

(19) World Intellectual Property Organization
International Bureau(43) International Publication Date
25 May 2001 (25.05.2001)(10) International Publication Number
PCT WO 01/36457 A2(51) International Patent Classification⁷: C07K 14/00

(21) International Application Number: PCT/CA00/01346

(22) International Filing Date:
10 November 2000 (10.11.2000)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
60/165,615 15 November 1999 (15.11.1999) US(71) Applicant (for all designated States except US): AVEN-
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Ontario K1P 5Y6 (CA).(81) Designated States (national): AE, AG, AL, AM, AT, AU,
AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ,
DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR,
HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,
LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ,

[Continued on next page]

(54) Title: CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS AND USES THEREOF

Nucleotide and amino acid sequences (SEQ ID Nos. 1
and 2) of the amino acid transporter from *C. pneumoniae*.

caamptccccc tatccaggaag catcccaattc ttaaacctgg tccaagatat ctattagatg 60
ctctaatatta caatcgcttta acctttccaa ggaagctctt atg cac tcc cac tca
Met His Ser His Ser 115
1 5

aaa cca aag aaa cag ttg gga aca ttc aag gtc agc atg tta tca ctt 163
Lys Pro Thr Lys Pro Leu Gly Thr Phe Thr Val Gly Met Leu Ser Leu 20
10 15 20

gct gta gta att agt ttg cgt aat ctc ccg tta aca gaa aat ggt 211
Ala Val Val Ile Ser Leu Arg Asn Leu Pro Leu Thr Ala Lys His Gly 30
25 30 35

ctt tcc act ctg ttt ttt tat gga cta gca gtc ata tgc ttt atg att 259
Leu Ser Thr Leu Phe Phe Tyr Gly Leu Ala Val Ile Cys Phe Met Ile 40
45 50

ccg tat gct ctg att tct gct gaa ctt gct tct ttc aag ctt cag gga 307
Pro Tyr Ala Leu Ile Ser Ala Gly Leu Ala Ser Phe Lys Pro Gln Gly 55
60 65

att tat att tgg gca cgt gac cgt cta ggc aca tgg tgg gga ttc ttt 355
Ile Tyr Ile Trp Ala Arg Asp Ala Leu Gly Lys Trp Tyr Gly Phe Phe 70
75 80 85

gct ata tgg atg aca tgg ttc cag aac atg acg tgg tat ctt ccc ctg 403
Ala Ile Trp Met Gln Trp Phe His Asn Met Thr Trp Tyr Pro Ala Val 90
95 100

tta gct ttt ata ggc agt aac att gta tat aac atc aat cca gaa ctc 451
Leu Ala Phe Ile Ala Ser Thr Ile Val Tyr Lys Ile Asn Pro Gln Gly 110
115 120

gct ccc aac aaa cag tgc tac att gca acc gtc atc ctt gct ttt tgg 499
Ala His Asn Lys Val Tyr Ile Ala Thr Val Ile Leu Ala Gly Phe Trp 125
130 135

ata ctt aca ttt ttt aat ttt tta gga att act tcc tcc gaa tta ttc 547
Ile Leu Thr Phe Phe Asn Phe Leu Gly Ile Thr Ser Ser Ala Leu Phe 140
145 150

agc tct att tgt gta atc ata gga aca tta att cca gca ttc atc tta 595
Ser Ser Ile Cys Val Ile Ile Gly Thr Leu Ile Pro Gly Val Ile Leu 155
160 165

ggt agt ttg gct ctc ttt tgg att ttt tcc ggc aac ccc att gct att 643
Val Ser Leu Ala Leu Phe Thr Phe Ser Gly Asn Pro Ile Ala Ile 170
175 180

tct ctt tct tgg gga aat ctt ctt cct aat ttc agt aac gta tcc tca 691
Ser Leu Ser Trp Trp Gly Asn Leu Leu Pro Asn Phe Ser Asn Val Ser Ser 185
190 195

ctt gta cta ata gct gga atg tta ctt ggc tta tgc ggt cta gag gct 739
Leu Val Leu Leu Ala Gly Met Leu Leu Leu Cys Gly Leu Glu Ala 200
205 210

aat ccg aac ctt gct tct gat atg gta aat ccc aag aac aat tat cca 787
Asn Ala Asn Leu Ala Ser Asp Met Val Asn Pro Arg Lys Asn Tyr Pro 215
220 225

aag gca gtc ttc att gct gca ata gca aca ctc att tta gct ctg 835
Lys Ala Val Phe Ile Gly Ala Ile Ala Thr Leu Thr Ile Leu Val Leu 230
235 240 245

ggt tct tta tcc ata gca ata gta gtt ccc aag aca gaa att agt tta 883
Gly Ser Leu Ser Ile Ala Ile Val Ile Pro Lys Glu Glu Ile Ser Leu 250
255 260

gtc tct gga cta gta aca acg ttt acc ttg ttc tct gat aac tat aac 931
Thr Leu Phe Phe Asn Arg Lys Tyr Asn 265
270 275

ctc tcc tgg atg act gca acc gtt gta gtc atg acc att gca gaa tgc 979
Leu Ser Trp Met Thr Gly Ile Val Val Val Met Thr Ile Ala Gly Ser 280
285 290

cta ggc gaa ctt aat gct tgg atg ttt gca gga cca aag cgg ctt ttt 1027
Leu Gly Glu Leu Asn Ala Trp Met Phe Ala Gly Thr Lys Gly Leu Phe 295
300 305

att tcc act cag aat gac tgc ttt ccc cga ctc ttt aag aac gta aat 1075
Ile Ser Thr Gln Asn Asp Cys Leu Pro Arg Leu Phe Lys Val Asn 310
315 320 325

agc aca aat gct cca acg aac tta atg tta ttc cca ggt att gtt ctg 1123
Ser Lys Asn Val Pro Thr Asn Leu Met Leu Phe Gln Gly Ile Val Val 330
335 340

aca ata ttc aca ctt tta ttt cta tgc ctt gat tca gca gac ctg ctg 1171
Thr Ile Phe Thr Leu Leu Phe Cys Leu Asp Ser Ala Asp Leu Val 345
350 355

tat tgg att tta aat gca ctc agc gtc cag atg tat ctt ccg atg tac 1219
Tyr Trp Ile Leu Thr Ala Leu Ser Val Gln Met Tyr Leu Ala Met Tyr 360
365 370

atc tgt ctg ttt ctt gca gga cag atc tta cgt atc aca gaa cca aag 1267
Ile Cys Leu Phe Leu Ala Gly Pro Ile Leu Arg Ile Lys Glu Pro Arg 375
380

gct aca cgc ctc tat tct gca cca gga aag ttt ttg gga atc tgc agt 1315
Ala Gln Arg Leu Tyr Ser Val Pro Gly Lys Thr Leu Gly Ile Cys Thr 390
395 400 405

atg tct ata tta gga att ctc tcc tgc gct ttt gct ctt tgg gtc agc 1363
Met Ser Ile Leu Gly Ile Leu Ser Cys Ala Phe Ala Leu Trp Val Ser 410
415 420

tcc ctg cct cct aca gaa ctt gct cag ata tcc gaa ggc agc aac ata 1411
Phe Leu Pro Pro Arg Glu Leu Ala Gln Ile Ser Glu Gly Ser Lys Ile 425
430 435

gga tat act aca ttc ctg ctt tta gca ttt agc ttg aat tgc tta att 1459
Gly Tyr Thr Thr Phe Leu Leu Ala Phe Ser Leu Asn Cys Leu Ile 440
445 450

ctt ttc gga atc tat ttc acg cat aac cgc tta tcc aca aag agc 1504
Pro Phe Gly Ile Tyr Phe Thr His Lys Arg Leu Ser Lys Lys Ser 455
460 465

caactcaaaa gacttttgg gaaagaaaa gaaagaagcc ttcttggtg tatggcagcc 1564
tggaagactt ctggaatcna attgctcttc ctgcaaaaag ttt 1607

(57) Abstract: The present invention provides a method of nucleic acid, including DNA, immunization of a host, including humans, against disease caused by infection by a strain of *Chlamydia*, specifically *C. pneumoniae*, employing a vector containing a nucleotide sequence encoding an amino acid transporter of a strain of *Chlamydia pneumoniae* and a promoter to effect expression of the amino acid transporter in the host. Modifications are possible within the scope of this invention.



NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM,
TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

(84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published:

— Without international search report and to be republished upon receipt of that report.

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

TITLE OF INVENTION

CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS
AND USES THEREOF

REFERENCE TO RELATED APPLICATIONS

5 This application claims the benefit of U.S.
Provisional Application No. 60/165,615, filed November 15,
1999.

FIELD OF INVENTION

10 The present invention relates to the *Chlamydia* amino
acid transporter and corresponding DNA molecules, which can be
used to prevent and treat *Chlamydia* infection in mammals, such
as humans.

BACKGROUND OF THE INVENTION

15 *Chlamydia* are prokaryotes. They exhibit morphologic
and structural similarities to gram-negative bacteria including
a trilaminar outer membrane, which contains lipopolysaccharide
and several membrane proteins that are structurally and
functionally analogous to proteins found in *E coli*. They are
obligate intra-cellular parasites with a unique biphasic life
20 cycle consisting of a metabolically inactive but infectious
extracellular stage and a replicating but non-infectious
intracellular stage. The replicative stage of the life-cycle
takes place within a membrane-bound inclusion which sequesters
the bacteria away from the cytoplasm of the infected host cell.

25 .*C. pneumoniae* is a common human pathogen, originally
described as the TWAR strain of *Chlamydia psittaci* but
subsequently recognised to be a new species. *C. pneumoniae* is
antigenically, genetically and morphologically distinct from

other *chlamydia* species (*C. trachomatis*, *C. pecorum* and *C. psittaci*). It shows 10% or less DNA sequence homology with either of *C. trachomatis* or *C. psittaci*.

C. pneumoniae is the third most common cause of
5 community acquired pneumonia, only less frequent than
Streptococcus pneumoniae and *Mycoplasma pneumoniae* (Grayston et
al. (1995) Journal of Infectious Diseases 168:1231; Campos et
al. (1995) Investigation of Ophthalmology and Visual Science
36:1477). It can also cause upper respiratory tract symptoms
10 and disease, including bronchitis and sinusitis (Grayston et
al. (1995) Journal of Infectious Diseases 168:1231; Grayston et
al (1990) Journal of Infectious Diseases 161:618-625; Marrie
(1993) Clinical Infectious Diseases. 18:501-513; Wang et al
(1986) Chlamydial infections Cambridge University Press,
15 Cambridge. p. 329. The great majority of the adult population
(over 60%) has antibodies to *C. pneumoniae* (Wang et al (1986)
Chlamydial infections. Cambridge University Press, Cambridge.
p. 329), indicating past infection which was unrecognized or
asymptomatic.

20 *C. pneumoniae* infection usually presents as an acute
respiratory disease (i.e., cough, sore throat, hoarseness, and
fever; abnormal chest sounds on auscultation). For most
patients, the cough persists for 2 to 6 weeks, and recovery is
slow. In approximately 10% of these cases, upper respiratory
25 tract infection is followed by bronchitis or pneumonia.
Furthermore, during a *C. pneumoniae* epidemic, subsequent co-
infection with pneumococcus has been noted in about half of
these pneumonia patients, particularly in the infirm and the
elderly. As noted above, there is more and more evidence that
30 *C. pneumoniae* infection is also linked to diseases other than
respiratory infections.

The reservoir for the organism is presumably people. In contrast to *C. psittaci* infections, there is no known bird or animal reservoir. Transmission has not been clearly defined. It may result from direct contact with secretions, from fomites, or from airborne spread. There is a long incubation period, which may last for many months. Based on analysis of epidemics, *C. pneumoniae* appears to spread slowly through a population (case-to-case interval averaging 30 days) because infected persons are inefficient transmitters of the organism. Susceptibility to *C. pneumoniae* is universal. Reinfections occur during adulthood, following the primary infection as a child. *C. pneumoniae* appears to be an endemic disease throughout the world, noteworthy for superimposed intervals of increased incidence (epidemics) that persist for 2 to 3 years. *C. trachomatis* infection does not confer cross-immunity to *C. pneumoniae*. Infections are easily treated with oral antibiotics, tetracycline or erythromycin (2 g/d, for at least 10 to 14 d). A recently developed drug, azithromycin, is highly effective as a single-dose therapy against chlamydial infections.

In most instances, *C. pneumoniae* infection is often mild and without complications, and up to 90% of infections are subacute or unrecognized. Among children in industrialized countries, infections have been thought to be rare up to the age of 5 y, although a recent study (E Normann et al, *Chlamydia pneumoniae* in children with acute respiratory tract infections, *Acta Paediatrica*, 1998, Vol 87, Iss 1, pp 23-27) has reported that many children in this age group show PCR evidence of infection despite being seronegative, and estimates a prevalence of 17-19% in 2-4 y olds. In developing countries, the seroprevalence of *C. pneumoniae* antibodies among young children is elevated, and there are suspicions that *C. pneumoniae* may be an important cause of acute lower respiratory

tract disease and mortality for infants and children in tropical regions of the world.

From seroprevalence studies and studies of local epidemics, the initial *C. pneumoniae* infection usually happens
5 between the ages of 5 and 20 y. In the USA, for example, there are estimated to be 30,000 cases of childhood pneumonia each year caused by *C. pneumoniae*. Infections may cluster among groups of children or young adults (e.g., school pupils or military conscripts).

10 *C. pneumoniae* causes 10 to 25% of community-acquired lower respiratory tract infections (as reported from Sweden, Italy, Finland, and the USA). During an epidemic, *C. pneumoniae* infection may account for 50 to 60% of the cases of pneumonia. During these periods, also, more episodes of mixed infections
15 with *S. pneumoniae* have been reported.

Reinfection during adulthood is common; the clinical presentation tends to be milder. Based on population seroprevalence studies, there tends to be increased exposure with age, which is particularly evident among men. Some
20 investigators have speculated that a persistent, asymptomatic *C. pneumoniae* infection state is common.

In adults of middle age or older, *C. pneumoniae* infection may progress to chronic bronchitis and sinusitis. A study in the USA revealed that the incidence of pneumonia
25 caused by *C. pneumoniae* in persons younger than 60 years is 1 case per 1,000 persons per year; but in the elderly, the disease incidence rose three-fold. *C. pneumoniae* infection rarely leads to hospitalization, except in patients with an underlying illness.

Of considerable importance is the association of atherosclerosis and *C. pneumoniae* infection. There are several epidemiological studies showing a correlation of previous infections with *C. pneumoniae* and heart attacks, coronary artery and carotid artery disease (Saikku et al. (1988) Lancet;ii:983-986; Thom et al. (1992) JAMA 268:68-72; Linnanmaki et al. (1993), Circulation 87:1030; Saikku et al. (1992) Annals Internal Medicine 116:273-287; Melnick et al (1993) American Journal of Medicine 95:499). Moreover, the organisms has been detected in atheromas and fatty streaks of the coronary, carotid, peripheral arteries and aorta (Shor et al. (1992) South African. Medical Journal 82:158-161; Kuo et al. (1993) Journal of Infectious Diseases 167:841-849; Kuo et al. (1993) Arteriosclerosis and Thrombosis 13:1501-1504; Campbell et al (1995) Journal of Infectious Diseases 172:585; Chiu et al. Circulation, 1997. Circulation. 96:2144-2148). Viable *C. pneumoniae* has been recovered from the coronary and carotid artery (Ramirez et al (1996) Annals of Internal Medicine 125:979-982; Jackson et al. 1997. J. Infect. Dis. 176:292-295). Furthermore, it has been shown that *C. pneumoniae* can induce changes of atherosclerosis in a rabbit model (Fong et al. 1997. Journal of Clinical Microbiolology 35:48 and Laitinen et al. 1997. Infect. Immun. 65:4832-4835). Taken together, these results indicate that it is highly probable that *C. pneumoniae* can cause atherosclerosis in humans, though the epidemiological importance of chlamydial atherosclerosis remains to be demonstrated.

A number of recent studies have also indicated an association between *C. pneumoniae* infection and asthma. Infection has been linked to wheezing, asthmatic bronchitis, adult-onset asthma and acute exacerbations of asthma in adults, and small-scale studies have shown that prolonged antibiotic treatment was effective at greatly reducing the severity of the

disease in some individuals (Hahn DL, et al. Evidence for *Chlamydia pneumoniae* infection in steroid-dependent asthma. Ann Allergy Asthma Immunol. 1998 Jan; 80(1): 45-49.; Hahn DL, et al. Association of *Chlamydia pneumoniae* IgA antibodies with recently symptomatic asthma. Epidemiol Infect. 1996 Dec; 117(3): 513-517; Bjornsson E, et al. Serology of *chlamydia* in relation to asthma and bronchial hyperresponsiveness. Scand J Infect Dis. 1996; 28(1): 63-69.; Hahn DL. Treatment of *Chlamydia pneumoniae* infection in adult asthma: a before-after trial. J Fam Pract. 1995 Oct; 41(4): 345-351.; Allegra L, et al. Acute exacerbations of asthma in adults: role of *Chlamydia pneumoniae* infection. Eur Respir J. 1994 Dec; 7(12): 2165-2168.; Hahn DL, et al. Association of *Chlamydia pneumoniae* (strain TWAR) infection with wheezing, asthmatic bronchitis, and adult-onset asthma. JAMA. 1991 Jul 10; 266(2): 225-230).

In light of these results a protective vaccine against *C. pneumoniae* infection would be of considerable importance. There is not yet an effective vaccine for any human chlamydial infection. It is conceivable that an effective vaccine can be developed using physically or chemically inactivated *Chlamydiae*. However, such a vaccine does not have a high margin of safety. In general, safer vaccines are made by genetically manipulating the organism by attenuation or by recombinant means. Accordingly, a major obstacle in creating an effective and safe vaccine against human chlamydial infection has been the paucity of genetic information regarding *Chlamydia*, specifically *C. pneumoniae*.

Studies with *C. trachomatis* and *C. psittaci* indicate that safe and effective vaccine against *Chlamydia* is an attainable goal. For example, mice which have recovered from a lung infection with *C. trachomatis* are protected from infertility induced by a subsequent vaginal challenge (Pal

et al.(1996) Infection and Immunity.64:5341). Similarly, sheep immunized with inactivated *C. psittaci* were protected from subsequent chlamydial-induced abortions and stillbirths (Jones et al. (1995) Vaccine 13:715). In a mouse model, protection from chlamydial infections has been associated with Th1 immune responses, particularly CD8+ CTL response (Rottenberg et al. 1999. J. Immunol. 162:2829-2836 and Pentttila et al. 1999. Immunology. 97:490-496) and it is unlikely that similar responses will need to be induced in humans to confer protection. However, antigens able to elicit a protective immune response against *C. pneumoniae* are largely unknown. The presence of sufficiently high titres of neutralising antibody at mucosal surfaces can also exert a protective effect (Cotter et al. (1995) Infection and Immunity 63:4704).

Antigenic variation within the species *C. pneumoniae* is not well documented due to insufficient genetic information, though variation is expected to exist based on *C. trachomatis*. Serovars of *C. trachomatis* are defined on the basis of antigenic variation in the major outer membrane protein (MOMP), but published *C. pneumoniae* MOMP gene sequences show no variation between several diverse isolates of the organism (Campbell et al. Infection and Immunity (1990) 58:93; McCafferty et al Infection and Immunity (1995) 63:2387-9; Gaydos et al. Infection and Immunity.(1992) 60(12):5319-5323). The gene encoding a 76 kDa antigen has been cloned from a single strain of *C. pneumoniae* and the sequence published (Perez Melgosa et al. Infection and Immunity.(1994) 62:880). An operon encoding the 9 kDa and 60 kDa cyteine-rich outer membrane protein genes has been described (Watson et al., Nucleic Acids Res (1990) 18:5299; Watson et al., Microbiology (1995) 141:2489). Many antigens recognized by immune sera to *C. pneumoniae* are conserved across all *chlamydiae*, but 98 kDa, 76 kDa and several other proteins may be *C. pneumoniae*-specific

(Knudsen et al. Infect. Immun. 1999. 67:375-383; Perez Melgosa et al. Infection and Immunity. 1994. 62:880; Melgosa et al., FEMS Microbiol Lett 1993. 112 :199;, Campbell et al., J. Clin. Microbiol. 1990. 28 :1261; Iijima et al., J. Clin. Microbiol. 1994. 32:583). Antisera to 76kDa and 54kDa antigens have been reported to neutralize *C. pneumoniae in vitro* (Perez Melgosa et al. 1994. Infect. Immun. 62:880-886 and Wiedman-Al-Ahmad et al. 1997. Clin. Diagn. Lab. Immunol. 4:700-704). An assessment of the number and relative frequency of any *C. pneumoniae* serotypes, and the defining antigens, is not yet possible. The entire genome sequence of *C. pneumoniae* strain CWL-029 is now known (<http://chlamydia-www.berkeley.edu:4231/>) and as further sequences become available a better understanding of antigenic variation may be gained.

Many antigens recognised by immune sera to *C. pneumoniae* are conserved across all *chlamydiae*, but 98kDa, 76 kDa and 54 kDa proteins appear to be *C. pneumoniae*-specific (Campos et al. (1995) Investigation of Ophthalmology and Visual Science 36:1477; Marrie (1993) Clinical Infectious Diseases. 18:501-513; Wiedmann-Al-Ahmad M, et al. Reactions of polyclonal and neutralizing anti-p54 monoclonal antibodies with an isolated, species-specific 54-kilodalton protein of *Chlamydia pneumoniae*. Clin Diagn Lab Immunol. 1997 Nov; 4(6): 700-704).

Immunoblotting of isolates with sera from patients does show variation of blotting patterns between isolates, indicating that serotypes *C. pneumoniae* may exist (Grayston et al. (1995) Journal of Infectious Diseases 168:1231; Ramirez et al (1996) Annals of Internal Medicine 125:979-982). However, the results are potentially confounded by the infection status of the patients, since immunoblot profiles of a patient's sera change with time post-infection. An assessment of the number

and relative frequency of any serotypes, and the defining antigens, is not yet possible.

The use of DNA immunization to elicit a protective immune response in Balb/c mice against pulmonary infection with the mouse pneumonitis (MoPn) strain of *Chlamydia trachomatis* has recently been described (Zhang et al. 1997. J. Infect. Dis. 76:1035-1040 and Zhang et al. 1999. Immunology. 96:314-321).

Accordingly, a need exists for identifying and isolating polynucleotide sequences of *C. pneumoniae* for use in preventing and treating *Chlamydia* infection.

SUMMARY OF THE INVENTION

The present invention provides purified and isolated polynucleotide molecules that encode the *Chlamydia* polypeptides designated amino acid transporter (SEQ ID No: 1) which can be used in methods to prevent, treat, and diagnose *Chlamydia* infection. In one form of the invention, the polynucleotide molecules are DNA that encode the polypeptide of SEQ ID No: 2.

Another form of the invention provides polypeptides corresponding to the isolated DNA molecules. The amino acid sequence of the corresponding encoded polypeptide is shown as SEQ ID No: 2.

Those skilled in the art will readily understand that the invention, having provided the polynucleotide sequences encoding the *Chlamydia* amino acid transporter, also provides polynucleotides encoding fragments derived from such a polypeptide. Moreover, the invention is understood to provide mutants and derivatives of such polypeptides and fragments derived therefrom, which result from the addition, deletion, or substitution of non-essential amino acids as described herein. Those skilled in the art would also readily understand that the

invention, having provided the polynucleotide sequences encoding *Chlamydia* polypeptides, further provides monospecific antibodies that specifically bind to such polypeptides.

The present invention has wide application and includes expression cassettes, vectors, and cells transformed or transfected with the polynucleotides of the invention. Accordingly, the present invention further provides (i) a method for producing a polypeptide of the invention in a recombinant host system and related expression cassettes, vectors, and transformed or transfected cells; (ii) a vaccine, or a live vaccine vector such as a pox virus, *Salmonella typhimurium*, or *Vibrio cholerae* vector, containing a polynucleotide of the invention, such vaccines and vaccine vectors being useful for, e.g., preventing and treating *Chlamydia* infection, in combination with a diluent or carrier, and related pharmaceutical compositions and associated therapeutic and/or prophylactic methods; (iii) a therapeutic and/or prophylactic use of an RNA or DNA molecule of the invention, either in a naked form or formulated with a delivery vehicle, a polypeptide or combination of polypeptides, or a monospecific antibody of the invention, and related pharmaceutical compositions; (iv) a method for diagnosing the presence of *Chlamydia* in a biological sample, which can involve the use of a DNA or RNA molecule, a monospecific antibody, or a polypeptide of the invention; and (v) a method for purifying a polypeptide of the invention by antibody-based affinity chromatography.

BRIEF DESCRIPTION OF THE DRAWINGS

The present invention will be further understood from the following description with reference to the drawings, in which:

Figure 1 shows the nucleotide sequence of the amino acid transporter gene (SEQ ID No: 1) and the deduced amino acid sequence of the amino acid transporter from *Chlamydia pneumoniae* (SEQ ID No: 2).

5 Figure 2 shows the restriction enzyme analysis of the *C. pneumoniae* amino acid transporter gene.

Figure 3 shows the construction and elements of plasmid pCABk297.

10 Figure 4 illustrates protection against *C. pneumoniae* infection by pCABk297 following DNA immunization.

DETAILED DESCRIPTION OF INVENTION

An open reading frame (ORF) encoding the Chlamydial amino acid transporter has been identified from the *C. pneumoniae* genome. The gene encoding this protein has been
15 inserted into an expression plasmid and shown to confer immune protection against chlamydial infection. Accordingly, this amino acid transporter and related polypeptides can be used to prevent and treat *Chlamydia* infection.

According to a first aspect of the invention,
20 isolated polynucleotides are provided which encode *Chlamydia* polypeptides, whose amino acid sequences are shown in SEQ ID No: 2.

The term "isolated polynucleotide" is defined as a polynucleotide removed from the environment in which it
25 naturally occurs. For example, a naturally-occurring DNA molecule present in the genome of a living bacteria or as part of a gene bank is not isolated, but the same molecule separated from the remaining part of the bacterial genome, as a result of, e.g., a cloning event (amplification), is isolated.

Typically, an isolated DNA molecule is free from DNA regions (e.g., coding regions) with which it is immediately contiguous at the 5' or 3' end, in the naturally occurring genome. Such isolated polynucleotides may be part of a vector or a
5 composition and still be defined as isolated in that such a vector or composition is not part of the natural environment of such polynucleotide.

The polynucleotide of the invention is either RNA or DNA (cDNA, genomic DNA, or synthetic DNA), or modifications,
10 variants, homologs or fragments thereof. The DNA is either double-stranded or single-stranded, and, if single-stranded, is either the coding strand or the non-coding (anti-sense) strand. Any one of the sequences that encode the polypeptides of the invention as shown in SEQ ID No: 1 is (a) a coding sequence,
15 (b) a ribonucleotide sequence derived from transcription of (a), or (c) a coding sequence which uses the redundancy or degeneracy of the genetic code to encode the same polypeptides. By "polypeptide" or "protein" is meant any chain of amino acids, regardless of length or post-translational modification
20 (e.g., glycosylation or phosphorylation). Both terms are used interchangeably in the present application.

Consistent with the first aspect of the invention, amino acid sequences are provided which are homologous to SEQ ID No: 2. As used herein, "homologous amino acid sequence" is
25 any polypeptide which is encoded, in whole or in part, by a nucleic acid sequence which hybridizes at 25-35°C below critical melting temperature (T_m), to any portion of the nucleic acid sequence of SEQ ID No: 1. A homologous amino acid sequence is one that differs from an amino acid sequence shown in SEQ ID
30 No: 2 by one or more conservative amino acid substitutions. Such a sequence also encompass serotypic variants (defined below) as well as sequences containing deletions or insertions

which retain inherent characteristics of the polypeptide such as immunogenicity. Preferably, such a sequence is at least 75%, more preferably 80%, and most preferably 90% identical to SEQ ID No: 2.

5 Homologous amino acid sequences include sequences that are identical or substantially identical to SEQ ID No: 2. By "amino acid sequence substantially identical" is meant a sequence that is at least 90%, preferably 95%, more preferably 97%, and most preferably 99% identical to an amino acid
10 sequence of reference and that preferably differs from the sequence of reference by a majority of conservative amino acid substitutions.

Conservative amino acid substitutions are substitutions among amino acids of the same class. These
15 classes include, for example, amino acids having uncharged polar side chains, such as asparagine, glutamine, serine, threonine, and tyrosine; amino acids having basic side chains, such as lysine, arginine, and histidine; amino acids having acidic side chains, such as aspartic acid and glutamic acid;
20 and amino acids having nonpolar side chains, such as glycine, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan, and cysteine.

Homology is measured using sequence analysis software such as Sequence Analysis Software Package of the Genetics
25 Computer Group, University of Wisconsin Biotechnology Center, 1710 University Avenue, Madison, WI 53705. Amino acid sequences are aligned to maximize identity. Gaps may be artificially introduced into the sequence to attain proper alignment. Once the optimal alignment has been set up, the
30 degree of homology is established by recording all of the

positions in which the amino acids of both sequences are identical, relative to the total number of positions.

Homologous polynucleotide sequences are defined in a similar way. Preferably, a homologous sequence is one that is
5 at least 45%, more preferably 60%, and most preferably 85% identical to the coding sequence of SEQ ID No: 1.

Consistent with the first aspect of the invention, polypeptides having a sequence homologous to SEQ ID No: 2 include naturally-occurring allelic variants, as well as
10 mutants or any other non-naturally occurring variants that retain the inherent characteristics of the polypeptide of SEQ ID No: 2.

As is known in the art, an allelic variant is an alternate form of a polypeptide that is characterized as having
15 a substitution, deletion, or addition of one or more amino acids that does not alter the biological function of the polypeptide. By "biological function" is meant the function of the polypeptide in the cells in which it naturally occurs, even if the function is not necessary for the growth or survival of
20 the cells. For example, the biological function of a porin is to allow the entry into cells of compounds present in the extracellular medium. Biological function is distinct from antigenic property. A polypeptide can have more than one biological function.

25 Allelic variants are very common in nature. For example, a bacterial species such as *C. pneumoniae*, is usually represented by a variety of strains that differ from each other by minor allelic variations. Indeed, a polypeptide that fulfills the same biological function in different strains can
30 have an amino acid sequence (and polynucleotide sequence) that is not identical in each of the strains. Despite this

variation, an immune response directed generally against many allelic variants has been demonstrated. In studies of the *Chlamydial* MOMP antigen, cross-strain antibody binding plus neutralization of infectivity occurs despite amino acid sequence variation of MOMP from strain to strain, indicating that the MOMP, when used as an immunogen, is tolerant of amino acid variations.

Polynucleotides encoding homologous polypeptides or allelic variants are retrieved by polymerase chain reaction (PCR) amplification of genomic bacterial DNA extracted by conventional methods. This involves the use of synthetic oligonucleotide primers matching upstream and downstream of the 5' and 3' ends of the encoding domain. Suitable primers are designed according to the nucleotide sequence information provided in SEQ ID No:1. The procedure is as follows: a primer is selected which consists of 10 to 40, preferably 15 to 25 nucleotides. It is advantageous to select primers containing C and G nucleotides in a proportion sufficient to ensure efficient hybridization; i.e., an amount of C and G nucleotides of at least 40%, preferably 50% of the total nucleotide content. A standard PCR reaction contains typically 0.5 to 5 Units of Taq DNA polymerase per 100 μ L, 20 to 200 μ M deoxynucleotide each, preferably at equivalent concentrations, 0.5 to 2.5 mM magnesium over the total deoxynucleotide concentration, 10^5 to 10^6 target molecules, and about 20 pmol of each primer. About 25 to 50 PCR cycles are performed, with an annealing temperature 15°C to 5°C below the true T_m of the primers. A more stringent annealing temperature improves discrimination against incorrectly annealed primers and reduces incorporation of incorrect nucleotides at the 3' end of primers. A denaturation temperature of 95°C to 97°C is typical, although higher temperatures may be appropriate for dematuration of G+C-

rich targets. The number of cycles performed depends on the starting concentration of target molecules, though typically more than 40 cycles is not recommended as non-specific background products tend to accumulate.

5 An alternative method for retrieving polynucleotides encoding homologous polypeptides or allelic variants is by hybridization screening of a DNA or RNA library. Hybridization procedures are well-known in the art and are described in Ausubel *et al.*, (Ausubel *et al.*, Current Protocols in Molecular
10 Biology, John Wiley & Sons Inc., 1994), Silhavy *et al.* (Silhavy *et al.* Experiments with Gene Fusions, Cold Spring Harbor Laboratory Press, 1984), and Davis *et al.* (Davis *et al.* A Manual for Genetic Engineering: Advanced Bacterial Genetics, Cold Spring Harbor Laboratory Press, 1980)). Important
15 parameters for optimizing hybridization conditions are reflected in a formula used to obtain the critical melting temperature above which two complementary DNA strands separate from each other (Casey & Davidson, Nucl. Acid Res. (1977) 4:1539). For polynucleotides of about 600 nucleotides or
20 larger, this formula is as follows: $T_m = 81.5 + 0.41 \times (\% \text{ G+C}) + 16.6 \log (\text{cation ion concentration}) - 0.63 \times (\% \text{ formamide}) - 600/\text{base number}$. Under appropriate stringency conditions, hybridization temperature (T_h) is approximately 20 to 40°C, 20 to 25°C, or, preferably 30 to 40°C below the calculated T_m .
25 Those skilled in the art will understand that optimal temperature and salt conditions can be readily determined.

For the polynucleotides of the invention, stringent conditions are achieved for both pre-hybridizing and hybridizing incubations (i) within 4-16 hours at 42°C, in 6 x
30 SSC containing 50% formamide, or (ii) within 4-16 hours at 65°C in an aqueous 6 x SSC solution (1 M NaCl, 0.1 M sodium citrate (pH 7.0)). Typically, hybridization experiments are performed

at a temperature from 60 to 68°C, e.g. 65°C. At such a temperature, stringent hybridization conditions can be achieved in 6xSSC, preferably in 2xSSC or 1xSSC, more preferably in 0.5xSSC, 0.3xSSC or 0.1xSSC (in the absence of formamide).

5 1xSSC contains 0.15 M NaCl and 0.015 M sodium citrate.

Useful homologs and fragments thereof that do not occur naturally are designed using known methods for identifying regions of an antigen that are likely to tolerate amino acid sequence changes and/or deletions. As an example, 10 homologous polypeptides from different species are compared; conserved sequences are identified. The more divergent sequences are the most likely to tolerate sequence changes. Homology among sequences may be analyzed using, as an example, the BLAST homology searching algorithm of Altschul et al., 15 Nucleic Acids Res.; 25:3389-3402 (1997). Alternatively, sequences are modified such that they become more reactive to T- and/or B-cells, based on computer-assisted analysis of probable T- or B-cell epitopes. Yet another alternative is to mutate a particular amino acid residue or sequence within the 20 polypeptide *in vitro*, then screen the mutant polypeptides for their ability to prevent or treat *Chlamydia* infection according to the method outlined below.

A person skilled in the art will readily understand that by following the screening process of this invention, it 25 will be determined without undue experimentation whether a particular homolog of SEQ ID No. 2 may be useful in the prevention or treatment of *Chlamydia* infection. The screening procedure comprises the steps:

(i) immunizing an animal, preferably mouse, 30 with the test homolog or fragment;

(ii) inoculating the immunized animal with *Chlamydia*; and

(iii) selecting those homologs or fragments which confer protection against *Chlamydia*.

5 By "conferring protection" is meant that there is a reduction in severity of any of the effects of *Chlamydia* infection, in comparison with a control animal which was not immunized with the test homolog or fragment.

Consistent with the first aspect of the invention,
10 polypeptide derivatives are provided that are partial sequences of SEQ ID No. 2, partial sequences of polypeptide sequences homologous to SEQ ID No. 2, polypeptides derived from full-length polypeptides by internal deletion, and fusion proteins.

It is an accepted practice in the field of immunology
15 to use fragments and variants of protein immunogens as vaccines, as all that is required to induce an immune response to a protein is a small (e.g., 8 to 10 amino acid) immunogenic region of the protein. Various short synthetic peptides corresponding to surface-exposed antigens of pathogens other
20 than *Chlamydia* have been shown to be effective vaccine antigens against their respective pathogens, e.g. an 11-residue peptide of murine mammary tumor virus (Casey & Davidson, Nucl. Acid Res. (1977) 4:1539), a 16-residue peptide of Semliki Forest virus (Snijders et al., 1991. J. Gen. Virol. 72:557-565), and
25 two overlapping peptides of 15 residues each from canine parvovirus (Langeveld et al., Vaccine 12(15):1473-1480, 1994).

Accordingly, it will be readily apparent to one skilled in the art, having read the present description, that partial sequences of SEQ ID No: 2 or their homologous amino
30 acid sequences are inherent to the full-length sequences and

are taught by the present invention. Such polypeptide fragments preferably are at least 12 amino acids in length. Advantageously, they are at least 20 amino acids, preferably at least 50 amino acids, more preferably at least 75 amino acids, and most preferably at least 100 amino acids in length.

Polynucleotides of 30 to 600 nucleotides encoding partial sequences of sequences homologous to SEQ ID No: 2 are retrieved by PCR amplification using the parameters outlined above and using primers matching the sequences upstream and downstream of the 5' and 3' ends of the fragment to be amplified. The template polynucleotide for such amplification is either the full length polynucleotide homologous to SEQ ID No: 1, or a polynucleotide contained in a mixture of polynucleotides such as a DNA or RNA library. As an alternative method for retrieving the partial sequences, screening hybridization is carried out under conditions described above and using the formula for calculating T_m . Where fragments of 30 to 600 nucleotides are to be retrieved, the calculated T_m is corrected by subtracting $(600/\text{polynucleotide size in base pairs})$ and the stringency conditions are defined by a hybridization temperature that is 5 to 10°C below T_m . Where oligonucleotides shorter than 20-30 bases are to be obtained, the formula for calculating the T_m is as follows: $T_m = 4 \times (G+C) + 2 (A+T)$. For example, an 18 nucleotide fragment of 50% G+C would have an approximate T_m of 54°C. Short peptides that are fragments of SEQ ID No: 2 or its homologous sequences, are obtained directly by chemical synthesis (E. Gross and H. J. Meinhofer, 4 The Peptides: Analysis, Synthesis, Biology; Modern Techniques of Peptide Synthesis, John Wiley & Sons (1981), and M. Bodanzki, Principles of Peptide Synthesis, Springer -Verlag (1984)).

Useful polypeptide derivatives, e.g., polypeptide fragments, are designed using computer-assisted analysis of amino acid sequences. This would identify probable surface-exposed, antigenic regions (Hughes et al., 1992. *Infect. Immun.* 5 60(9):3497). Analysis of 6 amino acid sequences contained in SEQ ID No: 2, based on the product of flexibility and hydrophobicity propensities using the program SEQSEE (Wishart DS, et al. "SEQSEE: a comprehensive program suite for protein sequence analysis." *Comput Appl Biosci.* 1994 Apr;10(2):121-32), 10 can reveal potential B- and T-cell epitopes which may be used as a basis for selecting useful immunogenic fragments and variants. This analysis uses a reasonable combination of external surface features that is likely to be recognized by antibodies. Probable T-cell epitopes for HLA-A0201 MHC 15 subclass may be revealed by an algorithms that emulate an approach developed at the NIH (Parker KC, et al. "Peptide binding to MHC class I molecules: implications for antigenic peptide prediction." *Immunol Res* 1995;14(1):34-57).

Epitopes which induce a protective T cell-dependent 20 immune response are present throughout the length of the polypeptide. However, some epitopes may be masked by secondary and tertiary structures of the polypeptide. To reveal such masked epitopes large internal deletions are created which remove much of the original protein structure and exposes the 25 masked epitopes. Such internal deletions sometimes effect the additional advantage of removing immunodominant regions of high variability among strains.

Polynucleotides encoding polypeptide fragments and polypeptides having large internal deletions are constructed 30 using standard methods (Ausubel et al., *Current Protocols in Molecular Biology*, John Wiley & Sons Inc., 1994). Such methods include standard PCR, inverse PCR, restriction enzyme treatment

of cloned DNA molecules, or the method of Kunkel *et al.*
(Kunkel *et al.* Proc. Natl. Acad. Sci. USA (1985) 82:448).
Components for these methods and instructions for their use are
readily available from various commercial sources such as
5 Stratagene. Once the deletion mutants have been constructed,
they are tested for their ability to prevent or treat *Chlamydia*
infection as described above.

As used herein, a fusion polypeptide is one that
contains a polypeptide or a polypeptide derivative of the
10 invention fused at the N- or C-terminal end to any other
polypeptide (hereinafter referred to as a peptide tail). A
simple way to obtain such a fusion polypeptide is by
translation of an in-frame fusion of the polynucleotide
sequences, *i.e.*, a hybrid gene. The hybrid gene encoding the
15 fusion polypeptide is inserted into an expression vector which
is used to transform or transfect a host cell. Alternatively,
the polynucleotide sequence encoding the polypeptide or
polypeptide derivative is inserted into an expression vector in
which the polynucleotide encoding the peptide tail is already
20 present. Such vectors and instructions for their use are
commercially available, *e.g.* the pMal-c2 or pMal-p2 system from
New England Biolabs, in which the peptide tail is a maltose
binding protein, the glutathione-S-transferase system of
Pharmacia, or the His-Tag system available from Novagen. These
25 and other expression systems provide convenient means for
further purification of polypeptides and derivatives of the
invention.

An advantageous example of a fusion polypeptide is
one where the polypeptide or homolog or fragment of the
30 invention is fused to a polypeptide having adjuvant activity,
such as subunit B of either cholera toxin or *E. coli* heat-
labile toxin. Another advantageous fusion is one where the

polypeptide, homolog or fragment is fused to a strong T-cell epitope or B-cell epitope. Such an epitope may be one known in the art (e.g. the Hepatitis B virus core antigen, D.R. Millich *et al.*, "Antibody production to the nucleocapsid and envelope of the Hepatitis B virus primed by a single synthetic T cell site", *Nature*. 1987. 329:547-549), or one which has been identified in another polypeptide of the invention based on computer-assisted analysis of probable T- or B-cell epitopes. Consistent with this aspect of the invention is a fusion polypeptide comprising T- or B-cell epitopes from SEQ ID No: 2 or its homolog or fragment, wherein the epitopes are derived from multiple variants of said polypeptide or homolog or fragment, each variant differing from another in the location and sequence of its epitope within the polypeptide. Such a fusion is effective in the prevention and treatment of *Chlamydia* infection since it optimizes the T- and B-cell response to the overall polypeptide, homolog or fragment.

To effect fusion, the polypeptide of the invention is fused to the N-, or preferably, to the C-terminal end of the polypeptide having adjuvant activity or T- or B-cell epitope. Alternatively, a polypeptide fragment of the invention is inserted internally within the amino acid sequence of the polypeptide having adjuvant activity. The T- or B-cell epitope may also be inserted internally within the amino acid sequence of the polypeptide of the invention.

Consistent with the first aspect, the polynucleotides of the invention also encode hybrid precursor polypeptides containing heterologous signal peptides, which mature into polypeptides of the invention. By "heterologous signal peptide" is meant a signal peptide that is not found in naturally-occurring precursors of polypeptides of the invention.

Polynucleotide molecules according to the invention, including RNA, DNA, or modifications or combinations thereof, have various applications. A DNA molecule is used, for example, (i) in a process for producing the encoded polypeptide in a recombinant host system, (ii) in the construction of vaccine vectors such as poxviruses, which are further used in methods and compositions for preventing and/or treating *Chlamydia* infection, (iii) as a vaccine agent (as well as an RNA molecule), in a naked form or formulated with a delivery vehicle and, (iv) in the construction of attenuated *Chlamydia* strains that can over-express a polynucleotide of the invention or express it in a non-toxic, mutated form.

Accordingly, a second aspect of the invention encompasses (i) an expression cassette containing a DNA molecule of the invention placed under the control of the elements required for expression, in particular under the control of an appropriate promoter; (ii) an expression vector containing an expression cassette of the invention; (iii) a procaryotic or eucaryotic cell transformed or transfected with an expression cassette and/or vector of the invention, as well as (iv) a process for producing a polypeptide or polypeptide derivative encoded by a polynucleotide of the invention, which involves culturing a procaryotic or eucaryotic cell transformed or transfected with an expression cassette and/or vector of the invention, under conditions that allow expression of the DNA molecule of the invention and, recovering the encoded polypeptide or polypeptide derivative from the cell culture.

A recombinant expression system is selected from procaryotic and eucaryotic hosts. Eucaryotic hosts include yeast cells (e.g., *Saccharomyces cerevisiae* or *Pichia pastoris*), mammalian cells (e.g., COS1, NIH3T3, or JEG3 cells), arthropods cells (e.g., *Spodoptera frugiperda* (SF9) cells), and

plant cells. A preferred expression system is a procaryotic host such as *E. coli*. Bacterial and eucaryotic cells are available from a number of different sources including commercial sources to those skilled in the art, e.g., the
5 American Type Culture Collection (ATCC; Rockville, Maryland). Commercial sources of cells used for recombinant protein expression also provide instructions for usage of the cells.

The choice of the expression system depends on the features desired for the expressed polypeptide. For example,
10 it may be useful to produce a polypeptide of the invention in a particular lipidated form or any other form.

One skilled in the art would readily understand that not all vectors and expression control sequences and hosts would be expected to express equally well the polynucleotides
15 of this invention. With the guidelines described below, however, a selection of vectors, expression control sequences and hosts may be made without undue experimentation and without departing from the scope of this invention.

In selecting a vector, the host must be chosen that
20 is compatible with the vector which is to exist and possibly replicate in it. Considerations are made with respect to the vector copy number, the ability to control the copy number, expression of other proteins such as antibiotic resistance. In selecting an expression control sequence, a number of variables
25 are considered. Among the important variable are the relative strength of the sequence (e.g. the ability to drive expression under various conditions), the ability to control the sequence's function, compatibility between the polynucleotide to be expressed and the control sequence (e.g. secondary
30 structures are considered to avoid hairpin structures which prevent efficient transcription). In selecting the host,

unicellular hosts are selected which are compatible with the selected vector, tolerant of any possible toxic effects of the expressed product, able to secrete the expressed product efficiently if such is desired, to be able to express the product in the desired conformation, to be easily scaled up, and to which ease of purification of the final product.

The choice of the expression cassette depends on the host system selected as well as the features desired for the expressed polypeptide. Typically, an expression cassette includes a promoter that is functional in the selected host system and can be constitutive or inducible; a ribosome binding site; a start codon (ATG) if necessary; a region encoding a signal peptide, e.g., a lipidation signal peptide; a DNA molecule of the invention; a stop codon; and optionally a 3' terminal region (translation and/or transcription terminator). The signal peptide encoding region is adjacent to the polynucleotide of the invention and placed in proper reading frame. The signal peptide-encoding region is homologous or heterologous to the DNA molecule encoding the mature polypeptide and is compatible with the secretion apparatus of the host used for expression. The open reading frame constituted by the DNA molecule of the invention, solely or together with the signal peptide, is placed under the control of the promoter so that transcription and translation occur in the host system. Promoters and signal peptide encoding regions are widely known and available to those skilled in the art and include, for example, the promoter of *Salmonella typhimurium* (and derivatives) that is inducible by arabinose (promoter araB) and is functional in Gram-negative bacteria such as *E. coli* (as described in U.S. Patent No. 5,028,530 and in Cagnon et al., (Cagnon et al., Protein Engineering (1991) 4(7):843)); the promoter of the gene of bacteriophage T7 encoding RNA polymerase, that is functional in a number of *E. coli* strains

expressing T7 polymerase (described in U.S. Patent No. 4,952,496); OspA lipidation signal peptide ; and RlpB lipidation signal peptide (Takase et al., J. Bact. (1987) 169:5692).

5 The expression cassette is typically part of an expression vector, which is selected for its ability to replicate in the chosen expression system. Expression vectors (e.g., plasmids or viral vectors) can be chosen, for example, from those described in Pouwels et al. (Cloning Vectors: A
10 Laboratory Manual 1985, Supp. 1987). Suitable expression vectors can be purchased from various commercial sources.

 Methods for transforming/transfecting host cells with expression vectors are well-known in the art and depend on the host system selected as described in Ausubel et al., (Ausubel
15 et al., Current Protocols in Molecular Biology, John Wiley & Sons Inc., 1994).

 Upon expression, a recombinant polypeptide of the invention (or a polypeptide derivative) is produced and remains in the intracellular compartment, is secreted/excreted in the
20 extracellular medium or in the periplasmic space, or is embedded in the cellular membrane. The polypeptide is recovered in a substantially purified form from the cell extract or from the supernatant after centrifugation of the recombinant cell culture. Typically, the recombinant
25 polypeptide is purified by antibody-based affinity purification or by other well-known methods that can be readily adapted by a person skilled in the art, such as fusion of the polynucleotide encoding the polypeptide or its derivative to a small affinity binding domain. Antibodies useful for purifying by
30 immunoaffinity the polypeptides of the invention are obtained as described below.

A polynucleotide of the invention can also be useful as a vaccine. There are two major routes, either using a viral or bacterial host as gene delivery vehicle (live vaccine vector) or administering the gene in a free form, e.g.,
5 inserted into a plasmid. Therapeutic or prophylactic efficacy of a polynucleotide of the invention is evaluated as described below.

Accordingly, a third aspect of the invention provides (i) a vaccine vector such as a poxvirus, containing a DNA
10 molecule of the invention, placed under the control of elements required for expression; (ii) a composition of matter comprising a vaccine vector of the invention, together with a diluent or carrier; specifically (iii) a pharmaceutical composition containing a therapeutically or prophylactically
15 effective amount of a vaccine vector of the invention; (iv) a method for inducing an immune response against *Chlamydia* in a mammal (e.g., a human; alternatively, the method can be used in veterinary applications for treating or preventing *Chlamydia* infection of animals, e.g., cats or birds), which involves
20 administering to the mammal an immunogenically effective amount of a vaccine vector of the invention to elicit a protective or therapeutic immune response to *Chlamydia* ; and particularly, (v) a method for preventing and/or treating a *Chlamydia* (e.g., *C. trachomatis*, *C. psittaci*, *C. pneumonia*, *C. pecorum*)
25 infection, which involves administering a prophylactic or therapeutic amount of a vaccine vector of the invention to an infected individual. Additionally, the third aspect of the invention encompasses the use of a vaccine vector of the invention in the preparation of a medicament for preventing
30 and/or treating *Chlamydia* infection.

As used herein, a vaccine vector expresses one or several polypeptides or derivatives of the invention. The

vaccine vector may express additionally a cytokine, such as interleukin-2 (IL-2) or interleukin-12 (IL-12), that enhances the immune response (adjuvant effect). It is understood that each of the components to be expressed is placed under the control of elements required for expression in a mammalian cell.

Consistent with the third aspect of the invention is a composition comprising several vaccine vectors, each of them capable of expressing a polypeptide or derivative of the invention. A composition may also comprise a vaccine vector capable of expressing an additional *Chlamydia* antigen, or a subunit, fragment, homolog, mutant, or derivative thereof; optionally together with or a cytokine such as IL-2 or IL-12.

Vaccination methods for treating or preventing infection in a mammal comprises use of a vaccine vector of the invention to be administered by any conventional route, particularly to a mucosal (e.g., ocular, intranasal, oral, gastric, pulmonary, intestinal, rectal, vaginal, or urinary tract) surface or via the parenteral (e.g., subcutaneous, intradermal, intramuscular, intravenous, or intraperitoneal) route. Preferred routes depend upon the choice of the vaccine vector. Treatment may be effected in a single dose or repeated at intervals. The appropriate dosage depends on various parameters understood by skilled artisans such as the vaccine vector itself, the route of administration or the condition of the mammal to be vaccinated (weight, age and the like).

Live vaccine vectors available in the art include viral vectors such as adenoviruses and poxviruses as well as bacterial vectors, e.g., *Shigella*, *Salmonella*, *Vibrio cholerae*, *Lactobacillus*, Bacille bilié de Calmette-Guérin (BCG), and *Streptococcus*.

An example of an adenovirus vector, as well as a method for constructing an adenovirus vector capable of expressing a DNA molecule of the invention, are described in U.S. Patent No. 4,920,209. Poxvirus vectors include vaccinia and canary pox virus, described in U.S. Patent No. 4,722,848 and U.S. Patent No. 5,364,773, respectively. (Also see, e.g., Tartaglia et al., Virology (1992) 188:217) for a description of a vaccinia virus vector and Taylor et al, Vaccine (1995) 13:539 for a reference of a canary pox.) Poxvirus vectors capable of expressing a polynucleotide of the invention are obtained by homologous recombination as described in Kieny et al., Nature (1984) 312:163 so that the polynucleotide of the invention is inserted in the viral genome under appropriate conditions for expression in mammalian cells. Generally, the dose of vaccine viral vector, for therapeutic or prophylactic use, can be of from about 1×10^4 to about 1×10^{11} , advantageously from about 1×10^7 to about 1×10^{10} , preferably of from about 1×10^7 to about 1×10^9 plaque-forming units per kilogram. Preferably, viral vectors are administered parenterally; for example, in 3 doses, 4 weeks apart. It is preferable to avoid adding a chemical adjuvant to a composition containing a viral vector of the invention and thereby minimizing the immune response to the viral vector itself.

Non-toxicogenic *Vibrio cholerae* mutant strains that are useful as a live oral vaccine are known. Mekalanos et al., Nature (1983) 306:551 and U.S. Patent No. 4,882,278 describe strains which have a substantial amount of the coding sequence of each of the two *ctxA* alleles deleted so that no functional *cholerae* toxin is produced. WO 92/11354 describes a strain in which the *irgA* locus is inactivated by mutation; this mutation can be combined in a single strain with *ctxA* mutations. WO 94/01533 describes a deletion mutant lacking functional *ctxA* and *attRS1* DNA sequences. These mutant strains are genetically

engineered to express heterologous antigens, as described in WO 94/19482. An effective vaccine dose of a *Vibrio cholerae* strain capable of expressing a polypeptide or polypeptide derivative encoded by a DNA molecule of the invention contains
5 about 1×10^5 to about 1×10^9 , preferably about 1×10^6 to about 1×10^8 , viable bacteria in a volume appropriate for the selected route of administration. Preferred routes of administration include all mucosal routes; most preferably, these vectors are administered intranasally or orally.

10 Attenuated *Salmonella typhimurium* strains, genetically engineered for recombinant expression of heterologous antigens or not, and their use as oral vaccines are described in Nakayama et al. (Bio/Technology (1988) 6:693) and WO 92/11361. Preferred routes of administration include
15 all mucosal routes; most preferably, these vectors are administered intranasally or orally.

Other bacterial strains used as vaccine vectors in the context of the present invention are described for *Shigella flexneri* in High et al., EMBO (1992) 11:1991 and Sizemore et
20 al., Science (1995) 270:299; for *Streptococcus gordonii* in Medaglini et al., Proc. Natl. Acad. Sci. USA (1995) 92:6868; and for Bacille Calmette Guerin in Flynn J.L., Cell. Mol. Biol. (1994) 40 (suppl. I):31, WO 88/06626, WO 90/00594, WO 91/13157, WO 92/01796, and WO 92/21376.

25 In bacterial vectors, the polynucleotide of the invention is inserted into the bacterial genome or remains in a free state as part of a plasmid.

The composition comprising a vaccine bacterial vector of the present invention may further contain an adjuvant. A
30 number of adjuvants are known to those skilled in the art. Preferred adjuvants are selected as provided below.

Accordingly, a fourth aspect of the invention provides (i) a composition of matter comprising a polynucleotide of the invention, together with a diluent or carrier; (ii) a pharmaceutical composition comprising a therapeutically or prophylactically effective amount of a polynucleotide of the invention; (iii) a method for inducing an immune response against *Chlamydia* in a mammal by administration of an immunogenically effective amount of a polynucleotide of the invention to elicit a protective immune response to *Chlamydia*; and particularly, (iv) a method for preventing and/or treating a *Chlamydia* (e.g., *C. trachomatis*, *C. psittaci*, *C. pneumoniae*, or *C. pecorum*) infection, by administering a prophylactic or therapeutic amount of a polynucleotide of the invention to an infected individual. Additionally, the fourth aspect of the invention encompasses the use of a polynucleotide of the invention in the preparation of a medicament for preventing and/or treating *Chlamydia* infection. A preferred use includes the use of a DNA molecule placed under conditions for expression in a mammalian cell, especially in a plasmid that is unable to replicate in mammalian cells and to substantially integrate in a mammalian genome.

Use of the polynucleotides of the invention include their administration to a mammal as a vaccine, for therapeutic or prophylactic purposes. Such polynucleotides are used in the form of DNA as part of a plasmid that is unable to replicate in a mammalian cell and unable to integrate into the mammalian genome. Typically, such a DNA molecule is placed under the control of a promoter suitable for expression in a mammalian cell. The promoter functions either ubiquitously or tissue-specifically. Examples of non-tissue specific promoters include the early Cytomegalovirus (CMV) promoter (described in U.S. Patent No. 4,168,062) and the Rous Sarcoma Virus promoter (described in Norton & Coffin, *Molec. Cell Biol.* (1985) 5:281).

An example of a tissue-specific promoter is the desmin promoter which drives expression in muscle cells (Li et al., Gene (1989) 78:243, Li & Paulin, J. Biol. Chem. (1991) 266:6562 and Li & Paulin, J. Biol. Chem. (1993) 268:10403). Use of promoters is well-known to those skilled in the art. Useful vectors are described in numerous publications, specifically WO 94/21797 and Hartikka et al., Human Gene Therapy (1996) 7:1205.

Polynucleotides of the invention which are used as vaccines encode either a precursor or a mature form of the corresponding polypeptide. In the precursor form, the signal peptide is either homologous or heterologous. In the latter case, a eucaryotic leader sequence such as the leader sequence of the tissue-type plasminogen factor (tPA) is preferred.

As used herein, a composition of the invention contains one or several polynucleotides with optionally at least one additional polynucleotide encoding another *Chlamydia* antigen such as urease subunit A, B, or both, or a fragment, derivative, mutant, or analog thereof. The composition may also contain an additional polynucleotide encoding a cytokine, such as interleukin-2 (IL-2) or interleukin-12 (IL-12) so that the immune response is enhanced. These additional polynucleotides are placed under appropriate control for expression. Advantageously, DNA molecules of the invention and/or additional DNA molecules to be included in the same composition, are present in the same plasmid.

Standard techniques of molecular biology for preparing and purifying polynucleotides are used in the preparation of polynucleotide therapeutics of the invention. For use as a vaccine, a polynucleotide of the invention is formulated according to various methods outlined below.

One method utilizes the polynucleotide in a naked form, free of any delivery vehicles. Such a polynucleotide is simply diluted in a physiologically acceptable solution such as sterile saline or sterile buffered saline, with or without a carrier. When present, the carrier preferably is isotonic, hypotonic, or weakly hypertonic, and has a relatively low ionic strength, such as provided by a sucrose solution, e.g., a solution containing 20% sucrose.

An alternative method utilizes the polynucleotide in association with agents that assist in cellular uptake. Examples of such agents are (i) chemicals that modify cellular permeability, such as bupivacaine (see, e.g., WO 94/16737), (ii) liposomes for encapsulation of the polynucleotide, or (iii) cationic lipids or silica, gold, or tungsten microparticles which associate themselves with the polynucleotides.

Anionic and neutral liposomes are well-known in the art (see, e.g., Liposomes: A Practical Approach, RPC New Ed, IRL press (1990), for a detailed description of methods for making liposomes) and are useful for delivering a large range of products, including polynucleotides.

Cationic lipids are also known in the art and are commonly used for gene delivery. Such lipids include LipofectinTM also known as DOTMA (N-[1-(2,3-dioleyloxy)propyl]-N,N,N-trimethylammonium chloride), DOTAP (1,2-bis(oleyloxy)-3-(trimethylammonio)propane), DDAB (dimethyldioctadecylammonium bromide), DOGS (dioctadecylamidologlycyl spermine) and cholesterol derivatives such as DC-Chol (3 beta-(N-(N',N'-dimethyl aminomethane)-carbamoyl) cholesterol). A description of these cationic lipids can be found in EP 187,702, WO 90/11092, U.S. Patent No. 5,283,185, WO 91/15501,

WO 95/26356, and U.S. Patent No. 5,527,928. Cationic lipids for gene delivery are preferably used in association with a neutral lipid such as DOPE (dioleoyl phosphatidylethanolamine), as described in WO 90/11092 as an example.

5 Formulation containing cationic liposomes may optionally contain other transfection-facilitating compounds. A number of them are described in WO 93/18759, WO 93/19768, WO 94/25608, and WO 95/02397. They include spermine derivatives useful for facilitating the transport of DNA through the
10 nuclear membrane (see, for example, WO 93/18759) and membrane-permeabilizing compounds such as GALA, Gramicidine S, and cationic bile salts (see, for example, WO 93/19768).

 Gold or tungsten microparticles are used for gene delivery, as described in WO 91/00359, WO 93/17706, and Tang et
15 *al.* Nature (1992) 356:152. The microparticle-coated polynucleotide is injected via intradermal or intraepidermal routes using a needleless injection device ("gene gun"), such as those described in U.S. Patent No. 4,945,050, U.S. Patent No. 5,015,580, and WO 94/24263.

20 The amount of DNA to be used in a vaccine recipient depends, *e.g.*, on the strength of the promoter used in the DNA construct, the immunogenicity of the expressed gene product, the condition of the mammal intended for administration (*e.g.*, the weight, age, and general health of the mammal), the mode of
25 administration, and the type of formulation. In general, a therapeutically or prophylactically effective dose from about 1 µg to about 1 mg, preferably, from about 10 µg to about 800 µg and, more preferably, from about 25 µg to about 250 µg, can be administered to human adults. The administration can be
30 achieved in a single dose or repeated at intervals.

The route of administration is any conventional route used in the vaccine field. As general guidance, a polynucleotide of the invention is administered via a mucosal surface, e.g., an ocular, intranasal, pulmonary, oral, intestinal, rectal, vaginal, and urinary tract surface; or via a parenteral route, e.g., by an intravenous, subcutaneous, intraperitoneal, intradermal, intraepidermal, or intramuscular route. The choice of administration route depends on the formulation that is selected. A polynucleotide formulated in association with bupivacaine is advantageously administered into muscles. When a neutral or anionic liposome or a cationic lipid, such as DOTMA or DC-Chol, is used, the formulation can be advantageously injected via intravenous, intranasal (aerosolization), intramuscular, intradermal, and subcutaneous routes. A polynucleotide in a naked form can advantageously be administered via the intramuscular, intradermal, or subcutaneous routes.

Although not absolutely required, such a composition can also contain an adjuvant. If so, a systemic adjuvant that does not require concomitant administration in order to exhibit an adjuvant effect is preferable such as, e.g., QS21, which is described in U.S. Patent No. 5,057,546.

The sequence information provided in the present application enables the design of specific nucleotide probes and primers that are used for diagnostic purposes. Accordingly, a fifth aspect of the invention provides a nucleotide probe or primer having a sequence found in or derived by degeneracy of the genetic code from a sequence shown in SEQ ID No:1.

The term "probe" as used in the present application refers to DNA (preferably single stranded) or RNA molecules (or

modifications or combinations thereof) that hybridize under the stringent conditions, as defined above, to nucleic acid molecules having SEQ ID No:1 or to sequences homologous to SEQ ID No:1, or to its complementary or anti-sense sequence.

5 Generally, probes are significantly shorter than full-length sequences. Such probes contain from about 5 to about 100, preferably from about 10 to about 80, nucleotides. In particular, probes have sequences that are at least 75%, preferably at least 85%, more preferably 95% homologous to a

10 portion of SEQ ID No:1 or that are complementary to such sequences. Probes may contain modified bases such as inosine, methyl-5-deoxycytidine, deoxyuridine, dimethylamino-5-deoxyuridine, or diamino-2, 6-purine. Sugar or phosphate residues may also be modified or substituted. For example, a

15 deoxyribose residue may be replaced by a polyamide (Nielsen *et al.*, Science (1991) 254:1497) and phosphate residues may be replaced by ester groups such as diphosphate, alkyl, arylphosphonate and phosphorothioate esters. In addition, the 2'-hydroxyl group on ribonucleotides may be modified by

20 including such groups as alkyl groups.

Probes of the invention are used in diagnostic tests, as capture or detection probes. Such capture probes are conventionally immobilized on a solid support, directly or indirectly, by covalent means or by passive adsorption. A

25 detection probe is labelled by a detection marker selected from: radioactive isotopes, enzymes such as peroxidase, alkaline phosphatase, and enzymes able to hydrolyze a chromogenic, fluorogenic, or luminescent substrate, compounds that are chromogenic, fluorogenic, or luminescent, nucleotide

30 base analogs, and biotin.

Probes of the invention are used in any conventional hybridization technique, such as dot blot (Maniatis *et al.*,

Molecular Cloning: A Laboratory Manual (1982) Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York), Southern blot (Southern, J. Mol. Biol. (1975) 98:503), northern blot (identical to Southern blot with the exception that RNA is used as a target), or the sandwich technique (Dunn et al., Cell (1977) 12:23). The latter technique involves the use of a specific capture probe and/or a specific detection probe with nucleotide sequences that at least partially differ from each other.

10 A primer is a probe of usually about 10 to about 40 nucleotides that is used to initiate enzymatic polymerization of DNA in an amplification process (e.g., PCR), in an elongation process, or in a reverse transcription method. Primers used in diagnostic methods involving PCR are labeled by
15 methods known in the art.

As described herein, the invention also encompasses (i) a reagent comprising a probe of the invention for detecting and/or identifying the presence of *Chlamydia* in a biological material; (ii) a method for detecting and/or identifying the presence of *Chlamydia* in a biological material, in which (a) a sample is recovered or derived from the biological material, (b) DNA or RNA is extracted from the material and denatured, and (c) exposed to a probe of the invention, for example, a capture, detection probe or both, under stringent hybridization
20 conditions, such that hybridization is detected; and (iii) a method for detecting and/or identifying the presence of *Chlamydia* in a biological material, in which (a) a sample is recovered or derived from the biological material, (b) DNA is extracted therefrom, (c) the extracted DNA is primed with at least one, and preferably two, primers of the invention and
30 amplified by polymerase chain reaction, and (d) the amplified DNA fragment is produced.

It is apparent that disclosure of polynucleotide sequences of SEQ ID No:1, its homologs and partial sequences enable their corresponding amino acid sequences. Accordingly, a sixth aspect of the invention features a substantially
5 purified polypeptide or polypeptide derivative having an amino acid sequence encoded by a polynucleotide of the invention.

A "substantially purified polypeptide" as used herein is defined as a polypeptide that is separated from the environment in which it naturally occurs and/or that is free of
10 the majority of the polypeptides that are present in the environment in which it was synthesized. For example, a substantially purified polypeptide is free from cytoplasmic polypeptides. Those skilled in the art would readily understand that the polypeptides of the invention may be
15 purified from a natural source, *i.e.*, a *Chlamydia* strain, or produced by recombinant means.

Consistent with the sixth aspect of the invention are polypeptides, homologs or fragments which are modified or treated to enhance their immunogenicity in the target animal,
20 in whom the polypeptide, homolog or fragments are intended to confer protection against *Chlamydia*. Such modifications or treatments include: amino acid substitutions with an amino acid derivative such as 3-methylhistidine, 4-hydroxyproline, 5-hydroxylysine etc., modifications or deletions which are
25 carried out after preparation of the polypeptide, homolog or fragment, such as the modification of free amino, carboxyl or hydroxyl side groups of the amino acids.

Identification of homologous polypeptides or polypeptide derivatives encoded by polynucleotides of the
30 invention which have specific antigenicity is achieved by screening for cross-reactivity with an antiserum raised against

the polypeptide of reference having an amino acid sequence of SEQ ID No:1. The procedure is as follows: a monospecific hyperimmune antiserum is raised against a purified reference polypeptide, a fusion polypeptide (for example, an expression product of MBP, GST, or His-tag systems, the description and instructions for use of which are contained in Invitrogen product manuals for pcDNA3.1/Myc-His(+) A, B, and C and for the Xpress[™] System Protein Purification), or a synthetic peptide predicted to be antigenic. Where an antiserum is raised against a fusion polypeptide, two different fusion systems are employed. Specific antigenicity can be determined according to a number of methods, including Western blot (Towbin *et al.*, Proc. Natl. Acad. Sci. USA (1979) 76:4350), dot blot, and ELISA, as described below.

In a Western blot assay, the product to be screened, either as a purified preparation or a total *E. coli* extract, is submitted to SDS-Page electrophoresis as described by Laemmli (Nature (1970) 227:680). After transfer to a nitrocellulose membrane, the material is further incubated with the monospecific hyperimmune antiserum diluted in the range of dilutions from about 1:5 to about 1:5000, preferably from about 1:100 to about 1:500. Specific antigenicity is shown once a band corresponding to the product exhibits reactivity at any of the dilutions in the above range.

In an ELISA assay, the product to be screened is preferably used as the coating antigen. A purified preparation is preferred, although a whole cell extract can also be used. Briefly, about 100 µl of a preparation at about 10 µg protein/ml are distributed into wells of a 96-well polycarbonate ELISA plate. The plate is incubated for 2 hours at 37°C then overnight at 4°C. The plate is washed with phosphate buffer saline (PBS) containing 0.05% Tween 20

(PBS/Tween buffer). The wells are saturated with 250 μ l PBS containing 1% bovine serum albumin (BSA) to prevent non-specific antibody binding. After 1 hour incubation at 37°C, the plate is washed with PBS/Tween buffer. The antiserum is
5 serially diluted in PBS/Tween buffer containing 0.5% BSA. 100 μ l of dilutions are added per well. The plate is incubated for 90 minutes at 37°C, washed and evaluated according to standard procedures. For example, a goat anti-rabbit peroxidase conjugate is added to the wells when specific antibodies were
10 raised in rabbits. Incubation is carried out for 90 minutes at 37°C and the plate is washed. The reaction is developed with the appropriate substrate and the reaction is measured by colorimetry (absorbance measured spectrophotometrically). Under the above experimental conditions, a positive reaction is
15 shown by O.D. values greater than a non immune control serum.

In a dot blot assay, a purified product is preferred, although a whole cell extract can also be used. Briefly, a solution of the product at about 100 μ g/ml is serially two-fold
diluted in 50 mM Tris-HCl (pH 7.5). 100 μ l of each dilution
20 are applied to a nitrocellulose membrane 0.45 μ m set in a 96-well dot blot apparatus (Biorad). The buffer is removed by applying vacuum to the system. Wells are washed by addition of 50 mM Tris-HCl (pH 7.5) and the membrane is air-dried. The membrane is saturated in blocking buffer (50 mM Tris-HCl (pH
25 7.5) 0.15 M NaCl, 10 g/L skim milk) and incubated with an antiserum dilution from about 1:50 to about 1:5000, preferably about 1:500. The reaction is revealed according to standard procedures. For example, a goat anti-rabbit peroxidase conjugate is added to the wells when rabbit antibodies are
30 used. Incubation is carried out 90 minutes at 37°C and the blot is washed. The reaction is developed with the appropriate substrate and stopped. The reaction is measured visually by the appearance of a colored spot, e.g., by colorimetry. Under

the above experimental conditions, a positive reaction is shown once a colored spot is associated with a dilution of at least about 1:5, preferably of at least about 1:500.

Therapeutic or prophylactic efficacy of a polypeptide
5 or derivative of the invention can be evaluated as described below. A seventh aspect of the invention provides (i) a composition of matter comprising a polypeptide of the invention together with a diluent or carrier; specifically (ii) a pharmaceutical composition containing a therapeutically or
10 prophylactically effective amount of a polypeptide of the invention; (iii) a method for inducing an immune response against *Chlamydia* in a mammal, by administering to the mammal an immunogenically effective amount of a polypeptide of the invention to elicit a protective immune response to *Chlamydia*;
15 and particularly, (iv) a method for preventing and/or treating a *Chlamydia* (e.g., *C. trachomatis*, *C. psittaci*, *C. pneumoniae*, or *C. pecorum*) infection, by administering a prophylactic or therapeutic amount of a polypeptide of the invention to an infected individual. Additionally, the seventh aspect of the
20 invention encompasses the use of a polypeptide of the invention in the preparation of a medicament for preventing and/or treating *Chlamydia* infection.

As used herein, the immunogenic compositions of the invention are administered by conventional routes known the
25 vaccine field, in particular to a mucosal (e.g., ocular, intranasal, pulmonary, oral, gastric, intestinal, rectal, vaginal, or urinary tract) surface or via the parenteral (e.g., subcutaneous, intradermal, intramuscular, intravenous, or intraperitoneal) route. The choice of administration route
30 depends upon a number of parameters, such as the adjuvant associated with the polypeptide. If a mucosal adjuvant is used, the intranasal or oral route is preferred. If a lipid

formulation or an aluminum compound is used, the parenteral route is preferred with the sub-cutaneous or intramuscular route being most preferred. The choice also depends upon the nature of the vaccine agent. For example, a polypeptide of the invention fused to CTB or LTB is best administered to a mucosal surface.

As used herein, the composition of the invention contains one or several polypeptides or derivatives of the invention. The composition optionally contains at least one additional *Chlamydia* antigen, or a subunit, fragment, homolog, mutant, or derivative thereof.

For use in a composition of the invention, a polypeptide or derivative thereof is formulated into or with liposomes, preferably neutral or anionic liposomes, microspheres, ISCOMS, or virus-like-particles (VLPs) to facilitate delivery and/or enhance the immune response. These compounds are readily available to one skilled in the art; for example, see Liposomes: A Practical Approach, RCP New Ed, IRL press (1990).

Adjuvants other than liposomes and the like are also used and are known in the art. Adjuvants may protect the antigen from rapid dispersal by sequestering it in a local deposit, or they may contain substances that stimulate the host to secrete factors that are chemotactic for macrophages and other components of the immune system. An appropriate selection can conventionally be made by those skilled in the art, for example, from those described below (under the eleventh aspect of the invention).

Treatment is achieved in a single dose or repeated as necessary at intervals, as can be determined readily by one skilled in the art. For example, a priming dose is followed by

three booster doses at weekly or monthly intervals. An appropriate dose depends on various parameters including the recipient (e.g., adult or infant), the particular vaccine antigen, the route and frequency of administration, the
5 presence/absence or type of adjuvant, and the desired effect (e.g., protection and/or treatment), as can be determined by one skilled in the art. In general, a vaccine antigen of the invention is administered by a mucosal route in an amount from about 10 μ g to about 500 mg, preferably from about 1 mg to
10 about 200 mg. For the parenteral route of administration, the dose usually does not exceed about 1 mg, preferably about 100 μ g.

When used as vaccine agents, polynucleotides and polypeptides of the invention may be used sequentially as part
15 of a multistep immunization process. For example, a mammal is initially primed with a vaccine vector of the invention such as a pox virus, e.g., via the parenteral route, and then boosted twice with the polypeptide encoded by the vaccine vector, e.g., via the mucosal route. In another example, liposomes
20 associated with a polypeptide or derivative of the invention is also used for priming, with boosting being carried out mucosally using a soluble polypeptide or derivative of the invention in combination with a mucosal adjuvant (e.g., LT).

A polypeptide derivative of the invention is also
25 used in accordance with the seventh aspect as a diagnostic reagent for detecting the presence of anti-*Chlamydia* antibodies, e.g., in a blood sample. Such polypeptides are about 5 to about 80, preferably about 10 to about 50 amino acids in length. They are either labeled or unlabeled,
30 depending upon the diagnostic method. Diagnostic methods involving such a reagent are described below.

Upon expression of a DNA molecule of the invention, a polypeptide or polypeptide derivative is produced and purified using known laboratory techniques. As described above, the polypeptide or polypeptide derivative may be produced as a fusion protein containing a fused tail that facilitates purification. The fusion product is used to immunize a small mammal, e.g., a mouse or a rabbit, in order to raise antibodies against the polypeptide or polypeptide derivative (monospecific antibodies). Accordingly, an eighth aspect of the invention provides a monospecific antibody that binds to a polypeptide or polypeptide derivative of the invention.

By "monospecific antibody" is meant an antibody that is capable of reacting with a unique naturally-occurring *Chlamydia* polypeptide. An antibody of the invention is either polyclonal or monoclonal. Monospecific antibodies may be recombinant, e.g., chimeric (e.g., constituted by a variable region of murine origin associated with a human constant region), humanized (a human immunoglobulin constant backbone together with hypervariable region of animal, e.g., murine, origin), and/or single chain. Both polyclonal and monospecific antibodies may also be in the form of immunoglobulin fragments, e.g., F(ab)'₂ or Fab fragments. The antibodies of the invention are of any isotype, e.g., IgG or IgA, and polyclonal antibodies are of a single isotype or a mixture of isotypes.

Antibodies against the polypeptides, homologs or fragments of the present invention are generated by immunization of a mammal with a composition comprising said polypeptide, homolog or fragment. Such antibodies may be polyclonal or monoclonal. Methods to produce polyclonal or monoclonal antibodies are well known in the art. For a review, see "Antibodies, A Laboratory Manual, Cold Spring Harbor Laboratory, Eds. E. Harlow and D. Lane (1988), and D.E. Yelton

et al., 1981. Ann. Rev. Biochem. 50:657-680. For monoclonal antibodies, see Kohler & Milstein (1975) Nature 256:495-497.

The antibodies of the invention, which are raised to a polypeptide or polypeptide derivative of the invention, are produced and identified using standard immunological assays, e.g., Western blot analysis, dot blot assay, or ELISA (see, e.g., Coligan et al., Current Protocols in Immunology (1994) John Wiley & Sons, Inc., New York, NY). The antibodies are used in diagnostic methods to detect the presence of a *Chlamydia* antigen in a sample, such as a biological sample. The antibodies are also used in affinity chromatography for purifying a polypeptide or polypeptide derivative of the invention. As is discussed further below, such antibodies may be used in prophylactic and therapeutic passive immunization methods.

Accordingly, a ninth aspect of the invention provides (i) a reagent for detecting the presence of *Chlamydia* in a biological sample that contains an antibody, polypeptide, or polypeptide derivative of the invention; and (ii) a diagnostic method for detecting the presence of *Chlamydia* in a biological sample, by contacting the biological sample with an antibody, a polypeptide, or a polypeptide derivative of the invention, such that an immune complex is formed, and by detecting such complex to indicate the presence of *Chlamydia* in the sample or the organism from which the sample is derived.

Those skilled in the art will readily understand that the immune complex is formed between a component of the sample and the antibody, polypeptide, or polypeptide derivative, whichever is used, and that any unbound material is removed prior to detecting the complex. It is understood that a polypeptide reagent is useful for detecting the presence of

anti-*Chlamydia* antibodies in a sample, e.g., a blood sample, while an antibody of the invention is used for screening a sample, such as a gastric extract or biopsy, for the presence of *Chlamydia* polypeptides.

5 For diagnostic applications, the reagent (i.e., the antibody, polypeptide, or polypeptide derivative of the invention) is either in a free state or immobilized on a solid support, such as a tube, a bead, or any other conventional support used in the field. Immobilization is achieved using
10 direct or indirect means. Direct means include passive adsorption (non-covalent binding) or covalent binding between the support and the reagent. By "indirect means" is meant that an anti-reagent compound that interacts with a reagent is first attached to the solid support. For example, if a polypeptide
15 reagent is used, an antibody that binds to it can serve as an anti-reagent, provided that it binds to an epitope that is not involved in the recognition of antibodies in biological samples. Indirect means may also employ a ligand-receptor system, for example, where a molecule such as a vitamin is
20 grafted onto the polypeptide reagent and the corresponding receptor immobilized on the solid phase. This is illustrated by the biotin-streptavidin system. Alternatively, a peptide tail is added chemically or by genetic engineering to the reagent and the grafted or fused product immobilized by passive
25 adsorption or covalent linkage of the peptide tail.

Such diagnostic agents may be included in a kit which also comprises instructions for use. The reagent is labeled with a detection means which allows for the detection of the reagent when it is bound to its target. The detection means
30 may be a fluorescent agent such as fluorescein isocyanate or fluorescein isothiocyanate, or an enzyme such as horse radish

peroxidase or luciferase or alkaline phosphatase, or a radioactive element such as ^{125}I or ^{51}Cr .

Accordingly, a tenth aspect of the invention provides a process for purifying, from a biological sample, a polypeptide or polypeptide derivative of the invention, which involves carrying out antibody-based affinity chromatography with the biological sample, wherein the antibody is a monospecific antibody of the invention.

For use in a purification process of the invention, the antibody is either polyclonal or monospecific, and preferably is of the IgG type. Purified IgGs is prepared from an antiserum using standard methods (see, e.g., Coligan et al., Current Protocols in Immunology (1994) John Wiley & Sons, Inc., New York, NY.). Conventional chromatography supports, as well as standard methods for grafting antibodies, are described in, e.g., Antibodies: A Laboratory Manual, D. Lane, E. Harlow, Eds. (1988) and outlined below.

Briefly, a biological sample, such as an *C. pneumoniae* extract preferably in a buffer solution, is applied to a chromatography material, preferably equilibrated with the buffer used to dilute the biological sample so that the polypeptide or polypeptide derivative of the invention (i.e., the antigen) is allowed to adsorb onto the material. The chromatography material, such as a gel or a resin coupled to an antibody of the invention, is in either a batch form or a column. The unbound components are washed off and the antigen is then eluted with an appropriate elution buffer, such as a glycine buffer or a buffer containing a chaotropic agent, e.g., guanidine HCl, or high salt concentration (e.g., 3 M MgCl_2). Eluted fractions are recovered and the presence of the antigen is detected, e.g., by measuring the absorbance at 280 nm.

An eleventh aspect of the invention provides (i) a composition of matter comprising a monospecific antibody of the invention, together with a diluent or carrier; (ii) a pharmaceutical composition comprising a therapeutically or prophylactically effective amount of a monospecific antibody of the invention, and (iii) a method for treating or preventing a *Chlamydia* (e.g., *C. trachomatis*, *C. psittaci*, *C. pneumoniae* or *C. pecorum*) infection, by administering a therapeutic or prophylactic amount of a monospecific antibody of the invention to an infected individual. Additionally, the eleventh aspect of the invention encompasses the use of a monospecific antibody of the invention in the preparation of a medicament for treating or preventing *Chlamydia* infection.

The monospecific antibody is either polyclonal or monoclonal, preferably of the IgA isotype (predominantly). In passive immunization, the antibody is administered to a mucosal surface of a mammal, e.g., the gastric mucosa, e.g., orally or intragastrically, advantageously, in the presence of a bicarbonate buffer. Alternatively, systemic administration, not requiring a bicarbonate buffer, is carried out. A monospecific antibody of the invention is administered as a single active component or as a mixture with at least one monospecific antibody specific for a different *Chlamydia* polypeptide. The amount of antibody and the particular regimen used are readily determined by one skilled in the art. For example, daily administration of about 100 to 1,000 mg of antibodies over one week, or three doses per day of about 100 to 1,000 mg of antibodies over two or three days, are effective regimens for most purposes.

Therapeutic or prophylactic efficacy are evaluated using standard methods in the art, e.g., by measuring induction of a mucosal immune response or induction of protective and/or

therapeutic immunity, using, e.g., the *C. pneumoniae* mouse model. Those skilled in the art will readily recognize that the *C. pneumoniae* strain of the model may be replaced with another *Chlamydia* strain. For example, the efficacy of DNA
5 molecules and polypeptides from *C. pneumoniae* is preferably evaluated in a mouse model using *C. pneumoniae* strain. Protection is determined by comparing the degree of *Chlamydia* infection to that of a control group. Protection is shown when infection is reduced by comparison to the control group. Such
10 an evaluation is made for polynucleotides, vaccine vectors, polypeptides and derivatives thereof, as well as antibodies of the invention.

Adjuvants useful in any of the vaccine compositions described above are as follows.

15 Adjuvants for parenteral administration include aluminum compounds, such as aluminum hydroxide, aluminum phosphate, and aluminum hydroxy phosphate. The antigen is precipitated with, or adsorbed onto, the aluminum compound according to standard protocols. Other adjuvants, such as RIBI
20 (ImmunoChem, Hamilton, MT), are used in parenteral administration.

Adjuvants for mucosal administration include bacterial toxins, e.g., the cholera toxin (CT), the *E. coli* heat-labile toxin (LT), the *Clostridium difficile* toxin A and
25 the pertussis toxin (PT), or combinations, subunits, toxoids, or mutants thereof such as a purified preparation of native cholera toxin subunit B (CTB). Fragments, homologs, derivatives, and fusions to any of these toxins are also suitable, provided that they retain adjuvant activity.
30 Preferably, a mutant having reduced toxicity is used. Suitable mutants are described, e.g., in WO 95/17211 (Arg-7-Lys CT

mutant), WO 96/06627 (Arg-192-Gly LT mutant), and WO 95/34323 (Arg-9-Lys and Glu-129-Gly PT mutant). Additional LT mutants that are used in the methods and compositions of the invention include, e.g., Ser-63-Lys, Ala-69Gly, Glu-110-Asp, and Glu-112-
5 Asp mutants. Other adjuvants, such as a bacterial monophosphoryl lipid A (MPLA) of, e.g., *E. coli*, *Salmonella minnesota*, *Salmonella typhimurium*, or *Shigella flexneri*; saponins, or polylactide glycolide (PLGA) microspheres, is also be used in mucosal administration.

10 Adjuvants useful for both mucosal and parenteral administrations include polyphosphazene (WO 95/02415), DC-chol (3 b-(N-(N',N'-dimethyl aminomethane)-carbamoyl) cholesterol; U.S. Patent No. 5,283,185 and WO 96/14831) and QS-21 (WO 88/09336).

15 Any pharmaceutical composition of the invention containing a polynucleotide, a polypeptide, a polypeptide derivative, or an antibody of the invention, is manufactured in a conventional manner. In particular, it is formulated with a pharmaceutically acceptable diluent or carrier, e.g., water or
20 a saline solution such as phosphate buffer saline. In general, a diluent or carrier is selected on the basis of the mode and route of administration, and standard pharmaceutical practice. Suitable pharmaceutical carriers or diluents, as well as pharmaceutical necessities for their use in pharmaceutical
25 formulations, are described in *Remington's Pharmaceutical Sciences*, a standard reference text in this field and in the USP/NF.

 The invention also includes methods in which *Chlamydia* infection are treated by oral administration of a
30 *Chlamydia* polypeptide of the invention and a mucosal adjuvant, in combination with an antibiotic, an antacid, sucralfate, or a

combination thereof. Examples of such compounds that can be administered with the vaccine antigen and the adjuvant are antibiotics, including, e.g., macrolides, tetracyclines, and derivatives thereof (specific examples of antibiotics that can be used include azithromycin or doxycyclin or immunomodulators such as cytokines or steroids). In addition, compounds containing more than one of the above-listed components coupled together, are used. The invention also includes compositions for carrying out these methods, i.e., compositions containing a *Chlamydia* antigen (or antigens) of the invention, an adjuvant, and one or more of the above-listed compounds, in a pharmaceutically acceptable carrier or diluent.

It has recently been shown that the 60kDa cysteine rich membrane protein contains a sequence cross-reactive with the murine alpha-myosin heavy chain epitope M7A-alpha, an epitope conserved in humans (Bachmaier et al., Science (1999) 283:1335). This cross-reactivity is proposed to contribute to the development of cardiovascular disease, so it may be beneficial to remove this epitope, and any other epitopes cross-reactive with human antigens, from the protein if it is to be used as a vaccine. Accordingly, a further embodiment of the present invention includes the modification of the coding sequence, for example, by deletion or substitution of the nucleotides encoding the epitope from polynucleotides encoding the protein, as to improve the efficacy and safety of the protein as a vaccine. A similar approach may be appropriate for any protective antigen found to have unwanted homologies or cross-reactivities with human antigens.

Amounts of the above-listed compounds used in the methods and compositions of the invention are readily determined by one skilled in the art. Treatment/immunization schedules are also known and readily designed by one skilled in

the art. For example, the non-vaccine components can be administered on days 1-14, and the vaccine antigen + adjuvant can be administered on days 7, 14, 21, and 28.

EXAMPLES

5 The above disclosure generally describes the present invention. A more complete understanding can be obtained by reference to the following specific examples. These examples are described solely for purposes of illustration and are not intended to limit the scope of the invention. Changes in form
10 and substitution of equivalents are contemplated as circumstances may suggest or render expedient. Although specific terms have been employed herein, such terms are intended in a descriptive sense and not for purposes of limitation.

15 Example 1:

This example illustrates the preparation of plasmid vector pCABk297 containing the amino acid transporter gene.

The amino acid transporter gene was amplified from *Chlamydia pneumoniae* genomic DNA by polymerase chain reaction
20 (PCR) using a 5' primer:
5' ATAAGAATGCGGCCGCCACCATGCACTCCCACTCAAACCAACG 3'; SEQ ID No:3; and a 3' primer:
5' GCGCCGGATCCCCGCTCTTTTATAGATAAGCGTTTATGC 3'; SEQ ID No:4. The
5' primer contains a NotI restriction site, a ribosome binding
25 site, an initiation codon and a sequence at the 5' end of the amino acid transporter coding sequence. The 3' primer includes the sequence encoding the C-terminal sequence of the amino acid transporter and a BamHI restriction site. The stop codon was excluded and an additional nucleotide was inserted to obtain an
30 in-frame fusion with the Histidine tag.

After amplification, the PCR fragment was purified using QIAquick™ PCR purification kit (Qiagen), then digested with NotI and BamHI and cloned into the pCA-Myc-His eukaryotic expression vector describe in Example 2 (Figure 3) with
5 transcription under control of the human CMV promoter.

Example 2:

This example illustrates the preparation of the eukaryotic expression vector pCA/Myc-His.

Plasmid pcDNA3.1(-)Myc-His C (Invitrogen) was
10 restricted with SpeI and BamHI to remove the CMV promoter and the remaining vector fragment was isolated. The CMV promoter and intron A from plasmid VR-1012 (Vical) was isolated on a SpeI / BamHI fragment. The fragments were ligated together to produce plasmid pCA/Myc-His. The NotI/BamHI restricted PCR
15 fragment containing the amino acid transporter gene was ligated into the NotI and BamHI restricted plasmid pCA/Myc-His to produce plasmid pCABk297 (Figure 3).

The resulting plasmid, pCABk297, was transferred by electroporation into *E. coli* XL-1 blue (Stratagene) which was
20 grown in LB broth containing 50 µg/ml carbenicillin. The plasmid was isolated by the Endo Free Plasmid Giga Kit™ (Qiagen) large scale DNA purification system. DNA concentration was determined by absorbance at 260 nm and the plasmid was verified after gel electrophoresis and ethidium
25 bromide staining by comparison to molecular weight standards. The 5' and 3' ends of the gene were verified by sequencing using a LiCor model 4000 L DNA sequencer and IRD-800 labelled primers.

Example 3:

This example illustrates the immunization of mice to achieve protection against an intranasal challenge of *C. pneumoniae*.

5 It has been previously demonstrated (Yang et al. Infect. Immun. May 1993. 61(5):2037-40) that mice are susceptible to intranasal infection with different isolates of *C. pneumoniae*. Strain AR-39 (Grayston et al. 1990. J. Infect. Dis. 161:618-625) was used in Balb/c mice as a challenge
10 infection model to examine the capacity of *chlamydia* gene products delivered as naked DNA to elicit a protective response against a sublethal *C. pneumoniae* lung infection. Protective immunity is defined as an accelerated clearance of pulmonary infection.

15 Groups of 7 to 9 week old male Balb/c mice (8 to 10 per group) were immunized intramuscularly (i.m.) plus intranasally (i.n.) with plasmid DNA containing the coding sequence of *C.pneumoniae* amino acid transporter as described in Examples 1 and 2. Saline or the plasmid vector lacking an
20 inserted chlamydial gene was given to groups of control animals.

 For i.m. immunization, alternate left and right quadriceps were injected with 100µg of DNA in 50µl of PBS on three occasions at 0, 3 and 6 weeks. For i.n. immunization,
25 anaesthetized mice were aspirated 50µl of PBS containing 50 µg DNA on three occasions at 0, 3 and 6 weeks. At week 8, immunized mice were inoculated i.n. with 5×10^5 IFU of *C. pneumoniae*, strain AR39 in 100µl of SPG buffer to test their ability to limit the growth of a sublethal *C. pneumoniae*
30 challenge.

Lungs were taken from mice at days 9 post-challenge and immediately homogenised in SPG buffer (7.5% sucrose, 5mM glutamate, 12.5mM phosphate pH7.5). The homogenate was stored frozen at -70°C until assay. Dilutions of the homogenate were
5 assayed for the presence of infectious *chlamydia* by inoculation onto monolayers of susceptible cells. The inoculum was centrifuged onto the cells at 3000rpm for 1 hour, then the cells were incubated for three days at 35°C in the presence of 1µg/ml cycloheximide. After incubation the monolayers were
10 fixed with formalin and methanol then immunoperoxidase stained for the presence of chlamydial inclusions using convalescent sera from rabbits infected with *C.pneumoniae* and metal-enhanced DAB as a peroxidase substrate.

Figure 4 and Table 1 show that mice immunized i.n.
15 and i.m. with pCABk297 had chlamydial lung titers less than 60,000 in 4 of 6 cases at day 9 (mean 41,016) whereas the range of values for control mice sham immunized with saline was 16,1000-228,400 IFU/lung (mean 83,378) at day 9. DNA immunisation *per se* was not responsible for the observed
20 protective effect since another plasmid DNA construct, pCABk680, failed to protect, with lung titers in immunised mice (mean 60,733) similar to those obtained for saline-immunized control mice. The construct pCABk680 is identical to pCABk297 except that the nucleotide sequence encoding the amino acid
25 transporter is replaced with a *C. pneumoniae* nucleotide sequence encoding a secretion protein.

Table 1

MOUSE	BACTERIAL LOAD (INCLUSION FORMING UNITS PER LUNG) IN THE LUNGS OF BALB/C MICE IMMUNIZED WITH VARIOUS DNA IMMUNIZATION CONSTRUCTS		
	IMMUNIZING CONSTRUCT		
	Saline	pCABk680	pCABk297
	Day 9	Day 9	Day 9
1	41000	41200	55400
2	131200	44800	63800
3	136100	23300	70200
4	63000	119500	25800
5	71800	74900	1200
6	164000	60700	29700
7	60200		
8	104400		
9	33900		
10	97900		
11	40500		
12	164000		
13	63200		
14	74100		
15	16100		
16	46300		
17	26600		
18	67900		
19	228400		
20	79500		
21	40600		
22	92900		
23	74100		
24			
MEAN	83378.26	60733.33	41016.67
SD	51698.0	33736.90	26542.83
Wilcoxon p		0.404	0.0435

CLAIMS:

1. A nucleic acid molecule comprising a nucleic acid sequence which encodes a polypeptide selected from any one of:

(a) SEQ ID No: 2;

5 (b) an immunogenic fragment comprising at least 12 consecutive amino acids from a polypeptide of (a); and

(c) a polypeptide of (a) or (b) which has been modified to improve its immunogenicity, wherein said modified polypeptide is at least 75% identical in amino acid sequence to
10 the corresponding polypeptide of (a) or (b).

2. A nucleic acid molecule comprising a nucleic acid sequence selected from any one of:

(a) SEQ ID No: 1;

15 (b) a sequence which encodes a polypeptide encoded by SEQ ID No: 1;

(c) a sequence comprising at least 38 consecutive nucleotides from any one of the nucleic acid sequences of (a) and (b); and

20 (d) a sequence which encodes a polypeptide which is at least 75% identical in amino acid sequence to the polypeptides encoded by SEQ ID No: 1.

3. A nucleic acid molecule comprising a nucleic acid sequence which is anti-sense to the nucleic acid molecule of
25 claim 1.

4. A nucleic acid molecule comprising a nucleic acid sequence which encodes a fusion protein, said fusion protein comprising a polypeptide encoded by a nucleic acid molecule according to claim 1 and an additional polypeptide.
- 5 5. The nucleic acid molecule of claim 4 wherein the additional polypeptide is a heterologous signal peptide.
6. The nucleic acid molecule of claim 4 wherein the additional polypeptide has adjuvant activity.
7. A nucleic acid molecule according to any one of
10 claims 1 to 6, operatively linked to one or more expression control sequences.
8. A vaccine comprising at least one first nucleic acid according to any one of claims 1, 2, and 4 to 7 and a vaccine vector wherein each first nucleic acid is expressed as a
15 polypeptide, the vaccine optionally comprising a second nucleic acid encoding an additional polypeptide which enhances the immune response to the polypeptide expressed by said first nucleic acid.
9. The vaccine of claim 8 wherein the second nucleic
20 acid encodes an additional *Chlamydia* polypeptide.
10. A pharmaceutical composition comprising a nucleic acid according to any one of claims 1 to 7 and a pharmaceutically acceptable carrier.
11. A pharmaceutical composition comprising a vaccine
25 according to claim 8 or 9 and a pharmaceutically acceptable carrier.
12. A unicellular host transformed with the nucleic acid molecule of claim 7.

13. A nucleic acid probe of 5 to 100 nucleotides which hybridizes under stringent conditions to the nucleic acid molecule of SEQ ID No: 1, or to a homolog or complementary or anti-sense sequence of said nucleic acid molecule.

5 14. A primer of 10 to 40 nucleotides which hybridizes under stringent conditions to the nucleic acid molecules of SEQ ID No: 1, or to a homolog or complementary or anti-sense sequence of said nucleic acid molecule.

15. A polypeptide encoded by a nucleic acid sequence
10 according to any one of claims 1, 2 and 4 to 7.

16. A polypeptide comprising an amino acid sequence selected from any one of:

(a) SEQ ID No: 2;

(b) an immunogenic fragment comprising at least 12
15 consecutive amino acids from a polypeptide of (a); and

(c) a polypeptide of (a) or (b) which has been modified to improve its immunogenicity, wherein said modified polypeptide is at least 75% identical in amino acid sequence to the corresponding polypeptide of (a) or (b).

20 17. A fusion polypeptide comprising a polypeptide of claim 15 or 16 and an additional polypeptide.

18. The fusion polypeptide of claim 17 wherein the additional polypeptide is a heterologous signal peptide.

19. The fusion protein of claim 17 wherein the additional
25 polypeptide has adjuvant activity.

20. A method for producing a polypeptide of claim 15 or 16, comprising the step of culturing a unicellular host according to claim 12.

21. An antibody against the polypeptide of any one of
5 claims 15 to 19.

22. A vaccine comprising at least one first polypeptide according to any one of claims 15 to 19 and a pharmaceutically acceptable carrier, optionally comprising a second polypeptide which enhances the immune response to the first polypeptide.

10 23. The vaccine of claim 22 wherein the second polypeptide comprises an additional *Chlamydia* polypeptide.

24. A pharmaceutical composition comprising a polypeptide according to any one of claims 15 to 19 and a pharmaceutically acceptable carrier.

15 25. A pharmaceutical composition comprising a vaccine according to claim 22 or 23 and a pharmaceutically acceptable carrier.

26. A pharmaceutical composition comprising an antibody according to claim 21 and a pharmaceutically acceptable
20 carrier.

27. A method for preventing or treating *Chlamydia* infection using:

(a) the nucleic acid of any one of claims 1 to 7;

(b) the vaccine of any one of claims 8, 9, 22
25 and 23;

(c) the pharmaceutical composition of any one of claims 10, 11, 24 to 26;

(d) the polypeptide of any one of claims 15 to 19;

or

(e) the antibody of claim 21.

28. A method of detecting *Chlamydia* infection comprising
5 the step of assaying a body fluid of a mammal to be tested,
with a component selected from any one of:

(a) the nucleic acid of any one of claims 1 to 7;

(b) the polypeptide of any one of claims 15 to 19;

and

10 (c) the antibody of claim 21.

29. A diagnostic kit comprising instructions for use and
a component selected from any one of:

(a) the nucleic acid of any one of claims 1 to 7;

(b) the polypeptide of any one of claims 15 to 19;

15 and

(c) the antibody of claim 21.

30. A method for identifying a polypeptide of claims 15
to 19 which induces an immune response effective to prevent or
lessen the severity of *Chlamydia* infection in a mammal
20 previously immunized with polypeptide, comprising the steps of:

(a) immunizing a mouse with the polypeptide; and

(b) inoculating the immunized mouse with *Chlamydia*;

wherein the polypeptide which prevents or lessens the
severity of *Chlamydia* infection in the immunized mouse compared
25 to a non-immunized control mouse is identified.

31. Expression plasmid pCABk297.
32. A nucleic acid molecule of SEQ ID NO. 3 or 4.
33. An amino acid transporter from *Chlamydia*.
34. An amino acid transporter from *Chlamydia pneumoniae*.

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Figure 1 (Continued)

gtt agt ttg gct ctc ttt tgg att ttt tct ggc aat ccc att gct att	643
Val Ser Leu Ala Leu Phe Trp Ile Phe Ser Gly Asn Pro Ile Ala Ile	
170 175 180	
tct ctt tct tgg gga aat ctt ctt cct aat ttc agt aac gta tct tca	691
Ser Leu Ser Trp Gly Asn Leu Leu Pro Asn Phe Ser Asn Val Ser Ser	
185 190 195	
ctt gta cta cta gct gga atg tta ctt gcg tta tgt ggt cta gag gct	739
Leu Val Leu Leu Ala Gly Met Leu Leu Ala Leu Cys Gly Leu Glu Ala	
200 205 210	
aat gcg aac ctt gct tct gat atg gta aat cct aga aaa aat tat cca	787
Asn Ala Asn Leu Ala Ser Asp Met Val Asn Pro Arg Lys Asn Tyr Pro	
215 220 225	
aag gca gtc ttc att ggt gca ata gca aca ctc act att tta gtt ctg	835
Lys Ala Val Phe Ile Gly Ala Ile Ala Thr Leu Thr Ile Leu Val Leu	
230 235 240 245	
ggt tct tta tcc ata gca ata gtg att ccg aaa gaa gaa att agt tta	883
Gly Ser Leu Ser Ile Ala Ile Val Ile Pro Lys Glu Glu Ile Ser Leu	
250 255 260	
gtc tct gga cta gta aaa acg ttt acc ttg ttc ttt gat aaa tat aac	931
Val Ser Gly Leu Val Lys Thr Phe Thr Leu Phe Phe Asp Lys Tyr Asn	
265 270 275	
ctc tcc tgg atg act gga atc gtt gta gtc atg acc att gca gga tcg	979
Leu Ser Trp Met Thr Gly Ile Val Val Val Met Thr Ile Ala Gly Ser	
280 285 290	
cta ggc gaa ctt aat gct tgg atg ttt gca gga aca aag ggg ctt ttt	1027
Leu Gly Glu Leu Asn Ala Trp Met Phe Ala Gly Thr Lys Gly Leu Phe	
295 300 305	
att tcc act cag aat gac tgt ctt ccc cga ctc ttt aag aaa gta aat	1075
Ile Ser Thr Gln Asn Asp Cys Leu Pro Arg Leu Phe Lys Lys Val Asn	
310 315 320 325	
agc aaa aat gtt cca acg aac tta atg tta ttc caa ggt att gtt gtg	1123
Ser Lys Asn Val Pro Thr Asn Leu Met Leu Phe Gln Gly Ile Val Val	
330 335 340	
aca ata ttc aca ctt tta ttt cta tgc ctt gat tca gca gac ctg gtg	1171
Thr Ile Phe Thr Leu Leu Phe Leu Cys Leu Asp Ser Ala Asp Leu Val	
345 350 355	
tat tgg att tta act gca ctg agc gtg cag atg tat ctt gcg atg tac	1219
Tyr Trp Ile Leu Thr Ala Leu Ser Val Gln Met Tyr Leu Ala Met Tyr	
360 365 370	

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Figure 1 (Continued)

atc tgt ctg ttt ctt gca gga ccg atc tta cgt atc aaa gaa cca agg	1267
Ile Cys Leu Phe Leu Ala Gly Pro Ile Leu Arg Ile Lys Glu Pro Arg	
375 380 385	
gct caa cgc ctc tat tct gta cca gga aag ttt ttg gga atc tgt acg	1315
Ala Gln Arg Leu Tyr Ser Val Pro Gly Lys Phe Leu Gly Ile Cys Thr	
390 395 400 405	
atg tct atc tta gga att ctc tcc tgt gcg ttt gct ctt tgg gtg agc	1363
Met Ser Ile Leu Gly Ile Leu Ser Cys Ala Phe Ala Leu Trp Val Ser	
410 415 420	
ttc ctg cct cct aga gaa ctt gct cag ata tct gaa ggc agc aaa ata	1411
Phe Leu Pro Pro Arg Glu Leu Ala Gln Ile Ser Glu Gly Ser Lys Ile	
425 430 435	
gga tat act aca ttc ctg ctt tta gca ttt agc ttg aat tgc tta att	1459
Gly Tyr Thr Thr Phe Leu Leu Leu Ala Phe Ser Leu Asn Cys Leu Ile	
440 445 450	
cct ttc gga atc tat ttc acg cat aaa cgc tta tct aaa aag agc	1504
Pro Phe Gly Ile Tyr Phe Thr His Lys Arg Leu Ser Lys Lys Ser	
455 460 465	
taatctaaaa gcatttttgg gaaaagaaaa gaaagaagcc ttccttggtg tatggcagcc	1564
tggaaagctt ctggattcaa atttgctctc ctgcaaaaag ttt	1607

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Figure 2. Restriction enzyme analysis of the *C. pneumoniae* amino acid transporter

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Figure 2 (Continued)

```

                                MwoI
                                BsaAI |
                                MaeIII |
                                PmlI |
                                Tsp45I |
                                Bsp1286I |
                                BseMII ||
                                MnlI | MaeII |
                                ApoI | BmgI || HgaI HinfI
                                Tsp509I | BseSI || BfaI | TfiI SfaNI
                                | | | | | | |
TCAGGGAATTTATATTTGGGCACGTGACGCTCTAGGCAAATGGTGGGGATTCTTTGCTAT
301 -----+-----+-----+-----+-----+-----+-----+ 360
AGTCCCTTAAATATAAACCCGTGCACTGCGAGATCCGTTTACCACCCCTAAGAAACGATA

                                HaeIV
                                Hin4I
                                FokI BtrI | AluI
                                BsrDI | MaeII | CviJI
                                CjeI | NlaIII | CjeI |
                                CviRI | BceFI | MwoI |
                                | | | | | BciVI | MwoI
                                | | | | |
ATGGATGCAATGGTTTCACAACATGACGTGGTATCCTGCCGTGTTAGCTTTTATAGCGAG
361 -----+-----+-----+-----+-----+-----+-----+ 420
TACCTACGTTACCAAAGTGTTGTACTGCACCATAGGACGGCACAATCGAAAATATCGCTC

                                Sau3AI
                                TaaI |
                                AlwI | |
                                CviRI | | |
                                CjePI | | |
                                BsrDI || | |
                                RsaI || | |
                                BsrGI || | |
                                TatI || | |
RsaI PsiI Hpy178III
| | |
TACCATTGTTTATAAAATCAATCCAGAACTCGCTCACAACAAAGTGTTACATTGCAACCGT
421 -----+-----+-----+-----+-----+-----+-----+ 480
ATGGTAACAAATATTTTAGTTAGGTCTTGAGCGAGTGTTGTTTCACATGTAACGTTGGCA

                                XmnI
                                Tsp509I MboII |
                                DpnI BciVI CjePI MseI | Tsp509I | AciI
                                | | | | | | |
GATCCTTGCTGGTTTTTGGATACTTACATTTTTTAATTTTTTAGGAATTACTTCTCCGC
481 -----+-----+-----+-----+-----+-----+-----+ 540
CTAGGAACGACCAAAAACCTATGAATGTAAAAAATTAATAATCTTAATGAAGAAGGCG

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Figure 2 (Continued)

```

                                HinfI
                                ScrFI |
                                EcoRII | |
                                Tsp509I | | |
                                AhoI | | | |
                                MseI | | | |
                                VspI | | | |
                                AluI | | | | |
                                CviJI | | | | |
                                AceIII | | | | |
                                CjePI | | | | |
                                PleI | | | | |
                                DdeI | | | | |
ATTATTTCAGCTCTATTTGTGTAATCATAGGAACATTAATTCCAGGAGTCATCTTAGTTAG
541 -----+-----+-----+-----+-----+-----+-----+ 600
TAATAAGTCGAGATAAACACATTAGTATCCTTGTAATTAAGGTCCTCAGTAGAATCAATC

                                CjePI
                                CjePI |
                                CviJI | |
                                BsrDI | CjePI |
                                MboII |
                                TTTGGCTCTCTTTTGGATTTTTTCTGGCAATCCCATTTGCTATTTCTCTTTCTTGGGGAAA
601 -----+-----+-----+-----+-----+-----+-----+ 660
AAACCGAGAGAAAACCTAAAAAAGACCGTTAGGGTAACGATAAAGAGAAAGAACCCCTTT

                                MaeII
                                MboII |
                                Tsp509I MaeIII | |
                                RsaI | CviJI
                                TatI | BfaI | MaeIII
                                TCTTCTTCCTAATTTTCAGTAACGTATCTTCACTTGTACTACTAGCTGGAATGTTACTTGC
661 -----+-----+-----+-----+-----+-----+-----+ 720
AGAAGAAGGATTAAAGTCATTGCATAGAAGTGAACATGATGATCGACCTTACAATGAACG

                                Hpy178III
                                BfaI |
                                XbaI | |
                                MnlI | | | CviJI
                                MwoI | |
                                Tsp509I
                                Bsp24I |
                                CjePI |
                                BfaI CjeI | |
                                GTTATGTGGTCTAGAGGCTAATGCGAACCTTGCTTCTGATATGGTAAATCCTAGAAAAA
721 -----+-----+-----+-----+-----+-----+-----+ 780
CAATACACCAGATCTCCGATTACGCTTGGAACGAAGACTATAACATTTAGGATCTTTTTT

                                CjeI
                                CjePI
                                BbsI
                                Bsp24I |
                                MboII | CviRI | BsbI
                                TTATCCAAAGGCAGTCTTCATTGGTGCAATAGCAACACTCACTATTTTAGTTCTGGGTTC
781 -----+-----+-----+-----+-----+-----+-----+ 840
AATAGGTTTCCGTCAGAAGTAACCACGTTATCGTTGTGAGTGATAAAATCAAGACCCAAG

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Figure 2 (Continued)

```

                                     BfaI
                                     SpeI
                                     BspGI ||
                                     BsmAI ||
Hpy188IX
HinfI |
TfiI | Tsp509I MboII || ||
| | |
TTTATCCATAGCAATAGTGATTCCGAAAGAAGAAATTAGTTTAGTCTCTGGACTAGTAAA
841 -----+-----+-----+-----+-----+ 900
AAATAGGTATCGTTATCACTAAGGCTTCTCTTAATCAAATCAGAGACCTGATCATTT

                                     CjeI
                                     FokI |
                                     BsrI ||
AclI
MaeII
|
CjeI
|
ScrFI
|
EcoRII |MnlI
| | |
HinfI ||
TfiI ||
RcaI
|
AACGTTTACCTTGTTCTTTGATAAATATAACCTCTCCTGGATGACTGGAATCGTTGTAGT
901 -----+-----+-----+-----+-----+ 960
TTGCAAATGGAACAAGAACTATTTATATTGGAGAGGACCTACTGACCTTAGCAACATCA

DpnI
BsrDI BcgI |Tth111II
NlaIII | Sau3AI | AlwI |Tth111II
Hpy178III | |CviRI | |BfaI | |MseI | BcgI
| | | | | | | | |
CviRI |FokI
| |
CATGACCATTGCAGGATCGCTAGGCGAACTTAATGCTTGGATGTTTGCAGGAACAAAGGG
961 -----+-----+-----+-----+-----+ 1020
GTACTGGTAACGTCCTAGCGATCCGCTTGAATTACGAACCTACAAACGTCCTTGTTTCCC

BbsI
MboII
PleI
MseI
Hpy188IX | BseMII| Sth132I |
CviJI DdeI | | TaaI || HinfI | |
| | | | |
GCTTTTTTATTTCCACTCAGAATGACTGTCTTCCCCGACTCTTTAAGAAAGTAAATAGCAA
1021 -----+-----+-----+-----+-----+ 1080
CGAAAAATAAAGGTGAGTCTTACTGACAGAAGGGGCTGAGAAATCTTTTCATTTATCGTT

MmeI
BsaJI | MaeIII
MseI StyI | Tsp45I SspI
| |
AAATGTTCCAACGAACCTTAATGTTATTCCAAGGTATTGTTGTGACAATATTCACACTTTT
1081 -----+-----+-----+-----+-----+ 1140
TTTACAAGGTTGCTTGAATTACAATAAGGTTCCATAACAACACTGTTATAAGTGTGAAAA

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Figure 2 (Continued)

```

                                CviRI
                                Cac8I |
                                TspRI ||
                                ScrFI
                                HinfI   EcoRII |   BseMII   DdeI   |||
                                TfiI     SexAI |BsgI   MseI   CviRI |   |||
                                |         |||         |         |   |||
1141  ATTTCTATGCCTTGATTGAGCAGACCTGGTGTATTGGATTTTAACTGCACTGAGCGTGCA
-----+-----+-----+-----+-----+-----+-----+ 1200
TAAAGATACGGAACATAAGTCGTCTGGACCACATAACCTAAAATTGACGTGACTCGCACGT

                                BsaBI
                                BsgI
                                RsaI
                                BsrGI |
                                TatI |
                                | |
                                DpnI
                                Sau3AI |
                                AvaII   ||| BsaAI
                                Sau96I   ||| SnaBI
                                CviRI   | | MaeII|TaqII
                                | |   | | | |
1201  GATGTATCTTGCGATGTACATCTGTCTGTTTCTTGCAGGACCGATCTTACGTATCAAAGA
-----+-----+-----+-----+-----+-----+ 1260
CTACATAGAACGCTACATGTAGACAGACAAAGAACGTCTGGCTAGAATGCATAGTTTCT

                                BanII
                                Bsp1286I
                                BsaJI   |
                                StyI     |
                                DrdII| CviJI |
                                ||   ||
                                ScrFI
                                EcoRII |
                                RsaI|| |
                                MnlI||| |
                                CjePI ||| |
                                ||   ||| |
1261  ACCAAGGGCTCAACGCCTCTATTCTGTACCAGGAAAGTTTTTGGGAATCTGTACGATGTC
-----+-----+-----+-----+-----+-----+ 1320
TGGTTCCCGAGTTGCGGAGATAAGACATGGTCCTTTCAAAAACCCCTTAGACATGCTACAG

                                ApoI
                                EcoRI
                                Tsp509I
                                DdeI   |
                                |   |
                                TaqII   |
                                |   |
                                AluI
                                CviJI   |
                                HphI   BfaI   MnlI
                                |   |   |   |
1321  TATCTTAGGAATTCTCTCCTGTGCGTTTGTCTTTGGGTGAGCTTCCTGCCTCCTAGAGA
-----+-----+-----+-----+-----+-----+ 1380
ATAGAATCCTTAAGAGAGGACACGCAAACGAGAAACCCACTCGAAGGACGGAGGATCTCT

                                Fnu4HI
                                TseI|
                                BseMII||
                                Hpy188IX   |||
                                EcoRV   |   |||
                                Hpy188IX   | |   |||
                                DdeI   | |   |||
                                | |   | |   |||
                                Eco57I
                                BbvI   |
                                |   |
1381  ACTTGCTCAGATATCTGAAGGCAGCAAATAGGATATACTACATTCTGCTTTTAGCATT
-----+-----+-----+-----+-----+-----+ 1440
TGAACGAGTCTATAGACTTCGTCGTTTTATCCTATATGATGTAAGGACGAAAATCGTAA

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Figure 2 (Continued)

```

                Tsp509I
                MwoI      |
      Tsp509I |      |      HinfI
      AluI    | |      |      TfiI
      CviJI    | | MseI | Hpy188IX |
                | |      | |      |
      TAGCTTGAATTGCTTAATTCCTTTTCGGAATCTATTTACGCATAAACGCTTATCTAAAAA
1441 -----+-----+-----+-----+-----+-----+ 1500
      ATCGAACTTAACGAATTAAGGAAAGCCTTAGATAAAGTGCGTATTTGCGAATAGATTTTT

                                Fnu4HI
                                TseI|
      AluI                      CviJI          CjePI||
      CviJI                      |              |||
                |
      GAGCTAATCTAAAAGCATTTTTGGGAAAAGAAAAGAAAGAGCCTTCCTTGTTGTATGGC
1501 -----+-----+-----+-----+-----+-----+ 1560
      CTCGATTAGATTTTCGTAAAAACCCTTTTCTTTCTTCTTCGGAAGGAACAACATACCG

                                ApoI
                                Tsp509I
                                HinfI      |
                                TfiI      |
                                Hpy178III |
                                AluI      | |
                                BbvI      | |
                                CviJI      | |
                                HindIII   | |
                                ScrFI      | |
      CviJI |      | |      | |      |
      EcoRII |MwoI| |      | |      | CjePI CviRI
                | |      | |      |      |
      AGCCTGGAAAGCTTCTGGATTCAAATTTGCTCTCCTGCAAAAAGTTT
1561 -----+-----+-----+-----+-----+ 1607
      TCGGACCTTTTCGAAGACCTAAGTTTAAACGAGAGGACGTTTTTCAAA

```

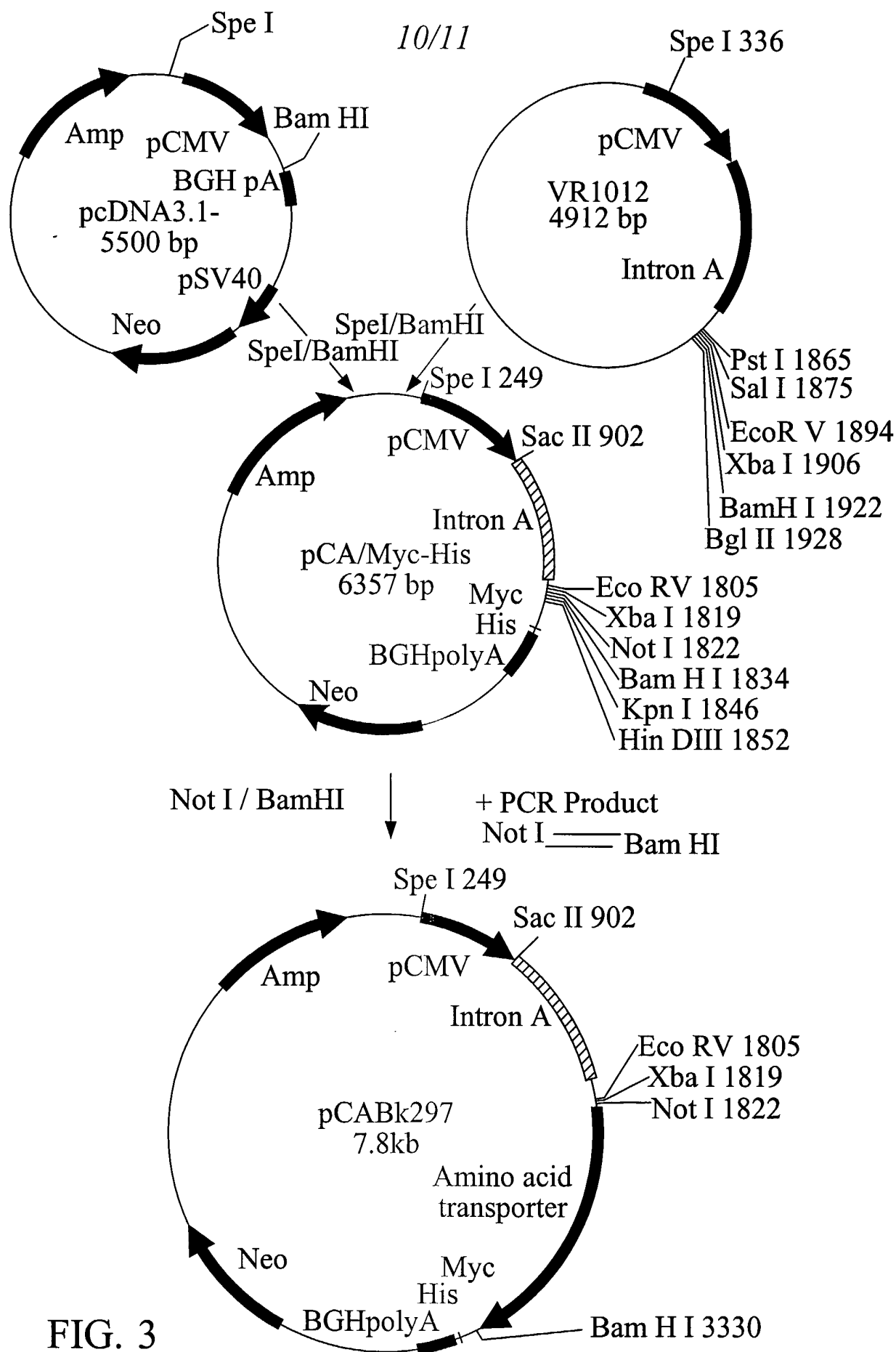
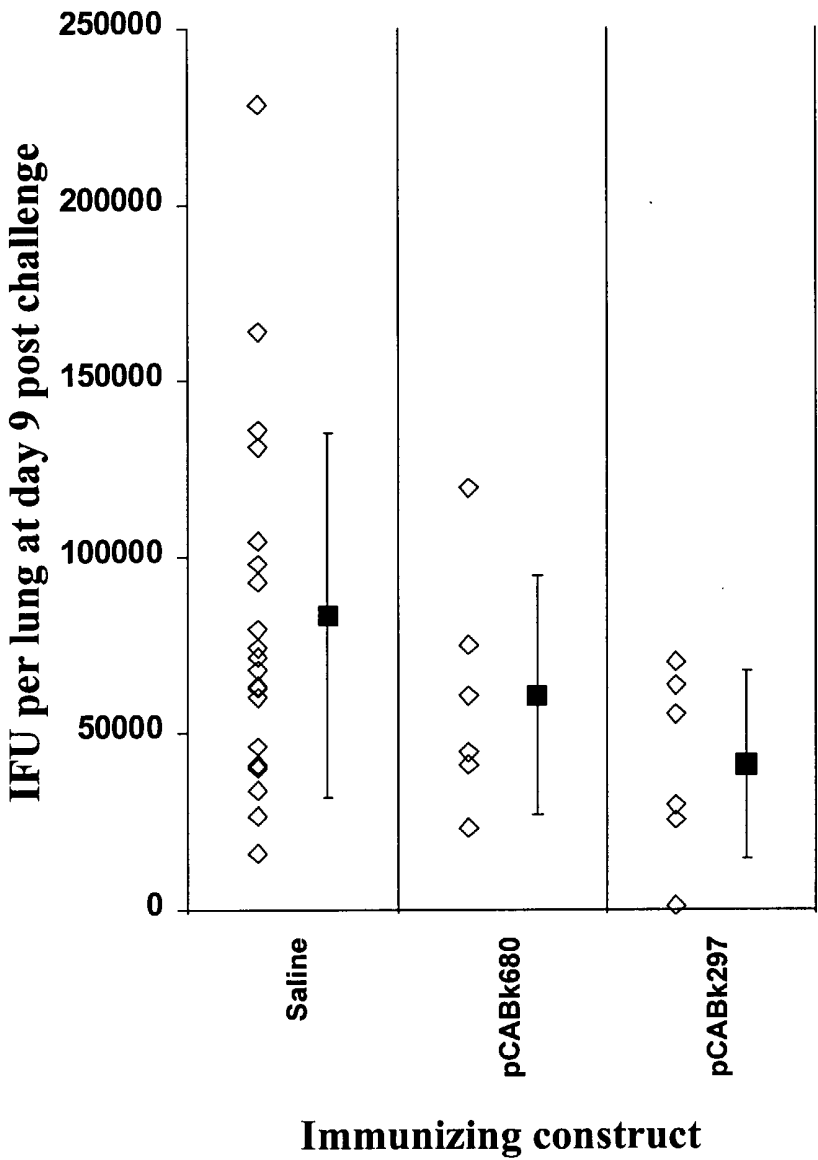


FIG. 3
Construction of pCABk297

Figure 4 Protective efficacy of DNA Immunisation with pCABk297



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SEQUENCE LISTING

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Met His Ser His Ser
1 5

aaa cca acg aaa ccg ttg gga aca ttc acg gtc ggc atg tta tca ctt 163
Lys Pro Thr Lys Pro Leu Gly Thr Phe Thr Val Gly Met Leu Ser Leu
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Ala Val Val Ile Ser Leu Arg Asn Leu Pro Leu Thr Ala Lys His Gly
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ctt tcc act ctg ttt ttt tat gga cta gca gtc ata tgt ttt atg att 259
Leu Ser Thr Leu Phe Phe Tyr Gly Leu Ala Val Ile Cys Phe Met Ile
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ccg tat gct ctg att tct gct gag ctt gct tct ttc aag cct cag gga 307
Pro Tyr Ala Leu Ile Ser Ala Glu Leu Ala Ser Phe Lys Pro Gln Gly
55 60 65

att tat att tgg gca cgt gac gct cta ggc aaa tgg tgg gga ttc ttt 355
Ile Tyr Ile Trp Ala Arg Asp Ala Leu Gly Lys Trp Trp Gly Phe Phe
70 75 80 85

gct ata tgg atg caa tgg ttt cac aac atg acg tgg tat cct gcc gtg 403
Ala Ile Trp Met Gln Trp Phe His Asn Met Thr Trp Tyr Pro Ala Val
90 95 100

tta gct ttt ata gcg agt acc att gtt tat aaa atc aat cca gaa ctc 451
Leu Ala Phe Ile Ala Ser Thr Ile Val Tyr Lys Ile Asn Pro Glu Leu
105 110 115

gct cac aac aaa gtg tac att gca acc gtg atc ctt gct ggt ttt tgg 499
Ala His Asn Lys Val Tyr Ile Ala Thr Val Ile Leu Ala Gly Phe Trp
120 125 130

60

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	Val Ser Leu Ala Leu Phe Trp Ile Phe Ser Gly Asn Pro Ile Ala Ile	
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	tct ctt tct tgg gga aat ctt ctt cct aat ttc agt aac gta tct tca	691
	Ser Leu Ser Trp Gly Asn Leu Leu Pro Asn Phe Ser Asn Val Ser Ser	
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	aag gca gtc ttc att ggt gca ata gca aca ctc act att tta gtt ctg	835
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	gtc tct gga cta gta aaa acg ttt acc ttg ttc ttt gat aaa tat aac	931
	Val Ser Gly Leu Val Lys Thr Phe Thr Leu Phe Phe Asp Lys Tyr Asn	
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	Leu Gly Glu Leu Asn Ala Trp Met Phe Ala Gly Thr Lys Gly Leu Phe	
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	att tcc act cag aat gac tgt ctt ccc cga ctc ttt aag aaa gta aat	1075
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	Ser Lys Asn Val Pro Thr Asn Leu Met Leu Phe Gln Gly Ile Val Val	
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	Tyr Trp Ile Leu Thr Ala Leu Ser Val Gln Met Tyr Leu Ala Met Tyr	
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gct caa cgc ctc tat tct gta cca gga aag ttt ttg gga atc tgt acg 1315
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ttc ctg cct cct aga gaa ctt gct cag ata tct gaa ggc agc aaa ata 1411
 Phe Leu Pro Pro Arg Glu Leu Ala Gln Ile Ser Glu Gly Ser Lys Ile
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 Gly Tyr Thr Thr Phe Leu Leu Leu Ala Phe Ser Leu Asn Cys Leu Ile
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cct ttc gga atc tat ttc acg cat aaa cgc tta tct aaa aag agc 1504
 Pro Phe Gly Ile Tyr Phe Thr His Lys Arg Leu Ser Lys Lys Ser
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 35 40 45

Ile Cys Phe Met Ile Pro Tyr Ala Leu Ile Ser Ala Glu Leu Ala Ser
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Phe Lys Pro Gln Gly Ile Tyr Ile Trp Ala Arg Asp Ala Leu Gly Lys
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Trp Tyr Pro Ala Val Leu Ala Phe Ile Ala Ser Thr Ile Val Tyr Lys
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Ile Asn Pro Glu Leu Ala His Asn Lys Val Tyr Ile Ala Thr Val Ile
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