gct t t agt t c t t gt t at t ga cggaggt ct a 360
 gcggaat t ag t ggcct ccgt t acagaaat t gat ct cggag ct t t at ccac t at at ccaca 420
 gt t cgt cagt t aat ggcgag ct acct cggg t t gacaact c t aacagct ga acaagaaaag 480
 gt t gt at t t t ccagct cct a t gt t cct t ca gaaaaaat c t cct t gaaca t gt aaaacaa 540
 gaaaaagct g ct gaaat cca agct aagcaa gaagaaat aa aagcagt at t agaagct aaa 600
 ggagt ct ct a ct gaagagat cgaagcgat a ct t aaggaat at cct gat at ct at gcagca 660
 gat t t ct t ca aagagt t t at agaagagcct t t acat acat at cgt gcaaa agt cggg gca 720
 ccgat ccaag agat gaat ga gaacgcat t cagct gct t c ct acacct cc t gcgat cact 780
 cct gacaat g t caat gaagt caacggaat g aacaccct ca gcact at t t t acaagct at a 840
 gat gat gct a t t aaacaagc t cct gcact t ggt ggggat c aggaaat cat t act at act a 900
 caaact t t gg t t ccct agt cgat aagacc acgt t t acaa aagct gaat t cgat ct t at t 960
 t acacagcaa cacaact t cc t aat acagca t ct t t aaaac t ct acct t ac ggat agacaa 1020
 at t gct gagt at cgagggaa aat cacgaaa gt at at caaa at t ct at cca aaat ct ct ct 1080
 gagacaaaac gt gt agt t ga aaacaaccga agcat gct ag aaacacaact ct ccat gt t c 1140
 caacaagcac aaaat t gct t t gt t act t gg at t agt caag ccaat gcact t aacat agcc 1200
 at cact aat a aat at at t t c t gct gt act t acgact t ct a t ggagat gt a cggaggt ct c 1260
 ct t t gcct t t ct t at at gt a cgaaaggt t a gccgat gat g aaaaagcaat t t t t gacaaa 1320
 agt gt gaat g agt at t t acc gat t cacat c gt t gt t ggt g gt t cat gggg aaat ggct gg 1380
 at agcaaaaa t ggcagcct a t caagaact c gcggaat act ct t t aggaac cgcagt t aca 1440
 agt caagat c aaat caaagc t t at t t acaa acacgagggga at gagt t t aa agct acgcgt 1500
 cat t t t t t cc at aat at t gg ggat caaat g t accaat t t g ct aat gagac t gt ct t t gga 1560
 aat t gt ct t a caacagcaaa t ggt gcgat a cagcccgat t t aggt ggt t t t at cagagaa 1620
 gcaat gacga at gt t ggaac t gt t gaagcc gat t at gt aa gcaat gct ca gaggat cct a 1680
 aat gaat t t a at acggct gc aact gcgcat gt t t t acaat t acaat t aca aat agct gag 1740
 t t acaaaaaga aagcagat ga ct t agaccga ggaaaagcct ct t t cact ga gaaccgt aaa 1800
 t t t gct gt t g ct gct t ggat cacat cggag agct t aggag at gct t t aat t t ct at gat t 1860
 t t aaact ct c agct accaaa gcaagaggct t t t t t aaaac ct t t gat cga agaaat t aac 1920
 t t caat aacc t cgcagcgaa t gcct t aac agct t gct ac agat t accaa t gaat t t t ct 1980
 acgact t ct g t ct act at ag cct ct ct t cc t at t t agt t c agagt aaaac t ggacaaaac 2040
 ct gt t t gct g gt gat t act a t gaaacact t ct agct gcag ct agagaacg ggagt at at t 2100
 t at cgcgaca ct gcgagat g t aaacaagcg at t aat ct ag t caat ggact t ct ccaaaaa 2160
 at t aact ct c t t ccaggggc t acct cagca caaaaacaag aaat gct t aa cgcaact acc 2220
 t at t at caat acagct t at c agt cact t t a aaccaact t a ct gt at t aga at ct t t act c 2280
 gcgggt ct ca aaat gact ct t cagacaact agt aat aaca aat acgacaa aagt gt gt t t 2340

aaaat t gaaa gt t t t gat ga ct ggat t cca act ct agct g ct t t ggaaag t t t t ct aact 2400
 agt ggat t cc ct aat at cag t gcgacagga ggcct aggt c ct t t at t t ac ccaggt gcaa 2460
 t ccgat cagc aaacgt at ac t t ct caagc cagacacagc agt t gaacct acaaaaccaa 2520
 at gaccact a t ccaacagga gt ggacat t a gt t t ccacat ccat gcaagt at t aaacggg 2580
 at t t t at cac agct t gct gg t gccat ct at t ccaact aa 2619

<210> 26
 <211> 2439
 <212> DNA
 <213> Chl amydi a pneumni ae

<400> 26
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 act acagcgg aacgt gacat act aaaacgg t t gat cgaag t t t t ggat ca gagggcgagc 120
 gagcgcct acc gct ct gccgt cgagaagct a cacaaat at g aagt ggagcg t gcgacagt a 180
 gcgaagt ct a t t cct gt ggc agccat t cat gagaaacct c t t t cct ct ac acat gcat ct 240
 gt t caggt t a cagcaagt ac gccagcagct acaggat ct g gagt cggggc ct at t at aac 300
 gcagt aaaac agaagt gggc gcaagat ct t at cgt t gagc t t aat acggg t at gaccact 360
 at cat ggcct cagt t aat ag t aagaat cct gcaaat aaag at gt ct t t ga t aaat t aaat 420
 act gaact t c aggc t t t agt cgct gcgggg aat aat t t aa cagaagagaa t t t t cagact 480
 ct ct acaat t t cccagagga gat ct t cact gcaat ccaac gagcagat ac gt t t act ggg 540
 ggaat gaaaa cagact t t ac gaaccagt t g gcaggcaaat at ggaaat ca agct act t t a 600
 act caaacgt t t gcagacgg t agagt cgaa ggg t caaag acat cct t ac agcggg acaa 660
 ggagt cct t a caccagagca gt t t act at c t t t gct gaga t t gcgacaga gct gcaggct 720
 t t agcagat c at gt aggt aa t t t t gat gaa gcaggat t ac aacggat t ga ggat gct gga 780
 gaaaaact cg ccgcat cat t aat t ct t ct gacct gact a gaaat gat aa aat t at gt t c 840
 t gt caacat a t aacagact t at act cagat caagt t gcgg ct t t aggat c ct t t gat acg 900
 gt act t gat g caagt at ct a t gt t aaccag cat caaggaa cgat gt t t t c caat t t gt ct 960
 agct t t gt t g gct ct t t aat t ggaact t t t gct ccaat t g at ct gagt t c ct ct caaggt 1020
 gat at t agt a gt gcggt t t agct ggagct ct acaaacag cccgaggg t aaat t ct cgt 1080
 t t caat gagt t aact gct ga gcaacagaaa ct gat t aat g agt gt at aaa at ct t t ggt t 1140
 acct t t aagt gt ggt gagca cct t ggt gct at ct gggct t at t t t acagc at ct act gt a 1200
 gt t gct t t aa acct act gc aacat ggac cacgt t aaag ct gct at cct t gaagaagct 1260
 aaagaat t ag at aact ct ag t t t t cagt t a gcat cat ct a t aaaat ccgc gat gact t ca 1320
 at t gt aaat t caagcgg t t c ct t t t ccgt a acggg gaact caagt acct t acaat at act 1380
 at at at t ct g agaaaaacgg caaagt t gag at t aat caaa t cct gt t aaa t t at ggat ct 1440
 acaggat t t t t gccagaaat t acgaaact a gcaaaaacaa acgccgaat c t acggcacga 1500
 agt t at t t t c ggt t t aaggc t ct t gct gct gt agaat cag aaaat gt aca gaacaaaat c 1560

gaagat ct t c agagt caat t gcaacaat t c accaat at ga aaacagaact gt t t gat ggg 1620
 caat t gt t at cacaggct ag t gaat t acgg gct ct ccccc t acct t cggc agt cgcct ct 1680
 gt gt t gat cg at cgt t at at gcct aaagag gt cgat t at c t aaat gaaat ct at aagaag 1740
 ct at at t at a gcaact t agg at ct t ct gt c ggaaat t cca t t at t gat gc gat t t ct caa 1800
 t at gt caat g gagct acgt a t t t caat t t t gct agt t at g t gggacaaca gccggcagt a 1860
 ggt gct gggg gagcgaat gc ct t cccagga t ct caagaaa gcgct caggc aaagt t ggat 1920
 caggagcgaa agcaagct gc t t t gt at ct c caagaaacac ggggagct ct t acagt t at t 1980
 gaagaacaaa gagct agagt gct t aaagat gat aaaat ca cgaat gagca gcgct ccacg 2040
 at t t t agat t cct t aaggaa ct acgaggac aacat caat t ct at ct cagg t t ct t t agt g 2100
 t t at t gcaaa at t act t aca gcct t t gt ct at agct ggag gt t ct gt agc aggaact t t t 2160
 gaagt t aaag aggggcaaga gcaat ggcaa gcgcgat t gc agat t ct t ga agaagct t t a 2220
 gt gt ccgggt t agt aggaaa t at gat t aat ggggggt at gt t cccact gca at ct acaat a 2280
 cagt cagacc agcaat ct t t t gcggat at g ggacagaact t ccagt t aga t t t gcagat g 2340
 cacct gact t ct at gcagca ggagt ggact gt agt cgcga ct t ct ct aca gct t t t aaat 2400
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<210> 27
 <211> 3273
 <212> DNA
 <213> Chl amydi a pneumoni ae

<400> 27
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 t t gt ct gggg t t gt t at t gc at t t gct gt g at t gcat t gc gt t t at ggt a t ct t gct gt t 120
 gt t gaacat g aacaaaagt t agaagaggca t acaagccac agat t cgagt gct t cct caa 180
 t at gt ggaaa gagcaacgat t t gt gat cgt t t t ggaaaga cat t ggct gt gaat cagt t g 240
 caat at gat g t gagcgt t gc t t at ggggcc at t cgt gat t t gcct act cg ggct t ggcgt 300
 gt cgat gagc at gggcat aa acagct cat t cct gt gcgt a agcat t at at aat gt gt t t g 360
 t ct gagct t t t at ct cagga at t gcat t t a gat cgcgagg cgat cgaaga t gcaat t cat 420
 gcaaaagct t ct gt at t agg t t cggc cct t at t t agt gg ct gct aat gt t t ct gagcgc 480
 acct at t t ga aact caaaat gt t at ct aaa gat t ggcct g gat t gcat gt agaggct gt a 540
 gt t cgt cgt c at t at cct ca agaaagcgt g gct t cagat a t t t t aggt t a t gt aggacct 600
 at cagt ct t c aagagt at aa gagagt cact caggagct ga gt caat t gcg t gagt gt gt g 660
 cgt gct t at g aagagggt ga agat cct aag t t gcct gaag gat t agcaag t at agat cag 720
 gt gcgt gct t t at t agagt c t gt ggagagc aacgct t at a gt t t aaat gc t t t agt agga 780
 aaaat ggggt g t t gaggcct g t t gggact ca aaat t acgag gt aagat cgg aaaaaaacgg 840
 at t t t agt ag at cgt cgt gg gaact t cat t caagaaat gg aggggt gct gt t cct gaagct 900
 cct ggaact a aat t gcagt t gact t t gt ct gct gagct ac aagcgt at gc ggat gcgt t a 960

ct t t t aga at	at gaaaaaac	ggagacgt t t	cgt agt gct a	agt cat t gaa	gaaacgagag	1020
aagct t cct c	ct t t gt t ccc	t t ggat t aaa	ggaggagcca	t t at t gcgt t	agat cct aat	1080
aacggagaga	t t t t agccat	ggct t ct t ct	ccccgt t at c	gt aacaat ga	t t t t gt gaat	1140
gCGaaggt t g	cggaagat t c	t aaagcgg t a	agat cgt ct a	t t t at cgat g	gt t agaaaat	1200
aaagagcat a	t t gcagaaat	t t at gat agg	aaagt ccct c	t aat t cgga	aagaaggaat	1260
cct ct t act g	gat t at gt t a	t gaagagat t	t t gccat t aa	cct t t gat t g	ct t cct t gat	1320
t t t ct t t t cc	ct gaaaact c	t gt gat t aaa	t t gcagt t aa	aaagaaacag	ct t t gt agga	1380
caggcgat ag	aggt t caaaa	ct t ggt gact	cgt t t gct t t	ct t t at t t cc	t t at gaagag	1440
gggacgt gt c	ct t gt t ccgc	t at t t t t gat	gcagt t t t cc	ct aat gaaga	ggggcat at c	1500
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gCGaat t acg	at aaaat ct t	gt at acggat	at cct t aggc	t gat t gt aga	t ccagagcgt	1680
t t t t ct cct g	t act t cct t c	agaggt t cat	aggct ct cgt	t at ct gaat t	t acagagct t	1740
caaggacgt t	at gt ggt gct	t cgct ct gca	t t ct ct act a	t t t t agaaga	t gct t t t at t	1800
gaggt gcat t	t t aagt cgt g	gcgt aagagt	gaat t t ct t c	aat at ct t gc	t gcgaaacgt	1860
caagaggaag	cat t aaggaa	acagaggt at	cct acacct t	at gt agat t a	ct t agaggaa	1920
gaaaaaacia	ggcaat at aa	aat gt t ct gc	caagaacat t	t ggat acat t	t ct t gcgt at	1980
t t at t t t ct a	aaaccct t a	t aaagaaggc	t t agagcct t	act at gat at	t t t agat t t a	2040
t ggat aaat g	aat t agat aa	t ggagcgc at	agagcgt t at	ct t ggaacga	acat t at ct t	2100
t t t ct aaaag	aacgt gt gt c	gcat ct t t ca	gaacat ct cc	ct gcact t t t	t t ct acat t t	2160
cgt gaat t ca	at gaat t gca	acgt cct ct a	t t aggcaaat	at cccat ct c	gat t gt gaga	2220
aat aagaggc	agacagaaca	agat t t agct	gct t ct t t t t	at ccagt at a	t ggat acgga	2280
t acct acgt c	ct cat gcct a	cgggcaagca	gct acct t ag	gt t ct at t t t	t aagt t agt a	2340
t ct gcat at t	ct gt gt t at c	t cagaggat c	t t at ggggac	at aat gagga	gcct gcgaat	2400
ccct t ggt ca	t t at t gat aa	aaat t cct t t	ggct at agga	gt t ct aagcc	t cacgt gggc	2460
t t t t t t aaag	at ggcacacc	gat t cccacg	t t t t t ccgt g	gggggag t t t	gccgggaaat	2520
gat t t cat gg	gaagaggct t	t at t gat t t a	gt ct cagcat	t agagat gt c	t agcaaccgg	2580
t act t t t cat	t at t ggt agg	ggaaggt ct t	ggggat cct g	aagat t t agc	agacgcggct	2640
t ct t t at t t g	gt t t t ggCGa	gaaaacaggt	t t aggat t gc	caggagagt a	t gcgggt agg	2700
gt gcct cat g	at t t ggcgt a	t aaccgt t cc	gg t t t at acg	caacagcgat	t ggacagcat	2760
act ct t gt t g	t aact cct t t	gcagacagca	gt gat gt t ag	ct t ct t t agt	t aat ggcgg t	2820
gt ggt t t at g	t ccccaagt t	at t gct t gga	gaat gggagg	gggagcat gt	t t ct t at ct c	2880
t ct t ct aaaa	agaagcgaac	gat t t t cat g	cct gat gct g	t agt agaggt	gct t aagact	2940
ggcat gcgca	at gt t at ct g	gggt caat ac	ggaacagct c	gagcaat aca	aagt caat t t	3000
cct ccacaac	t t t t gt ct cg	t at t at t gga	aagacaagt a	cagcagagt c	cat t at gcgt	3060

eol f - seq | . app

gt gggact gg at cgggaat a t ggt accat g aaaat gaaag acat ct ggt t t gct gcggt g 3120
 ggt t t t t ct g at caagat t t at ct ct t cct acgat cgt ag t cat agt ct a t t t acgct t a 3180
 ggagaat t t g gt cgagat gc ggct cct at g gcggt aaaaa t gat t gat at gt gggaaaaa 3240
 at t caacaaa gagaat ct t t t t aagggga t ag 3273

<210> 28
 <211> 1221
 <212> DNA
 <213> Chl amydi a pneumoni ae

<400> 28
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 t t t at t t at t t agat t cagc t gcaacgact cagaaacct c aacaggt gat agat gccgt t 120
 gct aact t t t at act t ct t c at at gcaact gt aaat cgt g cgat t t at ag t t cct ct agg 180
 aacgt cacgg aagcat acgc agct gt t cgc gaaaaagt gc gt aagt ggggt at ccgcagcc 240
 t ct gat agt g aaat cgt at t caccct ggg acaact gcag ggt t aaat t t at t agccat t 300
 t ct gt t aat g acct ct ggat ccct aagggg ggt gt t gt t c t ggt t t ct ga ggcagaacac 360
 cat gcgaat g t t t t at ct t g ggagat t gcc t gt cggcggc gaggt t ct t t agt aaaaaag 420
 at cagagt t c at gat t cagg gct t at agat ct t gat gat t t ggaaaagct t ct aaat gaa 480
 ggt gct caat t t gt aagcat t cct cat gt g agt aat gt t a cgggt t gt gt ccaacct ct c 540
 caacaagt t g ct gagct t gt ccaccgct at gacgct t acc t t gct gt t ga t ggt gct cag 600
 ggagct cct c at ct t cct at agacgt t cag ct t t gggat g t agat t t ct a t gt gt t t t cg 660
 t cacat aaga t t t at ggacc cacgggcat a ggagt ct t at at gggaaaaa agat ct at t a 720
 gat cagt t gc ct ccagt aga aggaggt ggt gat at ggt t g ct at ct acga t cat cagaat 780
 cct gaat at c t t cct gcacc t at gaaat t t gaagct ggga ct ccaaat at t gct ggagt t 840
 t t aggct t ag gggct gct t t agat t at ct c gat ggct t gt cagct aagt t t at ct acgac 900
 aaagagat t g ccct aact ac at at t t acat aaagagct gc t t gagat t cc aggt gt agag 960
 at t ct cggac ct t ct at aga ggaaccagg ggagct ct t a t aggcat gac aat cgat gga 1020
 gcccat cct t t ggat ct agg t t t t t at t a gat ct t agag gaat t gct gt gcgagcgggt 1080
 cat caat gt g cccaacct gc t at ggagcga t ggaat gt gg gt cat gt gt t gagagt gt cc 1140
 t t aggaat ct at aat gat ga ggat gat at c gat caat t ca t cct t gt t t t gcaggat t ct 1200
 t t agat aaga t t cgt agat g a 1221

<210> 29
 <211> 759
 <212> DNA
 <213> Chl amydi a pneumoni ae

<400> 29
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 cgt ct aaaaa at t acct acg gct cct aaaa caaaact t t g ct at t acct ccccaaagaa 120

cgaacct caa aaggacat t c gct aat gct c act t t t gact t cgcct cct t t gact t ct at 180
 acaaat at ct t t ccct t cct t gaggaacaa aagat t cct g ct gt t gt agg ggt agct t cc 240
 cgat at at t c cat caaat gc t gct caagac ct t caccct t cacat cgt t t aaaacct ct 300
 gaaact ct ag cat t ccaaga cgagat ct t c t ct aact aca t gccct t t t g t t gccaaaat 360
 gaact gat ag aaat ggcaaa gt ct ccct at at ccaat t ag cat cct cagg at t cgcaat t 420
 cggaat ct ca t gaat aat cc t ccgt at ct c act acagaaa t t t t act t t c gcgacat cac 480
 at agaaacaa t aacaggagc caagccct t g gcat t cct ct t ccct t cgg gaagt cagat 540
 cct acaagcc ggaagct t gc t gcagat cac t acccct at t ct t t cct gt t agggaat acc 600
 at t aacagaa aat t aaaaac t cat aacat c t accgct t ag acat aaaacc t at gcagt ac 660
 gt ct gcccga gt t t at t t ca gagct ct agg t at t t aaaa act ggat t aa agagaaaagt 720
 aaacagct gt at ct caaaaa acaact t cca aaaagat aa 759

<210> 30
 <211> 975
 <212> DNA
 <213> Chl amydi a pneumni ae

<400> 30
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 aagcgt t cct t t t ggt t t ca gggaaagaca at t gccagt c gt cct gt t ga cgacgt ct ct 120
 t t t t cact at act ccagacg t gct gt cggg ct t at t ggag aat ct ggat c agggaaaagt 180
 accct ggcgt t agct ct cgc aggt ct cct a cct ct cacct ct ggg t t ct t aact t t t aac 240
 ggcaccccaa t caagt t gca t t ct aaacac ggacgccat c aat t acgat c t caagt acgg 300
 t t ggt ct t t c aaaat ccaca agct t cat t a aaccgcgcaa aaact at cct agat agt t t a 360
 ggccact ct c t gct t t acca t aaact cgt c ccaaaagaaa aagt act agc aacggg aagg 420
 gaat at t t ag aat t ggt agg gt t at ct gag gagt at t t t t at cgt t at cc t caccagct t 480
 t ct ggaggac aacaacaacg agt ct ct at a gcgagagccc t at t aggagt ccct cagt t a 540
 at t at t t gt g acgaaat t gt t t ct gct ct a gat t t at ct a t t caagcaca aat t ct gaat 600
 at gct t gccg agct gcaaaa aaaact cagc ct cacat at c t ct t cat t t c gcat gat ct t 660
 gccgt t gt ac gct cgt t ct g cacagaggt a t t cat t at gt at aaggggca aat t gt agaa 720
 aaaggaaat a caaaacgcat t t t t t ct gat ccacaacat c ct t at acgcg cat gt t gt t a 780
 aat gcccaac t t ccagagac t cct gat caa aggcaat ct a aacct at at t ccaagaat at 840
 caciaagat t ct gaagaat c t t gct ct aca ggat gct act t t t acaat cg t t gt ccacia 900
 aaacaagaag ct t gcaagt c agagat cat c ccaaat caag gagacgcgca ccat acat ac 960
 cgt t gt at cc at t ga 975

<210> 31
 <211> 1311
 <212> DNA
 <213> Chl amydi a pneumni ae

eol f - seq | . app

<400> 31
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t c t t t acat g caggact ct c t t t cccagaa gt acgt ggag ct acggct gc t gt t gt ccat 120
gccgact ct g ggaaggt at t ct at gat aaa gacat agat g ct gt aat ct a t cct gccagc 180
at gacgaaaa t cgcaact gc cct ct t t at c ct aaagcact at cccacagt cct cgat act 240
ct cat caaag t caaacaaga t gcgat cgct t ccat cact c cgcaagcaaa aaaacaat ca 300
ggat at cgt a gt cct cccca ct ggt t agaa act gat ggat ct acaat aca gct ccat ct t 360
cgagaagagc t t t t aggt g ggacct gt t c cacgcct t ac t ggt ct gt t c t gct aat gat 420
gct gcgaat g t ct t agct at ggcat gt t gc ggat ct gt ag agaagt t t at ggat aagct g 480
aact t ct t ct t aaaagaaga aat cggct gc act cat accc at t t t aat aa t ccccat ggg 540
t t acat cat c cgaat cact a t act acaacc cgt gat ct t a t t agcat cat gcgt t gcgct 600
ct gaaagaac ct ccat t t cg aggggt cat c t ccacgacaa gct at aaaat aggggct aca 660
aacct gcat g gcgaacggat cct at cccca acaacaaat t gct t ct t cc t ggggt ct acc 720
t accact at c ccccagct t t aggggggaaa acagggacca ccaagact gc agggaaaaat 780
ct aat t at gg ct gct gaaaa aat aaccgc ct ct t ggt aa cgat cgcaac gggct at t cg 840
ggg cct gt ga gt gat ct ct a ccaagat gt c at t gct ct at gt gaaacggg at t t aacgag 900
ccgct at t aa gaaaagagct cgt cccccc t ccgact gt c t ccaat t aga aat agcgaat 960
ct t gggaagc t t t ct t gccc t ct t cct gag ggact ct act at gact t ct a t gcct ccgaa 1020
gat cgcgaac ct ct t t ct gt at ct t t t at t gcacat gcgg acgcct t ccc t at t gaacaa 1080
ggagat ct t c t t ggt cat t g ggt t t t t at gacgat gaag gcaagaaaat t t ct t cccag 1140
cct t t ct at g cccct t gt cg t t t t gagcgc act at caagc ct t ggaaact ct at at gaaa 1200
cgt gt ct t ca cat cgt at ag aacct at at g t ct at aacca t gct gct cat gt at t t t cgc 1260
at ccgcaagc accgcaagt a t aaaaat t t a aaacact at t ct aaaat ct a a 1311

<210> 32
<211> 708
<212> DNA
<213> Chl amydi a pneumoni ae

<400> 32
at gcccacca ct aact gt at t t t cct agat t t acgggggac act ct at t ct t caccaact g 60
caaat t gaag aggct t t act aagagt cgcg aat caaaat t t t t gcat t at aaat t caggt 120
gccaaagact ct at agt t t t aggaat t t ct cgaaact t ga at caagacgt t cat at t t ct 180
agagcacaag cagacat at t cct at cat a cgccgct at a gt ggaggggg gacggt at t c 240
at agat t cca at acct t gat ggt at ct t gg at t at gaaca gt t cagaagc t t ct gcccaa 300
cct caggaat t at t agcat g gact t at ggc at ct at agt c cact act t cc t aat acct t t 360
t ct at t cgag aaaacgact a t gt t ct t ggt cat aagaaaa t aggaggt aa t gcacaat at 420
at t caaagac at cgct gggg acat cacacg acat t t ct gt gggat at cga cct agat aag 480
t t gt cct act acct gccaat t cct caacaa caacct acct accgt aat ca acgct ct cac 540

eol f - seq| . app

gaagaat t t t t gact acgt t acgt cct t gg t t ccct ct c gcgat gact t ct t ggaaagg 600
at caaggcat ct ggt agt t t gt t gt t t acc t gggaagaat t t ct t gat aa t gagct agaa 660
gaaat t ct t g ct caacct ca t cgt aaagca act acagt ac t aaact aa 708

<210> 33
<211> 2379
<212> DNA
<213> Chl amydi a pneumni ae

<400> 33
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at t t t agaag cct gt gat ca t at t ggcat a gaagccgaga t t gaaaat ac t acct at ac 120
t ct t t cgct t ct gt gat t ac agcaaaaat t t t acat acga t t ccccat cc t aat gcggat 180
aaact ccggg t agct acct gaccgacggg gaaaaagagc accaagt ggt t t gcgagacc 240
cccaact gcg aagcaggat t gat t gt agct ct t gct ct ac ct ggagccaa at t at t t gat 300
agcgaaggac aagcct acac aat caaaaaa t ct aaact t c gt ggt gt aga at ct caaggg 360
at gt gct gcg gagccgacga gt t gggcct t gat gaact cc aaat t cagga gagagct ct t 420
t t agagct cc cagaagccac ccct t t aggt gaagat ct cg caacagt t t t agggaat act 480
t ct t t agaga t ct ct ct aac accgaat t t a ggccact gcg cct cct t cct aggat t ggcc 540
cgagaaat ct gccacgt cac t caggcaaac ct cgt cat cc ct aaggaat t ct cgt t cgaa 600
aat ct cccga ct acagccct agacat gggc aat gat cct g acat t t gcc ct t ct t t t ct 660
t at gt cgt ca t t acgggaat ct ct gcgcaa cct t caccaa t caagct t ca ggaat ct ct a 720
caagccct ca aacaaaagcc cat aaat gct at t gt cgat a t t acaaat t a cat cat gct t 780
t ct ct agggc aacct ct gca cgct t acgat gcgagt cacg t cgct t t aga ct ct ct gcga 840
gt agaaaagc t ct ccacccc agaat ct ct c accct at t ga acggagaaac cgt cct ct t g 900
ccct caggag t gcct gt agt ccgcat gat cat agt ct ct t ggggt ct t gg aggt gt t at g 960
ggagcgaaaag caccct cat t t caagaaacc acaaccact a cagt cat caa agct gcct at 1020
t t cct ccccg aagct ct ccg t gcct ct caa aaact t ct cc cgat t ccat c ggaat ct gcc 1080
t at agat t ca cccgggggat cgat ccacaa aat gt t gt ac cagcact aca agct gcaat t 1140
cact at at t t t agagat ct t ccccgaagct acaat ct ccc ccat ct at ag t t ct ggagaa 1200
at t t gt cgt g aat t aaaaga ggt cgct ct a cgccct aaaa ccct acagag aat t ct aggg 1260
aaat ct t t ct caat agagat cct ct ct caa aagt t acaga gct t aggggt t ct ct acgact 1320
ccacaagaaa ct t cct t act t gt aaaagt c cct t cct acc gccat gacat caat gaagaa 1380
at agat ct ag t agaagagat ct gt aggaca gaat ct t gga at at agaaac t caaaat cca 1440
gt at cct gct aact ccaat ct aaaaact a aaact gaaa ct gct ggggt t cct agcaaac 1500
gcaggact t c aagaat t ct t cact cct gac ct gct agat c ccgaaacagt ggct ct aaca 1560
agaaaagaaa aagaagaaat ct ct ct t cag ggct ccaaac at accact gt at t gagat cc 1620
t cact gct t c caggat t at t aaaaagt gct gcgacaaacc t aaat cgcca ggcaccct ct 1680

eol f - seq1 . app

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 t ct at agat g ct t t gacct t agagt ccagc gcgct ct gcg aat t t cacc ct accaacag 1920
 ggagt gt t gc gcat ccacaa acagagt t t t gct act t t ag gt caggt aca t cct gagt t a 1980
 gcaaaaaaag cacagat aaa acaccct gt g t t ct t t gcag aact caact t agacct t ct a 2040
 t gcaagat gc t aaaaaaac aacgaagct t t at aaacct t acgcat at a t cct t cat ct 2100
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 aaaagct t gg aaacacgaaa t aaaaat gt t t ct ct acgcc t cgt at t cca agat t at gag 2280
 cgaacat t at ct aaccaaga cat t gaagaa gaat act gt c gt t t ggt agc t t t act t aac 2340
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<210> 34
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 <212> DNA
 <213> Chl amydi a pneumni ae

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 ct ccaat gt g at t at cgaga aacct t gt c cccat at ct t t ggggaagt a t acgt t acat 180
 cgt aat ggct cacgcct t cc t aaact gacc cacggggat a t cct caat gc ct t cgaagca 240
 at caaacaaa cct acgct ct cct agaagct agt ggaaaaa t gat t caagc t ct t ct ggct 300
 t ct cagt gga aagaaaagcc t t cgc at aag ct ct t ct ct t t at t ct t gaa t t t cct ccac 360
 cgt at t cct g aaagcagcaa t ccagaat t t t t gcagcca t ct t t gt act t aaact t ct c 420
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 t at gcct gct at cgct acca aggccat aaa ct at gt aaga aacat cagca t aaacaagcc 540
 at ct ccat cg agaaagaaga agaacaaat c t t acaggct a t cat t cat gc gaagcagt t t 600
 t ct gaact t c t agct at t gc agaat t cccg at t gct at ag ct gaaaaaat t t t t at t t g 660
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<210> 35
 <211> 804
 <212> DNA
 <213> Chl amydi a pneumni ae

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act cgcact c cact aat t gc ct ct gggaga accgacgcag gcgt ccat gc ct acgggcaa 180
gt ggcgcat t t ccgagct cc t gat caccct ct at t t gcaa acgcgaacct t acaaaaaaa 240
gccct caat g cgat t ct ccc t aaagat at t gt aat cagag at gt t gct t t gt t t gat gat 300
aat t t ccat g cacgct at ct t accat t gct aaagaat at c gt t at t ccct at caagact t 360
gccaaacct c t t ccct ggca gcgccat t t c t gt t at accc ct cgccaccc t t t t t ct aca 420
gagct cat gc aggaaggt gc gaacct gct t at aggaact c at gact t t gc ct ct t t t gca 480
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aaaggagat t ct ct ct ccat aat at gcaga ggaaat ggct t cct t t at aa gat ggt acgg 600
aat ct t gt ag gagccct t t t agat gt gggg aaaggagcgt at ccacct ga acat ct cct a 660
gat at ct t ag aacagaaaa t cgt agagaa ggacct t cgg cggct cct gc ct acggcct t 720
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<210> 36

<211> 4209

<212> DNA

<213> Chl amydi a pneumoni ae

<400> 36

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aacgaagccg aacat at aat caaat ct t t t accaagcagg cccagcaagt t cgt aaggat 180
gt cat t cct c gcgt ct cagc gat cct t t cg t ccct acat t t acgt gggca cat acaacaa 240
cat cct gcga t t ccagat at t gt cagt gt g cgt t t t aaaa gaggt gaaga t gcagaggac 300
t t t at cggga acct cgt t ca t ggagagcct aacgt t ccca t aaagt ct gc aagact ccat 360
gt ggt t ggct at agt cgaga acacgacgac cat gt aat ac aagt agcaag ct ct at aaat 420
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at ggcct caa gt at t t t gca acgagt ct at t ct gcat gt a ct t t t ccgaa acaaaaagac 540
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gccaagaacc t t t ct t cagg at t t gaggt t t t t ct t cgc gact t t cagc gt t t t gccaa 660
cagt cct t t t ct t ccaacca agat agact t gcgt t t t t at cacgcct gt c t t cgt t gt ca 720
aacgacgcag caat cgat gt t gaagat caa aagct act ca agagt gt at a t gaaact ct t 780
t ct caaact g cat gcat t cg t agt t t agat t gccct t at a t t gaagggt t cgat t agat 840
t gt agt gagt cct cat t at t t t t agt t cc at agagt at t gccct aagga acgt aaaat t 900
t t cct gacac t acat t ct ga t t t gt t agca cagcgt acgt ct t t gt ct aa agaacaacgc 960
t t agat t t t g acagt cgt t t ggct gt t gaa aaacaaaagc t ct ct aagaa ct t aact gt t 1020
caagt agaag at t at acaa cggat t t t cc t t ccaat gga t ggat aaaga t act cagggga 1080
aagat t at t c t ccagggaga gcgt t t gct c caaggaat cg cagaacat ct cacggcat t a 1140

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t gcaaacact t t t ct aaagg ct ccgt t t ac	at ct t at t ga aaggact ccg t t ct at cgt c	1320
gcgaaat at c aacagggagg ggg t aaagaa	ct ccaaagt t t cgaaaaaga t ct acaaaat	1380
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eol f - seq | . app

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<210> 37
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 <212> DNA
 <213> Chl amydi a pneumoni ae

<400> 37
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 aacggagggg ggaaaagcac ct t aacgat g t t aat t t t gg gct t gct t ac t cct acat t c 180
 ggat cct t ga agact t t ccc t t cgcat t cc gcggggaaac aaacccat t c cat gat cggt 240
 t ggggt t cccc aacat t t ct c t t at gat cct t gt t t t cct a t ct cagt aaa agat gt t gt c 300
 ct ct caggaa gat t gt ct ca act ct cct gg cat ggaaaat at aaaaagaa agat t t t gaa 360
 gct gt agat c acgct t t gga t ct t gt t gga ct t t ct gacc accaccacca ct gct t cgcc 420
 cat ct ct cag gaggacaaat ccagcgt gt a ct t ct ggcaa gagcct t agc ct cct accct 480
 gaaat t t t aa t t ct t gat ga gccgacgaca aacat t gat c ct gacaat ca acaaagaat t 540
 t t aagt at cc t aaaaaagct caaccgt acg t gcacat t c t t at ggt aac t cacgat ct t 600
 caccat acga cgaat t act t t aat aaagt t t t t at at ga acaaaact t t gact t cat t g 660
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<210> 38
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 <212> DNA
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 cat acaggat ccggggat cc t acaagcgac gct gcct t aa caggat t t ac acaaagt t cc 180
 acagaaact g acggt act ac ct at accat t gt cggg gat a t cacct t ct c t act t t t acg 240
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 t t t gat t t t a caaaagat ag cgt gt t agac ct ct at cacc t t t t ct t t cc t t cagct t ca 420
 aat act ct ca at cct gcact cct t t ct t cc agt agcagcg gt ggat cct c gagcagcagt 480
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eol f - seq | . app

gacgat gt ca cgct aacgaa cct gacaggg aaaact at t t caagagaa t agcagt gag 1980
 aaacat ggag gt gggct ct c t ct cgcct ca ggaaaat ct c t gact at gac at cgt t agag 2040
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eol f - seq | . app

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aaagaagt at ct cgaaat t c t gact cat t c acct at cat g gcagaggct a t accgct gct	4440
gt ggat gcca aacct cgcca agaat t t at t t t aggagct g cct t cagt ca ggt t t t t ggt	4500
cacgccgagt ct gaat at ca cct t gacaac t at aagcat a aaggct cagg t cact ct aca	4560
caagcat ct c t t t at gct gg caat at ct t c t at t t t cct g cgat acggt c t cggcct at t	4620
ct at t ccaag gt gt ggcgac ct at ggt t at at gcaacat g acaccacaac ct act at cct	4680
t ct at t gaag aaaaaat at ggcaaact gg gat agcat t g ct t ggt t at t t gat ct gcgt	4740
t t cagt gt gg at ct t aaaga acct caacct cact ct acag caaggct t ac ct t ct at aca	4800
gaagct gagt at accagaat t cgccaggag aaat t cacag agct agact a t gat cct aga	4860
t ct t t ct ct g cat gct ct t a t ggaaact t a gcaat t cct a ct ggat t ct c t gt agacgga	4920
gcat t agct t ggcgt gagat t at t ct at at aat aaagt at cagct gcgt a cct ccct gt g	4980
at t ct cagga at aat ccaaa agcgacct at gaagt t ct ct ct acaaaaaga aaagggcaac	5040
gt agt caacg t t ct ccct ac aagaaacgca gct cgt gcag aggt gagct c t caaat t t at	5100
ct t ggaagt t act ggacact ct acggcacg t at act at t g at gct t caat gaat act t t a	5160
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<210> 39
 <211> 2844
 <212> DNA
 <213> Chl amydi a pneumni ae

<400> 39	
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ct acgagcaa acgat gt t ct cct ccct ct a t cagggat t c at t ct ggaga agacct t gaa	120
ct ct t t act c t acgcagt t c ct cccaaca aaaact acgt at t ct ct acg caaagat t t t	180
at t gt t t gt g at t t t gcagg aaat t ct at t cacaagcct g gagct gcat t cct gaact t a	240
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cact t aggag ct cgcggt gc t gggct ct t c t cggaat cca at gt gacct t caaaggcct g	360
cact ct ct cg t t ct cgaaaa caacgaaagt t ggggaggcg t cct caccac at ct ggcgac	420
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ggagcgct ac t ct t acaagg aagaaaaagc aaggct ct ct t t t t cagaga caat cgagga	540
acaat t ct at t t ct gaaaaa caaagccgt g aat caagat g aat cccat cc t ggggt acgga	600

ggagct gt aa gt agt at aag t cct ggct cc ccgat t acct t cgct gacaa ccaagaaat c 660
 ct at t ccaag agaat gaggg cgaact t ggt ggagccat t t at aacgat ca gggg gccat a 720
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 gct gt ct at a gccgct act g caat ct ct at t cacagt ggg gcgat acct at t cact aaa 840
 aacgct gct g caaaagt agg cggagccat c cat gcggat t at gt t cat at aagagact gt 900
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 caaggagat a t t gaat t t t g t ggaaat aaa gt acgat cgc agt t t cat t c acat at aaat 1140
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 gct gt t cgt t ct t t t at ca agaaggaggt ct t ct t gct c t cgggccagg t t ct aaact g 1500
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 cgt t ct t ccc t at t t ct cca agt cagcacc t cgt acat t a aagact t acg t cgggt caac 2640
 ccacaat ct t cagct t cct t ggt gt t aaat cact acacgt gggat at cca aggagt ccct 2700

ct agggaaag aagct ct aaa cat t acct t a aat agcacga t t aagt acaa gat t gt gact 2760
gcct at at gg ggat t t ct ag cacccaacga gaaggcagt a acct t t cggc aaat gct cat 2820
gcaggcct ct ccct t agt t t ct ag 2844

<210> 40
<211> 1182
<212> DNA
<213> Chl amydi a pneumni ae

<400> 40
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acggat aaaa t t gct acaga at t acct ct cct aaagcag gccgact ggt gcgt t t ct gc 180
gt caat gagg gagacgaggt t gct t ct ggg gat gt t t t ag gat t gat aga gct t gaggag 240
at t t ccgaag ct gat gat ga gagcacct ca t gt cct ct ga ct t ct t gt ga aacaaagt cg 300
gaggcgggt t ccagcagt t c t t cggt at gg t t t t ct cct g ccgt gct gag t t t agct caa 360
cgt gaaggca t t ggt ct t ga t aacct ccaa aagat t gccg gcacggggaa agggggacga 420
gt gact cgt c aggat t t aga agcgt at at t t cagaat cgc aacaagt t t c t at t cccgaa 480
at at t t caag gagaagt gaa t cgcat t cct at gt ct ccgc t acgt cgggc aat agct t ct 540
t ct ct ct cca agt ct t caga t gaggt t cct cacgcat ct t t ggt t gt t ga t gt cgat gt c 600
acagat ct t a t gaat ct gat t t ct ggt gaa cgccaacgct t ct t agat ac gcat ggggt g 660
aagct aacga t t acaagt t t cat t gt acag t gt t t agct c agact t t aag gcagt t t cct 720
t t at t gaat g gt t cct t aga t gggact acc at t gt t at ga agaaat ct gt gaat gt aggc 780
gt t gccgt ga acct caat aa ggaaggggt t gt t gt t cct g t cat ccacaa t t gt caagat 840
cgcggt t t ag t aagt at t gc aaaggcct t g gcggat ct at ct t caagggc t cggt t aaat 900
aaat t ggat c ct agt gaagt gcaagat ggc agcgt t act g t cacgaat t t t ggaat gacg 960
ggagct t t ga t t gggat gcc cat cat acgt t at cct gaag t t gct at t t t aggaat t ggc 1020
acaat acaaa aacgt gt t gt cgt ccgt gat gacgat t ct t t agccat t cg caaaat ggt c 1080
t at gt gacac t t acct t t ga ccat agagt a t t ggat ggt a t t t acggcag t gagt t t t t a 1140
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<210> 41
<211> 714
<212> DNA
<213> Chl amydi a pneumni ae

<400> 41
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t t cgat t cca t agcgagt aa gt at gat cgc acaaat acaa t act ct ct t t aggaat gcac 120
cat t t ct gga at cgct ct t t gat ccagat c ct aggggt cgg gat act ct ct cct ggat ct c 180
t gcgcaggaa caggaaaagt cgcaagcgt t at at t gccg cacaccct ca agcat cagt a 240

act ct cgt cg act t t t cct c agcaat gct c gacat t gcaa aacaacacct t ccccagggc 300
t ct t gct ct t t t at t cat ag cgat at t aat caact gccct t ggagaat ca t t ct t at ccc 360
ct agcagcga t ggcct at gg cct caggaac ct ct cggat c cacat aaagc cct acaagaa 420
at ct cccgag t gct t at gcc t t ct ggaaaa ct gggcat t c t agagct cac acct ccaaaa 480
aaaacacacc ct acct at ag t gccat aag ct ct at t t gc gt gct gt cgt cccct ggat t 540
ggaaagt ct g t t t ct aaaga t cccgacgcc t at agct at c t cagcaaaag t at ccagcaa 600
ct t ccaaagg accacgat ct t gaagacct a t t ct ct aaat caggat t t t a t at t gcgaaa 660
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<210> 42

<211> 1863

<212> DNA

<213> Chl amydi a pneumoni ae

<400> 42

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t t agcaggaa gt gggaaacc cacagat t gg gaagccccg cgacagat ct ct cccaaact 180
agaaacgt aa t ct acgcaga aat gccagaa ggcgaaat ca t cgaagcaac cgccat t cct 240
gt aaaagaca at cccgt t cc acaat t cgag t t t act ct cc cct acgaact t caagt agga 300
gaaaccct ca ct at t gt cat gggagcct ct ccaaaccat c ct caagt cga t gat gct ggg 360
aacggagccc aact t t t cgc acaacgt cgc aaaccct t t t acct ct acat cgat cct aca 420
ggagaaggaa act at gat ga acccgat gt c t t ct ct at gg at at ccgcgg aaacgt cct a 480
aaaaaaat ag agat ct t t ac t cct cct at gt cgt t aaaa acaaacgct t cgat at cacc 540
gt gcgat t t g aagacgaat t cgggaacct c accaact t ct ct cct gaaga gaccggaat c 600
gagct t t cct acgagcat ct t agagaaaat t t aaat t ggc agct ct t cat cccagaaaca 660
ggct t t gt t a t t ct t cct aa t ct ct at t t c aat gagcct g gaat t t at cg cat ccaat t g 720
aaaaacct ct ct acacaaga aat t t t cat c t ct gccct a t caaat gt t t cgct gact cc 780
gccccgaat c t t at gt gggg t ct cct ccac ggcgaaat ccg aacgcgt cga ct ct gaagaa 840
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t cat cat t cg aaaat caaga gaacct ct ct ccagat at t t ggaagct cat caat caaact 960
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acagt aat t g aaggat t aaa gaagaat ct c cgct t cggat t t gt t gct gg gggt ct cgac 1380

gat cgaggaa t t t at aaaga ct act t t gac t ct ccgcaag t gcaat at t c cccagggt t g 1440
 acggct at ca t t t gt aat aa at at acccga gagt ct ct t g t t gaagct t t at t cgcacgt 1500
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 ct aagt t cag t gaccct aaa agat ccaaac ggt aaagcac ct t t t gt at t ct act at ct c 1800
 agggc cact c aggcagacaa t gct at ggcc t ggagt t ccc caat ct gggg ggat t t aaat 1860
 t aa 1863

<210> 43
 <211> 1983
 <212> DNA
 <213> Chl amydi a pneumni ae

<400> 43
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 accacgcat cgat cgt t gc ct t caaaggt aat gagaaat t agt ggggat t ccagcaaaa 180
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 aagt act ct g aagt agct t c ggaaat ccaa accgt t cct t at acagt cac ct ccggat ct 300
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 caaat ct t aa t gaaaat gaa agagacagca gaagct t at c t aggcgaaac t gt cacagaa 420
 gcagt gat ca ccgt ccccg c at act t caat gat t ct caac gagcat ccac aaaagat gct 480
 ggacgcat t g caggt ct aga t gt aaaacgt at cat t ccag aacct accgc agcagct ct t 540
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 gaat t caaaa aacaagaagg cat t gat ct t agcaaagat a at at ggcct t acaaagact t 780
 aaagat gct g ct gagaaagc aaaaat agaa ct t t caggag t ct ct t ccac agaaat caat 840
 cagccat t ca t cacaat gga t gcacaagga cct aacacc t t gcat t gac act cacacgt 900
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 aacat caat a cagaagat t t gaaaaacat agt t t cagt a cgaagcct cc t t caaat aac 1920
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<210> 44

<211> 2859

<212> DNA

<213> Chl amydi a pneumoni ae

<400> 44

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 agggat gaag agt t t cgt ac gagct t t cct ct ct t agact ct ct ct ccac t ct t acagga 180
 t t t t ct ccaa t aact acgt t t gt t ggaaat agacat aat t cct ct caaga cat t gt act t 240
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 t cct gt aat a at t t ct t at t at caaat gt t gaagacat g cct t ct t cag t aaaaat ct c 360
 gcgat t ggga ct ggaggcgc gat t gct t gc cagggagcct gcacaat cac gaagaat aga 420
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 ct t at gct cc t acaggacag cacct gcct a ct ct t cgcgg aacaaggaaa t at cgcat t t 1080
 caaaaat aat g aggt t t t cct caccacat t t ggt agat aca acgccat aca t t gt acacca 1140

aat agcaact t acaact t gg agct aat aag gggg at acga ct gct t t t t t t gat cct at a 1200
gaacaccaac at ccaact ac aaat cct ct a at ct t t aat c ccaat gcgaa ccat cagga 1260
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ggcat ct ggt ct cct t at t g ggt agagacg at aacaaca caaat aacgc t t ct at agag 1860
acggcaaaca ccct ct acag agct ct gt at gccaat t gga ct ccct t agg at at aaggt c 1920
aat cct gaat accaaggaga t ct t gct acg act cccct at ggcaat cct t t cat act at g 1980
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gaaat t caag ggat t gccga cggcct ct t t gt t cat caaa at agcat ccc cggggct cca 2100
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<210> 45

<211> 2088

<212> DNA

<213> Chl amydi a pneumni ae

<400> 45

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<210> 46
 <211> 1545

<212> DNA

<213> Chl amydi a pneumoni ae

<400> 46

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t t a g a a c c t a a a a t t a c c t g t t a t c c a g a a g g a a c t t c t t a c a t c t t t c t a g a t g a c g t g      180
a g g a t t t c c a a c g t t a a g c a t g a t c a a g a a g a t g c t g g g g t t t t t a t a a a t c g a t c t g g g      240
a a t c t t t t t t t c a t g g g c a a c c g t t g c a a c t t c a c t t t t c a c a a c c t t a t g a c c g a g g g t      300
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g g t t c c g t g a t g a t c g a a a a t a g t g a g g a a g t g a c t t t c t g t g g g a a c t a c t c t t c g t g g      480
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c a t g c t t a t c a t g a c g t g a a t a g t a a t g g a g g a g c c a t t g c c a t t g c t c c t g g a g g a t c g      720
a t c t c t a t a t c c g t g a a a a g c g g a g a t c t c a t c t t c a a a g g a a a t a c a g c a t c a c a a g a c      780
g g a a a t a c a a t a c a c a a c t c c a t c c a t c t g c a a t c t g g a g c a c a g t t t a a g a a c c t a c g t      840
g c t g t t t c a g a a t c c g g a g t t t a t t t c t a t g a t c c t a t a a g c c a t a g c g a g t c g c a t a a a      900
a t t a c a g a t c t t g t a a t c a a t g c t c c t g a a g g a a a g g a a a c t t a t g a a g g a a c a a t t a g c      960
t t c t c a g g a c t a t g c c t g g a t g a t c a t g a a g t t t g t g c g g a a a a t c t t a c t t c c a c a a t c      1020
c t a c a a g a t g t c a c a t t a g c a g g a g g a a c t c t c t c t a t c g g a t g g g g t t a c c t t g c a a      1080
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<210> 47

<211> 2793

<212> DNA

<213> Chl amydi a pneumoni ae

<400> 47

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a g c a t t g c a a c t t a c g g a g c a g a t g c t t c t t t a t c c c c t a c a g a t a g c t t t g a t g g a g c g      120
g g c g g c t c t a c a t t t a c t c c a a a a t c t a c a g c a g a t g c c a t a t g g a a c g a a c t a t g t c t t a      180

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eol f - seq | . app

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<213> Chl amydi a pneumoni ae

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eol f - seq1 . app

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<211> 3831
<212> DNA
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eol f - seq | . app

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<210> 50

<211> 2727

<212> DNA

<213> Chl amydi a pneumni ae

<400> 50

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 act at t gct a t gct t caaga acaaaaat ct cagt t t ct at gt acgat t t a t cgt t at t at 240
 ggat at t t gc aaagt caaat t t caacgct t gccccaact a cagat t ct cg at t cat t cag 300
 gaaaagat cg ct aagat t ga t ct ggat gag caggt gcct t ct gcgggt ct act t cct aaa 360
 gct caggt t t cggt acgaga gct gat cgaa gct t t aaaaa aat gct at t g cggaagt ct t 420

act t t a g a a a c c c t a a c a t g t a c t c c t g a g t t g c a g g a g t t t g t t t g g a a t c t t a t g g a g 480
 a a g c g a c a a g t g g a g c g c t t t g c a g a g c a g c t c c t t c g c t c c t a t a a a g a c t t a t g t a a a 540
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 g g a a t t t c t a a c t a c g t t t t a g g a a t g g c c a t c g a g g t c g t t t g a a t g t a t t a a c g a a t 720
 g t t t t g g g a a g c c t t a c c g t t a t g t c t t t a t g g a g t t t g a a g a c g a t c c t g c a g c a c g t 780
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 a c a g c t c c c t t a c t c t a t g a t c a g a t t a a g a g a a a g a g a g t a t t c g c g a g c t g t t t a g g 1380
 c a a t a t c t g t t g g a a g g g c a g t t t g c a g a t a t t t c t g a a g a a a c t t t g g c a t c t a t t g a a 1440
 a a a g a g a t t c a a g a g a g t c t g a a t c g t g a g t t t c a a g t a t t g a a a g g g a c g g a t c c a g a a 1500
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 g a a g c g c a g t t t g g g g a t t t t g c t a a t g g t g c a c a a a t c a t t t t c g a t c a g t a t a t c t c t 2040
 t c g g g a a t t c a g a a g t g g g a t t t a c a c t c t g a c a t t g t t c t g c t t c t t c c c c a t g g g t a t 2100
 g a g g g c c a a g g a c c c g a g c a t t c t t c a t c t c g t a t a g a a c g t t a t t t g c a a t t a g c c g c g 2160
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 g a g c a t g c t a a g a g a g a t c t t t c t t t g c c t t t g g t g a t c t t a c t c c t a a g t t g c t g c t g 2280
 a g a t a t c c a c a a t g t g t a a g t a g t a t c g a g g a g t t c a c a g a a c c t g g g g g a t t c c g t g c t 2340
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 a t c t a t t a t g a t t a t g c a g a a a t g c t t c c t c a a g a t c g g c g t a a g g a c t t t t c t t g c t t g 2460
 c g t a t a g a g a g c t t g t a t c c t t t a g c t c t t g a g g a t t t a g t g a g c c t t a t c g a t a a g t a t 2520

eol f - seq1 . app

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<210> 51
 <211> 1035
 <212> DNA
 <213> Chl amydi a pneumoni ae

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 aat at t cct g t t at ct at t t cct cacagga at t t cat t t a t t gct gt t gt t ct t agcaac 240
 t t t at cct t t at aaacgagc aaccacct c t t aaaaccgc gt gct t gt gg caaacacaaa 300
 gaaat aaaac caaaaagggt ct ccaccaac ct acagt at t ct t ct at ct c t at cgcaat c 360
 aat cgt t ct a aagaaaact g ggaacaccaa cccaaggacc t acagaat ct ccccgaccc 420
 t ct gcat t ac t cacagat aa ccct t acgag at at ggaaag ct aaacat t c act gt t t t cc 480
 ct agt at ccc t cct accggg aggcaat cca gaacat ct ct t aat t t cagc t t ccgaaaat 540
 t t aggaaaga ct ct gt t aat t gaagaaacc t cgcaaaat g cgct at at c ct cct acgt a 600
 gat accact c cct ccccaaa at cct t gct c aat gaggcaa t t caggaaac cagggt agaa 660
 at aaat acag aact ccct gc gggagat t ca ggagaacgt t t at act ggca acccgat t t c 720
 cgaggccgcg t ct t cct ccc acaaat acca acaact cct g aagccat ct a ccaat act ac 780
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 at ccct t t at acagct t gag ggagcat ct c t at t ct agag aat t gcccc gcaat caaga 900
 at gcaacaat ct t t ggct at gat t acagca gt aaaat aca t ggccgagct gcaccagaa 960
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<210> 52
 <211> 1392
 <212> DNA
 <213> Chl amydi a pneumoni ae

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 accact at t c at at t gt t at cagt gccat c t t act ct gcg gagct t t gat agct t t ct t g 180
 t gt gt agcag ct cct gt t t c ct at at t ct a agt ggcgcat t gt t aggat t aggat t at t a 240
 at agcct t ga t t ggt gt gat t t t aggaat a aaaaaat ca cgct at gat t t cat caaaa 300

eol f - seq | . app

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gaacaagt at t cccccaaga act cgt aaat agaat caggg cgcact at cc t aaat t t gt c      360
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ct aaat caat t gcact ct ga agt t ggat ca t ct acaaat t acaacgt at c t gaagaact a      480
caacagaaaa t agat acgt t cgagggt at c gcacgct t aa aaaat gaagt ccgt act gcg      540
t ct ct t aaaa gact t gaaag cgct gct t ct t cccgt cccc t ct t cccct c t t t agcaaaa      600
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gt t gt agagc t ccat cgagt t aagaaaat t ggaggcagcc t cgaagaaga cct t agt gat      720
t at at aaaac cagagat gct t ccgacct at t ggt t gat t c ct t t agat t t t agaccaaca      780
aat t cct ct a t t ct aaat ct acacacat t a gt t t t agct a gagt ct t aac t cgt gat gt t      840
t t t caacat c t t aagt at gc agcat t aaat ggcgagt gga acct gaat ca t agt gat ct a      900
aat act at ga aacagcagct ct t t gct aaa t at cat gcgg cgt at caat c ct at aaacat      960
ct at ct caac cct ct ct t ca agaggat gaa t t ct at aacc t gct ct t gt g t at t t t aag      1020
cat aggt act cgt ggaagca gat gt cct t a at aaaaacag t cccggct ga t t t at gggaa      1080
aacct ct gt t gct t gact t t agaccat aca ggacgacccc aagacat gga at t t gcct ct      1140
ct aat t ggt a ct ct ct acac acaaggcct a at t cat aaag aaagcgaagc at t t ct t t ct      1200
t cat t gacac t cct t agt t t agat cagt t t aaaacgat cc gt cgt cagt c aaccaat at a      1260
gcgat gt t cc t t gagaat t t agcaact cat aat t ccacct t t agaagct t accacct at a      1320
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<210> 53
<211> 516
<212> DNA
<213> Chl amydi a pneumoni ae

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cct agcggcg gt t at at gca t cat t t cact ct aaaaaaga t gaaaagcgc t gct cccgaa      180
caact t t t aa aaat gt t aaa aacat t t at t t t agaat cgg aaaccccacg cacaat t aat      240
cct aagcct a gagct cct ag aggct ct aaa aaacgt cgt g act t t at t aa ct t t act aaa      300
acagat at t g aacgcgt t t t agaact ggca agacaagt t g gagacaaaga cct cct cgct      360
cgct t t agcc ct aaaaaacc gt t aact t ct t t aaaaaggg agt t aat t cg t t cgat t cgc      420
aacggat at cg t gagcgt aga gct at ggaat gcct acgt cg aagct gt gaa ggct gt aagc      480
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<210> 54
<211> 936
<212> DNA
<213> Chl amydi a pneumoni ae

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ggt ggccagc t t at gact ac aacagaagt t gagaat t t t c cagggt t t cc t gaagggat t 180
ct t gggccaa aact t at gaa t aat at gaag gagcaggct g t gcggt t t gg gaccaagaca 240
ct agct caag at at t at t t c cgt agat t t t t ct gt t cgcc ct t t t at t t t gaaat caaaa 300
gaagaaacct at t ct t gt ga t gcct gt at c at agct acag gagct t ct gc t aaacgt t t a 360
gaaat t cct g gagcaggaaa cgat gaat t t t ggcaaaaag gagt gact gc t t gt gccgt t 420
t gcgat gggg ct t ct cct at t t t t aaaaat aaagat ct t t at gt gat t gg gggaggggat 480
t ct gct t t ag aagaagct ct t t acct gact cgt t at ggaa gccacgt at a t gt agt t cat 540
cgt agagat a aact gcgggc t t ct aaagct at ggaagct c gggcgcaaaa caat gaaaaa 600
at t acat t t t t at ggaat ag cgagat t gt a aaaat t t ct g gagat agcat t gt ccgt t cc 660
gt agat at t a agaat gt t ca gact caagaa at t acaact a gagaagct gc ggggggt gt t c 720
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gct ggagat g t t caggat aa gt act at cgt caggcgggt t a ct t ct gcagg aagt ggt t gt 900
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<210> 55
<211> 516
<212> DNA
<213> Chl amydi a pneumni ae

<400> 55
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gaaact gaag aat t ggaagc t at gaaacag cagt t t gt aa aaaat gct ga gaaaaat agaa 180
gaagaact ca ct t ct at t t a t aat aagt t g caagat gaag at t acat gga aagcct at cg 240
gat t ct gcct ct gaagagt t gcgaaagaaa t t cgaagat c t t t caggaga gt acaat gcg 300
t accagt ct c agt act at ca at ct at caat caaagt aat g t aaaacgcat t caaaaact c 360
at t caagaag t aaaaat agc t gcagaat ca gt gcggt cca aagaaaaact agaagct at c 420
ct t aat gaag aagct gt ct t agcaat agca cct gggact g at aaaacaac cgaaat t at t 480
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<210> 56
<211> 2418
<212> DNA
<213> Chl amydi a pneumni ae

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ct agt ct at g aggt t gt aga caacagcat t gacgaagcca t ggcaggt t a t t gct ct agg 180
 at t gat gt t c gcat t t t aga ggacgggggt at t gt cat cg t agat aat gg ccgaggaat c 240
 cct at agaag t t cacgaaag agagt ct gca aaacaaggt a gagaggt ct c t gct t t agaa 300
 gt ggt t t t aa cagt cct t ca t gct ggagga aaat t cgat a aggat agct a t aaagt at cc 360
 ggaggct t gc acggagt t gg ggt t t ct t gc gt t aat gct c t t t cggagaa at t agt t gcc 420
 acggt ct t t a aagat aagaa gt gt t at caa at ggagt t ct ct aggggaat t cct gt aact 480
 ccat t gcagt at gt aagt gt t agt gat cgg caggaacag aaat cgt t t t ct accct gat 540
 cct aaaat at t t t cgact t g t act t t t gat cgct ct at t t t aat gaaacg ct t gcgagag 600
 ct t gct t t ct t aaat cgt gg gat cacaat a gt ct t t gaag at gat cgaga t gt t agct t t 660
 gacaaggt t a cct t ct t t t a t gagggagg at t caat ct t t t gt aagt t a cct gaat caa 720
 aat aaagaaa gcct t t t ct c t gaaccgat t t at at t t gt g gaact cgagt aggagat gat 780
 ggagaaat cg agt t t gaagc agcct t acaa t ggaat t cag ggt at t ct ga act t gt t t at 840
 t cct at gcca at aat at t cc t acacgcaa ggaggaacgc at ct t acagg gt t t t ct acc 900
 gcgct t act a gggat aat caa t acgt at at t aaagct cat a acct t gcgaa gaat aat aag 960
 ct t gcat t aa ccggagaaga t at t cgagaa ggt ct gacag ct gt gat t t c t gt aaaggt c 1020
 ccaaat ccac aat t t gaagg gcaaacaaaa cagaaat t ag gaaacagt ga t gt t agct ca 1080
 gt ggct caac aggt t gt agg ggaagct ct g acaat ct t t t t t gaagagaa t cct caaat t 1140
 gct aggat ga t t gt t gat aa ggt t t t t gt t gcagcgcaag ct agagaagc t gcaaaaaaa 1200
 gct cgagaat t gact t t aag gaaaagt gct t t agat agcg cacgct t acc t ggaaaact a 1260
 at t gat t gt t t agaaaaaga t cccgaaaag t gt gagat gt acat t gt gga gggggat t ct 1320
 gct ggaggat ct gcgaaaca aggt agagat cgaagat t t c aagcaat t ct gcct at t cga 1380
 ggt aaaat t c t gaacgt aga aaaagct cgt ct acagaaaa t t t t ccaaaa ccaagagat a 1440
 ggaaccat ca t agcagct t t aggct gt ggc at aggt gct g at aat t t t aa t ct cagt aaa 1500
 t t acgct at a gacgt at cat t at cat gaca gat gct gacg t ggacggt t c t cat at t cgt 1560
 accct act t c t cacat t ct t ct at cgt cat at gacagcgc t t at t gaaaa t gaat gt gt t 1620
 t at at t gct c aacct cct t t at acaaggt g agt aagaaaa aagact t ccg t t at at t ct t 1680
 t cagagaaag aaat ggacag ct at t t gct c at gt t aggca cgaat gagag ct ccat t ct c 1740
 t t t aaat ct a cggaagaga at t acgt gga gaggct t t ag agagt t t t at caacgt cat t 1800
 t t agat gt ag agagct t t at aaacact ct t gagaaaaaag cgat t ccct t ct ct gaat t t 1860
 t t agagat gt at aaagaggg gat aggct at cct t t gt act at ct t gct cc ggcaact gga 1920
 at gcagggag ggcgct at ct t t at t ct gat gaggaaaaag aagaagct t t agct caagaa 1980
 gaaact cat a agt t t aaaat cat agagct t t at aaagt t g ct gt gt t cgt agat at t caa 2040
 aat caact ca aagaat at gg t t t agat at t t ct agct at c t t at ccct ca gaaaaacgag 2100
 at t gt gat t g gaaat gaaga t t cccaagc t gt aact at a gct gct at ac ct t ggaagaa 2160
 gt cat t aact at ct t aaaaa t ct t ggaaga aaaggcat ag aaat t cagag gt at aaaggt 2220

eol f - seq | . app

ct t ggagaga t gaat gccga ccagct t t gg gat act act a t gaat cct ga gcagagaaca 2280
 ct cat t cat g t gt cat t gaa ggat gccgt a gaagcagacc at at t t t cac t at gt t gat g 2340
 ggggaagaag t ccct ccaag aagagaat t c at agaaagt c at gct t t gt c cat t aggat a 2400
 aat aat t t ag at at t t ag 2418

<210> 57
 <211> 864
 <212> DNA
 <213> Chl amydi a pneumni ae

<400> 57
 at gaaaagaa gaaacct aca aaaaat t ct a cct aat gct t ct act ccgt c t acaaat gt a 60
 gccgaaaat a ct ggaat aaa agat cagaac t t at t t ct t g at caagcgac t ct t aat gt g 120
 gat ggcaat g t cgat at aga aaact t t t t a gagact cgag at t t aaaagt t gcagat aca 180
 at cact t ct c cat gt gaat t t act gt cggg ggcggat t at cagcagaaaag t t ct caat t t 240
 aaagcgacaa cact t t ct aa aggt t t ggag at cact t ct g aagat cagga t ggccgagt t 300
 cct aagt t t a caaat gt t ag cgat ccccaa t ct ccaagag at gct t t aac at at aact at 360
 t at aggaaca ct ggat gcca ggccct t aat ct gt at acct act at agt t c at ct cagcct 420
 act act gt ag gt aaaccaat cgaaacggg g t gt caaaacc cgaat ccaga gacgt at cgc 480
 at t agcgct t cagct aaaat t t at gat gct gt aacgagat t cccct at at t cagt t caag 540
 gcacct ggaa t ct at caagt cacaat acaa at acgt cgcg agagcgggca acat agt gga 600
 ct t gat aat c ct aat t t at a t ct gaact t a at gat t ggga at aat aagac gct gct t t gt 660
 gct t cagat a cgagaggi t a ct caggagga cat aggact a gt at t gct gt aacaggcacg 720
 t t t act t t aa cagaaat t gt t gct accccc cct cat gat t accct t ggt t at t ct t agaa 780
 act act at t g gt t t agat at t aat ccat g t caacat gt g t t at t t ggt t t ccat t t caa 840
 gct aat t t t g cggaggt aga t t aa 864

<210> 58
 <211> 696
 <212> DNA
 <213> Chl amydi a pneumni ae

<400> 58
 at gt t gcaga gt t gcaaaaa ggcct t at t a t ccat agt ag t at cgat t t t agct t t t cac 60
 cct at ccct g gt at gggagt cgaagct aaa t ct ggt t t t t agggaaagt caaaggat gg 120
 t t ct caaaaa aagagat t ca ggaagaggct agaat t t t ac cagt t aaaga cagt ct t t ca 180
 t ggaaacgct at gact at ac at caagt t ct ggggt t t t ct g t ggaat t t cc t ggggagcct 240
 gat cat t cgg ggcaaat t gt agaagt ccct caat cagaga t t accat acg t t at gat acc 300
 t at gt aacag agact cat cc agacaacact gt gt at gt ag t ct ct gt t t g ggagt at cct 360
 gaaaaagt ag at at aagt cg t ccagagct c aat ct gcaag aggggt t t t c aggcat gat g 420
 caggct ct cc ct gaat ccca ggt t ct t t t c at gcaagcaa ggcagat t ca aggccat aag 480

eol f - seq | . app

gct t t ggaat t t t ggat t gt t t gcgaagat	gt t t at t t ca gagggat gt t gat t t ccgt a	540
aat cacact c t t t at caagt ct t t at ggt t t at aagaat a agaat cct ca ggcct t ggat		600
aaagaat acg aggcgt t t t c t cagt ct t t t aaaat t act a aaat acgaga accaagaacg		660
at t cct t ct t cagt gaaaaa gaaagt gagt ct gt aa		696

<210> 59
 <211> 1653
 <212> DNA
 <213> Chl amydi a pneumoni ae

<400> 59		
at gcat cct t t at acgt t ga t ct t gat act at t at cagct cct act ct cc t ccct t acct		60
aaagaat t t c aagaagcagc ct ct t t aat t gct gt t ccag at act t caca t t ct aagcct		120
gt cgt t ccag gagt gaaaac cct ct t t cca caaacct acc acct t ccct a t ct aaagt t t		180
gt ccaaggag aaaat gt cgt t cacact cct ct aaaagt ag gcgt aat gt t ct caggagga		240
cct gct ccag gaggacat aa t gt cat ccaa ggact ct t ca at agt ct aaa agat t t ccat		300
cccgat t cct ccct cgt ggg gt t cgt aat aat ggagacg gt ct t acaaa caat aaaagc		360
at agacat t a ct gaagagt t t ct ct ccaaa t t ccgaaat t ccggaggct t caact gt at a		420
ggaacaggaa ggaaaaaat t gt aact cca gaagct aaag aggct t gt ct aaagaccgca		480
gaggct ct gg at ct cgacgg act agt cat t at t ggcggt g at ggct ccaa t acagcaacc		540
gct at t ct t g cagagt at t t t gcaaaacga cgcccaaaaa cct ct at t gt cggagt t cct		600
aaaact at ag at ggggat ct acaacacacc t t ct t ggat c t gacct t cgg at t t gat act		660
gcaacaaaaat t ct act ct t c aat cat t agc aat at t t caa gagat gct ct t t cct gt aaa		720
gct cat t acc act t cat t aa act t at gggg cgct cagcat cccat at t gc t t t ggaat gt		780
gct ct ccaaa ct cat ccaaa t at t gccct t at cggcgaag aaat t gccga aaaaaat ct a		840
ccact aaaaa ccat cat cca t aaaat ct gc t ccgt aat t g cagat agagc cgct at ggaa		900
aaat act at g gcgt cat cct cat cccagaa ggcat t at cg agt t cat ccc agaaat cat c		960
aaact t aat t a cagaaat cga aagcct at ca gaat acgaag at aaaaat ct c caggct ct ct		1020
ccagaat ccc aacgcct act gaaaagct t c ccagcacct a t cat cgagca aat cct caat		1080
gaccgcat g ct cacggt aa t gt ct at gt t t ct aaaaat t a gt gt cgat aa act act cat c		1140
cacct ggt ca gcaat cat ct ccaacaat at t t ccct aacg t ccct t t caa t gcgat ct ca		1200
cat t t t ct ag gat at gaagg acgct cggga t t gcct acaa aat t cgat aa t acct acggc		1260
t at agcct cg gat acggcgc cggat at t ct c gt ccgcaat c act gcaacgg ct at ct ct ct		1320
act at agaat ccct agcat g ccct t t cat g aaat ggaaat t acgggcaat t cccgt agt g		1380
aaaaat gt t ca cagt aaaaca acaggcagat ggaact ct ac aacct aaaaat t aaaaaat ac		1440
ct cgt agat a t aggaagcac ggcat t t cgt aaat t t aagc t ct at aggaa aat t t gggcc		1500
ct cgaagact cct accgat t cct agggcct ct acaaat ag aaact cct cc agaaat gcac		1560
t ct gat aat t t ccct cct ct t acct t t t g ct t aat cat a act t t t ggca acgt caccag		1620

ggg t gcat ag aat ccct ga t act acgt at t aa 1653

<210> 60
 <211> 1587
 <212> DNA
 <213> Chl amydi a pneumoni ae

<400> 60
 at gaagat gc at aggct t aa acct acct t a aaaagt ct ga t ccct aat ct t ct t t t ct t a 60
 t t gct cact c t t t caagct g ct caaagcaa aaacaagaac cct t aggaaa acat ct cgt t 120
 at t gcgat ga gccat gat ct cgccgacct a gat cct cgca at gcct at t t aagcagagat 180
 gct t ccct ag caaaagccct ct at gaagga ct gacaagag aaact gat ca aggaat cgca 240
 ct ggct ct t g cagaaagt t a t acct gt ca aaagat cat a aggt ct at ac ct t t aaact c 300
 agacct t ct g t gt ggagcga t ggccact cca ct cact gct t at gact t t ga aaaat ct at a 360
 aaacaact gt act t cgaaga at t t t cacct t ccat acat a ct t t act cgg cgt gat t aaa 420
 aat t ct t cgg caat ccacaa t gct caaaaa t ct ct ggaaa ct ct t gggat acaggcaaaa 480
 gat gat ct t a ct t t ggt gat t acct agag caacct t t cc cat act t t ct cacact t at c 540
 gct cgccccg t at t ct cccc t gt t cat cac acct t aggg aat cct at aa gaaaggaaca 600
 cccccat cca cat acat ct c caat gggccc t t t gt ct t aa aaaaacat ga acacccaaaac 660
 t act t aat t t t agaaaaaaa t cct cact ac t at gat cat g aat cagt aaa gt t agaccga 720
 gt cacct t aa aaat t at ccc agacgcct cc acagccacga aact t t t caa aagt aaat ct 780
 at agat t gga t t ggct cacc t t ggagcgct cccgat at ct a acgaagacca aaaagt t ct c 840
 t cccaagaaa agat t ct t ac ct at t ct gt t t caagcacca ccct t ct t at ct at aacct g 900
 caaaaacct c t aat acaaaa t aaagccct c aggaaagcca t t gct cat gc t at t gat aga 960
 aaat ct at ct t aagact cgt gcct t cagga caagaagct g t aact ct agt t cccccaaat 1020
 ct t t cacaac t caat ct t ca aaaagagat c t caacagaag aacgacaaac aaaagccaga 1080
 gcat at t t t c aagaagct aa agaaacact t t ct gaaaaag aact cgcaga act cagcat c 1140
 ct ct at cct a t agat t cct c gaat t cct cc at cat agct c aagaaat cca aagacaact t 1200
 aaagat acct t aggat t gaa aat caaaat c caaggcat gg agt accact g ct t t t t aaag 1260
 aaacgt cgt c aaggagat t t ct t cat agcg acaggaggat ggat t gcgga at acgt aagc 1320
 cccgt agcct t cct at ct at t ct aggcaac cccagagacc t cacacaat g gagaaacagt 1380
 gat t acgaaa agact t t aga gaaact ct at ct ccct cat g cct acaaaga gaat t t aaaa 1440
 cgcgagaaa t gat aat aga agaagaaacc cccgat t at cc ccct gt at ca cggcaaat at 1500
 at t t acgct a t acat cct aa aat ccagaat acat t cggat ct ct t ct agg ccacacagat 1560
 ct caaaaat a t cgat at ct t aagt t ag 1587

<210> 61
 <211> 1860
 <212> DNA
 <213> Chl amydi a pneumoni ae

eol f - seq | . app

<400> 61
at ggaaagt g agaaagat at aggagct aag t t t t t aggt g act at aggat t ct ct at cgc 60
aaggggcaga gcct at ggag cgaagat ct t t t agccgaac at cgat t t at aaaaaaacgt 120
t acct t at t c gat t act t ct t cct gat ct a ggaagt t ct c aacctat t cat ggaagct t t t 180
cat gat gt t g t t gt t aaact agcaaaat t a aacctat ccag gcat cct cag t at agaaaat 240
gt t t ct gaat ct gagggaag at gt t t ct t g gt aacacaag agcaagacat ccccat cct t 300
t cact aacgc aat at t t aaa aagt at t ccc cgcaaact t a cagagct aga aat t gt agat 360
at t gt aagcc aact cgct t c t c t t t agat t at gt gcat t cagaaggact ggct caagaa 420
gagt ggaat c t t gat t ct gt ct at at t cat at t t t gaat g gt gt t cct aa agt cat act c 480
cct gat ct gg ggt t t gct t c at t gat aaaa gaacgt at t t t ggacgggt t t at t t cagat 540
gaggagaat c gagaat ct aa aat aaaagaa aggggt act ac t t cacact t c agaaggaaaa 600
caaggt agag aagat acgt a t gct t t t ggt gct at cacct at t at t t act t t t t ggt t t t 660
ct t cct caag gcat t t t ccc t at gcct t cg aaagt t t t t t ct gat t t t at ct at gat t gg 720
gat t t t t t aa t t agct ct t g t t t aagt t gt t t t at ggaag aaagggcaaa agaact t t t c 780
ccct t aat aa gaaaaaaaaac t t t aggagaa gagct gcaaa at gt t gt cac t aact gt at a 840
gaaagct ct t t aaggggaagt gccagat cct t t ggaat ct t ct cagaat ct t cct caagcg 900
gt cct t aaag t aggggaaac gaaggcaagt caccagcaga aggaat ct gc ggaacat t t a 960
gaat t t gt gt t agt ggaagc at gct ccat a gat gaagcca t ggat accgc t at agaat cc 1020
gaaagt agt t ct ggagt t ga ggaggaaggg t at t ccct ag ct ct acagt c t t t at t agt t 1080
cggaaccag t agt gagt cg t t at gt agaa gct gagaaag aagaacccaa accgcaaccc 1140
at act t acag aaat ggt t t t aat agagggga ggagaat t ct cccgaggaag t gt cgaaggg 1200
caacgt gat g agct t cct gt acat aaggt a at t t t acat a gct t t t t ct t agat gt t cat 1260
cct gt gacga acgaacagt t t at t cgt t at t t agaat gt t gt ggt agt ga acaggat aag 1320
t at t at aat g agt t aat ccg at t gcgagat t ct cgt at ac agcgt cgt t c ggggt aggct t 1380
gt t at agagc caggt t at gc t aagcacct gt cgt t gggg t t act t ggt a t ggagcct ca 1440
gggt at gcag aat ggat agg aaaacgcct g cct acagaag ct gaat gggga aat agct gct 1500
t ct ggcgggg t ggct gcgct acgct at ccc t gt ggggagg aaat cgaaaa aagccgggca 1560
aat t t t t t ca ct gcggat ac gacaacagt c at gagt t at c cacccaat cc t t at ggcct c 1620
t at gat at gg caggggaat gt ct acgagt gg t gccaagat t ggt at gggg a t gat t t t t at 1680
gaaat t t ct g ct caagagcc agagagt cct caaggt cct g ct caaggagt ct at cgggt g 1740
ct aagagggg gat gt t ggaa gagct t aaaa gat gat ct t c gct gt gct ca t cgccat cgt 1800
aat aat cct g gggct gt aaa t agt acgt at ggt t t t aggt gcgct aaaaa t at caat t aa 1860

<210> 62
<211> 1911
<212> DNA
<213> Chl amydi a pneumoni ae

<400> 62
 at gaaacaac act at t ct ct aaat aaaagt cgt cat at cc t ccgcagt ac t t at aagct t 60
 t t aaaaagt a aaaaact cgc ccat t ccct gcagat aaaa agcaact gca agaact act a 120
 gaacaact ag aagaggct at ct t t gaacat gat caagaaa ct gcaagcga ct t agct cag 180
 caagcat t ag cat t t t ccaa ccgt t at cct aat t cct t cg gacgcaaac ct at gagct t 240
 at caaggccc t t ct t t t gc t ggt gt t gt a gcct t ct t ag t t cggcaat t t t ggt t t gaa 300
 ct t t at gaag t gcct acagg at ccat gagg cct acaat t t t agaacagga t cggat t ct t 360
 gt at ccaaaa caacat t t gg t ct ccat t gc cct t t t gct a agaaaccact t gcct t caat 420
 cct gaat ccg t aact cgcgg ggggt ct t gt t gt t t t cact g t aggcgacct ccct at ccca 480
 gat gct gat a caaagt act t cggat t gat t ccaggaaaa agcgt t acat t aaacgt t gc 540
 at gggaagac ct ggggact t ct t at at t t c t at ggaggaa aaat t t at gg t ct t gat gat 600
 gcagg t aaac gcat agagt t t cct t ct gt c cat ggt t t ag aaaact t at a t cacgt cccc 660
 t at at at cct t t gat ggcac t accagcagc cat acagaag ggcagaaaac aat t at agat 720
 t t t aagcagt t caat caaag t t at ggt cgg ct gat t t t cc ct caaacct c cat gt at gga 780
 caat t ct t t g accat aaaga at ggcat caa gacgagcct a at aaat t aaa agat cct cat 840
 ct t t cgccag t cagct at gc cgat ct t t t t ggt at ggg t a act at gct at ggt gcgcat c 900
 t t aacagaac at caggcag aacat cccat ct act t ccga at ccaggaag t ccaact aaa 960
 gt ct act t ag aaat t t gcc a t acagcgaac ct t t cct acc caaagcct ct gt t gcgt cac 1020
 t at gagcat c agct ct cgcc t gcgat t caa cct at gaaga ct t t act t cc t t t gcgt aag 1080
 gaacat t t gc act t aat t cg gaacaat ct t act acct ct c gt t t t at t gt t gct caagga 1140
 t gt gcgt at a aat accat ca at t caagat t aacact t cag gaat t gccaa agcct at gca 1200
 at t ct cct gc ccaaggt ccc t gat ggt t gt t at gaat at t ct aaaggcga agcgt at caa 1260
 at t ggct t t g gagagat t cg t t at aagct a aaat ct t ct c accccct t ac t cagct caat 1320
 gat aagcaag t gat t gaact t t t t aact gc gggat caact t t agt t ct at t t at aat cct 1380
 gt gaat ccgc t gcaagcacc t t t acct aac cgt t at gcat t ct t t aacca agggat ct t 1440
 t at at cat gg at t ct cct gt at t t at aaag aat gat ccaa ct ct gcaaaa at t t gt gact 1500
 t ct gaaacgg aaaagcaaga ggggt ct t ca gagacacaac cct at at agc t t t t gt t gac 1560
 aagggact cc ct ccagaaga t t t t aaagaa t t cgt ggagt t t at acat aa t t t t ggt at t 1620
 caagt t cct a aaggt cat gt t ct cgt ct t g ggagat aact accct at gag t gcggat agt 1680
 cgagaat t t g gct t t gt t cc t at ggaaaat ct ct t aggat ct cct ct at g t acat t ct gg 1740
 cct at t ggac gcat gggacg gt t aact gga gt t t ct gct c caacaacact ct caggt t at 1800
 ct t gt t agt g ggat agcat t agcgacgggt ct ct ct ct ca t t ggat at gt ct act at caa 1860
 aaacgacgca gact ct t t cc t aagaaagag gagaaaaacc acaagaaat a a 1911

<210> 63
 <211> 5481
 <212> DNA

<213> Chl amydi a pneumni ae

<400> 63

at gaaat cac t t cct gt at a t gt t t ct ggg at caaagt t a gaaat ct aaa aaacgt t t ct	60
at ccat t t t a act ccgagga aat cgt t ct a ct cacaggag t t t cgggat c aggaaaat cc	120
t cgat agcct t t gat accct at at gct gct ggaagaaaac gct at at t t c aacact t ccg	180
acat t ct t cg ct act acgat aacgacgct g cccaat cct a aagt agaaga aat t cat ggt	240
ct ct caccaa caat agcaat aaaacagaac cact t t t cac act at agt ca t gcgact gt c	300
gggagcact a ct gaact t t t t t cgcacct t gct ct t ct ct t cagct aga aggacaggct	360
cgagat cct a agact aaaga agt ct t agat ct ct acagca aggagaaagt t ct t agt acc	420
at t at ggagc t ct ct gaagg t gt acagat c t ct at t t t ag ct cct ct gct acgt aaagat	480
at t gct gcaa t ccat gagt a t gcacaacag ggat t t acaa aagt acgt t g t aacggcacg	540
at ccaccca t t t act cct t cct aact t ca gggat t cct g aagact gct c t gt t gat at t	600
gt t at t gat a ct ct aat caa aagt gaaaat aat at t gcaa ggct caaagt t agcct at t c	660
acagct t t gg aat t cggaga ggggt cat t gc t cagt t ct t a gt gacgaaga gct cat gaca	720
t t ct ccacaa agcaacagat cgat gacgt c acct at accc ct ct aact ca acaat t at t t	780
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eol f - seq | . app

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eol f - seq | . app

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agt t t t aat c ccact gct ga gcaggaggct	ccgt t agt t c	ct aat ct t ct	t t ggggt t ct	1560
t t t at agat g t t cgt t cct t ccagaat t t t	at agagct ag	gt act gaagg	t gct cct t ac	1620
gaaaagagat t t t ggg t t gc aggcatt t t cc	aat gt t t t gc	at aggagcgg	t cgt gaaaat	1680
caaaggaat t ccgt cat gt gagt ggaggt	gct gt agt ag	gt gct agcac	gaggat gccg	1740
ggg ggt gat a cct t gt ct ct ggg t t t gct	cagct ct t t g	cgcgat gacaa	agact act t t	1800
at gaat acca at t t cgcaaa gacct acgca	ggat ct t t ac	gt t t gcagca	cgat gct t cc	1860
ct at act ct g t ggt gagt at cct t t t agga	gagggaggac	t ccgagat	cct gt t gcct	1920
t at gt t t cca agact ct gcc gt gct ct t t c	t at gggcagc	t t agct acgg	ccat acggat	1980
cat cgcat ga agaccgagt c t ct acccccc	ccccccccga	cgct ct cgac	ggat cat act	2040
t ct t ggggag gat at gt ct g ggct ggagag	ct gggaact c	gagt t gct gt	t gaaaat acc	2100
agcggcagag gat t t t t cca agagt acact	ccat t t gt aa	aagt ccaagc	t gt t t acgct	2160
cgccaagat a gct t t gt aga act aggagct	at cagt cgt g	at t t t agt ga	t t cgcat ct t	2220
t at aacct t g cgat t cct ct t ggaat caag	t t agagaaac	gg t t t gcaga	gcaat at t at	2280
cat gt t gt ag cgat gt at t c t ccagat gt t	t gt cgt agt a	accccaaat g	t acgact acc	2340
ct act t t cca accaagggag t t ggaagacc	aaaggt t cga	act t agcaag	acaggct ggt	2400
at t gt t cagg cct caggt t t t cgat ct t t g	ggagct gcag	cagagct t t t	cgggaaact t t	2460
ggct t t gaat ggcggggat c t t ct cgt agc	t at aat gt ag	at gcgggt ag	caaaat caaa	2520
t t t t ag				2526

<210> 67
 <211> 1935
 <212> DNA
 <213> Chl amydi a pneumni ae

<400> 67
 at gact t cgt ct t ct t gcc cct t t t agac ct gat at t gt ct cct gcaga t t t aaagaaa 60
 ct ct ct at t t ct cagct t cc t ggt t t agct gaagaaat cc gt t at cgcat cat ct ct gt a 120
 t t at caaaa caggaggcca ct t at ct t ca aat ct t ggaa t cgt agagct t act at agcc 180
 t t acat t acg t gt t ct ct t c cccaaaagat aaat t t at t t t t gat gt agg acat cagacc 240
 t at cct cat a aact act gac aggaagaaat aat gaaggat t t gaccat at acgcaat gac 300
 aacggcct ca gt ggt t t t ac caaccct acg gagagt gacc acgat t t at t t t t ct ct gga 360
 cat gcaggga cggcat t gt c t t t agct ct a ggaat ggct c aaacaacccc t t t agaat ca 420
 cgcacacacg t cat t cccat cct t ggagat gct gcat t ct ct t gt ggt ct t acct t agaa 480
 gcgt t gaaca at at t t caac agat t t at cg aagt t t gt t g t t at t t t gaa t gacaacaat 540
 at gt cgat ct ct aaaaacgt aggagccat g t ct cgaat ct t t t cccgat g gct acaccac 600
 cct gcaacca at aaact cac t aagcaagt g gaaaaat ggc t cgct aaaat t ccacgct at 660
 ggggat agct t agcaaagca cagt cggaga ct t t cacaat gt gt t aaaaa t ct ct t ct gt 720
 cccact cct t t at t t gaaca at t cggat t a gcgt at gt cg gccct at aga cgggcat aat 780
 gt t aaaaaac t gat ccccat cct t cagt cc gt t cgt aacc t ccct t t t cc t at t ct t gt c 840
 cacgt ct gt a caact aaggg gaagggcct a gaccaagccc aaaat aacc t gcaaagt at 900
 cacggagt ca gagcaaact t caat aagcga gaat ccgcaa aacat ct t cc ygcgat t aag 960
 cct aagcct t ct t t ccct ga t at at t t ggc caaacgct at gt gaact t gg agaggt t t cc 1020
 t cacgt ct cc at gt ggt gac t cct gcaat g t ct at aggat ct cgt t t gga aggt t t caaa 1080
 cagaagt t cc cagaacgct t ct t t gat gt a gggat t gct g aaggccat gc agt gact t t c 1140
 agt gcaggca t t gcaaaagc cggcaat cct gt gat ct gt t ct at at at t c t acat t t t t a 1200
 caccgt gct c t cgat aat gt t t t ccacgat gt t t gcat gc aagat ct t cc cgt gat t t t t 1260
 gct at agat c gt gcaggact t gcct at ggt gat ggacgt a gt cat cacgg cat ct at gat 1320
 at gagt t t cc t acgt gcgat gccccagat g at t at ct gt c agccacgt ag ccaggt ggt a 1380
 t t ccaacagc t act gt at t c t t ct ct acac t ggt cct ct c ct t ct gct at ccgct acccc 1440
 aat at cccag ct cct cat gg agaccact c act ggagat c caaat t t cct aagat cccca 1500
 ggcaat gct g agaccct ct c acaaggt gag gacgt t ct ca t cat agct ct t ggaaccct c 1560
 t gct t cacgg ccct at ct at aaaacat cag t t gct t gct t at ggc at ct c cgcaact gt t 1620
 gt agaccgga t ct t t at aaa acct t t t gat aacgat ct t t t cagt ct t t t act gat gagt 1680
 cact ct aagg t gat t accat agaagagcac t ccat t cgag gaggat t agc gt ccgagt t t 1740
 aat aat t t t g t agct acgt t caat t t t aag gt cgat at ct t aaat t t t gc aat ccccgat 1800
 acat t cct at cccat gggag t aaggaagcc ct caaaaat ct at aggcct t gat gagagt 1860
 agt at gacca accgcat t ct cact cat t t c aact t cagat caaaaaagca gact gt t gga 1920

gacgt cagag t t t aa

1935

<210> 68
 <211> 1080
 <212> DNA
 <213> Chl amydi a pneumoni ae

<400> 68
 at gaaaaat a gct t t ggct c t t t gt t t t ct t t t acaacat ggggagaat c ccacggg ccc 60
 t caat cggag t t gt aat cga t ggt t gt ccc gcaggact cg agct ccat ga at cagat t t t 120
 gt t cct gcca t gaagcggc t cgt ccagga aat ccaggaa cct cat cgcg caaagaaaac 180
 gat at cgt gc aaat cct ct c t ggagt t t at aaaggaaaga ccacaggcac t cccct at cc 240
 ct gcaaat cc t caat act ga cgt agat agc t cccct t at g aaaacagt ga aaggct ct ac 300
 cgt cct ggcc act cccaat a t acct at gaa aagaaat t cg gaat t gt aga t cct aacgga 360
 ggagggt cgct cct cagct cg agagacggca t gt cgcgt cg ct gct ggcgt agt t gcagag 420
 aaat t cct cg cgaat caaaa cat t t t t act t t agcct acc t ct cct cgt t aggat ct ct a 480
 accct ccct c act acct gaa gat ct cccc gagct cat cc acaagat t ca cacct cgcca 540
 t t ct at t cac cgt t acct aa t gagaaaat c caagagat cc t t act t ct ct acacgacgac 600
 t ct gat t ct c t aggt ggggt gat t t ct t t c at aacgt ct c caat ccacga ct t t ct aggg 660
 gaaccct ct t t gggaaagt gcacgccct c t t agcaagt g ct t t aat gag cat ccccgcc 720
 gct aaaggat t cgaaat agg aaaagggt t t gcct ct gct c aaat gagagg t t cacaat at 780
 act gat ccct t cgt cat gga aggagaaaac at t acct t ga agt ct aacaa ct gt ggaggc 840
 aact aggag gcat aact at aggagt t cct at agaagggc gcat agcat t t aaacct acc 900
 t ct t cgat aa agcgaccct g t gct acagt g acaaagacaa aaaaagaaac t acct at agg 960
 acacct caaa caggacgt ca t gat cct t gt gt cgccat ac gcgct gt ccc t gt t gt t gag 1020
 gct at gat aa acct t gt t ct t gcagat ct t gt at t at acc aacgat gct c caaact at ga 1080

<210> 69
 <211> 1860
 <212> DNA
 <213> Chl amydi a pneumoni ae

<400> 69
 at gaaaaaag ggaaat t agg agccat agt t t t t ggcct t c t at t t acaag t agt gt t gct 60
 ggt t t t t ct a aggat t t gac t aaagacaac gct t at caag at t t aaat gt cat agagcat 120
 t t aat at cgt t aaaaat at gc t cct t t acca t ggaaggaac t at t at t t gg t t gggat t t a 180
 t ct cagcaaa cacagcaagc t cgct t gcaa ct ggt ct t ag aagaaaaacc aacaaccaac 240
 t act gccaga aggt act ct c t aact acgt g agat cat t aa acgat t at ca t gcagggat t 300
 acgt t t t at c gt act gaaag t gcgt at at c cct t acgt at t gaagt t aag t gaagat ggt 360
 cat gt ct t t g t agt cgacgt acagact agc caaggggat a t t t act t agg ggat gaaat c 420
 ct t gaagt ag at ggaat ggg gat t cgt gag gct at cgaaa gcct t cgct t t ggacgaggg 480

agt gccacag act at t ct gc t gcagt t cgt t cct t gacat cgcgt t ccgc cgct t t t gga 540
 gat gcggt t c ct t caggaat t gccat gt t g aaact t cgcc gacccagt gg t t t gat ccgt 600
 t cgacaccgg t ccgt t ggcg t t at act cca gagcat at cg gagat t t t t c t t t agt t gct 660
 cct t t gat t c ct gaacat aa acct caat t a cct acacaaa gt t gt gt gct at t ccgt t cc 720
 ggggt aaat t cacagt ct t c t agt agct ct t t at t cagt t cct acat ggt gcct t at t t c 780
 t gggaagaat t gcgggt t ca aaat aagcag cgt t t t gaca gt aat cacca t at agggagc 840
 cgt aat ggat t t t t acct ac gt t t ggt cct at t ct t t ggg aacaagacaa ggggccct at 900
 cgt t cct at a t ct t t aaagc aaaagat t ct cagggcaat c cccat cgcat aggat t t t t a 960
 agaat t t ct t ct t at gt t t g gact gat t t a gaaggact t g aagaggat ca t aaggat agt 1020
 cct t gggagc t ct t t ggaga gat cat cgat cat t t ggaaa aagagact ga t gct t t gat t 1080
 at t gat caga cccat aat cc t ggaggcagt gt t t t ct at c t ct at t cgt t act at ct at g 1140
 t t aacagat c at cct t t aga t act cct aaa cat agaat ga t t t t cact ca ggat gaagt c 1200
 agct cggct t t gcact ggca agat ct act a gaagat gt ct t cacagat ga gcaggcagt t 1260
 gccgt gct ag gggaaact at ggaaggat at t gcat ggat a t gcat gct gt agcct ct ct t 1320
 caaaact t ct ct cagagt gt cct t t ct t cc t ggggt t t cag gt gat at t aa cct t t caaaa 1380
 cct at gcct t t gct aggat t t gcacaggt t cgacct cat c ct aaacat ca at at act aaa 1440
 cct t t gt t t a t gt t gat aga cgaggat gac t t ct ct t gt g gagat t t agc gcct gcaat t 1500
 t t gaaggat a at ggccgcgc t act ct cat t ggaaagccaa cagcaggagc t ggaggt t t t 1560
 gt at t ccaag t cact t t ccc t aaccgt t ct ggaat t aaag gt ct t t ct t t aacaggat ct 1620
 t t agct gt t a ggaaagat gg t gagt t t at t gaaaact t ag gagt ggct cc t cat at t gat 1680
 t t aggat t t a cct ccaggga t t t gcaaact t ccaggt t t a ct gat t acgt t gaggcagt g 1740
 aaaact at ag t t t t aact t c t t t gt ct gag aacgct aaga agagt gaaga gcagact t ct 1800
 ccgcaagaga cgcct gaagt t at t cgagt c t ct t at ccca caacgact t c t gct t t gt aa 1860

<210> 70

<211> 1032

<212> DNA

<213> Chl amydi a pneumni ae

<400> 70

at ggaagt t t at agt t t t t c ccct t cagt a agaact t cgt t t cagcaccg t gt aat ggcg 60
 gcaact agat a at t ggt t t t t t ct aggaggg cgccgt t t aa aagt agt t t c t ct agat agt 120
 t gt aact cag ggcaggct t g t gaagaat ac gt gcct at t t caacgacaga aaaggt ct t a 180
 aagat act ct ct t acct act cat accgat t gt cat aat ag ct ct gt t aat t cgt t at ct t 240
 t t gcat agca at t t t acggc aaaggt at ca cagaaacct t ggt t aaagac cct gcagt t a 300
 ggaat t gat a t aaaaagct t cat act t ccc ggt t ct cat g t aaacacgat ggat t cagct 360
 act t t gt t t a aagcaat t cg t t t ggaaggg aagcgt gt t g at gt agaat a t cat aggct a 420
 cat agcagcg at aaggt ggt t t t t at at c cct gct caga aact t ccaga t gat ct gcgt 480

eol f - seq | . app

t t gact cat t ggct t ccaga aaaagaaaca agaaagact g agt at gt gag acat at gct g	540
gccccat gt ca t ggg t t at ct aacat cacag ggt aaggaac ggct t caaca ggt agt gcaa	600
gact ct cgaa gcagt act t c ct t gggggct gaaaaagt cc t t caat acag at t cat t gat	660
cat ccacaga gt caaggaga at t t caacgt ct gct t aat g aaaat at aac gaccaaaggt	720
t ccgaggat a aggaagt t gt acagagt gat t t at t t gaca t ggct t t t ca gt gt t ggt gg	780
ccacagt t t a t t t cagt t at acaat ct ccg acct t cagt g aagaat t agt acacgaaat g	840
agt cagaaac t t gat t t aga t t gt at at ac ccagaagat g at gaat t t ga gcagaagt t c	900
ct t aat accc t t ct gaaagc agt ct t gcac cacgg t t t g aaggaat cag t gt t gcgagt	960
at ggg t gt t a t ct t cct gat t t gt ccggac t ct ct t gcat t acagat t cc ct t ct t aagg	1020
aat caaaaat ga	1032

<210> 71
 <211> 1101
 <212> DNA
 <213> Chl amydi a pneumoni ae

<400> 71	
t t gt caggaa t at t t t caaa t cct cat cca gt t t cct at t t t t cgt caac acacgccaaag	60
cagt t aagt g act t t agt aa gaagcacccc at act cacca aaat t gt t ac gat cat t gt t	120
aaaat t t t ca aact ct t aat cggt ct gat t at t ccgcccc t gggaat t t a t t ggt t at gt	180
caat t agt at gt t cct t ggc t ct t t t cccc cgt t ct t cga t gct t t acag cgt ct t gaaa	240
acct gct t t a aaaagt at cg t t t ggaacag gaaat acaag at t at t t t gt aaagaat ct a	300
gat ccct ct t t caaagacct agcagt ct cg gaaagt aaaa gaat cacgat ccaacaagac	360
cat ct t acca t t gat act t t agcaat acat t t cagt acgg caaggcct aa acgt t ggct g	420
ct gat t t ct c t aggaagt gg agat t t cct c gaagacat ga t aggcct gaa agat t cct t g	480
t t t ct ct cct ggaaagagt t agct aaact g ct aggcgct a at at cct aat t t acaact at	540
cct ggggt t a agt cgagcac aggaaaat t g aact t agaga acct agcgac agct cat aat	600
ct at gt gcaa agt acct aca agat aaaat t cagggccct g gggct aacga aat cat cacc	660
t acggat at t cct t aggagg ggt agt ccag t ct gcagct t t gcaaaaaaa t cct t t t aca	720
aat agcgaga ct t ct t ggg t agcagt caaa gaccgt gct c cccact ct t t acccgagct	780
gct aat agt t t ct t cgggcc aat aggaaaa ct cat cgcag t cct cgct cg at ggaaaat g	840
gat gcggaaa aaaacagccg agagct t cct t gccagaaa t t ct t gt t t a t t ct gcggat	900
cgat t t cgcc ct t cagaagt t ggt gat gat accgcat t gc t cccggagt t t act ct t gct	960
cat gcaat aa aacgaacccc at t t gccagg agt aaaaaat t t at aggaga ggt aat ct a	1020
ct ccaact caa gccct ct gaa acaccct aca at acaaaagc t t gct gaagc aat cct t gag	1080
agt ct ct ct a gaaaaaat t a a	1101

<210> 72
 <211> 978
 <212> DNA

<213> Chl amydi a pneumni ae

<400> 72

at gcact ccg agt t gcct aa ct at cagaac at cgt t gagt ct gt agt t ac ggaaat cact 60
acacaact ac t aaact at cg aagcgagcac cgt t t ggt t c ct t t t t ggga aaaat ccgat 120
gggt t ct t t t a t caccgct gc t gat t acggc agt caat at t at ct aaaaca acagct t gca 180
aaagcct t t c ccaat at t cc t t t t at t gga gaagaaact c t at at cct ga t caagacaac 240
gaaaaaat cc ct gaaat ct t aaaat t t aca cgcct gt t aa ct t ct t cagt ct caagagat 300
gact t aat t t ct accct ggt ccct cct cca t ct ccgact t ct t t at t t t g gct t gt cgac 360
cct at t gat g gt act gcagg t t t t at caga cat cgt gct t t t gccgt t gc t at at cact a 420
at t t at gagt at cgaccgat t t t gt cggc c at ggcat gcc ct gcct at aa t cagacat t t 480
aaact at at t cagcagct aa aggt cat ggt ct t t ct at t g t t cat t ct ca aaat ct agat 540
agacgct t t g t t t at gct ga t agaaaaca acaaaacaat t ct gt gaggc t t cgt t agct 600
gcat t gaat c aacagcat ca t gcaacacgt aagct aagcc t gggt ct ccc caaact ccg 660
agt cct cgt c gt gt agaaag ccaat at aag t at gct t t ag t t gct gaagg cgccgt agat 720
t t t t t cat t c gct accct t t t at t gat t ct cccgct cgt g ct t gggat ca cgt acct gga 780
gcct t cct cg t t gaagaagc t gggggt aga gt cacggat g ct t t aggagc ccct t t agaa 840
t at agaaaag aaagt t t ggt ct t aaat aat cacgcagt ga t t ct t gct t c t ggagaccag 900
gaaacccat g agacaacat t agcagcgt t a caaaaccaac t caat gt t gt ccccacggat 960
aagct t at t g ct ct at ga 978

<210> 73

<211> 1377

<212> DNA

<213> Chl amydi a pneumni ae

<400> 73

at gt t caacg t caact t t aa at t ct t agaa ggact t cat c aaccgcgcc cagat acaca 60
agct accct a cagct t t aga at gggaacct t ccgat gcgg ct ccagct ct t ct agcgt t c 120
caaagaat t a gagaaaat cc t cagcct ct c t ct ct t t at t t t cat at ccc ct t ct gccaa 180
t ccat gt gt t t gt at t gcgg t t gt t ct gt t gt t t t gaat c gt cgt gaaga t at t gt agaa 240
gct t at at ca acaccct aat ccaagagat g aaact t gt cg t t gagaccat aggat t ccgg 300
cct caggt at ccaggat t ca t t t t ggagga ggcaccct a gcagact ct c cagggagt t g 360
t t t accct gc t t t t t gacca cat ccat aag ct t t t t gat c t t t cacat gc t gaagaaat t 420
gct at t gaag t ggat cct cg t t ct t t aaga aacgacat gg aaaaagcaga t t t ct t t cag 480
aacgt aggt t t t aat aggt t agct t aggc gt t caagat a cccaagct ga t gt t caagaa 540
gct gt acgac gacgccaat c gcat gaggaa t ct t t aaagg cat acgaaaa at t t aaggaa 600
ct cgcct t cc aaagt at caa t at agact t a at t t at ggt c t t cccaaca aaccaaggag 660
t cct t t t ct a aaacaat t ca agat at ct t a gcgat gt at c cagat cgt ct t gct t t at t t 720
t ct t t t gcct cagt t ccat g gat caagccg caccaaaaag ccat gaaagc t t cggat at g 780

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cct t ct at gg aagagaaat t cgcgat t t at t ct caat ccc ggcat t t act t acaaaagca 840
 ggat at cagg ccat cggg at ggat cat t t c t ct ct t cccc at gat cct ct t accct cgct 900
 t t caaaaaca aaact ct aat ccgcaact t t caggggt at t ct ct accccc agaagaagat 960
 ct gct cgggt t aggaat gac t t ct acaagc t t cat t cgt g gaat t t at ct acaaaat gca 1020
 aaaaccct t g aggaat at ca caat acggg g ct t cgaggaa cat t t gccac t gt gaaaagt 1080
 aaaat t ct t a ccgaggat ga t cggat t aga aaat gggcaa t ccat aagct gat gt gcacg 1140
 t t t acgat ca at aaggaaga gt t t t t caac ct t t t t ggat at gagt t t ga t act t at t t t 1200
 at agaaagt c gt gat cgct t gat aagt at g gaaact acag gt ct cat cca t aacagt cct 1260
 ggct ct t t ga aagt aact cc t ct t ggagaa t t gt t t gt ca gagt cat t gc cacagct t t c 1320
 gat cact at t t t ct caat aa ggt at ct aaa aaagaat gt t t ct cagct t c t at at aa 1377

<210> 74
 <211> 1140
 <212> DNA
 <213> Chl amydi a pneumni ae

<400> 74
 at gagat at c at aaat at t t t cggg at gt g aat t ct t ggg t t t t t ct t gt cgt act t acc 60
 t t aat gct at t aagt gt t gt ggt cat t t ct t caat ggat c ct acagcgat gct ggt gacc 120
 t cct ccaaag gcct ct t gac caat aaaagt at cat gcagc t caggcat t t cgct ct agga 180
 t gggg cgt t t t t t t at ct g t gcct act t c gat t at cact t at t t aaacg at gggcat gg 240
 gt act ct act t t t t cat gat t t gt gct ct c gt gggcct t t t t t t gt t cc gt cagt ccaa 300
 aat gt ccat a gat ggt accg t at t cct t t c at ccat at ga gcgt acagcc ct cagaat at 360
 ggaaagct t g t gat cgt gat aat gct cagt t at at ct t gg aat cccgaaa agcagat at t 420
 acat cgaaaa caacagcat t cct t gct t gc t t agt t gt cg cact t ccgt t ct t t ct aat t 480
 t t aaaagagc ct gat t t agg aaccgcat t a gt ct t at gt c ct gt gacat t gacgat t t t c 540
 t at t t aagt a at gt ccat t c t t t act agt a aaat t t t gt a cagt ggt cgc t accat cgga 600
 at t at aggct cgt t at t gat t t t t t cagga at cgt ct cac at cagaaagt gaaaccct at 660
 gct ct gaaag t cat caagga at at caat ac gagcgact ca gcccgt caaa t cat caccaa 720
 cgcgcgct ct c t cat t t ct at agggct gggg ggaat t cgag gt cgt ggat g gaaaact ggg 780
 gagt t t gcag gt cgt ggat g gct accct ac ggct acacag act ct gt at t ct cggcat t a 840
 ggagaggaat t cgggt t gct ggggct act c t t t act ct ag ggct at t t t a t t gt ct t at c 900
 t gt t t t ggt t gt cgaact gt t gcagt cgcc act gat gact t t ggaaaact cct cgct gct 960
 ggcat t accg t at acct agc gat gcacgt c t t aat caat a t t agcat gat gt gcgggct g 1020
 ct acct at ca caggagt ccc t ct gat t ct a at t t cct at g ggggct ct t c ggt aat ct ct 1080
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<210> 75
 <211> 3501

<212> DNA

<213> Chl amydi a pneumoni ae

<400> 75

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aaact t t t t g agcagggggc t gt gat t gat gcgaaaat cc t t t cgat gaa t ggagagact	120
gt ct gcat ca gcgct caggt t cggggct t g t acgacaaca t t t at gagt g t gagat t gaa	180
gt t gat cgct cggaat ccga t act gt ggat t ccaact gt g at t gt t cgt a t aact acgac	240
t gccagcaca t cgt cgcact at t at t ct at t t agagcaat at t t t aat ga gat ggt agt a	300
gcct at gct c gt agt gct ga t t t agaaacg gat cacgaga t caacgagga agt aaaaaag	360
gagct caagg aaact t t t gt cgct gct gcc acaaaggaag aagagcgt aa agat cgt gag	420
cat caaaaag agat t t t aag agagt at gt t cacgct gcaa at gct t t aag t gcgaat cct	480
t t t t t cct ac ct t t agaata t t t agaaaag gat t ct gct g agct t gct gt at t at t t gt t	540
t ct gt aaat g aggat acgt t t gct cct gcc aat cagcct a t agagt t t ca at t agt act t	600
cgt t t accgt gt cgt t ccaa gcct t t t at at ct ct aat a t ccgt acct t t t ggaaggg	660
gt gt t gt at c aggagccaat t gt at t gaat gggcgt cggg t t t t ct t t ac gat gcaat cg	720
t t t aat gct t ccgat cgcaa gct aat agat t t at t gat t c gct at gt ccg t t accccaat	780
cat acaaccg aagagaagt t at t aaaaat ct gcgt at t t ga t gcct cct gc gt t aggt gt g	840
at t ct t gcaa agat gt t t ga acat caact g gcagat cgt g gaggaggaag t t t aggggaa	900
aaagagagt t t t caggggt t at t ct gt gga aat ct t gaag agcct ct gt g t t ggt cat t a	960
act ccggct a agat gaagt t t aact t agac t t ct t t gaca t gccct acaa agcgt t gt t a	1020
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gagt cggat g ct ccagggat t at t cat cat t t t gt t t at c at cggg t t t c t cct cagat c	1140
aagcgt gcgc at t t acgt t c ct t t agt cgt t t gcgagat a t agcaat t cc agaggct t t g	1200
t t t ggt t cgt t ccgt gagaa t gct ct t cct gt at t t cagg aat at gct ga aat t gcgaat	1260
gt t cacct t t t gaat t cct t t gt gacact t cct t at gt ag at gaggt ccg ggccat t t gt	1320
gat at gagct at t t ggacgg ggaat t agag gcaaaat t ac at t t cct t t a t ggt t ct t t a	1380
cgggt t ccag cagcat ct t t ggct t t gcaa t at caggat g t t cgt gcct t t at t agt gat	1440
gaggaat ct t agccagaaa t ct ggt t gaa gagcgt aaga t gt t ggaaga ggt ct t ct ca	1500
ggct t t at t t at gat gaacg cgat ggagct t t t cgt gt t a aaagt gagaa gaagat cgt g	1560
gaat t t at ga cggagacgat ccct gcgaat caacat cgca t t act t t t aa ct gt ccggaa	1620
aat ct t t cag gt cagt t t at t t at gat gag acgat ct t t g aat t at cgt t ccgagaaggg	1680
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ggg cagcaat ct aagggaac gcggcgcggt aaggt gaat t cgggt aagt t gcct t gt at t	1860
t t agt ct t ag act t agaaaa aat t gct cct gt ggt gcaga t t t t t aat ga aat aggat t t	1920
aaagt t t t ag at gact t agt t cagaagt gt cct t t at gga gt t t aacggg aat t t cgt t a	1980

eol f - seq1 . app

gat cagt t t g aagcact t cc t gt gaact t t t ccat gt ct g aaaggct t at agagat t cag 2040
aagcaaat t c gt ggt gagat cgagt t t gat t t ccaagat g t t cct cagca gat t caggca 2100
acgt t acgt a gct at caaac cgagggcgt a cat t ggt t ag agcgt t t gag aaaaat gcat 2160
ct caacggga t t t t agct ga t gat at ggga ct t ggaaaga ct ct ccaggc gat t at t gct 2220
gt t act caga gt aaact aga gaaaggcagc ggct gt t ct t t gat t gt t t g t cct acct ct 2280
t t agt t t at a act ggaagga agagt t ccgt aaat t t aat c ct gaat t cag gact t t agt t 2340
at t gat ggag t t cct t ct ca aagacggaag cagt t aacgg ct t t agct ga t cgcgacgt c 2400
gcgat t act t cgt at aat t t at t acagaaa gacgt ggagt t at at aagag ct t t cgt t t t 2460
gact at gt t g t t t t agat ga agcgcaccac at t aagaat c gt acgact cg gaat gcaaaa 2520
t cggg gaaga t gat t caat c ggat cat cgg t t gat at t aa ct ggaacgcc gat agagaac 2580
t cgt t agaag agt t at ggag t ct t t t t gat t t ct t aat gc ct ggt t t at t gagcagct ac 2640
gat cgct t t g t t ggaaagt a cat acgt acg ggcaact at a t gggcaat aa agct gacaat 2700
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t t t agt cagt at acaaagat gct gggcat t at t aagaaag at t t agagt c t cgaggcat t 3120
cct t t t gt ct at ct agat gg t t ccaccaag aacagact ag at t t agt gaa t cagt t t aat 3180
gaagat cct a gct t gt t ggt t t t ct t aat t t cct t aaaag ct gggggcac gggct t gaat 3240
ct t gt cggg g ct gat acagt gat t cact ac gacat gt ggt ggaat cct gc t gt agagaat 3300
caagcgact g accgagt cca t cgt at t ggg cagagccgt t ct gt ct ct t c ct at aat t g 3360
gt aacct t ga acacgat t ga agaaaaat c ct t act t t gc agaacaggaa aaagagcct t 3420
gt aaagaaag t gat t aact c t gat gat gag gt t gt at cca agt t aact t g ggaagaagt a 3480
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<210> 76
<211> 2265
<212> DNA
<213> Chl amydi a pneumni ae

<400> 76
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t ct t ct ggag t ggct t t aac gat agccgag aagat ggct t ct t t agagca ct cggggaga 120
ggagcagacg at t at gaggg gat ggct t cg t t t aat gcca at at gagggga gt at agcct t 180
cagct gagca agt t gt at ga ggaagcacga aagct acgcg ct t ct ggaac t gaggat gaa 240
gct ct gt gga aggact t aat t cgacggat t ggt gaggt gc gaggct at ct t cgagagat c 300

eol f - seq| . app

gaggagct t t gggct gcaga aat t cgt gag aaagggggca at ct cgagga ct acgccct c 360
t ggaat cacc cagagact ac gat t t acaat ct t gt t accg at t acggaac cgaagact ct 420
at t t at t t ga t t cct caaga aat cggagcg at t aaaat cg caacct t at c gaaat t t gt a 480
gt t cct aaag agt ct t t cga agact gt ct c act cagat cc t at ct cgct t aggt at t ggc 540
gt gcgt cagg t caat t ct t g gat t aaggaa ct t t at at ga t gcgt aagga gggct gcagt 600
gt t gct ggag t t t t t t cct c cagaaaagat t t agaggcgc t cccagaaac agcct at at t 660
gg t t t t gt at t gaat t cgaa cgt agat gcg cat accaat c aacat gt ct t aaaaaagt t c 720
at t aaccct g aaacaacgca t gt agat gt g at t gcaggac gt gt gt ggat t t t t ggt t ct 780
gcgggggaag t cggcgagct t ct gaagat t t at aat t t t g t gcagt cgga gagcat acgt 840
caagagt at c ggg t gat t cc ct t aact aag at cgat ccag gggagat gat t t ccat t ct c 900
aacgcagcat t t cgt gagga t ct gact aaa gat gt t agt g aagaat ct t t aggcct t cgt 960
gt agt t cct t t acagt at ca agggcgt t cg t t gt t t t t aa gt ggaaccgc ggcgt t agt g 1020
cagcaagcgc t gact ct cat t cgagagct t gaagaagga t t gagaacc t acggat aaa 1080
acagt at t t t ggt at aacgt caagcact cc gat cccaag agt t ggcggc at t gct t t cc 1140
caagt ccat g at gt ct t ct c t ggcgagaat aaggcgagt g t cggagct gc agat ggat gt 1200
gggt cgcaat t aaat gcct c gat ccaaat t gat act acag t aagt t ct t c t gcgaaagat 1260
ggct cagt ga agt acggaaa ct t cat cgcg gat t ct aaga caggaact ct gat t at ggt g 1320
gt t gagaaag aagt t ct t cc acgt at t cag at gct act t a agaaact aga t gt ccct aaa 1380
aagat ggt cc gt at cgaggt gct gt t at t t gaaagaaaat t ggcacat ga gcagaaat ct 1440
gggt t aaat c t t ct acgt ct t ggt gaggaa gt t t gt aaaa aagggt gcag t cct t ct gt g 1500
t ct t gggccg ggggt act gg cat act agaa t t t t at t t a aaggaagt ac gggat ct t cg 1560
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gaaat gt caa t agcgggt gt c t t cagat aaa gat aaagcgc aat acaat cg t gcgcagt ac 1740
ggt at cat ga t aaaaaat gct ccccgt aat t aat gt gggag aggaagacgg aaaaagt t ac 1800
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gat gt t acaa ggcgt aat at t act aat aag gt gcgcat t g ct gacggaga gact gt gat t 1920
at t ggaggt t t gcgt t gcaa acagat gt ca gat t ct cat g at ggcat t cc t t t cct t gga 1980
gacat t cct g gt at agggaa gt t at t t gga at gagt t cca cat cagacag t ct cacggag 2040
at gt t t gt at t t at cact cc gaagat cct a gaaaat cct g t agagcaaca agaacgt aaa 2100
gaagaagct t t act ct ct t c gcgccct gga gagagagaag aat act at ca ggct t t agca 2160
gct agt gagg ct gcagcacg agcagct cat aaaaaat t ag agat gt t ccc ggcacat cagga 2220
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<211> 1467

<212> DNA

<213> Chl amydi a pneumni ae

<400> 77

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 at acagcaaa cacgt caggg t aaaaacact gagat ggaaa gcgat gccac t at t gct ggt 180
 gct t ct ggaa aagacaaaac t t cct cgact acaaaaacag aaacagct cc acaacagggga 240
 gt t gct gct g ggaaagaat c ct cagaaagt caaaaggcag gt gct gat ac t ggagt at ca 300
 ggagcggct g ct act acagc at caaat act gcaacaaaaa t t gct at gca gacct ct at t 360
 gaagaggcga gcaaaagt at ggagt ct acc t t agagt cac t t caaagcct cagt gccgcg 420
 caaat gaaag aagt cgaagc ggt t gt t gt t gct gccct ct cagggaaaag t t cgggt t cc 480
 gcaaaat t gg aaacacct ga gct cccaag cccggggg ga caccaagat c agaggt t at c 540
 gaaat cggac t cgcgct t gc t aaagcaat t cagacat t gg gagaagccac aaaat ct gcc 600
 t t at ct aact at gcaagt ac acaagcaca gcagaccaa caaat aact aggt ct agaa 660
 aagcaagcga t aaaaat cga t aaagaacga gaagaat acc aagagat gaa ggct gccgaa 720
 cagaagt ct a aagat ct cga aggaacaat g gat act gt ca at act gt gat gat cgcggt t 780
 t ct gt t gcca t t acagt t at t t ct at t gt t gct gct at t t t t acat gcgg agct ggact c 840
 gct ggact cg ct gcgggagc t gct gt aggt gcagcggcag ct ggaggt gc agcaggagct 900
 gct gccgcaa ccacggt agc aacacaaat t acagt t caag ct gt t gt cca agcggg gaaa 960
 caagct gt t a t cacagct gt cagacaagcg at caccgcgg ct at aaaagc ggct gt caaa 1020
 t ct ggaat aa aagcat t t at caaaact t t a gt caaagcga t t gccaaagc cat t t ct aaa 1080
 ggaat ct ct a aggt t t t cg t aagggaact caaat gat t g cgaagaact t cccaagct c 1140
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 gcgggcct g ct ct cggt aa agggat t at g caaat gcagc t ct cggagat gcaacaaaac 1260
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 t t cact caat t t t ggcaaca ggcaagt aaa at t gcct caa acaaacagg cgagt ct aat 1380
 gaaat gact c aaaaagct ac caagct gggc gct caaat cc t t aaagcgt a t gccgcaat c 1440
 agcggagcca t cgct ggcgc agcat aa 1467

<210> 78

<211> 81

<212> DNA

<213> Chl amydi a pneumni ae

<400> 78

aagt t acct t t t cccgcct c t t t ct t t at c t t t ccaagga aat ccggt cc aaat ccat gg 60
 aacaat t cat ggggt at gca a 81

<210> 79

<211> 429

<212> DNA
 <213> Chl amydi a pneumni ae
 <400> 79
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 ct cct gt gt a agt t t c t t t t t g c c c t t c c c t t t c t t t a c t a g c t c g c t a g c t g g a a g 120
 t t t a g c a g a t c g c t t t c a g a a a c g g a a t a t t a t c t t a g c a a c c a g a t t t a t a g a g a t t t t 180
 a t g t a c a a t t c t c g g a a c g t a c t t t t t c t t t a t c c a a t c t g t a g t t g g g g g g t a t g t a g t 240
 c t t a a t t t t a a t g g c a t g t c a c a c a c a a t c t t t g g g c c a g c a a a g c t c g g g a t t c t t c c 300
 c g a a a t g c t a c c c t c a g a a c a g c t c t c c c a a g c c a a c g g g a t t a t g a c a g c a g c c a c c t a 360
 t a c a g g a a g t a t t t t a g g t t c t t g c c t t g c t c c t c t t c t t g t c g a t g t a a c t c a t c g t t t 420
 a g g t g t a a a 429

<210> 80
 <211> 123
 <212> DNA
 <213> Chl amydi a pneumni ae
 <400> 80
 a g a a t t g g g t t a c c t c g t t c a g a a t t t g a a a a t c a a a t t c c c a t t g g c g t g t g t g t a g a 60
 t a c t t g t c a t a t t t t g c t g c g g g g t a c g a c a t t a c c t c t c c a c a g g g g t g g g a a g a t g t 120
 t c t 123

<210> 81
 <211> 174
 <212> DNA
 <213> Chl amydi a pneumni ae
 <400> 81
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 a a a a a g a a a a a a a g a t c g g g a t t t a a g t g g t c t c t t t t t t t a g a t t t a g t t t t a c t 120
 t g g t g t a a g t t c c c a g a g g c c t a c a g a g a c c t c g g c a a a t g t a a a a c a c a a t c t 174

<210> 82
 <211> 60
 <212> DNA
 <213> Chl amydi a pneumni ae
 <400> 82
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<210> 83
 <211> 69
 <212> DNA
 <213> Chl amydi a pneumni ae
 <400> 83
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<210> 84
 <211> 117

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<212> DNA
<213> Chl amydi a pneumni ae

<400> 84
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<210> 85
<211> 102
<212> DNA
<213> Chl amydi a pneumni ae

<400> 85
gagagaagct ct agaggctt cagt aacaga t gcttt agt a tctt acgttt caaat t t aga      60
cat gat accg t acacaagt t ct cagggcat agt cat agaa ga      102

<210> 86
<211> 282
<212> DNA
<213> Chl amydi a pneumni ae

<400> 86
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t t t aggaagt t ct ggagt t g gaaagacaac t t t g t t cgt t t gct t gcgg g t t cct acc      120
t t t gcaagaa ggccaact t c t at ggaat gg gagccct ct a aat cgcaaag acgt t gcct a      180
t at gcagcaa aaagaagccc t gct t cct t g gcgt acggct t t aaaaaaca t gacgt t gt c      240
aacggagct t ggcat caat a caagt caca cgcct t at cc aa      282

<210> 87
<211> 207
<212> DNA
<213> Chl amydi a pneumni ae

<400> 87
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t at agct at g ggcaat at cg gct t gcct at act agaccac at gggacaac caggagt t cg      120
t g t t gt agaa at cagct cat t t cagct agc aaccaagag gaacat at cc cagcact t t c      180
t ggat ct gt g t t t t gaact t t t ct cg      207

<210> 88
<211> 102
<212> DNA
<213> Chl amydi a pneumni ae

<400> 88
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aagagt ggt c caaacct ac at gcagcaac t t c t t at t t t t      102

<210> 89
<211> 303
<212> DNA
<213> Chl amydi a pneumni ae

<400> 89

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cat ggaggcc agccccaccc t t ggaacat ccgt t t agt c cccaccaaaag agcaaat aat 180
acaat agagg at gacat ccc gaaaaagat g t t agt gagcc ct gt aat cat caat cct at a 240
gccat gaaat at ct aggat t ggat t ggt cg gacat gact c cgct aacaaa ct t act gat t 300
cca 303

<210> 90
<211> 108
<212> DNA
<213> Chl amydi a pneumoni ae

<400> 90
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cat gct ct at t ct t gt caag gccat cagaa acggt cggt a gt t gt ccg 108

<210> 91
<211> 141
<212> DNA
<213> Chl amydi a pneumoni ae

<400> 91
acaccaccga cat cacaaac at at t cacat t t cgat aat a cgacaggat c t cgagagcgt 60
at aat t t t at t t t cat ccac aagat cgaaa at aat aagga gagcacacgc t gt gacct ca 120
t ccgcat gga aagaacat c g 141

<210> 92
<211> 399
<212> DNA
<213> Chl amydi a pneumoni ae

<400> 92
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cgaat gt cag t aaagact cc ccat agggg a t t gcat act a acgcagat t t t ct t t cgggg 180
ct gggaacaa at cct gt t t t ggt ccaagt t gccgt ggcct ct t t t gt at t t gt agct gt a 240
t ccgt agt cc aat t aacat t ccat t gt cct t ggaat ccgt at t ct gaat t aggat cct ca 300
gcaggaacag ggat aaggct gct gat gt ca acgt t agt at caacat cagc at caaccgt g 360
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<210> 93
<211> 54
<212> DNA
<213> Chl amydi a pneumoni ae

<400> 93
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<210> 94
<211> 96

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<212> DNA
<213> Chl amydi a pneumni ae

<400> 94
agcagagacc tctctacctt gttttgcaga ctctctttcg tgaacttcta tagggattcc      60
tcggccattatctacgatga caataccccc gt cctc                                     96

<210> 95
<211> 159
<212> DNA
<213> Chl amydi a pneumni ae

<400> 95
tctactactc acacaaagca actctttttc caccaagtcc agcccttgag tttcaaactc      60
ttggatccgc tctcgcagtt gctctcgaca ggctcttact tccgactcca aaccggaatc     120
cccctggaat ctcttctgac actctgtgta ggctcgtcg                               159

<210> 96
<211> 69
<212> DNA
<213> Chl amydi a pneumni ae

<400> 96
gagtttcggc at aagaggaa atccaagag cgcagagtcc t gaaagt aaa agaaaacgaa     60
aggat at ca                                                                    69

<210> 97
<211> 216
<212> DNA
<213> Chl amydi a pneumni ae

<400> 97
gactccttat gcaat aaaaa ttgcacgat a atcgctgaag cgcaaatcac actaaaggca     60
cagaaaaaag ctcccaaacc taatgtcgac aaagaaat tt caggagccag ccgtgagcag     120
agcttcagaa acaatgcaa cacaaaacca aagcaacaga gactgcagaa aat aaagcag     180
aacctctgtt tattaataat attttaaat gcattt                                     216

<210> 98
<211> 96
<212> DNA
<213> Chl amydi a pneumni ae

<400> 98
atfccagtat tcaacaggaa caaagcatc aatagccttt tctcgatcta cgacaagctt     60
caaagctaca gattgcacac gccctgcaga tatccc                                     96

<210> 99
<211> 871
<212> PRT
<213> Chl amydi a pneumni ae

<400> 99

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Ser Thr Phe Ser Ile Gln Asn Arg Leu Arg Thr Ile Ser Gly Glu Ser
1          5          10          15

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eol f - seq1 . app

Thr Arg Ile Ile Lys Leu Asp His Lys Tyr Ser Gly Phe Asp Pro Arg
 20 25 30

Ser Val Pro Ala Ile Asn Leu Gu Gu Leu Asn Ser Gly Ile Tyr Ala
 35 40 45

Leu Arg His Leu Met Asn Ala Leu Gn Ser Gu Asn Thr Asn Val Ala
 50 55 60

Ala Leu Leu Asn Pro Asn Asn Thr Ile Phe Pro Thr Thr Ser Trp Thr
 65 70 75 80

Asp Tyr Lys His Ser Arg Pro Gn Ala Ser Ser Pro Arg Ala Pro Ser
 85 90 95

Ser Gn Thr Pro Thr Asp Ile Val Ser Ala Ala Ala Leu Ala Leu Val
 100 105 110

Leu Val Ile Asp Gly Gly Leu Ala Gu Leu Val Ala Ser Val Thr Gu
 115 120 125

Ile Asp Leu Gly Ala Leu Ser Thr Ile Ser Thr Val Arg Gn Leu Met
 130 135 140

Ala Ser Tyr Leu Gly Leu Thr Thr Leu Thr Ala Gu Gn Gu Lys Val
 145 150 155 160

Val Phe Ser Ser Ser Tyr Val Pro Ser Gu Lys Asn Leu Leu Gu His
 165 170 175

Val Lys Gn Gu Lys Ala Ala Gu Ile Gn Ala Lys Gn Gu Gu Ile
 180 185 190

Lys Ala Val Leu Gu Ala Lys Gy Val Ser Thr Gu Gu Ile Gu Ala
 195 200 205

Ile Leu Lys Gu Tyr Pro Asp Ile Tyr Ala Ala Asp Phe Phe Lys Gu
 210 215 220

Phe Ile Gu Gu Pro Leu His Thr Tyr Arg Ala Lys Val Gly Ala Pro
 225 230 235 240

Ile Gn Gu Met Asn Gu Asn Ala Ile Gn Leu Leu Pro Thr Pro Pro
 245 250 255

Ala Ile Thr Pro Asp Asn Val Asn Gu Val Asn Gy Met Asn Thr Leu
 260 265 270

Ser Thr Ile Leu Gn Ala Ile Asp Asp Ala Ile Lys Gn Ala Pro Ala
 275 280 285

Leu Gly Gly Asp Gln Gu Ile Ile Thr Ile Leu Gln Thr Leu Val Pro
 290 295 300

Leu Val Asp Lys Thr Thr Phe Thr Lys Ala Gu Phe Asp Leu Ile Tyr
 305 310 315

Thr Ala Thr Gln Leu Pro Asn Thr Ala Ser Leu Lys Leu Tyr Leu Thr
 325 330

Asp Arg Gln Ile Ala Gu Tyr Arg Gly Lys Ile Thr Lys Val Tyr Gln
 340 345

Asn Ser Ile Gln Asn Leu Ser Gu Thr Lys Arg Val Val Gu Asn Asn
 355 360 365

Arg Ser Met Leu Gu Thr Gln Leu Ser Met Phe Gln Gln Ala Gln Asn
 370

Cys Phe Val Thr Trp Ile Ser Gln Ala Asn Ala Leu Asn Ile Ala Ile
 385 390 395 400

Thr Asn Lys Tyr Ile Ser Ala Val Leu Thr Thr Ser Met Gu Met Tyr
 405 410 415

Gly Gly Leu Leu Cys Leu Ser Tyr Met Tyr Gu Arg Leu Ala Asp Asp
 420 425 430

Gu Lys Ala Ile Phe Asp Lys Ser Val Asn Gu Tyr Leu Pro Ile His
 435 440 445

Ile Val Val Gly Gly Ser Trp Val Asn Gly Trp Ile Ala Lys Met Ala
 450 455 460

Ala Tyr Gln Gu Leu Ala Gu Tyr Ser Leu Gly Thr Ala Val Thr Ser
 465 470 475 480

Gln Asp Gln Ile Lys Ala Tyr Leu Gln Thr Arg Gly Asn Gu Phe Lys
 485 490 495

Ala Thr Arg His Phe Phe His Asn Ile Gly Asp Gln Met Tyr Gln Phe
 500 505 510

Ala Asn Gu Thr Val Phe Gly Asn Cys Leu Thr Thr Ala Asn Gly Ala
 515 520 525

Ile Gln Pro Asp Leu Gly Gly Phe Ile Arg Gu Ala Met Thr Asn Val
 530 535 540

Gly Thr Val Gu Ala Asp Tyr Val Ser Asn Ala Gln Arg Ile Leu Asn
 545 550 555 560

Gu Phe Asn Thr Ala Ala Thr Ala His Val Leu Gln Leu Gln Leu Gln

I l e A l a G l u L e u G l n L y s L y s A l a A s p A s p L e u A s p P r o G l y L y s A l a
 580 585 590
 S e r P h e T h r G l u A s n A r g L y s P h e A l a V a l A l a A l a T r p I l e T h r S e r
 595 600 605
 G l u S e r L e u G l y A s p A l a L e u I l e S e r M e t I l e L e u A s n S e r G l n L e u
 610 615 620
 P r o L y s G l n G l u A l a P h e L e u L y s P r o L e u I l e G l u G l u I l e A s n P h e
 625 630 635
 A s n A s n L e u A l a A l a A s n A l a L e u A s n S e r L e u L e u G l n I l e T h r A s n
 645 650 655
 G l u P h e S e r T h r T h r S e r V a l T y r T y r S e r L e u S e r S e r T y r L e u V a l
 660 665 670
 G l n S e r L y s T h r G l y G l n A s n L e u P h e A l a G l y A s p T y r T y r G l u T h r
 675 680 685
 L e u L e u A l a A l a A l a A r g G l u A r g G l u T y r I l e T y r A r g A s p T h r A l a
 690 695 700
 A r g C y s L y s G l n A l a I l e A s n L e u V a l A s n G l y L e u L e u G l n L y s I l e
 705 710 715 720
 A s n S e r L e u P r o G l y A l a T h r S e r A l a G l n L y s G l n G l u M e t L e u A s n
 725 730 735
 A l a T h r T h r T y r T y r G l n T y r S e r L e u S e r V a l T h r L e u A s n G l n L e u
 740 745 750
 T h r V a l L e u G l u S e r L e u L e u A l a G l y L e u L y s M e t T h r L e u G l n T h r
 755 760 765
 T h r S e r A s n A s n L y s T y r A s p L y s S e r V a l P h e L y s I l e G l u S e r P h e
 770 775 780
 A s p A s p T r p I l e P r o T h r L e u A l a A l a L e u G l u S e r P h e L e u T h r S e r
 785 790 795 800
 G l y P h e P r o A s n I l e S e r A l a T h r G l y G l y L e u G l y P r o L e u P h e T h r
 805 810 815
 G l n V a l G l n S e r A s p G l n G l n T h r T y r T h r S e r G l n G l y G l n T h r G l n
 820 825 830
 G l n L e u A s n L e u G l n A s n G l n M e t T h r T h r I l e G l n G l n G l u T r p T h r
 835 840 845

eol f - seq| . app

Leu Val Ser Thr Ser Met G n Val Leu Asn Gly Ile Leu Ser G n Leu
850 855 860

Al a Gly Al a Ile Tyr Ser Asn
865 870

<210> 100
<211> 811
<212> PRT
<213> Chl amydi a pneumoni ae
<400> 100

His Ser Phe Al a G n Arg His Arg G u Ser Leu G u His Ile Al a Asn
1 5 10 15

Tyr G u Lys Thr Thr Al a G u Arg Asp Ile Leu Lys Arg Leu Ile G u
20 25 30

Val Leu Asp G n Arg Al a Ser G u Arg Tyr Arg Ser Al a Val G u Lys
35 40 45

Leu His Lys Tyr G u Val G u Arg Al a Thr Val Al a Lys Ser Ile Pro
50 55 60

Val Al a Al a Ile His G u Lys Pro Leu Ser Ser Thr His Al a Ser Val
65 70 75 80

G n Val Thr Al a Ser Thr Pro Al a Al a Thr Gly Ser Gly Val Gly Al a
85 90 95

Tyr Tyr Asn Al a Val Lys G n Lys Trp Al a G n Asp Leu Ile Val G u
100 105 110

Leu Asn Thr Val Met Thr Thr Ile Met Al a Ser Val Asn Ser Lys Asn
115 120 125

Pro Al a Asn Lys Asp Val Phe Asp Lys Leu Asn Thr G u Leu G n Al a
130 135 140

Leu Val Al a Al a Gly Asn Asn Leu Thr G u G u Asn Phe G n Thr Leu
145 150 155 160

Tyr Asn Phe Pro G u G u Ile Phe Thr Al a Ile G n Arg Al a Asp Thr
165 170 175

Phe Thr Gly Gly Met Lys Thr Asp Phe Thr Asn G n Leu Al a Gly Lys
180 185 190

Tyr Gly Asn G n Al a Thr Leu Thr G n Thr Phe Al a Asp Gly Arg Val
195 200 205

G u G y Phe Lys Asp Ile Leu Thr Ala Val G n G y Val Leu Thr Pro
 210 215 220

G u G n Phe Thr Ile Phe Ala G u Ile Ala Thr G u Leu G n Ala Leu
 225 230 235 240

Ala Asp His Val G y Asn Phe Asp G u Ala G y Leu G n Arg Ile G u
 245 250 255

Asp Ala G y G u Lys Leu Ala Ala Val Ile Asn Ser Ser Asp Leu Thr
 260 265 270

Arg Asn Asp Lys Ile Met Phe Cys G n His Ile Thr Asp Leu Tyr Ser
 275 280 285

Asp G n Val Ala Ala Leu G y Ser Phe Asp Thr Val Leu Asp Ala Ser
 290 295 300

Ile Tyr Val Asn G n His G n G y Thr Met Phe Ser Asn Leu Ser Ser
 305 310 315 320

Phe Val G y Ser Leu Ile G y Thr Phe Ala Pro Ile Asp Leu Ser Ser
 325 330 335

Ser G n G y Asp Ile Ser Ser Ala Ala Leu Ala G y Ala Leu G n Thr
 340 345 350

Ala Arg G y Leu Asn Ser Arg Phe Asn G u Leu Thr Ala G u G n G n
 355 360 365

Lys Leu Ile Asn G u Cys Ile Lys Ser Leu Val Thr Phe Lys Cys G y
 370 375 380

G u His Leu G y Ala Ile Trp Ala Tyr Phe Thr Ala Ser Thr Val Val
 385 390 395 400

Ala Leu Asn Pro Thr Ala Thr Met Asp His Val Lys Ala Ala Ile Leu
 405 410 415

G u G u Ala Lys G u Leu Asp Asn Ser Ser Phe G n Leu Ala Ser Ser
 420 425 430

Ile Lys Ser Ala Met Thr Ser Ile Val Asn Ser Ser G y Ser Phe Ser
 435 440 445

Val Thr Val Asn Ser Ser Thr Leu G n Tyr Thr Ile Tyr Ser G u Lys
 450 455 460

Asn G y Lys Val G u Ile Asn G n Ile Leu Leu Asn Tyr G y Ser Thr
 465 470 475 480

G y Phe Leu Pro G u Ile Thr Lys Leu Ala Lys Thr Asn Ala G u Ser

Thr Ala Arg Ser Tyr Phe Arg Phe Lys Ala Leu Ala Ala Val Gu Ser
 500 505 510

Gu Asn Val Gn Asn Lys Ile Gu Asp Leu Gn Ser Gn Leu Gn Gn
 515 520 525

Phe Thr Asn Met Lys Thr Gu Leu Phe Asp Gy Gn Leu Leu Ser Gn
 530 535 540

Ala Ser Gu Leu Arg Ala Leu Pro Leu Pro Ser Ala Val Ala Ser Val
 545 550 555 560 565

Leu Ile Asp Arg Tyr Met Pro Lys Gu Val Asp Tyr Leu Asn Gu Ile
 565 570 575

Tyr Lys Lys Leu Tyr Tyr Ser Asn Leu Gy Ser Ser Val Gy Asn Ser
 580 585 590

Ile Ile Asp Ala Ile Ser Gn Tyr Val Asn Gy Ala Thr Tyr Phe Asn
 595 600 605

Phe Ala Ser Tyr Val Gy Gn Gn Pro Ala Val Gy Ala Gy Gy Ala
 610 615 620

Asn Ala Phe Pro Gy Ser Gn Gu Ser Ala Gn Ala Lys Leu Asp Gn
 625 630 635 640

Gu Arg Lys Gn Ala Ala Leu Tyr Leu Gn Gu Thr Arg Gy Ala Leu
 645 650 655

Thr Val Ile Gu Gu Gn Arg Ala Arg Val Leu Lys Asp Asp Lys Ile
 660 665 670

Thr Asn Gu Gn Arg Ser Thr Ile Leu Asp Ser Leu Arg Asn Tyr Gu
 675 680 685

Asp Asn Ile Asn Ser Ile Ser Gy Ser Leu Val Leu Leu Gn Asn Tyr
 690 695 700

Leu Gn Pro Leu Ser Ile Ala Gy Gy Ser Val Ala Gy Thr Phe Gu
 705 710 715 720

Val Lys Gu Gy Gn Gu Gn Trp Gn Ala Arg Leu Gn Ile Leu Gu
 725 730 735

Gu Ala Leu Val Ser Gy Leu Val Gy Asn Met Ile Asn Gy Gy Met
 740 745 750

Phe Pro Leu Gn Ser Thr Ile Gn Ser Asp Gn Gn Ser Phe Ala Asp
 755 760 765

Met Gly Gln Asn Phe Gln Leu Asp Leu Gln Met His Leu Thr Ser Met
770 775 780

Gln Gln Glu Trp Thr Val Val Ala Thr Ser Leu Gln Leu Leu Asn Gln
785 790 795 800

Met Tyr Leu Ser Leu Ala Arg Ser Leu Thr Gly
805 810

<210> 101
<211> 513
<212> PRT
<213> Chl amydi a pneumoni ae
<400> 101

Lys Arg Pro Lys Lys Phe Pro Ile Tyr Leu Ser Ile Ala Gln Lys Thr
1 5 10 15

Asn Arg Leu Leu Ser Gly Ile Val Ile Ala Phe Ala Val Ile Ala Leu
20 25 30

Arg Leu Trp Tyr Leu Ala Val Val Gu His Gu Gln Lys Leu Gu Gu
35 40 45

Ala Tyr Lys Pro Gln Ile Arg Val Leu Pro Gln Tyr Val Gu Arg Ala
50 55 60

Thr Ile Cys Asp Arg Phe Gly Lys Thr Leu Ala Val Asn Gln Leu Gln
65 70 75 80

Tyr Asp Val Ser Val Ala Tyr Gly Ala Ile Arg Asp Leu Pro Thr Arg
85 90 95

Ala Trp Arg Val Asp Gu His Gly His Lys Gln Leu Ile Pro Val Arg
100 105 110

Lys His Tyr Ile Met Cys Leu Ser Gu Leu Leu Ser Gln Gu Leu His
115 120 125

Leu Asp Arg Gu Ala Ile Gu Asp Ala Ile His Ala Lys Ala Ser Val
130 135 140

Leu Gly Ser Val Pro Tyr Leu Val Ala Ala Asn Val Ser Gu Arg Thr
145 150 155 160

Tyr Leu Lys Leu Lys Met Leu Ser Lys Asp Trp Pro Gly Leu His Val
165 170 175

Gu Ala Val Val Arg Arg His Tyr Pro Gln Gu Ser Val Ala Ser Asp
180 185 190

Ile Leu Gly Tyr Val Gly Pro Ile Ser Leu Gln Gu Tyr Lys Arg Val
 195 200 205

Thr Gln Gu Leu Ser Gln Leu Arg Gu Cys Val Arg Ala Tyr Gu Gu
 210 215 220

Gly Gu Asp Pro Lys Leu Pro Gu Gly Leu Ala Ser Ile Asp Gln Val
 225 230 235

Arg Ala Leu Leu Gu Ser Val Gu Ser Asn Ala Tyr Ser Leu Asn Ala
 245 250 255

Leu Val Gly Lys Met Gly Val Gu Ala Cys Trp Asp Ser Lys Leu Arg
 260 265 270

Gly Lys Ile Gly Lys Lys Pro Ile Leu Val Asp Arg Arg Gly Asn Phe
 275 280 285

Ile Gln Gu Met Gu Gly Ala Val Pro Gu Ala Pro Gly Thr Lys Leu
 290 295 300

Gln Leu Thr Leu Ser Ala Gu Leu Gln Ala Tyr Ala Asp Ala Leu Leu
 305 310 315 320

Leu Gu Tyr Gu Lys Thr Gu Thr Phe Arg Ser Ala Lys Ser Leu Lys
 325 330 335

Lys Arg Gu Lys Leu Pro Pro Leu Phe Pro Trp Ile Lys Gly Gly Ala
 340 345 350

Ile Ile Ala Leu Asp Pro Asn Asn Gly Gu Ile Leu Ala Met Ala Ser
 355 360 365

Ser Pro Arg Tyr Arg Asn Asn Asp Phe Val Asn Ala Lys Val Ala Gu
 370 375 380

Asp Ser Lys Ala Val Arg Ser Ser Ile Tyr Arg Trp Leu Gu Asn Lys
 385 390 395 400

Gu His Ile Ala Gu Ile Tyr Asp Arg Lys Val Pro Leu Ile Arg Gu
 405 410 415

Arg Arg Asn Pro Leu Thr Gly Leu Cys Tyr Gu Gu Ile Leu Pro Leu
 420 425 430

Thr Phe Asp Cys Phe Leu Asp Phe Leu Phe Pro Gu Asn Ser Val Ile
 435 440 445

Lys Leu Gln Leu Lys Arg Asn Ser Phe Val Gly Gln Ala Ile Gu Val
 450 455 460

Gln Asn Leu Val Thr Arg Leu Leu Ser Leu Phe Pro Tyr Gu Gu Gly

465 470 480

Thr Oys Pro Oys Ser Ala Ile Phe Asp Ala Val Phe Pro Asn Glu Glu
485 490 495

Gly His Ile Leu Ile Gn Gu Val Ile Ser Leu Arg Glu Gn Lys Trp
500 505 510

Ile

<210> 102
<211> 575
<212> PRT
<213> Chl amydi a pneumoni ae
<400> 102

Glu Oys Leu Asn Gn His Lys Ala Asp Ile Gu Gu Leu Lys Glu Ala
1 5 10 15

Leu Asp Gn Val Phe Asn Gu Leu Pro Ala Asn Tyr Asp Lys Ile Leu
20 25 30

Tyr Thr Asp Ile Leu Arg Leu Ile Val Asp Pro Gu Arg Phe Ser Pro
35 40 45

Val Leu Pro Ser Gu Val His Arg Leu Ser Leu Ser Gu Phe Thr Gu
50 55 60

Leu Gn Gly Arg Tyr Val Val Leu Arg Ser Ala Phe Ser Thr Ile Leu
65 70 75 80

Glu Asp Ala Phe Ile Gu Val His Phe Lys Ser Trp Arg Lys Ser Gu
85 90 95

Phe Leu Gn Tyr Leu Ala Ala Lys Arg Gn Gu Gu Ala Leu Arg Lys
100 105 110

Gn Arg Tyr Pro Thr Pro Tyr Val Asp Tyr Leu Gu Gu Gu Lys Thr
115 120 125

Arg Gn Tyr Lys Met Phe Cys Gn Gu His Leu Asp Thr Phe Leu Ala
130 135 140

Tyr Leu Phe Ser Lys Thr Pro Tyr Lys Gu Gly Leu Gu Pro Tyr Tyr
145 150 155 160

Asp Ile Leu Asp Leu Trp Ile Asn Gu Leu Asp Asn Gly Ala His Arg
165 170 175

Ala Leu Ser Trp Asn Gu His Tyr Leu Phe Leu Lys Gu Arg Val Ser
180 185 190

eol f - seq1 . app

His Leu Ser 195 Gu His Leu Pro Ala 200 Leu Phe Ser Thr Phe 205 Arg Gu Phe
 Asn Gu 210 Leu Gn Arg Pro Leu 215 Leu Gy Lys Tyr Pro 220 Ile Ser Ile Val
 Arg 225 Asn Lys Arg Gn Thr 230 Gu Gn Asp Leu Ala 235 Ala Ser Phe Tyr Pro 240
 Val Tyr Gy Tyr Gy 245 Tyr Leu Arg Pro His 250 Ala Tyr Gy Gn Ala 255 Ala
 Thr Leu Gy Ser 260 Ile Phe Lys Leu Val 265 Ser Ala Tyr Ser Val 270 Leu Ser
 Gn Arg Ile 275 Leu Trp Gy His Asn 280 Gu Gu Pro Ala Asn 285 Pro Leu Val
 Ile Ile 290 Asp Lys Asn Ser Phe 295 Gy Tyr Arg Ser Ser 300 Lys Pro His Val
 Gy 305 Phe Phe Lys Asp Gy 310 Thr Pro Ile Pro Thr 315 Phe Phe Arg Gy Gy 320
 Ser Leu Pro Gy Asn 325 Asp Phe Met Gy Arg 330 Gy Phe Ile Asp Leu Val 335
 Ser Ala Leu Gu 340 Met Ser Ser Asn Pro 345 Tyr Phe Ser Leu Leu 350 Val Gy
 Gu Gy Leu 355 Gy Asp Pro Gu Asp 360 Leu Ala Asp Ala 365 Ala Ser Leu Phe
 Gy Phe 370 Gy Gu Lys Thr Gy 375 Leu Gy Leu Pro Gy 380 Gu Tyr Ala Gy
 Arg 385 Val Pro His Asp Leu 390 Ala Tyr Asn Arg Ser 395 Gy Leu Tyr Ala Thr 400
 Ala Ile Gy Gn His 405 Thr Leu Val Val Thr 410 Pro Leu Gn Thr Ala Val 415
 Met Leu Ala Ser 420 Leu Val Asn Gy Gy 425 Val Val Tyr Val Pro 430 Lys Leu
 Leu Leu Gy 435 Gu Trp Gu Gy Gu 440 His Val Ser Tyr Leu Ser Ser Lys 445
 Lys Lys 450 Arg Thr Ile Phe Met 455 Pro Asp Ala Val Val 460 Gu Val Leu Lys

Thr Gly Met Arg Asn Val Ile Trp Gly Gln Tyr Gly Thr Ala Arg Ala
465 470 475 480

Ile Gln Ser Gln Phe Pro Pro Gln Leu Leu Ser Arg Ile Ile Gly Lys
485 490 495

Thr Ser Thr Ala Gu Ser Ile Met Arg Val Gly Leu Asp Arg Gu Tyr
500 505 510 515

Gly Thr Met Lys Met Lys Asp Ile Trp Phe Ala Ala Val Gly Phe Ser
515 520 525

Asp Gln Asp Leu Ser Leu Pro Thr Ile Val Val Ile Val Tyr Leu Arg
530 535 540

Leu Gly Gu Phe Gly Arg Asp Ala Ala Pro Met Ala Val Lys Met Ile
545 550 555 560

Asp Met Trp Gu Lys Ile Gln Gln Arg Gu Ser Phe Leu Arg Gly
565 570 575

<210> 103
<211> 406
<212> PRT
<213> Chlamydia pneumoniae
<400> 103

Val Lys Asn Leu Lys Gu Asp Phe Pro Ile Phe Ala Ala Lys Ala Lys
1 5 10 15

Gu Asn Gu Pro Phe Ile Tyr Leu Asp Ser Ala Ala Thr Thr Gln Lys
20 25 30

Pro Gln Gln Val Ile Asp Ala Val Ala Asn Phe Tyr Thr Ser Ser Tyr
35 40 45

Ala Thr Val Asn Arg Ala Ile Tyr Ser Ser Ser Arg Asn Val Thr Gu
50 55 60

Ala Tyr Ala Ala Val Arg Gu Lys Val Arg Lys Trp Val Ser Ala Ala
65 70 75 80

Ser Asp Ser Gu Ile Val Phe Thr Arg Gly Thr Thr Ala Gly Leu Asn
85 90 95

Leu Leu Ala Ile Ser Val Asn Asp Leu Trp Ile Pro Lys Gly Gly Val
100 105 110

Val Leu Val Ser Gu Ala Gu His His Ala Asn Val Leu Ser Trp Gu
115 120 125

Ile Ala Cys Arg Arg Arg Gly Ser Leu Val Lys Lys Ile Arg Val His
130 135 140

eol f - seq | . app

Asp Ser Gly Leu Ile Asp Leu Asp Asp Leu Gu Lys Leu Leu Asn Gu
 145 150 155 160
 Gly Ala Gln Phe Val Ser Ile Pro His Val Ser Asn Val Thr Gly Cys
 165 170 175
 Val Gln Pro Leu Gln Gln Val Ala Gu Leu Val His Arg Tyr Asp Ala
 180 185 190
 Tyr Leu Ala Val Asp Gly Ala Gln Gly Ala Pro His Leu Pro Ile Asp
 195 200 205
 Val Gln Leu Trp Asp Val Asp Phe Tyr Val Phe Ser Ser His Lys Ile
 210 215 220
 Tyr Gly Pro Thr Gly Ile Gly Val Leu Tyr Gly Lys Lys Asp Leu Leu
 225 230 235 240
 Asp Gln Leu Pro Pro Val Gu Gly Gly Gly Asp Met Val Ala Ile Tyr
 245 250 255
 Asp His Gln Asn Pro Gu Tyr Leu Pro Ala Pro Met Lys Phe Gu Ala
 260 265 270
 Gly Thr Pro Asn Ile Ala Gly Val Leu Gly Leu Gly Ala Ala Leu Asp
 275 280 285
 Tyr Leu Asp Gly Leu Ser Ala Lys Phe Ile Tyr Asp Lys Gu Ile Ala
 290 295 300
 Leu Thr Thr Tyr Leu His Lys Gu Leu Leu Gu Ile Pro Gly Val Gu
 305 310 315 320
 Ile Leu Gly Pro Ser Ile Gu Gu Pro Arg Gly Ala Leu Ile Gly Met
 325 330 335
 Thr Ile Asp Gly Ala His Pro Leu Asp Leu Gly Phe Leu Leu Asp Leu
 340 345 350
 Arg Gly Ile Ala Val Arg Thr Gly His Gln Cys Ala Gln Pro Ala Met
 355 360 365
 Gu Arg Trp Asn Val Gly His Val Leu Arg Val Ser Leu Gly Ile Tyr
 370 375 380
 Asn Asp Gu Asp Asp Ile Asp Gln Phe Ile Leu Val Leu Gln Asp Ser
 385 390 395 400
 Leu Asp Lys Ile Arg Arg
 405

eol f - seq| . app

<210> 104
 <211> 251
 <212> PRT
 <213> Chl amydi a pneumoni ae

<400> 104

Leu Ile Val Leu Ala Phe Arg Gln Val Phe Phe Ser His Ser Arg Ser
 1 5 10 15

Gln Leu Asp Arg Leu Lys Asn Tyr Leu Arg Leu Leu Lys Gln Asn Phe
 20 25 30

Ala Ile Thr Leu Pro Lys Gu Arg Thr Ser Lys Gly His Ser Leu Met
 35 40 45

Leu Thr Phe Asp Phe Ala Ser Phe Asp Phe Tyr Thr Asn Ile Phe Pro
 50 55 60

Phe Leu Gu Gu Gln Lys Ile Pro Ala Val Val Gly Val Ala Ser Arg
 65 70 75 80

Tyr Ile Pro Ser Asn Ala Ala Gln Asp Leu His Pro Ser His Arg Leu
 85 90 95

Lys Pro Ser Gu Thr Leu Ala Phe Gln Asp Gu Ile Phe Ser Asn Tyr
 100 105 110

Met Pro Phe Cys Cys Gln Asn Gu Leu Ile Gu Met Ala Lys Ser Pro
 115 120 125

Tyr Ile Gln Leu Ala Ser Ser Gly Phe Ala Ile Arg Asn Leu Met Asn
 130 135 140

Asn Pro Pro Tyr Leu Thr Thr Gu Ile Leu Leu Ser Arg His His Ile
 145 150 155 160

Gu Thr Ile Thr Gly Ala Lys Pro Leu Ala Phe Leu Phe Pro Phe Gly
 165 170 175

Lys Ser Asp Pro Thr Ser Arg Lys Leu Ala Ala Asp His Tyr Pro Tyr
 180 185 190

Ser Phe Leu Leu Gly Asn Thr Ile Asn Arg Lys Leu Lys Thr His Asn
 195 200 205

Ile Tyr Arg Leu Asp Ile Lys Pro Met Gln Tyr Val Cys Pro Ser Leu
 210 215 220

Phe Gln Ser Ser Arg Tyr Leu Lys Asn Trp Ile Lys Gu Lys Ser Lys
 225 230 235 240

Gln Leu Tyr Leu Lys Lys Gln Leu Pro Lys Arg
 Page 90

<210> 105
 <211> 323
 <212> PRT
 <213> Chl amydi a pneumoni ae

<400> 105

Thr Thr Asn Phe Pro G n Pro Leu Ile G n Ala Thr Ser Leu Thr Lys
 1 5 10 15

Hi s Tyr Tyr Lys Arg Ser Phe Trp Phe G n Gly Lys Thr Ile Ala Ser
 20 25 30

Arg Pro Val Asp Asp Val Ser Phe Ser Leu Tyr Ser Arg Arg Ala Val
 35 40 45

Gly Leu Ile Gly Gu Ser Gly Ser Gly Lys Ser Thr Leu Ala Leu Ala
 50 55 60

Leu Ala Gly Leu Leu Pro Leu Thr Ser Gly Phe Leu Thr Phe Asn Gly
 65 70 75 80

Thr Pro Ile Lys Leu Hi s Ser Lys Hi s Gly Arg Hi s G n Leu Arg Ser
 85 90 95

G n Val Arg Leu Val Phe G n Asn Pro G n Ala Ser Leu Asn Pro Arg
 100 105 110

Lys Thr Ile Leu Asp Ser Leu Gly Hi s Ser Leu Leu Tyr Hi s Lys Leu
 115 120 125

Val Pro Lys Gu Lys Val Leu Ala Thr Val Arg Gu Tyr Leu Gu Leu
 130 135 140

Val Gly Leu Ser Gu Gu Tyr Phe Tyr Arg Tyr Pro Hi s G n Leu Ser
 145 150 155 160

Gly Gly G n G n G n Arg Val Ser Ile Ala Arg Ala Leu Leu Gly Val
 165 170 175

Pro G n Leu Ile Ile Cys Asp Gu Ile Val Ser Ala Leu Asp Leu Ser
 180 185 190

Ile G n Ala G n Ile Leu Asn Met Leu Ala Gu Leu G n Lys Lys Leu
 195 200 205

Ser Leu Thr Tyr Leu Phe Ile Ser Hi s Asp Leu Ala Val Val Arg Ser
 210 215 220

Phe Cys Thr Gu Val Phe Ile Met Tyr Lys Gly G n Ile Val Gu Lys
 225 230 235 240

eol f - seq| . app

Gly Asn Thr Lys Arg Ile Phe Ser Asp Pro Gln His Pro Tyr Thr Arg
245 250 255

Met Leu Leu Asn Ala Gln Leu Pro Glu Thr Pro Asp Gln Arg Gln Ser
260 265 270

Lys Pro Ile Phe Gln Glu Tyr His Lys Asp Ser Glu Glu Ser Cys Ser
275 280 285

Thr Gly Cys Tyr Phe Tyr Asn Arg Cys Pro Gln Lys Gln Glu Ala Cys
290 295 300

Lys Ser Glu Ile Ile Pro Asn Gln Gly Asp Ala His His Thr Tyr Arg
305 310 315 320

Cys Ile His

- <210> 106
- <211> 234
- <212> PRT
- <213> Chl amydi a pneumoni ae

<400> 106

Pro Thr Thr Asn Cys Ile Phe Leu Asp Leu Arg Gly His Ser Ile Leu
1 5 10 15

His Gln Leu Gln Ile Glu Glu Ala Leu Leu Arg Val Ala Asn Gln Asn
20 25 30

Phe Cys Ile Ile Asn Ser Gly Ala Lys Asp Ser Ile Val Leu Gly Ile
35 40 45

Ser Arg Asn Leu Asn Gln Asp Val His Ile Ser Arg Ala Gln Ala Asp
50 55 60

His Ile Pro Ile Ile Arg Arg Tyr Ser Gly Gly Gly Thr Val Phe Ile
65 70 75 80

Asp Ser Asn Thr Leu Met Val Ser Trp Ile Met Asn Ser Ser Glu Ala
85 90 95

Ser Ala Gln Pro Gln Glu Leu Leu Ala Trp Thr Tyr Gly Ile Tyr Ser
100 105 110

Pro Leu Leu Pro Asn Thr Phe Ser Ile Arg Glu Asn Asp Tyr Val Leu
115 120 125

Gly His Lys Lys Ile Gly Gly Asn Ala Gln Tyr Ile Gln Arg His Arg
130 135 140

Trp Val His His Thr Thr Phe Leu Trp Asp Ile Asp Leu Asp Lys Leu

145 150 160

Ser Tyr Tyr Leu Pro Ile Pro G n G n G n Pro Thr Tyr Arg Asn G n
165 170 175

Arg Ser His Gl u Gl u Phe Leu Thr Thr Leu Arg Pro Trp Phe Pro Ser
180 185 190

Arg Asp Asp Phe Leu Gl u Arg Ile Lys Ala Ser Gly Ser Leu Leu Phe
195 200 205

Thr Trp Gl u Gl u Phe Leu Asp Asn Gl u Leu Gl u Gl u Ile Leu Ala G n
210 215 220

Pro His Arg Lys Ala Thr Thr Val Leu Asn
225 230

<210> 107
<211> 791
<212> PRT
<213> Chl amydi a pneumni ae

<400> 107

Arg Ile Pro Ile Thr Leu Leu G n Thr Tyr Phe Ser Gl u Pro Leu Ser
1 5 10 15

Thr Lys Gl u Ile Leu Gl u Ala Cys Asp His Ile Gly Ile Gl u Ala Gl u
20 25 30

Ile Gl u Asn Thr Thr Leu Tyr Ser Phe Ala Ser Val Ile Thr Ala Lys
35 40 45

Ile Leu His Thr Ile Pro His Pro Asn Ala Asp Lys Leu Arg Val Ala
50 55 60

Thr Leu Thr Asp Gly Gl u Lys Gl u His G n Val Val Cys Gly Ala Pro
65 70 75 80

Asn Cys Gl u Ala Gly Leu Ile Val Ala Leu Ala Leu Pro Gly Ala Lys
85 90 95

Leu Phe Asp Ser Gl u Gly G n Ala Tyr Thr Ile Lys Lys Ser Lys Leu
100 105 110

Arg Gly Val Gl u Ser G n Gly Met Cys Cys Gly Ala Asp Gl u Leu Gly
115 120 125

Leu Asp Gl u Leu G n Ile G n Gl u Arg Ala Leu Leu Gl u Leu Pro Gl u
130 135 140

Ala Thr Pro Leu Gly Gl u Asp Leu Ala Thr Val Leu Gly Asn Thr Ser
145 150 155 160

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Leu G u I l l e Ser Leu Thr Pro Asn Leu G y H i s C y s A l a Ser P h e Leu
165 170 175

G y Leu A l a A r g G u I l l e C y s H i s V a l Thr G n A l a Asn Leu V a l I l l e
180 185 190

Pro L y s G u P h e Ser P h e G u A s n Leu Pro Thr Thr A l a Leu Asp M e t
195 200 205

G y A s n Asp Pro Asp I l l e C y s Pro P h e P h e Ser T y r V a l V a l I l l e Thr
210 215 220

G y I l l e Ser A l a G n Pro Ser Pro I l l e L y s Leu G n G u Ser Leu G n
225 230 235 240

A l a Leu L y s G n L y s Pro I l l e A s n A l a I l l e V a l Asp I l l e Thr A s n T y r
245 250 255

I l l e M e t Leu Ser Leu G y G n Pro Leu H i s A l a T y r Asp A l a Ser H i s
260 265 270

V a l A l a Leu Asp Ser Leu A r g V a l G u L y s Leu Ser Thr Pro G u Ser
275 280 285

Leu Thr Leu Leu A s n G y G u Thr V a l Leu Leu Pro Ser G y V a l Pro
290 295 300

V a l V a l A r g Asp Asp H i s Ser Leu Leu G y Leu G y G y V a l M e t G y
305 310 315 320

A l a L y s A l a Pro Ser P h e G n G u Thr Thr Thr Thr V a l I l l e L y s
325 330 335

A l a A l a T y r P h e Leu Pro G u A l a Leu A r g A l a Ser G n L y s Leu Leu
340 345 350

Pro I l l e Pro Ser G u Ser A l a T y r A r g P h e Thr A r g G y I l l e Asp Pro
355 360 365

G n A s n V a l V a l Pro A l a Leu G n A l a A l a I l l e H i s T y r I l l e Leu G u
370 375 380

I l l e P h e Pro G u A l a Thr I l l e Ser Pro I l l e T y r Ser Ser G y G u I l l e
385 390 395 400

C y s A r g G u Leu L y s G u V a l A l a Leu A r g Pro L y s Thr Leu G n A r g
405 410 415

I l l e Leu G y L y s Ser P h e Ser I l l e G u I l l e Leu Ser G n L y s Leu G n
420 425 430

Ser Leu Gly Phe Ser Thr Thr Pro 440 G n G u Thr Ser Leu Leu Val Lys
 435 445

Val Pro Ser Tyr Arg His Asp Ile Asn G u G u Ile Asp Leu Val G u
 450 455 460

G u Ile Oys Arg Thr G u Ser Trp Asn Ile G u Thr G n Asn Pro Val
 465 470 475 480

Ser Oys Tyr Thr Pro Ile Tyr Lys Leu Lys Arg G u Thr Ala Gly Phe
 485 490 495

Leu Ala Asn Ala Gly Leu G n G u Phe Phe Thr Pro Asp Leu Leu Asp
 500 505

Pro G u Thr Val Ala Leu Thr Arg Lys G u Lys G u G u Ile Ser Leu
 515 520 525

G n Gly Ser Lys His Thr Thr Val Leu Arg Ser Ser Leu Leu Pro Gly
 530 535 540

Leu Leu Lys Ser Ala Ala Thr Asn Leu Asn Arg G n Ala Pro Ser Val
 545 550 555 560

G n Ala Phe G u Ile Gly Thr Val Tyr Ala Lys His Gly G u G n Oys
 565 570 575

G n G u Thr G n Thr Leu Ala Ile Leu Leu Thr G u Asp Gly G u Ser
 580 585 590

Arg Ser Trp Leu Pro Lys Pro Ser Leu Ser Phe Tyr Ser Leu Lys Gly
 595 600 605

Trp Val G u Arg Leu Leu Tyr His His His Leu Ser Ile Asp Ala Leu
 610 615 620

Thr Leu G u Ser Ser Ala Leu Oys G u Phe His Pro Tyr G n G n Gly
 625 630 635 640

Val Leu Arg Ile His Lys G n Ser Phe Ala Thr Leu Gly G n Val His
 645 650 655

Pro G u Leu Ala Lys Lys Ala G n Ile Lys His Pro Val Phe Phe Ala
 660 665 670

G u Leu Asn Leu Asp Leu Leu Oys Lys Met Leu Lys Lys Thr Thr Lys
 675 680 685

Leu Tyr Lys Pro Tyr Ala Ile Tyr Pro Ser Ser Phe Arg Asp Leu Thr
 690 695 700

Leu Thr Val Pro G u Asp Ile Pro Ala Asn Leu Leu Arg G n Lys Leu

705 710 720

Leu His Glu Gly Ser₇₂₅ Lys Trp Leu Glu Ser₇₃₀ Val Thr Ile Ile Ser₇₃₅ Ile

Tyr Gln Asp Lys₇₄₀ Ser Leu Glu Thr Arg₇₄₅ Asn Lys Asn Val Ser₇₅₀ Leu Arg

Leu Val Phe₇₅₅ Gln Asp Tyr Glu Arg₇₆₀ Thr Leu Ser Asn Gln Asp Ile Glu

Glu Glu Tyr Cys Arg Leu Val₇₇₅ Ala Leu Leu Asn Glu₇₈₀ Leu Leu Thr Asp

Thr Lys Gly Thr Ile Asn Ser₇₉₀

<210> 108
<211> 251
<212> PRT
<213> Chlamydia pneumoniae

<400> 108

Gln Ile Cys Val Thr₅ Gly Val Val Leu Arg₁₀ Ser Arg Pro Leu Gly Lys₁₅

Asn His Thr₂₀ Leu Thr Thr Leu Phe Thr₂₅ Pro Glu Gly Leu Phe₃₀ Thr Phe

Phe Ala Lys₃₅ Gln Gly Gln Thr Leu₄₀ Gln Cys Asp Tyr Arg₄₅ Glu Thr Leu

Val Pro Ile Ser Leu Gly Lys₅₅ Tyr Thr Leu His Arg₆₀ Asn Gly Ser Arg

Leu Pro Lys Leu Thr His₇₀ Gly Asp Ile Leu Asn₇₅ Ala Phe Glu Ala Ile₈₀

Lys Gln Thr Tyr Ala₈₅ Leu Leu Glu Ala Ser₉₀ Gly Lys Met Ile Gln Ala₉₅

Leu Leu Ala Ser₁₀₀ Gln Trp Lys Glu Lys₁₀₅ Pro Ser His Lys Leu₁₁₀ Phe Ser

Leu Phe Leu₁₁₅ Asn Phe Leu His Arg₁₂₀ Ile Pro Glu Ser Ser₁₂₅ Asn Pro Glu

Phe Phe Ala Ala Ile Phe Val₁₃₅ Leu Lys Leu Leu Gln Tyr Glu Gly Ile

Leu Asp Leu Thr Pro Ala₁₅₀ Cys Ser Leu Cys Lys₁₅₅ Ala Ser Leu Pro Tyr₁₆₀

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Al a Cys Tyr Arg Tyr G n G y Hi s Lys Leu Cys Lys Lys Hi s G n Hi s
165 170 175

Lys G n Al a Il e Ser Il e G u Lys G u G u G u G n Il e Leu G n Al a
180 185 190

Il e Il e Hi s Al a Lys G n Phe Ser G u Leu Leu Al a Il e Al a G u Phe
195 200 205

Pro Il e Al a Il e Al a G u Lys Il e Phe Tyr Leu Phe Asp Ser Leu G n
210 215 220

G u G u Lys Lys Ser G u Arg Asn Ser Ser G u Asp Pro Tyr Hi s G u
225 230 235 240

Il e Leu Arg Leu Ser Lys Val Val Hi s Pro Tyr
245 250

<210> 109
<211> 238
<212> PRT
<213> Chl amydi a pneumoni ae

<400> 109

G u G y Leu Al a Phe Arg Tyr G y Ser Lys G y Pro Asn Il e Il e Hi s
1 5 10 15

Asp Val Ser Phe Ser Val Tyr Asp G y Asp Phe Il e G y Il e Il e G y
20 25 30

Pro Asn G y G y G y Lys Ser Thr Leu Thr Met Leu Il e Leu G y Leu
35 40 45

Leu Thr Pro Thr Phe G y Ser Leu Lys Thr Phe Pro Ser Hi s Ser Al a
50 55 60

G y Lys G n Thr Hi s Ser Met Il e G y Trp Val Pro G n Hi s Phe Ser
65 70 75 80

Tyr Asp Pro Cys Phe Pro Il e Ser Val Lys Asp Val Val Leu Ser G y
85 90 95

Arg Leu Ser G n Leu Ser Trp Hi s G y Lys Tyr Lys Lys Lys Asp Phe
100 105 110

G u Al a Val Asp Hi s Al a Leu Asp Leu Val G y Leu Ser Asp Hi s Hi s
115 120 125

Hi s Hi s Cys Phe Al a Hi s Leu Ser G y G y G n Il e G n Arg Val Leu
130 135 140

Leu Al a Arg Al a Leu Al a Ser Tyr Pro G u Il e Leu Il e Leu Asp G u
Page 97

145 150 160

Pro Thr Thr Asn Ile Asp Pro Asp Asn G n G n Arg Ile Leu Ser Ile
165 170 175

Leu Lys Lys Leu Asn Arg Thr Cys Thr Ile Leu Met Val Thr His Asp
180 185 190

Leu His His Thr Thr Asn Tyr Phe Asn Lys Val Phe Tyr Met Asn Lys
195 200 205

Thr Leu Thr Ser Leu Ala Asp Thr Ser Thr Leu Thr Asp G n Phe Cys
210 215 220

Cys His Pro Tyr Lys Asn G n G u Phe Ser Cys Ser Pro His
225 230 235

<210> 110
<211> 392
<212> PRT
<213> Chl amydi a pneumni ae
<400> 110

Ile Phe G u Phe Arg Phe Pro Lys Ile G y G u Thr Ser Ser G y G y
1 5 10 15

Ser Ile Val Arg Trp Leu Lys Asn Leu G y Asp His Val Ala Arg Asp
20 25 30

G u Pro Leu Ile G u Val Ser Thr Asp Lys Ile Ala Thr G u Leu Pro
35 40 45

Ser Pro Lys Ala G y Arg Leu Val Arg Phe Cys Val Asn G u G y Asp
50 55 60

G u Val Ala Ser G y Asp Val Leu G y Leu Ile G u Leu G u G u Ile
65 70 75 80

Ser G u Ala Asp Asp G u Ser Thr Ser Cys Pro Leu Thr Ser Cys G u
85 90 95

Thr Lys Ser G u Ala G y Ser Ser Ser Ser Val Trp Phe Ser Pro
100 105 110

Ala Val Leu Ser Leu Ala G n Arg G u G y Ile G y Leu Asp Asn Leu
115 120 125

G n Lys Ile Ala G y Thr G y Lys G y G y Arg Val Thr Arg G n Asp
130 135 140

Leu G u Ala Tyr Ile Ser G u Ser G n G n Val Ser Ile Pro G u Ile
145 150 155 160

eol f - seq| . app

Phe G n G y G u Val 165 Asn Arg Ile Pro Met 170 Ser Pro Leu Arg Arg Ala 175

Ile Ala Ser Ser 180 Leu Ser Lys Ser Ser 185 Asp G u Val Pro His Ala Ser 190

Leu Val Val 195 Asp Val Asp Val Thr 200 Asp Leu Met Asn Leu Ile Ser G y 205

G u Arg 210 G n Arg Phe Leu Asp 215 Thr His G y Val Lys 220 Leu Thr Ile Thr

Ser 225 Phe Ile Val G n Cys 230 Leu Ala G n Thr Leu 235 Arg G n Phe Pro Leu 240

Leu Asn G y Ser 245 Leu Asp G y Thr Thr Ile 250 Val Met Lys Lys Ser 255 Val

Asn Val G y Val 260 Ala Val Asn Leu Asn 265 Lys G u G y Val Val 270 Val Pro

Val Ile His 275 Asn Cys G n Asp Arg 280 G y Leu Val Ser Ile Ala Lys Ala 285

Leu Ala 290 Asp Leu Ser Ser Arg 295 Ala Arg Leu Asn Lys 300 Leu Asp Pro Ser

G u Val G n Asp G y Ser 310 Val Thr Val Thr Asn 315 Phe G y Met Thr G y 320

Ala Leu Ile G y Met 325 Pro Ile Ile Arg Tyr 330 Pro G u Val Ala Ile Leu 335

G y Ile G y Thr 340 Ile G n Lys Arg Val 345 Val Val Arg Asp Asp 350 Asp Ser

Leu Ala Ile 355 Arg Lys Met Val Tyr 360 Val Thr Leu Thr Phe Asp His Arg 365

Val Leu Asp G y Ile Tyr G y 375 Ser G u Phe Leu Thr 380 Ser Leu Lys Asn

Arg 385 Leu G u Ser Val Thr Met G y 390

<210> 111

<211> 236

<212> PRT

<213> Chl amydi a pneumoni ae

<400> 111

Lys Asn Ser G y Asn Ile Met G u Pro Ser Thr Asn Lys Pro Asp Cys

1 5 15

Lys Lys Ile Phe Asp Ser Ile Ala Ser Lys Tyr Asp Arg Thr Asn Thr
20 25 30

Ile Leu Ser Leu Gly Met His His Phe Trp Asn Arg Ser Leu Ile Gln
35 40 45

Ile Leu Gly Ser Gly Tyr Ser Leu Leu Asp Leu Cys Ala Gly Thr Gly
50 55 60

Lys Val Ala Lys Arg Tyr Ile Ala Ala His Pro Gln Ala Ser Val Thr
65 70 75 80

Leu Val Asp Phe Ser Ser Ala Met Leu Asp Ile Ala Lys Gln His Leu
85 90 95

Pro Gln Gly Ser Cys Ser Phe Ile His Ser Asp Ile Asn Gln Leu Pro
100 105 110

Leu Gu Asn His Ser Tyr Pro Leu Ala Ala Met Ala Tyr Gly Leu Arg
115 120 125

Asn Leu Ser Asp Pro His Lys Ala Leu Gln Gu Ile Ser Arg Val Leu
130 135 140

Met Pro Ser Gly Lys Leu Gly Ile Leu Gu Leu Thr Pro Pro Lys Lys
145 150 155 160

Thr His Pro Thr Tyr Ser Ala His Lys Leu Tyr Leu Arg Ala Val Val
165 170 175

Pro Trp Ile Gly Lys Ser Val Ser Lys Asp Pro Asp Ala Tyr Ser Tyr
180 185 190

Leu Ser Lys Ser Ile Gln Gln Leu Pro Lys Asp His Asp Leu Gu Asp
195 200 205

Leu Phe Ser Lys Ser Gly Phe Tyr Ile Ala Lys Lys Lys Lys Leu Phe
210 215 220

Leu Gly Ala Ala Thr Ile Trp Leu Leu Gu Lys Gln
225 230 235

<210> 112
<211> 605
<212> PRT
<213> Chl amydi a pneumoni ae
<400> 112

Gly Gln Ile Ser Thr Trp Lys Phe Leu Tyr Ser Leu Ala Thr Pro Leu
1 5 10 15

eol f - seq| . app

Pro Ala Gly Thr 20 Lys Cys Lys Phe Asp 25 Leu Ala Gly Ser 30 Gly Lys Pro
 Thr Asp 35 Trp Gu Ala Pro Ala Thr 40 Asp Leu Ser Gn Thr 45 Arg Asn Val
 Ile Tyr 50 Ala Gu Met Pro Gu 55 Gly Gu Ile Ile 60 Gu Ala Thr Ala Ile
 Pro Val 65 Lys Asp Asn 70 Pro Val Pro Gn Phe 75 Gu Phe Thr Leu Pro Tyr 80
 Gu Leu Gn Val 85 Gly Gu Thr Leu Thr 90 Ile Val Met Gly Ala Ser 95 Pro
 Asn His Pro 100 Gn Val Asp Asp Ala 105 Gly Asn Gly Ala Gn 110 Leu Phe Ala
 Gn Arg 115 Arg Lys Pro Phe Tyr Leu 120 Tyr Ile Asp Pro Thr 125 Gly Gu Gly
 Asn Tyr 130 Asp Gu Pro Asp Val 135 Phe Ser Met Asp 140 Ile Arg Gly Asn Val
 Leu 145 Lys Lys Ile Gu 150 Ile Phe Thr Pro Ser Tyr 155 Val Val Lys Asn Lys 160
 Arg Phe Asp 165 Ile Thr Val Arg Phe Gu 170 Asp Gu Phe Gly Asn Leu Thr 175
 Asn Phe Ser 180 Pro Gu Gu Thr Arg 185 Ile Gu Leu Ser Tyr Gu 190 His Leu
 Arg Gu 195 Asn Leu Asn Trp Gn Leu Phe 200 Ile Pro Gu Thr 205 Gly Phe Val
 Ile Leu 210 Pro Asn Leu Tyr Phe 215 Asn Gu Pro Gly 220 Ile Tyr Arg Ile Gn
 Leu 225 Lys Asn Leu Ser Thr 230 Gn Gu Ile Phe 235 Ile Ser Ala Pro Ile Lys 240
 Cys Phe Ala Asp 245 Ser Ala Pro Asn Leu Met 250 Trp Gly Leu Leu His Gly 255
 Gu Ser Gu 260 Arg Val Asp Ser Gu 265 Gu Asn Ile Gu Thr Cys 270 Met Arg
 Tyr Phe 275 Arg Asp Asp Arg Ala Leu 280 Asn Phe Tyr Ala Ser 285 Ser Ser Phe

G u Asn G n G u Asn Leu Ser Pro Asp Ile Trp Lys Leu Ile Asn G n
 290 295 300

Thr Val Ser Asp Phe Asn G u G u Asp Arg Phe Ile Thr Leu Ser G y
 305 310 315 320

Phe G n Tyr Ser G y G u Pro His Leu G u G y Val Arg His Ile Leu
 325 330 335

His Thr Lys G u Thr Lys Ser His Ser Lys His Lys G u Tyr Lys His
 340 345 350

Ile Pro Leu Ala Lys Leu Tyr Lys Ser Thr Val Asn His Asp Met Ile
 355 360 365

Ser Ile Pro Ser Phe Thr Ala Ser Lys G u His G y Phe Asp Phe G u
 370 375 380

Asn Phe Tyr Pro G u Phe G u Arg Val Val G u Ile Tyr Asn Ala Trp
 385 390 395 400

G y Ser Ser G u Thr Thr Ala Ala Leu Asn Asn Pro Phe Pro Ile G n
 405 410 415

G y Lys Asp Ser G u Asp Pro Arg G y Thr Val Ile G u G y Leu Lys
 420 425 430

Lys Asn Leu Arg Phe G y Phe Val Ala G y G y Leu Asp Asp Arg G y
 435 440 445

Ile Tyr Lys Asp Tyr Phe Asp Ser Pro G n Val G n Tyr Ser Pro G y
 450 455 460

Leu Thr Ala Ile Ile Cys Asn Lys Tyr Thr Arg G u Ser Leu Val G u
 465 470 475 480

Ala Leu Phe Ala Arg His Cys Tyr Ala Thr Thr G y Pro Arg Ile Val
 485 490 495

Leu Ser Phe Asn Ile Thr Ser Ala Pro Met G y Ser G u Leu Ser Thr
 500 505 510

G y Ser Lys Pro G y Leu Asn Val Asn Arg His Ile Ser G y His Val
 515 520 525

Ala G y Thr Ala Leu Leu Lys Thr Val G u Ile Ile Arg Asn G y G u
 530 535 540

Val Leu His Thr Phe Phe Pro Asp Ser Asn Asn Leu Asp Tyr G u Tyr
 545 550 555 560

Asp Asp Met Val Pro Leu Ser Ser Val Thr Leu Lys Asp Pro Asn G y
 Page 102

Lys Ala Pro Phe Val Phe Tyr Tyr Leu Arg Val Thr Gl n Ala Asp Asn
580 585 590

Ala Met Ala Trp Ser Ser Pro Ile Trp Val Asp Leu Asn
595 600 605

<210> 113
<211> 171
<212> PRT
<213> Chl amydi a pneumni ae

<400> 113

Val Gly Phe Met Ala Val Gu Gn Ser His Ile Lys Gu Gu Ile Gu
1 5 10 15

Lys Leu Ile Gly Lys Ala Ile Lys Arg Val Cys Gly Asn Lys Gu Asn
20 25 30

Asp Leu Cys Arg Tyr Leu Pro Gly Pro Ser Gly Gly Tyr Met His His
35 40 45

Phe Thr Leu Lys Lys Met Lys Ser Ala Ala Pro Gu Gn Leu Leu Lys
50 55 60

Met Leu Lys Thr Phe Ile Leu Gu Ser Gu Thr Pro Arg Thr Ile Asn
65 70 75 80

Pro Lys Pro Arg Ala Pro Arg Gly Ser Lys Lys Arg Arg Asp Phe Ile
85 90 95

Asn Phe Thr Lys Thr Asp Ile Gu Arg Val Leu Gu Leu Ala Arg Gn
100 105 110

Val Gly Asp Lys Asp Leu Leu Ala Arg Phe Ser Pro Lys Lys Pro Leu
115 120 125

Thr Ser Leu Lys Arg Gu Leu Ile Arg Ser Ile Arg Asn Gly Ile Val
130 135 140

Ser Val Gu Leu Trp Asn Ala Tyr Val Gu Ala Val Lys Ala Val Ser
145 150 155 160

Ser Pro Asn Leu Gu Val Thr Ser Pro Phe Val
165 170

<210> 114
<211> 286
<212> PRT
<213> Chl amydi a pneumni ae

<400> 114

Lys Arg Arg Asn Leu G n Lys Ile Leu Pro Asn Ala Ser Thr Pro Ser
 1 5 10 15

Thr Asn Val Ala Gu Asn Thr Gly Ile Lys Asp G n Asn Leu Phe Leu
 20 25 30

Asp G n Ala Thr Leu Asn Val Asp Gly Asn Val Asp Ile Gu Asn Phe
 35 40 45

Leu Gu Thr Arg Asp Leu Lys Val Ala Asp Thr Ile Thr Ser Pro Cys
 50 55 60

Gu Phe Thr Val Gly Gly Gly Leu Ser Ala Gu Ser Ser G n Phe Lys
 65 70 75 80

Ala Thr Thr Leu Ser Lys Gly Leu Gu Ile Thr Ser Gu Asp G n Asp
 85 90 95

Gly Arg Val Pro Lys Phe Thr Asn Val Ser Asp Pro G n Ser Pro Arg
 100 105 110

Asp Ala Leu Thr Tyr Asn Tyr Tyr Arg Asn Thr Gly Cys G n Ala Leu
 115 120 125

Asn Leu Tyr Thr Tyr Tyr Ser Ser Ser G n Pro Thr Thr Val Gly Lys
 130 135 140

Pro Ile Gu Thr Val Cys G n Asn Pro Asn Pro Gu Thr Tyr Arg Ile
 145 150 155 160

Ser Ala Ser Ala Lys Ile Tyr Asp Ala Val Thr Arg Phe Pro Tyr Ile
 165 170 175

G n Phe Lys Ala Pro Gly Ile Tyr G n Val Thr Ile G n Ile Arg Arg
 180 185 190

Gu Ser Gly G n His Ser Gly Leu Asp Asn Pro Asn Leu Tyr Leu Asn
 195 200 205

Leu Met Ile Gly Asn Asn Lys Thr Leu Leu Cys Ala Ser Asp Thr Arg
 210 215 220

Gly Tyr Ser Gly Gly His Arg Thr Ser Ile Ala Val Thr Gly Thr Phe
 225 230 235 240

Thr Leu Thr Gu Ile Val Ala Thr Pro Pro His Asp Tyr Pro Trp Leu
 245 250 255

Phe Leu Gu Thr Thr Ile Gly Leu Asp Ile Lys Ser Met Ser Thr Cys
 260 265 270

Val Ile Trp Phe Pro Phe G n Ala Asn Phe Ala Gu Val Asp

275

280

285

<210> 115
 <211> 205
 <212> PRT
 <213> Chl amydi a pneumoni ae

<400> 115

Val Gl u Ala Lys Ser Gly Phe Leu Gly Lys Val Lys Gly Trp Phe Ser
 1 5 10 15

Lys Lys Gl u Ile Gn Gu Gu Ala Arg Ile Leu Pro Val Lys Asp Ser
 20 25 30

Leu Ser Trp Lys Arg Tyr Asp Tyr Thr Ser Ser Ser Gly Phe Ser Val
 35 40 45

Gl u Phe Pro Gly Gu Pro Asp His Ser Gly Gn Ile Val Gl u Val Pro
 50 55 60

Gn Ser Gl u Ile Thr Ile Arg Tyr Asp Thr Tyr Val Thr Gl u Thr His
 65 70 75 80

Pro Asp Asn Thr Val Tyr Val Val Ser Val Trp Gl u Tyr Pro Gl u Lys
 85 90 95

Val Asp Ile Ser Arg Pro Gu Leu Asn Leu Gn Gl u Gly Phe Ser Gly
 100 105 110

Met Met Gn Ala Leu Pro Gu Ser Gn Val Leu Phe Met Gn Ala Arg
 115 120 125

Gn Ile Gn Gly His Lys Ala Leu Gu Phe Trp Ile Val Oys Gl u Asp
 130 135 140

Val Tyr Phe Arg Gly Met Leu Ile Ser Val Asn His Thr Leu Tyr Gn
 145 150 155 160

Val Phe Met Val Tyr Lys Asn Lys Asn Pro Gn Ala Leu Asp Lys Gl u
 165 170 175

Tyr Gl u Ala Phe Ser Gn Ser Phe Lys Ile Thr Lys Ile Arg Gl u Pro
 180 185 190

Arg Thr Ile Pro Ser Ser Val Lys Lys Lys Val Ser Leu
 195 200 205

<210> 116
 <211> 549
 <212> PRT
 <213> Chl amydi a pneumoni ae

<400> 116

His Pro Leu Tyr Val Asp Leu Asp Thr Ile Ile Ser Ser Tyr Ser Pro
 1 5 10 15

Pro Leu Pro Lys Gu Phe Gn Gu Ala Ala Ser Leu Ile Ala Val Pro
 20 25 30

Asp Thr Ser His Ser Lys Pro Val Val Pro Gly Val Lys Thr Leu Phe
 35 40 45

Pro Gn Thr Tyr His Leu Pro Tyr Leu Lys Phe Val Gn Gly Gu Asn
 50 55 60

Val Val His Thr Pro Leu Lys Val Gly Val Met Phe Ser Gly Gly Pro
 65 70 75 80

Ala Pro Gly Gly His Asn Val Ile Gn Gly Leu Phe Asn Ser Leu Lys
 85 90 95

Asp Phe His Pro Asp Ser Ser Leu Val Gly Phe Val Asn Asn Gly Asp
 100 105 110

Gly Leu Thr Asn Asn Lys Ser Ile Asp Ile Thr Gu Gu Phe Leu Ser
 115 120 125

Lys Phe Arg Asn Ser Gly Gly Phe Asn Cys Ile Gly Thr Gly Arg Lys
 130 135 140

Lys Ile Val Thr Pro Gu Ala Lys Gu Ala Cys Leu Lys Thr Ala Gu
 145 150 155 160

Ala Leu Asp Leu Asp Gly Leu Val Ile Ile Gly Gly Asp Gly Ser Asn
 165 170 175

Thr Ala Thr Ala Ile Leu Ala Gu Tyr Phe Ala Lys Arg Arg Pro Lys
 180 185 190

Thr Ser Ile Val Gly Val Pro Lys Thr Ile Asp Gly Asp Leu Gn His
 195 200 205

Thr Phe Leu Asp Leu Thr Phe Gly Phe Asp Thr Ala Thr Lys Phe Tyr
 210 215 220

Ser Ser Ile Ile Ser Asn Ile Ser Arg Asp Ala Leu Ser Cys Lys Ala
 225 230 235 240

His Tyr His Phe Ile Lys Leu Met Gly Arg Ser Ala Ser His Ile Ala
 245 250 255

Leu Gu Cys Ala Leu Gn Thr His Pro Asn Ile Ala Leu Ile Gly Gu
 260 265 270

Gu Ile Ala Gu Lys Asn Leu Pro Leu Lys Thr Ile Ile His Lys Ile

275

280

285

Cys Ser Val Ile Ala Asp Arg Ala Ala Met Gu Lys Tyr Tyr Gly Val
 290 295 300

Ile Leu Ile Pro Gu Gly Ile Ile Gu Phe Ile Pro Gu Ile Ile Asn
 305 310 315 320

Leu Ile Thr Gu Ile Gu Ser Leu Ser Gu Tyr Gu Asp Lys Ile Ser
 325 330 335

Arg Leu Ser Pro Gu Ser Gn Arg Leu Leu Lys Ser Phe Pro Ala Pro
 340 345 350

Ile Ile Gu Gn Ile Leu Asn Asp Arg Asp Ala His Gly Asn Val Tyr
 355 360 365

Val Ser Lys Ile Ser Val Asp Lys Leu Leu Ile His Leu Val Ser Asn
 370 375 380

His Leu Gn Gn Tyr Phe Pro Asn Val Pro Phe Asn Ala Ile Ser His
 385 390 395 400

Phe Leu Gly Tyr Gu Gly Arg Ser Gly Leu Pro Thr Lys Phe Asp Asn
 405 410 415

Thr Tyr Gly Tyr Ser Leu Gly Tyr Gly Ala Gly Ile Leu Val Arg Asn
 420 425 430

His Cys Asn Gly Tyr Leu Ser Thr Ile Gu Ser Leu Ala Cys Pro Phe
 435 440 445

Met Lys Trp Lys Leu Arg Ala Ile Pro Val Val Lys Met Phe Thr Val
 450 455 460

Lys Gn Gn Ala Asp Gly Thr Leu Gn Pro Lys Ile Lys Lys Tyr Leu
 465 470 475 480

Val Asp Ile Gly Ser Thr Ala Phe Arg Lys Phe Lys Leu Tyr Arg Lys
 485 490 495

Ile Trp Ala Leu Gu Asp Ser Tyr Arg Phe Leu Gly Pro Leu Gn Ile
 500 505 510

Gu Thr Pro Pro Gu Met His Ser Asp Asn Phe Pro Pro Leu Thr Leu
 515 520 525

Leu Leu Asn His Asn Phe Trp Gn Arg His Gn Gly Cys Ile Gu Ile
 530 535 540

Pro Asp Thr Thr Tyr
 545

<210> 117
 <211> 643
 <212> PRT
 <213> Chl amydi a pneumoni ae

<400> 117

Thr Ser Ser Ser Cys Pro Leu Leu Asp Leu Ile Leu Ser Pro Ala Asp
 1 5 10 15

Leu Lys Lys Leu Ser Ile Ser Gn Leu Pro Gly Leu Ala Glu Glu Ile
 20 25 30

Arg Tyr Arg Ile Ile Ser Val Leu Ser Gn Thr Gly Gly His Leu Ser
 35 40 45

Ser Asn Leu Gly Ile Val Gu Leu Thr Ile Ala Leu His Tyr Val Phe
 50 55 60

Ser Ser Pro Lys Asp Lys Phe Ile Phe Asp Val Gly His Gn Thr Tyr
 65 70 75 80

Pro His Lys Leu Leu Thr Gly Arg Asn Asn Gu Gly Phe Asp His Ile
 85 90 95

Arg Asn Asp Asn Gly Leu Ser Gly Phe Thr Asn Pro Thr Gu Ser Asp
 100 105 110

His Asp Leu Phe Phe Ser Gly His Ala Gly Thr Ala Leu Ser Leu Ala
 115 120 125

Leu Gly Met Ala Gn Thr Thr Pro Leu Gu Ser Arg Thr His Val Ile
 130 135 140

Pro Ile Leu Gly Asp Ala Ala Phe Ser Cys Gly Leu Thr Leu Gu Ala
 145 150 155 160

Leu Asn Asn Ile Ser Thr Asp Leu Ser Lys Phe Val Val Ile Leu Asn
 165 170 175

Asp Asn Asn Met Ser Ile Ser Lys Asn Val Gly Ala Met Ser Arg Ile
 180 185 190

Phe Ser Arg Trp Leu His His Pro Ala Thr Asn Lys Leu Thr Lys Gn
 195 200 205

Val Gu Lys Trp Leu Ala Lys Ile Pro Arg Tyr Gly Asp Ser Leu Ala
 210 215 220

Lys His Ser Arg Arg Leu Ser Gn Cys Val Lys Asn Leu Phe Cys Pro
 225 230 235 240

Thr Pro Leu Phe G u G n Phe G y Leu Al a Tyr Val G y Pro I l e Asp
 245 250 255
G y Hi s Asn Val Lys Lys Leu I l e Pro I l e Leu G n Ser Val Arg Asn
 260 265 270
Leu Pro Phe Pro I l e Leu Val Hi s Val Cys Thr Thr Lys G y Lys G y
 275 280 285
Leu Asp G n Al a G n Asn Asn Pro Al a Lys Tyr Hi s G y Val Arg Al a
 290 295 300
Asn Phe Asn Lys Arg G u Ser Al a Lys Hi s Leu Pro Al a I l e Lys Pro
 305 310 315 320
Lys Pro Ser Phe Pro Asp I l e Phe G y G n Thr Leu Cys G u Leu G y
 325 330 335
G u Val Ser Ser Arg Leu Hi s Val Val Thr Pro Al a Met Ser I l e G y
 340 345 350
Ser Arg Leu G u G y Phe Lys G n Lys Phe Pro G u Arg Phe Phe Asp
 355 360 365
Val G y I l e Al a G u G y Hi s Al a Val Thr Phe Ser Al a G y I l e Al a
 370 375 380
Lys Al a G y Asn Pro Val I l e Cys Ser I l e Tyr Ser Thr Phe Leu Hi s
 385 390 395 400
Arg Al a Leu Asp Asn Val Phe Hi s Asp Val Cys Met G n Asp Leu Pro
 405 410 415
Val I l e Phe Al a I l e Asp Arg Al a G y Leu Al a Tyr G y Asp G y Arg
 420 425 430
Ser Hi s Hi s G y I l e Tyr Asp Met Ser Phe Leu Arg Al a Met Pro G n
 435 440 445
Met I l e I l e Cys G n Pro Arg Ser G n Val Val Phe G n G n Leu Leu
 450 455 460
Tyr Ser Ser Leu Hi s Trp Ser Ser Pro Ser Al a I l e Arg Tyr Pro Asn
 465 470 480
I l e Pro Al a Pro Hi s G y Asp Pro Leu Thr G y Asp Pro Asn Phe Leu
 485 490 495
Arg Ser Pro G y Asn Al a G u Thr Leu Ser G n G y G u Asp Val Leu
 500 505 510
I l e I l e Al a Leu G y Thr Leu Cys Phe Thr Al a Leu Ser I l e Lys Hi s

515

520

525

Gln Leu Leu Ala Tyr Gly Ile Ser Ala Thr Val Val Asp Pro Ile Phe
530 535 540

Ile Lys Pro Phe Asp Asn Asp Leu Phe Ser Leu Leu Leu Met Ser His
545 550 555

Ser Lys Val Ile Thr Ile Gu Gu His Ser Ile Arg Gly Gly Leu Ala
565 570 575

Ser Gu Phe Asn Asn Phe Val Ala Thr Phe Asn Phe Lys Val Asp Ile
580 585 590

Leu Asn Phe Ala Ile Pro Asp Thr Phe Leu Ser His Gly Ser Lys Gu
595 600 605

Ala Leu Thr Lys Ser Ile Gly Leu Asp Gu Ser Ser Met Thr Asn Arg
610 615 620

Ile Leu Thr His Phe Asn Phe Arg Ser Lys Lys Gln Thr Val Gly Asp
625 630 635 640

Val Arg Val

<210> 118

<211> 342

<212> PRT

<213> Chlamydia pneumoniae

<400> 118

Gu Val Tyr Ser Phe Ser Pro Ser Val Arg Thr Ser Phe Gln His Arg
1 5 10 15

Val Met Ala Ala Leu Asp Asn Trp Phe Phe Leu Gly Gly Arg Arg Leu
20 25 30

Lys Val Val Ser Leu Asp Ser Cys Asn Ser Gly Gln Ala Cys Gu Gu
35 40 45

Tyr Val Pro Ile Ser Thr Thr Gu Lys Val Leu Lys Ile Leu Ser Tyr
50 55 60

Leu Leu Ile Pro Ile Val Ile Ile Ala Leu Leu Ile Arg Tyr Leu Leu
65 70 75 80

His Ser Asn Phe Thr Ala Lys Val Ser Gln Lys Pro Trp Leu Lys Thr
85 90 95

Leu Gln Leu Gly Ile Asp Ile Lys Ser Phe Ile Leu Pro Gly Ser His
100 105 110

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Val Asn Thr Met Asp Ser Ala Thr Leu Phe Lys Ala Ile Arg Leu Glu
115 120 125

Gly Lys Arg Val Asp Val Glu Tyr His Arg Leu His Ser Ser Asp Lys
130 135 140

Val Val Phe Tyr Ile Pro Ala Gn Lys Leu Pro Asp Asp Leu Arg Leu
145 150 155 160

Thr His Trp Leu Pro Glu Lys Glu Thr Arg Lys Thr Glu Tyr Val Arg
165 170 175

His Met Leu Ala His Val Met Gly Tyr Leu Thr Ser Gn Gly Lys Glu
180 185 190

Arg Leu Gn Gn Val Val Gn Asp Ser Arg Ser Ser Thr Ser Leu Gly
195 200 205

Ala Glu Lys Val Leu Gn Tyr Arg Phe Ile Asp His Pro Gn Ser Gn
210 215 220

Gly Glu Phe Gn Arg Leu Leu Asn Glu Asn Ile Thr Thr Lys Gly Ser
225 230 235 240

Glu Asp Lys Glu Val Val Gn Ser Asp Leu Phe Asp Met Ala Phe Gn
245 250 255

Cys Trp Trp Pro Gn Phe Ile Ser Val Ile Gn Ser Pro Thr Phe Ser
260 265 270

Glu Glu Leu Val His Glu Met Ser Gn Lys Leu Asp Leu Asp Cys Ile
275 280 285

Tyr Pro Glu Asp Asp Glu Phe Glu Gn Lys Phe Leu Asn Thr Leu Leu
290 295 300

Lys Ala Val Leu His His Gly Phe Glu Gly Ile Ser Val Ala Ser Met
305 310 315 320

Gly Val Ile Phe Leu Ile Cys Pro Asp Ser Leu Ala Leu Gn Ile Pro
325 330 335

Phe Leu Arg Asn Gn Lys
340

<210> 119
<211> 366
<212> PRT
<213> Chl amydi a pneumoni ae

<400> 119

Leu Ser Gly Ile Phe Ser Asn Pro His Pro Val Ser Tyr Phe Ser Ser
Page 111

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Leu Pro Cys Pro Glu Ile Leu Val Tyr Ser Ala Asp Arg Phe Arg Pro
290 295 300

Ser Glu Val Gly Asp Asp Thr Ala Leu Leu Pro Glu Phe Thr Leu Ala
305 310 315 320

His Ala Ile Lys Arg Thr Pro Phe Ala Arg Ser Lys Lys Phe Ile Gly
325 330 335

Glu Val Asn Leu Leu His Ser Ser Pro Leu Lys His Pro Thr Ile Gln
340 345 350

Lys Leu Ala Glu Ala Ile Leu Glu Ser Leu Ser Arg Lys Asn
355 360 365

<210> 120
<211> 324
<212> PRT
<213> Chl amydi a pneumni ae
<400> 120

His Ser Glu Leu Pro Asn Tyr Gln Asn Ile Val Glu Ser Val Val Thr
1 5 10 15

Glu Ile Thr Thr Gln Leu Leu Asn Tyr Arg Ser Glu His Arg Leu Val
20 25 30

Pro Phe Trp Glu Lys Ser Asp Gly Ser Phe Ile Thr Ala Ala Asp Tyr
35 40 45

Gly Ser Gln Tyr Tyr Leu Lys Gln Gln Leu Ala Lys Ala Phe Pro Asn
50 55 60

Ile Pro Phe Ile Gly Glu Glu Thr Leu Tyr Pro Asp Gln Asp Asn Glu
65 70 75 80

Lys Ile Pro Glu Ile Leu Lys Phe Thr Arg Leu Leu Thr Ser Ser Val
85 90 95

Ser Arg Asp Asp Leu Ile Ser Thr Leu Val Pro Pro Pro Ser Pro Thr
100 105 110

Ser Leu Phe Trp Leu Val Asp Pro Ile Asp Gly Thr Ala Gly Phe Ile
115 120 125

Arg His Arg Ala Phe Ala Val Ala Ile Ser Leu Ile Tyr Glu Tyr Arg
130 135 140

Pro Ile Leu Ser Val Met Ala Cys Pro Ala Tyr Asn Gln Thr Phe Lys
145 150 155 160

Leu Tyr Ser Ala Ala Lys Gly His Gly Leu Ser Ile Val His Ser Gln
 165 170 175

Asn Leu Asp Arg Arg Phe Val Tyr Ala Asp Arg Lys Gln Thr Lys Gln
 180 185 190

Phe Cys Gu Ala Ser Leu Ala Ala Leu Asn Gln Gln His His Ala Thr
 195 200 205

Arg Lys Leu Ser Leu Gly Leu Pro Asn Thr Pro Ser Pro Arg Arg Val
 210 215 220

Gu Ser Gln Tyr Lys Tyr Ala Leu Val Ala Gu Gly Ala Val Asp Phe
 225 230 235 240

Phe Ile Arg Tyr Pro Phe Ile Asp Ser Pro Ala Arg Ala Trp Asp His
 245 250 255

Val Pro Gly Ala Phe Leu Val Gu Gu Ala Gly Gly Arg Val Thr Asp
 260 265 270

Ala Leu Gly Ala Pro Leu Gu Tyr Arg Lys Gu Ser Leu Val Leu Asn
 275 280 285

Asn His Ala Val Ile Leu Ala Ser Gly Asp Gln Gu Thr His Gu Thr
 290 295 300

Thr Leu Ala Ala Leu Gln Asn Gln Leu Asn Val Val Pro Thr Asp Lys
 305 310 315 320

Leu Ile Ala Leu

<210> 121
 <211> 457
 <212> PRT
 <213> Chlamydia pneumoniae

<400> 121

Phe Asn Val Asn Phe Lys Phe Leu Gu Gly Leu His Gln Pro Ala Pro
 1 5 10 15

Arg Tyr Thr Ser Tyr Pro Thr Ala Leu Gu Trp Gu Pro Ser Asp Ala
 20 25 30

Ala Pro Ala Leu Leu Ala Phe Gln Arg Ile Arg Gu Asn Pro Gln Pro
 35 40 45

Leu Ser Leu Tyr Phe His Ile Pro Phe Cys Gln Ser Met Cys Leu Tyr
 50 55 60

Cys Gly Cys Ser Val Val Leu Asn Arg Arg Gu Asp Ile Val Gu Ala
 65 70 75 80

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Tyr Ile Asn Thr Leu Ile G n G u Met Lys Leu Val Val G u Thr Ile
 85 90 95
 Gly Phe Arg Pro G n Val Ser Arg Ile His Phe Gly Gly Gly Thr Pro
 100 105 110
 Ser Arg Leu Ser Arg G u Leu Phe Thr Leu Leu Phe Asp His Ile His
 115 120 125
 Lys Leu Phe Asp Leu Ser His Ala G u G u Ile Ala Ile G u Val Asp
 130 135 140
 Pro Arg Ser Leu Arg Asn Asp Met G u Lys Ala Asp Phe Phe G n Asn
 145 150 155 160
 Val Gly Phe Asn Arg Val Ser Leu Gly Val G n Asp Thr G n Ala Asp
 165 170 175
 Val G n G u Ala Val Arg Arg Arg G n Ser His G u G u Ser Leu Lys
 180 185 190
 Ala Tyr G u Lys Phe Lys G u Leu Ala Phe G n Ser Ile Asn Ile Asp
 195 200 205
 Leu Ile Tyr Gly Leu Pro Lys G n Thr Lys G u Ser Phe Ser Lys Thr
 210 215 220
 Ile G n Asp Ile Leu Ala Met Tyr Pro Asp Arg Leu Ala Leu Phe Ser
 225 230 235 240
 Phe Ala Ser Val Pro Trp Ile Lys Pro His G n Lys Ala Met Lys Ala
 245 250 255
 Ser Asp Met Pro Ser Met G u G u Lys Phe Ala Ile Tyr Ser G n Ser
 260 265 270
 Arg His Leu Leu Thr Lys Ala Gly Tyr G n Ala Ile Gly Met Asp His
 275 280 285
 Phe Ser Leu Pro His Asp Pro Leu Thr Leu Ala Phe Lys Asn Lys Thr
 290 295 300
 Leu Ile Arg Asn Phe G n Gly Tyr Ser Leu Pro Pro G u G u Asp Leu
 305 310 315 320
 Leu Gly Leu Gly Met Thr Ser Thr Ser Phe Ile Arg Gly Ile Tyr Leu
 325 330 335
 G n Asn Ala Lys Thr Leu G u G u Tyr His Asn Thr Val Leu Arg Gly
 340 345 350

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Thr Phe Ala Thr Val Lys Ser Lys Ile Leu Thr Gu Asp Asp Arg Ile
355 360 365

Arg Lys Trp Ala Ile His Lys Leu Met Cys Thr Phe Thr Ile Asn Lys
370 375 380

Gu Gu Phe Phe Asn Leu Phe Gy Tyr Gu Phe Asp Thr Tyr Phe Ile
385 390 395 400

Gu Ser Arg Asp Arg Leu Ile Ser Met Gu Thr Thr Gy Leu Ile His
405 410 415

Asn Ser Pro Gy Ser Leu Lys Val Thr Pro Leu Gy Gu Leu Phe Val
420 425 430

Arg Val Ile Ala Thr Ala Phe Asp His Tyr Phe Leu Asn Lys Val Ser
435 440 445

Lys Lys Gu Cys Phe Ser Ala Ser Ile
450 455

<210> 122

<211> 349

<212> PRT

<213> Chl amydi a pneumoni ae

<400> 122

Ser Met Asp Pro Thr Ala Met Leu Val Thr Ser Ser Lys Gy Leu Leu
1 5 10 15

Thr Asn Lys Ser Ile Met Gn Leu Arg His Phe Ala Leu Gy Trp Val
20 25 30

Val Phe Phe Ile Cys Ala Tyr Phe Asp Tyr His Leu Phe Lys Arg Trp
35 40 45

Ala Trp Val Leu Tyr Phe Phe Met Ile Cys Ala Leu Val Gy Leu Phe
50 55 60

Phe Val Pro Ser Val Gn Asn Val His Arg Trp Tyr Arg Ile Pro Phe
65 70 75 80

Ile His Met Ser Val Gn Pro Ser Gu Tyr Gy Lys Leu Val Ile Val
85 90 95

Ile Met Leu Ser Tyr Ile Leu Gu Ser Arg Lys Ala Asp Ile Thr Ser
100 105 110

Lys Thr Thr Ala Phe Leu Ala Cys Leu Val Val Ala Leu Pro Phe Phe
115 120 125

Leu Ile Leu Lys Gu Pro Asp Leu Gy Thr Ala Leu Val Leu Cys Pro
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130

135

Val Thr Leu Thr Ile Phe Tyr Leu Ser Asn Val His Ser Leu Leu Val
145 150 155 160

Lys Phe Cys Thr Val Val Ala Thr Ile Gly Ile Ile Gly Ser Leu Leu
165 170 175

Ile Phe Ser Gly Ile Val Ser His Gn Lys Val Lys Pro Tyr Ala Leu
180 185 190

Lys Val Ile Lys Gu Tyr Gn Tyr Gu Arg Leu Ser Pro Ser Asn His
195 200 205

His Gn Arg Ala Ser Leu Ile Ser Ile Gly Leu Gly Gly Ile Arg Gly
210 215 220

Arg Gly Trp Lys Thr Gly Gu Phe Ala Gly Arg Gly Trp Leu Pro Tyr
225 230 235 240

Gly Tyr Thr Asp Ser Val Phe Ser Ala Leu Gly Gu Gu Phe Gly Leu
245 250 255

Leu Gly Leu Leu Phe Thr Leu Gly Leu Phe Tyr Cys Leu Ile Cys Phe
260 265 270

Gly Cys Arg Thr Val Ala Val Ala Thr Asp Asp Phe Gly Lys Leu Leu
275 280 285

Ala Ala Gly Ile Thr Val Tyr Leu Ala Met His Val Leu Ile Asn Ile
290 295 300

Ser Met Met Cys Gly Leu Leu Pro Ile Thr Gly Val Pro Leu Ile Leu
305 310 315 320

Ile Ser Tyr Gly Gly Ser Ser Val Ile Ser Thr Met Ala Ser Leu Gly
325 330 335

Val Leu Gn Ser Ile Tyr Ser His Arg Phe Ala Lys Tyr
340 345

<210> 123
<211> 872
<212> PRT
<213> Chl amydi a pneumni ae

<400> 123

Met Ser Thr Phe Ser Ile Gn Asn Arg Leu Arg Thr Ile Ser Gly Gu
1 5 10 15

Ser Thr Arg Ile Ile Lys Leu Asp His Lys Tyr Ser Gly Phe Asp Pro
20 25 30

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Arg Ser Val Pro Ala Ile Asn Leu Gu Gu Leu Asn Ser Gly Ile Tyr
 35 40 45

Ala Leu Arg His Leu Met Asn Ala Leu Gn Ser Gu Asn Thr Asn Val
 50 55 60

Ala Ala Leu Leu Asn Pro Asn Asn Thr Ile Phe Pro Thr Thr Ser Trp
 65 70 75 80

Thr Asp Tyr Lys His Ser Arg Pro Gn Ala Ser Ser Pro Arg Ala Pro
 85 90 95

Ser Ser Gn Thr Pro Thr Asp Ile Val Ser Ala Ala Ala Leu Ala Leu
 100 105 110

Val Leu Val Ile Asp Gly Gly Leu Ala Gu Leu Val Ala Ser Val Thr
 115 120 125

Gu Ile Asp Leu Gly Ala Leu Ser Thr Ile Ser Thr Val Arg Gn Leu
 130 135 140

Met Ala Ser Tyr Leu Gly Leu Thr Thr Leu Thr Ala Gu Gn Gu Lys
 145 150 155 160

Val Val Phe Ser Ser Ser Tyr Val Pro Ser Gu Lys Asn Leu Leu Gu
 165 170 175

His Val Lys Gn Gu Lys Ala Ala Gu Ile Gn Ala Lys Gn Gu Gu
 180 185 190

Ile Lys Ala Val Leu Gu Ala Lys Gly Val Ser Thr Gu Gu Ile Gu
 195 200 205

Ala Ile Leu Lys Gu Tyr Pro Asp Ile Tyr Ala Ala Asp Phe Phe Lys
 210 215 220

Gu Phe Ile Gu Gu Pro Leu His Thr Tyr Arg Ala Lys Val Gly Ala
 225 230 235 240

Pro Ile Gn Gu Met Asn Gu Asn Ala Ile Gn Leu Leu Pro Thr Pro
 245 250 255

Pro Ala Ile Thr Pro Asp Asn Val Asn Gu Val Asn Gly Met Asn Thr
 260 265 270

Leu Ser Thr Ile Leu Gn Ala Ile Asp Asp Ala Ile Lys Gn Ala Pro
 275 280 285

Ala Leu Gly Gly Asp Gn Gu Ile Ile Thr Ile Leu Gn Thr Leu Val
 290 295 300

Pro Leu Val Asp Lys Thr Thr Phe Thr Lys Ala Glu Phe Asp Leu Ile
 305 310 315 320

Tyr Thr Ala Thr Gl n Leu Pro Asn Thr Ala Ser Leu Lys Leu Tyr Leu
 325 330 335

Thr Asp Arg Gl n Ile Ala Gl u Tyr Arg Gl y Lys Ile Thr Lys Val Tyr
 340 345 350

Gl n Asn Ser Ile Gl n Asn Leu Ser Gl u Thr Lys Arg Val Val Gl u Asn
 355 360 365

Asn Arg Ser Met Leu Gl u Thr Gl n Leu Ser Met Phe Gl n Gl n Ala Gl n
 370 375 380

Asn Cys Phe Val Thr Trp Ile Ser Gl n Ala Asn Ala Leu Asn Ile Ala
 385 390 400

Ile Thr Asn Lys Tyr Ile Ser Ala Val Leu Thr Thr Ser Met Gl u Met
 405 410 415

Tyr Gl y Gl y Leu Leu Cys Leu Ser Tyr Met Tyr Gl u Arg Leu Ala Asp
 420 425 430

Asp Gl u Lys Ala Ile Phe Asp Lys Ser Val Asn Gl u Tyr Leu Pro Ile
 435 440 445

His Ile Val Val Gl y Gl y Ser Trp Val Asn Gl y Trp Ile Ala Lys Met
 450 455 460

Ala Ala Tyr Gl n Gl u Leu Ala Gl u Tyr Ser Leu Gl y Thr Ala Val Thr
 465 470 475 480

Ser Gl n Asp Gl n Ile Lys Ala Tyr Leu Gl n Thr Arg Gl y Asn Gl u Phe
 485 490 495

Lys Ala Thr Arg His Phe Phe His Asn Ile Gl y Asp Gl n Met Tyr Gl n
 500 505 510

Phe Ala Asn Gl u Thr Val Phe Gl y Asn Cys Leu Thr Thr Ala Asn Gl y
 515 520 525

Ala Ile Gl n Pro Asp Leu Gl y Gl y Phe Ile Arg Gl u Ala Met Thr Asn
 530 535 540

Val Gl y Thr Val Gl u Ala Asp Tyr Val Ser Asn Ala Gl n Arg Ile Leu
 545 550 555 560

Asn Gl u Phe Asn Thr Ala Ala Thr Ala His Val Leu Gl n Leu Gl n Leu
 565 570 575

Gl n Ile Ala Gl u Leu Gl n Lys Lys Ala Asp Asp Leu Asp Pro Gl y Lys

Al a Ser Phe Thr Gu Asn Arg Lys Phe Al a Val Al a Al a Trp Ile Thr
595 600 605

Ser Gu Ser Leu Gy Asp Al a Leu Ile Ser Met Ile Leu Asn Ser Gn
610 615 620

Leu Pro Lys Gn Gu Al a Phe Leu Lys Pro Leu Ile Gu Gu Ile Asn
625 630 635 640

Phe Asn Asn Leu Al a Al a Asn Al a Leu Asn Ser Leu Leu Gn Ile Thr
645 650 655

Asn Gu Phe Ser Thr Thr Ser Val Tyr Tyr Ser Leu Ser Ser Tyr Leu
660 665 670

Val Gn Ser Lys Thr Gy Gn Asn Leu Phe Al a Gy Asp Tyr Tyr Gu
675 680 685

Thr Leu Leu Al a Al a Al a Arg Gu Arg Gu Tyr Ile Tyr Arg Asp Thr
690 695 700

Al a Arg Cys Lys Gn Al a Ile Asn Leu Val Asn Gy Leu Leu Gn Lys
705 710 715 720

Ile Asn Ser Leu Pro Gy Al a Thr Ser Al a Gn Lys Gn Gu Met Leu
725 730 735

Asn Al a Thr Thr Tyr Tyr Gn Tyr Ser Leu Ser Val Thr Leu Asn Gn
740 745 750

Leu Thr Val Leu Gu Ser Leu Leu Al a Gy Leu Lys Met Thr Leu Gn
755 760 765

Thr Thr Ser Asn Asn Lys Tyr Asp Lys Ser Val Phe Lys Ile Gu Ser
770 775 780

Phe Asp Asp Trp Ile Pro Thr Leu Al a Al a Leu Gu Ser Phe Leu Thr
785 790 795 800

Ser Gy Phe Pro Asn Ile Ser Al a Thr Gy Gy Leu Gy Pro Leu Phe
805 810 815

Thr Gn Val Gn Ser Asp Gn Gn Thr Tyr Thr Ser Gn Gy Gn Thr
820 825 830

Gn Gn Leu Asn Leu Gn Asn Gn Met Thr Thr Ile Gn Gn Gu Trp
835 840 845

Thr Leu Val Ser Thr Ser Met Gn Val Leu Asn Gy Ile Leu Ser Gn
850 855 860

Leu Ala Gly Ala Ile Tyr Ser Asn
865 870

<210> 124
<211> 812
<212> PRT
<213> Chl amydi a pneumoni ae

<400> 124

Met His Ser Phe Ala Gln Arg His Arg Glu Ser Leu Glu His Ile Ala
1 5 10 15

Asn Tyr Glu Lys Thr Thr Ala Glu Arg Asp Ile Leu Lys Arg Leu Ile
20 25 30

Glu Val Leu Asp Gln Arg Ala Ser Glu Arg Tyr Arg Ser Ala Val Glu
35 40 45

Lys Leu His Lys Tyr Glu Val Glu Arg Ala Thr Val Ala Lys Ser Ile
50 55 60

Pro Val Ala Ala Ile His Glu Lys Pro Leu Ser Ser Thr His Ala Ser
65 70 75 80

Val Gln Val Thr Ala Ser Thr Pro Ala Ala Thr Gly Ser Gly Val Gly
85 90 95

Ala Tyr Tyr Asn Ala Val Lys Gln Lys Trp Ala Gln Asp Leu Ile Val
100 105 110

Glu Leu Asn Thr Val Met Thr Thr Ile Met Ala Ser Val Asn Ser Lys
115 120 125

Asn Pro Ala Asn Lys Asp Val Phe Asp Lys Leu Asn Thr Glu Leu Gln
130 135 140

Ala Leu Val Ala Ala Gly Asn Asn Leu Thr Glu Glu Asn Phe Gln Thr
145 150 155 160

Leu Tyr Asn Phe Pro Glu Glu Ile Phe Thr Ala Ile Gln Arg Ala Asp
165 170 175

Thr Phe Thr Gly Gly Met Lys Thr Asp Phe Thr Asn Gln Leu Ala Gly
180 185 190

Lys Tyr Gly Asn Gln Ala Thr Leu Thr Gln Thr Phe Ala Asp Gly Arg
195 200 205

Val Glu Gly Phe Lys Asp Ile Leu Thr Ala Val Gln Gly Val Leu Thr
210 215 220

Pro 225 G u G n Phe Thr Ile Phe Ala G u Ile Ala Thr G u Leu G n Ala 240
 230 235
 Leu Ala Asp His Val Gly Asn Phe Asp G u Ala Gly Leu G n Arg Ile 255
 245 250
 G u Asp Ala Gly G u Lys Leu Ala Ala Val Ile Asn Ser Ser Asp Leu 270
 260 265
 Thr Arg Asn Asp Lys Ile Met Phe Cys G n His Ile Thr Asp Leu Tyr 285
 275 280
 Ser Asp G n Val Ala Ala Leu Gly Ser Phe Asp Thr Val Leu Asp Ala 300
 290
 Ser Ile Tyr Val Asn G n His G n Gly Thr Met Phe Ser Asn Leu Ser 320
 305 310
 Ser Phe Val Gly Ser Leu Ile Gly Thr Phe Ala Pro Ile Asp Leu Ser 335
 325 330
 Ser Ser G n Gly Asp Ile Ser Ser Ala Ala Leu Ala Gly Ala Leu G n 350
 340
 Thr Ala Arg Gly Leu Asn Ser Arg Phe Asn G u Leu Thr Ala G u G n 365
 355 360
 G n Lys Leu Ile Asn G u Cys Ile Lys Ser Leu Val Thr Phe Lys Cys 380
 370 375
 Gly G u His Leu Gly Ala Ile Trp Ala Tyr Phe Thr Ala Ser Thr Val 400
 385 390
 Val Ala Leu Asn Pro Thr Ala Thr Met Asp His Val Lys Ala Ala Ile 415
 405 410
 Leu G u G u Ala Lys G u Leu Asp Asn Ser Ser Phe G n Leu Ala Ser 430
 420 425
 Ser Ile Lys Ser Ala Met Thr Ser Ile Val Asn Ser Ser Gly Ser Phe 445
 435 440
 Ser Val Thr Val Asn Ser Ser Thr Leu G n Tyr Thr Ile Tyr Ser G u 460
 450
 Lys Asn Gly Lys Val G u Ile Asn G n Ile Leu Leu Asn Tyr Gly Ser 480
 465 470 475
 Thr Gly Phe Leu Pro G u Ile Thr Lys Leu Ala Lys Thr Asn Ala G u 495
 485 490
 Ser Thr Ala Arg Ser Tyr Phe Arg Phe Lys Ala Leu Ala Ala Val G u

Ser G u Asn Val G n Asn Lys Ile G u Asp Leu G n Ser G n Leu G n
 515 520 525
 G n Phe Thr Asn Met Lys Thr G u Leu Phe Asp G y G n Leu Leu Ser
 530 535 540
 G n Al a Ser G u Leu Arg Al a Leu Pro Leu Pro Ser Al a Val Al a Ser
 545 550 555 560 565
 Val Leu Ile Asp Arg Tyr Met Pro Lys G u Val Asp Tyr Leu Asn G u
 565 570 575
 Ile Tyr Lys Lys Leu Tyr Tyr Ser Asn Leu G y Ser Ser Val G y Asn
 580 585 590
 Ser Ile Ile Asp Al a Ile Ser G n Tyr Val Asn G y Al a Thr Tyr Phe
 595 600 605
 Asn Phe Al a Ser Tyr Val G y G n G n Pro Al a Val G y Al a G y G y
 610 615 620
 Al a Asn Al a Phe Pro G y Ser G n G u Ser Al a G n Al a Lys Leu Asp
 625 630 635 640
 G n G u Arg Lys G n Al a Al a Leu Tyr Leu G n G u Thr Arg G y Al a
 645 650 655
 Leu Thr Val Ile G u G u G n Arg Al a Arg Val Leu Lys Asp Asp Lys
 660 665 670
 Ile Thr Asn G u G n Arg Ser Thr Ile Leu Asp Ser Leu Arg Asn Tyr
 675 680 685
 G u Asp Asn Ile Asn Ser Ile Ser G y Ser Leu Val Leu Leu G n Asn
 690 695 700
 Tyr Leu G n Pro Leu Ser Ile Al a G y G y Ser Val Al a G y Thr Phe
 705 710 715 720
 G u Val Lys G u G y G n G u G n Trp G n Al a Arg Leu G n Ile Leu
 725 730 735
 G u G u Al a Leu Val Ser G y Leu Val G y Asn Met Ile Asn G y G y
 740 745 750
 Met Phe Pro Leu G n Ser Thr Ile G n Ser Asp G n G n Ser Phe Al a
 755 760 765
 Asp Met G y G n Asn Phe G n Leu Asp Leu G n Met Hi s Leu Thr Ser
 770 775 780

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Met 785 G n G n G u Trp Thr 790 Val Val Ala Thr Ser 795 Leu G n Leu Leu Asn 800

G n Met Tyr Leu Ser 805 Leu Ala Arg Ser Leu 810 Thr Gly

<210> 125
 <211> 1090
 <212> PRT
 <213> Chl amydi a pneumoni ae
 <400> 125

Met 1 Lys Arg Pro Lys 5 Lys Phe Pro Ile Tyr 10 Leu Ser Ile Ala G n Lys 15

Thr Asn Arg Leu 20 Leu Ser Gly Ile Val 25 Ile Ala Phe Ala Val 30 Ile Ala

Leu Arg Leu 35 Trp Tyr Leu Ala Val 40 Val Gu His Gu G n Lys Leu Gu

Gu Ala Tyr Lys Pro G n Ile 55 Arg Val Leu Pro G n Tyr Val Gu Arg 60

Ala Thr Ile Cys Asp Arg 70 Phe Gly Lys Thr Leu 75 Ala Val Asn G n Leu 80

G n Tyr Asp Val Ser 85 Val Ala Tyr Gly Ala 90 Ile Arg Asp Leu Pro Thr 95

Arg Ala Trp Arg 100 Val Asp Gu His Gly 105 His Lys G n Leu Ile Pro Val 110

Arg Lys His 115 Tyr Ile Met Cys Leu 120 Ser Gu Leu Leu Ser 125 G n Gu Leu

His Leu 130 Asp Arg Gu Ala Ile 135 Gu Asp Ala Ile His 140 Ala Lys Ala Ser

Val Leu Gly Ser Val Pro Tyr Leu Val Ala 155 Ala Asn Val Ser Gu Arg 160

Thr Tyr Leu Lys Leu 165 Lys Met Leu Ser Lys 170 Asp Trp Pro Gly Leu His 175

Val Gu Ala Val 180 Val Arg Arg His Tyr 185 Pro G n Gu Ser Val 190 Ala Ser

Asp Ile Leu 195 Gly Tyr Val Gly Pro 200 Ile Ser Leu G n Gu 205 Tyr Lys Arg

Val Thr G n G u Leu Ser G n Leu Arg G u Cys Val Arg Ala Tyr G u
 210 215 220

G u G y G u Asp Pro Lys Leu Pro G u G y Leu Ala Ser Ile Asp G n
 225 230 235 240

Val Arg Ala Leu Leu G u Ser Val G u Ser Asn Ala Tyr Ser Leu Asn
 245 250 255

Ala Leu Val G y Lys Met G y Val G u Ala Cys Trp Asp Ser Lys Leu
 260 265 270

Arg G y Lys Ile G y Lys Lys Pro Ile Leu Val Asp Arg Arg G y Asn
 275 280 285

Phe Ile G n G u Met G u G y Ala Val Pro G u Ala Pro G y Thr Lys
 290 295 300

Leu G n Leu Thr Leu Ser Ala G u Leu G n Ala Tyr Ala Asp Ala Leu
 305 310 315 320

Leu Leu G u Tyr G u Lys Thr G u Thr Phe Arg Ser Ala Lys Ser Leu
 325 330 335

Lys Lys Arg G u Lys Leu Pro Pro Leu Phe Pro Trp Ile Lys G y G y
 340 345 350

Ala Ile Ile Ala Leu Asp Pro Asn Asn G y G u Ile Leu Ala Met Ala
 355 360 365

Ser Ser Pro Arg Tyr Arg Asn Asn Asp Phe Val Asn Ala Lys Val Ala
 370 375 380

G u Asp Ser Lys Ala Val Arg Ser Ser Ile Tyr Arg Trp Leu G u Asn
 385 390 395 400

Lys G u His Ile Ala G u Ile Tyr Asp Arg Lys Val Pro Leu Ile Arg
 405 410 415

G u Arg Arg Asn Pro Leu Thr G y Leu Cys Tyr G u G u Ile Leu Pro
 420 425 430

Leu Thr Phe Asp Cys Phe Leu Asp Phe Leu Phe Pro G u Asn Ser Val
 435 440 445

Ile Lys Leu G n Leu Lys Arg Asn Ser Phe Val G y G n Ala Ile G u
 450 455 460

Val G n Asn Leu Val Thr Arg Leu Leu Ser Leu Phe Pro Tyr G u G u
 465 470 475 480

G y Thr Cys Pro Cys Ser Ala Ile Phe Asp Ala Val Phe Pro Asn G u

G u G y H i s I l e L e u I l e G n G u V a l I l e S e r L e u A r g G u G n L y s
 500 505 510

T r p I l e M e t G u C y s L e u A s n G n H i s L y s A l a A s p I l e G u G u L e u
 515 520 525

L y s G u A l a L e u A s p G n V a l P h e A s n G u L e u P r o A l a A s n T y r A s p
 530 535 540

L y s I l e L e u T y r T h r A s p I l e L e u A r g L e u I l e V a l A s p P r o G u A r g
 545 550 555 560

P h e S e r P r o V a l L e u P r o S e r G u V a l H i s A r g L e u S e r L e u S e r G u
 565 570 575

P h e T h r G u L e u G n G y A r g T y r V a l V a l L e u A r g S e r A l a P h e S e r
 580 585 590

T h r I l e L e u G u A s p A l a P h e I l e G u V a l H i s P h e L y s S e r T r p A r g
 595 600 605

L y s S e r G u P h e L e u G n T y r L e u A l a A l a L y s A r g G n G u G u A l a
 610 615 620

L e u A r g L y s G n A r g T y r P r o T h r P r o T y r V a l A s p T y r L e u G u G u
 625 630 635 640

G u L y s T h r A r g G n T y r L y s M e t P h e C y s G n G u H i s L e u A s p T h r
 645 650 655

P h e L e u A l a T y r L e u P h e S e r L y s T h r P r o T y r L y s G u G y L e u G u
 660 665 670

P r o T y r T y r A s p I l e L e u A s p L e u T r p I l e A s n G u L e u A s p A s n G y
 675 680 685

A l a H i s A r g A l a L e u S e r T r p A s n G u H i s T y r L e u P h e L e u L y s G u
 690 695 700

A r g V a l S e r H i s L e u S e r G u H i s L e u P r o A l a L e u P h e S e r T h r P h e
 705 710 715 720

A r g G u P h e A s n G u L e u G n A r g P r o L e u L e u G y L y s T y r P r o I l e
 725 730 735

S e r I l e V a l A r g A s n L y s A r g G n T h r G u G n A s p L e u A l a A l a S e r
 740 745 750

P h e T y r P r o V a l T y r G y T y r G y T y r L e u A r g P r o H i s A l a T y r G y
 755 760 765

G n Ala Ala Thr Leu Gly Ser Ile Phe Lys Leu Val Ser Ala Tyr Ser
 770 775 780

Val Leu Ser G n Arg Ile Leu Trp Gly His Asn Gu Gu Pro Ala Asn
 785 790 795 800

Pro Leu Val Ile Ile Asp Lys Asn Ser Phe Gly Tyr Arg Ser Ser Lys
 805 810 815

Pro His Val Gly Phe Phe Lys Asp Gly Thr Pro Ile Pro Thr Phe Phe
 820 825 830

Arg Gly Gly Ser Leu Pro Gly Asn Asp Phe Met Gly Arg Gly Phe Ile
 835 840 845

Asp Leu Val Ser Ala Leu Gu Met Ser Ser Asn Pro Tyr Phe Ser Leu
 850 855 860

Leu Val Gly Gu Gly Leu Gly Asp Pro Gu Asp Leu Ala Asp Ala Ala
 865 870 875 880

Ser Leu Phe Gly Phe Gly Gu Lys Thr Gly Leu Gly Leu Pro Gly Gu
 885 890 895

Tyr Ala Gly Arg Val Pro His Asp Leu Ala Tyr Asn Arg Ser Gly Leu
 900 905 910

Tyr Ala Thr Ala Ile Gly G n His Thr Leu Val Val Thr Pro Leu G n
 915 920 925

Thr Ala Val Met Leu Ala Ser Leu Val Asn Gly Gly Val Val Tyr Val
 930 935 940

Pro Lys Leu Leu Leu Gly Gu Trp Gu Gly Gu His Val Ser Tyr Leu
 945 950 955 960

Ser Ser Lys Lys Lys Arg Thr Ile Phe Met Pro Asp Ala Val Val Gu
 965 970 975

Val Leu Lys Thr Gly Met Arg Asn Val Ile Trp Gly G n Tyr Gly Thr
 980 985 990

Ala Arg Ala Ile G n Ser G n Phe Pro Pro G n Leu Leu Ser Arg Ile
 995 1000 1005

Ile Gly Lys Thr Ser Thr Ala Gu Ser Ile Met Arg Val Gly Leu
 1010 1015 1020

Asp Arg Gu Tyr Gly Thr Met Lys Met Lys Asp Ile Trp Phe Ala
 1025 1030 1035

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Al a Val Gly Phe Ser Asp G n Asp Leu Ser Leu Pro Thr Ile Val
1040 1045 1050

Val Ile Val Tyr Leu Arg Leu Gly Gu Phe Gly Arg Asp Al a Al a
1055 1060 1065

Pro Met Al a Val Lys Met Ile Asp Met Trp Gu Lys Ile G n G n
1070 1075 1080

Arg Gu Ser Phe Leu Arg Gly
1085 1090

<210> 126
<211> 406
<212> PRT
<213> Chl amydi a pneumoni ae

<400> 126

Val Lys Asn Leu Lys Gu Asp Phe Pro Ile Phe Al a Al a Lys Al a Lys
1 5 10 15

Gu Asn Gu Pro Phe Ile Tyr Leu Asp Ser Al a Al a Thr Thr G n Lys
20 25 30

Pro G n G n Val Ile Asp Al a Val Al a Asn Phe Tyr Thr Ser Ser Tyr
35 40 45

Al a Thr Val Asn Arg Al a Ile Tyr Ser Ser Ser Arg Asn Val Thr Gu
50 55 60

Al a Tyr Al a Al a Val Arg Gu Lys Val Arg Lys Trp Val Ser Al a Al a
65 70 75 80

Ser Asp Ser Gu Ile Val Phe Thr Arg Gly Thr Thr Al a Gly Leu Asn
85 90 95

Leu Leu Al a Ile Ser Val Asn Asp Leu Trp Ile Pro Lys Gly Gly Val
100 105 110

Val Leu Val Ser Gu Al a Gu His His Al a Asn Val Leu Ser Trp Gu
115 120 125

Ile Al a Cys Arg Arg Arg Gly Ser Leu Val Lys Lys Ile Arg Val His
130 135 140

Asp Ser Gly Leu Ile Asp Leu Asp Asp Leu Gu Lys Leu Leu Asn Gu
145 150 155 160

Gly Al a G n Phe Val Ser Ile Pro His Val Ser Asn Val Thr Gly Cys
165 170 175

Val G n Pro Leu G n G n Val Al a Gu Leu Val His Arg Tyr Asp Al a

Tyr Leu Ala Val Asp Gly Ala Gn Gly Ala Pro His Leu Pro Ile Asp
195 200 205

Val Gn Leu Trp Asp Val Asp Phe Tyr Val Phe Ser Ser His Lys Ile
210 215 220

Tyr Gly Pro Thr Gly Ile Gly Val Leu Tyr Gly Lys Lys Asp Leu Leu
225 230 235 240

Asp Gn Leu Pro Pro Val Gu Gly Gly Gly Asp Met Val Ala Ile Tyr
245 250 255

Asp His Gn Asn Pro Gu Tyr Leu Pro Ala Pro Met Lys Phe Gu Ala
260 265 270

Gly Thr Pro Asn Ile Ala Gly Val Leu Gly Leu Gly Ala Ala Leu Asp
275 280 285

Tyr Leu Asp Gly Leu Ser Ala Lys Phe Ile Tyr Asp Lys Gu Ile Ala
290 295 300

Leu Thr Thr Tyr Leu His Lys Gu Leu Leu Gu Ile Pro Gly Val Gu
305 310 315 320

Ile Leu Gly Pro Ser Ile Gu Gu Pro Arg Gly Ala Leu Ile Gly Met
325 330 335

Thr Ile Asp Gly Ala His Pro Leu Asp Leu Gly Phe Leu Leu Asp Leu
340 345 350

Arg Gly Ile Ala Val Arg Thr Gly His Gn Cys Ala Gn Pro Ala Met
355 360 365

Gu Arg Trp Asn Val Gly His Val Leu Arg Val Ser Leu Gly Ile Tyr
370 375 380

Asn Asp Gu Asp Asp Ile Asp Gn Phe Ile Leu Val Leu Gn Asp Ser
385 390 395 400

Leu Asp Lys Ile Arg Arg
405

<210> 127
<211> 252
<212> PRT
<213> Chl amydi a pneumoni ae
<400> 127

Met Leu Ile Val Leu Ala Phe Arg Gn Val Phe Phe Ser His Ser Arg
1 5 10 15

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Ser G n Leu Asp Arg Leu Lys Asn Tyr Leu Arg Leu Leu Lys G n Asn
20 25 30

Phe Ala Ile Thr Leu Pro Lys Gu Arg Thr Ser Lys Gly His Ser Leu
35 40 45

Met Leu Thr Phe Asp Phe Ala Ser Phe Asp Phe Tyr Thr Asn Ile Phe
50 55 60

Pro Phe Leu Gu Gu G n Lys Ile Pro Ala Val Val Gly Val Ala Ser
65 70 75 80

Arg Tyr Ile Pro Ser Asn Ala Ala G n Asp Leu His Pro Ser His Arg
85 90 95

Leu Lys Pro Ser Gu Thr Leu Ala Phe G n Asp Gu Ile Phe Ser Asn
100 105 110

Tyr Met Pro Phe Cys Cys G n Asn Gu Leu Ile Gu Met Ala Lys Ser
115 120 125

Pro Tyr Ile G n Leu Ala Ser Ser Gly Phe Ala Ile Arg Asn Leu Met
130 135 140

Asn Asn Pro Pro Tyr Leu Thr Thr Gu Ile Leu Leu Ser Arg His His
145 150 155 160

Ile Gu Thr Ile Thr Gly Ala Lys Pro Leu Ala Phe Leu Phe Pro Phe
165 170 175

Gly Lys Ser Asp Pro Thr Ser Arg Lys Leu Ala Ala Asp His Tyr Pro
180 185 190

Tyr Ser Phe Leu Leu Gly Asn Thr Ile Asn Arg Lys Leu Lys Thr His
195 200 205

Asn Ile Tyr Arg Leu Asp Ile Lys Pro Met G n Tyr Val Cys Pro Ser
210 215 220

Leu Phe G n Ser Ser Arg Tyr Leu Lys Asn Trp Ile Lys Gu Lys Ser
225 230 235 240

Lys G n Leu Tyr Leu Lys Lys G n Leu Pro Lys Arg
245 250

<210> 128
<211> 324
<212> PRT
<213> Chl amydi a pneumoni ae

<400> 128

Met Thr Thr Asn Phe Pro G n Pro Leu Ile G n Ala Thr Ser Leu Thr

Ser Thr Gly Cys Tyr Phe Tyr Asn Arg Cys Pro Gl n Lys Gl n Gl u Ala
 290 295 300

Cys Lys Ser Gl u Ile Ile Pro Asn Gl n Gly Asp Ala His His Thr Tyr
 305 310 315 320

Arg Cys Ile His

<210> 129
 <211> 436
 <212> PRT
 <213> Chl amydi a pneumoni ae
 <400> 129

Met Lys Arg Pro Phe Phe Thr Tyr Leu Cys Ile Ile Phe Tyr Gly Ser
 1 5 10 15

Cys Ala Ser Leu Ser Leu His Ala Gly Leu Ser Phe Pro Gl u Val Arg
 20 25 30

Gly Ala Thr Ala Ala Val Val His Ala Asp Ser Gly Lys Val Phe Tyr
 35 40 45

Asp Lys Asp Ile Asp Ala Val Ile Tyr Pro Ala Ser Met Thr Lys Ile
 50 55 60

Ala Thr Ala Leu Phe Ile Leu Lys His Tyr Pro Thr Val Leu Asp Thr
 65 70 75 80

Leu Ile Lys Val Lys Gl n Asp Ala Ile Ala Ser Ile Thr Pro Gl n Ala
 85 90 95

Lys Lys Gl n Ser Gly Tyr Arg Ser Pro Pro His Trp Leu Gl u Thr Asp
 100 105 110

Gly Ser Thr Ile Gl n Leu His Leu Arg Gl u Gl u Leu Leu Gly Trp Asp
 115 120 125

Leu Phe His Ala Leu Leu Val Cys Ser Ala Asn Asp Ala Ala Asn Val
 130 135 140

Leu Ala Met Ala Cys Cys Gly Ser Val Gl u Lys Phe Met Asp Lys Leu
 145 150 155 160

Asn Phe Phe Leu Lys Gl u Gl u Ile Gly Cys Thr His Thr His Phe Asn
 165 170 175

Asn Pro His Gly Leu His His Pro Asn His Tyr Thr Thr Thr Arg Asp
 180 185 190

Leu Ile Ser Ile Met Arg Cys Ala Leu Lys Gu Pro Pro Phe Arg Gly
 195 200 205
 Val Ile Ser Thr Thr Ser Tyr Lys Ile Gly Ala Thr Asn Leu His Gly
 210 215 220
 Gu Arg Ile Leu Ser Pro Thr Asn Lys Leu Leu Leu Pro Gly Ser Thr
 225 230 235 240
 Tyr His Tyr Pro Pro Ala Leu Gly Gly Lys Thr Gly Thr Thr Lys Thr
 245 250 255
 Ala Gly Lys Asn Leu Ile Met Ala Ala Gu Lys Asn Asn Arg Leu Leu
 260 265 270
 Val Thr Ile Ala Thr Gly Tyr Ser Gly Pro Val Ser Asp Leu Tyr Gn
 275 280 285
 Asp Val Ile Ala Leu Cys Gu Thr Val Phe Asn Gu Pro Leu Leu Arg
 290 295 300
 Lys Gu Leu Val Pro Pro Ser Asp Cys Leu Gn Leu Gu Ile Ala Asn
 305 310 315 320
 Leu Gly Lys Leu Ser Cys Pro Leu Pro Gu Gly Leu Tyr Tyr Asp Phe
 325 330 335
 Tyr Ala Ser Gu Asp Arg Gu Pro Leu Ser Val Ser Phe Ile Ala His
 340 345 350
 Ala Asp Ala Phe Pro Ile Gu Gn Gly Asp Leu Leu Gly His Trp Val
 355 360 365
 Phe Tyr Asp Asp Gu Gly Lys Lys Ile Ser Ser Gn Pro Phe Tyr Ala
 370 375 380
 Pro Cys Arg Phe Gu Arg Thr Ile Lys Pro Trp Lys Leu Tyr Met Lys
 385 390 395 400
 Arg Val Phe Thr Ser Tyr Arg Thr Tyr Met Ser Ile Thr Met Leu Leu
 405 410 415
 Met Tyr Phe Arg Ile Arg Lys His Arg Lys Tyr Lys Asn Leu Lys His
 420 425 430
 Tyr Ser Lys Ile
 435

<210> 130
 <211> 235
 <212> PRT
 <213> Chl amydi a pneumoni ae

<400> 130

Met Pro Thr Thr Asn Cys Ile Phe Leu Asp Leu Arg Gly His Ser Ile
1 5 10 15Leu His Gln Leu Gln Ile Gu Gu Ala Leu Leu Arg Val Ala Asn Gln
20 25 30Asn Phe Cys Ile Ile Asn Ser Gly Ala Lys Asp Ser Ile Val Leu Gly
35 40 45Ile Ser Arg Asn Leu Asn Gln Asp Val His Ile Ser Arg Ala Gln Ala
50 55 60Asp His Ile Pro Ile Ile Arg Arg Tyr Ser Gly Gly Gly Thr Val Phe
65 70 75 80Ile Asp Ser Asn Thr Leu Met Val Ser Trp Ile Met Asn Ser Ser Gu
85 90 95Ala Ser Ala Gln Pro Gln Gu Leu Leu Ala Trp Thr Tyr Gly Ile Tyr
100 105 110Ser Pro Leu Leu Pro Asn Thr Phe Ser Ile Arg Gu Asn Asp Tyr Val
115 120 125Leu Gly His Lys Lys Ile Gly Gly Asn Ala Gln Tyr Ile Gln Arg His
130 135 140Arg Trp Val His His Thr Thr Phe Leu Trp Asp Ile Asp Leu Asp Lys
145 150 155 160Leu Ser Tyr Tyr Leu Pro Ile Pro Gln Gln Gln Pro Thr Tyr Arg Asn
165 170 175Gln Arg Ser His Gu Gu Phe Leu Thr Thr Leu Arg Pro Trp Phe Pro
180 185 190Ser Arg Asp Asp Phe Leu Gu Arg Ile Lys Ala Ser Gly Ser Leu Leu
195 200 205Phe Thr Trp Gu Gu Phe Leu Asp Asn Gu Leu Gu Gu Ile Leu Ala
210 215 220Gln Pro His Arg Lys Ala Thr Thr Val Leu Asn
225 230 235

<210> 131

<211> 792

<212> PRT

<213> Chlamydia pneumoniae

<400> 131

Met Arg Ile Pro Ile Thr Leu Leu Gln Thr Tyr Phe Ser Glu Pro Leu
1 5 10 15
Ser Thr Lys Glu Ile Leu Gu Ala Cys Asp His Ile Gly Ile Glu Ala
20 25 30
Glu Ile Glu Asn Thr Thr Leu Tyr Ser Phe Ala Ser Val Ile Thr Ala
35 40 45
Lys Ile Leu His Thr Ile Pro His Pro Asn Ala Asp Lys Leu Arg Val
50 55 60
Ala Thr Leu Thr Asp Gly Gu Lys Gu His Gln Val Val Cys Gly Ala
65 70 75 80
Pro Asn Cys Glu Ala Gly Leu Ile Val Ala Leu Ala Leu Pro Gly Ala
85 90 95
Lys Leu Phe Asp Ser Gu Gly Gln Ala Tyr Thr Ile Lys Lys Ser Lys
100 105
Leu Arg Gly Val Gu Ser Gln Gly Met Cys Cys Gly Ala Asp Glu Leu
115 120 125
Gly Leu Asp Glu Leu Gln Ile Gln Gu Arg Ala Leu Leu Glu Leu Pro
130 135 140
Glu Ala Thr Pro Leu Gly Gu Asp Leu Ala Thr Val Leu Gly Asn Thr
145 150 155 160
Ser Leu Glu Ile Ser Leu Thr Pro Asn Leu Gly His Cys Ala Ser Phe
165 170 175
Leu Gly Leu Ala Arg Gu Ile Cys His Val Thr Gln Ala Asn Leu Val
180 185 190
Ile Pro Lys Glu Phe Ser Phe Gu Asn Leu Pro Thr Thr Ala Leu Asp
195 200 205
Met Gly Asn Asp Pro Asp Ile Cys Pro Phe Phe Ser Tyr Val Val Ile
210 215 220
Thr Gly Ile Ser Ala Gln Pro Ser Pro Ile Lys Leu Gln Glu Ser Leu
225 230 235 240
Gln Ala Leu Lys Gln Lys Pro Ile Asn Ala Ile Val Asp Ile Thr Asn
245 250 255
Tyr Ile Met Leu Ser Leu Gly Gln Pro Leu His Ala Tyr Asp Ala Ser
260 265 270
His Val Ala Leu Asp Ser Leu Arg Val Gu Lys Leu Ser Thr Pro Glu
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275

280

285

Ser Leu Thr Leu Leu Asn Gly Gu Thr Val Leu Leu Pro Ser Gly Val
 290 295 300

Pro Val Val Arg Asp Asp His Ser Leu Leu Gly Leu Gly Gly Val Met
 305 310 315 320

Gly Ala Lys Ala Pro Ser Phe Gn Gu Thr Thr Thr Thr Val Ile
 325 330 335

Lys Ala Ala Tyr Phe Leu Pro Gu Ala Leu Arg Ala Ser Gn Lys Leu
 340 345 350

Leu Pro Ile Pro Ser Gu Ser Ala Tyr Arg Phe Thr Arg Gly Ile Asp
 355 360 365

Pro Gn Asn Val Val Pro Ala Leu Gn Ala Ala Ile His Tyr Ile Leu
 370 375 380

Gu Ile Phe Pro Gu Ala Thr Ile Ser Pro Ile Tyr Ser Ser Gly Gu
 385 390 395 400

Ile Cys Arg Gu Leu Lys Gu Val Ala Leu Arg Pro Lys Thr Leu Gn
 405 410 415

Arg Ile Leu Gly Lys Ser Phe Ser Ile Gu Ile Leu Ser Gn Lys Leu
 420 425 430

Gn Ser Leu Gly Phe Ser Thr Thr Pro Gn Gu Thr Ser Leu Leu Val
 435 440 445

Lys Val Pro Ser Tyr Arg His Asp Ile Asn Gu Gu Ile Asp Leu Val
 450 455 460

Gu Gu Ile Cys Arg Thr Gu Ser Trp Asn Ile Gu Thr Gn Asn Pro
 465 470 475 480

Val Ser Cys Tyr Thr Pro Ile Tyr Lys Leu Lys Arg Gu Thr Ala Gly
 485 490 495

Phe Leu Ala Asn Ala Gly Leu Gn Gu Phe Phe Thr Pro Asp Leu Leu
 500 505 510

Asp Pro Gu Thr Val Ala Leu Thr Arg Lys Gu Lys Gu Gu Ile Ser
 515 520 525

Leu Gn Gly Ser Lys His Thr Thr Val Leu Arg Ser Ser Leu Leu Pro
 530 535 540

Gly Leu Leu Lys Ser Ala Ala Thr Asn Leu Asn Arg Gn Ala Pro Ser
 545 550 555 560

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Val G n Ala Phe G u Ile G y Thr Val Tyr Ala Lys His G y G u G n
565 570 575

Oys G n G u Thr G n Thr Leu Ala Ile Leu Leu Thr G u Asp G y G u
580 585 590

Ser Arg Ser Trp Leu Pro Lys Pro Ser Leu Ser Phe Tyr Ser Leu Lys
595 600 605

G y Trp Val G u Arg Leu Leu Tyr His His His Leu Ser Ile Asp Ala
610 615 620

Leu Thr Leu G u Ser Ser Ala Leu Oys G u Phe His Pro Tyr G n G n
625 630 635 640

G y Val Leu Arg Ile His Lys G n Ser Phe Ala Thr Leu G y G n Val
645 650 655

His Pro G u Leu Ala Lys Lys Ala G n Ile Lys His Pro Val Phe Phe
660 665 670

Ala G u Leu Asn Leu Asp Leu Leu Oys Lys Met Leu Lys Lys Thr Thr
675 680 685

Lys Leu Tyr Lys Pro Tyr Ala Ile Tyr Pro Ser Ser Phe Arg Asp Leu
690 695 700

Thr Leu Thr Val Pro G u Asp Ile Pro Ala Asn Leu Leu Arg G n Lys
705 710 715 720

Leu Leu His G u G y Ser Lys Trp Leu G u Ser Val Thr Ile Ile Ser
725 730 735

Ile Tyr G n Asp Lys Ser Leu G u Thr Arg Asn Lys Asn Val Ser Leu
740 745 750

Arg Leu Val Phe G n Asp Tyr G u Arg Thr Leu Ser Asn G n Asp Ile
755 760 765

G u G u G u Tyr Oys Arg Leu Val Ala Leu Leu Asn G u Leu Leu Thr
770 775 780

Asp Thr Lys G y Thr Ile Asn Ser
785 790

- <210> 132
- <211> 252
- <212> PRT
- <213> Chl amydi a pneumoni ae
- <400> 132

Met 1 G n 1 I l e 5 C y s 5 V a l 5 T h r 5 G y 5 V a l 5 V a l 10 L e u 10 A r g 10 S e r 10 A r g 10 P r o 10 L e u 15 G y 15
L y s 20 A s n 20 H i s 20 T h r 20 L e u 20 T h r 20 T h r 20 L e u 25 P h e 25 T h r 25 P r o 25 G l u 25 G y 25 L e u 30 P h e 30 T h r 30
P h e 35 P h e 35 A l a 35 L y s 35 G n 35 G y 35 G n 35 T h r 40 L e u 40 G n 40 C y s 40 A s p 40 T y r 45 A r g 45 G l u 45 T h r 45
L e u 50 V a l 50 P r o 50 I l e 50 S e r 50 L e u 55 G y 55 L y s 55 T y r 55 T h r 55 L e u 60 H i s 60 A r g 60 A s n 60 G y 60 S e r 60
A r g 65 L e u 65 P r o 65 L y s 65 L e u 70 T h r 70 H i s 70 G y 70 A s p 70 I l e 75 L e u 75 A s n 75 A l a 75 P h e 75 G l u 75 A l a 80
I l e 85 L y s 85 G n 85 T h r 85 T y r 85 A l a 85 L e u 85 L e u 85 G l u 85 A l a 85 S e r 85 G y 85 L y s 85 M e t 85 I l e 85 G n 85
A l a 90 L e u 90 L e u 90 A l a 95 S e r 95 G n 95 T r p 95 L y s 95 G l u 95 L y s 95 P r o 95 S e r 95 H i s 95 L y s 95 L e u 95 P h e 95
S e r 100 L e u 100 P h e 100 L e u 100 A s n 100 P h e 100 L e u 100 H i s 100 A r g 100 I l e 100 P r o 100 G l u 100 S e r 100 S e r 100 A s n 100 P r o 100
G l u 105 P h e 105 P h e 105 A l a 110 A l a 110 I l e 110 P h e 110 V a l 110 L e u 110 L y s 110 L e u 110 L e u 110 G n 110 T y r 110 G l u 110 G y 110
I l e 115 L e u 115 A s p 115 L e u 115 T h r 115 P r o 115 A l a 115 C y s 115 S e r 115 L e u 115 C y s 115 L y s 115 A l a 115 S e r 115 L e u 115 P r o 115
T y r 120 A l a 120 C y s 120 T y r 120 A r g 120 T y r 120 G n 120 G y 120 H i s 120 L y s 120 L e u 120 C y s 120 L y s 120 L y s 120 H i s 120 G n 120
H i s 125 L y s 125 G n 125 A l a 130 I l e 130 S e r 130 I l e 130 G l u 130 L y s 130 G l u 130 G l u 130 G l u 130 G n 130 I l e 130 L e u 130 G n 130
A l a 135 I l e 135 I l e 135 H i s 135 A l a 140 L y s 140 G n 140 P h e 140 S e r 140 G l u 140 L e u 140 L e u 140 A l a 140 I l e 140 A l a 140 G l u 140
P h e 145 P r o 145 I l e 145 A l a 145 I l e 145 A l a 150 G l u 150 L y s 150 I l e 150 P h e 150 T y r 150 L e u 150 P h e 150 A s p 150 S e r 150 L e u 150
G n 155 G l u 155 G l u 155 L y s 155 L y s 155 S e r 155 G l u 155 A r g 155 A s n 155 S e r 155 S e r 155 G l u 155 A s p 155 P r o 155 T y r 155 H i s 155
G l u 160 I l e 160 L e u 160 A r g 160 L e u 160 S e r 160 L y s 160 V a l 160 V a l 160 H i s 160 P r o 160 T y r 160

<210> 133

<211> 267

<212> PRT

<213> Chl amydi a pneumoni ae

<400> 133

Met Thr Lys Val Ala Leu Leu Ile Ala Tyr Gln Gly Thr Ala Tyr Ser
 1 5 10 15
 Gly Trp Gln Gln Gln Pro Asn Asp Leu Ser Ile Gln Glu Val Ile Glu
 20 25 30
 Ser Ser Leu Lys Lys Ile Thr Lys Thr Arg Thr Pro Leu Ile Ala Ser
 35 40 45
 Gly Arg Thr Asp Ala Gly Val His Ala Tyr Gly Gln Val Ala His Phe
 50 55 60
 Arg Ala Pro Asp His Pro Leu Phe Ala Asn Ala Asn Leu Thr Lys Lys
 65 70 75 80
 Ala Leu Asn Ala Ile Leu Pro Lys Asp Ile Val Ile Arg Asp Val Ala
 85 90 95
 Leu Phe Asp Asp Asn Phe His Ala Arg Tyr Leu Thr Ile Ala Lys Glu
 100 105 110
 Tyr Arg Tyr Ser Leu Ser Arg Leu Ala Lys Pro Leu Pro Trp Gln Arg
 115 120 125
 His Phe Cys Tyr Thr Pro Arg His Pro Phe Ser Thr Glu Leu Met Gln
 130 135 140
 Glu Gly Ala Asn Leu Leu Ile Gly Thr His Asp Phe Ala Ser Phe Ala
 145 150 155 160
 Asn His Gly Arg Asp Tyr Asn Ser Thr Val Arg Thr Ile Tyr Thr Leu
 165 170 175
 Asp Ile Val Asp Lys Gly Asp Ser Leu Ser Ile Ile Cys Arg Gly Asn
 180 185 190
 Gly Phe Leu Tyr Lys Met Val Arg Asn Leu Val Gly Ala Leu Leu Asp
 195 200 205
 Val Gly Lys Gly Ala Tyr Pro Pro Glu His Leu Leu Asp Ile Leu Glu
 210 215 220
 Gln Lys Asn Arg Arg Glu Gly Pro Ser Ala Ala Pro Ala Tyr Gly Leu
 225 230 235 240
 Ser Leu His His Val Cys Tyr Ser Ser Pro Tyr Asn Asn Phe Cys Cys
 245 250 255
 Glu Gln Cys Ser Val Ser Thr Ser Asn Glu Gly
 260 265

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<210> 134
 <211> 1402
 <212> PRT
 <213> Chl amydi a pneumoni ae

<400> 134

Met Lys G n Lys Val Lys Arg Asn Phe Ala Ile Ile Ile Cys Val Phe
 1 5 10 15

Ala Leu Ala Leu Tyr Tyr Val Leu Pro Thr Cys Leu Tyr Tyr Ala Lys
 20 25 30

Pro Leu Asp Lys Lys Ile Asp Gly Asn Gu Ala Gu His Ile Ile Lys
 35 40 45

Ser Phe Thr Lys G n Ala G n G n Val Arg Lys Asp Val Ile Pro Arg
 50 55 60

Val Ser Ala Ile Leu Ser Ser Leu His Leu Arg Gly His Ile G n G n
 65 70 75 80

His Pro Ala Ile Pro Asp Ile Val Ser Val Arg Phe Lys Arg Gly Gu
 85 90 95

Asp Ala Gu Asp Phe Ile Gly Asn Leu Val His Gly Gu Pro Asn Val
 100 105 110

Pro Ile Lys Ser Ala Arg Leu His Val Val Gly Tyr Ser Arg Gu His
 115 120 125

Asp Asp His Val Ile G n Val Ala Ser Ser Ile Asn Thr Ser Leu Val
 130 135 140

Gu Ser Asp Phe Ser Phe Val Ser Tyr Ser Ser Gu Asn Gu G n Gu
 145 150 155 160

Met Ala Ser Ser Ile Leu G n Arg Val Tyr Ser Ala Cys Thr Phe Pro
 165 170 175

Lys G n Lys Asp Cys Ser Cys Ser Tyr Pro Ser Ile Trp Gu Thr Ala
 180 185 190

Pro Lys Gu G n Leu Leu G n Tyr Ala Lys Asn Leu Ser Ser Gly Phe
 195 200 205

Gu Val Phe Ser Ser Arg Leu Ser Ala Phe Cys G n G n Ser Phe Ser
 210 215 220

Ser Asn G n Asp Arg Leu Ala Phe Leu Ser Arg Leu Ser Ser Leu Ser
 225 230 235 240

Asn Asp Ala Ala Ile Asp Val Gu Asp G n Lys Leu Leu Lys Ser Val

Tyr G u Thr Leu Ser G n Thr Al a Cys Ile Arg Ser Leu Asp Cys Pro
 260 265 270
 Tyr Ile G u G y Leu Arg Leu Asp Cys Ser G u Ser Ser Leu Phe Phe
 275 280 285
 Ser Ser Ile G u Tyr Cys Pro Lys G u Arg Lys Ile Phe Leu Thr Leu
 290 295 300
 His Ser Asp Leu Leu Al a G n Arg Thr Ser Leu Ser Lys G u G n Arg
 305 310 315 320
 Leu Asp Phe Asp Ser Arg Leu Al a Val G u Lys G n Lys Leu Ser Lys
 325 330 335
 Asn Leu Thr Val G n Val G u Asp Tyr Asn Asn G y Phe Ser Phe G n
 340 345
 Trp Met Asp Lys Asp Thr G n G y Lys Ile Ile Leu G n G y G u Arg
 355 360 365
 Leu Leu G n G y Ile Al a G u His Leu Thr Al a Leu Thr Leu His Arg
 370 375 380
 Pro Al a Al a G u Ser Cys Asp Leu Ile Pro G u Asn Phe Pro Val Phe
 385 390 400
 Cys Arg G n Pro Arg G u Ser G u Al a Phe G y Cys Tyr Ile Phe Ser
 405 410 415
 Pro Asn Thr Asp Cys Lys His Phe Ser Lys G y Ser Val Tyr Ile Leu
 420 425 430
 Leu Lys G y Leu Arg Ser Ile Val Al a Lys Tyr G n G n G y G y G y
 435 440 445
 Lys G u Leu G n Ser Phe G u Lys Asp Leu G n Asn Leu Tyr Asn Cys
 450 455 460
 Phe Ser His Thr G u Al a Ile Ser Trp Thr Leu G y G u Asp G n Val
 465 470 475 480
 Leu G u Ile Arg His Pro Leu G n G n Phe Leu Asp Val Trp G y G u
 485 490 495
 G y Phe Val Ile G y Lys G u G y Cys Al a Phe Leu G u Val Lys Asp
 500 505 510
 Ile G n Asp Arg Leu Al a Thr Val Asn G n Ile G u Lys Asn Arg G n
 515 520 525

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Ser Asp Leu Val Arg Trp His Glu Gln Tyr Arg His Ala Lys Cys Ser
530 535 540

Met Asp Leu Gln Glu Arg Leu Ser Ala Pro Ile Pro Tyr Gln Asn Leu
545 550 555 560

Phe Leu Glu Asn Met Lys Leu Asn Met Arg Lys Phe Ser Arg Gly Glu
565 570 575

Asn Ile Leu Arg Leu Gly Ile Asp Phe Val Gly Gly Arg Gln Leu Leu
580 585 590

Leu Ser Phe Lys Asp His Gln Gly Lys Gln Leu Thr Asp Lys Glu Asp
595 600 605

Ile Leu Lys Val Ser Asp Glu Leu Cys Ala Arg Leu Asn Lys Leu Gly
610 615 620

Val Ser Glu Ile Glu Leu Arg Arg Glu Gly Asp Tyr Ile His Leu Ser
625 630 635 640

Val Pro Gly Ser Ser Thr Ile Ser Ser Ser Glu Ile Leu Gly Thr Ser
645 650 655

Lys Met Ser Phe His Val Val Asn Glu Arg Phe Ser Ser Tyr Ser Ala
660 665 670

Ser Arg Tyr Glu Val Gln Arg Phe Leu Asp Tyr Leu Trp Phe Thr Ser
675 680 685

Gln Ala Gln Gly Lys Thr Ser Pro Glu Glu Ile Asn Thr Phe Ala Ser
690 695 700

Ala Leu Phe Asn Glu Glu Val Asp Val Pro Pro Ser Val His Glu Ala
705 710 715 720

Ile Thr Lys Leu Lys Ser Glu Gly Leu Ala Phe Ser Pro Ser Gly Cys
725 730 735

Glu Thr Pro Ser Thr Asp Leu Asp Thr Thr Phe Ser Met Ile Ala Ile
740 745 750

Gly Lys Asp Ala Glu Gln Lys Ala Asn Pro Leu Val Ile Val Phe Arg
755 760 765

Asn Tyr Ala Leu Asp Gly Ala Ser Leu Lys Asp Ile Arg Pro Glu Phe
770 775 780

Ala Ala Gly Glu Gly Tyr Val Leu Asn Phe Ser Val Lys Asp Thr Ser
785 790 795 800

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Pro Lys Lys Met Ala Gu Lys Leu Ser Pro Thr Gu Ser Phe His Thr
 805 810 815
 Trp Thr Ser Ala Tyr Cys Gn Gu Gly Ile Ser Gly Thr Ala Asn Gly
 820 825 830
 Gn Tyr Ser Ala Asn Arg Gly Trp Arg Met Ala Val Val Ile Asp Gly
 835 840 845
 Tyr Met Val Ser Ser Pro Ile Leu Asn Val Pro Leu Lys Asn His Ala
 850 855 860
 Ser Val Ser Gly Lys Phe Thr His Arg Gu Val Ser Lys Leu Ala Ser
 865 870 875 880
 Asp Leu Lys Ser Gly Ala Met Ser Phe Val Pro Gu Val Leu Ser Gu
 885 890 895
 Gu Thr Ile Ser Ser Asp Leu Gly Lys Lys Gn Cys Thr Gn Gly Ile
 900 905 910
 Ile Ser Ala Cys Cys Gly Leu Ala Met Leu Ile Val Leu Met Ser Val
 915 920 925
 Tyr Tyr Arg Phe Gly Gly Val Ile Ala Ser Gly Ala Val Leu Leu Asn
 930 935 940
 Leu Leu Leu Ile Trp Ala Ala Leu Gn Tyr Leu Asp Ala Pro Leu Thr
 945 950 955 960
 Leu Ser Gly Leu Ala Gly Ile Val Leu Ala Met Gly Met Ala Val Asp
 965 970 975
 Ala Asn Val Leu Val Phe Gu Arg Ile Arg Gu Gu Phe Leu Leu Ser
 980 985 990
 Gn Ser Leu Lys Lys Ser Val Gu Lys Gly Tyr Thr Lys Ala Phe Gly
 995 1000 1005
 Ala Ile Phe Asp Ser Asn Leu Thr Thr Val Leu Ala Ser Ala Leu
 1010 1015 1020
 Leu Phe Phe Leu Asp Thr Gly Pro Ile Lys Gly Phe Ala Leu Thr
 1025 1030 1035
 Leu Ile Leu Gly Ile Phe Ser Ser Met Phe Thr Ala Leu Phe Met
 1040 1045 1050
 Thr Lys Phe Phe Phe Met Leu Trp Met Asn Lys Thr Gn His Thr
 1055 1060 1065

G n Leu His Met Met Asn Lys Phe Val Gly Ile Lys His Asp Phe
 1070 1075 1080
 Leu Arg Gly Cys Lys Lys Leu Trp Ala Val Ser Gly Ser Val Phe
 1085 1090 1095
 Leu Leu Gly Cys Val Ala Leu Gly Phe Gly Ala Trp Asn Ser Val
 1100 1105 1110
 Leu Gly Met Asp Phe Lys Gly Gly Tyr Ala Phe Thr Phe Asn Pro
 1115 1120 1125
 Lys Gu His Gly Ile Ser Asp Val Ala G n Met Arg Gly Lys Val
 1130 1135 1140
 Val His Lys Leu G n Gu Ala Gly Leu Ser Ser Arg Asp Phe Arg
 1145 1150 1155
 Ile G n Thr Phe Gly Ser Ser Gu Lys Ile Lys Ile Tyr Phe Ser
 1160 1165 1170
 Asp Lys Ala Leu Ser Tyr Thr Lys Ala Asp Thr Ser Leu Ser Pro
 1175 1180 1185
 Lys Ile Asn Asp His Gu Leu Ala Leu Ala Val Gly Leu Leu Ser
 1190 1195 1200
 Gu Thr Gly Leu Asp Phe Ser Thr Gu Thr Leu Asn Gu Thr G n
 1205 1210 1215
 Asn Phe Trp Ser Lys Val Ser Ser Lys Leu Ser Lys Lys Met Arg
 1220 1225 1230
 Tyr G n Ala Thr Ile Gly Leu Leu Gly Ala Leu Ala Ile Ile Leu
 1235 1240 1245
 Leu Tyr Val Ser Leu Arg Phe Gu Trp G n Tyr Ala Phe Ser Ala
 1250 1255 1260
 Val Cys Ala Leu Ile His Asp Leu Leu Ala Thr Cys Ala Val Leu
 1265 1270 1275
 Phe Ile Ala His Phe Phe Leu Lys Lys Ile G n Ile Asp Leu G n
 1280 1285 1290
 Ala Ile Gly Ala Leu Met Thr Val Leu Gly Tyr Ser Leu Asn Asn
 1295 1300 1305
 Thr Leu Ile Ile Phe Asp Arg Ile Arg Gu Asp Arg G n Ala Asn
 1310 1315 1320
 Leu Phe Thr Pro Met His Val Leu Val Asn Asp Ala Leu G n Lys
 1325 1330 1335

1325

1330

1335

Thr Phe Ser Arg Thr Val Met Thr Thr Ala Thr Thr Leu Ser Val
 1340 1345 1350

Leu Leu Met Leu Leu Phe Ile Gly Gly Ser Ser Val Phe Asn Phe
 1355 1360 1365

Ala Phe Ile Met Thr Ile Gly Ile Leu Leu Gly Thr Leu Ser Ser
 1370 1375 1380

Leu Tyr Ile Ala Pro Pro Leu Leu Leu Phe Met Val Arg Lys Gu
 1385 1390 1395

Asn Arg Ser Lys
 1400

<210> 135

<211> 245

<212> PRT

<213> Chl amydi a pneumni ae

<400> 135

Met Thr Ile Arg Ile Leu Ala Gu Gly Leu Ala Phe Arg Tyr Gly Ser
 1 5 10 15

Lys Gly Pro Asn Ile Ile His Asp Val Ser Phe Ser Val Tyr Asp Gly
 20 25 30

Asp Phe Ile Gly Ile Ile Gly Pro Asn Gly Gly Gly Lys Ser Thr Leu
 35 40 45

Thr Met Leu Ile Leu Gly Leu Leu Thr Pro Thr Phe Gly Ser Leu Lys
 50 55 60

Thr Phe Pro Ser His Ser Ala Gly Lys Gn Thr His Ser Met Ile Gly
 65 70 75 80

Trp Val Pro Gn His Phe Ser Tyr Asp Pro Cys Phe Pro Ile Ser Val
 85 90 95

Lys Asp Val Val Leu Ser Gly Arg Leu Ser Gn Leu Ser Trp His Gly
 100 105 110

Lys Tyr Lys Lys Lys Asp Phe Gu Ala Val Asp His Ala Leu Asp Leu
 115 120 125

Val Gly Leu Ser Asp His His His His Cys Phe Ala His Leu Ser Gly
 130 135 140

Gly Gn Ile Gn Arg Val Leu Leu Ala Arg Ala Leu Ala Ser Tyr Pro
 145 150 155 160

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G u l l e Leu l l e Leu Asp G u Pro Thr Thr Asn l l e Asp Pro Asp Asn
165 170 175

G n G n Arg l l e Leu Ser l l e Leu Lys Lys Leu Asn Arg Thr Cys Thr
180 185 190

l l e Leu Met Val Thr His Asp Leu His His Thr Thr Asn Tyr Phe Asn
195 200 205

Lys Val Phe Tyr Met Asn Lys Thr Leu Thr Ser Leu Ala Asp Thr Ser
210 215 220

Thr Leu Thr Asp G n Phe Cys Cys His Pro Tyr Lys Asn G n G u Phe
225 230 235 240

Ser Cys Ser Pro His
245

<210> 136
<211> 1732
<212> PRT
<213> Chl amydi a pneumoni ae

<400> 136

Val Asn l l e Ser Asp Arg Phe Ser Ser Met Lys Trp Leu Pro Ala Thr
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Al a Val Phe Al a Al a Val Leu Pro Al a Leu Thr Al a Phe Gly Asp Pro
20 25 30

Al a Ser Val G u l l e Ser Thr Ser His Thr Gly Ser Gly Asp Pro Thr
35 40 45

Ser Asp Al a Al a Leu Thr Gly Phe Thr G n Ser Ser Thr G u Thr Asp
50 55 60

Gly Thr Thr Tyr Thr l l e Val Gly Asp l l e Thr Phe Ser Thr Phe Thr
65 70 75 80

Asn l l e Pro Val Pro Val Val Thr Pro Asp Al a Asn Asp Ser Ser Ser
85 90 95

Asn Ser Ser Lys Gly Gly Ser Ser Ser Ser Gly Al a Thr Ser Leu l l e
100 105 110

Arg Ser Ser Asn Leu His Ser Asp Phe Asp Phe Thr Lys Asp Ser Val
115 120 125

Leu Asp Leu Tyr His Leu Phe Phe Pro Ser Al a Ser Asn Thr Leu Asn
130 135 140

Pro Al a Leu Leu Ser Ser Ser Ser Ser Gly Gly Ser Ser Ser Ser Ser
Page 146

Ile G n Ile G n G n Cys Thr Gly Thr Thr Leu Phe Ser Gly Asn Thr
 435 440 445
 Ala Asn Lys Ser Gly Gly Gly Ile Tyr Ala Val Gly G n Val Thr Leu
 450 455 460
 Gu Asp Ile Ala Asn Leu Lys Met Thr Asn Asn Thr Cys Lys Gly Gu
 465 470 475 480
 Gly Gly Ala Ile Tyr Thr Lys Lys Ala Leu Thr Ile Asn Asn Gly Ala
 485 490 495
 Ile Leu Thr Thr Phe Ser Gly Asn Thr Ser Thr Asp Asn Gly Gly Ala
 500 505 510 515
 Ile Phe Ala Val Gly Gly Ile Thr Leu Ser Asp Leu Val Gu Val Arg
 515 520 525
 Phe Ser Lys Asn Lys Thr Gly Asn Tyr Ser Ala Pro Ile Thr Lys Ala
 530 535 540 545
 Ala Ser Asn Thr Ala Pro Val Val Ser Ser Ser Thr Thr Ala Ala Ser
 545 550 555 560 565
 Pro Ala Val Pro Ala Ala Ala Ala Ala Pro Val Thr Asn Ala Ala Lys
 565 570 575
 Gly Gly Ala Leu Tyr Ser Thr Gu Gly Leu Thr Val Ser Gly Ile Thr
 580 585 590
 Ser Ile Leu Ser Phe Gu Asn Asn Gu Cys G n Asn G n Gly Gly Gly
 595 600 605
 Ala Tyr Val Thr Lys Thr Phe G n Cys Ser Asp Ser His Arg Leu G n
 610 615 620
 Phe Thr Ser Asn Lys Ala Ala Asp Gu Gly Gly Gly Leu Tyr Cys Gly
 625 630 635 640
 Asp Asp Val Thr Leu Thr Asn Leu Thr Gly Lys Thr Leu Phe G n Gu
 645 650 655
 Asn Ser Ser Gu Lys His Gly Gly Gly Leu Ser Leu Ala Ser Gly Lys
 660 665 670
 Ser Leu Thr Met Thr Ser Leu Gu Ser Phe Cys Leu Asn Ala Asn Thr
 675 680 685
 Ala Lys Gu Asn Gly Gly Gly Ala Asn Val Pro Gu Asn Ile Val Leu
 690 695 700

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Thr Phe Thr Tyr Thr Pro Thr Pro Asn Gu Pro Ala Pro Val Gn Gn
705 710 715 720

Pro Val Tyr Gy Gu Ala Leu Val Thr Gy Asn Thr Ala Thr Lys Ser
725 730 735

Gy Gy Gy Ile Tyr Thr Lys Asn Ala Ala Phe Ser Asn Leu Ser Ser
740 745 750

Val Thr Phe Asp Gn Asn Thr Ser Ser Gu Asn Gy Gy Ala Leu Leu
755 760 765

Thr Gn Lys Ala Ala Asp Lys Thr Asp Cys Ser Phe Thr Tyr Ile Thr
770 775 780

Asn Val Asn Ile Thr Asn Asn Thr Ala Thr Gy Asn Gy Gy Gy Ile
785 790 800

Ala Gy Gy Lys Ala His Phe Asp Arg Ile Asp Asn Leu Thr Val Gn
805 810 815

Ser Asn Gn Ala Lys Lys Gy Gy Gy Val Tyr Leu Gu Asp Ala Leu
820 825 830

Ile Leu Gu Lys Val Ile Thr Gy Ser Val Ser Gn Asn Thr Ala Thr
835 840 845

Gu Ser Gy Gy Gy Ile Tyr Ala Lys Asp Ile Gn Leu Gn Ala Leu
850 855 860

Pro Gy Ser Phe Thr Ile Thr Asp Asn Lys Val Gu Thr Ser Leu Thr
865 870 875 880

Thr Ser Thr Asn Leu Tyr Gy Gy Gy Ile Tyr Ser Ser Gy Ala Val
885 890 895

Thr Leu Thr Asn Ile Ser Gy Thr Phe Gy Ile Thr Gy Asn Ser Val
900 905 910

Ile Asn Thr Ala Thr Ser Gn Asp Ala Asp Ile Gn Gy Gy Gy Ile
915 920 925

Tyr Ala Thr Thr Ser Leu Ser Ile Asn Gn Cys Asn Thr Pro Ile Leu
930 935 940

Phe Ser Asn Asn Ser Ala Ala Thr Lys Lys Thr Ser Thr Thr Lys Gn
945 950 955 960

Ile Ala Gy Gy Ala Ile Phe Ser Ala Ala Val Thr Ile Gu Asn Asn
965 970 975

Ser G n Pro Ile Ile Phe Leu Asn Asn Ser Ala Lys Ser Glu Ala Thr
 980 985 990

Thr Ala Ala Thr Ala Gly Asn Lys Asp Ser Cys Gly Gly Ala Ile Ala
 995 1000 1005

Ala Asn Ser Val Thr Leu Thr Asn Asn Pro Glu Ile Thr Phe Lys
 1010 1015 1020

Gly Asn Tyr Ala Glu Thr Gly Gly Ala Ile Gly Cys Ile Asp Leu
 1025 1030 1035

Thr Asn Gly Ser Pro Pro Arg Lys Val Ser Ile Ala Asp Asn Gly
 1040 1045 1050

Ser Val Leu Phe G n Asp Asn Ser Ala Leu Asn Arg Gly Gly Ala
 1055 1060 1065

Ile Tyr Gly Glu Thr Ile Asp Ile Ser Arg Thr Gly Ala Thr Phe
 1070 1075 1080

Ile Gly Asn Ser Ser Lys His Asp Gly Ser Ala Ile Cys Cys Ser
 1085 1090 1095

Thr Ala Leu Thr Leu Ala Pro Asn Ser G n Leu Ile Phe Glu Asn
 1100 1105 1110

Asn Lys Val Thr Glu Thr Thr Ala Thr Thr Lys Ala Ser Ile Asn
 1115 1120 1125

Asn Leu Gly Ala Ala Ile Tyr Gly Asn Asn Glu Thr Ser Asp Ile
 1130 1135 1140

Thr Ile Ser Leu Ser Ala Glu Asn Gly Ser Ile Phe Phe Lys Asn
 1145 1150 1155

Asn Leu Cys Thr Ala Thr Asn Lys Tyr Cys Ser Ile Ala Gly Asn
 1160 1165 1170

Val Lys Phe Thr Ala Ile Glu Ala Ser Ala Gly Lys Ala Ile Ser
 1175 1180 1185

Phe Tyr Asp Ala Val Asn Val Ser Thr Lys Glu Thr Asn Ala G n
 1190 1195 1200

Glu Leu Lys Leu Asn Glu Lys Ala Thr Ser Thr Gly Thr Ile Leu
 1205 1210 1215

Phe Ser Gly Glu Leu His Glu Asn Lys Ser Tyr Ile Pro G n Lys
 1220 1225 1230

Val Thr Phe Ala His Gly Asn Leu Ile Leu Gly Lys Asn Ala Glu
 1235 1240 1245

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Ser Gu Tyr His Leu Asp Asn Tyr Lys His Lys Gly Ser Gly His
 1505 1510 1515

Ser Thr Gn Ala Ser Leu Tyr Ala Gly Asn Ile Phe Tyr Phe Pro
 1520 1525 1530

Ala Ile Arg Ser Arg Pro Ile Leu Phe Gn Gly Val Ala Thr Tyr
 1535 1540 1545

Gly Tyr Met Gn His Asp Thr Thr Thr Tyr Tyr Pro Ser Ile Gu
 1550 1555 1560

Gu Lys Asn Met Ala Asn Trp Asp Ser Ile Ala Trp Leu Phe Asp
 1565 1570 1575

Leu Arg Phe Ser Val Asp Leu Lys Gu Pro Gn Pro His Ser Thr
 1580 1585 1590

Ala Arg Leu Thr Phe Tyr Thr Gu Ala Gu Tyr Thr Arg Ile Arg
 1595 1600 1605

Gn Gu Lys Phe Thr Gu Leu Asp Tyr Asp Pro Arg Ser Phe Ser
 1610 1615 1620

Ala Cys Ser Tyr Gly Asn Leu Ala Ile Pro Thr Gly Phe Ser Val
 1625 1630 1635

Asp Gly Ala Leu Ala Trp Arg Gu Ile Ile Leu Tyr Asn Lys Val
 1640 1645 1650

Ser Ala Ala Tyr Leu Pro Val Ile Leu Arg Asn Asn Pro Lys Ala
 1655 1660 1665

Thr Tyr Gu Val Leu Ser Thr Lys Gu Lys Gly Asn Val Val Asn
 1670 1675 1680

Val Leu Pro Thr Arg Asn Ala Ala Arg Ala Gu Val Ser Ser Gn
 1685 1690 1695

Ile Tyr Leu Gly Ser Tyr Trp Thr Leu Tyr Gly Thr Tyr Thr Ile
 1700 1705 1710

Asp Ala Ser Met Asn Thr Leu Val Gn Met Ala Asn Gly Gly Ile
 1715 1720 1725

Arg Phe Val Phe
 1730

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<213> Chl amydi a pneumni ae

<400> 137

Met Lys Gln Met Arg Leu Trp Gly Phe Leu Phe Leu Ser Ser Phe Cys
1 5 10 15Gln Val Ser Tyr Leu Arg Ala Asn Asp Val Leu Leu Pro Leu Ser Gly
20 25 30Ile His Ser Gly Glu Asp Leu Glu Leu Phe Thr Leu Arg Ser Ser Ser
35 40 45Pro Thr Lys Thr Thr Tyr Ser Leu Arg Lys Asp Phe Ile Val Cys Asp
50 55 60Phe Ala Gly Asn Ser Ile His Lys Pro Gly Ala Ala Phe Leu Asn Leu
65 70 75 80Lys Gly Asp Leu Phe Phe Ile Asn Ser Thr Pro Leu Ala Ala Leu Thr
85 90 95Phe Lys Asn Ile His Leu Gly Ala Arg Gly Ala Gly Leu Phe Ser Glu
100 105 110Ser Asn Val Thr Phe Lys Gly Leu His Ser Leu Val Leu Glu Asn Asn
115 120 125Glu Ser Trp Gly Gly Val Leu Thr Thr Ser Gly Asp Leu Ser Phe Ile
130 135 140Asn Asn Thr Ser Val Leu Cys Gln Asn Asn Ile Ser Tyr Gly Pro Gly
145 150 155 160Gly Ala Leu Leu Leu Gln Gly Arg Lys Ser Lys Ala Leu Phe Phe Arg
165 170 175Asp Asn Arg Gly Thr Ile Leu Phe Leu Lys Asn Lys Ala Val Asn Gln
180 185 190Asp Glu Ser His Pro Gly Tyr Gly Gly Ala Val Ser Ser Ile Ser Pro
195 200 205Gly Ser Pro Ile Thr Phe Ala Asp Asn Gln Glu Ile Leu Phe Gln Glu
210 215 220Asn Glu Gly Glu Leu Gly Gly Ala Ile Tyr Asn Asp Gln Gly Ala Ile
225 230 235 240Thr Phe Glu Asn Asn Phe Gln Thr Thr Ser Phe Phe Ser Asn Lys Ala
245 250 255Ser Phe Gly Gly Ala Val Tyr Ser Arg Tyr Cys Asn Leu Tyr Ser Gln
Page 153

Trp Gly Asp Thr Leu Phe Thr Lys Asn Ala Ala Ala Lys Val Gly Gly
 275 280 285
 Ala Ile His Ala Asp Tyr Val His Ile Arg Asp Cys Lys Gly Ser Ile
 290 300
 Val Phe Gu Gu Asn Ser Ala Thr Ala Gly Gly Ala Ile Ala Val Asn
 305 310 315 320
 Ala Val Cys Asp Ile Asn Ala Gn Gly Pro Val Arg Phe Ile Asn Asn
 325 330 335
 Ser Ala Leu Gly Leu Asn Gly Gly Ala Ile Tyr Met Gn Ala Thr Gly
 340 345
 Ser Ile Leu Arg Leu His Ala Asn Gn Gly Asp Ile Gu Phe Cys Gly
 355 360 365
 Asn Lys Val Arg Ser Gn Phe His Ser His Ile Asn Ser Thr Ser Asn
 370 375 380
 Phe Thr Asn Asn Ala Ile Thr Ile Gn Gly Ala Pro Arg Gu Phe Ser
 385 390 395 400
 Leu Ser Ala Asn Gu Gly His Arg Ile Cys Phe Tyr Asp Pro Ile Ile
 405 410 415
 Ser Ala Thr Gu Asn Tyr Asn Ser Leu Tyr Ile Asn His Gn Arg Leu
 420 425 430
 Leu Gu Ala Gly Gly Ala Val Ile Phe Ser Gly Ala Arg Leu Ser Pro
 435 440 445
 Gu His Lys Lys Gu Asn Lys Asn Lys Thr Ser Ile Ile Asn Gn Pro
 450 455 460
 Val Arg Leu Cys Ser Gly Val Leu Ser Ile Gu Gly Gly Ala Ile Leu
 465 470 475 480
 Ala Val Arg Ser Phe Tyr Gn Gu Gly Gly Leu Leu Ala Leu Gly Pro
 485 490 495
 Gly Ser Lys Leu Thr Thr Gn Gly Lys Asn Ser Gu Lys Asp Lys Ile
 500 505 510
 Val Ile Thr Asn Leu Gly Phe Asn Leu Gu Asn Leu Asp Ser Ser Asp
 515 520 525
 Pro Ala Gu Ile Arg Ala Thr Gu Lys Ala Ser Ile Gu Ile Ser Gly
 530 535 540

Val Pro Arg Val Tyr Gly His Thr Glu Ser Phe Tyr Glu Asn His Glu
 545 550 555 560 565 570 575 580 585 590 595 600 605 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 815 820 825 830 835 840 845 850 855 860 865 870 875 880 885 890 895 900 905 910 915 920 925 930 935 940 945 950 955 960 965 970 975 980 985 990 995

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Leu G n Tyr Thr 820 Lys Leu Val G n Asn Pro Phe Val G u Thr G y Tyr 830

Asp Pro Arg 835 Tyr Phe Ser Ser Ser 840 G u Met Thr Asn Leu Ser Leu Pro 845

Ile G y Ile Ala Leu G u Met 855 Arg Phe Ile G y Ser 860 Arg Ser Ser Leu

Phe Leu G n Val Ser Thr 870 Ser Tyr Ile Lys Asp 875 Leu Arg Arg Val Asn 880

Pro G n Ser Ser Ala 885 Ser Leu Val Leu Asn 890 His Tyr Thr Trp Asp Ile 895

G n G y Val Pro 900 Leu G y Lys G u Ala 905 Leu Asn Ile Thr Leu Asn Ser 910

Thr Ile Lys 915 Tyr Lys Ile Val Thr 920 Ala Tyr Met G y Ile Ser Ser Thr 925

G n Arg G u G y Ser Asn 935 Leu Ser Ala Asn Ala His 940 Ala G y Leu Ser

Leu Ser Phe 945

<210> 138
 <211> 393
 <212> PRT
 <213> Chl amydi a pneumoni ae

<400> 138

Met Ile Phe G u Phe Arg Phe Pro Lys Ile G y G u Thr Ser Ser G y 1 5 10 15

G y Ser Ile Val Arg Trp Leu Lys Asn Leu G y Asp His Val Ala Arg 20 25 30

Asp G u Pro Leu Ile G u Val Ser Thr Asp Lys Ile Ala Thr G u Leu 35 40 45

Pro Ser Pro Lys Ala G y Arg Leu Val Arg Phe Cys Val Asn G u G y 50 55 60

Asp G u Val Ala Ser G y Asp Val Leu G y Leu Ile G u Leu G u G u 65 70 75 80

Ile Ser G u Ala Asp Asp G u Ser Thr Ser Cys Pro Leu Thr Ser Cys 85 90 95

G u Thr Lys Ser G u Ala G y Ser Ser Ser Ser Val Trp Phe Ser

Pro Ala Val Leu Ser Leu Ala Gln Arg Gu Gly Ile Gly Leu Asp Asn
 115 120 125
 Leu Gln Lys Ile Ala Gly Thr Gly Lys Gly Gly Arg Val Thr Arg Gln
 130 135 140
 Asp Leu Gu Ala Tyr Ile Ser Gu Ser Gln Gln Val Ser Ile Pro Gu
 145 150 155 160
 Ile Phe Gln Gly Gu Val Asn Arg Ile Pro Met Ser Pro Leu Arg Arg
 165 170 175
 Ala Ile Ala Ser Ser Leu Ser Lys Ser Ser Asp Gu Val Pro His Ala
 180
 Ser Leu Val Val Asp Val Asp Val Thr Asp Leu Met Asn Leu Ile Ser
 195 200 205
 Gly Gu Arg Gln Arg Phe Leu Asp Thr His Gly Val Lys Leu Thr Ile
 210 215 220
 Thr Ser Phe Ile Val Gln Cys Leu Ala Gln Thr Leu Arg Gln Phe Pro
 225 230 235 240
 Leu Leu Asn Gly Ser Leu Asp Gly Thr Thr Ile Val Met Lys Lys Ser
 245 250 255
 Val Asn Val Gly Val Ala Val Asn Leu Asn Lys Gu Gly Val Val Val
 260 265 270
 Pro Val Ile His Asn Cys Gln Asp Arg Gly Leu Val Ser Ile Ala Lys
 275 280 285
 Ala Leu Ala Asp Leu Ser Ser Arg Ala Arg Leu Asn Lys Leu Asp Pro
 290 295 300
 Ser Gu Val Gln Asp Gly Ser Val Thr Val Thr Asn Phe Gly Met Thr
 305 310 315 320
 Gly Ala Leu Ile Gly Met Pro Ile Ile Arg Tyr Pro Gu Val Ala Ile
 325 330 335
 Leu Gly Ile Gly Thr Ile Gln Lys Arg Val Val Val Arg Asp Asp Asp
 340 345 350
 Ser Leu Ala Ile Arg Lys Met Val Tyr Val Thr Leu Thr Phe Asp His
 355 360 365
 Arg Val Leu Asp Gly Ile Tyr Gly Ser Gu Phe Leu Thr Ser Leu Lys
 370 375 380

Asn Arg Leu Glu Ser Val Thr Met Gly
385 390

<210> 139
<211> 237
<212> PRT
<213> Chlamydia pneumoniae

<400> 139

Leu Lys Asn Ser Gly Asn Ile Met Glu Pro Ser Thr Asn Lys Pro Asp
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Cys Lys Lys Ile Phe Asp Ser Ile Ala Ser Lys Tyr Asp Arg Thr Asn
20 25 30

Thr Ile Leu Ser Leu Gly Met His His Phe Trp Asn Arg Ser Leu Ile
35 40 45

Gln Ile Leu Gly Ser Gly Tyr Ser Leu Leu Asp Leu Cys Ala Gly Thr
50 55 60

Gly Lys Val Ala Lys Arg Tyr Ile Ala Ala His Pro Gln Ala Ser Val
65 70 75 80

Thr Leu Val Asp Phe Ser Ser Ala Met Leu Asp Ile Ala Lys Gln His
85 90 95

Leu Pro Gln Gly Ser Cys Ser Phe Ile His Ser Asp Ile Asn Gln Leu
100 105 110

Pro Leu Glu Asn His Ser Tyr Pro Leu Ala Ala Met Ala Tyr Gly Leu
115 120 125

Arg Asn Leu Ser Asp Pro His Lys Ala Leu Gln Glu Ile Ser Arg Val
130 135 140

Leu Met Pro Ser Gly Lys Leu Gly Ile Leu Glu Leu Thr Pro Pro Lys
145 150 155 160

Lys Thr His Pro Thr Tyr Ser Ala His Lys Leu Tyr Leu Arg Ala Val
165 170 175

Val Pro Trp Ile Gly Lys Ser Val Ser Lys Asp Pro Asp Ala Tyr Ser
180 185 190

Tyr Leu Ser Lys Ser Ile Gln Gln Leu Pro Lys Asp His Asp Leu Glu
195 200 205

Asp Leu Phe Ser Lys Ser Gly Phe Tyr Ile Ala Lys Lys Lys Lys Leu
210 215 220

Phe Leu Gly Ala Ala Thr Ile Trp Leu Leu Glu Lys Gn
 225 230 235

<210> 140
 <211> 620
 <212> PRT
 <213> Chl amydi a pneumoni ae

<400> 140

Met Arg Arg Ser Val Cys Tyr Val Asn Pro Ser Ile Ala Arg Ala Gly
 1 5 10 15

Gn Ile Ser Thr Trp Lys Phe Leu Tyr Ser Leu Ala Thr Pro Leu Pro
 20 25 30

Ala Gly Thr Lys Cys Lys Phe Asp Leu Ala Gly Ser Gly Lys Pro Thr
 35 40 45

Asp Trp Glu Ala Pro Ala Thr Asp Leu Ser Gn Thr Arg Asn Val Ile
 50 55 60

Tyr Ala Glu Met Pro Glu Gly Glu Ile Ile Glu Ala Thr Ala Ile Pro
 65 70 75 80

Val Lys Asp Asn Pro Val Pro Gn Phe Glu Phe Thr Leu Pro Tyr Glu
 85 90 95

Leu Gn Val Gly Glu Thr Leu Thr Ile Val Met Gly Ala Ser Pro Asn
 100 105 110

His Pro Gn Val Asp Asp Ala Gly Asn Gly Ala Gn Leu Phe Ala Gn
 115 120 125

Arg Arg Lys Pro Phe Tyr Leu Tyr Ile Asp Pro Thr Gly Glu Gly Asn
 130 135 140

Tyr Asp Glu Pro Asp Val Phe Ser Met Asp Ile Arg Gly Asn Val Leu
 145 150 155 160

Lys Lys Ile Glu Ile Phe Thr Pro Ser Tyr Val Val Lys Asn Lys Arg
 165 170 175

Phe Asp Ile Thr Val Arg Phe Glu Asp Glu Phe Gly Asn Leu Thr Asn
 180 185 190

Phe Ser Pro Glu Glu Thr Arg Ile Glu Leu Ser Tyr Glu His Leu Arg
 195 200 205

Glu Asn Leu Asn Trp Gn Leu Phe Ile Pro Glu Thr Gly Phe Val Ile
 210 215 220

Leu Pro Asn Leu Tyr Phe Asn Glu Pro Gly Ile Tyr Arg Ile Gn Leu
 225 230 235 240

eol f - seq1 . app

Lys Asn Leu Ser Thr 245 Gln Gu Ile Phe Ile Ser Ala Pro Ile Lys Cys 255
 Phe Ala Asp Ser 260 Ala Pro Asn Leu Met 265 Trp Gly Leu Leu His Gly Gu 270
 Ser Gu Arg Val Asp Ser Gu Gu Asn Ile Gu Thr Cys 285 Met Arg Tyr 275
 Phe Arg Asp Asp Arg Ala Leu Asn Phe Tyr Ala Ser 300 Ser Ser Phe Gu 290
 Asn Gln Gu Asn Leu Ser 310 Pro Asp Ile Trp Lys 315 Leu Ile Asn Gln Thr 320
 Val Ser Asp Phe Asn 325 Gu Gu Asp Arg Phe Ile Thr Leu Ser Gly Phe 335
 Gln Tyr Ser Gly Gu Pro His Leu Gu Gly Val Arg His Ile Leu His 340
 Thr Lys Gu Thr Lys Ser His Ser 360 Lys His Lys Gu Tyr Lys His Ile 355
 Pro Leu Ala Lys Leu Tyr Lys 375 Ser Thr Val Asn His 380 Asp Met Ile Ser 370
 Ile Pro Ser Phe Thr Ala Ser Lys Gu His Gly Phe Asp Phe Gu Asn 385 390 400
 Phe Tyr Pro Gu Phe Gu Arg Val Val Gu Ile Tyr Asn Ala Trp Gly 405 410 415
 Ser Ser Gu Thr Thr Ala Ala Leu Asn 425 Asn Pro Phe Pro Ile Gln Gly 420 430
 Lys Asp Ser Gu Asp Pro Arg Gly Thr Val Ile Gu Gly Leu Lys Lys 435 440 445
 Asn Leu Arg Phe Gly Phe Val Ala Gly Gly Leu Asp Asp Arg Gly Ile 450 455 460
 Tyr Lys Asp Tyr Phe Asp Ser Pro Gln Val Gln Tyr Ser Pro Gly Leu 465 470 475 480
 Thr Ala Ile Ile Cys Asn Lys Tyr Thr Arg Gu Ser Leu Val Gu Ala 485 490 495
 Leu Phe Ala Arg His Cys Tyr Ala Thr Thr Gly Pro Arg Ile Val Leu 500 505 510

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Ser Phe Asn Ile Thr Ser Ala Pro Met Gly Ser Gu Leu Ser Thr Gly
515 520 525

Ser Lys Pro Gly Leu Asn Val Asn Arg His Ile Ser Gly His Val Ala
530 535 540 545

Gly Thr Ala Leu Leu Lys Thr Val Gu Ile Ile Arg Asn Gly Gu Val
545 550 555 560 565

Leu His Thr Phe Phe Pro Asp Ser Asn Asn Leu Asp Tyr Gu Tyr Asp
565 570 575

Asp Met Val Pro Leu Ser Ser Val Thr Leu Lys Asp Pro Asn Gly Lys
580 585 590

Ala Pro Phe Val Phe Tyr Tyr Leu Arg Val Thr Gn Ala Asp Asn Ala
595 600 605

Met Ala Trp Ser Ser Pro Ile Trp Val Asp Leu Asn
610 615 620

<210> 141
<211> 660
<212> PRT
<213> Chlamydia pneumoniae
<400> 141

Met Ser Gu His Lys Lys Ser Ser Lys Ile Ile Gly Ile Asp Leu Gly
1 5 10 15

Thr Thr Asn Ser Cys Val Ser Val Met Gu Gly Gly Gn Ala Lys Val
20 25 30

Ile Thr Ser Ser Gu Gly Thr Arg Thr Thr Pro Ser Ile Val Ala Phe
35 40 45

Lys Gly Asn Gu Lys Leu Val Gly Ile Pro Ala Lys Arg Gn Ala Val
50 55 60

Thr Asn Pro Gu Lys Thr Leu Gly Ser Thr Lys Arg Phe Ile Gly Arg
65 70 75 80

Lys Tyr Ser Gu Val Ala Ser Gu Ile Gn Thr Val Pro Tyr Thr Val
85 90 95

Thr Ser Gly Ser Lys Gly Asp Ala Val Phe Gu Val Asp Gly Lys Gn
100 105 110

Tyr Thr Pro Gu Gu Ile Gly Ala Gn Ile Leu Met Lys Met Lys Gu
115 120 125

Thr Ala Gu Ala Tyr Leu Gly Gu Thr Val Thr Gu Ala Val Ile Thr

130

135

Val 145 Pro Ala Tyr Phe Asn 150 Asp Ser Gln Arg Ala 155 Ser Thr Lys Asp Ala 160
 Gly Arg Ile Ala Gly 165 Leu Asp Val Lys Arg 170 Ile Ile Pro Glu Pro 175 Thr
 Ala Ala Ala Leu 180 Ala Tyr Gly Ile Asp 185 Lys Val Gly Asp Lys 190 Lys Ile
 Ala Val Phe 195 Asp Leu Gly Gly Gly Thr Phe Asp Ile Ser 205 Ile Leu Glu
 Ile Gly 210 Asp Gly Val Phe Gu 215 Val Leu Ser Thr Asn 220 Gly Asp Thr Leu
 Leu Gly Gly Asp Asp Phe 230 Asp Gu Val Ile Ile 235 Lys Trp Met Ile Glu 240
 Gu Phe Lys Lys Gln Gu Gly Ile Asp Leu 250 Ser Lys Asp Asn Met 255 Ala
 Leu Gln Arg Leu 260 Lys Asp Ala Ala Gu 265 Lys Ala Lys Ile Gu 270 Leu Ser
 Gly Val Ser 275 Ser Thr Gu Ile Asn 280 Gln Pro Phe Ile Thr Met Asp Ala
 Gln Gly 290 Pro Lys His Leu Ala 295 Leu Thr Leu Thr Arg Ala Gln Phe Glu 300
 Lys 305 Leu Ala Ala Ser Leu 310 Ile Gu Arg Thr Lys 315 Ser Pro Cys Ile Lys 320
 Ala Leu Ser Asp Ala 325 Lys Leu Ser Ala Lys 330 Asp Ile Asp Asp Val Leu 335
 Leu Val Gly Gly 340 Met Ser Arg Met Pro Ala Val Gln Gu Thr 350 Val Lys
 Gu Leu Phe 355 Gly Lys Gu Pro Asn 360 Lys Gly Val Asn 365 Pro Asp Gu Val
 Val Ala Ile Gly Ala Ala Ile 375 Gln Gly Gly Val Leu 380 Gly Gly Gu Val
 Lys 385 Asp Val Leu Leu Leu 390 Asp Val Ile Pro Leu 395 Ser Leu Gly Ile Gu 400
 Thr Leu Gly Gly 405 Val Met Thr Thr Leu Val 410 Gu Arg Asn Thr Thr 415 Ile

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Pro Thr G n Lys Lys G n Ile Phe Ser Thr Ala Ala Asp Asn G n Pro
 420 425 430

Ala Val Thr Ile Val Val Leu G n G y G u Arg Pro Met Ala Lys Asp
 435 440 445

Asn Lys G u Ile G y Arg Phe Asp Leu Thr Asp Ile Pro Pro Ala Pro
 450 455 460

Arg G y His Pro G n Ile G u Val Ser Phe Asp Ile Asp Ala Asn G y
 465 470 475 480

Ile Phe His Val Ser Ala Lys Asp Val Ala Ser G y Lys G u G n Lys
 485 490 495

Ile Arg Ile G u Ala Ser Ser G y Leu G n G u Asp G u Ile G n Arg
 500 505 510

Met Val Arg Asp Ala G u Ile Asn Lys G u G u Asp Lys Lys Arg Arg
 515 520 525

G u Ala Ser Asp Ala Lys Asn G u Ala Asp Ser Met Ile Phe Arg Ala
 530 535 540

G u Lys Ala Ile Lys Asp Tyr Lys G u G n Ile Pro G u Thr Leu Val
 545 550 555 560

Lys G u Ile G u G u Arg Ile G u Asn Val Arg Asn Ala Leu Lys Asp
 565 570 575

Asp Ala Pro Ile G u Lys Ile Lys G u Val Thr G u Asp Leu Ser Lys
 580 585 590

His Met G n Lys Ile G y G u Ser Met G n Ser G n Ser Ala Ser Ala
 595 600 605

Ala Ala Ser Ser Ala Ala Asn Ala Lys G y G y Pro Asn Ile Asn Thr
 610 615 620

G u Asp Leu Lys Lys His Ser Phe Ser Thr Lys Pro Pro Ser Asn Asn
 625 630 635 640

G y Ser Ser G u Asp His Ile G u G u Ala Asp Val G u Ile Ile Asp
 645 650 655

Asn Asp Asp Lys
 660

<210> 142
 <211> 952
 <212> PRT

<213> Chl amydi a pneumni ae

<400> 142

Val Ser Lys Thr Pro Pro Lys Phe Leu Phe Tyr Leu Gly Asn Phe Thr
 1 5 10 15
 Ala Cys Met Phe Gly Met Thr Pro Ala Val Tyr Ser Leu Gl n Thr Asp
 20 25 30
 Ser Leu Gl u Lys Phe Ala Leu Gl u Arg Asp Gl u Gl u Phe Arg Thr Ser
 35 40 45
 Phe Pro Leu Leu Asp Ser Leu Ser Thr Leu Thr Gly Phe Ser Pro Ile
 50 55 60
 Thr Thr Phe Val Gly Asn Arg His Asn Ser Ser Gl n Asp Ile Val Leu
 65 70 75 80
 Ser Asn Tyr Lys Ser Ile Asp Asn Ile Leu Leu Leu Trp Thr Ser Ala
 85 90 95
 Gly Gly Ala Val Ser Cys Asn Asn Phe Leu Leu Ser Asn Val Gl u Asp
 100 105 110
 His Ala Phe Phe Ser Lys Asn Leu Ala Ile Gly Thr Gly Gly Ala Ile
 115 120 125
 Ala Cys Gl n Gly Ala Cys Thr Ile Thr Lys Asn Arg Gly Pro Leu Ile
 130 135 140
 Phe Phe Ser Asn Arg Gly Leu Asn Asn Ala Ser Thr Gly Gly Gl u Thr
 145 150 155 160
 Arg Gly Gly Ala Ile Ala Cys Asn Gly Asp Phe Thr Ile Ser Gl n Asn
 165 170 175
 Gl n Gly Thr Phe Tyr Phe Val Asn Asn Ser Val Asn Asn Trp Gly Gly
 180 185 190
 Ala Leu Ser Thr Asn Gly His Cys Arg Ile Gl n Ser Asn Arg Ala Pro
 195 200 205
 Leu Leu Phe Phe Asn Asn Thr Ala Pro Ser Gly Gly Gly Ala Leu Arg
 210 215 220
 Ser Gl u Asn Thr Thr Ile Ser Asp Asn Thr Arg Pro Ile Tyr Phe Lys
 225 230 235 240
 Asn Asn Cys Gly Asn Asn Gly Gly Ala Ile Gl n Thr Ser Val Thr Val
 245 250 255
 Ala Ile Lys Asn Asn Ser Gly Ser Val Ile Phe Asn Asn Asn Thr Ala
 Page 164

Leu Ser Gly Ser Ile Asn Ser Gly Asn Gly Ser Gly Gly Ala Ile Tyr
 275 280 285
 Thr Thr Asn Leu Ser Ile Asp Asp Asn Pro Gly Thr Ile Leu Phe Asn
 290 295 300
 Asn Asn Tyr Cys Ile Arg Asp Gly Gly Ala Ile Cys Thr Gl n Phe Leu
 305 310 315 320
 Thr Ile Lys Asn Ser Gly His Val Tyr Phe Thr Asn Asn Gl n Gly Asn
 325 330 335
 Trp Gly Gly Ala Leu Met Leu Leu Gl n Asp Ser Thr Cys Leu Leu Phe
 340 345 350
 Ala Gu Gl n Gly Asn Ile Ala Phe Gl n Asn Asn Gu Val Phe Leu Thr
 355 360 365
 Thr Phe Gly Arg Tyr Asn Ala Ile His Cys Thr Pro Asn Ser Asn Leu
 370 375 380
 Gl n Leu Gly Ala Asn Lys Gly Tyr Thr Thr Ala Phe Phe Asp Pro Ile
 385 390 395 400
 Gu His Gl n His Pro Thr Thr Asn Pro Leu Ile Phe Asn Pro Asn Ala
 405 410 415
 Asn His Gl n Gly Thr Ile Leu Phe Ser Ser Ala Tyr Ile Pro Gu Ala
 420 425 430
 Ser Asp Tyr Gu Asn Asn Phe Ile Ser Ser Ser Lys Asn Thr Ser Gu
 435 440 445
 Leu Arg Asn Gly Val Leu Ser Ile Gu Asp Arg Ala Gly Trp Gl n Phe
 450 455 460
 Tyr Lys Phe Thr Gl n Lys Gly Gly Ile Leu Lys Leu Gly His Ala Ala
 465 470 475 480
 Ser Ile Ala Thr Thr Ala Asn Ser Gu Thr Pro Ser Thr Ser Val Gly
 485 490 495
 Ser Gl n Val Ile Ile Asn Asn Leu Ala Ile Asn Leu Pro Ser Ile Leu
 500 505 510
 Ala Lys Gly Lys Ala Pro Thr Leu Trp Ile Arg Pro Leu Gl n Ser Ser
 515 520 525
 Ala Pro Phe Thr Gu Asp Asn Asn Pro Thr Ile Thr Leu Ser Gly Pro
 530 535 540

Leu Thr Leu Leu Asn Gu Gu Asn Arg Asp Pro Tyr Asp Ser Ile Asp
 545 550 555 560

Leu Ser Gu Pro Leu Gn Asn Ile His Leu Leu Ser Leu Ser Asp Val
 565 570 575

Thr Ala Arg His Ile Asn Thr Asp Asn Phe His Pro Gu Ser Leu Asn
 580 585 590

Ala Thr Gu His Tyr Gy Tyr Gn Gy Ile Trp Ser Pro Tyr Trp Val
 595 600 605

Gu Thr Ile Thr Thr Thr Asn Asn Ala Ser Ile Gu Thr Ala Asn Thr
 610 615 620

Leu Tyr Arg Ala Leu Tyr Ala Asn Trp Thr Pro Leu Gy Tyr Lys Val
 625 630 635 640

Asn Pro Gu Tyr Gn Gy Asp Leu Ala Thr Thr Pro Leu Trp Gn Ser
 645 650 655

Phe His Thr Met Phe Ser Leu Leu Arg Ser Tyr Asn Arg Thr Gy Asp
 660 665 670

Ser Asp Ile Gu Arg Pro Phe Leu Gu Ile Gn Gy Ile Ala Asp Gy
 675 680 685

Leu Phe Val His Gn Asn Ser Ile Pro Gy Ala Pro Gy Phe Arg Ile
 690 695 700

Gn Ser Thr Gy Tyr Ser Leu Gn Ala Ser Ser Gu Thr Ser Leu His
 705 710 715 720

Gn Lys Ile Ser Leu Gy Phe Ala Gn Phe Phe Thr Arg Thr Lys Gu
 725 730 735

Ile Gy Ser Ser Asn Asn Val Ser Ala His Asn Thr Val Ser Ser Leu
 740 745 750

Tyr Val Gu Leu Pro Trp Phe Gn Gu Ala Phe Ala Thr Ser Thr Val
 755 760 765

Leu Ala Tyr Gy Tyr Gy Asp His His Leu His Ser Leu His Pro Ser
 770 775 780

His Gn Gu Gn Ala Gu Gy Thr Cys Tyr Ser His Thr Leu Ala Ala
 785 790 795 800

Ala Ile Gy Cys Ser Phe Pro Trp Gn Gn Lys Ser Tyr Leu His Leu
 805 810 815

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Ser Pro Phe Val G n Ala Ile Ala Ile Arg Ser His G n Thr Ala Phe
820 825 830

G u G u Ile Gly Asp Asn Pro Arg Lys Phe Val Ser G n Lys Pro Phe
835 840 845

Tyr Asn Leu Thr Leu Pro Leu Gly Ile G n Gly Lys Trp G n Ser Lys
850 855 860

Phe His Val Pro Thr G u Trp Thr Leu G u Leu Ser Tyr G n Pro Val
865 870 875 880

Leu Tyr G n G n Asn Pro G n Ile Gly Val Thr Leu Leu Ala Ser Gly
885 890 895

Gly Ser Trp Asp Ile Leu Gly His Asn Tyr Val Arg Asn Ala Leu Gly
900 905 910

Tyr Lys Val His Asn G n Thr Ala Leu Phe Arg Ser Leu Asp Leu Phe
915 920 925

Leu Asp Tyr G n Gly Ser Val Ser Ser Ser Thr Ser Thr His His Leu
930 935 940

G n Ala Gly Ser Thr Leu Lys Phe
945 950

<210> 143
<211> 695
<212> PRT
<213> Chl amydi a pneumoni ae

<400> 143

Leu Phe Val Ser Asn Phe Ile Phe Phe Val Val Met Pro Ile Pro Tyr
1 5 10 15

Ile Ser Ser Trp Ile Ser Thr Val Arg G n His Phe Val Lys Ala Phe
20 25 30

Asp Phe Ser Arg Pro Phe Cys Ser Arg Val Thr Asn Phe Ala Leu Gly
35 40 45

Val Ile Lys Ala Ile Pro Ile Val Gly His Ile Val Met Gly Met G u
50 55 60

Trp Leu Val Ser Ser Cys Val Ala Gly Ile Ile Thr Arg Ser Ser Phe
65 70 75 80

Thr Ser Asp Val Val G n Ile Val Lys Thr G u Lys Ala Leu Gly Arg
85 90 95

Asp His Ile Ser Arg Val Ala G u Ile Leu G n Arg G u Arg Gly Thr
Page 167

I l e Thr Pro G u Asn G n Asp Lys Val Hi s G y Lys Phe Pro Val Cys
 115 120 125

Pro Phe G y Arg Leu Lys Ser G u G u Thr Leu Lys Leu Lys Pro G y
 130 135 140

G u Arg G y G y Thr Leu Asp Thr Val Phe Ser Pro I l e Arg Thr Arg
 145 150 155 160

Val Thr Arg Ala Tyr Leu G n Ala Pro Arg Pro G u I l e Arg Thr I l e
 165 170 175

Ser I l e Val G y Ser Lys Leu Lys Thr Pro G n Asp Phe Ser G n Phe
 180 185 190

Val Ser Leu Ala Asn G u Thr G n Arg Leu Hi s Pro G u Ala Leu Val
 195 200 205

Cys Leu Tyr Leu Thr G y Leu Asn Arg G u Ser G n Met Cys Asp Thr
 210 215 220

Thr Thr Ala G u Lys Lys G n Tyr Leu Hi s Asn Ser G y Leu Asp Ser
 225 230 235 240

Arg I l e G n Cys Lys Asp Ser Lys G u Asp Asp Ala G y Ser Pro G u
 245 250 255

Asn Pro G u Leu Trp I l e G y Tyr Tyr Ser Arg G u G n G n Hi s Asn
 260 265 270

I l e Asp G y G n Tyr I l e G n G n Cys Leu G y Lys Ser Ala Asp Pro
 275 280 285

I l e Pro Trp I l e Hi s Val Thr G u Asp Thr Lys Asp Phe Tyr Tyr Pro
 290 295 300

Pro Asn Phe Thr Ser Tyr Ser Hi s Thr Arg G n Ser Thr Asp Pro Thr
 305 310 315 320

Ser Pro Pro Arg Leu Pro G u Ser G u G y Asp Lys Asp Ser Leu Tyr
 325 330 335

G y G n Leu Ser Arg Ser Tyr Hi s Hi s G u Tyr Met Leu G y Leu G y
 340 345 350

Leu Lys Pro G u Asp Ala G y Leu Leu Met Asp Pro Asp Arg I l e Tyr
 355 360 365

Ala Pro Leu Ser G n G y Hi s Tyr Cys Hi s Ser Tyr Leu Ala Asp I l e
 370 375 380

G u Asn G u Asp Leu Arg Thr Leu Val Leu Ser Pro Phe Leu Asp Pro
 385 390 395 400
 G y Asn Leu Ser Ser G u Asp Leu Arg Pro Val Al a Phe Asn Ile Al a
 405 410 415
 Arg Leu Pro Leu G u Leu Asp Ser Leu Phe Phe Arg Leu Val Al a G y
 420 425 430
 G n G n G u G y Arg Asn Ile Val Thr Leu Al a Hi s G y Thr Pro Arg
 435 440 445
 Pro G u Asp Leu Asp Pro Asp Ser Met Asn Ile Leu Thr Arg Arg Leu
 450 455 460
 G n Met Ser G y Tyr Ser Tyr Leu Asn Ile Phe Ser Tyr Lys Ser Arg
 465 470 475 480
 Lys Met Ile Val Lys G u Arg G n Phe Phe G y Asp Arg Ser G u G y
 485 490 495
 Lys Ser Phe Thr Leu Ile Leu Phe G u Asp Pro Ile Ser Al a Al a Asp
 500 505 510
 Phe Arg Cys Leu G n Leu Al a Al a G u G y Met Val Al a Lys Asp Leu
 515 520 525
 Pro Ser Val Al a Asp Ile Cys Al a Ser G y Cys Ser Cys Ile G n Phe
 530 535 540
 Ser G u Met G n Ser Pro G n Al a Ile G u Tyr Arg G n Trp G u Al a
 545 550 555 560
 Arg Val G u Asp G u Al a G y G u G u Al a Arg G u Pro Val Ile Tyr
 565 570 575
 Ser G n Asp G n Leu Ser Ser Met Leu Thr Thr G n G n Asn Phe Val
 580 585 590
 Phe Ser Leu Asp Al a Val Val Lys G n Al a Ile Trp Arg Phe Arg Ser
 595 600 605
 Lys G y Leu Leu Thr Met G u Arg Lys Al a Leu G y G u G u Phe Leu
 610 615 620
 Thr Al a Ile Phe Ser Tyr Leu G y Ser G n G u Arg Asn G u Asn Met
 625 630 635 640
 G y Lys Arg Thr Thr G u G u Hi s G u Val Val Ile Ser Phe G u G u
 645 650 655

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Leu Asp Arg Met Val Gln Val Leu Pro Ala Glu Val Pro Ala Asp Ser
660 665 670

Gly Asn Asp Pro Thr His Pro Val Pro Asn Pro Asp Ser Asn Pro Asp
675 680 685

Ser Ser Gln Asn Glu Gly Ser
690 695

<210> 144
<211> 514
<212> PRT
<213> Chlamydia pneumoniae

<400> 144

Met Thr Ile Leu Arg Asn Phe Leu Thr Cys Ser Ala Leu Phe Leu Ala
1 5 10 15

Leu Pro Ala Ala Ala Gln Val Val Tyr Leu His Glu Ser Asp Gly Tyr
20 25 30

Asn Gly Ala Ile Asn Asn Lys Ser Leu Glu Pro Lys Ile Thr Cys Tyr
35 40 45

Pro Glu Gly Thr Ser Tyr Ile Phe Leu Asp Asp Val Arg Ile Ser Asn
50 55 60

Val Lys His Asp Gln Glu Asp Ala Gly Val Phe Ile Asn Arg Ser Gly
65 70 75 80

Asn Leu Phe Phe Met Gly Asn Arg Cys Asn Phe Thr Phe His Asn Leu
85 90 95

Met Thr Glu Gly Phe Gly Ala Ala Ile Ser Asn Arg Val Gly Asp Thr
100 105 110

Thr Leu Thr Leu Ser Asn Phe Ser Tyr Leu Ala Phe Thr Ser Ala Pro
115 120 125

Leu Leu Pro Gln Gly Gln Gly Ala Ile Tyr Ser Leu Gly Ser Val Met
130 135 140

Ile Glu Asn Ser Glu Glu Val Thr Phe Cys Gly Asn Tyr Ser Ser Trp
145 150 155 160

Ser Gly Ala Ala Ile Tyr Thr Pro Tyr Leu Leu Gly Ser Lys Ala Ser
165 170 175

Arg Pro Ser Val Asn Leu Ser Gly Asn Arg Tyr Leu Val Phe Arg Asp
180 185 190

Asn Val Ser Gln Gly Tyr Gly Gly Ala Ile Ser Thr His Asn Leu Thr
Page 170

195

200

205

Leu Thr Thr Arg Gly Pro Ser Cys Phe Glu Asn Asn His Ala Tyr His
 210 215 220

Asp Val Asn Ser Asn Gly Gly Ala Ile Ala Ile Ala Pro Gly Gly Ser
 225 230 235 240

Ile Ser Ile Ser Val Lys Ser Gly Asp Leu Ile Phe Lys Gly Asn Thr
 245 250 255

Ala Ser Gln Asp Gly Asn Thr Ile His Asn Ser Ile His Leu Gln Ser
 260 265 270

Gly Ala Gln Phe Lys Asn Leu Arg Ala Val Ser Glu Ser Gly Val Tyr
 275 280 285

Phe Tyr Asp Pro Ile Ser His Ser Glu Ser His Lys Ile Thr Asp Leu
 290 295 300

Val Ile Asn Ala Pro Glu Gly Lys Glu Thr Tyr Glu Gly Thr Ile Ser
 305 310 315 320

Phe Ser Gly Leu Cys Leu Asp Asp His Glu Val Cys Ala Glu Asn Leu
 325 330 335

Thr Ser Thr Ile Leu Gln Asp Val Thr Leu Ala Gly Gly Thr Leu Ser
 340 345 350

Leu Ser Asp Gly Val Thr Leu Gln Leu His Ser Phe Lys Gln Glu Ala
 355 360 365

Ser Ser Thr Leu Thr Met Ser Pro Gly Thr Thr Leu Leu Cys Ser Gly
 370 375 380

Asp Ala Arg Val Gln Asn Leu His Ile Leu Ile Glu Asp Thr Asp Asn
 385 390 395 400

Phe Val Pro Val Arg Ile Arg Ala Glu Asp Lys Asp Ala Leu Val Ser
 405 410 415

Leu Glu Lys Leu Lys Val Ala Phe Glu Ala Tyr Trp Ser Val Tyr Asp
 420 425 430

Phe Pro Gln Phe Lys Glu Ala Phe Thr Ile Pro Leu Leu Glu Leu Leu
 435 440 445

Gly Pro Ser Phe Asp Ser Leu Leu Leu Gly Glu Thr Thr Leu Glu Arg
 450 455 460

Thr Gln Val Thr Thr Glu Asn Asp Ala Val Arg Gly Phe Trp Ser Leu
 465 470 475 480

Ser Trp Glu Glu Tyr Pro Pro Ser Leu Asp Lys Asp Arg Arg Ile Thr
485 490 495

Pro Thr Lys Lys Thr Val Phe Leu Thr Trp Asn Pro Glu Ile Thr Ser
500 505 510

Thr Pro

<210> 145

<211> 930

<212> PRT

<213> Chl amydi a pneumoni ae

<400> 145

Met Lys Ile Pro Leu His Lys Leu Leu Ile Ser Ser Thr Leu Val Thr
1 5 10 15

Pro Ile Leu Leu Ser Ile Ala Thr Tyr Gly Ala Asp Ala Ser Leu Ser
20 25 30

Pro Thr Asp Ser Phe Asp Gly Ala Gly Gly Ser Thr Phe Thr Pro Lys
35 40 45

Ser Thr Ala Asp Ala Asn Gly Thr Asn Tyr Val Leu Ser Gly Asn Val
50 55 60

Tyr Ile Asn Asp Ala Gly Lys Gly Thr Ala Leu Thr Gly Cys Cys Phe
65 70 75 80

Thr Glu Thr Thr Gly Asp Leu Thr Phe Thr Gly Lys Gly Tyr Ser Phe
85 90 95

Ser Phe Asn Thr Val Asp Ala Gly Ser Asn Ala Gly Ala Ala Ala Ser
100 105 110

Thr Thr Ala Asp Lys Ala Leu Thr Phe Thr Gly Phe Ser Asn Leu Ser
115 120 125

Phe Ile Ala Ala Pro Gly Thr Thr Val Ala Ser Gly Lys Ser Thr Leu
130 135 140

Ser Ser Ala Gly Ala Leu Asn Leu Thr Asp Asn Gly Thr Ile Leu Phe
145 150 155 160

Ser Gn Asn Val Ser Asn Gu Ala Asn Asn Asn Gly Gly Ala Ile Thr
165 170 175

Ala Lys Thr Leu Ser Ile Ser Gly Asn Thr Ser Ser Ile Thr Phe Thr
180 185 190

Ser Asn Ser Ala Lys Lys Leu Gly Gly Ala Ile Tyr Ser Ser Ala Ala
195 200 205

Ala Ser Ile Ser Gly Asn Thr Gly Gn Leu Val Phe Met Asn Asn Lys
210 215 220

Gly Gu Thr Gly Gly Gly Ala Leu Gly Phe Gu Ala Ser Ser Ser Ile
225 230 235 240

Thr Gn Asn Ser Ser Leu Phe Phe Ser Gly Asn Thr Ala Thr Asp Ala
245 250 255

Ala Gly Lys Gly Gly Ala Ile Tyr Cys Gu Lys Thr Gly Gu Thr Pro
260 265 270

Thr Leu Thr Ile Ser Gly Asn Lys Ser Leu Thr Phe Ala Gu Asn Ser
275 280 285

Ser Val Thr Gn Gly Gly Ala Ile Cys Ala His Gly Leu Asp Leu Ser
290 295 300

Ala Ala Gly Pro Thr Leu Phe Ser Asn Asn Arg Cys Gly Asn Thr Ala
305 310 315 320

Ala Gly Lys Gly Gly Ala Ile Ala Ile Ala Asp Ser Gly Ser Leu Ser
325 330 335

Leu Ser Ala Asn Gn Gly Asp Ile Thr Phe Leu Gly Asn Thr Leu Thr
340 345 350

Ser Thr Ser Ala Pro Thr Ser Thr Arg Asn Ala Ile Tyr Leu Gly Ser
355 360 365

Ser Ala Lys Ile Thr Asn Leu Arg Ala Ala Gn Gly Gn Ser Ile Tyr
370 375 380

Phe Tyr Asp Pro Ile Ala Ser Asn Thr Thr Gly Ala Ser Asp Val Leu
385 390 395 400

Thr Ile Asn Gn Pro Asp Ser Asn Ser Pro Leu Asp Tyr Ser Gly Thr
405 410 415

Ile Val Phe Ser Gly Gu Lys Leu Ser Ala Asp Gu Ala Lys Ala Ala
420 425 430

Asp Asn Phe Thr Ser Ile Leu Lys Gn Pro Leu Ala Leu Ala Ser Gly
435 440 445

Thr Leu Ala Leu Lys Gly Asn Val Gu Leu Asp Val Asn Gly Phe Thr
450 455 460

Gn Thr Gu Gly Ser Thr Leu Leu Met Gn Pro Gly Thr Lys Leu Lys

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Asn Asp Met Asp Thr Arg Tyr Thr Ser Tyr Pro Glu Ala Gln Gly Ser
755 760 765

Trp Thr Asn Asn Ser Gly Ala Leu Glu Leu Gly Gly Ser Leu Ala Leu
770 775 780

Tyr Leu Pro Lys Glu Ala Pro Phe Phe Gln Gly Tyr Phe Pro Phe Leu
785 790 795 800

Lys Phe Gln Ala Val Tyr Ser Arg Gln Gln Asn Phe Lys Glu Ser Gly
805 810 815

Ala Glu Ala Arg Ala Phe Asp Asp Gly Asp Leu Val Asn Cys Ser Ile
820 825 830

Pro Val Gly Ile Arg Leu Glu Lys Ile Ser Glu Asp Glu Lys Asn Asn
835 840 845

Phe Glu Ile Ser Leu Ala Tyr Ile Gly Asp Val Tyr Arg Lys Asn Pro
850 855 860

Arg Ser Arg Thr Ser Leu Met Val Ser Gly Ala Ser Trp Thr Ser Leu
865 870 875 880

Cys Lys Asn Leu Ala Arg Gln Ala Phe Leu Ala Ser Ala Gly Ser His
885 890 895

Leu Thr Leu Ser Pro His Val Glu Leu Ser Gly Glu Ala Ala Tyr Glu
900 905 910

Leu Arg Gly Ser Ala His Ile Tyr Asn Val Asp Cys Gly Leu Arg Tyr
915 920 925

Ser Phe
930

<210> 146
<211> 936
<212> PRT
<213> Chlamydia pneumoniae

<400> 146

Met Lys Ser Ser Val Ser Trp Leu Phe Phe Ser Ser Ile Pro Leu Phe
1 5 10 15

Ser Ser Leu Ser Ile Val Ala Ala Glu Val Thr Leu Asp Ser Ser Asn
20 25 30

Asn Ser Tyr Asp Gly Ser Asn Gly Thr Thr Phe Thr Val Phe Ser Thr
35 40 45

Thr Asp Ala Ala Ala Gly Thr Thr Tyr Ser Leu Leu Ser Asp Val Ser
 50 55 60

Phe Gln Asn Ala Gly Ala Leu Gly Ile Pro Leu Ala Ser Gly Cys Phe
 65 70 75 80

Leu Gu Ala Gly Gly Asp Leu Thr Phe Gln Gly Asn Gln His Ala Leu
 85 90 95

Lys Phe Ala Phe Ile Asn Ala Gly Ser Ser Ala Gly Thr Val Ala Ser
 100 105 110

Thr Ser Ala Ala Asp Lys Asn Leu Leu Phe Asn Asp Phe Ser Arg Leu
 115 120 125

Ser Ile Ile Ser Cys Pro Ser Leu Leu Leu Ser Pro Thr Gly Gln Cys
 130 135 140

Ala Leu Lys Ser Val Gly Asn Leu Ser Leu Thr Gly Asn Ser Gln Ile
 145 150 155 160

Ile Phe Thr Gln Asn Phe Ser Ser Asp Asn Gly Gly Val Ile Asn Thr
 165 170 175

Lys Asn Phe Leu Leu Ser Gly Thr Ser Gln Phe Ala Ser Phe Ser Arg
 180 185 190

Asn Gln Ala Phe Thr Gly Lys Gln Gly Gly Val Val Tyr Ala Thr Gly
 195 200 205

Thr Ile Thr Ile Gu Asn Ser Pro Gly Ile Val Ser Phe Ser Gln Asn
 210 215 220

Leu Ala Lys Gly Ser Gly Gly Ala Leu Tyr Ser Thr Asp Asn Cys Ser
 225 230 235 240

Ile Thr Asp Asn Phe Gln Val Ile Phe Asp Gly Asn Ser Ala Trp Gu
 245 250 255

Ala Ala Gln Ala Gln Gly Gly Ala Ile Cys Cys Thr Thr Thr Asp Lys
 260 265 270

Thr Val Thr Leu Thr Gly Asn Lys Asn Leu Ser Phe Thr Asn Asn Thr
 275 280 285

Ala Leu Thr Tyr Gly Gly Ala Ile Ser Gly Leu Lys Val Ser Ile Ser
 290 295 300

Ala Gly Gly Pro Thr Leu Phe Gln Ser Asn Ile Ser Gly Ser Ser Ala
 305 310 315 320

Gly Gln Gly Gly Gly Gly Ala Ile Asn Ile Ala Ser Ala Gly Gu Leu

Al a Leu Ser Al a Thr Ser Gly Asp Ile Thr Phe Asn Asn Asn G n Val
340 345 350

Thr Asn Gly Ser Thr Ser Thr Arg Asn Al a Ile Asn Ile Ile Asp Thr
355 360

Al a Lys Val Thr Ser Ile Arg Al a Al a Thr Gly G n Ser Ile Tyr Phe
370 375 380

Tyr Asp Pro Ile Thr Asn Pro Gly Thr Al a Al a Ser Thr Asp Thr Leu
385 390 400

Asn Leu Asn Leu Al a Asp Al a Asn Ser Gu Ile Gu Tyr Gly Gly Al a
405 410 415

Ile Val Phe Ser Gly Gu Lys Leu Ser Pro Thr Gu Lys Al a Ile Al a
420 425 430

Al a Asn Val Thr Ser Thr Ile Arg G n Pro Al a Val Leu Al a Arg Gly
435 440 445

Asp Leu Val Leu Arg Asp Gly Val Thr Val Thr Phe Lys Asp Leu Thr
450 455 460

G n Ser Pro Gly Ser Arg Ile Leu Met Asp Gly Gly Thr Thr Leu Ser
465 470 475 480

Al a Lys Gu Al a Asn Leu Ser Leu Asn Gly Leu Al a Val Asn Leu Ser
485 490 495

Ser Leu Asp Gly Thr Asn Lys Al a Al a Leu Lys Thr Gu Al a Al a Asp
500 505 510

Lys Asn Ile Ser Leu Ser Gly Thr Ile Al a Leu Ile Asp Thr Gu Gly
515 520 525

Ser Phe Tyr Gu Asn His Asn Leu Lys Ser Al a Ser Thr Tyr Pro Leu
530 535 540

Leu Gu Leu Thr Thr Al a Gly Al a Asn Gly Thr Ile Thr Leu Gly Al a
545 550 555 560

Leu Ser Thr Leu Thr Leu G n Gu Pro Gu Thr His Tyr Gly Tyr G n
565 570 575

Gly Asn Trp G n Leu Ser Trp Al a Asn Al a Thr Ser Ser Lys Ile Gly
580 585 590

Ser Ile Asn Trp Thr Arg Thr Gly Tyr Ile Pro Ser Pro Gu Arg Lys
595 600 605

Ser Asn Leu Pro Leu Asn Ser Leu Trp Gly Asn Phe Ile Asp Ile Arg
 610 615 620

Ser Ile Asn Gln Leu Ile Gu Thr Lys Ser Ser Gly Gu Pro Phe Gu
 625 630 635 640

Arg Gu Leu Trp Leu Ser Gly Ile Ala Asn Phe Phe Tyr Arg Asp Ser
 645 650 655

Met Pro Thr Arg His Gly Phe Arg His Ile Ser Gly Gly Tyr Ala Leu
 660 665 670

Gly Ile Thr Ala Thr Thr Pro Ala Gu Asp Gln Leu Thr Phe Ala Phe
 675 680 685

Cys Gln Leu Phe Ala Arg Asp Arg Asn His Ile Thr Gly Lys Asn His
 690 695 700

Gly Asp Thr Tyr Gly Ala Ser Leu Tyr Phe His His Thr Gu Gly Leu
 705 710 715 720

Phe Asp Ile Ala Asn Phe Leu Trp Gly Lys Ala Thr Arg Ala Pro Trp
 725 730 735

Val Leu Ser Gu Ile Ser Gln Ile Ile Pro Leu Ser Phe Asp Ala Lys
 740 745 750

Phe Ser Tyr Leu His Thr Asp Asn His Met Lys Thr Tyr Tyr Thr Asp
 755 760 765

Asn Ser Ile Ile Lys Gly Ser Trp Arg Asn Asp Ala Phe Cys Ala Asp
 770 775 780

Leu Gly Ala Ser Leu Pro Phe Val Ile Ser Val Pro Tyr Leu Leu Lys
 785 790 795 800

Gu Val Gu Pro Phe Val Lys Val Gln Tyr Ile Tyr Ala His Gln Gln
 805 810 815

Asp Phe Tyr Gu Arg Tyr Ala Gu Gly Arg Ala Phe Asn Lys Ser Gu
 820 825 830

Leu Ile Asn Val Gu Ile Pro Ile Gly Val Thr Phe Gu Arg Asp Ser
 835 840 845

Lys Ser Gu Lys Gly Thr Tyr Asp Leu Thr Leu Met Tyr Ile Leu Asp
 850 855 860

Ala Tyr Arg Arg Asn Pro Lys Cys Gln Thr Ser Leu Ile Ala Ser Asp
 865 870 875 880

eol f - seq | . app

Al a Asn Trp Met Al a Tyr Gly Thr Asn Leu Al a Arg G n Gly Phe Ser
885 890 895

Val Arg Al a Al a Asn His Phe G n Val Asn Pro His Met Gl u Ile Phe
900 905 910

Gly G n Phe Al a Phe Gl u Val Arg Ser Ser Ser Arg Asn Tyr Asn Thr
915 920 925

Asn Leu Gly Ser Lys Phe Cys Phe
930 935

<210> 147

<211> 1276

<212> PRT

<213> Chl amydi a pneumoni ae

<400> 147

Met Lys Tyr Ser Leu Pro Trp Leu Leu Thr Ser Ser Al a Leu Val Phe
1 5 10 15

Ser Leu His Pro Leu Met Al a Al a Asn Thr Asp Leu Ser Ser Ser Asp
20 25 30

Asn Tyr Gl u Asn Gly Ser Ser Gly Ser Al a Al a Phe Thr Al a Lys Gl u
35 40 45

Thr Ser Asp Al a Ser Gly Thr Thr Tyr Thr Leu Thr Ser Asp Val Ser
50 55 60

Ile Thr Asn Val Ser Al a Ile Thr Pro Al a Asp Lys Ser Cys Phe Thr
65 70 75 80

Asn Thr Gly Gly Al a Leu Ser Phe Val Gly Al a Asp His Ser Leu Val
85 90 95

Leu G n Thr Ile Al a Leu Thr His Asp Gly Al a Al a Ile Asn Asn Thr
100 105 110

Asn Thr Al a Leu Ser Phe Ser Gly Phe Ser Ser Leu Leu Ile Asp Ser
115 120 125

Al a Pro Al a Thr Gly Thr Ser Gly Gly Lys Gly Al a Ile Cys Val Thr
130 135 140

Asn Thr Gl u Gly Gly Thr Al a Thr Phe Thr Asp Asn Al a Ser Val Thr
145 150 155 160

Leu G n Lys Asn Thr Ser Gl u Lys Asp Gly Al a Al a Val Ser Al a Tyr
165 170 175

Ser Ile Asp Leu Al a Lys Thr Thr Thr Al a Al a Leu Leu Asp G n Asn

Thr Ser Thr Lys Asn Gly Gly Ala Leu Cys Ser Thr Ala Asn Thr Thr
 195 200 205
 Val Gln Gly Asn Ser Gly Thr Val Thr Phe Ser Ser Asn Thr Ala Thr
 210 215 220
 Asp Lys Gly Gly Gly Ile Tyr Ser Lys Gu Lys Asp Ser Thr Leu Asp
 225 230 235 240
 Ala Asn Thr Gly Val Val Thr Phe Lys Ser Asn Thr Ala Lys Thr Gly
 245 250 255
 Gly Ala Trp Ser Ser Asp Asp Asn Leu Ala Leu Thr Gly Asn Thr Gln
 260 265
 Val Leu Phe Gln Gu Asn Lys Thr Thr Gly Ser Ala Ala Gln Ala Asn
 275 280 285
 Asn Pro Gu Gly Cys Gly Gly Ala Ile Cys Cys Tyr Leu Ala Thr Ala
 290 295 300
 Thr Asp Lys Thr Gly Leu Ala Ile Ser Gln Asn Gln Gu Met Ser Phe
 305 310 315 320
 Thr Ser Asn Thr Thr Thr Ala Asn Gly Gly Ala Ile Tyr Ala Thr Lys
 325 330 335
 Cys Thr Leu Asp Gly Asn Thr Thr Leu Thr Phe Asp Gln Asn Thr Ala
 340 345 350
 Thr Ala Gly Cys Gly Gly Ala Ile Tyr Thr Gu Thr Gu Asp Phe Ser
 355 360 365
 Leu Lys Gly Ser Thr Gly Thr Val Thr Phe Ser Thr Asn Thr Ala Lys
 370 375 380
 Thr Gly Gly Ala Leu Tyr Ser Lys Gly Asn Ser Ser Leu Thr Gly Asn
 385 390 395 400
 Thr Asn Leu Leu Phe Ser Gly Asn Lys Ala Thr Gly Pro Ser Asn Ser
 405 410 415
 Ser Ala Asn Gln Gu Gly Cys Gly Gly Ala Ile Leu Ser Phe Leu Gu
 420 425 430
 Ser Ala Ser Val Ser Thr Lys Lys Gly Leu Trp Ile Gu Asp Asn Gu
 435 440 445
 Asn Val Ser Leu Ser Gly Asn Thr Ala Thr Val Ser Gly Gly Ala Ile
 450 455 460

Tyr Ala Thr Lys Cys Ala Leu His Gly Asn Thr Thr Leu Thr Phe Asp
 465 470 475 480
 Gly Asn Thr Ala Gu Thr Ala Gly Gly Ala Ile Tyr Thr Gu Thr Gu
 485 490 495
 Asp Phe Thr Leu Thr Gly Ser Thr Gly Thr Val Thr Phe Ser Thr Asn
 500 505 510
 Thr Ala Lys Thr Ala Gly Ala Leu His Thr Lys Gly Asn Thr Ser Phe
 515 520 525
 Thr Lys Asn Lys Ala Leu Val Phe Ser Gly Asn Ser Ala Thr Ala Thr
 530 535 540
 Ala Thr Thr Thr Thr Asp Gn Gu Gly Cys Gly Ala Ile Leu Cys
 545 550 555 560
 Asn Ile Ser Gu Ser Asp Ile Ala Thr Lys Ser Leu Thr Leu Thr Gu
 565 570 575
 Asn Gu Ser Leu Ser Phe Ile Asn Asn Thr Ala Lys Arg Ser Gly Gly
 580 585 590
 Gly Ile Tyr Ala Pro Lys Cys Val Ile Ser Gly Ser Gu Ser Ile Asn
 595 600 605
 Phe Asp Gly Asn Thr Ala Gu Thr Ser Gly Gly Ala Ile Tyr Ser Lys
 610 615 620
 Asn Leu Ser Ile Thr Ala Asn Gly Pro Val Ser Phe Thr Asn Asn Ser
 625 630 635 640
 Gly Gly Lys Gly Gly Ala Ile Tyr Ile Ala Asp Ser Gly Gu Leu Ser
 645 650 655
 Leu Gu Ala Ile Asp Gly Asp Ile Thr Phe Ser Gly Asn Arg Ala Thr
 660 665 670
 Gu Gly Thr Ser Thr Pro Asn Ser Ile His Leu Gly Ala Gly Ala Lys
 675 680 685
 Ile Thr Lys Leu Ala Ala Ala Pro Gly His Thr Ile Tyr Phe Tyr Asp
 690 695 700
 Pro Ile Thr Met Gu Ala Pro Ala Ser Gly Gly Thr Ile Gu Gu Leu
 705 710 715 720
 Val Ile Asn Pro Val Val Lys Ala Ile Val Pro Pro Pro Gn Pro Lys
 725 730 735

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Asn Gly Pro Ile Ala Ser Val Pro Val Val Pro Val Ala Pro Ala Asn
740 745 750

Pro Asn Thr Gly Thr Ile Val Phe Ser Ser Gly Lys Leu Pro Ser Gln
755 760 765

Asp Ala Ser Ile Pro Ala Asn Thr Thr Thr Ile Leu Asn Gln Lys Ile
770 775 780

Asn Leu Ala Gly Gly Asn Val Val Leu Lys Glu Gly Ala Thr Leu Gln
785 790 800

Val Tyr Ser Phe Thr Gln Gln Pro Asp Ser Thr Val Phe Met Asp Ala
805 810 815

Gly Thr Thr Leu Glu Thr Thr Thr Thr Asn Asn Thr Asp Gly Ser Ile
820 825 830

Asp Leu Lys Asn Leu Ser Val Asn Leu Asp Ala Leu Asp Gly Lys Arg
835 840 845

Met Ile Thr Ile Ala Val Asn Ser Thr Ser Gly Gly Leu Lys Ile Ser
850 855 860

Gly Asp Leu Lys Phe His Asn Asn Glu Gly Ser Phe Tyr Asp Asn Pro
865 870 875 880

Gly Leu Lys Ala Asn Leu Asn Leu Pro Phe Leu Asp Leu Ser Ser Thr
885 890 895

Ser Gly Thr Val Asn Leu Asp Asp Phe Asn Pro Ile Pro Ser Ser Met
900 905 910

Ala Ala Pro Asp Tyr Gly Tyr Gln Gly Ser Trp Thr Leu Val Pro Lys
915 920 925

Val Gly Ala Gly Gly Lys Val Thr Leu Val Ala Glu Trp Gln Ala Leu
930 935 940

Gly Tyr Thr Pro Lys Pro Glu Leu Arg Ala Thr Leu Val Pro Asn Ser
945 950 955 960

Leu Trp Asn Ala Tyr Val Asn Ile His Ser Ile Gln Gln Glu Ile Ala
965 970 975

Thr Ala Met Ser Asp Ala Pro Ser His Pro Gly Ile Trp Ile Gly Gly
980 985 990

Ile Gly Asn Ala Phe His Gln Asp Lys Gln Lys Glu Asn Ala Gly Phe
995 1000 1005

Arg Leu Ile Ser Arg Gly Tyr Ile Val Gly Gly Ser Met Thr Thr
1010 1015 1020

Pro Gln Glu Tyr Thr Phe Ala Val Ala Phe Ser Gln Leu Phe Gly
1025 1030 1035

Lys Ser Lys Asp Tyr Val Val Ser Asp Ile Lys Ser Gln Val Tyr
1040 1045 1050

Ala Gly Ser Leu Cys Ala Gln Ser Ser Tyr Val Ile Pro Leu His
1055 1060 1065

Ser Ser Leu Arg Arg His Val Leu Ser Lys Val Leu Pro Glu Leu
1070 1075 1080

Pro Gly Glu Thr Pro Leu Val Leu His Gly Gln Val Ser Tyr Gly
1085 1090 1095

Arg Asn His His Asn Met Thr Thr Lys Leu Ala Asn Asn Thr Gln
1100 1105 1110

Gly Lys Ser Asp Trp Asp Ser His Ser Phe Ala Val Glu Val Gly
1115 1120 1125

Gly Ser Leu Pro Val Asp Leu Asn Tyr Arg Tyr Leu Thr Ser Tyr
1130 1135 1140

Ser Pro Tyr Val Lys Leu Gln Val Val Ser Val Asn Gln Lys Gly
1145 1150 1155

Phe Gln Glu Val Ala Ala Asp Pro Arg Ile Phe Asp Ala Ser His
1160 1165 1170

Leu Val Asn Val Ser Ile Pro Met Gly Leu Thr Phe Lys His Glu
1175 1180 1185

Ser Ala Lys Pro Pro Ser Ala Leu Leu Leu Thr Leu Gly Tyr Ala
1190 1195 1200

Val Asp Ala Tyr Arg Asp His Pro His Cys Leu Thr Ser Leu Thr
1205 1210 1215

Asn Gly Thr Ser Trp Ser Thr Phe Ala Thr Asn Leu Ser Arg Gln
1220 1225 1230

Ala Phe Phe Ala Glu Ala Ser Gly His Leu Lys Leu Leu His Gly
1235 1240 1245

Leu Asp Cys Phe Ala Ser Gly Ser Cys Glu Leu Arg Ser Ser Ser
1250 1255 1260

Arg Ser Tyr Asn Ala Asn Cys Gly Thr Arg Tyr Ser Phe

1265

1270

<210> 148
<211> 908
<212> PRT
<213> Chl amydi a pneumoni ae

<400> 148

Met Asp Ser Gu Phe Val Gly Gn Val Tyr Ser Ser Asp Met Asp Trp
1 5 10 15

Ile Gu Ser Met Tyr Gn Arg Phe Met Asn His Gu Thr Leu Asp Pro
20 25 30

Ser Trp Lys Tyr Phe Phe Gu Gly Tyr Gn Leu Gly Gn Ala Ala Ser
35 40 45

Pro Ser Gu Ala Ser Thr Lys Ile Ser Gly Asn Gu Thr Ile Ala Met
50 55 60

Leu Gn Gu Gn Lys Ser Gn Phe Leu Cys Thr Ile Tyr Arg Tyr Tyr
65 70 75 80

Gly Tyr Leu Gn Ser Gn Ile Ser Thr Leu Ala Pro Thr Thr Asp Ser
85 90 95

Arg Phe Ile Gn Gu Lys Ile Ala Lys Ile Asp Leu Asp Gu Gn Val
100 105 110

Pro Ser Ala Gly Leu Leu Pro Lys Ala Gn Val Ser Val Arg Gu Leu
115 120 125

Ile Gu Ala Leu Lys Lys Cys Tyr Cys Gly Ser Leu Thr Leu Gu Thr
130 135 140

Leu Thr Cys Thr Pro Gu Leu Gn Gu Phe Val Trp Asn Leu Met Gu
145 150 155 160

Lys Arg Gn Val Gu Arg Phe Ala Gu Gn Leu Leu Arg Ser Tyr Lys
165 170 175

Asp Leu Cys Lys Ala Thr Phe Phe Gu Gu Phe Leu Gn Ile Lys Phe
180 185 190

Thr Gly Gn Lys Arg Phe Ser Leu Gu Gly Gly Gu Thr Leu Val Pro
195 200 205

Met Leu Gu His Leu Val His Tyr Gly Ser Ala Leu Gly Ile Ser Asn
210 215 220

Tyr Val Leu Gly Met Ala His Arg Gly Arg Leu Asn Val Leu Thr Asn
225 230 235 240

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Val Leu Gly Lys Pro Tyr Arg Tyr Val Phe Met Gu Phe Gu Asp Asp
 245 250 255

Pro Ala Ala Arg Gly Leu Gu Ser Val Gly Asp Val Lys Tyr His Lys
 260 265 270

Gly Tyr Val Leu Lys Ser His Gn Lys Asp Arg Gu Thr Thr Phe Val
 275 280 285

Met Leu Pro Asn Ala Ser His Leu Gu Ser Val Asp Pro Ile Val Gu
 290 295 300

Gly Val Val Ala Ala Leu Gn His Gn Gly His Ala Gly Lys Gu Gn
 305 310 315 320

Ser Ser Leu Ala Ile Leu Val His Gly Asp Ala Ala Phe Ser Gly Gn
 325 330 335

Gly Val Val Tyr Gu Thr Leu Gn Leu Ser Arg Val Pro Gly Tyr Ser
 340 345 350

Thr Gu Gly Thr Leu His Ile Val Val Asn Asn Tyr Ile Gly Phe Thr
 355 360 365

Ala Val Pro Arg Gu Ser Arg Ser Thr Pro Tyr Cys Thr Asp Ile Ala
 370 375 380

Lys Met Leu Gly Ile Pro Val Phe Arg Val Asn Ser Gu Asp Val Val
 385 390 400

Ala Cys Ile Gu Ala Ile Gu Tyr Ala Leu Gn Val Arg Gu Arg Phe
 405 410 415

Ser Cys Asp Val Ile Ile Asp Leu Cys Cys Tyr Arg Lys Tyr Gly His
 420 425 430

Asn Gu Ser Asp Asp Pro Ser Val Thr Ala Pro Leu Leu Tyr Asp Gn
 435 440 445

Ile Lys Arg Lys Lys Ser Ile Arg Gu Leu Phe Arg Gn Tyr Leu Leu
 450 455 460

Gu Gly Gn Phe Ala Asp Ile Ser Gu Gu Thr Leu Ala Ser Ile Gu
 465 470 475 480

Lys Gu Ile Gn Gu Ser Leu Asn Arg Gu Phe Gn Val Leu Lys Gly
 485 490 495

Thr Asp Pro Gu Pro Phe Pro Lys Lys Gu Cys His His Cys Asp Arg
 500 505 510

Leu Asn Asn Gly Gu Leu Ile Leu His Asp Cys Asp Val Ser Leu Asp
 515 520 525

Arg Gu Thr Leu Phe His Met Ser Ser Arg Leu Cys Gly Phe Pro Asp
 530 535 540

Asn Phe His Pro His Pro Lys Ile Lys Thr Leu Leu Gu Lys Arg Met
 545 550 555

Lys Met Ala Gu Gly Gly Val Gly Tyr Asp Trp Ala Met Ala Gu Gu
 565 570 575

Leu Ala Phe Ala Ser Leu Leu Ile Gu Gly Tyr Asn Leu Arg Leu Ser
 580 585 590

Gly Gn Asp Ser Ile Arg Gly Thr Phe Ser Gn Arg His Leu Val Trp
 595 600 605

Ser Asp Thr Val Thr Gly Asp Thr Tyr Ser Pro Leu Tyr His Leu Ser
 610 615 620

Ala Gu Gn Gly Ser Val Gu Met Tyr Asn Ser Pro Leu Ser Gu Tyr
 625 630 635 640

Ala Ile Leu Gly Phe Gu Tyr Gly Tyr Ala Gn Gn Ala Leu Lys Thr
 645 650 655

Leu Val Leu Trp Gu Ala Gn Phe Gly Asp Phe Ala Asn Gly Ala Gn
 660 665 670

Ile Ile Phe Asp Gn Tyr Ile Ser Ser Gly Ile Gn Lys Trp Asp Leu
 675 680 685

His Ser Asp Ile Val Leu Leu Leu Pro His Gly Tyr Gu Gly Gn Gly
 690 695 700

Pro Gu His Ser Ser Ser Arg Ile Gu Arg Tyr Leu Gn Leu Ala Ala
 705 710 715 720

Asn Trp Asn Phe Gn Val Val Leu Pro Ser Thr Pro Val Gn Tyr Phe
 725 730 735

Arg Ile Leu Arg Gu His Ala Lys Arg Asp Leu Ser Leu Pro Leu Val
 740 745 750

Ile Phe Thr Pro Lys Leu Leu Leu Arg Tyr Pro Gn Cys Val Ser Ser
 755 760 765

Ile Gu Gu Phe Thr Gu Pro Gly Gly Phe Arg Ala Ile Leu Gu Asp
 770 775 780

Ala Asp Pro Asn Tyr Asp Ala Ser Ile Leu Val Leu Cys Ser Gly Lys
 Page 186

785 790 800

I l e Tyr Tyr Asp Tyr 805 Al a G u Met Leu Pro G n Asp Arg Arg Lys Asp 815

Phe Ser Cys Leu 820 Arg I l e G u Ser Leu 825 Tyr Pro Leu Al a Leu 830 G u Asp

Leu Val Ser 835 Leu I l e Asp Lys Tyr 840 Ser Hi s Leu Lys Hi s 845 Phe Val Trp

Leu G n G u G u Ser Lys Asn 855 Met G y Al a Tyr Asp 860 Tyr Met Phe Met

Al a Leu G n Asp I l e Leu 870 Pro G u Lys Leu Leu 875 Tyr I l e G y Arg Pro 880

Arg Ser Ser Ser Thr 885 Al a Ser G y Ser Al a 890 Lys Leu Ser Arg G n G u 895

Leu Val Thr Cys 900 Met G u Thr Leu Phe 905 Ser Leu Arg

<210> 149

<211> 344

<212> PRT

<213> Chl amydi a pneumoni ae

<400> 149

Val Asn Ser Leu I l e Met Al a Thr I l e Ser 10 Pro I l e Ser Leu Thr Val 15

Asp Hi s Pro Leu 20 Val Asp Thr Lys Lys 25 Lys Ser Cys Ser Asn Phe Asp 30

Lys I l e G n Ser Arg I l e Leu Leu 40 I l e Thr Al a I l e Phe Al a Val Leu 45

Val Thr I l e G y Thr Leu Leu 55 I l e G y Leu Leu Leu 60 Asn I l e Pro Val

I l e Tyr Phe Leu Thr G y I l e Ser Phe I l e Al a Val Val Leu Ser Asn 65 70 75 80

Phe I l e Leu Tyr Lys 85 Arg Al a Thr Thr Leu Leu Lys Pro Arg Al a Cys 90 95

G y Lys Hi s Lys 100 G u I l e Lys Pro Lys 105 Arg Val Ser Thr Asn Leu G n 110

Tyr Ser Ser I l e Ser I l e Al a I l e Asn Arg Ser Lys G u Asn Trp G u 115 120 125

eol f - seq| . app

His Gln Pro Lys Asp Leu Gln Asn Leu Pro Ala Pro Ser Ala Leu Leu
130 135 140

Thr Asp Asn Pro Tyr Glu Ile Trp Lys Ala Lys His Ser Leu Phe Ser
145 150 155 160

Leu Val Ser Leu Leu Pro Gly Gly Asn Pro Glu His Leu Leu Ile Ser
165 170 175

Ala Ser Glu Asn Leu Gly Lys Thr Leu Leu Ile Glu Glu Thr Ser Gln
180 185 190

Asn Ala Pro Ile Ser Ser Tyr Val Asp Thr Thr Pro Ser Pro Lys Ser
195 200 205

Leu Leu Asn Glu Ala Ile Gln Glu Thr Arg Val Glu Ile Asn Thr Glu
210 215 220

Leu Pro Ala Gly Asp Ser Gly Glu Arg Leu Tyr Trp Gln Pro Asp Phe
225 230 235 240

Arg Gly Arg Val Phe Leu Pro Gln Ile Pro Thr Thr Pro Glu Ala Ile
245 250 255

Tyr Gln Tyr Tyr Tyr Ala Leu Tyr Val Thr Tyr Ile Gln Thr Ala Ile
260 265 270

Asn Thr Asn Thr Gln Ile Ile Gln Ile Pro Leu Tyr Ser Leu Arg Glu
275 280 285

His Leu Tyr Ser Arg Glu Leu Pro Pro Gln Ser Arg Met Gln Gln Ser
290 295 300

Leu Ala Met Ile Thr Ala Val Lys Tyr Met Ala Glu Leu His Pro Glu
305 310 315 320

Tyr Pro Leu Thr Ile Ala Cys Val Glu Arg Ser Leu Ala Gln Leu Pro
325 330 335

Gln Glu Ser Ile Glu Asp Leu Ser
340

- <210> 150
- <211> 463
- <212> PRT
- <213> Chlamydia pneumoniae
- <400> 150

Leu Leu Asn Leu Arg Tyr Asn Thr Gln Ile Asp Glu Pro Arg Lys Cys
1 5 10 15

Met Ser Asn Ile Thr Ser Pro Val Ile Gln Asn Asn Arg Ser Cys Asn
Page 188

Tyr Tyr Phe 35 Gl u Leu Lys Asn Ser 40 Thr Thr Ile His Ile 45 Val Ile Ser
 Ala Ile 50 Leu Leu Cys Gly Ala 55 Leu Ile Ala Phe Leu 60 Cys Val Ala Ala
 Pro 65 Val Ser Tyr Ile Leu 70 Ser Gly Ala Leu 75 Gly Leu Gly Leu 80
 Ile Ala Leu Ile 85 Gly Val Ile Leu Gly 90 Ile Lys Lys Ile Thr Pro Met 95
 Ile Ser Ser Lys 100 Gl u Gn Val Phe Pro 105 Gn Gl u Leu Val Asn Arg Ile 110
 Arg Ala His 115 Tyr Pro Lys Phe Val 120 Ser Asp Phe Val Ser 125 Gl u Ala Lys
 Pro Asn 130 Leu Lys Asp Leu Ile 135 Ser Phe Ile Asp Leu 140 Leu Asn Gn Leu
 His 145 Ser Gl u Val Gly Ser 150 Ser Thr Asn Tyr Asn 155 Val Ser Gl u Gl u Leu 160
 Gn Gn Lys Ile Asp 165 Thr Phe Gl u Gly Ile 170 Ala Arg Leu Lys Asn Gl u 175
 Val Arg Thr Ala 180 Ser Leu Lys Arg Leu 185 Gl u Ser Ala Ala Ser 190 Ser Arg
 Pro Leu Phe 195 Pro Ser Leu Ala Lys 200 Ile Leu Gn Lys Val 205 Phe Pro Phe
 Phe Trp 210 Leu Gly Gl u Phe Ile 215 Ser Ala Gly Ser Lys 220 Val Val Gl u Leu
 His 225 Arg Val Lys Lys Ile 230 Gly Gly Ser Leu Gl u Gl u Asp Leu Ser Asp 240
 Tyr Ile Lys Pro Gl u 245 Met Leu Pro Thr Tyr 250 Trp Leu Ile Pro Leu Asp 255
 Phe Arg Pro Thr 260 Asn Ser Ser Ile Leu Asn Leu His Thr Leu 270 Val Leu
 Ala Arg Val 275 Leu Thr Arg Asp Val 280 Phe Gn His Leu Lys Tyr Ala Ala 285
 Leu Asn Gly Gl u Trp Asn Leu 295 Asn His Ser Asp Leu 300 Asn Thr Met Lys

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G n G n Leu Phe Ala Lys Tyr His Ala Ala Tyr G n Ser Tyr Lys His
305 310 315 320

Leu Ser G n Pro Ser Leu G n G u Asp G u Phe Tyr Asn Leu Leu Leu
325 330 335

Cys Ile Phe Lys His Arg Tyr Ser Trp Lys G n Met Ser Leu Ile Lys
340 345 350

Thr Val Pro Ala Asp Leu Trp G u Asn Leu Cys Cys Leu Thr Leu Asp
355 360 365

His Thr Gly Arg Pro G n Asp Met G u Phe Ala Ser Leu Ile Gly Thr
370 375 380

Leu Tyr Thr G n Gly Leu Ile His Lys G u Ser G u Ala Phe Leu Ser
385 390 395 400

Ser Leu Thr Leu Leu Ser Leu Asp G n Phe Lys Thr Ile Arg Arg G n
405 410 415

Ser Thr Asn Ile Ala Met Phe Leu G u Asn Leu Ala Thr His Asn Ser
420 425 430

Thr Phe Arg Ser Leu Pro Pro Ile Thr Val His Pro Leu Lys Arg Ser
435 440 445

Val Phe Ser G n Pro G u G u Asp G u Ser Ser Leu Leu Ile Gly
450 455 460

<210> 151
<211> 171
<212> PRT
<213> Chl amydi a pneumoni ae
<400> 151

Val Gly Phe Met Ala Val G u G n Ser His Ile Lys G u G u Ile G u
1 5 10 15

Lys Leu Ile Gly Lys Ala Ile Lys Arg Val Cys Gly Asn Lys G u Asn
20 25 30

Asp Leu Cys Arg Tyr Leu Pro Gly Pro Ser Gly Gly Tyr Met His His
35 40 45

Phe Thr Leu Lys Lys Met Lys Ser Ala Ala Pro G u G n Leu Leu Lys
50 55 60

Met Leu Lys Thr Phe Ile Leu G u Ser G u Thr Pro Arg Thr Ile Asn
65 70 75 80

Pro Lys Pro Arg Ala Pro Arg Gly Ser Lys Lys Arg Arg Asp Phe Ile
85 90 95

Asn Phe Thr Lys Thr Asp Ile Gu Arg Val Leu Gu Leu Ala Arg Gn
100 105 110

Val Gly Asp Lys Asp Leu Leu Ala Arg Phe Ser Pro Lys Lys Pro Leu
115 120 125

Thr Ser Leu Lys Arg Gu Leu Ile Arg Ser Ile Arg Asn Gly Ile Val
130 135 140

Ser Val Gu Leu Trp Asn Ala Tyr Val Gu Ala Val Lys Ala Val Ser
145 150 155 160

Ser Pro Asn Leu Gu Val Thr Ser Pro Phe Val
165 170

<210> 152
<211> 311
<212> PRT
<213> Chl amydi a pneumoni ae

<400> 152

Met Ile His Ser Arg Leu Ile Ile Ile Gly Ser Gly Pro Ser Gly Tyr
1 5 10 15

Thr Ala Ala Ile Tyr Ala Ser Arg Ala Leu Leu His Pro Leu Leu Phe
20 25 30

Gu Gly Phe Phe Ser Gly Ile Ser Gly Gly Gn Leu Met Thr Thr Thr
35 40 45

Gu Val Gu Asn Phe Pro Gly Phe Pro Gu Gly Ile Leu Gly Pro Lys
50 55 60

Leu Met Asn Asn Met Lys Gu Gn Ala Val Arg Phe Gly Thr Lys Thr
65 70 75 80

Leu Ala Gn Asp Ile Ile Ser Val Asp Phe Ser Val Arg Pro Phe Ile
85 90 95

Leu Lys Ser Lys Gu Gu Thr Tyr Ser Cys Asp Ala Cys Ile Ile Ala
100 105 110

Thr Gly Ala Ser Ala Lys Arg Leu Gu Ile Pro Gly Ala Gly Asn Asp
115 120 125

Gu Phe Trp Gn Lys Gly Val Thr Ala Cys Ala Val Cys Asp Gly Ala
130 135 140

Ser Pro Ile Phe Lys Asn Lys Asp Leu Tyr Val Ile Gly Gly Gly Asp
145 150 155 160

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Ser Ala Leu Gu Gu Ala Leu Tyr Leu Thr Arg Tyr Gly Ser His Val
165 170 175

Tyr Val Val His Arg Arg Asp Lys Leu Arg Ala Ser Lys Ala Met Gu
180 185 190

Ala Arg Ala Gn Asn Asn Gu Lys Ile Thr Phe Leu Trp Asn Ser Gu
195 200 205

Ile Val Lys Ile Ser Gly Asp Ser Ile Val Arg Ser Val Asp Ile Lys
210 215 220

Asn Val Gn Thr Gn Gu Ile Thr Thr Arg Gu Ala Ala Gly Val Phe
225 230 235 240

Phe Ala Ile Gly His Lys Pro Asn Thr Asp Phe Leu Gly Gly Gn Leu
245 250 255

Thr Leu Asp Gu Ser Gly Tyr Ile Val Thr Gu Lys Gly Thr Ser Lys
260 265 270

Thr Ser Val Pro Gly Val Phe Ala Ala Gly Asp Val Gn Asp Lys Tyr
275 280 285

Tyr Arg Gn Ala Val Thr Ser Ala Gly Ser Gly Cys Ile Ala Ala Leu
290 295 300

Asp Ala Gu Arg Phe Leu Gly
305 310

<210> 153
<211> 171
<212> PRT
<213> Chl amydi a pneumoni ae
<400> 153

Met Lys Lys Leu Leu Phe Ser Thr Phe Leu Leu Val Leu Gly Ser Thr
1 5 10 15

Ser Ala Ala His Ala Asn Leu Gly Tyr Val Asn Leu Lys Arg Cys Leu
20 25 30

Gu Gu Ser Asp Leu Gly Lys Lys Gu Thr Gu Gu Leu Gu Ala Met
35 40 45

Lys Gn Gn Phe Val Lys Asn Ala Gu Lys Ile Gu Gu Gu Leu Thr
50 55 60

Ser Ile Tyr Asn Lys Leu Gn Asp Gu Asp Tyr Met Gu Ser Leu Ser
65 70 75 80

Asp Ser Ala Ser Gu Gu Leu Arg Lys Lys Phe Gu Asp Leu Ser Gly
85 90 95

Gu Tyr Asn Ala Tyr Gn Ser Gn Tyr Tyr Gn Ser Ile Asn Gn Ser
100 105 110

Asn Val Lys Arg Ile Gn Lys Leu Ile Gn Gu Val Lys Ile Ala Ala
115 120 125

Gu Ser Val Arg Ser Lys Gu Lys Leu Gu Ala Ile Leu Asn Gu Gu
130 135 140

Ala Val Leu Ala Ile Ala Pro Gly Thr Asp Lys Thr Thr Gu Ile Ile
145 150 155 160 165

Ala Ile Leu Asn Gu Ser Phe Lys Lys Gn Asn
165 170

<210> 154

<211> 805

<212> PRT

<213> Chl amydi a pneumoni ae

<400> 154

Met Asp Pro Lys Gu Lys Asn Tyr Asp Ala Ser Ala Ile Thr Val Leu
1 5 10 15

Gu Gly Leu Gn Ala Val Arg Gu Arg Pro Gly Met Tyr Ile Gly Asp
20 25 30

Thr Gly Ile Thr Gly Leu His His Leu Val Tyr Gu Val Val Asp Asn
35 40 45

Ser Ile Asp Gu Ala Met Ala Gly Tyr Cys Ser Arg Ile Asp Val Arg
50 55 60

Ile Leu Gu Asp Gly Gly Ile Val Ile Val Asp Asn Gly Arg Gly Ile
65 70 75 80

Pro Ile Gu Val His Gu Arg Gu Ser Ala Lys Gn Gly Arg Gu Val
85 90 95

Ser Ala Leu Gu Val Val Leu Thr Val Leu His Ala Gly Gly Lys Phe
100 105 110

Asp Lys Asp Ser Tyr Lys Val Ser Gly Gly Leu His Gly Val Gly Val
115 120 125

Ser Cys Val Asn Ala Leu Ser Gu Lys Leu Val Ala Thr Val Phe Lys
130 135 140

Asp Lys Lys Cys Tyr Gn Met Gu Phe Ser Arg Gly Ile Pro Val Thr
145 150 155 160

eol f - seq1 . app

Pro Leu Gln Tyr Val Ser Val Ser Asp Arg Gln Gly Thr Glu Ile Val
 165 170 175
 Phe Tyr Pro Asp Pro Lys Ile Phe Ser Thr Cys Thr Phe Asp Arg Ser
 180 185 190
 Ile Leu Met Lys Arg Leu Arg Glu Leu Ala Phe Leu Asn Arg Gly Ile
 195 200 205
 Thr Ile Val Phe Glu Asp Asp Arg Asp Val Ser Phe Asp Lys Val Thr
 210 215 220
 Phe Phe Tyr Glu Gly Gly Ile Gln Ser Phe Val Ser Tyr Leu Asn Gln
 225 230 235 240
 Asn Lys Glu Ser Leu Phe Ser Glu Pro Ile Tyr Ile Cys Gly Thr Arg
 245 250 255
 Val Gly Asp Asp Gly Glu Ile Glu Phe Glu Ala Ala Leu Gln Trp Asn
 260 265 270
 Ser Gly Tyr Ser Glu Leu Val Tyr Ser Tyr Ala Asn Asn Ile Pro Thr
 275 280 285
 Arg Gln Gly Gly Thr His Leu Thr Gly Phe Ser Thr Ala Leu Thr Arg
 290 295 300
 Val Ile Asn Thr Tyr Ile Lys Ala His Asn Leu Ala Lys Asn Asn Lys
 305 310 315 320
 Leu Ala Leu Thr Gly Glu Asp Ile Arg Glu Gly Leu Thr Ala Val Ile
 325 330 335
 Ser Val Lys Val Pro Asn Pro Gln Phe Glu Gly Gln Thr Lys Gln Lys
 340 345 350
 Leu Gly Asn Ser Asp Val Ser Ser Val Ala Gln Gln Val Val Gly Glu
 355 360 365
 Ala Leu Thr Ile Phe Phe Glu Glu Asn Pro Gln Ile Ala Arg Met Ile
 370 375 380
 Val Asp Lys Val Phe Val Ala Ala Gln Ala Arg Glu Ala Ala Lys Lys
 385 390 395 400
 Ala Arg Glu Leu Thr Leu Arg Lys Ser Ala Leu Asp Ser Ala Arg Leu
 405 410 415
 Pro Gly Lys Leu Ile Asp Cys Leu Glu Lys Asp Pro Glu Lys Cys Glu
 420 425 430

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Mèt Tyr Ile Val Gu Gy Asp Ser Ala Gy Gy Ser Ala Lys Gn Gy
 435 440 445

Arg Asp Arg Arg Phe Gn Ala Ile Leu Pro Ile Arg Gy Lys Ile Leu
 450 455 460

Asn Val Gu Lys Ala Arg Leu Gn Lys Ile Phe Gn Asn Gn Gu Ile
 465 470 475 480

Gy Thr Ile Ile Ala Ala Leu Gy Cys Gy Ile Gy Ala Asp Asn Phe
 485 490 495

Asn Leu Ser Lys Leu Arg Tyr Arg Arg Ile Ile Ile Mèt Thr Asp Ala
 500 505 510

Asp Val Asp Gy Ser His Ile Arg Thr Leu Leu Leu Thr Phe Phe Tyr
 515 520 525

Arg His Mèt Thr Ala Leu Ile Gu Asn Gu Cys Val Tyr Ile Ala Gn
 530 535 540

Pro Pro Leu Tyr Lys Val Ser Lys Lys Lys Asp Phe Arg Tyr Ile Leu
 545 550 555 560

Ser Gu Lys Gu Mèt Asp Ser Tyr Leu Leu Mèt Leu Gy Thr Asn Gu
 565 570 575

Ser Ser Ile Leu Phe Lys Ser Thr Gu Arg Gu Leu Arg Gy Gu Ala
 580 585 590

Leu Gu Ser Phe Ile Asn Val Ile Leu Asp Val Gu Ser Phe Ile Asn
 595 600 605

Thr Leu Gu Lys Lys Ala Ile Pro Phe Ser Gu Phe Leu Gu Mèt Tyr
 610 615 620

Lys Gu Gy Ile Gy Tyr Pro Leu Tyr Tyr Leu Ala Pro Ala Thr Gy
 625 630 635 640

Mèt Gn Gy Gy Arg Tyr Leu Tyr Ser Asp Gu Gu Lys Gu Gu Ala
 645 650 655

Leu Ala Gn Gu Gu Thr His Lys Phe Lys Ile Ile Gu Leu Tyr Lys
 660 665 670

Val Ala Val Phe Val Asp Ile Gn Asn Gn Leu Lys Gu Tyr Gy Leu
 675 680 685

Asp Ile Ser Ser Tyr Leu Ile Pro Gn Lys Asn Gu Ile Val Ile Gy
 690 695 700

Asn 705 Gl u Asp Ser Pro Ser 710 Cys Asn Tyr Ser Cys 715 Tyr Thr Leu Gl u Gl u 720

Val Ile Asn Tyr Leu 725 Lys Asn Leu Gl y Arg 730 Lys Gl y Ile Gl u Ile Gl n 735

Arg Tyr Lys Gl y 740 Leu Gl y Gl u Met Asn 745 Ala Asp Gl n Leu Trp Asp Thr 750

Thr Met Asn 755 Pro Gl u Gl n Arg Thr 760 Leu Ile His Val Ser 765 Leu Lys Asp

Ala Val 770 Gl u Ala Asp His Ile 775 Phe Thr Met Leu Met 780 Gl y Gl u Gl u Val

Pro 785 Pro Arg Arg Gl u Phe 790 Ile Gl u Ser His Ala 795 Leu Ser Ile Arg Ile 800

Asn Asn Leu Asp Ile 805

- <210> 155
- <211> 287
- <212> PRT
- <213> Chl amydi a pneumoni ae
- <400> 155

Met 1 Lys Arg Arg Asn 5 Leu Gl n Lys Ile Leu 10 Pro Asn Ala Ser Thr Pro 15

Ser Thr Asn Val 20 Ala Gl u Asn Thr Gl y 25 Ile Lys Asp Gl n Asn 30 Leu Phe

Leu Asp Gl n 35 Ala Thr Leu Asn Val 40 Asp Gl y Asn Val Asp 45 Ile Gl u Asn

Phe Leu 50 Gl u Thr Arg Asp Leu 55 Lys Val Ala Asp Thr 60 Ile Thr Ser Pro

Cys 65 Gl u Phe Thr Val Gl y 70 Gl y Gl y Leu Ser Ala 75 Gl u Ser Ser Gl n Phe 80

Lys Ala Thr Thr Leu 85 Ser Lys Gl y Leu Gl u 90 Ile Thr Ser Gl u Asp Gl n 95

Asp Gl y Arg Val 100 Pro Lys Phe Thr Asn 105 Val Ser Asp Pro Gl n 110 Ser Pro

Arg Asp Ala 115 Leu Thr Tyr Asn Tyr 120 Tyr Arg Asn Thr Gl y 125 Cys Gl n Ala

Leu Asn 130 Leu Tyr Thr Tyr Tyr 135 Ser Ser Ser Gl n Pro 140 Thr Thr Val Gl y

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Lys Pro Ile Glu Thr Val Cys Gln Asn Pro Asn Pro Glu Thr Tyr Arg
145 150 155 160

Ile Ser Ala Ser Ala Lys Ile Tyr Asp Ala Val Thr Arg Phe Pro Tyr
165 170 175

Ile Gln Phe Lys Ala Pro Gly Ile Tyr Gln Val Thr Ile Gln Ile Arg
180 185 190

Arg Glu Ser Gly Gln His Ser Gly Leu Asp Asn Pro Asn Leu Tyr Leu
195 200 205

Asn Leu Met Ile Gly Asn Asn Lys Thr Leu Leu Cys Ala Ser Asp Thr
210 215 220

Arg Gly Tyr Ser Gly Gly His Arg Thr Ser Ile Ala Val Thr Gly Thr
225 230 235 240

Phe Thr Leu Thr Glu Ile Val Ala Thr Pro Pro His Asp Tyr Pro Trp
245 250 255

Leu Phe Leu Glu Thr Thr Ile Gly Leu Asp Ile Lys Ser Met Ser Thr
260 265 270

Cys Val Ile Trp Phe Pro Phe Gln Ala Asn Phe Ala Glu Val Asp
275 280 285

<210> 156
<211> 231
<212> PRT
<213> Chlamydia pneumoniae

<400> 156

Met Leu Gln Ser Cys Lys Lys Ala Leu Leu Ser Ile Val Val Ser Ile
1 5 10 15

Leu Ala Phe His Pro Ile Pro Gly Met Gly Val Glu Ala Lys Ser Gly
20 25 30

Phe Leu Gly Lys Val Lys Gly Trp Phe Ser Lys Lys Glu Ile Gln Glu
35 40 45

Glu Ala Arg Ile Leu Pro Val Lys Asp Ser Leu Ser Trp Lys Arg Tyr
50 55 60

Asp Tyr Thr Ser Ser Ser Gly Phe Ser Val Glu Phe Pro Gly Glu Pro
65 70 75 80

Asp His Ser Gly Gln Ile Val Glu Val Pro Gln Ser Glu Ile Thr Ile
85 90 95

Arg Tyr Asp Thr Tyr Val Thr Gu Thr His Pro Asp Asn Thr Val Tyr
 100 105 110
 Val Val Ser Val Trp Gu Tyr Pro Gu Lys Val Asp Ile Ser Arg Pro
 115 120 125
 Gu Leu Asn Leu Gn Gu Gy Phe Ser Gy Met Met Gn Ala Leu Pro
 130 135 140
 Gu Ser Gn Val Leu Phe Met Gn Ala Arg Gn Ile Gn Gy His Lys
 145 150 155
 Ala Leu Gu Phe Trp Ile Val Cys Gu Asp Val Tyr Phe Arg Gy Met
 165 170 175
 Leu Ile Ser Val Asn His Thr Leu Tyr Gn Val Phe Met Val Tyr Lys
 180 185 190
 Asn Lys Asn Pro Gn Ala Leu Asp Lys Gu Tyr Gu Ala Phe Ser Gn
 195 200 205
 Ser Phe Lys Ile Thr Lys Ile Arg Gu Pro Arg Thr Ile Pro Ser Ser
 210 215 220
 Val Lys Lys Lys Val Ser Leu
 225 230
 <210> 157
 <211> 550
 <212> PRT
 <213> Chl amydi a pneumoni ae
 <400> 157
 Met His Pro Leu Tyr Val Asp Leu Asp Thr Ile Ile Ser Ser Tyr Ser
 1 5 10 15
 Pro Pro Leu Pro Lys Gu Phe Gn Gu Ala Ala Ser Leu Ile Ala Val
 20 25 30
 Pro Asp Thr Ser His Ser Lys Pro Val Val Pro Gy Val Lys Thr Leu
 35 40 45
 Phe Pro Gn Thr Tyr His Leu Pro Tyr Leu Lys Phe Val Gn Gy Gu
 50 55 60
 Asn Val Val His Thr Pro Leu Lys Val Gy Val Met Phe Ser Gy Gy
 65 70 75 80
 Pro Ala Pro Gy Gy His Asn Val Ile Gn Gy Leu Phe Asn Ser Leu
 85 90 95
 Lys Asp Phe His Pro Asp Ser Ser Leu Val Gy Phe Val Asn Asn Gy
 100 105 110

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Asp Gly Leu Thr Asn Asn Lys Ser Ile Asp Ile Thr Glu Glu Phe Leu
 115 120 125
 Ser Lys Phe Arg Asn Ser Gly Gly Phe Asn Cys Ile Gly Thr Gly Arg
 130 135 140
 Lys Lys Ile Val Thr Pro Glu Ala Lys Glu Ala Cys Leu Lys Thr Ala
 145 150 155 160
 Glu Ala Leu Asp Leu Asp Gly Leu Val Ile Ile Gly Gly Asp Gly Ser
 165 170 175
 Asn Thr Ala Thr Ala Ile Leu Ala Glu Tyr Phe Ala Lys Arg Arg Pro
 180 185 190
 Lys Thr Ser Ile Val Gly Val Pro Lys Thr Ile Asp Gly Asp Leu Gn
 195 200 205
 His Thr Phe Leu Asp Leu Thr Phe Gly Phe Asp Thr Ala Thr Lys Phe
 210 215 220
 Tyr Ser Ser Ile Ile Ser Asn Ile Ser Arg Asp Ala Leu Ser Cys Lys
 225 230 235 240
 Ala His Tyr His Phe Ile Lys Leu Met Gly Arg Ser Ala Ser His Ile
 245 250 255
 Ala Leu Glu Cys Ala Leu Gn Thr His Pro Asn Ile Ala Leu Ile Gly
 260 265 270
 Glu Glu Ile Ala Glu Lys Asn Leu Pro Leu Lys Thr Ile Ile His Lys
 275 280 285
 Ile Cys Ser Val Ile Ala Asp Arg Ala Ala Met Glu Lys Tyr Tyr Gly
 290 295 300
 Val Ile Leu Ile Pro Glu Gly Ile Ile Glu Phe Ile Pro Glu Ile Ile
 305 310 315 320
 Asn Leu Ile Thr Glu Ile Glu Ser Leu Ser Glu Tyr Glu Asp Lys Ile
 325 330 335
 Ser Arg Leu Ser Pro Glu Ser Gn Arg Leu Leu Lys Ser Phe Pro Ala
 340 345 350
 Pro Ile Ile Glu Gn Ile Leu Asn Asp Arg Asp Ala His Gly Asn Val
 355 360 365
 Tyr Val Ser Lys Ile Ser Val Asp Lys Leu Leu Ile His Leu Val Ser
 370 375 380

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Asn His Leu Gln Gln Tyr Phe Pro Asn Val Pro Phe Asn Ala Ile Ser
385 390 395 400

His Phe Leu Gly Tyr Gu Gly Arg Ser Gly Leu Pro Thr Lys Phe Asp
405 410 415

Asn Thr Tyr Gly Tyr Ser Leu Gly Tyr Gly Ala Gly Ile Leu Val Arg
420 425 430

Asn His Cys Asn Gly Tyr Leu Ser Thr Ile Gu Ser Leu Ala Cys Pro
435 440 445

Phe Met Lys Trp Lys Leu Arg Ala Ile Pro Val Val Lys Met Phe Thr
450 455 460

Val Lys Gln Gln Ala Asp Gly Thr Leu Gln Pro Lys Ile Lys Lys Tyr
465 470 475 480

Leu Val Asp Ile Gly Ser Thr Ala Phe Arg Lys Phe Lys Leu Tyr Arg
485 490 495

Lys Ile Trp Ala Leu Gu Asp Ser Tyr Arg Phe Leu Gly Pro Leu Gln
500 505 510

Ile Gu Thr Pro Pro Gu Met His Ser Asp Asn Phe Pro Pro Leu Thr
515 520 525

Leu Leu Leu Asn His Asn Phe Trp Gln Arg His Gln Gly Cys Ile Gu
530 535 540

Ile Pro Asp Thr Thr Tyr
545 550

<210> 158
<211> 528
<212> PRT
<213> Chlamydia pneumoniae

<400> 158

Met Lys Met His Arg Leu Lys Pro Thr Leu Lys Ser Leu Ile Pro Asn
1 5 10 15

Leu Leu Phe Leu Leu Leu Thr Leu Ser Ser Cys Ser Lys Gln Lys Gln
20 25 30

Gu Pro Leu Gly Lys His Leu Val Ile Ala Met Ser His Asp Leu Ala
35 40 45

Asp Leu Asp Pro Arg Asn Ala Tyr Leu Ser Arg Asp Ala Ser Leu Ala
50 55 60

Lys Ala Leu Tyr Gu Gly Leu Thr Arg Gu Thr Asp Gln Gly Ile Ala

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G u G u Arg G n Thr Lys Ala Arg Ala Tyr Phe G n G u Ala Lys G u
355 360 365

Thr Leu Ser G u Lys G u Leu Ala G u Leu Ser Ile Leu Tyr Pro Ile
370 375 380

Asp Ser Ser Asn Ser Ser Ile Ile Ala G n G u Ile G n Arg G n Leu
385 390 400

Lys Asp Thr Leu G y Leu Lys Ile Lys Ile G n G y Met G u Tyr Hi s
405 410 415

Cys Phe Leu Lys Lys Arg Arg G n G y Asp Phe Phe Ile Ala Thr G y
420 425 430

G y Trp Ile Ala G u Tyr Val Ser Pro Val Ala Phe Leu Ser Ile Leu
435 440 445

G y Asn Pro Arg Asp Leu Thr G n Trp Arg Asn Ser Asp Tyr G u Lys
450 455 460

Thr Leu G u Lys Leu Tyr Leu Pro Hi s Ala Tyr Lys G u Asn Leu Lys
465 470 475 480

Arg Ala G u Met Ile Ile G u G u G u Thr Pro Ile Ile Pro Leu Tyr
485 490 495

Hi s G y Lys Tyr Ile Tyr Ala Ile Hi s Pro Lys Ile G n Asn Thr Phe
500 505 510

G y Ser Leu Leu G y Hi s Thr Asp Leu Lys Asn Ile Asp Ile Leu Ser
515 520 525

<210> 159
<211> 619
<212> PRT
<213> Chl amydi a pneumoni ae

<400> 159

Met G u Ser G u Lys Asp Ile G y Ala Lys Phe Leu G y Asp Tyr Arg
1 5 10 15

Ile Leu Tyr Arg Lys G y G n Ser Leu Trp Ser G u Asp Leu Leu Ala
20 25 30

G u Hi s Arg Phe Ile Lys Lys Arg Tyr Leu Ile Arg Leu Leu Leu Pro
35 40 45

Asp Leu G y Ser Ser G n Pro Phe Met G u Ala Phe Hi s Asp Val Val
50 55 60

Val Lys Leu Ala Lys Leu Asn His Pro Gly Ile Leu Ser Ile Gu Asn
65 70 75 80

Val Ser Gu Ser Gu Gy Arg Cys Phe Leu Val Thr Gn Gu Gn Asp
85 90 95

Ile Pro Ile Leu Ser Leu Thr Gn Tyr Leu Lys Ser Ile Pro Arg Lys
100 105 110

Leu Thr Gu Leu Gu Ile Val Asp Ile Val Ser Gn Leu Ala Ser Leu
115 120 125

Leu Asp Tyr Val His Ser Gu Gy Leu Ala Gn Gu Gu Trp Asn Leu
130 135 140

Asp Ser Val Tyr Ile His Ile Leu Asn Gy Val Pro Lys Val Ile Leu
145 150 155 160

Pro Asp Leu Gy Phe Ala Ser Leu Ile Lys Gu Arg Ile Leu Asp Gy
165 170 175

Phe Ile Ser Asp Gu Gu Asn Arg Gu Ser Lys Ile Lys Gu Arg Val
180 185 190

Leu Leu His Thr Ser Gu Gy Lys Gn Gy Arg Gu Asp Thr Tyr Ala
195 200 205

Phe Gy Ala Ile Thr Tyr Tyr Leu Leu Phe Gy Phe Leu Pro Gn Gy
210 215 220

Ile Phe Pro Met Pro Ser Lys Val Phe Ser Asp Phe Ile Tyr Asp Trp
225 230 235 240

Asp Phe Leu Ile Ser Ser Cys Leu Ser Cys Phe Met Gu Gu Arg Ala
245 250 255

Lys Gu Leu Phe Pro Leu Ile Arg Lys Lys Thr Leu Gy Gu Gu Leu
260 265 270

Gn Asn Val Val Thr Asn Cys Ile Gu Ser Ser Leu Arg Gu Val Pro
275 280 285

Asp Pro Leu Gu Ser Ser Gn Asn Leu Pro Gn Ala Val Leu Lys Val
290 295 300

Gy Gu Thr Lys Ala Ser His Gn Gn Lys Gu Ser Ala Gu His Leu
305 310 315 320

Gu Phe Val Leu Val Gu Ala Cys Ser Ile Asp Gu Ala Met Asp Thr
325 330 335

Ala Ile Gu Ser Gu Ser Ser Ser Gy Val Gu Gu Gu Gy Tyr Ser
Page 203

Leu Ala Leu Gn Ser Leu Leu Val Arg Gu Pro Val Val Ser Arg Tyr
 355 360 365

Val Gu Ala Gu Lys Gu Gu Pro Lys Pro Gn Pro Ile Leu Thr Gu
 370 375 380

Met Val Leu Ile Gu Gy Gy Gu Phe Ser Arg Gy Ser Val Gu Gy
 385 390 400

Gn Arg Asp Gu Leu Pro Val His Lys Val Ile Leu His Ser Phe Phe
 405 410 415

Leu Asp Val His Pro Val Thr Asn Gu Gn Phe Ile Arg Tyr Leu Gu
 420 425 430

Cys Cys Gy Ser Gu Gn Asp Lys Tyr Tyr Asn Gu Leu Ile Arg Leu
 435 440 445

Arg Asp Ser Arg Ile Gn Arg Arg Ser Gy Arg Leu Val Ile Gu Pro
 450 455 460

Gy Tyr Ala Lys His Pro Val Val Gy Val Thr Trp Tyr Gy Ala Ser
 465 470 475 480

Gy Tyr Ala Gu Trp Ile Gy Lys Arg Leu Pro Thr Gu Ala Gu Trp
 485 490 495

Gu Ile Ala Ala Ser Gy Gy Val Ala Ala Leu Arg Tyr Pro Cys Gy
 500 505 510

Gu Gu Ile Gu Lys Ser Arg Ala Asn Phe Phe Thr Ala Asp Thr Thr
 515 520 525

Thr Val Met Ser Tyr Pro Pro Asn Pro Tyr Gy Leu Tyr Asp Met Ala
 530 535 540

Gy Asn Val Tyr Gu Trp Cys Gn Asp Trp Tyr Gy Tyr Asp Phe Tyr
 545 550 555 560

Gu Ile Ser Ala Gn Gu Pro Gu Ser Pro Gn Gy Pro Ala Gn Gy
 565 570 575

Val Tyr Arg Val Leu Arg Gy Gy Cys Trp Lys Ser Leu Lys Asp Asp
 580 585 590

Leu Arg Cys Ala His Arg His Arg Asn Asn Pro Gy Ala Val Asn Ser
 595 600 605

Thr Tyr Gy Phe Arg Cys Ala Lys Asn Ile Asn
 610 615

<210> 160
 <211> 636
 <212> PRT
 <213> Chlamydia pneumoniae

<400> 160

Met Lys Gln His Tyr Ser Leu Asn Lys Ser Arg His Ile Leu Arg Ser
 1 5 10 15

Thr Tyr Lys Leu Leu Lys Ser Lys Lys Leu Ala His Ser Pro Ala Asp
 20 25 30

Lys Lys Gln Leu Gln Gu Leu Leu Gu Gln Leu Gu Gu Ala Ile Phe
 35 40 45

Gu His Asp Gln Gu Thr Ala Ser Asp Leu Ala Gln Gln Ala Leu Ala
 50 55 60

Phe Ser Asn Arg Tyr Pro Asn Ser Phe Gly Arg Lys Thr Tyr Gu Leu
 65 70 75 80

Ile Lys Ala Leu Leu Phe Ala Gly Val Val Ala Phe Leu Val Arg Gln
 85 90 95

Phe Trp Phe Gu Leu Tyr Gu Val Pro Thr Gly Ser Met Arg Pro Thr
 100 105 110

Ile Leu Gu Gln Asp Arg Ile Leu Val Ser Lys Thr Thr Phe Gly Leu
 115 120 125

His Cys Pro Phe Ala Lys Lys Pro Leu Ala Phe Asn Pro Gu Ser Val
 130 135 140

Thr Arg Gly Gly Leu Val Val Phe Thr Val Gly Asp Leu Pro Ile Pro
 145 150 155 160

Asp Ala Asp Thr Lys Tyr Phe Gly Leu Ile Pro Gly Lys Lys Arg Tyr
 165 170 175

Ile Lys Arg Cys Met Gly Arg Pro Gly Asp Phe Leu Tyr Phe Tyr Gly
 180 185 190

Gly Lys Ile Tyr Gly Leu Asp Asp Ala Gly Lys Arg Ile Gu Phe Pro
 195 200 205

Ser Val His Gly Leu Gu Asn Leu Tyr His Val Pro Tyr Ile Ser Phe
 210 215 220

Asp Gly Thr Thr Ser Ser His Thr Gu Gly Gln Lys Thr Ile Ile Asp
 225 230 235 240

Phe Lys Gln Phe Asn 245 Gln Ser Tyr Gly Arg 250 Leu Ile Phe Pro Gln Thr 255

Ser Met Tyr Gly 260 Gln Phe Phe Asp His 265 Lys Glu Trp His Gln Asp Glu 270

Pro Asn Lys 275 Leu Lys Asp Pro His 280 Leu Ser Pro Val Ser 285 Tyr Ala Asp

Leu Phe Gly 290 Met Gly Asn Tyr 295 Ala Met Val Arg Ile 300 Leu Thr Glu His

Gln Ala Arg Thr Ser His 310 Leu Leu Pro Asn Pro 315 Gly Ser Pro Thr Lys 320

Val Tyr Leu Glu Ile 325 Cys His Thr Ala Asn 330 Leu Ser Tyr Pro Lys 335 Pro

Leu Leu Arg His 340 Tyr Glu His Gln Leu Ser Pro Ala Ile Gln Pro Met 350

Lys Thr Leu 355 Leu Pro Leu Arg Lys 360 Glu His Leu His Leu Ile Arg Asn 365

Asn Leu Thr Thr Ser Arg Phe 375 Ile Val Ala Gln Gly 380 Cys Ala Tyr Lys

Tyr His Gln Phe Lys Ile 390 Asn Thr Ser Gly Ile 395 Ala Lys Ala Tyr Ala 400

Ile Leu Leu Pro Lys 405 Val Pro Asp Gly Cys 410 Tyr Glu Tyr Ser Lys Glu 415

Glu Ala Tyr Gln Ile Gly Phe Gly Glu 425 Ile Arg Tyr Lys Leu Lys Ser 430

Ser His Pro 435 Leu Thr Gln Leu Asn 440 Asp Lys Gln Val Ile Glu Leu Phe 445

Asn Cys Gly Ile Asn Phe Ser 455 Ser Ile Tyr Asn Pro Val Asn Pro Leu 460

Gln Ala Pro Leu Pro Asn Arg Tyr Ala Phe Phe Asn Gln Gly Asn Leu 470 480

Tyr Ile Met Asp Ser 485 Pro Val Phe Ile Lys Asn Asp Pro Thr Leu Gln 495

Lys Phe Val Thr Ser Glu Thr Glu Lys 505 Gln Glu Gly Ser Ser Glu Thr 510

Gln Pro Tyr Ile Ala Phe Val Asp Lys Gly Leu Pro Pro Glu Asp Phe

515

520

525

Lys Glu Phe Val Glu Phe Ile His Asn Phe Gly Ile Gn Val Pro Lys
530 535 540

Gly His Val Leu Val Leu Gly Asp Asn Tyr Pro Met Ser Ala Asp Ser
545 550 555 560

Arg Glu Phe Gly Phe Val Pro Met Glu Asn Leu Leu Gly Ser Pro Leu
565 570 575

Cys Thr Phe Trp Pro Ile Gly Arg Met Gly Arg Leu Thr Gly Val Ser
580 585 590

Ala Pro Thr Thr Leu Ser Gly Tyr Leu Val Ser Gly Ile Ala Leu Ala
595 600 605

Thr Gly Leu Ser Leu Ile Gly Tyr Val Tyr Tyr Gn Lys Arg Arg Arg
610 615 620

Leu Phe Pro Lys Lys Glu Glu Lys Asn His Lys Lys
625 630 635

<210> 161

<211> 1826

<212> PRT

<213> Chl amydi a pneumoni ae

<400> 161

Met Lys Ser Leu Pro Val Tyr Val Ser Gly Ile Lys Val Arg Asn Leu
1 5 10 15

Lys Asn Val Ser Ile His Phe Asn Ser Glu Glu Ile Val Leu Leu Thr
20 25 30

Gly Val Ser Gly Ser Gly Lys Ser Ser Ile Ala Phe Asp Thr Leu Tyr
35 40 45

Ala Ala Gly Arg Lys Arg Tyr Ile Ser Thr Leu Pro Thr Phe Phe Ala
50 55 60

Thr Thr Ile Thr Thr Leu Pro Asn Pro Lys Val Glu Glu Ile His Gly
65 70 75 80

Leu Ser Pro Thr Ile Ala Ile Lys Gn Asn His Phe Ser His Tyr Ser
85 90 95

His Ala Thr Val Gly Ser Thr Thr Glu Leu Phe Ser His Leu Ala Leu
100 105 110

Leu Phe Thr Leu Glu Gly Gn Ala Arg Asp Pro Lys Thr Lys Glu Val
115 120 125

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Leu Asp Leu Tyr Ser Lys Gu Lys Val Leu Ser Thr Ile Met Gu Leu
 130 135 140

Ser Gu Gly Val Gn Ile Ser Ile Leu Ala Pro Leu Leu Arg Lys Asp
 145 150 155 160

Ile Ala Ala Ile His Gu Tyr Ala Gn Gn Gly Phe Thr Lys Val Arg
 165 170 175

Cys Asn Gly Thr Ile His Pro Ile Tyr Ser Phe Leu Thr Ser Gly Ile
 180 185 190

Pro Gu Asp Cys Ser Val Asp Ile Val Ile Asp Thr Leu Ile Lys Ser
 195 200 205

Gu Asn Asn Ile Ala Arg Leu Lys Val Ser Leu Phe Thr Ala Leu Gu
 210 215 220

Phe Gly Gu Gly His Cys Ser Val Leu Ser Asp Gu Gu Leu Met Thr
 225 230 235 240

Phe Ser Thr Lys Gn Gn Ile Asp Asp Val Thr Tyr Thr Pro Leu Thr
 245 250 255

Gn Gn Leu Phe Ser Pro His Ala Leu Gu Ser Arg Cys Ser Leu Cys
 260 265 270

Gn Gly Ser Gly Ile Phe Ile Ser Ile Asp Asn Pro Leu Leu Ile Asp
 275 280 285

Gu Asn Leu Ser Ile Lys Gu Asn Cys Cys Ser Phe Ala Gly Asn Cys
 290 295 300

Ser Ser Tyr Leu Tyr His Thr Ile Tyr Gn Ala Leu Ala Asp Ala Leu
 305 310 315 320

Asn Phe Asn Leu Gu Thr Pro Trp Lys Asp Leu Ser Pro Gu Ile Gn
 325 330 335

Asn Ile Phe Leu Arg Gly Lys Asn Asn Leu Val Leu Pro Val Arg Leu
 340 345 350

Phe Asp Gn Thr Leu Gly Lys Lys Asn Leu Thr Tyr Lys Val Trp Arg
 355 360 365

Gly Val Leu Asn Asp Ile Gly Asp Lys Val Arg Tyr Thr Thr Lys Pro
 370 375 380

Ser Arg Tyr Leu Ser Lys Gly Met Ser Ala His Ser Cys Ser Leu Cys
 385 390 395 400

Lys Gly Thr Gly Leu₄₀₅ Gly Asp Tyr Ala Ser Val Ala Thr Trp Glu Gly₄₁₅
 Lys Thr Phe Thr₄₂₀ Glu Phe Gn Gn Met₄₂₅ Ser Leu Asn Asn Trp His Val₄₃₀
 Phe Phe Ser₄₃₅ Lys Val Lys Ser Pro₄₄₀ Ser Leu Ser Ile Gn Glu Ile Leu₄₄₅
 Gn Gly₄₅₀ Leu Lys Gn Arg Leu Ser Phe Leu Ile Asp₄₆₀ Leu Gly Leu Gly
 Tyr₄₆₅ Leu Thr Pro Asn Arg₄₇₀ Ala Leu Ala Thr Leu₄₇₅ Ser Gly Gly Glu Gn₄₈₀
 Glu Arg Thr Ala Ile₄₈₅ Ala Lys His Leu Gly Gly Glu Leu Phe Gly Ile₄₉₅
 Thr Tyr Ile Leu₅₀₀ Asp Glu Pro Ser Ile Gly Leu His Pro Gn Asp Thr₅₁₀
 Glu Lys Leu Ile Gly Val Ile Lys₅₂₀ Lys Leu Arg Asp Gn Gly Asn Thr₅₂₅
 Val Ile₅₃₀ Leu Val Glu His Gu Gu Arg Met Ile Ser₅₄₀ Leu Ala Asp Arg
 Ile Ile Asp Ile Gly Pro₅₅₀ Gly Ala Gly Ile Phe Gly Gly Glu Val Leu₅₆₀
 Phe Asn Gly Lys Pro₅₆₅ Glu Asp Phe Leu Met₅₇₀ Asn Ser Ser Ser Leu Thr₅₇₅
 Ala Lys Tyr Leu₅₈₀ Arg Gn Gu Leu Thr₅₈₅ Ile Pro Ile Pro Glu Ser Arg₅₉₀
 Glu Ala Pro₅₉₅ Thr Ser Trp Leu Leu Leu Thr Glu Ala Thr Ile His Asn₆₀₀
 Leu Lys₆₁₀ Asn Leu Ser Ile Arg₆₁₅ Leu Pro Leu Ala Arg₆₂₀ Leu Ile Gly Val
 Thr Gly Val Ser Gly Ser₆₃₀ Gly Lys Ser Ser Leu Ile Asn Asn Thr Leu₆₄₀
 Val Pro Ala Ile Glu₆₄₅ Ser Phe Leu Lys Gn Gu Asn Pro Lys Asn Leu₆₅₅
 His Phe Glu Trp₆₆₀ Gly Cys Ile Gly Arg₆₆₅ Leu Ile His Ile Thr Arg Asp₆₇₀
 Leu Pro Gly Arg Ser Gn Arg Ser Ile Pro Leu Thr Tyr Ile Lys Ala

675

680

685

Phe Asp Asp Ile Arg Gu Leu Phe Ala Ser Gn Pro Arg Ser Leu Arg
 690 695 700
 Gn Gy Leu Thr Lys Ala His Phe Ser Phe Asn Gn Pro Gn Gy Ala
 705 710 715
 Cys Ile Gn Cys Gn Gy Leu Gy Thr Met Thr Ile Ser Asp Asp Asp
 725 730 735
 Thr Pro Ile Pro Cys Ser Gu Cys Gn Gy Lys Arg Tyr His Ser Gu
 740 745 750
 Val Leu Gu Ile Leu Tyr Gu Gy Lys Asn Ile Ala Asp Ile Leu Asp
 755 760 765
 Met Thr Ala Tyr Gu Ala Gu Lys Phe Phe Ile Ser His Pro Lys Ile
 770 775 780
 His Gu Lys Ile His Ala Leu Cys Ser Leu Arg Leu Asp Tyr Leu Pro
 785 790 795 800
 Leu Gy Arg Pro Leu Ser Thr Leu Ser Gy Gy Gu Ile Gn Arg Leu
 805 810 815
 Lys Leu Ala His Gu Leu Leu Phe Ala Ser Pro Lys Gn Thr Leu Tyr
 820 825 830
 Val Leu Asp Gu Pro Thr Thr Gy Leu His Thr His Asp Ile Gn Ala
 835 840 845
 Leu Ile Gu Val Leu Leu Ser Leu Thr Tyr Leu Gy His Thr Val Leu
 850 855 860
 Val Ile Gu His Asn Met His Val Val Lys Val Cys Asp Tyr Val Leu
 865 870 875 880
 Gu Leu Gy Pro Gu Gy Gy Asp Leu Gy Gy Tyr Leu Leu Ala Ser
 885 890 895
 Cys Thr Pro Lys Asp Leu Ile Gn Leu Asn Thr Pro Thr Ala Lys Ala
 900 905 910
 Leu Ala Pro Tyr Ile Gu Gy Ser Leu Asp Ile Pro Val Val Lys Ser
 915 920 925
 Gu Pro Pro Ser Ser Pro Lys Ser Cys Asp Ile Leu Ile Lys Asp Ala
 930 935 940
 Tyr Gn Asn Asn Leu Lys His Ile Asp Leu Ala Leu Pro Arg Asn Ser
 945 950 955 960

eol f - seq| . app

Leu Ile Ala Ile Ala Gly Pro Gly Ala Ser Gly Lys His Ser Leu Val
 965 970 975

Phe Asp Ile Leu Tyr Ala Ser Gly Asn Ile Ala Tyr Ala Glu Leu Phe
 980 985 990

Pro Pro Tyr Ile Arg Gln Gly Leu Leu Lys Glu Thr Pro Leu Pro Ser
 995 1000 1005

Val Gly Glu Val Lys Gly Leu Ser Pro Val Ile Ser Val Arg Lys
 1010 1015 1020

Cys Ser Ser Ser Asn Arg Ser Tyr His Thr Ile Ala Ser Ala Leu
 1025 1030 1035

Gly Leu Ser Asn Gly Leu Glu Lys Leu Phe Ala Ile Leu Gly Glu
 1040 1045 1050

Pro Phe Ser Pro Leu Thr Glu Glu Lys Leu Ser Lys Thr Thr Pro
 1055 1060 1065

Gln Thr Ile Ile Asp Ser Leu Leu Lys Ser Tyr Lys Asp Asp Tyr
 1070 1075 1080

Val Thr Ile Thr Ser Pro Ile Pro Leu Gly Ser Asp Leu Glu Ile
 1085 1090 1095

Phe Leu Gln Glu Lys Gln Lys Glu Gly Phe Ile Lys Leu Tyr Ser
 1100 1105 1110

Glu Gly Asn Leu Tyr Asp Leu Asp Glu Arg Leu Pro Leu Asn Leu
 1115 1120 1125

Ile Glu Pro Ala Ile Val Ile Gln His Thr Lys Val Ser Pro Lys
 1130 1135 1140

Asn Ser Ser Ser Leu Leu Ser Ala Ile Ser Val Ala Phe Ser Leu
 1145 1150 1155

Ser Ser Glu Ile Trp Ile Tyr Ile Ser Gln Lys Lys Gln Arg Lys
 1160 1165 1170

Leu Ser Tyr Ser Leu Gly Trp Lys Asp Lys Lys Gly Arg Leu Tyr
 1175 1180 1185

Pro Glu Ile Thr His Gln Leu Leu Ser Ser Asp His Pro Glu Gly
 1190 1195 1200

Arg Cys Leu Thr Cys Gly Gly Arg Gly Glu Ile Leu Lys Ile Ser
 1205 1210 1215

eol f - seq1 . app

Leu Gu Gu His Lys Gu Lys Ile Ala His Tyr Thr Pro Leu Gu
1220 1225 1230

Phe Phe Ser Leu Phe Phe Pro Lys Ser Tyr Met Lys Pro Val Gn
1235 1240 1245

Lys Leu Leu Lys Asp Gu Asn Ala Ser Gn Pro Leu Lys Leu Leu
1250 1255 1260

Thr Thr Lys Gu Phe Leu Asn Phe Cys Arg Gly Ser Ser Gu Phe
1265 1270 1275

Pro Gly Met Asn Ala Leu Leu Met Gu Gn Leu Asp Thr Gu Ser
1280 1285 1290

Asp Ser Pro Leu Ile Lys Pro Leu Leu Ala Leu Thr Ser Cys Pro
1295 1300 1305

Ala Cys Lys Gly Ser Gly Leu Asn Asp Tyr Ala Asn Tyr Val Arg
1310 1315 1320

Ile Asn Asn Thr Ser Leu Leu Asp Ile Tyr Gn Gu Asp Ala Thr
1325 1330 1335

Phe Leu Gu Ser Phe Leu Asn Thr Ile Gly Thr Asp Asp Thr Arg
1340 1345 1350

Ser Ile Ile Gn Asp Leu Met Asn Arg Leu Thr Phe Ile Ser Lys
1355 1360 1365

Val Gly Leu Ser Tyr Ile Thr Leu Gly Gn Arg Gn Asp Thr Leu
1370 1375 1380

Ser Asp Gly Gu Asn Tyr Arg Leu His Leu Ala Lys Lys Ile Ser
1385 1390 1395

Ile Asn Leu Thr Asn Ile Val Tyr Leu Phe Gu Gu Pro Leu Ser
1400 1405 1410

Gly Leu His Pro Gn Asp Leu Pro Thr Ile Val Gn Leu Leu Lys
1415 1420 1425

Gu Leu Val Ala Asn Asn Asn Thr Val Ile Ala Thr Asp Arg Ser
1430 1435 1440

Cys Ser Leu Ile Pro His Ala Asp His Ala Ile Phe Leu Gly Pro
1445 1450 1455

Gly Ser Gly Pro Gn Gly Gly Phe Leu Met Asp Ser Asp Thr Gu
1460 1465 1470

Val Cys Pro Ser Val Asp Leu His Ala Asn Val Pro Gl n Thr Gl u
 1475 1480 1485
 Val Cys Pro Lys Ala Pro Leu Ser Ile Ser Lys Ala Asn His Thr
 1490 1495 1500
 Arg Gly Ser Asp Arg Thr Leu Lys Val Asn Leu Ser Ile His His
 1505 1510 1515
 Ile Gl n Asn Leu Lys Val Ser Ala Pro Leu His Ala Leu Val Ala
 1520 1525 1530
 Ile Gly Gly Val Ser Gly Ser Gly Lys Thr Ser Leu Leu Leu Gl u
 1535 1540 1545
 Gly Phe Lys Lys Gl n Ala Gl u Leu Leu Ile Ala Lys Gly Thr Thr
 1550 1555 1560
 Thr Phe Ser Asp Leu Val Val Ile Asp Ser His Pro Ile Ala Ser
 1565 1570 1575
 Ser Gl n Arg Ser Asp Ile Ser Thr Tyr Phe Asp Ile Ala Pro Ser
 1580 1585 1590
 Leu Arg Ala Phe Tyr Ala Ser Leu Thr Gl n Ala Lys Ala Leu Asn
 1595 1600 1605
 Ile Ser Ser Thr Met Phe Ser Thr Asn Thr Lys Gl n Gly Gl n Cys
 1610 1615 1620
 Ser Asp Cys Gl n Gly Leu Gly Tyr Gl n Trp Ile Asp Arg Ala Phe
 1625 1630 1635
 Tyr Ala Leu Gl u Lys Arg Pro Cys Pro Thr Cys Ser Gly Phe Arg
 1640 1645 1650
 Ile Gl n Pro Leu Ala Gl n Gl u Val Leu Tyr Gl u Gly Lys His Phe
 1655 1660 1665
 Gly Gl u Leu Leu His Thr Pro Ile Gl u Thr Val Ala Leu Arg Phe
 1670 1675 1680
 Pro Phe Ile Lys Lys Ile Gl n Lys Pro Leu Lys Ala Leu Leu Asp
 1685 1690 1695
 Ile Gly Leu Gly Tyr Leu Pro Ile Gly Gl n Lys Leu Ser Ser Leu
 1700 1705 1710
 Ser Val Ser Gl u Lys Thr Ala Leu Lys Thr Ala Tyr Phe Leu Tyr
 1715 1720 1725
 Gl n Thr Pro Gl u Thr Pro Thr Leu Phe Leu Ile Asp Gl u Leu Phe

1730

1735

1740

Ser Ser Leu Asp Pro Ile Lys Lys G n H i s Leu Pro G u Lys Leu
1745 1750 1755

Arg Ser Leu Ile Asn Ser G y H i s Ser Val Ile Tyr Ile Asp H i s
1760 1765 1770

Asp Val Lys Leu Leu Lys Ser Ala Asp Tyr Leu Ile G u Ile G y
1775 1780 1785

Pro G y Ser G y Lys G n G y G y Lys Leu Leu Phe Ser G y Ser
1790 1795 1800

Pro Lys Asp Ile Tyr Ala Ser Lys Asp Ser Leu Leu Lys Lys Tyr
1805 1810 1815

Ile Cys Asn G u G u Leu Asp Ser
1820 1825

<210> 162

<211> 1262

<212> PRT

<213> Chl amydi a pneumni ae

<400> 162

Leu Ser H i s G n Asn Ser Arg Arg Thr Arg Met Leu Lys Cys Pro G u
1 5 10 15

Arg Val Ser Val Lys Lys Lys G u Asp Ile Pro Asp Leu Pro Asn Leu
20 25 30

Ile G u Ile G n Ile Lys Ser Tyr Lys G n Phe Leu G n Ile G y Lys
35 40 45

Leu Ala G u G u Arg G u Asn Ile G y Leu G u G u Val Phe Arg G u
50 55 60

Ile Phe Pro Ile Lys Ser Tyr Asn G u Ala Thr Val Leu G u Tyr Leu
65 70 75 80

Ser Tyr Asn Leu G y Val Pro Lys Tyr Ser Pro G u G u Cys Ile Arg
85 90 95

Arg G y Ile Thr Tyr Ser Val Thr Leu Lys Val Arg Phe Arg Leu Thr
100 105 110

Asp G u Thr G y Ile Lys G u G u G u Val Tyr Met G y Thr Ile Pro
115 120 125

Leu Met Thr Asp Lys G y Thr Phe Ile Ile Asn G y Ala G u Arg Val
130 135 140

eol f - seq| . app

Val Val Ser G n Val His Arg Ser Pro Gly Ile Asn Phe Gl u G n Gl u
 145 150 155 160

Lys His Ser Lys Gly Asn Ile Leu Phe Ser Phe Arg Ile Ile Pro Tyr
 165 170 175

Arg Gly Ser Trp Leu Gl u Ala Ile Phe Asp Ile Asn Asp Leu Ile Tyr
 180 185 190

Ile His Ile Asp Arg Lys Lys Arg Arg Arg Lys Ile Leu Ala Ile Thr
 195 200 205

Phe Ile Arg Ala Leu Gly Tyr Ser Ser Asp Ala Asp Ile Ile Gl u Gl u
 210 215 220

Phe Phe Thr Ile Gly Gl u Ser Ser Leu Arg Ser Gl u Lys Asp Phe Ala
 225 230 235 240

Leu Leu Val Gly Arg Ile Leu Ala Asp Asn Ile Ile Asp Gl u Ala Ser
 245 250 255

Ser Leu Val Tyr Gly Lys Ala Gly Gl u Lys Leu Ser Thr Ala Met Leu
 260 265 270

Lys Arg Met Leu Asp Ala Gly Ile Ala Ser Val Lys Ile Ala Val Asp
 275 280 285

Ala Asp Gl u Asn His Pro Ile Ile Lys Met Leu Ala Lys Asp Pro Thr
 290 295 300

Asp Ser Tyr Gl u Ala Ala Leu Lys Asp Phe Tyr Arg Arg Leu Arg Pro
 305 310 315 320

Gly Gl u Pro Ala Thr Leu Ala Asn Ala Arg Ser Thr Ile Met Arg Leu
 325 330 335

Phe Phe Asp Pro Lys Arg Tyr Asn Leu Gly Arg Val Gly Arg Tyr Lys
 340 345 350

Leu Asn Arg Lys Leu Gly Phe Ser Ile Asp Asp Gl u Ala Leu Ser G n
 355 360 365

Val Thr Leu Arg Lys Gl u Asp Val Ile Gly Ala Leu Lys Tyr Leu Ile
 370 375 380

Arg Leu Lys Met Gly Asp Gl u Lys Ala Cys Val Asp Asp Ile Asp His
 385 390 395 400

Leu Ala Asn Arg Arg Val Arg Ser Val Gly Gl u Leu Ile G n Asn G n
 405 410 415

Cys Arg Ser Gly Leu Ala Arg Met Gu Lys Ile Val Arg Gu Arg Met
 420 425 430

Asn Leu Phe Asp Phe Ser Ser Asp Thr Leu Thr Pro Gly Lys Val Val
 435 440 445

Ser Ala Lys Gly Leu Ala Ser Val Leu Lys Asp Phe Phe Gly Arg Ser
 450 455 460

Gn Leu Ser Gn Phe Met Asp Gn Thr Asn Pro Val Ala Gu Leu Thr
 465 470 475 480

His Lys Arg Arg Leu Ser Ala Leu Gly Pro Gly Gly Leu Asn Arg Gu
 485 490 495

Arg Ala Gly Phe Gu Val Arg Asp Val His Ala Ser His Tyr Gly Arg
 500 505

Ile Cys Pro Ile Gu Thr Pro Gu Gly Pro Asn Ile Gly Leu Ile Thr
 515 520 525

Ser Leu Ser Ser Phe Ala Lys Ile Asn Gu Phe Gly Phe Ile Gu Thr
 530 535 540

Pro Tyr Arg Ile Val Arg Asp Gly Ile Val Thr Asp Gu Ile Gu Tyr
 545 550 555 560 565

Met Thr Ala Asp Val Gu Gu Gu Cys Val Ile Ala Gn Ala Ser Ala
 565 570 575

Ser Leu Asp Gu Tyr Asn Met Phe Thr Gu Pro Val Cys Trp Val Arg
 580 585 590

Tyr Ala Gly Gu Ala Phe Gu Ala Asp Thr Ser Thr Val Thr His Met
 595 600 605

Asp Val Ser Pro Lys Gn Leu Val Ser Ile Val Thr Gly Leu Ile Pro
 610 615 620

Phe Leu Gu His Asp Asp Ala Asn Arg Ala Leu Met Gly Ser Asn Met
 625 630 635 640

Gn Arg Gn Ala Val Pro Leu Leu Lys Thr Gu Ala Pro Val Val Gly
 645 650 655

Thr Gly Leu Gu Cys Arg Ala Ala Lys Asp Ser Gly Ala Ile Val Val
 660 665 670

Ala Gu Gu Asp Gly Val Val Asp Phe Val Asp Gly Tyr Lys Val Val
 675 680 685

Val Ala Ala Lys His Asn Pro Thr Ile Lys Arg Thr Tyr His Leu Lys

690

695

Lys Phe Leu Arg Ser Asn Ser Gly Thr Cys Ile Asn Gl n Gl n Pro Leu
 705 710 715 720
 Cys Ala Val Gly Asp Val Ile Thr Lys Gly Asp Val Ile Ala Asp Gly
 725 730 735
 Pro Ala Thr Asp Arg Gly Gu Leu Ala Leu Gly Lys Asn Val Leu Val
 740 745 750
 Ala Phe Met Pro Trp Tyr Gly Tyr Asn Phe Gu Asp Ala Ile Ile Ile
 755 760 765
 Ser Gu Lys Leu Ile Arg Gu Asp Ala Tyr Thr Ser Ile Tyr Ile Gu
 770 775 780
 Gu Phe Gu Leu Thr Ala Arg Asp Thr Lys Leu Gly Lys Gu Gu Ile
 785 790 795 800
 Thr Arg Asp Ile Pro Asn Val Ser Asp Gu Val Leu Ala Asn Leu Gly
 805 810 815
 Gu Asp Gly Ile Ile Arg Ile Gly Ala Gu Val Lys Pro Gly Asp Ile
 820 825 830
 Leu Val Gly Lys Ile Thr Pro Lys Ser Gu Thr Gu Leu Ala Pro Gu
 835 840 845
 Gu Arg Leu Leu Arg Ala Ile Phe Gly Gu Lys Ala Ala Asp Val Lys
 850 855 860
 Asp Ala Ser Leu Thr Val Pro Pro Gly Thr Gu Gly Val Val Met Asp
 865 870 875 880
 Val Lys Val Phe Ser Arg Lys Asp Arg Leu Ser Lys Ser Asp Asp Gu
 885 890 895
 Leu Val Gu Gu Ala Val His Leu Lys Asp Leu Gl n Lys Gly Tyr Lys
 900 905
 Asn Gl n Val Ala Thr Leu Lys Thr Gu Tyr Arg Gu Lys Leu Gly Ala
 915 920 925
 Leu Leu Leu Asn Gu Lys Ala Pro Ala Ala Ile Ile His Arg Arg Thr
 930 935 940
 Ala Gu Ile Val Val His Gu Gly Leu Leu Phe Asp Gl n Gu Thr Ile
 945 950 955 960
 Gu Arg Ile Gu Gl n Gu Asp Leu Val Asp Leu Leu Met Pro Asn Cys
 965 970 975

eol f - seq1 . app

G u M e t T y r G u V a l L e u L y s G y L e u L e u S e r A s p T y r G u T h r A l a
 980 985 990
 L e u G n A r g L e u G u I l e A s n T y r L y s T h r G u V a l G u H i s I l e A r g
 995 1000 1005
 G u G y A s p A l a A s p L e u A s p H i s G y V a l I l e A r g G n V a l L y s
 1010 1015 1020
 V a l T y r V a l A l a S e r L y s A r g L y s L e u G n V a l G y A s p L y s M e t
 1025 1030 1035
 A l a G y A r g H i s G y A s n L y s G y V a l V a l S e r L y s I l e V a l P r o
 1040 1045
 G u A l a A s p M e t P r o T y r L e u S e r A s n G y G u T h r V a l G n M e t
 1055 1060 1065
 I l e L e u A s n P r o L e u G y V a l P r o S e r A r g M e t A s n L e u G y G n
 1070 1075 1080
 V a l L e u G u T h r H i s L e u G y T y r A l a A l a L y s T h r A l a G y I l e
 1085 1090 1095
 T y r V a l L y s T h r P r o V a l P h e G u G y P h e P r o G u G n A r g I l e
 1100 1105 1110
 T r p A s p M e t M e t I l e G u G n G y L e u P r o G u A s p G y L y s S e r
 1115 1120 1125
 P h e L e u T y r A s p G y L y s T h r G y G u A r g P h e A s p A s n L y s V a l
 1130 1135 1140
 V a l I l e G y T y r I l e T y r M e t L e u L y s L e u S e r H i s L e u I l e A l a
 1145 1150 1155
 A s p L y s I l e H i s A l a A r g S e r I l e G y P r o T y r S e r L e u V a l T h r
 1160 1165 1170
 G n G n P r o L e u G y G y L y s A l a G n M e t G y G y G n A r g P h e
 1175 1180 1185
 G y G u M e t G u V a l T r p A l a L e u G u A l a T y r G y V a l A l a H i s
 1190 1195 1200
 M e t L e u G n G u I l e L e u T h r V a l L y s S e r A s p A s p V a l S e r G y
 1205 1210 1215
 A r g T h r A r g I l e T y r G u S e r I l e V a l L y s G y G u A s n L e u L e u
 1220 1225 1230

eol f - seq| . app

Arg Ser Gly Thr Pro Glu Ser Phe Asn Val Leu Ile Lys Glu Met
1235 1240 1245

Gln Gly Leu Gly Leu Asp Val Arg Pro Met Val Val Asp Ala
1250 1255 1260

<210> 163
<211> 598
<212> PRT
<213> Chl amydi a pneumoni ae

<400> 163

Met Lys Glu Val Glu Gln Arg Ile Arg Ser Leu Tyr Asp Ala Val Thr
1 5 10 15

Ala Glu Asn Ile Cys Arg Trp Leu Ser Asn Asp Cys Thr Gln Gln Asp
20 25 30

Ala Lys Thr Ile Leu Gly Trp Leu Asp Thr Asp Pro Ala Gln Leu Glu
35 40 45

Asp Leu Phe Gly Ala Thr Leu Thr Phe Gly Thr Gly Gly Leu Arg Ser
50 55 60

Leu Met Gly Ile Gly Thr Asn Arg Ile Asn Leu Phe Thr Ile Arg Arg
65 70 75 80

Thr Thr Gln Gly Leu Val Gln Val Leu Arg Ala His Leu Pro His Pro
85 90 95

Gly Asp Pro Met Arg Val Val Val Gly Cys Asp Thr Arg His Asn Ser
100 105 110

Ile Glu Phe Ala Gln Glu Thr Ala Lys Val Leu Ala Gly Asn Gly Cys
115 120 125

Glu Val Phe Leu Phe Gln Tyr Pro Glu Pro Leu Ala Leu Val Ser Phe
130 135 140

Thr Val Arg Tyr Glu Arg Ala Ile Gly Gly Val Met Ile Thr Ala Ser
145 150 155 160

His Asn Pro Pro Asn Tyr Asn Gly Tyr Lys Val Tyr Met Ala Ser Gly
165 170 175

Gly Gln Val Leu Pro Pro Leu Asp Gln Glu Ile Val Ala Ala Cys Ser
180 185 190

Ala Val Asn Glu Ile Leu Ser Val Pro Ser Ile Asp His Pro Asn Ile
195 200 205

His Leu Ile Gly Lys Glu Tyr Glu Ala Leu Tyr Arg Asp Thr Leu Lys

210

215

G n Leu G n Leu Tyr Pro G u Ala Asn Arg Ile Ser G y Arg Ser Leu
225 230 235 240

Ser Ile Ser Tyr Ser Pro Leu His G y Thr G y Ile Ser Leu Val Pro
245 250 255

His Val Leu Lys Asp Trp G y Phe Leu Ser Val His Leu Val G u Lys
260 265 270

G n Ala Ile G y Asp G y Asp Phe Pro Thr Val G n Leu Pro Asn Pro
275 280 285

G u Asp Pro G u Ala Leu Thr Leu G y Thr G u G n Met Leu Ala Asn
290 295 300

Asp Asp Asp Leu Phe Ile Ala Thr Asp Pro Asp Ala Asp Arg Val G y
305 310 315 320

Val Val Cys Leu G u Asp G y G n Pro Tyr Arg Phe Asn G y Asn G n
325 330 335

Met Ala Ser Leu Leu Ala Asp His Ile Leu G y Ala Trp Ser Lys Thr
340 345

Arg His Leu G y G u His Asp Lys Leu Val Lys Ser Leu Val Thr Thr
355 360 365

G u Met Leu Ser Ala Ile Ala Lys His Tyr His Val Asp Leu Ile Asn
370 375 380

Val G y Thr G y Phe Lys Tyr Ile G y G u Lys Ile G u Ser Trp Arg
385 390 395 400

Asn Ser Thr Asn Lys Phe Val Phe G y Ala G u G u Ser Tyr G y Cys
405 410 415

Leu Tyr G y Thr His Val G u Asp Lys Asp Ala Ile Ile Ala Ser Ala
420 425 430

Leu Ile Ala G u Ala Ala Leu G n G n Lys Leu G n G y Lys Thr Leu
435 440 445

Cys Asp Ala Leu Leu Ser Leu Tyr G u Thr Tyr G y Tyr Phe Ala Asn
450 455 460

Lys Thr G u Ser Val Val Phe Ser Ala Lys Thr Asp G u G n G u Ile
465 470 475 480

Arg Lys Lys Leu Ser His Leu G u G u Ile Ser Ser Ala Asn Phe Phe
485 490 495

eol f - seq1 . app

Ser Gly Lys Tyr Gln Val Gu Lys Phe Gu Asn Tyr Lys Gln Gly Ile
500 505 510

Gly Phe Asn Leu Leu Ser Lys Asp Ser Tyr Ala Leu Thr Leu Pro Lys
515 520 525

Thr Ser Met Leu Cys Tyr Tyr Phe Ser Gly Gly Gly Arg Val Ile Ile
530 535 540

Arg Pro Ser Gly Thr Gu Pro Lys Ile Lys Phe Tyr Phe Gu Met Ser
545 550 555 560 565

Thr His Tyr Pro Gu Arg Val Thr Asp Lys Gu Ile Gln Lys Gln Arg
565 570 575

Gu Ala Gu Ser Phe Gln His Leu Asp Asp Phe Ile Phe Asp Phe Lys
580 585 590

Gu Lys Phe Ser Asn Leu
595

<210> 164
<211> 841
<212> PRT
<213> Chlamydia pneumoniae
<400> 164

Met Lys Ile Pro Leu Arg Phe Leu Leu Ile Ser Leu Val Pro Thr Leu
1 5 10 15

Ser Met Ser Asn Leu Leu Gly Ala Ala Thr Thr Gu Gu Leu Ser Ala
20 25 30

Ser Asn Ser Phe Asp Gly Thr Thr Ser Thr Thr Ser Phe Ser Ser Lys
35 40 45

Thr Ser Ser Ala Thr Asp Gly Thr Asn Tyr Val Phe Lys Asp Ser Val
50 55 60

Val Ile Gu Asn Val Pro Lys Thr Gly Gu Thr Gln Ser Thr Ser Cys
65 70 75 80

Phe Lys Asn Asp Ala Ala Ala Gly Asp Leu Asn Phe Leu Gly Gly Gly
85 90 95

Phe Ser Phe Thr Phe Ser Asn Ile Asp Ala Thr Thr Ala Ser Gly Ala
100 105 110

Ala Ile Gly Ser Gu Ala Ala Asn Lys Thr Val Thr Leu Ser Gly Phe
115 120 125

Ser Ala Leu Ser Phe Leu Lys Ser Pro Ala Ser Thr Val Thr Asn Gly
 130 135 140

Leu Gly Ala Ile Asn Val Lys Gly Asn Leu Ser Leu Leu Asp Asn Asp
 145 150 155 160

Lys Val Leu Ile Gln Asp Asn Phe Ser Thr Gly Asp Gly Gly Ala Ile
 165 170 175

Asn Cys Ala Gly Ser Leu Lys Ile Ala Asn Asn Lys Ser Leu Ser Phe
 180 185 190

Ile Gly Asn Ser Ser Ser Thr Arg Gly Gly Ala Ile His Thr Lys Asn
 195 200 205

Leu Thr Leu Ser Ser Gly Gly Gu Thr Leu Phe Gln Gly Asn Thr Ala
 210 215 220

Pro Thr Ala Ala Gly Lys Gly Gly Ala Ile Ala Ile Ala Asp Ser Gly
 225 230 235 240

Thr Leu Ser Ile Ser Gly Asp Ser Gly Asp Ile Ile Phe Gu Gly Asn
 245 250 255

Thr Ile Gly Ala Thr Gly Thr Val Ser His Ser Ala Ile Asp Leu Gly
 260 265 270

Thr Ser Ala Lys Ile Thr Ala Leu Arg Ala Ala Gln Gly His Thr Ile
 275 280 285

Tyr Phe Tyr Asp Pro Ile Thr Val Thr Gly Ser Thr Ser Val Ala Asp
 290 300

Ala Leu Asn Ile Asn Ser Pro Asp Thr Gly Asp Asn Lys Gu Tyr Thr
 305 310 315 320

Gly Thr Ile Val Phe Ser Gly Gu Lys Leu Thr Gu Ala Gu Ala Lys
 325 330 335

Asp Gu Lys Asn Arg Thr Ser Lys Leu Leu Gln Asn Val Ala Phe Lys
 340 345 350

Asn Gly Thr Val Val Leu Lys Gly Asp Val Val Leu Ser Ala Asn Gly
 355 360 365

Phe Ser Gln Asp Ala Asn Ser Lys Leu Ile Met Asp Leu Gly Thr Ser
 370 375 380

Leu Val Ala Asn Thr Gu Ser Ile Gu Leu Thr Asn Leu Gu Ile Asn
 385 390 395 400

Ile Asp Ser Leu Arg Asn Gly Lys Lys Ile Lys Leu Ser Ala Ala Thr

Al a G n Lys Asp 420 Ile Arg Ile Asp Arg 425 Pro Val Val Leu Al a Ile Ser
Asp Gu Ser 435 Phe Tyr G n Asn Gly 440 Phe Leu Asn Gu Asp 445 His Ser Tyr
Asp Gly 450 Ile Leu Gu Leu Asp 455 Al a Gly Lys Asp Ile 460 Val Ile Ser Al a
Asp Ser Arg Ser Ile Asp 470 Al a Val G n Ser Pro Tyr Gly Tyr G n Gly 480
Lys Trp Thr Ile Asn 485 Trp Ser Thr Asp Asp 490 Lys Lys Al a Thr Val Ser 495
Trp Al a Lys G n Ser Phe Asn Pro Thr 505 Al a Gu G n Gu Al a Pro Leu 510
Val Pro Asn 515 Leu Leu Trp Gly Ser 520 Phe Ile Asp Val Arg 525 Ser Phe G n
Asn Phe 530 Ile Gu Leu Gly Thr 535 Gu Gly Al a Pro Tyr 540 Gu Lys Arg Phe
Trp Val Al a Gly Ile Ser 550 Asn Val Leu His Arg 555 Ser Gly Arg Gu Asn 560
G n Arg Lys Phe Arg 565 His Val Ser Gly Gly 570 Al a Val Val Gly Al a Ser 575
Thr Arg Met Pro 580 Gly Gly Asp Thr Leu 585 Ser Leu Gly Phe Al a G n Leu 590
Phe Al a Arg 595 Asp Lys Asp Tyr Phe Met Asn Thr Asn Phe Al a Lys Thr 605
Tyr Al a Gly Ser Leu Arg Leu G n His Asp Al a Ser 620 Leu Tyr Ser Val 610
Val Ser Ile Leu Leu Gly 630 Gu Gly Gly Leu Arg 635 Gu Ile Leu Leu Pro 640
Tyr Val Ser Lys Thr 645 Leu Pro Cys Ser Phe Tyr Gly G n Leu Ser Tyr 655
Gly His Thr Asp 660 His Arg Met Lys Thr 665 Gu Ser Leu Pro Pro Pro Pro 670
Pro Thr Leu Ser Thr Asp His Thr 680 Ser Trp Gly Gly Tyr Val Trp Al a 685

Gly Gu Leu Gly Thr Arg Val Ala Val Gu Asn Thr Ser Gly Arg Gly
690 695 700

Phe Phe Gn Gu Tyr Thr Pro Phe Val Lys Val Gn Ala Val Tyr Ala
705 710 715 720

Arg Gn Asp Ser Phe Val Gu Leu Gly Ala Ile Ser Arg Asp Phe Ser
725 730 735

Asp Ser His Leu Tyr Asn Leu Ala Ile Pro Leu Gly Ile Lys Leu Gu
740 745 750

Lys Arg Phe Ala Gu Gn Tyr Tyr His Val Val Ala Met Tyr Ser Pro
755 760 765

Asp Val Cys Arg Ser Asn Pro Lys Cys Thr Thr Thr Leu Leu Ser Asn
770 775 780

Gn Gly Ser Trp Lys Thr Lys Gly Ser Asn Leu Ala Arg Gn Ala Gly
785 790 800

Ile Val Gn Ala Ser Gly Phe Arg Ser Leu Gly Ala Ala Ala Gu Leu
805 810 815

Phe Gly Asn Phe Gly Phe Gu Trp Arg Gly Ser Ser Arg Ser Tyr Asn
820 825 830

Val Asp Ala Gly Ser Lys Ile Lys Phe
835 840

<210> 165
<211> 644
<212> PRT
<213> Chl amydi a pneumoni ae
<400> 165

Met Thr Ser Ser Ser Cys Pro Leu Leu Asp Leu Ile Leu Ser Pro Ala
1 5 10 15

Asp Leu Lys Lys Leu Ser Ile Ser Gn Leu Pro Gly Leu Ala Gu Gu
20 25 30

Ile Arg Tyr Arg Ile Ile Ser Val Leu Ser Gn Thr Gly Gly His Leu
35 40 45

Ser Ser Asn Leu Gly Ile Val Gu Leu Thr Ile Ala Leu His Tyr Val
50 55 60

Phe Ser Ser Pro Lys Asp Lys Phe Ile Phe Asp Val Gly His Gn Thr
65 70 75 80

Tyr Pro His Lys Leu₈₅ Leu Thr Gly Arg Asn₉₀ Asn Glu Gly Phe Asp₉₅ His
 Ile Arg Asn Asp₁₀₀ Asn Gly Leu Ser Gly₁₀₅ Phe Thr Asn Pro Thr₁₁₀ Glu Ser
 Asp His Asp₁₁₅ Leu Phe Phe Ser Gly₁₂₀ His Ala Gly Thr Ala₁₂₅ Leu Ser Leu
 Ala Leu Gly Met Ala Gln Thr₁₃₅ Thr Pro Leu Glu Ser₁₄₀ Arg Thr His Val
 Ile Pro Ile Leu Gly Asp₁₅₀ Ala Ala Phe Ser Cys₁₅₅ Gly Leu Thr Leu Glu₁₆₀
 Ala Leu Asn Asn Ile Ser Thr Asp Leu Ser₁₇₀ Lys Phe Val Val Ile Leu₁₇₅
 Asn Asp Asn Asn Met Ser Ile Ser Lys₁₈₅ Asn Val Gly Ala Met₁₉₀ Ser Arg
 Ile Phe Ser₁₉₅ Arg Trp Leu His His₂₀₀ Pro Ala Thr Asn Lys₂₀₅ Leu Thr Lys
 Gln Val Glu Lys Trp Leu Ala₂₁₅ Lys Ile Pro Arg Tyr₂₂₀ Gly Asp Ser Leu
 Ala Lys His Ser Arg Arg₂₃₀ Leu Ser Gln Cys Val₂₃₅ Lys Asn Leu Phe Cys₂₄₀
 Pro Thr Pro Leu Phe₂₄₅ Glu Gln Phe Gly Leu Ala Tyr Val Gly Pro Ile₂₅₅
 Asp Gly His Asn₂₆₀ Val Lys Lys Leu Ile₂₆₅ Pro Ile Leu Gln Ser₂₇₀ Val Arg
 Asn Leu Pro Phe Pro Ile Leu Val₂₈₀ His Val Cys Thr Thr₂₈₅ Lys Gly Lys
 Gly Leu Asp Gln Ala Gln Asn₂₉₅ Asn Pro Ala Lys Tyr₃₀₀ His Gly Val Arg
 Ala Asn Phe Asn Lys Arg₃₁₀ Glu Ser Ala Lys His₃₁₅ Leu Pro Ala Ile Lys₃₂₀
 Pro Lys Pro Ser Phe₃₂₅ Pro Asp Ile Phe Gly₃₃₀ Gln Thr Leu Cys Glu Leu₃₃₅
 Gly Glu Val Ser₃₄₀ Ser Arg Leu His Val₃₄₅ Val Thr Pro Ala Met₃₅₀ Ser Ile
 Gly Ser Arg Leu Glu Gly Phe Lys Gln Lys Phe Pro Glu Arg Phe Phe

355

360

365

Asp Val Gly Ile Ala Gu Gly His Ala Val Thr Phe Ser Ala Gly Ile
370 375 380

Ala Lys Ala Gly Asn Pro Val Ile Cys Ser Ile Tyr Ser Thr Phe Leu
385 390 395 400

His Arg Ala Leu Asp Asn Val Phe His Asp Val Cys Met Gln Asp Leu
405 410 415

Pro Val Ile Phe Ala Ile Asp Arg Ala Gly Leu Ala Tyr Gly Asp Gly
420 425 430

Arg Ser His His Gly Ile Tyr Asp Met Ser Phe Leu Arg Ala Met Pro
435 440 445

Gln Met Ile Ile Cys Gln Pro Arg Ser Gln Val Val Phe Gln Gln Leu
450 455 460

Leu Tyr Ser Ser Leu His Trp Ser Ser Pro Ser Ala Ile Arg Tyr Pro
465 470 475 480

Asn Ile Pro Ala Pro His Gly Asp Pro Leu Thr Gly Asp Pro Asn Phe
485 490 495

Leu Arg Ser Pro Gly Asn Ala Gu Thr Leu Ser Gln Gly Glu Asp Val
500 505 510 515

Leu Ile Ile Ala Leu Gly Thr Leu Cys Phe Thr Ala Leu Ser Ile Lys
515 520 525

His Gln Leu Leu Ala Tyr Gly Ile Ser Ala Thr Val Val Asp Pro Ile
530 535 540

Phe Ile Lys Pro Phe Asp Asn Asp Leu Phe Ser Leu Leu Leu Met Ser
545 550 555 560 565

His Ser Lys Val Ile Thr Ile Gu Gu His Ser Ile Arg Gly Gly Leu
565 570 575

Ala Ser Gu Phe Asn Asn Phe Val Ala Thr Phe Asn Phe Lys Val Asp
580 585 590

Ile Leu Asn Phe Ala Ile Pro Asp Thr Phe Leu Ser His Gly Ser Lys
595 600 605

Gu Ala Leu Thr Lys Ser Ile Gly Leu Asp Gu Ser Ser Met Thr Asn
610 615 620

Arg Ile Leu Thr His Phe Asn Phe Arg Ser Lys Lys Gln Thr Val Gly
625 630 635 640

Asp Val Arg Val

<210> 166
 <211> 359
 <212> PRT
 <213> Chl amydi a pneumoni ae
 <400> 166

Met Lys Asn Ser Phe Gly Ser Leu Phe Ser Phe Thr Thr Trp Gly Glu
 1 5 10 15

Ser His Gly Pro Ser Ile Gly Val Val Ile Asp Gly Cys Pro Ala Gly
 20 25 30

Leu Glu Leu His Glu Ser Asp Phe Val Pro Ala Met Lys Arg Arg Arg
 35 40 45

Pro Gly Asn Pro Gly Thr Ser Ser Arg Lys Glu Asn Asp Ile Val Glu
 50 55 60

Ile Leu Ser Gly Val Tyr Lys Gly Lys Thr Thr Gly Thr Pro Leu Ser
 65 70 75 80

Leu Glu Ile Leu Asn Thr Asp Val Asp Ser Ser Pro Tyr Glu Asn Ser
 85 90 95

Glu Arg Leu Tyr Arg Pro Gly His Ser Glu Tyr Thr Tyr Glu Lys Lys
 100 105 110

Phe Gly Ile Val Asp Pro Asn Gly Gly Gly Arg Ser Ser Ala Arg Glu
 115 120 125

Thr Ala Cys Arg Val Ala Ala Gly Val Val Ala Glu Lys Phe Leu Ala
 130 135 140

Asn Glu Asn Ile Phe Thr Leu Ala Tyr Leu Ser Ser Leu Gly Ser Leu
 145 150 155 160

Thr Leu Pro His Tyr Leu Lys Ile Ser Pro Glu Leu Ile His Lys Ile
 165 170 175

His Thr Ser Pro Phe Tyr Ser Pro Leu Pro Asn Glu Lys Ile Glu Glu
 180 185 190

Ile Leu Thr Ser Leu His Asp Asp Ser Asp Ser Leu Gly Gly Val Ile
 195 200 205

Ser Phe Ile Thr Ser Pro Ile His Asp Phe Leu Gly Glu Pro Leu Phe
 210 215 220

Gly Lys Val His Ala Leu Leu Ala Ser Ala Leu Met Ser Ile Pro Ala
225 230 235 240

Ala Lys Gly Phe Gu Ile Gly Lys Gly Phe Ala Ser Ala Gln Met Arg
245 250 255

Gly Ser Gln Tyr Thr Asp Pro Phe Val Met Gu Gly Gu Asn Ile Thr
260 265 270

Leu Lys Ser Asn Asn Cys Gly Gly Thr Leu Gly Gly Ile Thr Ile Gly
275 280 285

Val Pro Ile Gu Gly Arg Ile Ala Phe Lys Pro Thr Ser Ser Ile Lys
290 295 300

Arg Pro Cys Ala Thr Val Thr Lys Thr Lys Lys Gu Thr Thr Tyr Arg
305 310 315 320

Thr Pro Gln Thr Gly Arg His Asp Pro Cys Val Ala Ile Arg Ala Val
325 330 335

Pro Val Val Gu Ala Met Ile Asn Leu Val Leu Ala Asp Leu Val Leu
340 345 350

Tyr Gln Arg Cys Ser Lys Leu
355

<210> 167
<211> 619
<212> PRT
<213> Chl amydi a pneumoni ae

<400> 167

Met Lys Lys Gly Lys Leu Gly Ala Ile Val Phe Gly Leu Leu Phe Thr
1 5 10 15

Ser Ser Val Ala Gly Phe Ser Lys Asp Leu Thr Lys Asp Asn Ala Tyr
20 25 30

Gln Asp Leu Asn Val Ile Gu His Leu Ile Ser Leu Lys Tyr Ala Pro
35 40 45

Leu Pro Trp Lys Gu Leu Leu Phe Gly Trp Asp Leu Ser Gln Gln Thr
50 55 60

Gln Gln Ala Arg Leu Gln Leu Val Leu Gu Gu Lys Pro Thr Thr Asn
65 70 75 80

Tyr Cys Gln Lys Val Leu Ser Asn Tyr Val Arg Ser Leu Asn Asp Tyr
85 90 95

His Ala Gly Ile Thr Phe Tyr Arg Thr Gu Ser Ala Tyr Ile Pro Tyr
100 105 110

Val Leu Lys Leu Ser Gu Asp Gy His Val Phe Val Val Asp Val Gn
 115 120 125
 Thr Ser Gn Gy Asp Ile Tyr Leu Gy Asp Gu Ile Leu Gu Val Asp
 130 135 140
 Gy Met Gy Ile Arg Gu Ala Ile Gu Ser Leu Arg Phe Gy Arg Gy
 145 150 155 160 165
 Ser Ala Thr Asp Tyr Ser Ala Ala Val Arg Ser Leu Thr Ser Arg Ser
 165 170 175
 Ala Ala Phe Gy Asp Ala Val Pro Ser Gy Ile Ala Met Leu Lys Leu
 180 185 190
 Arg Arg Pro Ser Gy Leu Ile Arg Ser Thr Pro Val Arg Trp Arg Tyr
 195 200 205
 Thr Pro Gu His Ile Gy Asp Phe Ser Leu Val Ala Pro Leu Ile Pro
 210 215 220
 Gu His Lys Pro Gn Leu Pro Thr Gn Ser Cys Val Leu Phe Arg Ser
 225 230 235 240
 Gy Val Asn Ser Gn Ser Ser Ser Ser Ser Leu Phe Ser Ser Tyr Met
 245 250 255
 Val Pro Tyr Phe Trp Gu Gu Leu Arg Val Gn Asn Lys Gn Arg Phe
 260 265 270
 Asp Ser Asn His His Ile Gy Ser Arg Asn Gy Phe Leu Pro Thr Phe
 275 280 285
 Gy Pro Ile Leu Trp Gu Gn Asp Lys Gy Pro Tyr Arg Ser Tyr Ile
 290 295 300
 Phe Lys Ala Lys Asp Ser Gn Gy Asn Pro His Arg Ile Gy Phe Leu
 305 310 315 320
 Arg Ile Ser Ser Tyr Val Trp Thr Asp Leu Gu Gy Leu Gu Gu Asp
 325 330 335
 His Lys Asp Ser Pro Trp Gu Leu Phe Gy Gu Ile Ile Asp His Leu
 340 345 350
 Gu Lys Gu Thr Asp Ala Leu Ile Ile Asp Gn Thr His Asn Pro Gy
 355 360 365
 Gy Ser Val Phe Tyr Leu Tyr Ser Leu Leu Ser Met Leu Thr Asp His
 370 375 380

eol f - seq| . app

Pro Leu Asp Thr Pro Lys His Arg Met Ile Phe Thr Gln Asp Glu Val
385 390 395 400

Ser Ser Ala Leu His Trp Gln Asp Leu Leu Glu Asp Val Phe Thr Asp
405 410 415

Glu Gln Ala Val Ala Val Leu Gly Glu Thr Met Glu Gly Tyr Cys Met
420 425 430

Asp Met His Ala Val Ala Ser Leu Gln Asn Phe Ser Gln Ser Val Leu
435 440 445

Ser Ser Trp Val Ser Gly Asp Ile Asn Leu Ser Lys Pro Met Pro Leu
450 455 460

Leu Gly Phe Ala Gln Val Arg Pro His Pro Lys His Gln Tyr Thr Lys
465 470 475 480

Pro Leu Phe Met Leu Ile Asp Glu Asp Asp Phe Ser Cys Gly Asp Leu
485 490 495

Ala Pro Ala Ile Leu Lys Asp Asn Gly Arg Ala Thr Leu Ile Gly Lys
500 505 510

Pro Thr Ala Gly Ala Gly Gly Phe Val Phe Gln Val Thr Phe Pro Asn
515 520 525

Arg Ser Gly Ile Lys Gly Leu Ser Leu Thr Gly Ser Leu Ala Val Arg
530 535 540

Lys Asp Gly Glu Phe Ile Glu Asn Leu Gly Val Ala Pro His Ile Asp
545 550 555 560

Leu Gly Phe Thr Ser Arg Asp Leu Gln Thr Ser Arg Phe Thr Asp Tyr
565 570 575

Val Glu Ala Val Lys Thr Ile Val Leu Thr Ser Leu Ser Glu Asn Ala
580 585 590

Lys Lys Ser Glu Glu Gln Thr Ser Pro Gln Glu Thr Pro Glu Val Ile
595 600 605

Arg Val Ser Tyr Pro Thr Thr Thr Ser Ala Leu
610 615

<210> 168
<211> 343
<212> PRT
<213> Chlamydia pneumoniae

<400> 168

Met Glu Val Tyr Ser Phe Ser Pro Ser Val Arg Thr Ser Phe Gln His
Page 230

1 5 15

Arg Val Met Ala Ala Leu Asp Asn Trp Phe Phe Leu Gly Gly Arg Arg
20 25 30

Leu Lys Val Val Ser Leu Asp Ser Cys Asn Ser Gly Gln Ala Cys Glu
35 40 45

Glu Tyr Val Pro Ile Ser Thr Thr Glu Lys Val Leu Lys Ile Leu Ser
50 55 60

Tyr Leu Leu Ile Pro Ile Val Ile Ile Ala Leu Leu Ile Arg Tyr Leu
65 70 75 80

Leu His Ser Asn Phe Thr Ala Lys Val Ser Gln Lys Pro Trp Leu Lys
85 90 95

Thr Leu Gln Leu Gly Ile Asp Ile Lys Ser Phe Ile Leu Pro Gly Ser
100 105 110

His Val Asn Thr Met Asp Ser Ala Thr Leu Phe Lys Ala Ile Arg Leu
115 120 125

Glu Gly Lys Arg Val Asp Val Glu Tyr His Arg Leu His Ser Ser Asp
130 135 140

Lys Val Val Phe Tyr Ile Pro Ala Gln Lys Leu Pro Asp Asp Leu Arg
145 150 155 160

Leu Thr His Trp Leu Pro Glu Lys Glu Thr Arg Lys Thr Glu Tyr Val
165 170 175

Arg His Met Leu Ala His Val Met Gly Tyr Leu Thr Ser Gln Gly Lys
180 185 190

Glu Arg Leu Gln Gln Val Val Gln Asp Ser Arg Ser Ser Thr Ser Leu
195 200 205

Gly Ala Glu Lys Val Leu Gln Tyr Arg Phe Ile Asp His Pro Gln Ser
210 215 220

Gln Gly Glu Phe Gln Arg Leu Leu Asn Glu Asn Ile Thr Thr Lys Gly
225 230 235 240

Ser Glu Asp Lys Glu Val Val Gln Ser Asp Leu Phe Asp Met Ala Phe
245 250 255

Gln Cys Trp Trp Pro Gln Phe Ile Ser Val Ile Gln Ser Pro Thr Phe
260 265 270

Ser Glu Glu Leu Val His Glu Met Ser Gln Lys Leu Asp Leu Asp Cys
275 280 285

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I l l e T y r P r o G u A s p A s p G u P h e G u G n L y s P h e L e u A s n T h r L e u
290 295 300

L e u L y s A l a V a l L e u H i s H i s G y P h e G u G y I l l e S e r V a l A l a S e r
305 310 315 320

M e t G y V a l I l l e P h e L e u I l l e C y s P r o A s p S e r L e u A l a L e u G n I l l e
325 330 335

P r o P h e L e u A r g A s n G n L y s
340

<210> 169

<211> 366

<212> PRT

<213> Chl amydi a pneumoni ae

<400> 169

L e u S e r G y I l l e P h e S e r A s n P r o H i s P r o V a l S e r T y r P h e S e r S e r
1 5 10 15

T h r H i s A l a L y s G n L e u S e r A s p P h e S e r L y s L y s H i s P r o I l l e L e u
20 25 30

T h r L y s I l l e V a l T h r I l l e I l l e V a l L y s I l l e P h e L y s L e u L e u I l l e G y
35 40 45

L e u I l l e I l l e P r o P r o L e u G y I l l e T y r T r p L e u C y s G n L e u V a l C y s
50 55 60

S e r L e u A l a L e u P h e P r o A r g S e r S e r M e t L e u T y r S e r V a l L e u L y s
65 70 75 80

T h r C y s P h e L y s L y s T y r A r g L e u G u G n G u I l l e G n A s p T y r P h e
85 90 95

V a l L y s A s n L e u A s p P r o S e r P h e L y s A s p P r o A l a V a l S e r G u S e r
100 105 110

L y s A r g I l l e T h r I l l e G n G n A s p H i s L e u T h r I l l e A s p T h r L e u A l a
115 120 125

I l l e H i s P h e S e r T h r A l a A r g P r o L y s A r g T r p L e u L e u I l l e S e r L e u
130 135 140

G y S e r G y A s p P h e L e u G u A s p M e t I l l e G y L e u L y s A s p S e r L e u
145 150 155 160

P h e L e u S e r T r p L y s G u L e u A l a L y s L e u L e u G y A l a A s n I l l e L e u
165 170 175

I l e Tyr Asn Tyr Pro Gly Val Lys Ser Ser Thr Gly Lys Leu Asn Leu
180 185 190

G u Asn Leu Ala Thr Ala His Asn Leu Cys Ala Lys Tyr Leu G n Asp
195 200 205

Lys I l e G n Gly Pro Gly Ala Asn G u I l e I l e Thr Tyr Gly Tyr Ser
210 215 220

Leu Gly Gly Val Val G n Ser Ala Ala Leu G n Lys Asn Pro Phe Thr
225 230 235 240

Asn Ser G u Thr Ser Trp Val Ala Val Lys Asp Arg Ala Pro His Ser
245 250 255

Leu Pro Ala Ala Ala Asn Ser Phe Phe Gly Pro I l e Gly Lys Leu I l e
260 265 270

Ala Val Leu Ala Arg Trp Lys Met Asp Ala G u Lys Asn Ser Arg G u
275 280 285

Leu Pro Cys Pro G u I l e Leu Val Tyr Ser Ala Asp Arg Phe Arg Pro
290 295 300

Ser G u Val Gly Asp Asp Thr Ala Leu Leu Pro G u Phe Thr Leu Ala
305 310 315 320

His Ala I l e Lys Arg Thr Pro Phe Ala Arg Ser Lys Lys Phe I l e Gly
325 330 335

G u Val Asn Leu Leu His Ser Ser Pro Leu Lys His Pro Thr I l e G n
340 345 350

Lys Leu Ala G u Ala I l e Leu G u Ser Leu Ser Arg Lys Asn
355 360 365

<210> 170

<211> 325

<212> PRT

<213> Chl amydi a pneumoni ae

<400> 170

Met His Ser G u Leu Pro Asn Tyr G n Asn I l e Val G u Ser Val Val
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Thr G u I l e Thr Thr G n Leu Leu Asn Tyr Arg Ser G u His Arg Leu
20 25 30

Val Pro Phe Trp G u Lys Ser Asp Gly Ser Phe I l e Thr Ala Ala Asp
35 40 45

Tyr Gly Ser G n Tyr Tyr Leu Lys G n G n Leu Ala Lys Ala Phe Pro
50 55 60

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Asn Ile Pro Phe Ile Gly Gu Gu Thr Leu Tyr Pro Asp Gln Asp Asn
 65 70 75 80
 Gu Lys Ile Pro Gu Ile Leu Lys Phe Thr Arg Leu Leu Thr Ser Ser
 85 90 95
 Val Ser Arg Asp Asp Leu Ile Ser Thr Leu Val Pro Pro Pro Ser Pro
 100 105 110
 Thr Ser Leu Phe Trp Leu Val Asp Pro Ile Asp Gly Thr Ala Gly Phe
 115 120 125
 Ile Arg His Arg Ala Phe Ala Val Ala Ile Ser Leu Ile Tyr Gu Tyr
 130 135 140
 Arg Pro Ile Leu Ser Val Met Ala Cys Pro Ala Tyr Asn Gln Thr Phe
 145 150 155 160
 Lys Leu Tyr Ser Ala Ala Lys Gly His Gly Leu Ser Ile Val His Ser
 165 170 175
 Gln Asn Leu Asp Arg Arg Phe Val Tyr Ala Asp Arg Lys Gln Thr Lys
 180 185 190
 Gln Phe Cys Gu Ala Ser Leu Ala Ala Leu Asn Gln Gln His His Ala
 195 200 205
 Thr Arg Lys Leu Ser Leu Gly Leu Pro Asn Thr Pro Ser Pro Arg Arg
 210 215 220
 Val Gu Ser Gln Tyr Lys Tyr Ala Leu Val Ala Gu Gly Ala Val Asp
 225 230 235 240
 Phe Phe Ile Arg Tyr Pro Phe Ile Asp Ser Pro Ala Arg Ala Trp Asp
 245 250 255
 His Val Pro Gly Ala Phe Leu Val Gu Gu Ala Gly Gly Arg Val Thr
 260 265 270
 Asp Ala Leu Gly Ala Pro Leu Gu Tyr Arg Lys Gu Ser Leu Val Leu
 275 280 285
 Asn Asn His Ala Val Ile Leu Ala Ser Gly Asp Gln Gu Thr His Gu
 290 295 300
 Thr Thr Leu Ala Ala Leu Gln Asn Gln Leu Asn Val Val Pro Thr Asp
 305 310 315 320
 Lys Leu Ile Ala Leu
 325

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<210> 171
 <211> 458
 <212> PRT
 <213> Chl amydi a pneumni ae

<400> 171

Met Phe Asn Val Asn Phe Lys Phe Leu Gl u Gl y Leu Hi s Gl n Pro Ala
 1 5 10 15

Pro Arg Tyr Thr Ser Tyr Pro Thr Ala Leu Gl u Trp Gl u Pro Ser Asp
 20 25 30

Ala Ala Pro Ala Leu Leu Ala Phe Gl n Arg Ile Arg Gl u Asn Pro Gl n
 35 40 45

Pro Leu Ser Leu Tyr Phe Hi s Ile Pro Phe Cys Gl n Ser Met Cys Leu
 50 55 60

Tyr Cys Gl y Cys Ser Val Val Leu Asn Arg Arg Gl u Asp Ile Val Gl u
 65 70 75 80

Ala Tyr Ile Asn Thr Leu Ile Gl n Gl u Met Lys Leu Val Val Gl u Thr
 85 90 95

Ile Gl y Phe Arg Pro Gl n Val Ser Arg Ile Hi s Phe Gl y Gl y Gl y Thr
 100 105 110

Pro Ser Arg Leu Ser Arg Gl u Leu Phe Thr Leu Leu Phe Asp Hi s Ile
 115 120 125

Hi s Lys Leu Phe Asp Leu Ser Hi s Ala Gl u Gl u Ile Ala Ile Gl u Val
 130 135 140

Asp Pro Arg Ser Leu Arg Asn Asp Met Gl u Lys Ala Asp Phe Phe Gl n
 145 150 155 160

Asn Val Gl y Phe Asn Arg Val Ser Leu Gl y Val Gl n Asp Thr Gl n Ala
 165 170 175

Asp Val Gl n Gl u Ala Val Arg Arg Arg Gl n Ser Hi s Gl u Gl u Ser Leu
 180 185 190

Lys Ala Tyr Gl u Lys Phe Lys Gl u Leu Ala Phe Gl n Ser Ile Asn Ile
 195 200 205

Asp Leu Ile Tyr Gl y Leu Pro Lys Gl n Thr Lys Gl u Ser Phe Ser Lys
 210 215 220

Thr Ile Gl n Asp Ile Leu Ala Met Tyr Pro Asp Arg Leu Ala Leu Phe
 225 230 235 240

Ser Phe Ala Ser Val Pro Trp Ile Lys Pro Hi s Gl n Lys Ala Met Lys

Al a Ser Asp Met Pro Ser Met Gu Gu Lys Phe Al a Ile Tyr Ser G n
260 265 270

Ser Arg His Leu Leu Thr Lys Al a Gy Tyr G n Al a Ile Gy Met Asp
275 280 285

His Phe Ser Leu Pro His Asp Pro Leu Thr Leu Al a Phe Lys Asn Lys
290 295 300

Thr Leu Ile Arg Asn Phe G n Gy Tyr Ser Leu Pro Pro Gu Gu Asp
305 310 315 320

Leu Leu Gy Leu Gy Met Thr Ser Thr Ser Phe Ile Arg Gy Ile Tyr
325 330 335

Leu G n Asn Al a Lys Thr Leu Gu Gu Tyr His Asn Thr Val Leu Arg
340 345 350

Gy Thr Phe Al a Thr Val Lys Ser Lys Ile Leu Thr Gu Asp Asp Arg
355 360 365

Ile Arg Lys Trp Al a Ile His Lys Leu Met Cys Thr Phe Thr Ile Asn
370 375 380

Lys Gu Gu Phe Phe Asn Leu Phe Gy Tyr Gu Phe Asp Thr Tyr Phe
385 390 395 400

Ile Gu Ser Arg Asp Arg Leu Ile Ser Met Gu Thr Thr Gy Leu Ile
405 410 415

His Asn Ser Pro Gy Ser Leu Lys Val Thr Pro Leu Gy Gu Leu Phe
420 425 430

Val Arg Val Ile Al a Thr Al a Phe Asp His Tyr Phe Leu Asn Lys Val
435 440 445

Ser Lys Lys Gu Cys Phe Ser Al a Ser Ile
450 455

<210> 172
<211> 379
<212> PRT
<213> Chl amydi a pneumni ae

<400> 172

Met Arg Tyr His Lys Tyr Phe Arg Tyr Val Asn Ser Trp Val Phe Leu
1 5 10 15

Val Val Leu Thr Leu Met Leu Leu Ser Val Val Val Ile Ser Ser Met
20 25 30

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Asp Pro Thr Ala Met Leu Val Thr Ser Ser Lys Gly Leu Leu Thr Asn
 35 40 45
 Lys Ser Ile Met Gln Leu Arg His Phe Ala Leu Gly Trp Val Val Phe
 50 55 60
 Phe Ile Cys Ala Tyr Phe Asp Tyr His Leu Phe Lys Arg Trp Ala Trp
 65 70 75 80
 Val Leu Tyr Phe Phe Met Ile Cys Ala Leu Val Gly Leu Phe Phe Val
 85 90 95
 Pro Ser Val Gln Asn Val His Arg Trp Tyr Arg Ile Pro Phe Ile His
 100 105 110
 Met Ser Val Gln Pro Ser Gu Tyr Gly Lys Leu Val Ile Val Ile Met
 115 120 125
 Leu Ser Tyr Ile Leu Gu Ser Arg Lys Ala Asp Ile Thr Ser Lys Thr
 130 135 140
 Thr Ala Phe Leu Ala Cys Leu Val Val Ala Leu Pro Phe Phe Leu Ile
 145 150 155 160
 Leu Lys Gu Pro Asp Leu Gly Thr Ala Leu Val Leu Cys Pro Val Thr
 165 170 175
 Leu Thr Ile Phe Tyr Leu Ser Asn Val His Ser Leu Leu Val Lys Phe
 180 185 190
 Cys Thr Val Val Ala Thr Ile Gly Ile Ile Gly Ser Leu Leu Ile Phe
 195 200 205
 Ser Gly Ile Val Ser His Gln Lys Val Lys Pro Tyr Ala Leu Lys Val
 210 215 220
 Ile Lys Gu Tyr Gln Tyr Gu Arg Leu Ser Pro Ser Asn His His Gln
 225 230 235 240
 Arg Ala Ser Leu Ile Ser Ile Gly Leu Gly Gly Ile Arg Gly Arg Gly
 245 250 255
 Trp Lys Thr Gly Gu Phe Ala Gly Arg Gly Trp Leu Pro Tyr Gly Tyr
 260 265 270
 Thr Asp Ser Val Phe Ser Ala Leu Gly Gu Gu Phe Gly Leu Leu Gly
 275 280 285
 Leu Leu Phe Thr Leu Gly Leu Phe Tyr Cys Leu Ile Cys Phe Gly Cys
 290 295 300

Arg Thr Val Ala Val Ala Thr Asp Asp Phe Gly Lys Leu Leu Ala Ala
 305 310 315 320

Gly Ile Thr Val Tyr Leu Ala Met His Val Leu Ile Asn Ile Ser Met
 325 330 335

Met Cys Gly Leu Leu Pro Ile Thr Gly Val Pro Leu Ile Leu Ile Ser
 340 345 350

Tyr Gly Gly Ser Ser Val Ile Ser Thr Met Ala Ser Leu Gly Val Leu
 355 360 365

Gln Ser Ile Tyr Ser His Arg Phe Ala Lys Tyr
 370 375

<210> 173
 <211> 1166
 <212> PRT
 <213> Chl amydi a pneumoni ae

<400> 173

Met Leu Asn Phe Arg Lys Leu Arg Arg Asp Phe Ser Ala Asn Ile Leu
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Gln Asp Gly Lys Lys Leu Phe Gu Gln Gly Ala Val Ile Asp Ala Lys
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Ile Leu Ser Met Asn Gly Gu Thr Val Cys Ile Ser Ala Gln Val Arg
 35 40 45

Gly Leu Tyr Asp Asn Ile Tyr Gu Cys Gu Ile Gu Val Asp Arg Ser
 50 55 60

Gu Ser Asp Thr Val Asp Ser Asn Cys Asp Cys Ser Tyr Asn Tyr Asp
 65 70 75 80

Cys Gln His Ile Val Ala Leu Leu Phe Tyr Leu Gu Gln Tyr Phe Asn
 85 90 95

Gu Met Val Val Ala Tyr Ala Arg Ser Ala Asp Leu Gu Thr Asp His
 100 105 110

Gu Ile Asn Gu Gu Val Lys Lys Gu Leu Lys Gu Thr Phe Val Ala
 115 120 125

Ala Ala Thr Lys Gu Gu Gu Arg Lys Asp Arg Gu His Gln Lys Gu
 130 135 140

Ile Leu Arg Gu Tyr Val His Ala Ala Asn Ala Leu Ser Ala Asn Pro
 145 150 155 160

Phe Phe Leu Pro Leu Gu Tyr Leu Gu Lys Asp Ser Ala Gu Leu Ala
 165 170 175

eol f - seq | . app

Val Leu Phe Val Ser Val Asn Gu Asp Thr Phe Ala Pro Ala Asn Gn
 180 185 190
 Pro Ile Gu Phe Gn Leu Val Leu Arg Leu Pro Cys Arg Ser Lys Pro
 195 200 205
 Phe Tyr Ile Ser Asn Ile Arg Thr Phe Leu Gu Gly Val Leu Tyr Gn
 210 215 220
 Gu Pro Ile Val Leu Asn Gy Arg Arg Phe Phe Phe Thr Met Gn Ser
 225 230 235
 Phe Asn Ala Ser Asp Arg Lys Leu Ile Asp Leu Leu Ile Arg Tyr Val
 245 250
 Arg Tyr Pro Asn His Thr Thr Gu Gu Lys Leu Leu Lys Ser Ala Tyr
 260 265 270
 Leu Met Pro Pro Ala Leu Gy Val Ile Leu Ala Lys Met Phe Gu His
 275 280 285
 Gn Leu Ala Asp Arg Gy Gy Gy Ser Leu Gy Gu Lys Gu Ser Phe
 290 295 300
 Ser Gy Leu Phe Cys Gy Asn Leu Gu Gu Pro Leu Cys Trp Ser Leu
 305 310 315
 Thr Pro Ala Lys Met Lys Phe Asn Leu Asp Phe Phe Asp Met Pro Tyr
 325 330 335
 Lys Ala Leu Leu Met Thr Pro Val Ile Leu Val Asp Asp Asp Gu Val
 340 345 350
 Gn Pro Gu Gn Thr Met Leu Leu Gu Ser Asp Ala Pro Gly Ile Ile
 355 360 365
 His His Phe Val Tyr His Arg Phe Ser Pro Gn Ile Lys Arg Ala His
 370 375 380
 Leu Arg Ser Phe Ser Arg Leu Arg Asp Ile Ala Ile Pro Gu Ala Leu
 385 390 395 400
 Phe Gy Ser Phe Arg Gu Asn Ala Leu Pro Val Phe Gn Gu Tyr Ala
 405 410 415
 Gu Ile Ala Asn Val His Leu Leu Asn Ser Phe Val Thr Leu Pro Tyr
 420 425 430
 Val Asp Gu Val Arg Ala Ile Cys Asp Met Ser Tyr Leu Asp Gy Gu
 435 440 445

eol f - seq1 . app

Leu 450 G u A l a L y s L e u H i s P h e 455 L e u T y r G y S e r L e u 460 A r g V a l P r o A l a
 A l a 465 S e r L e u A l a L e u G n 470 T y r G n A s p V a l A r g 475 A l a P h e I l e S e r A s p 480
 G u G y I l e L e u A l a 485 A r g A s n L e u V a l G u 490 G u A r g L y s M e t L e u G u 495
 G u V a l P h e 500 S e r G y P h e I l e T y r A s p 505 G u A r g A s p G y A l a 510 P h e A r g
 V a l L y s 515 S e r G u L y s L y s I l e V a l 520 G u P h e M e t T h r G u 525 T h r I l e P r o
 A l a 530 A s n G n H i s A r g I l e T h r 535 P h e A s n C y s P r o G u 540 A s n L e u S e r G y
 G n 545 P h e I l e T y r A s p G u 550 T h r I l e P h e G u L e u 555 S e r P h e A r g G u G y 560
 S e r A s p I l e A s n 565 T y r T y r G u A l a A s p L e u 570 L y s V a l H i s G y L e u 575 L e u
 L y s G y V a l P r o 580 L e u A s p L e u L e u T r p 585 A s p C y s I l e S e r A l a 590 L y s L y s
 A r g P h e L e u 595 G u L e u P r o L y s A l a 600 G y G n G n S e r L y s 605 G y T h r A r g
 A r g G y 610 L y s V a l A s n S e r G y 615 L y s L e u P r o C y s I l e 620 L e u V a l L e u A s p
 L e u 625 G u L y s I l e A l a P r o 630 V a l V a l G n I l e P h e 635 A s n G u I l e G y P h e 640
 L y s V a l L e u A s p 645 A s p L e u V a l G n L y s C y s 650 P r o L e u T r p S e r L e u 655 T h r
 G y I l e S e r L e u 660 A s p G n P h e G u A l a 665 L e u P r o V a l A s n P h e 670 S e r M e t
 S e r G u 675 A r g L e u I l e G u I l e G n 680 L y s G n I l e A r g G y 685 G u I l e G u
 P h e 690 A s p P h e G n A s p V a l P r o 695 G n G n I l e G n A l a 700 T h r L e u A r g S e r
 T y r 705 G n T h r G u G y V a l 710 H i s T r p L e u G u 715 A r g L e u A r g L y s M e t H i s 720

Leu Asn Gly Ile Leu Ala Asp Asp Met Gly Leu Gly Lys Thr Leu Gn
 725 730 735
 Ala Ile Ile Ala Val Thr Gn Ser Lys Leu Gu Lys Gly Ser Gly Cys
 740 745 750
 Ser Leu Ile Val Cys Pro Thr Ser Leu Val Tyr Asn Trp Lys Gu Gu
 755 760 765
 Phe Arg Lys Phe Asn Pro Gu Phe Arg Thr Leu Val Ile Asp Gly Val
 770 775 780
 Pro Ser Gn Arg Arg Lys Gn Leu Thr Ala Leu Ala Asp Arg Asp Val
 785 790 795 800
 Ala Ile Thr Ser Tyr Asn Leu Leu Gn Lys Asp Val Gu Leu Tyr Lys
 805 810 815
 Ser Phe Arg Phe Asp Tyr Val Val Leu Asp Gu Ala His His Ile Lys
 820 825 830
 Asn Arg Thr Thr Arg Asn Ala Lys Ser Val Lys Met Ile Gn Ser Asp
 835 840 845
 His Arg Leu Ile Leu Thr Gly Thr Pro Ile Gu Asn Ser Leu Gu Gu
 850 855 860
 Leu Trp Ser Leu Phe Asp Phe Leu Met Pro Gly Leu Leu Ser Ser Tyr
 865 870 875 880
 Asp Arg Phe Val Gly Lys Tyr Ile Arg Thr Gly Asn Tyr Met Gly Asn
 885 890 895
 Lys Ala Asp Asn Met Val Ala Leu Lys Lys Lys Val Ser Pro Phe Ile
 900 905 910
 Leu Arg Arg Met Lys Gu Asp Val Leu Lys Asp Leu Pro Pro Val Ser
 915 920 925
 Gu Ile Leu Tyr His Cys His Leu Thr Gu Ser Gn Lys Gu Leu Tyr
 930 935 940
 Gn Ser Tyr Ala Ala Ser Ala Lys Gn Gu Leu Ser Arg Leu Val Lys
 945 950 955 960
 Gn Gu Gly Phe Gu Arg Ile His Ile His Val Leu Ala Thr Leu Thr
 965 970 975
 Arg Leu Lys Gn Ile Cys Cys His Pro Ala Ile Phe Ala Lys Asp Ala
 980 985 990
 Pro Gu Pro Gly Asp Ser Ala Lys Tyr Asp Met Leu Met Asp Leu Leu

995

1000

1005

Ser Ser Leu Val Asp Ser Gly His Lys Thr Val Val Phe Ser Gln
 1010 1015 1020
 Tyr Thr Lys Met Leu Gly Ile Ile Lys Lys Asp Leu Glu Ser Arg
 1025 1030 1035
 Gly Ile Pro Phe Val Tyr Leu Asp Gly Ser Thr Lys Asn Arg Leu
 1040 1045 1050
 Asp Leu Val Asn Gln Phe Asn Glu Asp Pro Ser Leu Leu Val Phe
 1055 1060 1065
 Leu Ile Ser Leu Lys Ala Gly Gly Thr Gly Leu Asn Leu Val Gly
 1070 1075 1080
 Ala Asp Thr Val Ile His Tyr Asp Met Trp Trp Asn Pro Ala Val
 1085 1090 1095
 Glu Asn Gln Ala Thr Asp Arg Val His Arg Ile Gly Gln Ser Arg
 1100 1105 1110
 Ser Val Ser Ser Tyr Lys Leu Val Thr Leu Asn Thr Ile Glu Glu
 1115 1120 1125
 Lys Ile Leu Thr Leu Gln Asn Arg Lys Lys Ser Leu Val Lys Lys
 1130 1135 1140
 Val Ile Asn Ser Asp Asp Glu Val Val Ser Lys Leu Thr Trp Glu
 1145 1150 1155
 Glu Val Leu Glu Leu Leu Gln Ile
 1160 1165

<210> 174

<211> 754

<212> PRT

<213> Chl amydi a pneumni ae

<400> 174

Met Val Phe Phe Arg Asn Ser Leu Leu His Leu Val Ala Leu Ser Gly
 1 5 10 15
 Met Leu Cys Cys Ser Ser Gly Val Ala Leu Thr Ile Ala Glu Lys Met
 20 25 30
 Ala Ser Leu Glu His Ser Gly Arg Gly Ala Asp Asp Tyr Glu Gly Met
 35 40 45
 Ala Ser Phe Asn Ala Asn Met Arg Glu Tyr Ser Leu Gln Leu Ser Lys
 50 55 60

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Leu Tyr Gu Gu Ala Arg Lys Leu Arg Ala Ser Gy Thr Gu Asp Gu
 65 70 75 80
 Ala Leu Trp Lys Asp Leu Ile Arg Arg Ile Gy Gu Val Arg Gy Tyr
 85 90 95
 Leu Arg Gu Ile Gu Gu Leu Trp Ala Ala Gu Ile Arg Gu Lys Gy
 100 105 110
 Gy Asn Leu Gu Asp Tyr Ala Leu Trp Asn His Pro Gu Thr Thr Ile
 115 120 125
 Tyr Asn Leu Val Thr Asp Tyr Gy Thr Gu Asp Ser Ile Tyr Leu Ile
 130 135 140
 Pro Gn Gu Ile Gy Ala Ile Lys Ile Ala Thr Leu Ser Lys Phe Val
 145 150 155 160
 Val Pro Lys Gu Ser Phe Gu Asp Cys Leu Thr Gn Ile Leu Ser Arg
 165 170 175
 Leu Gy Ile Gy Val Arg Gn Val Asn Ser Trp Ile Lys Gu Leu Tyr
 180 185 190
 Met Met Arg Lys Gu Gy Cys Ser Val Ala Gy Val Phe Ser Ser Arg
 195 200 205
 Lys Asp Leu Gu Ala Leu Pro Gu Thr Ala Tyr Ile Gy Phe Val Leu
 210 215 220
 Asn Ser Asn Val Asp Ala His Thr Asn Gn His Val Leu Lys Lys Phe
 225 230 235 240
 Ile Asn Pro Gu Thr Thr His Val Asp Val Ile Ala Gy Arg Val Trp
 245 250 255
 Ile Phe Gy Ser Ala Gy Gu Val Gy Gu Leu Leu Lys Ile Tyr Asn
 260 265 270
 Phe Val Gn Ser Gu Ser Ile Arg Gn Gu Tyr Arg Val Ile Pro Leu
 275 280 285
 Thr Lys Ile Asp Pro Gy Gu Met Ile Ser Ile Leu Asn Ala Ala Phe
 290 295 300
 Arg Gu Asp Leu Thr Lys Asp Val Ser Gu Gu Ser Leu Gy Leu Arg
 305 310 315 320
 Val Val Pro Leu Gn Tyr Gn Gy Arg Ser Leu Phe Leu Ser Gy Thr
 325 330 335

Al a Al a Leu Val G n G n Al a Leu Thr Leu Ile Arg G u Leu G u G u
340 345 350

G y Ile G u Asn Pro Thr Asp Lys Thr Val Phe Trp Tyr Asn Val Lys
355 360 365

Hi s Ser Asp Pro G n G u Leu Al a Al a Leu Leu Ser G n Val Hi s Asp
370 375 380

Val Phe Ser G y G u Asn Lys Al a Ser Val G y Al a Al a Asp G y Cys
385 390 400

G y Ser G n Leu Asn Al a Ser Ile G n Ile Asp Thr Thr Val Ser Ser
405 410 415

Ser Al a Lys Asp G y Ser Val Lys Tyr G y Asn Phe Ile Al a Asp Ser
420 425 430

Lys Thr G y Thr Leu Ile Met Val Val G u Lys G u Val Leu Pro Arg
435 440 445

Ile G n Met Leu Leu Lys Lys Leu Asp Val Pro Lys Lys Met Val Arg
450 455 460

Ile G u Val Leu Leu Phe G u Arg Lys Leu Al a Hi s G u G n Lys Ser
465 470 475 480

G y Leu Asn Leu Leu Arg Leu G y G u G u Val Cys Lys Lys G y Cys
485 490 495

Ser Pro Ser Val Ser Trp Al a G y G y Thr G y Ile Leu G u Phe Leu
500 505 510 515

Phe Lys G y Ser Thr G y Ser Ser Ile Val Pro G y Tyr Asp Leu Al a
515 520 525

Tyr G n Phe Leu Met Al a G n G u Asp Val Arg Ile Asn Al a Ser Pro
530 535 540

Ser Val Val Thr Met Asn G n Thr Pro Al a Arg Ile Al a Val Val Asp
545 550 555 560

G u Met Ser Ile Al a Val Ser Ser Asp Lys Asp Lys Al a G n Tyr Asn
565 570 575

Arg Al a G n Tyr G y Ile Met Ile Lys Met Leu Pro Val Ile Asn Val
580 585 590

G y G u G u Asp G y Lys Ser Tyr Ile Thr Leu G u Thr Asp Ile Thr
595 600 605

Phe Asp Thr Thr G y Lys Asn Hi s Asp Asp Arg Pro Asp Val Thr Arg
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610

615

Arg Asn Ile Thr Asn Lys Val Arg Ile Ala Asp Gly Gu Thr Val Ile
625 630 635 640

Ile Gly Gly Leu Arg Cys Lys Gn Met Ser Asp Ser His Asp Gly Ile
645 650 655

Pro Phe Leu Gly Asp Ile Pro Gly Ile Gly Lys Leu Phe Gly Met Ser
660 665 670

Ser Thr Ser Asp Ser Leu Thr Gu Met Phe Val Phe Ile Thr Pro Lys
675 680 685

Ile Leu Gu Asn Pro Val Gu Gn Gn Gu Arg Lys Gu Gu Ala Leu
690 695 700

Leu Ser Ser Arg Pro Gly Gu Arg Gu Gu Tyr Tyr Gn Ala Leu Ala
705 710 715 720

Ala Ser Gu Ala Ala Ala Arg Ala Ala His Lys Lys Leu Gu Met Phe
725 730 735

Pro Ala Ser Gly Val Ser Leu Ser Gn Val Gu Arg Gn Gu Tyr Asp
740 745 750

Gly Cys

- <210> 175
- <211> 488
- <212> PRT
- <213> Chl amydi a pneumoni ae
- <400> 175

Met Ser Ile Ser Ser Ser Ser Gly Pro Asp Asn Gn Lys Asn Ile Met
1 5 10 15

Ser Gn Val Leu Thr Ser Thr Pro Gn Gly Val Pro Gn Gn Asp Lys
20 25 30

Leu Ser Gly Asn Gu Thr Lys Gn Ile Gn Gn Thr Arg Gn Gly Lys
35 40 45

Asn Thr Gu Met Gu Ser Asp Ala Thr Ile Ala Gly Ala Ser Gly Lys
50 55 60

Asp Lys Thr Ser Ser Thr Thr Lys Thr Gu Thr Ala Pro Gn Gn Gly
65 70 75 80

Val Ala Ala Gly Lys Gu Ser Ser Gu Ser Gn Lys Ala Gly Ala Asp
85 90 95

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Thr Gly Val Ser 100 Gly Ala Ala Ala Thr 105 Thr Ala Ser Asn Thr 110 Ala Thr

Lys Ile Ala 115 Met Gln Thr Ser Ile 120 Gu Gu Ala Ser Lys 125 Ser Met Gu

Ser Thr 130 Leu Gu Ser Leu Gln 135 Ser Leu Ser Ala Ala 140 Gln Met Lys Gu

Val 145 Gu Ala Val Val Val 150 Ala Ala Leu Ser Gly 155 Lys Ser Ser Gly Ser 160

Ala Lys Leu Gu Thr 165 Pro Gu Leu Pro Lys 170 Pro Gly Val Thr Pro 175 Arg

Ser Gu Val 180 Ile Gu Ile Gly Leu Ala 185 Leu Ala Lys Ala 190 Ile Gln Thr

Leu Gly Gu 195 Ala Thr Lys Ser Ala 200 Leu Ser Asn Tyr Ala 205 Ser Thr Gln

Ala Gln 210 Ala Asp Gln Thr Asn 215 Lys Leu Gly Leu Gu 220 Lys Gln Ala Ile

Lys 225 Ile Asp Lys Gu Arg 230 Gu Gu Tyr Gln Gu 235 Met Lys Ala Ala Gu 240

Gln Lys Ser Lys Asp 245 Leu Gu Gly Thr Met 250 Asp Thr Val Asn Thr 255 Val

Met Ile Ala 260 Val Ser Val Ala Ile Thr 265 Val Ile Ser Ile Val 270 Ala Ala

Ile Phe Thr 275 Cys Gly Ala Gly Leu 280 Ala Gly Leu Ala 285 Ala Gly Ala Ala

Val Gly 290 Ala Ala Ala Ala Gly 295 Gly Ala Ala Gly Ala 300 Ala Ala Ala Thr

Thr 305 Val Ala Thr Gln Ile Thr 310 Val Gln Ala Val 315 Val Gln Ala Val Lys 320

Gln Ala Val 325 Ile Thr Ala Val Arg Gln Ala 330 Ile Thr Ala Ala 335 Ile Lys

Ala Ala Val 340 Lys Ser Gly Ile Lys Ala 345 Phe Ile Lys Thr Leu 350 Val Lys

Ala Ile Ala 355 Lys Ala Ile Ser Lys 360 Gly Ile Ser Lys Val 365 Phe Ala Lys

Gly Thr Gln Met Ile Ala Lys Asn Phe Pro Lys Leu Ser Lys Val Ile
370 375 380

Ser Ser Leu Thr Ser Lys Trp Val Thr Val Gly Val Gly Val Val Val
385 390 400

Ala Ala Pro Ala Leu Gly Lys Gly Ile Met Gln Met Gln Leu Ser Gly
405 410 415

Met Gln Gln Asn Val Ala Gln Phe Gln Lys Gly Val Gly Lys Leu Gln
420 425 430

Ala Ala Ala Asp Met Ile Ser Met Phe Thr Gln Phe Trp Gln Gln Ala
435 440 445

Ser Lys Ile Ala Ser Lys Gln Thr Gly Gu Ser Asn Gu Met Thr Gln
450 455 460

Lys Ala Thr Lys Leu Gly Ala Gln Ile Leu Lys Ala Tyr Ala Ala Ile
465 470 475 480

Ser Gly Ala Ile Ala Gly Ala Ala
485

<210> 176
<211> 27
<212> PRT
<213> Chl amydi a pneumoni ae

<400> 176

Lys Leu Pro Phe Pro Ala Ser Phe Phe Ile Phe Pro Arg Lys Ser Gly
1 5 10 15

Pro Asn Pro Trp Asn Asn Ser Trp Gly Met Gln
20 25

<210> 177
<211> 143
<212> PRT
<213> Chl amydi a pneumoni ae

<400> 177

Ile Ser Phe Ser Val Phe Pro Ile Gly Arg Gln Asn Ser Asn Arg Gu
1 5 10 15

Cys Lys Asp Ser Leu Leu Cys Lys Phe Leu Phe Cys Pro Ser Leu Ser
20 25 30

Phe Thr Ser Ser Ala Ser Trp Lys Phe Ser Arg Ser Leu Ser Gu Thr
35 40 45

Gu Tyr Tyr Leu Ser Asn Gln Ile Tyr Arg Asp Phe Met Tyr Asn Ser
50 55 60

eol f - seq1 . app

Arg Asn Val Leu Phe Leu Tyr Pro Ile Cys Ser Trp Gly Val Cys Ser
65 70 75 80

Leu Asn Phe Asn Gly Met Ser His His Asn Leu Trp Ala Ser Lys Ala
85 90 95

Arg Asp Ser Ser Arg Asn Ala Thr Leu Arg Thr Ala Leu Pro Ser Gln
100 105 110

Arg Asp Tyr Asp Ser Ser His Leu Tyr Arg Lys Tyr Phe Arg Phe Leu
115 120 125

Pro Cys Ser Ser Ser Cys Arg Cys Asn Ser Ser Phe Arg Cys Lys
130 135 140

<210> 178
<211> 41
<212> PRT
<213> Chl amydi a pneumni ae

<400> 178

Arg Ile Gly Leu Pro Arg Ser Gu Phe Gu Lys Ser Asn Ser His Trp
1 5 10 15

Arg Val Cys Arg Tyr Leu Ser Tyr Phe Cys Cys Gly Val Arg His Tyr
20 25 30

Leu Ser Thr Gly Val Gly Arg Cys Ser
35 40

<210> 179
<211> 58
<212> PRT
<213> Chl amydi a pneumni ae

<400> 179

Lys Gu Ser Gly Gu Asn Cys Asp Ile Gu His Trp Lys Lys Asn Leu
1 5 10 15

Ala Arg His Gln Lys Lys Gu Lys Lys Asp Arg Asp Phe Lys Trp Ser
20 25 30

Leu Phe Phe Arg Phe Ser Phe Thr Trp Cys Lys Phe Pro Gu Ala Tyr
35 40 45

Arg Asp Leu Gly Lys Cys Lys Thr Gln Ser
50 55

<210> 180
<211> 20
<212> PRT
<213> Chl amydi a pneumni ae

<400> 180

eol f - seq1 . app

Arg Asp Thr Phe Asn Tyr Phe Pro Arg Ser Thr His Arg Lys His Ala
1 5 10 15

Asn Thr Ile Tyr
20

<210> 181
<211> 23
<212> PRT
<213> Chl amydi a pneumoni ae

<400> 181

Cys Arg Asp Pro Arg Tyr Thr Pro Phe Trp Cys Tyr Ser Thr Arg Ser
1 5 10 15

Ser Trp Trp Arg Asp Leu Leu
20

<210> 182
<211> 39
<212> PRT
<213> Chl amydi a pneumoni ae

<400> 182

Pro Thr Arg Tyr Pro Ala Leu Leu Gly Lys Arg Ser Arg Lys Gly His
1 5 10 15

Arg Asn Lys Tyr Leu Pro Met Gn Ser Gly Ile His Thr Pro Gly Trp
20 25 30

Ala Ile Asp Ser Leu Arg Gly
35

<210> 183
<211> 34
<212> PRT
<213> Chl amydi a pneumoni ae

<400> 183

Glu Arg Ser Ser Arg Gly Phe Ser Asn Arg Cys Phe Ser Ile Leu Arg
1 5 10 15

Phe Lys Phe Arg His Asp Thr Val His Lys Phe Ser Gly His Ser His
20 25 30

Arg Arg

<210> 184
<211> 94
<212> PRT
<213> Chl amydi a pneumoni ae

<400> 184

Gln Ser Ser His Phe Lys Gly Cys Phe Phe Pro Ser Val Ser Arg Asp
1 5 10 15

Asn Tyr Asp Tyr Phe Arg Lys Phe Trp Ser Trp Lys Asp Asn Phe Val
20 25 30

Ser Phe Ala Cys Gly Phe Pro Thr Phe Ala Arg Arg Arg Thr Ser Met
35 40 45

Glu Trp Glu Pro Ser Lys Ser Gln Arg Arg Cys Leu Tyr Ala Ala Lys
50 55 60

Arg Ser Pro Ala Ser Leu Ala Tyr Gly Phe Lys Lys His Asp Val Val
65 70 75 80

Asn Gly Ala Trp His Gln Tyr Lys Ser Gln Arg Leu Ile Gln
85 90

<210> 185
<211> 69
<212> PRT
<213> Chlamydia pneumoniae

<400> 185

Trp Gln Asp Asn Asn Asp Ile Ile Ser Tyr Pro Ser Leu Lys Tyr Phe
1 5 10 15

Arg Asp Pro Cys Tyr Ser Tyr Gly Gln Tyr Arg Leu Ala Tyr Thr Arg
20 25 30

Pro His Gly Thr Thr Arg Ser Ser Cys Cys Arg Asn Gln Leu Ile Ser
35 40 45

Ala Ser Asn Pro Arg Gly Thr Tyr Pro Ser Thr Phe Trp Ile Cys Val
50 55 60

Phe Glu Leu Phe Ser
65

<210> 186
<211> 34
<212> PRT
<213> Chlamydia pneumoniae

<400> 186

Ile Ser Ser Leu Cys Leu Gly Lys Asn Ser Phe Leu Tyr Val Gly Val
1 5 10 15

Ser Asn Leu Arg Lys Ser Gly Pro Asn Pro Thr Cys Ser Asn Phe Leu
20 25 30

Phe Phe

eol f - seq1 . app

<210> 187
 <211> 101
 <212> PRT
 <213> Chl amydi a pneumni ae

<400> 187

Ser Ile Met Asn Pro Val Arg Ile Gly Ile Ser Ala Pro Pro Ile Leu
 1 5 10 15

Trp Gu Val Leu His Thr Leu His Gn Val Pro Arg Ser Asp Phe Ala
 20 25 30

Tyr Gn Trp Val Ser Arg Arg Ala His Gly Gly Gn Pro His Pro Trp
 35 40 45

Asn His Pro Phe Ser Pro His Gn Arg Ala Asn Asn Thr Ile Gu Asp
 50 55 60

Asp Ile Pro Lys Lys Met Leu Val Ser Pro Val Ile Ile Asn Pro Ile
 65 70 75 80

Ala Met Lys Tyr Leu Gly Leu Asp Trp Ser Asp Met Thr Pro Leu Thr
 85 90 95

Asn Leu Leu Ile Pro
 100

<210> 188
 <211> 36
 <212> PRT
 <213> Chl amydi a pneumni ae

<400> 188

His Lys Gn Tyr Lys Gly Leu Gn Val Ala Pro Ser Cys Cys Asn Pro
 1 5 10 15

Arg Gly Gly Ala His Ala Leu Phe Leu Ser Arg Pro Ser Gu Thr Val
 20 25 30

Gly Ser Cys Pro
 35

<210> 189
 <211> 47
 <212> PRT
 <213> Chl amydi a pneumni ae

<400> 189

Thr Pro Pro Thr Ser Gn Thr Tyr Ser His Phe Asp Asn Thr Thr Gly
 1 5 10 15

Ser Arg Gu Arg Ile Ile Leu Phe Ser Ser Thr Arg Ser Lys Ile Ile
 20 25 30

eol f - seq1 . app

Arg Arg Ala His Ala Val Thr Ser Ser Ala Trp Lys Glu Pro Ser
35 40 45

<210> 190
<211> 133
<212> PRT
<213> Chl amydi a pneumni ae

<400> 190

Arg Lys Pro Leu Arg Phe Ser Ser Pro Val Leu Cys Arg Lys Phe Val
1 5 10 15

Met Glu Glu Thr Gn Lys Pro Cys Leu Cys Ser Ile Pro Val Ala Pro
20 25 30

Ile Ser Thr Ser Cys Cys Arg Glu Arg Met Ser Val Lys Thr Pro His
35 40 45

Arg Val Leu His Thr Asn Ala Asp Phe Leu Ser Gly Leu Gly Thr Asn
50 55 60

Pro Val Leu Val Gn Val Ala Val Ala Ser Phe Val Phe Val Ala Val
65 70 75 80

Ser Val Val Gn Leu Thr Phe His Cys Pro Trp Asn Pro Tyr Ser Glu
85 90 95

Leu Gly Ser Ser Ala Gly Thr Gly Ile Arg Leu Leu Met Ser Thr Leu
100 105 110

Val Ser Thr Ser Ala Ser Thr Val Ile Phe Asn Arg Glu Lys Ser Trp
115 120 125

Ser Trp Leu Asn Ile
130

<210> 191
<211> 18
<212> PRT
<213> Chl amydi a pneumni ae

<400> 191

Ser Gn Tyr Pro Leu Ala Lys Ile Met Pro Asn Ser Leu Gly Ile Pro
1 5 10 15

Asn Gly

<210> 192
<211> 32
<212> PRT
<213> Chl amydi a pneumni ae

<400> 192

eol f - seq1 . app

Ser Arg Asp Leu Ser Thr Leu Phe Cys Arg Leu Ser Phe Val Asn Phe
1 5 10 15

Tyr Arg Asp Ser Ser Ala Ile Ile Tyr Asp Asp Asn Thr Pro Val Leu
20 25 30

<210> 193
<211> 53
<212> PRT
<213> Chl amydi a pneumoni ae

<400> 193

Ser Thr Thr His Thr Lys Gn Leu Phe Phe His Gn Val Gn Pro Leu
1 5 10 15

Ser Phe Lys Leu Leu Asp Pro Leu Ser Gn Leu Leu Ser Thr Gly Ser
20 25 30

Tyr Phe Arg Leu Gn Thr Arg Ile Pro Leu Gu Ser Leu Leu Thr Leu
35 40 45

Oys Val Gly Ser Ser
50

<210> 194
<211> 23
<212> PRT
<213> Chl amydi a pneumoni ae

<400> 194

Gu Phe Arg His Lys Arg Lys Phe Gn Gu Arg Arg Val Leu Lys Val
1 5 10 15

Lys Gu Asn Gu Arg Ile Ser
20

<210> 195
<211> 72
<212> PRT
<213> Chl amydi a pneumoni ae

<400> 195

Asp Ser Leu Cys Asn Lys Asn Cys Thr Ile Ile Ala Gu Ala Gn Ile
1 5 10 15

Thr Leu Lys Ala Gn Lys Lys Ala Pro Lys Pro Asn Val Asp Lys Gu
20 25 30

Ile Ser Gly Ala Ser Arg Gu Gn Ser Phe Arg Asn Asn Ala Asn Thr
35 40 45

Lys Pro Lys Gn Gn Arg Leu Gn Lys Ile Lys Gn Asn Leu Cys Leu
50 55 60

eol f - seq1 . app

Leu Lys Ile Phe Leu Asn Ala Phe
65 70

<210> 196
<211> 32
<212> PRT
<213> Chl amydi a pneumni ae

<400> 196

Ile Pro Val Phe Asn Arg Asn Lys Ser Ile Asn Ser Leu Phe Ser Ile
1 5 10 15

Tyr Asp Lys Leu Gln Ser Tyr Arg Leu His Thr Pro Cys Arg Tyr Pro
20 25 30