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(54) **SEQUENCE GENOMIQUE ET POLYPEPTIDES DE CHLAMYDIA PNEUMONIAE, LEURS FRAGMENTS ET LEURS UTILISATIONS, EN PARTICULIER POUR LE DIAGNOSTIC, LA PREVENTION OU LE TRAITEMENT D'UNE INFECTION**

(54) **CHLAMYDIA PNEUMONIAE GENOMIC SEQUENCE AND POLYPEPTIDES, FRAGMENTS THEREOF AND USES THEREOF, IN PARTICULAR FOR THE DIAGNOSIS, PREVENTION AND TREATMENT OF INFECTION**

(57) L'objet de l'invention est la séquence génomique et les séquences nucléotidiques codant des polypeptides de Chlamydia pneumoniae, tels que des polypeptides d'enveloppe cellulaire, sécrétés ou spécifiques, ou intervenant dans le métabolisme, dans le processus de réplication ou dans la virulence, des polypeptides codés par de telles séquences, ainsi que des vecteurs incluant lesdites séquences et des cellules ou animaux manipulés au moyen desdits vecteurs. L'invention concerne des produits géniques transcriptionnels du génome de Chlamydia pneumoniae, tels que, par exemple, des molécules antisens ou ribozymatiques pouvant être utilisés pour réguler la croissance du micro-organisme. L'invention concerne aussi des procédés de détection desdits acides nucléiques ou polypeptides et des trousses permettant de diagnostiquer une infection à Chlamydia pneumoniae. L'invention concerne en outre un procédé de sélection de composés pouvant moduler une infection bactérienne, et un procédé mettant en oeuvre ces séquences nucléotidiques ou ces polypeptides pour réaliser la biosynthèse ou la biodégradation de molécules d'étude. L'invention concerne enfin des produits pharmaceutiques, en particulier des vaccins, et des compositions servant à la prévention et/ou au traitement d'infections bactériennes, notamment d'infections à Chlamydia pneumoniae.

(57) The subject of the invention is the genomic sequence and the nucleotide sequences encoding polypeptides of Chlamydia pneumoniae, such as cellular envelope polypeptides, which are secreted or specific, or which are involved in metabolism, in the replication process or in virulence, polypeptides encoded by such sequences, as well as vectors including the said sequences and cells or animals transformed with these vectors. The invention also relates to transcriptional gene products of the Chlamydia pneumoniae genome, such as, for example, antisense and ribozyme molecules, which can be used to control growth of the microorganism. The invention also relates to methods of detecting these nucleic acids or polypeptides and kits for diagnosing Chlamydia pneumoniae infection. The invention also relates to a method of selecting compounds capable of modulating bacterial infection and a method for the biosynthesis or biodegradation of molecules of interest using the said nucleotide sequences or the said polypeptides. The invention finally comprises, pharmaceutical, in particular vaccine, compositions for the prevention and/or treatment of bacterial, in particular Chlamydia pneumoniae, infections.

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(54) Title: *CHLAMYDIA PNEUMONIAE* GENOMIC SEQUENCE AND POLYPEPTIDES, FRAGMENTS THEREOF AND USES THEREOF, IN PARTICULAR FOR THE DIAGNOSIS, PREVENTION AND TREATMENT OF INFECTION

(57) Abstract

The subject of the invention is the genomic sequence and the nucleotide sequences encoding polypeptides of *Chlamydia pneumoniae*, such as cellular envelope polypeptides, which are secreted or specific, or which are involved in metabolism, in the replication process or in virulence, polypeptides encoded by such sequences, as well as vectors including the said sequences and cells or animals transformed with these vectors. The invention also relates to transcriptional gene products of the *Chlamydia pneumoniae* genome, such as, for example, antisense and ribozyme molecules, which can be used to control growth of the microorganism. The invention also relates to methods of detecting these nucleic acids or polypeptides and kits for diagnosing *Chlamydia pneumoniae* infection. The invention also relates to a method of selecting compounds capable of modulating bacterial infection and a method for the biosynthesis or biodegradation of molecules of interest using the said nucleotide sequences or the said polypeptides. The invention finally comprises, pharmaceutical, in particular vaccine, compositions for the prevention and/or treatment of bacterial, in particular *Chlamydia pneumoniae*, infections.

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CHLAMYDIA PNEUMONIAE GENOMIC SEQUENCE AND POLYPEPTIDES, FRAGMENTS THEREOF AND USES THEREOF, IN PARTICULAR FOR THE DIAGNOSIS, PREVENTION AND TREATMENT OF INFECTION

The subject of the invention is the genomic sequence and the nucleotide sequences encoding polypeptides of *Chlamydia pneumoniae*, such as cellular envelope polypeptides, which are secreted or specific, or which are involved in metabolism, in the replication process or in virulence, polypeptides encoded by such sequences, as well as vectors including the said sequences and cells or animals transformed with these vectors. The invention also relates to transcriptional gene products of the *Chlamydia pneumoniae* genome, such as, for example, antisense and ribozyme molecules, which can be used to control growth of the microorganism. The invention also relates to methods of detecting these nucleic acids or polypeptides and kits for diagnosing *Chlamydia pneumoniae* infection. The invention also relates to a method of selecting compounds capable of modulating bacterial infection and a method for the biosynthesis or biodegradation of molecules of interest using the said nucleotide sequences or the said polypeptides. The invention finally comprises, pharmaceutical, in particular vaccine, compositions for the prevention and/or treatment of bacterial, in particular *Chlamydia pneumoniae*, infections.

Comparative analysis of the sequence of the gene encoding the ribosomal 16S RNA has been widely used for the phylogenetic study of prokaryotes. This approach has made it possible to classify the Chlamydiae among the eubacteria, among which they represent a well-isolated group, with, nevertheless, a very weak link with the planctomyces. The Chlamydiae thus exhibit some unique characteristics within the eubacteria, in particular their development cycle and the structure of their membranes. They have a unique two-phase cell cycle: the elementary body, a small extracellular form, attaches to the host and is phagocytosed; in the phagosome, it is converted to the replicative intracellular form, the reticulate body. The Chlamydiae are obligate intracellular bacteria which multiply in eukaryotic cells at the expense of their energy reserves and nucleotide pools; they are responsible for a wide variety of diseases in mammals and birds. The Chlamydiae are the only members of the order Chlamydiales, of the family Chlamydiaceae and of the genus Chlamydia. Within the genus *Chlamydia*, four species are currently described: *Chlamydia trachomatis*, *Chlamydia psittaci*, *Chlamydia pneumoniae* and *Chlamydia pecorum*. These bacteria are grouped together and share biological and biochemical properties. Among them, only the first three infect humans, *Chlamydia pecorum* being a pathogen of ruminants.

The species *Chlamydia psittaci* infects many animals, in particular birds, and is transmissible to humans. It is responsible for atypical pneumonia, for hepatic and renal dysfunction, for endocarditis and for conjunctivitis.

The species *Chlamydia trachomatis* is the best characterized. Besides a murine strain, it is divided into two groups which are distinguishable by the nature of the diseases for which they are responsible: trachoma, genital attack and venereal lymphogranulomatosis. There are fifteen human serotypes of *Chlamydia trachomatis* (A, K) and LGV (L1, L2, L3). Strains A to C are mainly found in eye infections, whereas strains D to K and LGV are essentially responsible for genital entry infections. It should be mentioned that the LGV strains are responsible for systemic diseases. Historically, it was in 1906 that Halberstaeder and Von Provaseck discovered, in trachoma patients, the presence of inclusions in the cytoplasm of the cells derived from conjunctival scrapings. In 1940, Rake and Jones described these same inclusions in certain cells obtained by puncturing the ganglia from a patient suffering from venereal granulomatosis. Characterization of the *Chlamydia trachomatis* microorganism was only successfully carried out in 1957, after a series of isolations in cell cultures.

It was in 1983 that *Chlamydia pneumoniae* was recognized as a human pathogen (Grayston JT et al., 1986); since then, special attention has been paid to this bacterium and it is estimated (Gaydos CA et al., 1994) that 10% of pneumonias, and 5% of bronchitides and sinusites are attributable to *Chlamydia pneumoniae* (Aldous MB et al., 1992). More recently, the association of this bacterium with the pathogenesis of asthmatic disease and of cardiovascular impairments is increasingly of interest.

Serological studies have made it possible to observe that *Chlamydia pneumoniae* infection is common in children between 5 and 16 years of age. Before this age, it is rare to find antibodies; the increase in the number of individuals carrying antibodies is then correlated with age up to 20 years. Accordingly, 50% of adults are carriers of antibodies, it being possible for this prevalence to be as high as 75%. These figures are all the more striking since a first infection induces antibody levels of which the persistence over time is limited to 3 or at most 5 years, which suggests frequent reinfection during the entire lifespan. The annual seroconversion rate is about 8% between 8 and 12 years and about 6% between 12 and 16 years (Haidl et al., 1994). Before the age of 15 years, the seroprevalence of the disease is identical between both sexes. After this age, men are more frequently infected than women; this is true in all regions worldwide where such studies have been carried out.

These infections are geographically highly widespread, as shown by numerous studies carried out throughout the world (Kanamoto Y et al., 1991; Tong CY et al., 1993). Developed countries of the north such as Canada, Denmark and Norway have the lowest infection rates; conversely, the highest prevalence rates are found in the less developed countries of tropical regions where the infection may occur before the age of 5 years.

Humans are the only known reservoir for *Chlamydia pneumoniae* and it is probable that the infection is caused by direct transmission, respiratory secretions probably being responsible for this low-yield transmission (Aldous et al., 1992). The chain of transmission may also appear to be indirect (Kleemola M et al., 1988), suggesting that the infection is caused by an effective transmission, but also that asymptomatic carriers exist, which could explain the high prevalence of the disease.

Other studies (Mordhorst CH et al., 1992) show that the efficiency of the transmission varies according to the individuals and list cases of infection affecting all or the majority of members of one family or of a group of families. The period of incubation is several weeks, significantly longer in this regard than that of many other respiratory pathogenic agents. Although under conditions of high relative humidity the infectivity of *Chlamydia pneumoniae* in the open air decreases rapidly, suggesting a direct mode of transmission under these conditions, it is probable that the transmission occurs in some cases indirectly since the microorganism can survive for up to 30 hours in a hostile environment (Falsey et al., 1993).

Clinical manifestations due to *Chlamydia pneumoniae* are essentially respiratory diseases. Pneumonia and bronchitis are the most frequent because they are clinically patent: since etiological diagnosis is evoked in this case, the infectious agent is identified. The asymptomatic diseases are probably numerous (Grayston JT et al., 1992; Grayston JT et al., 1986; Thom DH et al., 1990). The disease then progresses via bronchitis or pneumonia; fever is absent at the time of examination but is sometimes reported by the patient. The degree of seriousness of the disease is variable and in hospitalized patients, it is common to observe pleural effusion; a generalized infection may also be observed and, in severe cases, anatomicopathological examination shows *Chlamydia pneumoniae* diseases.

Other syndromes such as sinusitis (Hashiguchi K et al., 1992), purulent otitis media (Ogawa H et al., 1992), or pharyngitis (Huovinen P et al., 1989) have been described, as well as infections with respiratory impairments similar to asthma (Hahn DL et al., 1991). *Chlamydia pneumoniae* has also been associated with sarcoidosis, with erythema nodosum (Sundelof et al., 1993) and one case of Guillain-Barré syndrome has even been described (Haidl et al., 1992). The involvement of *Chlamydia pneumoniae* in Reiter's syndrome has also been evaluated (Braun J et al., 1994).

The association of *Chlamydia pneumoniae* with coronary diseases and with myocardial infarction was first suspected from the observation of the high antibody level in 71% of patients having a heart disease (Shor A et al., 1992; Kuo CC et al., 1993; Puolakkainen M et al., 1993; Thomas GN et al., 1997). Studies carried out in several countries have shown similar results in patients with atheromatous impairments (Shor A et al., 1992; Kuo CC et al., 1993; Puolakkainen M et al., 1993; Grayston JT et al., 1996; Casas-Ciria J et al., 1996; Thomas GN et al., 1997; Jackson LA et al., 1997) and in patients with carotid impairments. Anatomicopathological and microbiological studies have detected *Chlamydia pneumoniae* in the vessels. The electron microscope has made it possible to visualize the bacterium (Ladany S et al., 1989), which has in fact been demonstrated by other techniques such as PCR (Campbell LA et al., 1992; Kuo CC et al., 1993; Kuo CC et al., 1988). It also appears that the bacterium is more frequently found in old atheromatous lesions. Other studies carried out on young subjects from 15 to 35 years have given the opportunity to study the coronary arteries of people without atherosclerosis, this observation not being possible in older subjects (the onset of the atheromatous disease is early). In these young subjects, the PCR studies did not find *Chlamydia pneumoniae* in subjects free of atheromatous disease, but revealed the presence of *Chlamydia pneumoniae* in two of the eleven subjects who showed early lesions and in six of the seven subjects who developed atheroma plaques. These studies therefore show that the atheroma plaque is very strongly correlated with the presence of *Chlamydia pneumoniae*, but the role played by the bacterium in vascular pathology is not yet defined.

The data relating to controlled clinical studies analysing the effect of treatments in *Chlamydia pneumoniae* infections are limited in number. Unlike penicillin, ampicillin or the sulphamides, erythromycin, tetracycline or doxycycline show an antibiotic activity *in vitro* against *Chlamydia pneumoniae*. However, a treatment at high doses should be continued for several weeks in order to avoid a recurrence of the infection. Accordingly, the use of two new macrolides, clarithromycin and azithromycin, whose diffusion, bioavailability and half-life allow shorter and better tolerated cures, is nowadays preferred. In the absence of definitive proof based on the results of clinical studies, an effective, without recurrences, and well-tolerated treatment of *Chlamydia pneumoniae* infections therefore remains desirable.

An even more important need up until now relates to a specific and sensitive diagnosis, which can be carried out conveniently and rapidly, allowing early screening for the infection. Methods based on *Chlamydia pneumoniae* culture are slow and require a considerable know-how because of the difficulty involved in the collection, preservation and storage of the strain under appropriate conditions. Methods based on antigen detection (EIA, DFA) or on nucleic acid amplification (PCR) provide tests which are more suitable for laboratory practice. A reliable, sensitive and convenient test, which allows distinction between serogroups and a fortiori between *Chlamydia pneumoniae* species is therefore highly desirable.

This is all the more important since the symptoms of *Chlamydia pneumoniae* infection appear slowly, since all the pathologies associated with these infections have not yet been identified, and since, as has been mentioned above, an association is suspected between these infections and serious chronic infections, asthma or atherosclerosis.

No vaccine is yet available against *Chlamydia pneumoniae*: this is due to the labile nature of the antigens specific to the strain, which has so far prevented their specific identification.

Although the number of studies and of animal models developed is high, the antigens used have not induced sufficient protective immunity to lead to the development of human vaccines. In the case of *Chlamydia pneumoniae*, the role of the immune defense in the physiology and pathology of the disease should probably be understood in order to develop satisfactory vaccines.

More detailed information relating to the biology of these strains, their interactions with their hosts, the associated phenomena of infectivity and those of escaping the immune defenses of the host in particular, and finally their involvement in the development of the these associated pathologies, will allow a better understanding of these mechanisms. In the light of the preceding text which shows in particular the limitations of the means of controlling *Chlamydia pneumoniae* infection, it is therefore at present essential, on the one hand, to develop molecular tools, in particular from a better genetic knowledge of *Chlamydia pneumoniae*, but also to develop new preventive and therapeutic treatments, new diagnostic methods and new vaccine strategies which are specific, effective and tolerated. This is precisely the object of the present invention.

The subject of the present invention is the nucleotide sequence having the sequence SEQ ID No. 1 of the *Chlamydia pneumoniae* genome. However, the invention is not limited to SEQ ID No. 1, but encompasses genomes and nucleotides encoding polypeptides of strain variants, polymorphisms, allelic variants, and mutants.

Thus, the subject of the present invention encompasses nucleotide sequences characterized in that they are chosen from:

a) the nucleotide sequence of SEQ ID No. 1, a nucleotide sequence exhibiting at least 99.9% identity with the sequence SEQ ID No. 1, the nucleotide sequence of the genomic DNA contained within ATCC Deposit No. ___, the nucleotide sequence of a clone insert within ATCC Deposit No. __;

b) a nucleotide sequence homologous to the sequence SEQ ID No. 1;

c) a polynucleotide sequence that hybridizes to the nucleotide sequence of a) under conditions of high or intermediate stringency as described below:

(i) By way of example and not limitation, procedures using conditions of high stringency are as follows: Prehybridization of filters containing DNA is carried out for 8 h to overnight at 65EC in buffer composed of 6X SSC, 50 mM Tris-HCl (pH 7.5), 1 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.02% BSA, and 500 µg/ml denatured salmon sperm DNA. Filters are hybridized for 48 h at 65EC, the preferred hybridization temperature, in prehybridization mixture containing 100 µg/ml denatured salmon sperm DNA and 5-20 X 10^6 cpm of ^{32}P-labeled probe. Alternatively, the hybridization step can be performed at 65EC in the presence of SSC buffer, 1 x SSC corresponding to 0.15M NaCl and 0.05 M Na citrate. Subsequently, filter washes can be done at 37EC for 1 h in a solution containing 2X SSC, 0.01% PVP, 0.01% Ficoll, and 0.01% BSA, followed by a wash in 0.1X SSC at 50EC for 45 min. Alternatively, filter washes can be performed in a solution containing 2 x SSC and 0.1% SDS, or 0.5 x SSC and 0.1% SDS, or 0.1 x SSC and 0.1% SDS at 68EC for 15 minute intervals. Following the wash steps, the hybridized probes are detectable by autoradiography. Other conditions of high stringency which may be used are well known in the art and as cited in Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, Second Edition, Cold Spring Harbor Press, N.Y., pp. 9.47-9.57; and Ausubel et al., 1989, Current Protocols in Molecular Biology, Green Publishing Associates and Wiley Interscience, N.Y. are incorporated herein in their entirety.

(ii) By way of example and not limitation, procedures using conditions of intermediate stringency are as follows: Filters containing DNA are prehybridized, and then hybridized at a temperature of 60EC in the presence of a 5 x SSC buffer and labeled probe. Subsequently, filters washes are performed in a solution containing 2x SSC at 50EC and the hybridized probes are detectable by autoradiography. Other conditions of intermediate stringency which may be used are well known in the art and as cited in Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, Second Edition, Cold Spring Harbor Press, N.Y., pp. 9.47-9.57; and Ausubel et al., 1989, Current Protocols in Molecular Biology, Green Publishing Associates and Wiley Interscience, N.Y. are incorporated herein in their entirety.

d) a nucleotide sequence complementary to the sequence SEQ ID No. 1 or complementary to a nucleotide sequence as defined in a), b) or c) and a nucleotide sequence of their corresponding RNA;

e) a nucleotide sequence of a representative fragment of the sequence SEQ ID No. 1, or of a representative fragment of the nucleotide sequence as defined in a), b), c) or d);

f) a nucleotide sequence comprising a sequence as defined in a), b), c), d) or e);

g) a nucleotide sequence capable of being obtained from a nucleotide sequence as defined in a), b), c), d), e) or f); and

h) a modified nucleotide sequence of a nucleotide sequence as defined in a), b), c), d), e), f) or g).

Nucleotide sequence, polynucleotide or nucleic acid are understood to mean, according to the present invention, either a double-stranded DNA, a single-stranded DNA or products of transcription of the said DNAs.

It should be understood that the present invention does not relate to the genomic nucleotide sequences of *Chlamydia pneumoniae* taken in their natural environment, that is to say in the natural state. They are sequences which may have been isolated, purified or partially purified, by separation methods such as, for example, ion-exchange chromatography, molecular size exclusion chromatography or affinity chromatography, or alternatively fractionation techniques based on solubility in various solvents, or by genetic engineering methods such as amplification, cloning or subcloning, it being possible for the sequences of the invention to be carried by vectors.

The nucleotide sequence SEQ ID No. 1 was obtained by sequencing the *Chlamydia pneumoniae* genome by the method of directed sequencing after fluorescent automated sequencing of the inserts of clones and assembling of these sequences of nucleotide fragments (inserts) by means of softwares (cf. Examples). In spite of the high precision of the sequence SEQ ID No. 1, it is possible that it does not perfectly, 100% represent the nucleotide sequence of the *Chlamydia pneumoniae* genome and that a few rare sequencing errors or uncertainties still remain in the sequence SEQ ID No. 1. In the present invention, the presence of an uncertainty for an amino acid is designated by "Xaa" and that for a nucleotide is designated by "N" in the sequence listing below. These few rare errors or uncertainties could be easily detected and corrected by persons skilled in the art using the entire chromosome and/or its representative fragments according to the invention and standard amplification, cloning and sequencing methods, it being possible for the sequences obtained to be easily compared, in particular by means of a computer software and using computer-readable media for recording the sequences according to the invention as described, for example, below. After correcting these possible rare errors or uncertainties, the corrected nucleotide sequence obtained would still exhibit at least 99.9% identity with the sequence SEQ ID No. 1. Such rare sequencing uncertainties are not present within the DNA contained within ATCC Deposit No. __ or ___, and whatever rare sequence uncertainties that exist within SEQ ID No. 1 can routinely be corrected utilizing the DNA of the ATCC deposits.

Homologous nucleotide sequence for the purposes of the present invention is understood to mean a nucleotide sequence having a percentage identity with the bases of the nucleotide sequence SEQ ID No. 1 of at least 80%, preferably 90% and 95%, this percentage being purely statistical and it being possible for the differences between the two nucleotide sequences to be distributed randomly and over their entire length. The said homologous sequences exhibiting a percentage identity with the bases of the nucleotide sequence SEQ ID No. 1 of at least 80%, preferably 90% and 95%, may comprise, for example, the sequences corresponding to the genomic sequence or to the sequences of its representative fragments of a bacterium belonging to the Chlamydia family, including the species *Chlamydia trachomatis*, *Chlamydia psittaci* and *Chlamydia pecorum* mentioned above, as well as the sequences corresponding to the genomic sequence or to the sequences of its representative fragments of a bacterium belonging to the variants of the species *Chlamydia pneumoniae*. In the present invention, the terms family and genus are mutually interchangeable, the terms variant, serotype, strain and subspecies are also mutually interchangeable. These homologous sequences may thus correspond to variations linked to mutations within the same species or between species and may correspond in particular to truncations, substitutions, deletions and/or additions of at least one nucleotide. The said homologous sequences may also correspond to variations linked to the degeneracy of the genetic code or to a bias in the genetic code which is specific to the family, to the species or to the variant and which are likely to be present in *Chlamydia*.

Protein and/or nucleic acid sequence homologies may be evaluated using any of the variety of sequence comparison algorithms and programs known in the art. Such algorithms and programs include, but are by no means limited to, TBLASTN, BLASTP, FASTA, TFASTA, and CLUSTALW (Pearson and Lipman, 1988, *Proc. Natl. Acad. Sci. USA 85(8)*:2444-2448; Altschul *et al.*, 1990, *J. Mol. Biol. 215(3)*:403-410; Thompson *et al.*, 1994, *Nucleic Acids Res. 22(2)*:4673-4680; Higgins *et al.*, 1996, *Methods Enzymol. 266*:383-402; Altschul *et al.*, 1990, *J. Mol. Biol. 215(3)*:403-410; Altschul *et al.*, 1993, *Nature Genetics 3*:266-272).

In a particularly preferred embodiment, protein and nucleic acid sequence homologies are evaluated using the Basic Local Alignment Search Tool ("BLAST") which is well known in the art (see, *e.g.*, Karlin and Altschul, 1990, *Proc. Natl. Acad. Sci. USA 87*:2267-2268; Altschul *et al.*, 1990, *J. Mol. Biol. 215*:403-410; Altschul *et al.*, 1993, *Nature Genetics 3*:266-272; Altschul *et al.*, 1997, *Nuc. Acids Res.* *25*:3389-3402). In particular, five specific BLAST programs are used to perform the following task:

(1)BLASTP and BLAST3 compare an amino acid query sequence against a protein sequence database;

(2)BLASTN compares a nucleotide query sequence against a nucleotide sequence database;

(3)BLASTX compares the six-frame conceptual translation products of a query nucleotide sequence (both strands) against a protein sequence database;

(4)TBLASTN compares a query protein sequence against a nucleotide sequence database translated in all six reading frames (both strands); and

(5)TBLASTX compares the six-frame translations of a nucleotide query sequence against the six-frame translations of a nucleotide sequence database.

The BLAST programs identify homologous sequences by identifying similar segments, which are referred to herein as "high-scoring segment pairs," between a query amino or nucleic acid sequence and a test sequence which is preferably obtained from a protein or nucleic acid sequence database. High-scoring segment pairs are preferably identified (*i.e.*, aligned) by means of a scoring matrix, many of which are known in the art. Preferably, the scoring matrix used is the BLOSUM62 matrix (Gonnet *et al.*, 1992, *Science* *256*:1443-1445; Henikoff and Henikoff, 1993, *Proteins* *17*:49-61). Less preferably, the PAM or PAM250 matrices may also be used (see, *e.g.*, Schwartz and Dayhoff, eds., 1978, *Matrices for Detecting Distance Relationships: Atlas of Protein Sequence and Structure*, Washington: National Biomedical Research Foundation)

The BLAST programs evaluate the statistical significance of all high-scoring segment pairs identified, and preferably selects those segments which satisfy a user-specified threshold of significance, such as a user-specified percent homology. Preferably, the statistical significance of a high-scoring segment pair is evaluated using the statistical significance formula of Karlin (see, *e.g.*, Karlin and Altschul, 1990, *Proc. Natl. Acad. Sci. USA* *87*:2267-2268).

Nucleotide sequence complementary to a sequence of the invention is understood to mean any DNA whose nucleotides are complementary to those of the sequence of the invention, and whose orientation is reversed (antiparallel sequence).

The present invention further comprises fragments of the sequences of a) through f), above. Representative fragments of the sequences according to the invention will be understood to mean any nucleotide fragment having at least 8 successive nucleotides, preferably at least 12 successive nucleotides, and still more preferably at least 15 or at least 20 successive nucleotides of the sequence from which it is derived. It is understood that such fragments refer only to portions of SEQ ID No. 1 that are not currently listed in a publicly available database.

Among these representative fragments, those capable of hybridizing under stringent conditions with a nucleotide sequence according to the invention are preferred. Hybridization under stringent conditions means that the temperature and ionic strength conditions are chosen such that they allow hybridization to be maintained between two complementary DNA fragments.

By way of illustration, high stringency conditions for the hybridization step for the purposes of defining the nucleotide fragments described above, are advantageously the following.

The hybridization is carried out at a preferred temperature of 65EC in the presence of SSC buffer, 1 × SSC corresponding to 0.15 M NaCl and 0.05 M Na citrate. The washing steps may be, for example, the following:

2 × SSC, 0.1% SDS at room temperature followed by three washes with 1 × SSC, 0.1% SDS; 0.5 × SSC, 0.1% SDS; 0.1 × SSC, 0.1% SDS at 68EC for 15 minutes.

Intermediate stringency conditions, using, for example, a temperature of 60EC in the presence of a 5 × SSC buffer, or of low stringency, for example a temperature of 50EC in the presence of a 5 × SSC buffer, respectively require a lower overall complementarity for the hybridization between the two sequences.

The stringent hybridization conditions described above for a polynucleotide of about 300 bases in size will be adapted by persons skilled in the art for larger- or smaller-sized oligonucleotides, according to the teaching of Sambrook et al., 1989.

Among the representative fragments according to the invention, those which can be used as primer or probe in methods which make it possible to obtain homologous sequences or their representative fragments according to the invention, or to reconstitute a genomic fragment found to be incomplete in the sequence SEQ ID No. 1 or carrying an error or an uncertainty, are also preferred, these methods, such as the polymerase chain reaction (PCR), cloning and sequencing of nucleic acid being well known to persons skilled in the art. These homologous nucleotide sequences corresponding to mutations or to inter- or intra-species variations, as well as the complete genomic sequence or one of its representative fragments capable of being reconstituted, of course form part of the invention.

Among the said representative fragments, those which can be used as primer or probe in methods allowing diagnosis of the presence of *Chlamydia pneumoniae* or one of its associated microorganisms as defined below are also preferred.

The representative fragments capable of modulating, regulating, inhibiting or inducing the expression of a gene of *Chlamydia pneumoniae* or one of its associated microorganisms, and/or capable of modulating the replication cycle of *Chlamydia pneumoniae* or one of its associated microorganisms in the host cell and/or organism, are also preferred. Replication cycle is intended to designate invasion, multiplication, intracellular localization, in particular retention in the vacuole and inhibition of the process of fusion to the lysosome, and propagation of *Chlamydia pneumoniae* or one of its associated microorganisms from host cells to host cells.

Among the said representative fragments, those corresponding to nucleotide sequences corresponding to open reading frames, called ORF sequences (ORF for open reading frame), and encoding polypeptides, such as for example, but without being limited thereto, the ORF sequences which will be later described, are finally preferred.

The representative fragments according to the invention may be obtained, for example, by specific amplification, such as PCR, or after digestion, with appropriate restriction enzymes, of nucleotide sequences according to the invention; these methods are in particular described in the manual by Sambrook et al., 1989. The said representative fragments may also be obtained by chemical synthesis when they are not too large in size and according to methods well known to persons skilled in the art. For example, such fragments can be obtained by isolating fragments of the genomic DNA of ATCC Deposit No. ___ or a clone insert present at this ATCC Deposit No. __.

The representative fragments according to the invention may be used, for example, as primer, to reconstitute some of the said representative fragments, in particular those in which a portion of the sequence is likely to be missing or imperfect, by methods well known to persons skilled in the art such as amplification, cloning or sequencing techniques.

Modified nucleotide sequence will be understood to mean any nucleotide sequence obtained by mutagenesis according to techniques well known to persons skilled in the art, and exhibiting modifications in relation to the normal sequences, for example mutations in the regulatory and/or promoter sequences for the expression of a polypeptide, in particular leading to a modification of the level of expression of the said polypeptide or to a modulation of the replicative cycle.

Modified nucleotide sequence will also be understood to mean any nucleotide sequence encoding a modified polypeptide as defined below.

The subject of the present invention also includes *Chlamydia pneumoniae* nucleotide sequences characterized in that they are chosen from a nucleotide sequence of an open reading frame (ORF), that is, the ORF2 to ORF1297 sequences.

The ORF2 to ORF1297 nucleotide sequences are defined in Tables 1 and 2, *infra*, by their position on the sequence SEQ ID No. 1. For example, the ORF2 sequence is defined by the nucleotide sequence between the nucleotides at position 42 and 794 on the sequence SEQ ID No. 1, ends included. ORF2 to ORF1297 have been identified via homology analyses as well as via analyses of potential ORF start sites, as discussed in the examples below. It is to be understood that each identified ORF of the invention comprises a nucleotide sequence that spans the contiguous nucleotide sequence from the ORF stop codon immediately 3' to the stop codon of the preceding ORF and through the 5' codon to the next stop codon of SEQ ID No.:1 in-frame to the ORF nucleotide sequence. Table 2, *infra*, lists the beginning, end and potential start site of each of ORFs 1-1297. In one embodiment, the ORF comprises the contiguous nucleotide sequence spanning from the potential ORF start site downstream (that is, 3') to the ORF stop codon (or the ORF codon immediately adjacent to and upstream of the ORF stop codon). ORF2 to ORF1297 encode the polypeptides of SEQ ID No. 2 to SEQ ID No. 1291 and of SEQ ID No. 6844 to SEQ ID No. 6849, respectively.

Upon introduction of minor frameshifts, certain individual ORFs can comprise larger "combined" ORFs. A list of such putative "combined" ORFs is shown in Table 3, below. For example, a combined ORF can comprise ORF 25, ORF 26 and ORF 27, including intervening in-frame, nucleotide sequences. The order of ORFs (5' to 3'), within each "combined" ORF is as listed. It is to be understood that when ORF2 to ORF1297 are referred to herein, such reference is also meant to include "combined" ORFs. Polypeptide sequences encoded by such "combined" ORFs are also part of the present invention.

Table 3

ORF 25, ORF 26, ORF 27;
ORF 28, ORF 29, ORF 30;
ORF 31, ORF 32;
ORF 33, ORF 35;
ORF 466, ORF 467;
ORF 468, ORF 469;
ORF 477, ORF 476, ORF 474;
ORF 480, ORF 482;
ORF 483, ORF 485, ORF 486, ORF 500;
ORF 503, ORF 504, ORF 505;
ORF 506, ORF 507;
ORF 1211, ORF 647;
ORF 1286, ORF 1039;
ORF 691, ORF 690;
ORF 105, ORF 106;
ORF 170, ORF 171;ORF 394, ORF 393;
ORF 453, ORF 452, ORF 451;
ORF 526, ORF 525;
ORF 757, ORF 756, ORF 755;
ORF 856, ORF 855;
ORF 958, ORF 957;
ORF 915, ORF 914, ORF 913;
ORF 543, ORF 544;
ORF 1266, ORF 380;
ORF 745, ORF 744;
ORF 777, ORF 776;
ORF 343, ORF 1297, and representative fragments.

Table 1 also depicts the results of homology searches that compared the sequences of the polypeptides encoded by each of the ORFs to sequences present in public published databases. It is understood that those polypeptides listed in Table 1 as exhibiting greater than about 95% identity to a polypeptide present in a publicly disclosed database are not considered part of the present invention; likewise in this embodiment, those nucleotide sequences encoding such polypeptides are not considered part of the invention. In another embodiment, it is understood that those polypeptides listed in Table 1 as exhibiting greater than about 99% identity to a polypeptide present in a publicly disclosed database are not considered part of the invention; likewise, in this embodiment, those nucleotide sequences encoding such polypeptides are not considered part of the invention.

The invention also relates to the nucleotide sequences characterized in that they comprise a nucleotide sequence chosen from:

a) an ORF2 to ORF1297, a "combined" ORF nucleotide sequence, the nucleotide sequence of the genomic DNA contained within ATCC Deposit No. _______ or the nucleotide sequence of a clone insert in ATCC Deposit No. _______ according to the invention;

b) a homologous nucleotide sequence exhibiting at least 80% identity across an entire ORF2 to ORF1297 nucleotide sequence according to the invention or as defined in a);

c) a polynucleotide sequence that hybridizes to ORF2 to ORF1297 under conditions of high or intermediate stringency as described below:

(i) By way of example and not limitation, procedures using conditions of high stringency are as follows: Prehybridization of filters containing DNA is carried out for 8 h to overnight at 65EC in buffer composed of 6X SSC, 50 mM Tris-HCl (pH 7.5), 1 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.02% BSA, and 500 μg/ml denatured salmon sperm DNA. Filters are hybridized for 48 h at 65EC, the preferred hybridization temperature, in prehybridization mixture containing 100 μg/ml denatured salmon sperm DNA and 5-20 X 10^6 cpm of ^{32}P-labeled probe. Alternatively, the hybridization step can be performed at 65EC in the presence of SSC buffer, 1 x SSC corresponding to 0.15M NaCl and 0.05 M Na citrate. Subsequently, filter washes can be done at 37EC for 1 h in a solution containing 2X SSC, 0.01% PVP, 0.01% Ficoll, and 0.01% BSA, followed by a wash in 0.1X SSC at 50EC for 45 min. Alternatively, filter washes can be performed in a solution containing 2 x SSC and 0.1% SDS, or 0.5 x SSC and 0.1% SDS, or 0.1 x SSC and 0.1% SDS at 68EC for 15 minute intervals. Following the wash steps, the hybridized probes are detectable by autoradiography. Other conditions of high stringency which may be used are well known in the art and as cited in Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, Second Edition, Cold Spring Harbor Press, N.Y., pp. 9.47-9.57; and Ausubel et al., 1989, Current Protocols in Molecular Biology, Green Publishing Associates and Wiley Interscience, N.Y. are incorporated herein in their entirety. Preferably, such sequences encode a homolog of a polypeptide encoded by one of ORF2 to ORF1297. In one embodiment, such sequences encode a *Chlamydia pneumoniae* polypeptide.

(ii) By way of example and not limitation, procedures using conditions of intermediate stringency are as follows: Filters containing DNA are prehybridized, and then hybridized at a temperature of 60EC in the presence of a 5 x SSC buffer and labeled probe. Subsequently, filters washes are performed in a solution containing 2x SSC at 50EC and the hybridized probes are detectable by autoradiography. Other conditions of intermediate stringency which may be used are well known in the art and as cited in Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, Second Edition, Cold Spring Harbor Press, N.Y., pp. 9.47-9.57; and Ausubel et al., 1989, Current Protocols in Molecular Biology, Green Publishing Associates and Wiley Interscience, N.Y. are incorporated herein in their entirety. Preferably, such sequences encode a homolog of a polypeptide encoded by one of ORF2 to ORF1297. In one embodiment, such sequences encode a *Chlamydia pneumoniae* polypeptide.

d) complementary or RNA nucleotide sequence corresponding to an ORF2 to ORF1297 sequence according to the invention or as defined in a), b) or c);

e) a nucleotide sequence of a representative fragment of an ORF2 to ORF1297 sequence according to the invention or of a sequence as defined in a), b), c) or d);

f) a nucleotide sequence capable of being obtained from an ORF2 to ORF1297 sequence according to the invention or as defined in a), b), c), d) or e); and

g) a modified nucleotide sequence of an ORF2 to ORF1297 sequence according to the invention or as defined in a), b), c), d), e) or f);

As regards the homology with the ORF2 to ORF1297 nucleotide sequences, the homologous sequences exhibiting a percentage identity with the bases of one of the ORF2 to ORF1297 nucleotide sequences of at least 80%, preferably 90% and 95%, are preferred. Such homologous sequences are identified routinely via, for example, the algorithms described above and in the examples below. The said homologous sequences correspond to the homologous sequences as defined above and may comprise, for example, the sequences corresponding to the ORF sequences of a bacterium belonging to the Chlamydia family, including the species *Chlamydia trachomatis*, *Chlamydia psittaci* and *Chlamydia pecorum* mentioned above, as well as the sequences corresponding to the ORF sequences of a bacterium belonging to the variants of the species *Chlamydia pneumoniae*. These homologous sequences may likewise correspond to variations linked to mutations within the same species or between species and may correspond in particular to truncations, substitutions, deletions and/or additions of at least one nucleotide. The said homologous sequences may also correspond to variations linked to the degeneracy of the genetic code or to a bias in the genetic code which is specific to the family, to the species or to the variant and which are likely to be present in *Chlamydia*.

The invention comprises polypeptides encoded by a nucleotide sequence according to the invention, preferably by a representative fragment of the sequence SEQ ID No. 1 and corresponding to an ORF sequence, in particular the *Chlamydia pneumoniae* polypeptides, characterized in that they are chosen from the sequences SEQ ID No. 2 to SEQ ID No. 1291 or SEQ ID No. 6844 to SEQ ID No.

6849 and representative fragments thereof. However, the invention is not limited to polypeptides encoded by ORFs in SEQ ID No. 1 and its corresponding ORF sequences, but encompasses polypeptides of strain variants, polymorphisms, allelic variants, and mutants.

Thus, the invention also comprises the polypeptides characterized in that they comprise a polypeptide chosen from:

a) a polypeptide encoded by a polynucleotide sequence in SEQ ID No. 1 (*e.g.*, any polypeptide encoded by a polynucleotide sequence corresponding to ORF2 to ORF1297 and/or representative fragments thereof) according to the invention;

b) a polypeptide homologous to a polypeptide according to the invention, or as defined in a);

c) a polypeptide encoded by a polynucleotide sequence that hybridizes to SEQ ID No. 1 or ORF2 to ORF1297 under high or intermediate stringency as described below:

(i) By way of example and not limitation, procedures using conditions of high stringency are as follows: Prehybridization of filters containing DNA is carried out for 8 h to overnight at 65EC in buffer composed of 6X SSC, 50 mM Tris-HCl (pH 7.5), 1 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.02% BSA, and 500 μg/ml denatured salmon sperm DNA. Filters are hybridized for 48 h at 65EC, the preferred hybridization temperature, in prehybridization mixture containing 100 μg/ml denatured salmon sperm DNA and 5-20 X 10^6 cpm of ^{32}P-labeled probe. Alternatively, the hybridization step can be performed at 65EC in the presence of SSC buffer, 1 x SSC corresponding to 0.15M NaCl and 0.05 M Na citrate. Subsequently, filter washes can be done at 37EC for 1 h in a solution containing 2X SSC, 0.01% PVP, 0.01% Ficoll, and 0.01% BSA, followed by a wash in 0.1X SSC at 50EC for 45 min. Alternatively, filter washes can be performed in a solution containing 2 x SSC and 0.1% SDS, or 0.5 x SSC and 0.1% SDS, or 0.1 x SSC and 0.1% SDS at 68EC for 15 minute intervals. Following the wash steps, the hybridized probes are detectable by autoradiography. Other conditions of high stringency which may be used are well known in the art and as cited in Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, Second Edition, Cold Spring Harbor Press, N.Y., pp. 9.47-9.57; and Ausubel et al., 1989, Current Protocols in Molecular Biology, Green Publishing Associates and Wiley Interscience, N.Y. are incorporated herein in their entirety. Preferably such polypeptide represents a homolog of a polypeptide encoded by ORF2 to ORF1297. Preferably, such sequences encode a homolog of a polypeptide encoded by one of ORF2 to ORF1297. In one embodiment, such sequences encode a *Chlamydia pneumoniae* polypeptide.

(ii) By way of example and not limitation, procedures using conditions of intermediate stringency are as follows: Filters containing DNA are prehybridized, and then hybridized at a temperature of 60EC in the presence of a 5 x SSC buffer and labeled probe. Subsequently, filters washes are performed in a solution containing 2x SSC at 50EC and the hybridized probes are detectable by autoradiography. Other conditions of intermediate stringency which may be used are well known in the art and as cited in Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, Second Edition, Cold Spring Harbor Press, N.Y., pp. 9.47-9.57; and Ausubel et al., 1989, Current Protocols in Molecular Biology, Green Publishing Associates and Wiley Interscience, N.Y. are incorporated herein in their entirety. Preferably, such sequences encode a homolog of a polypeptide encoded by one of ORF2 to ORF1297. In one embodiment, such sequences encode a *Chlamydia pneumoniae* polypeptide.

d) a fragment of at least 5 amino acids of a polypeptide according to the invention, or as defined in a), b) or c);

e) a biologically active fragment of a polypeptide according to the invention, or as defined in a), b), c) or d); and

f) a modified polypeptide of a polypeptide according to the invention, as defined in a), b), c),d) or e).

In the present description, the terms polypeptide, peptide and protein are interchangeable.

It should be understood that the invention does not relate to the polypeptides in natural form, that is to say that they are not taken in their natural environment but that they may have been isolated or obtained by purification from natural sources, or alternatively obtained by genetic recombination, or else by chemical synthesis and that they may, in this case, comprise nonnatural amino acids, as will be described below.

Homologous polypeptide will be understood to designate the polypeptides exhibiting, in relation to the natural polypeptide, certain modifications such as in particular a deletion, addition or substitution of at least one amino acid, a truncation, an extension, a chimeric fusion, and/or a mutation, or polypeptides exhibiting post-translational modifications. Among the homologous polypeptides, those whose amino acid sequence exhibits at least 80%, preferably 90%, homology or identity with the amino acid sequences of the polypeptides according to the invention are preferred. In the case of a substitution, one or more consecutive or nonconsecutive amino acids are replaced by "equivalent" amino acids. The expression "equivalent" amino acid is intended here to designate any amino acid capable of being substituted for one of the amino acids in the basic structure without, however, essentially modifying the biological activities of the corresponding peptides and as will be defined later.

Protein and/or nucleic acid sequence homologies may be evaluated using any of the variety of sequence comparison algorithms and programs known in the art. Such algorithms and programs include, but are by no means limited to, TBLASTN, BLASTP, FASTA, TFASTA, and CLUSTALW (Pearson and Lipman, 1988, *Proc. Natl. Acad. Sci. USA 85(8)*:2444-2448; Altschul *et al.*, 1990, *J. Mol. Biol. 215(3)*:403-410; Thompson *et al.*, 1994, *Nucleic Acids Res. 22(2)*:4673-4680; Higgins *et al.*, 1996, *Methods Enzymol. 266*:383-402; Altschul *et al.*, 1990, *J. Mol. Biol. 215(3)*:403-410; Altschul *et al.*, 1993, *Nature Genetics 3*:266-272).

In a particularly preferred embodiment, protein and nucleic acid sequence homologies are evaluated using the Basic Local Alignment Search Tool ("BLAST") which is well know in the art (see, *e.g.*, Karlin and Altschul, 1990, *Proc. Natl. Acad. Sci. USA 87*:2267-2268; Altschul *et al.*, 1990, *J. Mol. Biol. 215*:403-410; Altschul *et al.*, 1993, *Nature Genetics 3*:266-272; Altschul *et al.*, 1997, *Nuc. Acids Res. 25*:3389-3402). In particular, five specific BLAST programs are used to perform the following task:

(1)BLASTP and BLAST3 compare an amino acid query sequence against a protein sequence database;

(2)BLASTN compares a nucleotide query sequence against a nucleotide sequence database;

(3)BLASTX compares the six-frame conceptual translation products of a query nucleotide sequence (both strands) against a protein sequence database;

(4)TBLASTN compares a query protein sequence against a nucleotide sequence database translated in all six reading frames (both strands); and

(5)TBLASTX compares the six-frame translations of a nucleotide query sequence against the six-frame translations of a nucleotide sequence database.

The BLAST programs identify homologous sequences by identifying similar segments, which are referred to herein as "high-scoring segment pairs," between a query amino or nucleic acid sequence and a test sequence which is preferably obtained from a protein or nucleic acid sequence database. High-scoring segment pairs are preferably identified (*i.e.*, aligned) by means of a scoring matrix, many of which are known in the art. Preferably, the scoring matrix used is the BLOSUM62 matrix (Gonnet *et al.*, 1992, *Science 256*:1443-1445; Henikoff and Henikoff, 1993, *Proteins 17*:49-61). Less preferably, the PAM or PAM250 matrices may also be used (see, *e.g.*, Schwartz and Dayhoff, eds., 1978, *Matrices for Detecting Distance Relationships: Atlas of Protein Sequence and Structure*, Washington: National Biomedical Research Foundation)

The BLAST programs evaluate the statistical significance of all high-scoring segment pairs identified, and preferably selects those segments which satisfy a user-specified threshold of significance, such as a user-specified percent homology. Preferably, the statistical significance of a high-scoring segment pair is evaluated using the statistical significance formula of Karlin (see, *e.g.*, Karlin and Altschul, 1990, *Proc. Natl. Acad. Sci. USA 87*:2267-2268).

Equivalent amino acids may be determined either based on their structural homology with the amino acids for which they are substituted, or on results of comparative tests of biological activity between the various polypeptides which may be carried out.

By way of example, there may be mentioned the possibilities of substitutions which may be carried out without resulting in a substantial modification of the biological activity of the corresponding modified polypeptides; the replacements, for example, of leucine with valine or isoleucine, of aspartic acid with glutamic acid, of glutamine with asparagine, of arginine with lysine, and the like, the reverse substitutions naturally being feasible under the same conditions.

The homologous polypeptides also correspond to the polypeptides encoded by the homologous nucleotide sequences as defined above and thus comprise in the present definition the mutated polypeptides or polypeptides corresponding to inter- or intra-species variations which may exist in *Chlamydia*, and which correspond in particular to truncations, substitutions, deletions and/or additions of at least one amino acid residue.

Biologically active fragment of a polypeptide according to the invention will be understood to designate in particular a polypeptide fragment, as defined below, exhibiting at least one of the characteristics of the polypeptides according to the invention, in particular in that it is:

- capable of eliciting an immune response directed against *Chlamydia pneumoniae*; and/or
- capable of being recognized by an antibody specific for a polypeptide according to the invention; and/or
- capable of binding to a polypeptide or to a nucleotide sequence of *Chlamydia pneumoniae*; and/or
- capable of modulating, regulating, inducing or inhibiting the expression of a gene of *Chlamydia pneumoniae* or one of its associated microorganisms, and/or capable of modulating the replication cycle of *Chlamydia pneumoniae* or one of its associated microorganisms in the host cell and/or organism; and/or
- capable of generally exerting an even partial physiological activity, such as for example a structural activity (cellular envelope, ribosome), an enzymatic (metabolic) activity, a transport activity, an activity in the secretion or in the virulence.

A polypeptide fragment according to the invention is understood to designate a polypeptide comprising a minimum of 5 amino acids, preferably 10 amino acids or preferably 15 amino acids. It is to be understood that such fragments refer only to portions of polypeptides encoded by ORF2 to ORF1297 that are not currently listed in a publicly available database.

The polypeptide fragments according to the invention may correspond to isolated or purified fragments which are naturally present in *Chlamydia pneumoniae* or which are secreted by *Chlamydia pneumoniae,* or may correspond to fragments capable of being obtained by cleaving the said polypeptide with a proteolytic enzyme, such as trypsin or chymotrypsin or collagenase, or with a chemical reagent, such as cyanogen bromide (CNBr) or alternatively by placing the said polypeptide in a highly acidic environment, for example at pH 2.5. Such polypeptide fragments may be equally well prepared by chemical synthesis, using hosts transformed with an expression vector according to the invention containing a nucleic acid allowing the expression of the said fragments, placed under the control of appropriate elements for regulation and/or expression.

"Modified polypeptide" of a polypeptide according to the invention is understood to designate a polypeptide obtained by genetic recombination or by chemical synthesis as will be described below, exhibiting at least one modification in relation to the normal sequence. These modifications may in particular affect amino acids responsible for a specificity or for the efficiency of the activity, or responsible for the structural conformation, for the charge or for the hydrophobicity, and for the capacity for multimerization and for membrane insertion of the polypeptide according to the invention. It is thus possible to create polypeptides with an equivalent, an increased or a reduced activity, and with an equivalent, a narrower or a broader specificity. Among the modified polypeptides, there may be mentioned the polypeptides in which up to 5 amino acids may be modified, truncated at the N- or C-terminal end, or alternatively deleted, or else added.

As is indicated, the modifications of the polypeptide may have in particular the objective:

- of making it capable of modulating, regulating, inhibiting or inducing the expression of a gene of *Chlamydia*, in particular of *Chlamydia pneumoniae* and its variants, or one of its associated microorganisms, and/or capable of modulating the replication cycle of *Chlamydia*, in particular of *Chlamydia pneumoniae* and its variants, or one of its associated microorganisms, in the host cell and/or organism,
- of allowing its use in methods of biosynthesis or of biodegradation, or its incorporation into vaccine compositions,
- of modifying its bioavailability as a compound for therapeutic use.

The said modified polypeptides may also be used on any cell or microorganism for which the said modified polypeptides will be capable of modulating, regulating, inhibiting or inducing gene expression, or of modulating the growth or the replication cycle of the said cell or of the said microorganism. The methods allowing demonstration of the said modulations on eukaryotic or prokaryotic cells are well known to persons skilled in the art. The said cells or microorganisms will be chosen, in particular, from tumour cells or infectious microorganisms and the said modified polypeptides may be used for the prevention or treatment of pathologies linked to the presence of the said cells or of the said microorganisms. It is also clearly understood that the nucleotide sequences encoding the said modified polypeptides may be used for the said modulations, for example by the intermediacy of vectors according to the invention and which are described below, so as to prevent or to treat the said pathologies.

The above modified polypeptides may be obtained using combinatory chemistry, in which it is possible to systematically vary portions of the polypeptide before testing them on models, cell cultures or microorganisms for example, so as to select the compounds which are the most active or which exhibit the desired properties.

Chemical synthesis also has the advantage of being able to use:

- nonnatural amino acids, or
- nonpeptide bonds.

Accordingly, in order to extend the life of the polypeptides according to the invention, it may be advantageous to use nonnatural amino acids, for example in the D form, or alternatively amino acid analogues, in particular sulphur-containing forms for example.

Finally, the structure of the polypeptides according to the invention, its homologous or modified forms, as well as the corresponding fragments may be integrated into chemical structures of the polypeptide type and the like. Accordingly, it may be advantageous to provide at the N- and C-terminal ends compounds which are not recognized by proteases.

Also forming part of the invention are the nucleotide sequences encoding a polypeptide according to the invention. Described below are ORF nucleotide sequences encoding polypeptides exhibiting particularly preferable characteristics. For each group of preferred ORFS described below, it is to be understood that in addition to the individual ORFs listed, in instances wherein such ORFS are present as part of "combined" ORFs, the "combined" ORFs are also to be included within the preferred group.

More particularly, the subject of the invention is nucleotide sequences, characterized in that they encode a polypeptide of the cellular envelope, preferably of the outer cellular envelope of *Chlamydia pneumoniae* or one of its representative fragments, such as for example the predominant proteins of the outer membrane, the adhesion proteins or the proteins entering into the composition of the Chlamydia wall. Among these sequences, the sequences comprising a nucleotide sequence chosen from the following sequences are most preferred:

ORF15; ORF25; ORF26; ORF27; ORF28; ORF29; ORF30; ORF31; ORF32; ORF33; ORF35; ORF68; ORF124; ORF275; ORF291; ORF294; ORF327; ORF342; ORF364; ORF374; ORF380; ORF414; ORF439; ORF466; ORF467; ORF468; ORF469; ORF470; ORF472; ORF474; ORF476; ORF477; ORF478; ORF479; ORF480; ORF482; ORF485; ORF500; ORF501; ORF503; ORF504; ORF505; ORF506; ORF520; ORF578; ORF580; ORF581; ORF595; ORF596; ORF597; ORF737; ORF830; ORF834; ORF836; ORF893; ORF917; ORF932; ORF976; ORF1035; ORF1045; ORF1090 and one of their representative fragments.

The structure of the cytoplasmic membranes and of the wall of bacteria is dependent on the associated proteins. The structure of the cytoplasmic membrane makes it impermeable to water, to water-soluble substances and to small-sized molecules (ions, small inorganic molecules, peptides or proteins). To enter into or to interfere with a cell or a bacterium, a ligand must establish a special relationship with a protein anchored in the cytoplasmic membrane (the receptor). These proteins which are anchored on the membrane play an important role in metabolism since they control the exchanges in the bacterium. These exchanges apply to molecules of interest for the bacterium (small molecules such as sugars and small peptides) as well as undesirable molecules for the bacterium such as antibiotics or heavy metals.

The double lipid layer structure of the membrane requires the proteins which are inserted therein to have hydrophobic domains of about twenty amino acids forming an alpha helix. Predominantly hydrophobic and potentially transmembrane regions may be predicted from the primary sequence of the proteins, itself deduced from the nucleotide sequence. The presence of one or more putative transmembrane domains raises the possibility for a protein to be associated with the cytoplasmic membrane and to be able to play an important metabolic role therein or alternatively for the protein thus exposed to be able to exhibit potentially protective epitopes.

If the proteins inserted into the membrane exhibit several transmembrane domains capable of interacting with one another via electrostatic bonds, it then becomes possible for these proteins to form pores which go across the membrane which becomes permeable for a number of substances. It should be noted that proteins which do not have transmembrane domains may also be anchored by the intermediacy of fatty acids in the cytoplasmic membrane, it being possible for the breaking of the bond between the protein and its anchor in some cases to be responsible for the release of the peptide outside the bacterium.

Preferably, the invention relates to the nucleotide sequences according to the invention, characterized in that they encode a *Chlamydia pneumoniae* transmembrane polypeptide or one of its representative fragments, having between 1 and 3 transmembrane domains and in that they comprise a nucleotide sequence chosen from the following sequences:

ORF2; ORF3; ORF6; ORF9; ORF10; ORF11; ORF13; ORF14; ORF16; ORF18; ORF19; ORF20; ORF21; ORF22; ORF25; ORF27; ORF28; ORF29; ORF30; ORF31; ORF32; ORF33; ORF34; ORF35; ORF37; ORF39; ORF41; ORF42; ORF44; ORF45; ORF46; ORF47; ORF48; ORF49; ORF50; ORF53; ORF54; ORF56; ORF57; ORF59; ORF60; ORF61; ORF62; ORF63; ORF64; ORF65; ORF66; ORF69;; ORF72; ORF73; ORF74; ORF76; ORF77; ORF78; ORF79; ORF80; ORF82; ORF84; ORF85; ORF86; ORF88; ORF89; ORF90; ORF91; ORF92; ORF93; ORF95; ORF96; ORF98; ORF99; ORF100; ORF101; ORF102; ORF103; ORF104; ORF105; ORF106; ORF107; ORF108; ORF114; ORF117; ORF118; ORF122; ORF123; ORF124; ORF125; ORF129; ORF130; ORF131; ORF132; ORF133; ORF134; ORF135; ORF137; ORF138; ORF139; ORF140; ORF141; ORF142; ORF143; ORF145; ORF146; ORF147; ORF150; ORF151; ORF152; ORF156; ORF157; ORF158; ORF159; ORF160; ORF161; ORF162; ORF164; ORF166; ORF167; ORF170; ORF173; ORF175; ORF176; ORF178; ORF179; ORF180; ORF182; ORF183; ORF184; ORF185; ORF186; ORF187; ORF188; ORF189; ORF190; ORF191; ORF192; ORF194; ORF195; ORF196; ORF197; ORF198; ORF199; ORF200; ORF201; ORF202; ORF205; ORF207; ORF208; ORF209; ORF210; ORF212; ORF215; ORF219; ORF220; ORF224; ORF226; ORF227; ORF228; ORF231; ORF232; ORF233; ORF234; ORF235; ORF236; ORF238; ORF239; ORF240; ORF241; ORF242; ORF244; ORF247; ORF251; ORF252; ORF253; ORF255; ORF256; ORF257; ORF258; ORF260; ORF262; ORF263; ORF266; ORF267; ORF268; ORF269; ORF270; ORF273; ORF274; ORF276; ORF278; ORF279; ORF280; ORF281; ORF282; ORF283; ORF284; ORF286; ORF287; ORF289; ORF290; ORF291; ORF293; ORF294; ORF297; ORF304; ORF305; ORF307; ORF308; ORF309; ORF310; ORF311; ORF313; ORF314; ORF315; ORF316; ORF318; ORF319; ORF320; ORF321; ORF322; ORF323; ORF324; ORF325; ORF326; ORF331; ORF332; ORF336; ORF338; ORF339; ORF341; ORF344; ORF345; ORF346; ORF350; ORF352; ORF353; ORF356; ORF357; ORF358; ORF359; ORF360; ORF362; ORF365; ORF366; ORF367; ORF370; ORF372; ORF373; ORF376; ORF377; ORF378; ORF379; ORF381; ORF382; ORF383; ORF384; ORF385; ORF386; ORF387; ORF390; ORF392; ORF393; ORF394; ORF396; ORF398; ORF399; ORF400; ORF404; ORF408; ORF410; ORF411; ORF413; ORF416; ORF417; ORF418; ORF420; ORF422; ORF424; ORF427;

ORF428; ORF429; ORF430; ORF431; ORF433; ORF434; ORF437; ORF440; ORF441; ORF442; ORF443; ORF444; ORF445; ORF447; ORF450; ORF451; ORF452; ORF455; ORF456; ORF459; ORF460; ORF461; ORF462; ORF463; ORF464; ORF465; ORF467; ORF469; ORF471; ORF474; ORF475; ORF476; ORF477; ORF479; ORF482; ORF483; ORF484; ORF485; ORF486; ORF487; ORF488; ORF491; ORF493; ORF494; ORF497; ORF498; ORF499; ORF503; ORF508; ORF509; ORF510; ORF512; ORF514; ORF515; ORF516; ORF517; ORF518; ORF520; ORF521; ORF523; ORF525; ORF527; ORF528; ORF529; ORF530; ORF531; ORF533; ORF534; ORF535; ORF536; ORF537; ORF540; ORF541; ORF543; ORF544; ORF545; ORF546; ORF548; ORF549; ORF551; ORF553; ORF554; ORF555; ORF556; ORF557; ORF558; ORF559; ORF560; ORF562; ORF563; ORF564; ORF565; ORF566; ORF569; ORF571; ORF573; ORF576; ORF577; ORF581; ORF583; ORF584; ORF585; ORF586; ORF588; ORF591; ORF592; ORF594; ORF595; ORF596; ORF597; ORF599; ORF600; ORF603; ORF605; ORF608; ORF614; ORF615; ORF620; ORF621; ORF622; ORF623; ORF624; ORF625; ORF629; ORF630; ORF631; ORF633; ORF634; ORF637; ORF642; ORF644; ORF645; ORF647; ORF648; ORF652; ORF654; ORF655; ORF657; ORF658; ORF659; ORF660; ORF661; ORF664; ORF665; ORF666; ORF667; ORF670; ORF671; ORF672; ORF673; ORF674; ORF676; ORF679; ORF681; ORF684; ORF687; ORF688; ORF689; ORF690; ORF693; ORF694; ORF695; ORF696; ORF697; ORF698; ORF699; ORF700; ORF701; ORF703; ORF705; ORF706; ORF707; ORF708; ORF710; ORF712; ORF715; ORF716; ORF717; ORF718; ORF719; ORF721; ORF722; ORF723; ORF725; ORF726; ORF727; ORF728; ORF729; ORF730; ORF731; ORF733; ORF736; ORF737; ORF738; ORF740; ORF741; ORF742; ORF743; ORF747; ORF748; ORF750; ORF752; ORF754; ORF755; ORF756; ORF757; ORF759; ORF760; ORF761; ORF762; ORF763; ORF764; ORF765; ORF766; ORF767; ORF768; ORF772; ORF774; ORF775; ORF777; ORF781; ORF783; ORF788; ORF791; ORF792; ORF793; ORF794; ORF795; ORF796; ORF797; ORF798; ORF799; ORF802; ORF803; ORF806; ORF807; ORF808; ORF809; ORF810; ORF811; ORF813; ORF814; ORF815; ORF816; ORF817; ORF819; ORF820; ORF821; ORF823; ORF824; ORF827; ORF829; ORF830; ORF831; ORF833; ORF834; ORF835; ORF837; ORF844; ORF845; ORF846; ORF847; ORF848; ORF849; ORF850; ORF851; ORF852; ORF854; ORF855; ORF856; ORF857; ORF859; ORF860; ORF862; ORF865; ORF866; ORF868; ORF869; ORF870; ORF871; ORF872; ORF874; ORF877; ORF878; ORF879; ORF880; ORF881; ORF882; ORF884; ORF885; ORF888; ORF889; ORF890; ORF891; ORF892; ORF894; ORF895; ORF896; ORF897; ORF899; ORF900; ORF902; ORF903; ORF904; ORF905; ORF909; ORF910; ORF912; ORF913; ORF914; ORF915; ORF917; ORF918; ORF919; ORF921; ORF923; ORF924; ORF926; ORF927; ORF928; ORF929; ORF930; ORF931; ORF937; ORF938; ORF939; ORF941; ORF943; ORF948; ORF951; ORF952; ORF953; ORF958; ORF960; ORF963; ORF964; ORF965; ORF968; ORF970; ORF974; ORF975; ORF977; ORF979; ORF980; ORF981; ORF983; ORF984; ORF985; ORF987; ORF989; ORF992; ORF993; ORF997; ORF998; ORF999; ORF1001; ORF1002; ORF1004; ORF1005; ORF1009; ORF1013; ORF1014; ORF1015; ORF1016; ORF1019; ORF1021; ORF1023; ORF1024;

ORF1029; ORF1031; ORF1033; ORF1034; ORF1039; ORF1041; ORF1042; ORF1045; ORF1047; ORF1049; ORF1051; ORF1052; ORF1053; ORF1054; ORF1056; ORF1059; ORF1061; ORF1062; ORF1063; ORF1064; ORF1065; ORF1067; ORF1075; ORF1077; ORF1078; ORF1079; ORF1080; ORF1081; ORF1089; ORF1095; ORF1097; ORF1098; ORF1099; ORF1101; ORF1102; ORF1103; ORF1106; ORF1107; ORF1108; ORF1109; ORF1110; ORF1113; ORF1116; ORF1118; ORF1119; ORF1121; ORF1123; ORF1124; ORF1126; ORF1128; ORF1130; ORF1131; ORF1133; ORF1134; ORF1136; ORF1137 and one of their representative fragments.

Preferably, the invention relates to the nucleotide sequences according to the invention, characterized in that they encode a *Chlamydia pneumoniae* transmembrane polypeptide or one of its representative fragments, having between 4 and 6 transmembrane domains and in that they comprise a nucleotide sequence chosen from the following sequences:

ORF5; ORF7; ORF8; ORF15; ORF36; ORF38; ORF51; ORF55; ORF58; ORF67; ORF70; ORF81; ORF97; ORF110; ORF111; ORF115; ORF119; ORF126; ORF128; ORF148; ORF155; ORF163; ORF165; ORF168; ORF169; ORF171; ORF172; ORF174; ORF177; ORF181; ORF193; ORF203; ORF213; ORF214; ORF216; ORF217; ORF221; ORF222; ORF225; ORF229; ORF243; ORF246; ORF248; ORF254; ORF261; ORF285; ORF288; ORF292; ORF296; ORF298; ORF299; ORF301; ORF303; ORF317; ORF328; ORF329; ORF351; ORF354; ORF355; ORF364; ORF371; ORF374; ORF375; ORF391; ORF395; ORF401; ORF403; ORF405; ORF409; ORF414; ORF419; ORF421; ORF423; ORF425; ORF438; ORF448; ORF453; ORF458; ORF466; ORF468; ORF470; ORF480; ORF489; ORF490; ORF496; ORF501; ORF504; ORF505; ORF506; ORF511; ORF513; ORF519; ORF526; ORF532; ORF538; ORF539; ORF547; ORF550; ORF561; ORF568; ORF570; ORF574; ORF578; ORF579; ORF580; ORF582; ORF589; ORF593; ORF598; ORF601; ORF604; ORF610; ORF613; ORF617; ORF626; ORF632; ORF635; ORF638; ORF640; ORF641; ORF646; ORF649; ORF650; ORF651; ORF686; ORF711; ORF724; ORF732; ORF734; ORF744; ORF745; ORF749; ORF751; ORF769; ORF770; ORF771; ORF773; ORF776; ORF779; ORF780; ORF785; ORF787; ORF789; ORF801; ORF805; ORF812; ORF822; ORF825; ORF826; ORF839; ORF841; ORF843; ORF853; ORF861; ORF875; ORF876; ORF886; ORF893; ORF898; ORF906; ORF907; ORF908; ORF920; ORF922; ORF925; ORF933; ORF935; ORF936; ORF944; ORF946; ORF947; ORF954; ORF959; ORF961; ORF966; ORF967; ORF972; ORF978; ORF995; ORF996; ORF1000; ORF1003; ORF1010; ORF1011; ORF1012; ORF1017; ORF1020; ORF1030; ORF1036; ORF1038; ORF1043; ORF1046; ORF1048; ORF1050; ORF1058; ORF1071; ORF1073; ORF1084; ORF1085; ORF1086; ORF1087; ORF1091; ORF1092; ORF1094; ORF1096; ORF1100; ORF1104; ORF1111; ORF1112; ORF1114; ORF1117; ORF1122; ORF1125 and one of their representative fragments.

Preferably, the invention also relates to the nucleotide sequences according to the invention, characterized in that they encode a *Chlamydia pneumoniae* transmembrane polypeptide or one of its representative fragments, having at least 7 transmembrane domains and in that they comprise a nucleotide sequence chosen from the following sequences:

ORF17; ORF52; ORF68; ORF83; ORF87; ORF109; ORF112; ORF113; ORF120; ORF121; ORF127; ORF153; ORF204; ORF211; ORF218; ORF223; ORF275; ORF277; ORF295; ORF300; ORF302; ORF306; ORF327; ORF335; ORF342; ORF343; ORF347; ORF349; ORF361; ORF363; ORF369; ORF380; ORF388; ORF389; ORF397; ORF415; ORF432; ORF439; ORF446; ORF449; ORF472; ORF478; ORF500; ORF522; ORF524; ORF567; ORF575; ORF602; ORF606; ORF609; ORF636; ORF639; ORF643; ORF653; ORF668; ORF692; ORF702; ORF704; ORF713; ORF720; ORF778; ORF784; ORF800; ORF836; ORF838; ORF842; ORF864; ORF867; ORF883; ORF901; ORF916; ORF932; ORF934; ORF940; ORF942; ORF950; ORF956; ORF971; ORF973; ORF976; ORF988; ORF994; ORF1018; ORF1028; ORF1035; ORF1037; ORF1044; ORF1055; ORF1057; ORF1068; ORF1069; ORF1070; ORF1072; ORF1082; ORF1088; ORF1105; ORF1132; ORF1135 and one of their representative fragments.

Preferably, the invention relates to the nucleotide sequences according to the invention, characterized in that they encode a *Chlamydia pneumoniae* surface exposed polypeptide (*e.g.*, an outer membrane protein) or one of its representative fragments, said nucleotide sequences comprising a nucleotide sequence chosen from the following sequences:

ORF 15, ORF 25, ORF 26, ORF 27, ORF 28, ORF 29, ORF 30, ORF 31, ORF 32, ORF 33, ORF 35, ORF 36, ORF 1257, ORF 280, ORF 291, ORF 314, ORF 354, ORF 380, ORF 1266, ORF 466, ORF 467, ORF 468, ORF 469, ORF 470, ORF 472, ORF 474, ORF 476, ORF 477, ORF 478, ORF 479, ORF 480, ORF 482, ORF 483, ORF 485, ORF 486, ORF 500, ORF 501, ORF 503, ORF 504, ORF 505, ORF 506, ORF 507, ORF 1268, ORF 1269, ORF 543, ORF 544, ORF 578, ORF 579, ORF 580, ORF 581, ORF 595, ORF 596, ORF 597, ORF 1271, ORF 633, ORF 637, ORF 699, ORF 706, ORF 737, ORF 744, ORF 1273, ORF 751, ORF 775, ORF 776, ORF 777, ORF 793, ORF 815, ORF 830, ORF 1221, ORF 849, ORF 851, ORF 852, ORF 874, ORF 891, ORF 922, ORF 940, ORF 1231, ORF 1281, ORF 1035, ORF 1079, ORF 1087, ORF 1108, and one of their representative fragments.

Preferably, the invention relates to the nucleotide sequences according to the invention, characterized in that they encode a *Chlamydia pneumoniae* lipoprotein or one of its representative fragments, said nucleotide sequences comprising a nucleotide sequence chosen from the following sequences:

ORF 3, ORF 10, ORF 11, ORF 16, ORF 1254, ORF 1255, ORF 38, ORF 1256, ORF 62, ORF 85, ORF 1258, ORF 115, ORF 1151, ORF 151, ORF 1259, ORF 173, ORF 1261, ORF 186, ORF 194, ORF 205, ORF 214, ORF 216, ORF 217, ORF 238, ORF 1177, ORF 280, ORF 291, ORF 317, ORF 327, ORF 354, ORF 364, ORF 367, ORF 414, ORF 432, ORF 1192, ORF 460, ORF 1267, ORF 1268, ORF 520, ORF 536, ORF 1270, ORF 576, ORF 597, ORF 603, ORF 609, ORF 637, ORF 1272, ORF 652, ORF 1213, ORF 699, ORF 705, ORF 706, ORF 708, ORF 711, ORF 727, ORF 1274, ORF 800, ORF 814, ORF 825, ORF 829, ORF 830, ORF 831, ORF 844, ORF 849, ORF 1275, ORF 1276, ORF 1277, ORF 872, ORF 878, ORF 880, ORF 891, ORF 892, ORF 1278, ORF 1279, ORF 1280, ORF 941, ORF 942, ORF 1282, ORF 1283, ORF 952, ORF 988, ORF 998, ORF 1009, ORF 1285, ORF

1235, ORF 1028, ORF 1056, ORF 1070, ORF 1287, ORF 1087, ORF 1288, ORF 1289, ORF 1098, ORF 1246, ORF 1291, ORF 1108, ORF 1109, ORF 1112, ORF 1133, and one of their representative fragments.

Preferably, the invention relates to the nucleotide sequences according to the invention, characterized in that they encode a *Chlamydia pneumoniae* polypeptide involved in lipopolysaccharide (LPS) biosynthesis, said nucleotide sequences comprising a nucleotide sequence chosen from the following sequences: ORF 316, ORF 564, ORF 610, ORF 647, ORF 1211, ORF 688, ORF 924, and one of their representative fragments.

Preferably the invention relates to additional LPS-related nucleotide sequences according to the invention, characterized in that they encode:

(a) a *Chlamydia pneumoniae* KDO (3-deoxy-D-manno-octulosonic acid)-related polypeptide or one of its representative fragments, said nucleotide sequences comprising a nucleotide sequence chosen from the following sequences: ORF 177, ORF 1156, ORF 245, ORF 767, and one of their representative fragments;

(b) a *Chlamydia pneumoniae* phosphomannomutase-related polypeptide or one of its representative fragments, said nucleotide sequences comprising a nucleotide sequence chosen from the following sequences: ORF 74, and one of its representative fragments;

(c) a *Chlamydia pneumoniae* phosphoglucomutase-related polypeptide or one of its representative fragments, said nucleotide sequences comprising a nucleotide sequence chosen from the following sequences: ORF 1286, ORF 1039, and one of their representative fragments; and

(d) a *Chlamydia pneumoniae* lipid A component-related polypeptide or one of its representative fragments, said nucleotide sequences comprising a nucleotide sequence chosen from the following sequences: ORF 689, ORF 690, ORF 691, ORF 1037, and one of their representative fragments.

Preferably, the invention relates to the nucleotide sequences according to the invention, characterized in that they encode a *Chlamydia pneumoniae* polypeptide containing RGD (Arg-Gly-Asp) attachment sites or one of its representative fragments.

(a) RGD-containing proteins that are outer membrane proteins, are more likely to play a role in cell attachment. ORFs that encoded a protein containing an RGD sequence and also were classified as outer membrane proteins are ORF 468 and its representative fragments.

(b) An RGD-encoding ORF that showed homology to cds1, cds2, and copN type III virulence loci in *Chlamydia psittaci* (Hsia, R. et al. (1997), Type III secretion genes identity a putative virulence locus of Chlamydia. Molecular Microbiology 25:351-359) is ORF 350, and its representative fragments.

(c) The outer membrane of Chlamydia is made of cysteine-rich proteins that form a network of both intra and inter molecular disulfide links. This contributes to the integrity of the membrane since Chlamydia lacks the peptidoglycan layer that other gram-negative bacteria have. Cysteine-rich proteins that have the RGD sequence are also considered to be potential vaccine candidates. Cysteine-rich proteins were defined as proteins that had more than 3.0% cysteine in their primary amino acid sequence, above the mean genomic ORF cysteine content. The corresponding ORFs are: ORF 1290, ORF 1294, ORF 1296, and one of their representative fragments.

(d) The outer membrane of Chlamydia may also contain small proteins that have cysteines in their N– and C-terminus that may contribute to the network formed by disulfide linkages. These proteins may be anchored in the outer membrane via their N-terminus and may have their C-terminus exposed, which then can interact with the host cells. Alternatively, these proteins may be anchored in the outer membrane via both N-and C-terminus and may have regions in the middle that may be exposed which can in turn interact with the host cells. ORFs encoding polypeptides that contain cysteines in their first 30 amino acids and also contain an RGD sequence are: ORF 105, ORF 106, ORF 114, ORF 170, ORF 171, ORF 1264, ORF 268, ORF 1265, ORF 350, ORF 393, ORF 394, ORF 451, ORF 452, ORF 453, ORF 473, ORF 499, ORF 515, ORF 519, ORF 525, ORF 526, ORF 538, ORF 611, ORF 645, ORF 686, ORF 700, ORF 746, ORF 755, ORF 756, ORF 757, ORF 789, ORF 814, ORF 855, ORF 856, ORF 878, ORF 957, ORF 958, ORF 989, ORF 1290, and one of their representative fragments.

(e) RGD-containing ORFs homologous to RGD-containing ORFs from *Chlamydia trachomatis* are:
ORF 114, ORF 468, ORF 755, ORF 756, ORF 757, ORF 855, ORF 856, ORF 905, ORF 913, ORF 914, ORF 915, and one of their representative fragments.

Preferably, the invention relates to the nucleotide sequences according to the invention, characterized in that they encode a *Chlamydia pneumoniae* Type III or other, non-type III secreted polypeptide or one of its representative fragments, said nucleotide sequences comprising a nucleotide sequence chosen from the following sequences:

ORF 25, ORF 28, ORF 29, ORF 33, ORF 308, ORF 309, ORF 343, ORF 344, ORF 345, ORF 367, ORF 414, ORF 415, ORF 480, ORF 550, ORF 579, ORF 580, ORF 581, ORF 597, ORF 699, ORF 744, ORF 751, ORF 776, ORF 866, ORF 874, ORF 883, ORF 884, ORF 888, ORF 891, ORF 1293, and one of their representative fragments.

Preferably, the invention relates to the nucleotide sequences according to the invention, characterized in that they encode a *Chlamydia pneumoniae* cell wall anchored surface polypeptide or one of its representative fragments, said nucleotide sequences comprising a nucleotide sequence chosen from the following sequences: ORF 267, ORF 271, ORF 419, ORF 590, ORF 932, ORF 1292, ORF 1295, and one of their representative fragments.

Preferably, the invention relates to the nucleotide sequences according to the invention, characterized in that they encode *Chlamydia pneumoniae* polypeptides not found in *Chlamydia trachomatis* (Blastp. $P>e^{-10}$), said nucleotide sequences comprising a nucleotide sequence chosen from the following sequences: ORF 7, ORF 8, ORF 9, ORF 16, ORF 17, ORF 18, ORF 19, ORF 20, ORF 21, ORF 22, ORF 1254, ORF 23, ORF 1255, ORF 24, ORF 1139, ORF 1140, ORF 46, ORF 47, ORF 51, ORF 60, ORF 1256, ORF 61, ORF 62, ORF 63, ORF 64, ORF 1257, ORF 65, ORF 66, ORF 67, ORF 68, ORF 1143, ORF 1145, ORF 83, ORF 84, ORF 1146, ORF 85, ORF 86, ORF 87, ORF 1258, ORF 116, ORF 117, ORF 125, ORF 1148, ORF 143, ORF 1150, ORF 1151, ORF 144, ORF 145, ORF 147, ORF 148, ORF 149, ORF 150, ORF 152, ORF 1259, ORF 162, ORF 166, ORF 1154, ORF 167, ORF 1261, ORF 1156, ORF 1157, ORF 178, ORF 179, ORF 1158, ORF 182, ORF 183, ORF 184, ORF 185, ORF 1159, ORF 186, ORF 1160, ORF 187, ORF 188, ORF 189, ORF 190, ORF 1161, ORF 1162, ORF 191, ORF 192, ORF 194, ORF 195, ORF 1163, ORF 196, ORF 201, ORF 202, ORF 209, ORF 212, ORF 221, ORF 224, ORF 1167, ORF 226, ORF 227, ORF 228, ORF 229, ORF 230, ORF 231, ORF 232, ORF 1169, ORF 1170, ORF 1171, ORF 234, ORF 235, ORF 236, ORF 1172, ORF 243, ORF 251, ORF 252, ORF 1176, ORF 253, ORF 255, ORF 254, ORF 256, ORF 1177, ORF 1178, ORF 262, ORF 263, ORF 1264, ORF 278, ORF 279, ORF 1180, ORF 280, ORF 290, ORF 291, ORF 292, ORF 296, ORF 1181, ORF 297, ORF 298, ORF 300, ORF 1265, ORF 322, ORF 324, ORF 325, ORF 370, ORF 1186, ORF 371, ORF 372, ORF 1187, ORF 373, ORF 378, ORF 1266, ORF 382, ORF 383, ORF 384, ORF 385, ORF 386, ORF 1188, ORF 1189, ORF 391, ORF 392, ORF 398, ORF 400, ORF 403, ORF 1191, ORF 423, ORF 435, ORF 445, ORF 450, ORF 1193, ORF 456, ORF 460, ORF 461, ORF 465, ORF 1196, ORF 471, ORF 473, ORF 475, ORF 481, ORF 484, ORF 487, ORF 488, ORF 489, ORF 490, ORF 491, ORF 492, ORF 493, ORF 494, ORF 495, ORF 496, ORF 497, ORF 498, ORF 499, ORF 502, ORF 1267, ORF 1268, ORF 508, ORF 510, ORF 509, ORF 512, ORF 515, ORF 519, ORF 1197, ORF 521, ORF 1198, ORF 522, ORF 524, ORF 528, ORF 534, ORF 537, ORF 1269, ORF 1270, ORF 548, ORF 551, ORF 557, ORF 1201, ORF 1203, ORF 562, ORF 566, ORF 593, ORF 595, ORF 600, ORF 1271, ORF 604, ORF 611, ORF 612, ORF 614, ORF 616, ORF 625, ORF 627, ORF 628, ORF 629, ORF 631, ORF 641, ORF 1272, ORF 648, ORF 1212, ORF 663, ORF 685, ORF 707, ORF 714, ORF 715, ORF 716, ORF 717, ORF 722, ORF 746, ORF 1273, ORF 761, ORF 764, ORF 770, ORF 1217, ORF 783, ORF 1274, ORF 803, ORF 815, ORF 1220, ORF 835, ORF 1221, ORF 844, ORF 845, ORF 846, ORF 847, ORF 848, ORF 849, ORF 850, ORF 851, ORF 1275, ORF 852, ORF 862, ORF 1276, ORF 1277, ORF 873, ORF 1223, ORF 892, ORF 919, ORF 1225,

ORF 1278, ORF 926, ORF 1228, ORF 1229, ORF 1230, ORF 1279, ORF 1281, ORF 1282, ORF 1283, ORF 948, ORF 950, ORF 949, ORF 951, ORF 980, ORF 982, ORF 1233, ORF 999, ORF 1000, ORF 1001, ORF 1002, ORF 1008, ORF 1285, ORF 1235, ORF 1016, ORF 1019, ORF 1027, ORF 1036, ORF 1241, ORF 1048, ORF 1049, ORF 1050, ORF 1053, ORF 1054, ORF 1064, ORF 1076, ORF 1091, ORF 1288, ORF 1093, ORF 1289, ORF 1101, ORF 1103, ORF 1245, ORF 1246, ORF 1247, ORF 1290, ORF 1291, ORF 1115, ORF 1116, ORF 1118, ORF 1120, ORF 1249, ORF 1121, ORF 1250, ORF 1126, ORF 1251, ORF 1127, ORF 1128, ORF 1130, ORF 1129, ORF 1131, ORF 1136, ORF 1253, ORF 1292, ORF 1294, ORF 1295, ORF 1296, and one of their representative fragments.

Preferably, the invention also relates to the nucleotide sequences according to the invention, characterized in that they encode a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the intermediate metabolism, in particular in the metabolism of sugars and/or of cofactors, such as for example triose phosphate isomerase or pyruvate kinase, and in that they comprise a nucleotide sequence chosen from the following sequences: ORF2; ORF55; ORF56; ORF69; ORF75; ORF80; ORF100; ORF110; ORF114; ORF120; ORF121; ORF157; ORF160; ORF161; ORF172; ORF180; ORF181; ORF198; ORF200; ORF225; ORF248; ORF249; ORF276; ORF277; ORF318; ORF319; ORF320; ORF323; ORF331; ORF347; ORF375; ORF376; ORF381; ORF393; ORF394; ORF395; ORF396; ORF409; ORF446; ORF447; ORF448; ORF449; ORF513; ORF516; ORF571; ORF647; ORF662; ORF697; ORF718; ORF793; ORF794; ORF808; ORF809; ORF838; ORF839; ORF840; ORF853; ORF854; ORF918; ORF923; ORF929; ORF931; ORF938; ORF939; ORF958; ORF959; ORF960; ORF966; ORF995; ORF1021; ORF1040; ORF1041; ORF1042; ORF1085; ORF1100; ORF1102; ORF1117; ORF1118; ORF1119; ORF1120; ORF1135 and one of their representative fragments.

Preferably, the invention also relates to the nucleotide sequences according to the invention, characterized in that they encode a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the intermediate metabolism of nucleotides or nucleic acids, such as for example CTP synthetase or GMP synthetase, and in that they comprise a nucleotide sequence chosen from the following sequences:

ORF77; ORF78; ORF138; ORF189; ORF190; ORF233; ORF246; ORF338; ORF412; ORF421; ORF438; ORF607; ORF648; ORF657; ORF740; ORF783; ORF967; ORF989; ORF990; ORF992; ORF1011; ORF1058; ORF1059; ORF1073; ORF1074 and one of their representative fragments.

Preferably, the invention also relates to the nucleotide sequences according to the invention, characterized in that they encode a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the metabolism of nucleic acids, such as for example DNA polymerases or DNA topoisomerases, and in that they comprise a nucleotide sequence chosen from the following sequences:

ORF14; ORF59; ORF70; ORF71; ORF97; ORF113; ORF137; ORF141; ORF169; ORF285; ORF287;

ORF288; ORF313; ORF326; ORF358; ORF411; ORF443; ORF548; ORF569; ORF601; ORF651; ORF654; ORF658; ORF659; ORF664; ORF665; ORF694; ORF698; ORF704; ORF760; ORF762; ORF763; ORF786; ORF787; ORF788; ORF801; ORF802; ORF812; ORF819; ORF822; ORF870; ORF897; ORF898; ORF902; ORF908; ORF916; ORF954; ORF955; ORF961; ORF983; ORF996; ORF1007; ORF1012; ORF1013; ORF1014; ORF1015; ORF1038; ORF1137 and one of their representative fragments.

Preferably, the invention also relates to the nucleotide sequences according to the invention, characterized in that they encode a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the metabolism of amino acids or polypeptides, such as for example serine hydroxymethyl transferase or the proteins which load amino acids onto transfer RNAs, and in that they comprise a nucleotide sequence chosen from the following sequences:

ORF99; ORF111; ORF127; ORF134; ORF140; ORF174; ORF175; ORF176; ORF353; ORF377; ORF404; ORF523; ORF539; ORF559; ORF561; ORF586; ORF598; ORF609; ORF636; ORF687; ORF700; ORF701; ORF759; ORF790; ORF857; ORF861; ORF904; ORF936; ORF952; ORF962; ORF963; ORF964; ORF965; ORF991; ORF1003; ORF1004; ORF1005; ORF1018; ORF1067; ORF1110; ORF1111; ORF1112; ORF1114; ORF1121; ORF1122; ORF1123; ORF1124; ORF1125 and one of their representative fragments.

Preferably, the invention also relates to the nucleotide sequences according to the invention, characterized in that they encode a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the metabolism of polypeptides, such as for example protein kinases or proteases, and in that they comprise a nucleotide sequence chosen from the following sequences:

ORF4; ORF44; ORF45; ORF48; ORF54; ORF112; ORF130; ORF155; ORF163; ORF212; ORF257; ORF307; ORF343; ORF405; ORF416; ORF458; ORF540; ORF541; ORF542; ORF543; ORF544; ORF560; ORF594; ORF652; ORF699; ORF723; ORF747; ORF817; ORF827; ORF871; ORF909; ORF910; ORF911; ORF912; ORF1023; ORF1051; ORF1052; ORF1081 and one of their representative fragments.

Preferably, the invention also relates to the nucleotide sequences according to the invention, characterized in that they encode a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the metabolism of fatty acids, such as for example succinyl-CoA-synthesizing proteins or phosphatidylserine synthetase, and in that they comprise a nucleotide sequence chosen from the following sequences:

ORF76; ORF284; ORF308; ORF309; ORF310; ORF311; ORF312; ORF425; ORF433; ORF565; ORF688; ORF690; ORF691; ORF767; ORF797; ORF894; ORF895; ORF994; ORF1020; ORF1030; ORF1033; ORF1034; ORF1046; ORF1047; ORF1057 and one of their representative fragments.

Preferably, the invention also relates to the nucleotide sequences according to the invention, characterized in that they encode a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the synthesis of the wall, such as for example KDO transferase, and the proteins responsible for the attachment of certain sugars onto the exposed proteins, and in that they comprise a nucleotide sequence chosen from the following sequences: ORF49; ORF50; ORF177; ORF178; ORF245; ORF610; ORF972; ORF974; ORF978; ORF1037 and one of their representative fragments.

Preferably, the invention also relates to the nucleotide sequences according to the invention, characterized in that they encode a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the transcription, translation and/or maturation process, such as for example initiation factors, RNA polymerases or certain chaperone proteins, and in that they comprise a nucleotide sequence chosen from the following sequences: ORF90; ORF92; ORF131; ORF151; ORF199; ORF333; ORF334; ORF336; ORF379; ORF589; ORF590; ORF619; ORF630; ORF649; ORF739; ORF741; ORF806; ORF821; ORF843; ORF968; ORF971; ORF1061 and one of their representative fragments.

Preferably, the invention also relates to the nucleotide sequences according to the invention, characterized in that they encode a *Chlamydia pneumoniae* ribosomal polypeptide or one of its representative fragments, such as for example the ribosomal proteins L21, L27 and S10, and in that they comprise a nucleotide sequence chosen from the following sequences: ORF93; ORF94; ORF95; ORF136; ORF259; ORF332; ORF348; ORF583; ORF584; ORF588; ORF591; ORF592; ORF663; ORF666; ORF667; ORF669; ORF670; ORF671; ORF672; ORF673; ORF674; ORF675; ORF676; ORF677; ORF678; ORF679; ORF680; ORF681; ORF683; ORF684; ORF738; ORF781; ORF1008; ORF1024; ORF1025; ORF1066 and one of their representative fragments.

Preferably, the invention also relates to the nucleotide sequences according to the invention, characterized in that they encode a *Chlamydia pneumoniae* transport polypeptide or one of its representative fragments, such as for example the proteins for transporting amino acids, sugars and certain oligopeptides, and in that they comprise a nucleotide sequence chosen from the following sequences: ORF40; ORF41; ORF52; ORF105; ORF106; ORF107; ORF109; ORF133; ORF210; ORF211; ORF214; ORF215; ORF216; ORF217; ORF218; ORF219; ORF220; ORF223; ORF242; ORF260; ORF293; ORF299; ORF366; ORF369; ORF575; ORF602; ORF638; ORF639; ORF640; ORF643; ORF653; ORF702; ORF703; ORF724; ORF732; ORF855; ORF856; ORF901; ORF906; ORF933; ORF942; ORF1043; ORF1086; ORF1105 and one of their representative fragments.

Preferably, the invention also relates to the nucleotide sequences according to the invention, characterized in that they encode a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the virulence process, such as for example the proteins analogous to the *Escherichia coli* vacB protein, and in that they comprise a nucleotide sequence chosen from the following sequences:

ORF546; ORF550; ORF778; ORF779; ORF886 and one of their representative fragments.

Preferably, the invention also relates to the nucleotide sequences according to the invention, characterized in that they encode a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the secretory system and/or which is secreted, such as for example proteins homologous to proteins in the secretory system of certain bacteria such as the Salmonellae or the Yersiniae, and in that they comprise a nucleotide sequence chosen from the following sequences:

ORF751; ORF874; ORF875; ORF876; ORF883; ORF884; ORF885 and one of their representative fragments.

Preferably, the invention also relates to a nucleotide sequence according to the invention, characterized in that they encode a polypeptide specific to *Chlamydia pneumoniae* or one of its representative fragments (with a Blast E value of $>10^{-5}$), and in that they comprise a nucleotide sequence chosen from the following sequences:

ORF7; ORF8; ORF17; ORF18; ORF19; ORF20; ORF22; ORF23; ORF24; ORF51; ORF60; ORF63; ORF65; ORF66; ORF67; ORF83; ORF84; ORF86; ORF87; ORF125; ORF143; ORF144; ORF179; ORF182; ORF184; ORF185; ORF187; ORF221; ORF252; ORF254;; ORF278; ORF279; ORF387; ORF388; ORF397; ORF1048; ORF1049; ORF1050; ORF1128; ORF1130; ORF1131 and one of their representative fragments.

Also forming part of the invention are polypeptides encoded by the polynucleotides of the invention, as well as fusion polypeptides comprising such polypeptides. In one embodiment, the polypeptides and fusion polypeptides immunoreact with seropositive serum of an individual infected with *Chlamydia pneumoniae*. For example, described below, are polypeptide sequences exhibiting particularly preferable characteristics. For each group of preferred polypeptides described below, it is to be understood that in addition to the individual polypeptides listed, in instances wherein such polypeptides are encoded as part of "combined" ORFs, such "combined" polypeptides are also to be included within the preferred group.

The subject of the invention is also a polypeptide according to the invention, characterized in that it is a polypeptide of the cellular envelope, preferably of the outer cellular envelope, of *Chlamydia pneumoniae* or one of its representative fragments. According to the invention, the said polypeptide is preferably chosen from the polypeptides having the following sequences:

SEQ ID No. 15; SEQ ID No. 25; SEQ ID No. 26; SEQ ID No. 27; SEQ ID No. 28; SEQ ID No. 29; SEQ ID No. 30; SEQ ID No. 31; SEQ ID No. 32; SEQ ID No. 33; SEQ ID No. 35; SEQ ID No. 68; SEQ ID No. 124; SEQ ID No. 275; SEQ ID No. 291; SEQ ID No. 294; SEQ ID No. 327; SEQ ID No. 342; SEQ ID No. 364; SEQ ID No. 374; SEQ ID No. 380; SEQ ID No. 414; SEQ ID No. 439; SEQ ID No. 466; SEQ ID No. 467; SEQ ID No. 468; SEQ ID No. 469; SEQ ID No. 470; SEQ ID No. 472; SEQ ID No. 474; SEQ ID No. 476; SEQ ID No. 477; SEQ ID No. 478; SEQ ID No. 479;

SEQ ID No. 480; SEQ ID No. 482; SEQ ID No. 485; SEQ ID No. 500; SEQ ID No. 501; SEQ ID No. 503; SEQ ID No. 504; SEQ ID No. 505; SEQ ID No. 506; SEQ ID No. 520; SEQ ID No. 578; SEQ ID No. 580; SEQ ID No. 581; SEQ ID No. 595; SEQ ID No. 596; SEQ ID No. 597; SEQ ID No. 737; SEQ ID No. 830; SEQ ID No. 834; SEQ ID No. 836; SEQ ID No. 893; SEQ ID No. 917; SEQ ID No. 932; SEQ ID No. 976; SEQ ID No. 1035; SEQ ID No. 1045; SEQ ID No. 1090 and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, characterized in that it is a *Chlamydia pneumoniae* transmembrane polypeptide or one of its representative fragments, having between 1 and 3 transmembrane domains, and in that it is chosen from the polypeptides having the following sequences:

SEQ ID No. 2; SEQ ID No. 3; SEQ ID No. 6; SEQ ID No. 9; SEQ ID No. 10; SEQ ID No. 11; SEQ ID No. 13; SEQ ID No. 14; SEQ ID No. 16; SEQ ID No. 18; SEQ ID No. 19; SEQ ID No. 20; SEQ ID No. 21; SEQ ID No. 22; SEQ ID No. 25; SEQ ID No. 27; SEQ ID No. 28; SEQ ID No. 29; SEQ ID No. 30; SEQ ID No. 31; SEQ ID No. 32; SEQ ID No. 33; SEQ ID No. 34; SEQ ID No. 35; SEQ ID No. 37; SEQ ID No. 39; SEQ ID No. 41; SEQ ID No. 42; SEQ ID No. 44; SEQ ID No. 45; SEQ ID No. 46; SEQ ID No. 47; SEQ ID No. 48; SEQ ID No. 49; SEQ ID No. 50; SEQ ID No. 53; SEQ ID No. 54; SEQ ID No. 56; SEQ ID No. 57; SEQ ID No. 59; SEQ ID No. 60; SEQ ID No. 61; SEQ ID No. 62; SEQ ID No. 63; SEQ ID No. 64; SEQ ID No. 65; SEQ ID No. 66; SEQ ID No. 69;; SEQ ID No. 72; SEQ ID No. 73; SEQ ID No. 74; SEQ ID No. 76; SEQ ID No. 77; SEQ ID No. 78; SEQ ID No. 79; SEQ ID No. 80; SEQ ID No. 82; SEQ ID No. 84; SEQ ID No. 85; SEQ ID No. 86; SEQ ID No. 88; SEQ ID No. 89; SEQ ID No. 90; SEQ ID No. 91; SEQ ID No. 92; SEQ ID No. 93; SEQ ID No. 95; SEQ ID No. 96; SEQ ID No. 98; SEQ ID No. 99; SEQ ID No. 100; SEQ ID No. 101; SEQ ID No. 102; SEQ ID No. 103; SEQ ID No. 104; SEQ ID No. 105; SEQ ID No. 106; SEQ ID No. 107; SEQ ID No. 108; SEQ ID No. 114; SEQ ID No. 117; SEQ ID No. 118; SEQ ID No. 122; SEQ ID No. 123; SEQ ID No. 124; SEQ ID No. 125; SEQ ID No. 129; SEQ ID No. 130; SEQ ID No. 131; SEQ ID No. 132; SEQ ID No. 133; SEQ ID No. 134; SEQ ID No. 135; SEQ ID No. 137; SEQ ID No. 138; SEQ ID No. 139; SEQ ID No. 140; SEQ ID No. 141; SEQ ID No. 142; SEQ ID No. 143; SEQ ID No. 145; SEQ ID No. 146; SEQ ID No. 147; SEQ ID No. 150; SEQ ID No. 151; SEQ ID No. 152; SEQ ID No. 156; SEQ ID No. 157; SEQ ID No. 158; SEQ ID No. 159; SEQ ID No. 160; SEQ ID No. 161; SEQ ID No. 162; SEQ ID No. 164; SEQ ID No. 166; SEQ ID No. 167; SEQ ID No. 170; SEQ ID No. 173; SEQ ID No. 175; SEQ ID No. 176; SEQ ID No. 178; SEQ ID No. 179; SEQ ID No. 180; SEQ ID No. 182; SEQ ID No. 183; SEQ ID No. 184; SEQ ID No. 185; SEQ ID No. 186; SEQ ID No. 187; SEQ ID No. 188; SEQ ID No. 189; SEQ ID No. 190; SEQ ID No. 191; SEQ ID No. 192; SEQ ID No: 194; SEQ ID No. 195; SEQ ID No. 196; SEQ ID No. 197; SEQ ID No. 198; SEQ ID No. 199; SEQ ID No. 200; SEQ ID No. 201; SEQ ID No. 202; SEQ ID No. 205; SEQ ID No. 207; SEQ ID No. 208; SEQ ID No. 209; SEQ ID No. 210; SEQ ID No. 212; SEQ ID

No. 215; SEQ ID No. 219; SEQ ID No. 220; SEQ ID No. 224; SEQ ID No. 226; SEQ ID No. 227; SEQ ID No. 228; SEQ ID No. 231; SEQ ID No. 232; SEQ ID No. 233; SEQ ID No. 234; SEQ ID No. 235; SEQ ID No. 236; SEQ ID No. 238; SEQ ID No. 239; SEQ ID No. 240; SEQ ID No. 241; SEQ ID No. 242; SEQ ID No. 244; SEQ ID No. 247; SEQ ID No. 251; SEQ ID No. 252; SEQ ID No. 253; SEQ ID No. 255; SEQ ID No. 256; SEQ ID No. 257; SEQ ID No. 258; SEQ ID No. 260; SEQ ID No. 262; SEQ ID No. 263; SEQ ID No. 266; SEQ ID No. 267; SEQ ID No. 268; SEQ ID No. 269; SEQ ID No. 270; SEQ ID No. 273; SEQ ID No. 274; SEQ ID No. 276; SEQ ID No. 278; SEQ ID No. 279; SEQ ID No. 280; SEQ ID No. 281; SEQ ID No. 282; SEQ ID No. 283; SEQ ID No. 284; SEQ ID No. 286; SEQ ID No. 287; SEQ ID No. 289; SEQ ID No. 290; SEQ ID No. 291; SEQ ID No. 293; SEQ ID No. 294; SEQ ID No. 297; SEQ ID No. 304; SEQ ID No. 305; SEQ ID No. 307; SEQ ID No. 308; SEQ ID No. 309; SEQ ID No. 310; SEQ ID No. 311; SEQ ID No. 313; SEQ ID No. 314; SEQ ID No. 315; SEQ ID No. 316; SEQ ID No. 318; SEQ ID No. 319; SEQ ID No. 320; SEQ ID No. 321; SEQ ID No. 322; SEQ ID No. 323; SEQ ID No. 324; SEQ ID No. 325; SEQ ID No. 326; SEQ ID No. 331; SEQ ID No. 332; SEQ ID No. 336; SEQ ID No. 338; SEQ ID No. 339; SEQ ID No. 341; SEQ ID No. 344; SEQ ID No. 345; SEQ ID No. 346; SEQ ID No. 350; SEQ ID No. 352; SEQ ID No. 353; SEQ ID No. 356; SEQ ID No. 357; SEQ ID No. 358; SEQ ID No. 359; SEQ ID No. 360; SEQ ID No. 362; SEQ ID No. 365; SEQ ID No. 366; SEQ ID No. 367; SEQ ID No. 370; SEQ ID No. 372; SEQ ID No. 373; SEQ ID No. 376; SEQ ID No. 377; SEQ ID No. 378; SEQ ID No. 379; SEQ ID No. 381; SEQ ID No. 382; SEQ ID No. 383; SEQ ID No. 384; SEQ ID No. 385; SEQ ID No. 386; SEQ ID No. 387; SEQ ID No. 390; SEQ ID No. 392; SEQ ID No. 393; SEQ ID No. 394; SEQ ID No. 396; SEQ ID No. 398; SEQ ID No. 399; SEQ ID No. 400; SEQ ID No. 404; SEQ ID No. 408; SEQ ID No. 410; SEQ ID No. 411; SEQ ID No. 413; SEQ ID No. 416; SEQ ID No. 417; SEQ ID No. 418; SEQ ID No. 420; SEQ ID No. 422; SEQ ID No. 424; SEQ ID No. 427; SEQ ID No. 428; SEQ ID No. 429; SEQ ID No. 430; SEQ ID No. 431; SEQ ID No. 433; SEQ ID No. 434; SEQ ID No. 437; SEQ ID No. 440; SEQ ID No. 441; SEQ ID No. 442; SEQ ID No. 443; SEQ ID No. 444; SEQ ID No. 445; SEQ ID No. 447; SEQ ID No. 450; SEQ ID No. 451; SEQ ID No. 452; SEQ ID No. 455; SEQ ID No. 456; SEQ ID No. 459; SEQ ID No. 460; SEQ ID No. 461; SEQ ID No. 462; SEQ ID No. 463; SEQ ID No. 464; SEQ ID No. 465; SEQ ID No. 467; SEQ ID No. 469; SEQ ID No. 471; SEQ ID No. 474; SEQ ID No. 475; SEQ ID No. 476; SEQ ID No. 477; SEQ ID No. 479; SEQ ID No. 482; SEQ ID No. 483; SEQ ID No. 484; SEQ ID No. 485; SEQ ID No. 486; SEQ ID No. 487; SEQ ID No. 488; SEQ ID No. 491; SEQ ID No. 493; SEQ ID No. 494; SEQ ID No. 497; SEQ ID No. 498; SEQ ID No. 499; SEQ ID No. 503; SEQ ID No. 508; SEQ ID No. 509; SEQ ID No. 510; SEQ ID No. 512; SEQ ID No. 514; SEQ ID No. 515; SEQ ID No. 516; SEQ ID No. 517; SEQ ID No. 518; SEQ ID No. 520; SEQ ID No. 521; SEQ ID No. 523; SEQ ID No. 525; SEQ ID No. 527; SEQ ID No. 528; SEQ ID No. 529; SEQ ID No. 530; SEQ ID No. 531; SEQ ID No. 533; SEQ ID No. 534; SEQ ID No. 535; SEQ ID No. 536; SEQ ID No. 537; SEQ ID No. 540; SEQ ID No. 541; SEQ ID No. 543; SEQ ID No. 544; SEQ ID

No. 545; SEQ ID No. 546; SEQ ID No. 548; SEQ ID No. 549; SEQ ID No. 551; SEQ ID No. 553; SEQ ID No. 554; SEQ ID No. 555; SEQ ID No. 556; SEQ ID No. 557; SEQ ID No. 558; SEQ ID No. 559; SEQ ID No. 560; SEQ ID No. 562; SEQ ID No. 563; SEQ ID No. 564; SEQ ID No. 565; SEQ ID No. 566; SEQ ID No. 569; SEQ ID No. 571; SEQ ID No. 573; SEQ ID No. 576; SEQ ID No. 577; SEQ ID No. 581; SEQ ID No. 583; SEQ ID No. 584; SEQ ID No. 585; SEQ ID No. 586; SEQ ID No. 588; SEQ ID No. 591; SEQ ID No. 592; SEQ ID No. 594; SEQ ID No. 595; SEQ ID No. 596; SEQ ID No. 597; SEQ ID No. 599; SEQ ID No. 600; SEQ ID No. 603; SEQ ID No. 605; SEQ ID No. 608; SEQ ID No. 614; SEQ ID No. 615; SEQ ID No. 620; SEQ ID No. 621; SEQ ID No. 622; SEQ ID No. 623; SEQ ID No. 624; SEQ ID No. 625; SEQ ID No. 629; SEQ ID No. 630; SEQ ID No. 631; SEQ ID No. 633; SEQ ID No. 634; SEQ ID No. 637; SEQ ID No. 642; SEQ ID No. 644; SEQ ID No. 645; SEQ ID No. 647; SEQ ID No. 648; SEQ ID No. 652; SEQ ID No. 654; SEQ ID No. 655; SEQ ID No. 657; SEQ ID No. 658; SEQ ID No. 659; SEQ ID No. 660; SEQ ID No. 661; SEQ ID No. 664; SEQ ID No. 665; SEQ ID No. 666; SEQ ID No. 667; SEQ ID No. 670; SEQ ID No. 671; SEQ ID No. 672; SEQ ID No. 673; SEQ ID No. 674; SEQ ID No. 676; SEQ ID No. 679; SEQ ID No. 681; SEQ ID No. 684; SEQ ID No. 687; SEQ ID No. 688; SEQ ID No. 689; SEQ ID No. 690; SEQ ID No. 693; SEQ ID No. 694; SEQ ID No. 695; SEQ ID No. 696; SEQ ID No. 697; SEQ ID No. 698; SEQ ID No. 699; SEQ ID No. 700; SEQ ID No. 701; SEQ ID No. 703; SEQ ID No. 705; SEQ ID No. 706; SEQ ID No. 707; SEQ ID No. 708; SEQ ID No. 710; SEQ ID No. 712; SEQ ID No. 715; SEQ ID No. 716; SEQ ID No. 717; SEQ ID No. 718; SEQ ID No. 719; SEQ ID No. 721; SEQ ID No. 722; SEQ ID No. 723; SEQ ID No. 725; SEQ ID No. 726; SEQ ID No. 727; SEQ ID No. 728; SEQ ID No. 729; SEQ ID No. 730; SEQ ID No. 731; SEQ ID No. 733; SEQ ID No. 736; SEQ ID No. 737; SEQ ID No. 738; SEQ ID No. 740; SEQ ID No. 741; SEQ ID No. 742; SEQ ID No. 743; SEQ ID No. 747; SEQ ID No. 748; SEQ ID No. 750; SEQ ID No. 752; SEQ ID No. 754; SEQ ID No. 755; SEQ ID No. 756; SEQ ID No. 757; SEQ ID No. 759; SEQ ID No. 760; SEQ ID No. 761; SEQ ID No. 762; SEQ ID No. 763; SEQ ID No. 764; SEQ ID No. 765; SEQ ID No. 766; SEQ ID No. 767; SEQ ID No. 768; SEQ ID No. 772; SEQ ID No. 774; SEQ ID No. 775; SEQ ID No. 777; SEQ ID No. 781; SEQ ID No. 783; SEQ ID No. 788; SEQ ID No. 791; SEQ ID No. 792; SEQ ID No. 793; SEQ ID No. 794; SEQ ID No. 795; SEQ ID No. 796; SEQ ID No. 797; SEQ ID No. 798; SEQ ID No. 799; SEQ ID No. 802; SEQ ID No. 803; SEQ ID No. 806; SEQ ID No. 807; SEQ ID No. 808; SEQ ID No. 809; SEQ ID No. 810; SEQ ID No. 811; SEQ ID No. 813; SEQ ID No. 814; SEQ ID No. 815; SEQ ID No. 816; SEQ ID No. 817; SEQ ID No. 819; SEQ ID No. 820; SEQ ID No. 821; SEQ ID No. 823; SEQ ID No. 824; SEQ ID No. 827; SEQ ID No. 829; SEQ ID No. 830; SEQ ID No. 831; SEQ ID No. 833; SEQ ID No. 834; SEQ ID No. 835; SEQ ID No. 837; SEQ ID No. 844; SEQ ID No. 845; SEQ ID No. 846; SEQ ID No. 847; SEQ ID No. 848; SEQ ID No. 849; SEQ ID No. 850; SEQ ID No. 851; SEQ ID No. 852; SEQ ID No. 854; SEQ ID No. 855; SEQ ID No. 856; SEQ ID No. 857; SEQ ID No. 859; SEQ ID No. 860; SEQ ID No. 862; SEQ ID No. 865; SEQ ID No. 866; SEQ ID No. 868; SEQ ID No. 869; SEQ ID

No. 870; SEQ ID No. 871; SEQ ID No. 872; SEQ ID No. 874; SEQ ID No. 877; SEQ ID No. 878; SEQ ID No. 879; SEQ ID No. 880; SEQ ID No. 881; SEQ ID No. 882; SEQ ID No. 884; SEQ ID No. 885; SEQ ID No. 888; SEQ ID No. 889; SEQ ID No. 890; SEQ ID No. 891; SEQ ID No. 892; SEQ ID No. 894; SEQ ID No. 895; SEQ ID No. 896; SEQ ID No. 897; SEQ ID No. 899; SEQ ID No. 900; SEQ ID No. 902; SEQ ID No. 903; SEQ ID No. 904; SEQ ID No. 905; SEQ ID No. 909; SEQ ID No. 910; SEQ ID No. 912; SEQ ID No. 913; SEQ ID No. 914; SEQ ID No. 915; SEQ ID No. 917; SEQ ID No. 918; SEQ ID No. 919; SEQ ID No. 921; SEQ ID No. 923; SEQ ID No. 924; SEQ ID No. 926; SEQ ID No. 927; SEQ ID No. 928; SEQ ID No. 929; SEQ ID No. 930; SEQ ID No. 931; SEQ ID No. 937; SEQ ID No. 938; SEQ ID No. 939; SEQ ID No. 941; SEQ ID No. 943; SEQ ID No. 948; SEQ ID No. 951; SEQ ID No. 952; SEQ ID No. 953; SEQ ID No. 958; SEQ ID No. 960; SEQ ID No. 963; SEQ ID No. 964; SEQ ID No. 965; SEQ ID No. 968; SEQ ID No. 970; SEQ ID No. 974; SEQ ID No. 975; SEQ ID No. 977; SEQ ID No. 979; SEQ ID No. 980; SEQ ID No. 981; SEQ ID No. 983; SEQ ID No. 984; SEQ ID No. 985; SEQ ID No. 987; SEQ ID No. 989; SEQ ID No. 992; SEQ ID No. 993; SEQ ID No. 997; SEQ ID No. 998; SEQ ID No. 999; SEQ ID No. 1001; SEQ ID No. 1002; SEQ ID No. 1004; SEQ ID No. 1005; SEQ ID No. 1009; SEQ ID No. 1013; SEQ ID No. 1014; SEQ ID No. 1015; SEQ ID No. 1016; SEQ ID No. 1019; SEQ ID No. 1021; SEQ ID No. 1023; SEQ ID No. 1024; SEQ ID No. 1029; SEQ ID No. 1031; SEQ ID No. 1033; SEQ ID No. 1034; SEQ ID No. 1039; SEQ ID No. 1041; SEQ ID No. 1042; SEQ ID No. 1045; SEQ ID No. 1047; SEQ ID No. 1049; SEQ ID No. 1051; SEQ ID No. 1052; SEQ ID No. 1053; SEQ ID No. 1054; SEQ ID No. 1056; SEQ ID No. 1059; SEQ ID No. 1061; SEQ ID No. 1062; SEQ ID No. 1063; SEQ ID No. 1064; SEQ ID No. 1065; SEQ ID No. 1067; SEQ ID No. 1075; SEQ ID No. 1077; SEQ ID No. 1078; SEQ ID No. 1079; SEQ ID No. 1080; SEQ ID No. 1081; SEQ ID No. 1089; SEQ ID No. 1095; SEQ ID No. 1097; SEQ ID No. 1098; SEQ ID No. 1099; SEQ ID No. 1101; SEQ ID No. 1102; SEQ ID No. 1103; SEQ ID No. 1106; SEQ ID No. 1107; SEQ ID No. 1108; SEQ ID No. 1109; SEQ ID No. 1110; SEQ ID No. 1113; SEQ ID No. 1116; SEQ ID No. 1118; SEQ ID No. 1119; SEQ ID No. 1121; SEQ ID No. 1123; SEQ ID No. 1124; SEQ ID No. 1126; SEQ ID No. 1128; SEQ ID No. 1130; SEQ ID No. 1131; SEQ ID No. 1133; SEQ ID No. 1134; SEQ ID No. 1136; SEQ ID No. 1137 and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, characterized in that it is a *Chlamydia pneumoniae* transmembrane polypeptide or one of its respective fragments, having between 4 and 6 transmembrane domains, and in that it is chosen from the polypeptides having the following sequences:

SEQ ID No. 5; SEQ ID No. 7; SEQ ID No. 8; SEQ ID No. 15; SEQ ID No. 36; SEQ ID No. 38; SEQ ID No. 51; SEQ ID No. 55; SEQ ID No. 58; SEQ ID No. 67; SEQ ID No. 70; SEQ ID No. 81; SEQ ID No. 97; SEQ ID No. 110; SEQ ID No. 111; SEQ ID No. 115; SEQ ID No. 119; SEQ ID No. 126; SEQ ID No. 128; SEQ ID No. 148; SEQ ID No. 155; SEQ ID No. 163; SEQ ID

No. 165; SEQ ID No. 168; SEQ ID No. 169; SEQ ID No. 171; SEQ ID No. 172; SEQ ID No. 174; SEQ ID No. 177; SEQ ID No. 181; SEQ ID No. 193; SEQ ID No. 203; SEQ ID No. 213; SEQ ID No. 214; SEQ ID No. 216; SEQ ID No. 217; SEQ ID No. 221; SEQ ID No. 222; SEQ ID No. 225; SEQ ID No. 229; SEQ ID No. 243; SEQ ID No. 246; SEQ ID No. 248; SEQ ID No. 254; SEQ ID No. 261; SEQ ID No. 285; SEQ ID No. 288; SEQ ID No. 292; SEQ ID No. 296; SEQ ID No. 298; SEQ ID No. 299; SEQ ID No. 301; SEQ ID No. 303; SEQ ID No. 317; SEQ ID No. 328; SEQ ID No. 329; SEQ ID No. 351; SEQ ID No. 354; SEQ ID No. 355; SEQ ID No. 364; SEQ ID No. 371; SEQ ID No. 374; SEQ ID No. 375; SEQ ID No. 391; SEQ ID No. 395; SEQ ID No. 401; SEQ ID No. 403; SEQ ID No. 405; SEQ ID No. 409; SEQ ID No. 414; SEQ ID No. 419; SEQ ID No. 421; SEQ ID No. 423; SEQ ID No. 425; SEQ ID No. 438; SEQ ID No. 448; SEQ ID No. 453; SEQ ID No. 458; SEQ ID No. 466; SEQ ID No. 468; SEQ ID No. 470; SEQ ID No. 480; SEQ ID No. 489; SEQ ID No. 490; SEQ ID No. 496; SEQ ID No. 501; SEQ ID No. 504; SEQ ID No. 505; SEQ ID No. 506; SEQ ID No. 511; SEQ ID No. 513; SEQ ID No. 519; SEQ ID No. 526; SEQ ID No. 532; SEQ ID No. 538; SEQ ID No. 539; SEQ ID No. 547; SEQ ID No. 550; SEQ ID No. 561; SEQ ID No. 568; SEQ ID No. 570; SEQ ID No. 574; SEQ ID No. 578; SEQ ID No. 579; SEQ ID No. 580; SEQ ID No. 582; SEQ ID No. 589; SEQ ID No. 593; SEQ ID No. 598; SEQ ID No. 601; SEQ ID No. 604; SEQ ID No. 610; SEQ ID No. 613; SEQ ID No. 617; SEQ ID No. 626; SEQ ID No. 632; SEQ ID No. 635; SEQ ID No. 638; SEQ ID No. 640; SEQ ID No. 641; SEQ ID No. 646; SEQ ID No. 649; SEQ ID No. 650; SEQ ID No. 651; SEQ ID No. 686; SEQ ID No. 711; SEQ ID No. 724; SEQ ID No. 732; SEQ ID No. 734; SEQ ID No. 744; SEQ ID No. 745; SEQ ID No. 749; SEQ ID No. 751; SEQ ID No. 769; SEQ ID No. 770; SEQ ID No. 771; SEQ ID No. 773; SEQ ID No. 776; SEQ ID No. 779; SEQ ID No. 780; SEQ ID No. 785; SEQ ID No. 787; SEQ ID No. 789; SEQ ID No. 801; SEQ ID No. 805; SEQ ID No. 812; SEQ ID No. 822; SEQ ID No. 825; SEQ ID No. 826; SEQ ID No. 839; SEQ ID No. 841; SEQ ID No. 843; SEQ ID No. 853; SEQ ID No. 861; SEQ ID No. 875; SEQ ID No. 876; SEQ ID No. 886; SEQ ID No. 893; SEQ ID No. 898; SEQ ID No. 906; SEQ ID No. 907; SEQ ID No. 908; SEQ ID No. 920; SEQ ID No. 922; SEQ ID No. 925; SEQ ID No. 933; SEQ ID No. 935; SEQ ID No. 936; SEQ ID No. 944; SEQ ID No. 946; SEQ ID No. 947; SEQ ID No. 954; SEQ ID No. 959; SEQ ID No. 961; SEQ ID No. 966; SEQ ID No. 967; SEQ ID No. 972; SEQ ID No. 978; SEQ ID No. 995; SEQ ID No. 996; SEQ ID No. 1000; SEQ ID No. 1003; SEQ ID No. 1010; SEQ ID No. 1011; SEQ ID No. 1012; SEQ ID No. 1017; SEQ ID No. 1020; SEQ ID No. 1030; SEQ ID No. 1036; SEQ ID No. 1038; SEQ ID No. 1043; SEQ ID No. 1046; SEQ ID No. 1048; SEQ ID No. 1050; SEQ ID No. 1058; SEQ ID No. 1071; SEQ ID No. 1073; SEQ ID No. 1084; SEQ ID No. 1085; SEQ ID No. 1086; SEQ ID No. 1087; SEQ ID No. 1091; SEQ ID No. 1092; SEQ ID No. 1094; SEQ ID No. 1096; SEQ ID No. 1100; SEQ ID No. 1104; SEQ ID No. 1111; SEQ ID No. 1112; SEQ ID No. 1114; SEQ ID No. 1117; SEQ ID No. 1122; SEQ ID No. 1125 and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, characterized in that it is a *Chlamydia pneumoniae* transmembrane polypeptide or one of its representative fragments, having at least 7 transmembrane domains, and in that it is chosen from the polypeptides having the following sequences:

SEQ ID No. 17; SEQ ID No. 52; SEQ ID No. 68; SEQ ID No. 83; SEQ ID No. 87; SEQ ID No. 109; SEQ ID No. 112; SEQ ID No. 113; SEQ ID No. 120; SEQ ID No. 121; SEQ ID No. 127; SEQ ID No. 153; SEQ ID No. 204; SEQ ID No. 211; SEQ ID No. 218; SEQ ID No. 223; SEQ ID No. 275; SEQ ID No. 277; SEQ ID No. 295; SEQ ID No. 300; SEQ ID No. 302; SEQ ID No. 306; SEQ ID No. 327; SEQ ID No. 335; SEQ ID No. 342; SEQ ID No. 343; SEQ ID No. 347; SEQ ID No. 349; SEQ ID No. 361; SEQ ID No. 363; SEQ ID No. 369; SEQ ID No. 380; SEQ ID No. 388; SEQ ID No. 389; SEQ ID No. 397; SEQ ID No. 415; SEQ ID No. 432; SEQ ID No. 439; SEQ ID No. 446; SEQ ID No. 449; SEQ ID No. 472; SEQ ID No. 478; SEQ ID No. 500; SEQ ID No. 522; SEQ ID No. 524; SEQ ID No. 567; SEQ ID No. 575; SEQ ID No. 602; SEQ ID No. 606; SEQ ID No. 609; SEQ ID No. 636; SEQ ID No. 639; SEQ ID No. 643; SEQ ID No. 653; SEQ ID No. 668; SEQ ID No. 692; SEQ ID No. 702; SEQ ID No. 704; SEQ ID No. 713; SEQ ID No. 720; SEQ ID No. 778; SEQ ID No. 784; SEQ ID No. 800; SEQ ID No. 836; SEQ ID No. 838; SEQ ID No. 842; SEQ ID No. 864; SEQ ID No. 867; SEQ ID No. 883; SEQ ID No. 901; SEQ ID No. 916; SEQ ID No. 932; SEQ ID No. 934; SEQ ID No. 940; SEQ ID No. 942; SEQ ID No. 950; SEQ ID No. 956; SEQ ID No. 971; SEQ ID No. 973; SEQ ID No. 976; SEQ ID No. 988; SEQ ID No. 994; SEQ ID No. 1018; SEQ ID No. 1028; SEQ ID No. 1035; SEQ ID No. 1037; SEQ ID No. 1044; SEQ ID No. 1055; SEQ ID No. 1057; SEQ ID No. 1068; SEQ ID No. 1069; SEQ ID No. 1070; SEQ ID No. 1072; SEQ ID No. 1082; SEQ ID No. 1088; SEQ ID No. 1105; SEQ ID No. 1132; SEQ ID No. 1135 and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, in that it is a *Chlamydia pneumoniae* surface exposed polypeptide or one of its representative fragments, and in that it is chosen from the polypeptides having the following sequences:

SEQ ID No. 15, SEQ ID No. 25, SEQ ID No. 26, SEQ ID No. 27, SEQ ID No. 28, SEQ ID No. 29, SEQ ID No. 30, SEQ ID No. 31, SEQ ID No. 32, SEQ ID No. 33, SEQ ID No. 35, SEQ ID No. 36, SEQ ID No. 1257, SEQ ID No. 280, SEQ ID No. 291, SEQ ID No. 314, SEQ ID No. 354, SEQ ID No. 380, SEQ ID No. 1266, SEQ ID No. 466, SEQ ID No. 467, SEQ ID No. 468, SEQ ID No. 469, SEQ ID No. 470, SEQ ID No. 472, SEQ ID No. 474, SEQ ID No. 476, SEQ ID No. 477, SEQ ID No. 478, SEQ ID No. 479, SEQ ID No. 480, SEQ ID No. 482, SEQ ID No. 483, SEQ ID No. 485, SEQ ID No. 486, SEQ ID No. 500, SEQ ID No. 501, SEQ ID No. 503, SEQ ID No. 504, SEQ ID No. 505, SEQ ID No. 506, SEQ ID No. 507, SEQ ID No. 1268, SEQ ID No. 1269, SEQ ID No. 543, SEQ ID No. 544, SEQ ID No. 578, SEQ ID No. 579, SEQ ID No. 580, SEQ ID No. 581, SEQ ID No. 595, SEQ ID No. 596, SEQ ID No. 597, SEQ ID No. 1271, SEQ ID No. 633, SEQ ID No. 637, SEQ ID No. 699, SEQ ID No. 706, SEQ ID No. 737, SEQ ID No. 744, SEQ ID No. 1273, SEQ ID No. 751, SEQ ID No. 775, SEQ ID No. 776, SEQ ID No. 777, SEQ ID No. 793, SEQ ID No. 815, SEQ ID No.

830, SEQ ID No. 1221, SEQ ID No. 849, SEQ ID No. 851, SEQ ID No. 852, SEQ ID No. 874, SEQ ID No. 891, SEQ ID No. 922, SEQ ID No. 940, SEQ ID No. 1231, SEQ ID No. 1281, SEQ ID No. 1035, SEQ ID No. 1079, SEQ ID No. 1087, SEQ ID No. 1108, and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, characterized in that it is a *Chlamydia pneumoniae* lipoprotein or one of its representative fragments, and in that it is chosen from the polypeptides having the following sequences:

SEQ ID No. 3, SEQ ID No. 10, SEQ ID No. 11, SEQ ID No. 16, SEQ ID No. 1254, SEQ ID No. 1255, SEQ ID No. 38, SEQ ID No. 1256, SEQ ID No. 62, SEQ ID No. 85, SEQ ID No. 1258, SEQ ID No. 115, SEQ ID No. 1151, SEQ ID No. 151, SEQ ID No. 1259, SEQ ID No. 173, SEQ ID No. 1261, SEQ ID No. 186, SEQ ID No. 194, SEQ ID No. 205, SEQ ID No. 214, SEQ ID No. 216, SEQ ID No. 217, SEQ ID No. 238, SEQ ID No. 1177, SEQ ID No. 280, SEQ ID No. 291, SEQ ID No. 317, SEQ ID No. 327, SEQ ID No. 354, SEQ ID No. 364, SEQ ID No. 367, SEQ ID No. 414, SEQ ID No. 432, SEQ ID No. 1192, SEQ ID No. 460, SEQ ID No. 1267, SEQ ID No. 1268, SEQ ID No. 520, SEQ ID No. 536, SEQ ID No. 1270, SEQ ID No. 576, SEQ ID No. 597, SEQ ID No. 603, SEQ ID No. 609, SEQ ID No. 637, SEQ ID No. 1272, SEQ ID No. 652, SEQ ID No. 1213, SEQ ID No. 699, SEQ ID No. 705, SEQ ID No. 706, SEQ ID No. 708, SEQ ID No. 711, SEQ ID No. 727, SEQ ID No. 1274, SEQ ID No. 800, SEQ ID No. 814, SEQ ID No. 825, SEQ ID No. 829, SEQ ID No. 830, SEQ ID No. 831, SEQ ID No. 844, SEQ ID No. 849, SEQ ID No. 1275, SEQ ID No. 1276, SEQ ID No. 1277, SEQ ID No. 872, SEQ ID No. 878, SEQ ID No. 880, SEQ ID No. 891, SEQ ID No. 892, SEQ ID No. 1278, SEQ ID No. 1279, SEQ ID No. 1280, SEQ ID No. 941, SEQ ID No. 942, SEQ ID No. 1282, SEQ ID No. 1283, SEQ ID No. 952, SEQ ID No. 988, SEQ ID No. 998, SEQ ID No. 1009, SEQ ID No. 1285, SEQ ID No. 1235, SEQ ID No. 1028, SEQ ID No. 1056, SEQ ID No. 1070, SEQ ID No. 1287, SEQ ID No. 1087, SEQ ID No. 1288, SEQ ID No. 1289, SEQ ID No. 1098, SEQ ID No. 1246, SEQ ID No. 1291, SEQ ID No. 1108, SEQ ID No. 1109, SEQ ID No. 1112, SEQ ID No. 1133, and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, in that it is a *Chlamydia pneumoniae* polypeptide involved in lipopolysaccharide (LPS) biosynthesis, and in that it is chosen from the polypeptides having the following sequences:

SEQ ID No. 316, SEQ ID No. 564, SEQ ID No. 610, SEQ ID No. 647, SEQ ID No. 1211, SEQ ID No. 688, SEQ ID No. 924, and one of their representative fragments.

Preferably, the invention relates to additional LPS-related polypeptides according to the invention, in that it is:

(a) a *Chlamydia pneumoniae* KDO (3-deoxy-D-manno-octylosonic acid)-related polypeptide or one of its representative fragments, and in that it is chosen from the polypeptides having the following sequences: SEQ ID No. 177, SEQ ID No. 1156, SEQ ID No. 245, SEQ ID No. 767, and one of their representative fragments;

(b) a *Chlamydia pneumoniae* phosphomannomutase-related polypeptide or one of its representative fragments, and in that it is chosen from the polypeptides having the following sequences: SEQ ID No. 74, and its representative fragment;

(c) a *Chlamydia pneumoniae* phosphoglucomutase-related polypeptide or one of its representative fragments, and in that it is chosen from the polypeptides having the following sequences: SEQ ID No. 1286, SEQ ID No. 1039, and its representative fragment; and

(d) a *Chlamydia pneumoniae* lipid A component-related polypeptide or one of its representative fragments, and in that it is chosen from the polypeptides having the following sequences: SEQ ID No. 689, SEQ ID No. 690, SEQ ID No. 691, SEQ ID No. 1037, and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, in that it is a *Chlamydia pneumoniae* polypeptide or one of its representative fragments that contains an RGD sequence and is also an outer membrane protein, and in that it is chosen from the polypeptides having the following sequences: SEQ ID No. 468 and its representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, in that it is a *Chlamydia pneumoniae* polypeptide or one of its representative fragments that contains an RGD sequence that shows homology to cds1, cds2, and copN type III virulence loci in *Chlamydia Psitacci*, and in that it is chosen from the polypeptides having the following sequences:
SEQ ID No. 350 and its representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, in that it is a *Chlamydia pneumoniae* polypeptide or one of its representative fragments that is cysteine-rich and contains RGD sequence, and in that it is chosen from the polypeptides having the following sequences: SEQ ID No. 1290, SEQ ID No. 6846, SEQ ID No. 6848, and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, in that it is a *Chlamydia pneumoniae* outer membrane polypeptide that contains cysteines in their first 30 amino acids and also contain an RGD sequence, and in that it is chosen from the polypeptides having the following sequences:
SEQ ID No. 105, SEQ ID No. 106, SEQ ID No. 114, SEQ ID No. 170, SEQ ID No. 171, SEQ ID No. 1264, SEQ ID No. 268, SEQ ID No. 1265, SEQ ID No. 350, SEQ ID No. 393, SEQ ID No. 394, SEQ ID No. 451, SEQ ID No. 452, SEQ ID No. 453, SEQ ID No. 473, SEQ ID No. 499, SEQ ID No. 515, SEQ ID No. 519, SEQ ID No. 525, SEQ ID No. 526, SEQ ID No. 538, SEQ ID No. 611, SEQ ID No. 645, SEQ ID No. 686, SEQ ID No. 700, SEQ ID No. 746, SEQ ID No. 755, SEQ ID No. 756, SEQ ID No. 757, SEQ ID No. 789, SEQ ID No. 814, SEQ ID No. 855, SEQ ID No. 856, SEQ ID No. 878, SEQ ID No. 957, SEQ ID No. 958, SEQ ID No. 989, SEQ ID No. 1290, and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, in that it is a

Chlamydia pneumoniae polypeptide or one of its representative fragments that contains RGD sequences homologous to *Chlamydia trachomatis* polypeptides containing RGD sequences, and in that it is chosen from the polypeptides having the following sequences:

SEQ ID No. 114, SEQ ID No. 468, SEQ ID No. 755, SEQ ID No. 756, SEQ ID No. 757, SEQ ID No. 855, SEQ ID No. 856, SEQ ID No. 905, SEQ ID No. 913, SEQ ID No. 914, SEQ ID No. 915, and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, in that it is a *Chlamydia pneumoniae* Type III and non-Type III secreted polypeptide or one of its representative fragments, and in that it is chosen from the polypeptides having the following sequences:

SEQ ID No. 25, SEQ ID No. 28, SEQ ID No. 29, SEQ ID No. 33, SEQ ID No. 308, SEQ ID No. 309, SEQ ID No. 343, SEQ ID No. 344, SEQ ID No. 345, SEQ ID No. 367, SEQ ID No. 414, SEQ ID No. 415, SEQ ID No. 480, SEQ ID No. 550, SEQ ID No. 579, SEQ ID No. 580, SEQ ID No. 581, SEQ ID No. 597, SEQ ID No. 699, SEQ ID No. 744, SEQ ID No. 751, SEQ ID No. 776, SEQ ID No. 866, SEQ ID No. 874, SEQ ID No. 883, SEQ ID No. 884, SEQ ID No. 888, SEQ ID No. 891, SEQ ID No. 6845, and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, in that it is a *Chlamydia pneumoniae* cell wall anchored surface polypeptide or one of its representative fragments, and in that it is chosen from the polypeptides having the following sequences:

SEQ ID No. 267, SEQ ID No. 271, SEQ ID No. 419, SEQ ID No. 590, SEQ ID No. 932, SEQ ID No. 6844, SEQ ID No. 6847, and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, in that it is a *Chlamydia pneumoniae* polypeptide or one of its representative fragments not found in *Chlamydia trachomatis* (Blastp $P>e^{-10}$), and in that it is chosen from the polypeptides having the following sequences:

SEQ ID No. 7, SEQ ID No. 8, SEQ ID No. 9, SEQ ID No. 16, SEQ ID No. 17, SEQ ID No. 18, SEQ ID No. 19, SEQ ID No. 20, SEQ ID No. 21, SEQ ID No. 22, SEQ ID No. 1254, SEQ ID No. 23, SEQ ID No. 1255, SEQ ID No. 24, SEQ ID No. 1139, SEQ ID No. 1140, SEQ ID No. 46, SEQ ID No. 47, SEQ ID No. 51, SEQ ID No. 60, SEQ ID No. 1256, SEQ ID No. 61, SEQ ID No. 62, SEQ ID No. 63, SEQ ID No. 64, SEQ ID No. 1257, SEQ ID No. 65, SEQ ID No. 66, SEQ ID No. 67, SEQ ID No. 68, SEQ ID No. 1143, SEQ ID No. 1145, SEQ ID No. 83, SEQ ID No. 84, SEQ ID No. 1146, SEQ ID No. 85, SEQ ID No. 86, SEQ ID No. 87, SEQ ID No. 1258, SEQ ID No. 116, SEQ ID No. 117, SEQ ID No. 125, SEQ ID No. 1148, SEQ ID No. 143, SEQ ID No. 1150, SEQ ID No. 1151, SEQ ID No. 144, SEQ ID No. 145, SEQ ID No. 147, SEQ ID No. 148, SEQ ID No. 149, SEQ ID No. 150, SEQ ID No. 152, SEQ ID No. 1259, SEQ ID No. 162, SEQ ID No. 166, SEQ ID No. 1154, SEQ ID No. 167, SEQ ID No. 1261, SEQ ID No. 1156, SEQ ID No. 1157, SEQ ID No. 178, SEQ ID No. 179, SEQ ID No. 1158, SEQ ID No. 182, SEQ ID No. 183, SEQ ID No. 184, SEQ ID No. 185, SEQ ID No. 1159, SEQ ID No. 186, SEQ ID No. 1160, SEQ ID No. 187, SEQ ID No. 188, SEQ ID No. 189, SEQ ID

No. 190, SEQ ID No. 1161, SEQ ID No. 1162, SEQ ID No. 191, SEQ ID No. 192, SEQ ID No. 194, SEQ ID No. 195, SEQ ID No. 1163, SEQ ID No. 196, SEQ ID No. 201, SEQ ID No. 202, SEQ ID No. 209, SEQ ID No. 212, SEQ ID No. 221, SEQ ID No. 224, SEQ ID No. 1167, SEQ ID No. 226, SEQ ID No. 227, SEQ ID No. 228, SEQ ID No. 229, SEQ ID No. 230, SEQ ID No. 231, SEQ ID No. 232, SEQ ID No. 1169, SEQ ID No. 1170, SEQ ID No. 1171, SEQ ID No. 234, SEQ ID No. 235, SEQ ID No. 236, SEQ ID No. 1172, SEQ ID No. 243, SEQ ID No. 251, SEQ ID No. 252, SEQ ID No. 1176, SEQ ID No. 253, SEQ ID No. 255, SEQ ID No. 254, SEQ ID No. 256, SEQ ID No. 1177, SEQ ID No. 1178, SEQ ID No. 262, SEQ ID No. 263, SEQ ID No. 1264, SEQ ID No. 278, SEQ ID No. 279, SEQ ID No. 1180, SEQ ID No. 280, SEQ ID No. 290, SEQ ID No. 291, SEQ ID No. 292, SEQ ID No. 296, SEQ ID No. 1181, SEQ ID No. 297, SEQ ID No. 298, SEQ ID No. 300, SEQ ID No. 1265, SEQ ID No. 322, SEQ ID No. 324, SEQ ID No. 325, SEQ ID No. 370, SEQ ID No. 1186, SEQ ID No. 371, SEQ ID No. 372, SEQ ID No. 1187, SEQ ID No. 373, SEQ ID No. 378, SEQ ID No. 1266, SEQ ID No. 382, SEQ ID No. 383, SEQ ID No. 384, SEQ ID No. 385, SEQ ID No. 386, SEQ ID No. 1188, SEQ ID No. 1189, SEQ ID No. 391, SEQ ID No. 392, SEQ ID No. 398, SEQ ID No. 400, SEQ ID No. 403, SEQ ID No. 1191, SEQ ID No. 423, SEQ ID No. 435, SEQ ID No. 445, SEQ ID No. 450, SEQ ID No. 1193, SEQ ID No. 456, SEQ ID No. 460, SEQ ID No. 461, SEQ ID No. 465, SEQ ID No. 1196, SEQ ID No. 471, SEQ ID No. 473, SEQ ID No. 475, SEQ ID No. 481, SEQ ID No. 484, SEQ ID No. 487, SEQ ID No. 488, SEQ ID No. 489, SEQ ID No. 490, SEQ ID No. 491, SEQ ID No. 492, SEQ ID No. 493, SEQ ID No. 494, SEQ ID No. 495, SEQ ID No. 496, SEQ ID No. 497, SEQ ID No. 498, SEQ ID No. 499, SEQ ID No. 502, SEQ ID No. 1267, SEQ ID No. 1268, SEQ ID No. 508, SEQ ID No. 510, SEQ ID No. 509, SEQ ID No. 512, SEQ ID No. 515, SEQ ID No. 519, SEQ ID No. 1197, SEQ ID No. 521, SEQ ID No. 1198, SEQ ID No. 522, SEQ ID No. 524, SEQ ID No. 528, SEQ ID No. 534, SEQ ID No. 537, SEQ ID No. 1269, SEQ ID No. 1270, SEQ ID No. 548, SEQ ID No. 551, SEQ ID No. 557, SEQ ID No. 1201, SEQ ID No. 1203, SEQ ID No. 562, SEQ ID No. 566, SEQ ID No. 593, SEQ ID No. 595, SEQ ID No. 600, SEQ ID No. 1271, SEQ ID No. 604, SEQ ID No. 611, SEQ ID No. 612, SEQ ID No. 614, SEQ ID No. 616, SEQ ID No. 625, SEQ ID No. 627, SEQ ID No. 628, SEQ ID No. 629, SEQ ID No. 631, SEQ ID No. 641, SEQ ID No. 1272, SEQ ID No. 648, SEQ ID No. 1212, SEQ ID No. 663, SEQ ID No. 685, SEQ ID No. 707, SEQ ID No. 714, SEQ ID No. 715, SEQ ID No. 716, SEQ ID No. 717, SEQ ID No. 722, SEQ ID No. 746, SEQ ID No. 1273, SEQ ID No. 761, SEQ ID No. 764, SEQ ID No. 770, SEQ ID No. 1217, SEQ ID No. 783, SEQ ID No. 1274, SEQ ID No. 803, SEQ ID No. 815, SEQ ID No. 1220, SEQ ID No. 835, SEQ ID No. 1221, SEQ ID No. 844, SEQ ID No. 845, SEQ ID No. 846, SEQ ID No. 847, SEQ ID No. 848, SEQ ID No. 849, SEQ ID No. 850, SEQ ID No. 851, SEQ ID No. 1275, SEQ ID No. 852, SEQ ID No. 862, SEQ ID No. 1276, SEQ ID No. 1277, SEQ ID No. 873, SEQ ID No. 1223, SEQ ID No. 892, SEQ ID No. 919, SEQ ID No. 1225, SEQ ID No. 1278, SEQ ID No. 926, SEQ ID No. 1228, SEQ ID No. 1229, SEQ ID No. 1230, SEQ ID No. 1279, SEQ ID No. 1281, SEQ ID No. 1282, SEQ ID No. 1283, SEQ ID No. 948, SEQ ID No. 950, SEQ ID No. 949, SEQ ID No. 951, SEQ ID No. 980, SEQ ID No.

982, SEQ ID No. 1233, SEQ ID No. 999, SEQ ID No. 1000, SEQ ID No. 1001, SEQ ID No. 1002, SEQ ID No. 1008, SEQ ID No. 1285, SEQ ID No. 1235, SEQ ID No. 1016, SEQ ID No. 1019, SEQ ID No. 1027, SEQ ID No. 1036, SEQ ID No. 1241, SEQ ID No. 1048, SEQ ID No. 1049, SEQ ID No. 1050, SEQ ID No. 1053, SEQ ID No. 1054, SEQ ID No. 1064, SEQ ID No. 1076, SEQ ID No. 1091, SEQ ID No. 1288, SEQ ID No. 1093, SEQ ID No. 1289, SEQ ID No. 1101, SEQ ID No. 1103, SEQ ID No. 1245, SEQ ID No. 1246, SEQ ID No. 1247, SEQ ID No. 1290, SEQ ID No. 1291, SEQ ID No. 1115, SEQ ID No. 1116, SEQ ID No. 1118, SEQ ID No. 1120, SEQ ID No. 1249, SEQ ID No. 1121, SEQ ID No. 1250, SEQ ID No. 1126, SEQ ID No. 1251, SEQ ID No. 1127, SEQ ID No. 1128, SEQ ID No. 1130, SEQ ID No. 1129, SEQ ID No. 1131, SEQ ID No. 1136, SEQ ID No. 1253, SEQ ID No. 6844, SEQ ID No. 6846, SEQ ID No. 6847, SEQ ID No. 6848, and one of their representative fragments

Preferably, the invention relates to a polypeptide according to the invention, characterized in that it is a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the intermediate metabolism, in particular in the metabolism of sugars and/or of cofactors, and in that it is chosen from the polypeptides having the following sequences:

SEQ ID No. 2; SEQ ID No. 55; SEQ ID No. 56; SEQ ID No. 69; SEQ ID No. 75; SEQ ID No. 80; SEQ ID No. 100; SEQ ID No. 110; SEQ ID No. 114; SEQ ID No. 120; SEQ ID No. 121; SEQ ID No. 157; SEQ ID No. 160; SEQ ID No. 161; SEQ ID No. 172; SEQ ID No. 180; SEQ ID No. 181; SEQ ID No. 198; SEQ ID No. 200; SEQ ID No. 225; SEQ ID No. 248; SEQ ID No. 249; SEQ ID No. 276; SEQ ID No. 277; SEQ ID No. 318; SEQ ID No. 319; SEQ ID No. 320; SEQ ID No. 323; SEQ ID No. 331; SEQ ID No. 347; SEQ ID No. 375; SEQ ID No. 376; SEQ ID No. 381; SEQ ID No. 393; SEQ ID No. 394; SEQ ID No. 395; SEQ ID No. 396; SEQ ID No. 409; SEQ ID No. 446; SEQ ID No. 447; SEQ ID No. 448; SEQ ID No. 449; SEQ ID No. 513; SEQ ID No. 516; SEQ ID No. 571; SEQ ID No. 647; SEQ ID No. 662; SEQ ID No. 697; SEQ ID No. 718; SEQ ID No. 793; SEQ ID No. 794; SEQ ID No. 808; SEQ ID No. 809; SEQ ID No. 838; SEQ ID No. 839; SEQ ID No. 840; SEQ ID No. 853; SEQ ID No. 854; SEQ ID No. 918; SEQ ID No. 923; SEQ ID No. 929; SEQ ID No. 931; SEQ ID No. 938; SEQ ID No. 939; SEQ ID No. 958; SEQ ID No. 959; SEQ ID No. 960; SEQ ID No. 966; SEQ ID No. 995; SEQ ID No. 1021; SEQ ID No. 1040; SEQ ID No. 1041; SEQ ID No. 1042; SEQ ID No. 1085; SEQ ID No. 1100; SEQ ID No. 1102; SEQ ID No. 1117; SEQ ID No. 1118; SEQ ID No. 1119; SEQ ID No. 1120; SEQ ID No. 1135 and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, characterized in that it is a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the intermediate metabolism of nucleotides or nucleic acids, and in that it is chosen from the polypeptides having the following sequences:

SEQ ID No. 77; SEQ ID No. 78; SEQ ID No. 138; SEQ ID No. 189; SEQ ID No. 190; SEQ ID No. 233; SEQ ID No. 246; SEQ ID No. 338; SEQ ID No. 412; SEQ ID No. 421; SEQ ID No. 438;

SEQ ID No. 607; SEQ ID No. 648; SEQ ID No. 657; SEQ ID No. 740; SEQ ID No. 783; SEQ ID No. 967; SEQ ID No. 989; SEQ ID No. 990; SEQ ID No. 992; SEQ ID No. 1011; SEQ ID No. 1058; SEQ ID No. 1059; SEQ ID No. 1073; SEQ ID No. 1074 and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, characterized in that it is a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the metabolism of nucleic acids, and in that it is chosen from the polypeptides having the following sequences:

SEQ ID No. 14; SEQ ID No. 59; SEQ ID No. 70; SEQ ID No. 71; SEQ ID No. 97; SEQ ID No. 113; SEQ ID No. 137; SEQ ID No. 141; SEQ ID No. 169; SEQ ID No. 285; SEQ ID No. 287; SEQ ID No. 288; SEQ ID No. 313; SEQ ID No. 326; SEQ ID No. 358; SEQ ID No. 411; SEQ ID No. 443; SEQ ID No. 548; SEQ ID No. 569; SEQ ID No. 601; SEQ ID No. 651; SEQ ID No. 654; SEQ ID No. 658; SEQ ID No. 659; SEQ ID No. 664; SEQ ID No. 665; SEQ ID No. 694; SEQ ID No. 698; SEQ ID No. 704; SEQ ID No. 760; SEQ ID No. 762; SEQ ID No. 763; SEQ ID No. 786; SEQ ID No. 787; SEQ ID No. 788; SEQ ID No. 801; SEQ ID No. 802; SEQ ID No. 812; SEQ ID No. 819; SEQ ID No. 822; SEQ ID No. 870; SEQ ID No. 897; SEQ ID No. 898; SEQ ID No. 902; SEQ ID No. 908; SEQ ID No. 916; SEQ ID No. 954; SEQ ID No. 955; SEQ ID No. 961; SEQ ID No. 983; SEQ ID No. 996; SEQ ID No. 1007; SEQ ID No. 1012; SEQ ID No. 1013; SEQ ID No. 1014; SEQ ID No. 1015; SEQ ID No. 1038; SEQ ID No. 1137 and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, characterized in that it is a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the metabolism of amino acids or polypeptides, and in that it is chosen from the polypeptides having the following sequences:

SEQ ID No. 99; SEQ ID No. 111; SEQ ID No. 127; SEQ ID No. 134; SEQ ID No. 140; SEQ ID No. 174; SEQ ID No. 175; SEQ ID No. 176; SEQ ID No. 353; SEQ ID No. 377; SEQ ID No. 404; SEQ ID No. 523; SEQ ID No. 539; SEQ ID No. 559; SEQ ID No. 561; SEQ ID No. 586; SEQ ID No. 598; SEQ ID No. 609; SEQ ID No. 636; SEQ ID No. 687; SEQ ID No. 700; SEQ ID No. 701; SEQ ID No. 759; SEQ ID No. 790; SEQ ID No. 857; SEQ ID No. 861; SEQ ID No. 904; SEQ ID No. 936; SEQ ID No. 952; SEQ ID No. 962; SEQ ID No. 963; SEQ ID No. 964; SEQ ID No. 965; SEQ ID No. 991; SEQ ID No. 1003; SEQ ID No. 1004; SEQ ID No. 1005; SEQ ID No. 1018; SEQ ID No. 1067; SEQ ID No. 1110; SEQ ID No. 1111; SEQ ID No. 1112; SEQ ID No. 1114; SEQ ID No. 1121; SEQ ID No. 1122; SEQ ID No. 1123; SEQ ID No. 1124; SEQ ID No. 1125 and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, characterized in that it is a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the metabolism of polypeptides, and in that it is chosen from the polypeptides having the following sequences:

SEQ ID No. 4; SEQ ID No. 44; SEQ ID No. 45; SEQ ID No. 48; SEQ ID No. 54; SEQ ID No. 112; SEQ ID No. 130; SEQ ID No. 155; SEQ ID No. 163; SEQ ID No. 212; SEQ ID No. 257; SEQ ID No. 307; SEQ ID No. 343; SEQ ID No. 405; SEQ ID No. 416; SEQ ID No. 458; SEQ ID No. 540; SEQ ID No. 541; SEQ ID No. 542; SEQ ID No. 543; SEQ ID No. 544; SEQ ID No. 560; SEQ ID No. 594; SEQ ID No. 652; SEQ ID No. 699; SEQ ID No. 723; SEQ ID No. 747; SEQ ID No. 817; SEQ ID No. 827; SEQ ID No. 871; SEQ ID No. 909; SEQ ID No. 910; SEQ ID No. 911; SEQ ID No. 912; SEQ ID No. 1023; SEQ ID No. 1051; SEQ ID No. 1052; SEQ ID No. 1081 and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, characterized in that it is a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the metabolism of fatty acids, and in that it is chosen from the polypeptides having the following sequences:

SEQ ID No. 76; SEQ ID No. 284; SEQ ID No. 308; SEQ ID No. 309; SEQ ID No. 310; SEQ ID No. 311; SEQ ID No. 312; SEQ ID No. 425; SEQ ID No. 433; SEQ ID No. 565; SEQ ID No. 688; SEQ ID No. 690; SEQ ID No. 691; SEQ ID No. 767; SEQ ID No. 797; SEQ ID No. 894; SEQ ID No. 895; SEQ ID No. 994; SEQ ID No. 1020; SEQ ID No. 1030; SEQ ID No. 1033; SEQ ID No. 1034; SEQ ID No. 1046; SEQ ID No. 1047; SEQ ID No. 1057 and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, characterized in that it is a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the synthesis of the wall, and in that it is chosen from the polypeptides having the following sequences:

SEQ ID No. 49; SEQ ID No. 50; SEQ ID No. 177; SEQ ID No. 178; SEQ ID No. 245; SEQ ID No. 610; SEQ ID No. 972; SEQ ID No. 974; SEQ ID No. 978; SEQ ID No. 1037 and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, characterized in that it is a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the transcription, translation and/or maturation process, and in that it is chosen from the polypeptides having the following sequences:

SEQ ID No. 90; SEQ ID No. 92; SEQ ID No. 131; SEQ ID No. 151; SEQ ID No. 199; SEQ ID No. 333; SEQ ID No. 334; SEQ ID No. 336; SEQ ID No. 379; SEQ ID No. 589; SEQ ID No. 590; SEQ ID No. 619; SEQ ID No. 630; SEQ ID No. 649; SEQ ID No. 739; SEQ ID No. 741; SEQ ID No. 806; SEQ ID No. 821; SEQ ID No. 843; SEQ ID No. 968; SEQ ID No. 971; SEQ ID No. 1061 and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, characterized in that it is a *Chlamydia pneumoniae* ribosomal polypeptide or one of its representative fragments, and in that it is chosen from the polypeptides having the following sequences: SEQ ID No. 93; SEQ ID No. 94; SEQ ID No. 95; SEQ ID No. 136; SEQ ID No. 259; SEQ ID No. 332; SEQ ID No. 348; SEQ ID No. 583; SEQ ID No. 584; SEQ ID No. 588; SEQ ID No. 591; SEQ ID No. 592; SEQ ID No. 663; SEQ ID No. 666; SEQ ID No. 667; SEQ ID No. 669; SEQ ID No. 670; SEQ ID No. 671; SEQ ID No. 672; SEQ ID No. 673; SEQ ID No. 674; SEQ ID No. 675; SEQ ID No. 676; SEQ ID No. 677; SEQ ID No. 678; SEQ ID No. 679; SEQ ID No. 680; SEQ ID No. 681; SEQ ID No. 683; SEQ ID No. 684; SEQ ID No. 738; SEQ ID No. 781; SEQ ID No. 1008; SEQ ID No. 1024; SEQ ID No. 1025; SEQ ID No. 1066 and one of their representative fragments.

Preferably, the invention also relates to a polypeptide according to the invention, characterized in that it is a *Chlamydia pneumoniae* transport polypeptide or one of its representative fragments, and in that it is chosen from the polypeptides having the following sequences: SEQ ID No. 40; SEQ ID No. 41; SEQ ID No. 52; SEQ ID No. 105; SEQ ID No. 106; SEQ ID No. 107; SEQ ID No. 109; SEQ ID No. 133; SEQ ID No. 210; SEQ ID No. 211; SEQ ID No. 214; SEQ ID No. 215; SEQ ID No. 216; SEQ ID No. 217; SEQ ID No. 218; SEQ ID No. 219; SEQ ID No. 220; SEQ ID No. 223; SEQ ID No. 242; SEQ ID No. 260; SEQ ID No. 293; SEQ ID No. 299; SEQ ID No. 366; SEQ ID No. 369; SEQ ID No. 575; SEQ ID No. 602; SEQ ID No. 638; SEQ ID No. 639; SEQ ID No. 640; SEQ ID No. 643; SEQ ID No. 653; SEQ ID No. 702; SEQ ID No. 703; SEQ ID No. 724; SEQ ID No. 732; SEQ ID No. 855; SEQ ID No. 856; SEQ ID No. 901; SEQ ID No. 906; SEQ ID No. 933; SEQ ID No. 942; SEQ ID No. 1043; SEQ ID No. 1086; SEQ ID No. 1105 and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, characterized in that it is a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the virulence process, and in that it is chosen from the polypeptides having the following sequences: SEQ ID No. 546; SEQ ID No. 550; SEQ ID No. 778; SEQ ID No. 779; SEQ ID No. 886 and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, characterized in that it is a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the secretory system and/or which is secreted, and in that it is chosen from the polypeptides having the following sequences: SEQ ID No. 751; SEQ ID No. 874; SEQ ID No. 875; SEQ ID No. 876; SEQ ID No. 883; SEQ ID No. 884; SEQ ID No. 885 and one of their representative fragments.

The secreted polypeptides, including the Type III and other, non-Type III secreted polypeptides, of the present invention, as well as the corresponding nucleotide sequences, may be detected by techniques known to persons skilled in the art, such as for example the techniques using cloning combined with vectors allowing the expression of the said polypeptides fused to export markers such as the *luc* gene for luciferase or the *PhoA* gene for alkaline phosphatase.

Preferably, the invention relates to a polypeptide according to the invention, characterized in that it is a polypeptide specific to *Chlamydia pneumoniae* or one of its representative fragments(with a Blast E value of $>10^{-5}$), and in that it is chosen from the polypeptides having the following sequences:

SEQ ID No. 7; SEQ ID No. 8; SEQ ID No. 17; SEQ ID No. 18; SEQ ID No. 19; SEQ ID No. 20; SEQ ID No. 22; SEQ ID No. 23; SEQ ID No. 24; SEQ ID No. 51; SEQ ID No. 60; SEQ ID No. 63; SEQ ID No. 65; SEQ ID No. 66; SEQ ID No. 67; SEQ ID No. 83; SEQ ID No. 84; SEQ ID No. 86; SEQ ID No. 87; SEQ ID No. 125; SEQ ID No. 143; SEQ ID No. 144; SEQ ID No. 179; SEQ ID No. 182; SEQ ID No. 184; SEQ ID No. 185; SEQ ID No. 187; SEQ ID No. 221; SEQ ID No. 252; SEQ ID No. 254;; SEQ ID No. 278; SEQ ID No. 279; SEQ ID No. 387; SEQ ID No. 388; SEQ ID No. 397; SEQ ID No. 1048; SEQ ID No. 1049; SEQ ID No. 1050; SEQ ID No. 1128; SEQ ID No. 1130; SEQ ID No. 1131 and one of their representative fragments.

In general, in the present invention, the functional group to which a polypeptide of the invention belongs, as well as its corresponding nucleotide sequence, may be determined either by comparative analogy with sequences already known, or by the use of standard techniques of biochemistry, of cytology combined with the techniques of genetic engineering such as immunoaffinity, localization by immunolabelling, differential extraction, measurement of enzymatic activity, study of the activity inducing or repressing expression or the study of expression in *E. coli*.

It is clearly understood, on the one hand, that, in the present invention, the nucleotide sequences (ORF) and the amino acid sequences (SEQ ID No. 2 to SEQ ID No. 1291 and SEQ ID No. 6844 to SEQ ID No. 6848) which are listed by functional group, are not exhaustive within the group considered. Moreover, it is also clearly understood that, in the present invention, a nucleotide sequence (ORF) or an amino acid sequence mentioned within a given functional group may also be part of another group taking into account, for example, the interrelationship between the groups listed. Accordingly, and as an example of this interrelationship, an exported and/or secreted polypeptide as well as its coding nucleotide sequence may also be involved in the *Chlamydia pneumoniae* virulence process by modifying the defense mechanism of the infected host cell, or a transmembrane polypeptide or its coding nucleotide sequence is also part of the polypeptides or coding nucleotide sequences of the cellular envelope.

The subject of the present invention is also the nucleotide and/or polypeptide sequences according to the invention, characterized in that the said sequences are recorded on a medium, called recording medium, whose type and nature facilitate the reading, the analysis and the exploitation of the said sequences. These media may of course also contain other information extracted from the present invention, such as in particular the analogies with already known sequences, such as those mentioned in Table 1 of the present description, and/or may contain, in addition, information relating to the nucleotide and/or polypeptide sequences of other microorganisms so as to facilitate the comparative analysis and the exploitation of the results obtained.

Among these recording media, computer-readable media, such as magnetic, optical, electrical and hybrid media such as, for example, floppy disks, CD-ROMs or recording cassettes, are preferred in particular.

The invention also relates to nucleotide sequences which can be used as primer or probe, characterized in that the said sequences are chosen from the nucleotide sequences according to the invention.

The invention relates, in addition, to the use of a nucleotide sequence according to the invention, as primer or probe, for the detection and/or amplification of nucleic acid sequences.

The nucleotide sequences according to the invention may thus be used to amplify nucleotide sequences, in particular by the PCR technique (polymerase chain reaction) (Erlich, 1989; Innis et al., 1990; Rolfs et al., 1991, and White et al., 1997).

These oligodeoxyribonucleotide or oligoribonucleotide primers correspond to representative nucleotide fragments, and are advantageously at least 8 nucleotides, preferably at least 12 nucleotides, 15 nucleotides and still more preferably at least 20 nucleotides long.

Other techniques for amplifying the target nucleic acid may be advantageously used as alternatives to PCR.

The nucleotide sequences of the invention, in particular the primers according to the invention, may also be used in other methods for amplifying a target nucleic acid, such as:

- the TAS (Transcription-based Amplification System) technique described by Kwoh et al. in 1989;
- the 3SR (Self-Sustained Sequence Replication) technique described by Guatelli et al. in 1990;
- the NASBA (Nucleic Acid Sequence Based Amplification) technique described by Kievitis et al. in 1991;
- the SDA (Strand Displacement Amplification) technique (Walker et al., 1992);
- the TMA (Transcription Mediated Amplification) technique.

The polynucleotides of the invention may also be used in techniques for amplifying or for modifying the nucleic acid serving as probe, such as:

- the LCR (Ligase Chain Reaction) technique described by Landegren et al. in 1988 and perfected by Barany et al. in 1991, which uses a thermostable ligase;
- the RCR (Repair Chain Reaction) technique described by Segev in 1992;
- the CPR (Cycling Probe Reaction) technique described by Duck et al. in 1990;
- the Q-beta-replicase amplification technique described by Miele et al. in 1983 and perfected in particular by Chu et al. in 1986, Lizardi et al. in 1988, and then by Burg et al. as well as by Stone et al. in 1996.

The invention also relates to the nucleotide sequences of fragments which can be obtained by amplification with the aid of at least one primer according to the invention. The present invention encompasses both hybridization probes and primers. In general, the complementary probes should be of a length sufficient to form a stable hybrid complex with the target sequences . Primers, while complementary to the target sequences need not form stable hybridization complexes with the target sequences alone. Rather, primers form stable complexes with the target sequences in the presence of polymerase to permit extension of the primer.

In the case where the target polynucleotide to be detected is possibly an RNA, for example an mRNA, it will be possible to use, prior to the use of an amplification reaction with the aid of at least one primer according to the invention or to the use of a method of detection with the aid of at least one probe of the invention, a reverse transcriptase-type enzyme so as to obtain a cDNA from the RNA contained in the biological sample. The cDNA obtained will then serve as target for the primer(s) or the probe(s) used in the amplification or detection method according to the invention.

The detection probe will be chosen so that it hybridizes with the target sequence or the amplicon generated from the target sequence. Such a detection probe will advantageously have as sequence a sequence of at least 12 nucleotides, in particular of at least 20 nucleotides, and preferably at least 100 nucleotides.

The invention also comprises the nucleotide sequences which can be used as probe or primer according to the invention, characterized in that they are labelled with a radioactive compound or with a nonradioactive compound.

The nonlabelled nucleotide sequences may be used directly as probes or primers; however, the sequences are generally labelled with a radioactive element (^{32}P, ^{35}S, ^{3}H, ^{125}I) or with a nonradioactive molecule (biotin, acetylaminofluorene, digoxigenin, 5-bromo-deoxyuridine, fluorescein) so as to obtain probes which can be used in numerous applications.

Examples of nonradioactive labelling of nucleotide sequences are described, for example, in French patent No. 78,10975 or by Urdea et al. or by Sanchez-Pescador et al. in 1988.

In the latter case, one of the labelling methods described in patents FR-2 422 956 and FR-2 518 755 may also be used.

The invention also relates to the nucleotide sequences of fragments which can be obtained by hybridization with the aid of at least one probe according to the invention.

The hybridization technique may be performed in various ways (Matthews et al., 1988). The most common method consists in immobilizing the nucleic acid extracted from *Chlamydia pneumoniae* cells on a support (such as nitrocellulose, nylon, polystyrene) and in incubating, under well-defined conditions, the target nucleic acid immobilized with the probe. After hybridization, the excess probe is removed and the hybrid molecules formed are detected by the appropriate method (measurement of the radioactivity, of the fluorescence or of the enzymatic activity linked to the probe).

The invention also comprises the nucleotide sequences according to the invention, characterized in that they are covalently or noncovalently immobilized on a support.

According to another advantageous embodiment of the nucleic sequences according to the invention, the latter may be used immobilized on a support and may thus serve to capture, through specific hybridization, the target nucleic acid obtained from the biological sample to be tested. If necessary, the solid support is separated from the sample and the hybridization complex formed between the so-called capture probe and the target nucleic acid is then detected by means of a second probe, called detection probe, labelled with an easily detectable element.

The nucleotide sequences according to the invention may also be used in new analytical systems, DNA chips, which allow sequencing, the study of mutations and of the expression of genes, and which are currently of interest given their very small size and their high capacity in terms of number of analyses.

The principle of the operation of these chips is based on molecular probes, most often oligonucleotides, which are attached onto a miniaturized surface, generally of the order of a few square centimetres. During an analysis, a sample containing fragments of a target nucleic acid to be analysed, for example DNA or RNA labelled, for example, after amplification, is deposited onto the DNA chip in which the support has been coated beforehand with probes. Bringing the labelled target sequences into contact with the probes leads to the formation, through hybridization, of a duplex according to the rule of pairing defined by J.D. Watson and F. Crick. After a washing step, analysis of the surface of the chip allows the effective hybridizations to be located by means of the signals emitted by the labels tagging the target. A hybridization fingerprint results from this analysis which, by appropriate computer processing, will make it possible to determine information such as the presence of specific fragments in the sample, the determination of sequences and the presence of mutations.

The chip consists of a multitude of molecular probes, precisely organized or arrayed on a solid support whose surface is miniaturized. It is at the centre of a system where other elements (imaging system, microcomputer) allow the acquisition and interpretation of a hybridization fingerprint.

The hybridization supports are provided in the form of flat or porous surfaces (pierced with wells) composed of various materials. The choice of a support is determined by its physicochemical properties, or more precisely, by the relationship between the latter and the conditions under which the support will be placed during the synthesis or the attachment of the probes or during the use of the chip. It is therefore necessary, before considering the use of a particular support (R.S. Matson et al., 1994), to consider characteristics such as its stability to pH, its physical strength, its reactivity and its chemical stability as well as its capacity to nonspecifically bind nucleic acids. Materials such as glass, silicon and polymers are commonly used. Their surface is, in a first step, called "functionalization", made reactive towards the groups which it is desired to attach thereon. After the functionalization, so-called spacer molecules are grafted onto the activated surface. Used as intermediates between the surface and the probe, these molecules of variable size render unimportant the surface properties of the supports, which often prove to be problematic for the synthesis or the attachment of the probes and for the hybridization.

Among the hybridization supports, there may be mentioned glass which is used, for example, in the method of in situ synthesis of oligonucleotides by photochemical addressing developed by the company Affymetrix (E.L. Sheldon, 1993), the glass surface being activated by silane. Genosensor Consortium (P. Mérel, 1994) also uses glass slides carrying wells 3 mm apart, this support being activated with epoxysilane.

Polymers or silicon may also be mentioned among these hybridization supports. For example, the Andrein Mirzabekov team has developed a chip consisting of polyacrylamide squares polymerized on a silanized glass surface (G. Yershov et al., 1996). Several teams use silicon, in particular the IFOS laboratory of Ecole Centrale of Lyon which uses a silicon semiconductor substrate which is p-doped by introducing it into its crystalline structure atoms whose valency is different from that of silicon. Various types of metals, in particular gold and platinum, may also be used as support (Genosensor Consortium (K. Beattie et al., 1993)).

The probes according to the invention may be synthesized directly in situ on the supports of the DNA chips. This in situ synthesis may be carried out by photochemical addressing (developed by the company Affymax (Amsterdam, Holland) and exploited industrially by its subsidiary Affymetrix (United States)) or based on the VLSIPS (very large scale immobilized polymer synthesis) technology (S.P.A. Fodor et al., 1991) which is based on a method of photochemically directed combinatory synthesis and the principle of which combines solid-phase chemistry, the use of photolabile protecting groups and photolithography.

The probes according to the invention may be attached to the DNA chips in various ways such as electrochemical addressing, automated addressing or the use of probe printers (T. Livache et al., 1994; G. Yershov et al., 1996; J. Derisi et al., 1996, and S. Borman, 1996).

The revealing of the hybridization between the probes of the invention, deposited or synthesized in situ on the supports of the DNA chips, and the sample to be analysed, may be determined, for example, by measurement of fluorescent signals, by radioactive counting or by electronic detection.

The use of fluorescent molecules such as fluorescein constitutes the most common method of labelling the samples. It allows direct or indirect revealing of the hybridization and allows the use of various fluorochromes.

Affymetrix currently provides an apparatus or a scanner designed to read its Gene Chip™ chips. It makes it possible to detect the hybridizations by scanning the surface of the chip in confocal microscopy (R.J. Lipshutz et al., 1995). Other methods of detecting fluorescent signals have been tested: coupling of an epifluorescence microscope and a CCD camera (G. Yershov et al., 1996), the use of an optical fibre collecting system (E.L. Sheldon, 1993). A conventional method consists in carrying out an end labelling, with phosphorus 32, of the target sequences, by means of an appropriate apparatus, the Phosphorimager (marketed by Molecular Dynamics). The electronic detection is based on the principle that the hybridization of two nucleic acid molecules is accompanied by physical phenomena which can be quantified under certain conditions (system developed by Ecole Centrale of

Lyon and called GEN-FET (GEN field effect transistor)). Genosensor Consortium and the company Beckman Instruments who are developing an electronic chip or Permittivity Chips™ may also be mentioned (K. Beattie et al., 1993).

The nucleotide sequences according to the invention may thus be used in DNA chips to carry out the analysis of mutations. This analysis is based on the production of chips capable of analysing each base of a nucleotide sequence according to the invention.

The nucleotide sequences according to the invention may also be used in DNA chips to carry out the analysis of the expression of the *Chlamydia pneumoniae* genes. This analysis of the expression of *Chlamydia pneumoniae* genes is based on the use of chips where probes of the invention, chosen for their specificity to characterize a given gene, are present (D.J. Lockhart et al., 1996; D.D. Shoemaker et al., 1996). For the methods of analysis of gene expression using the DNA chips, reference may, for example, be made to the methods described by D.J. Lockhart et al. (1996) and Sosnowsky et al. (1997) for the synthesis of probes in situ or for the addressing and the attachment of previously synthesized probes. The target sequences to be analysed are labelled and in general fragmented into sequences of about 50 to 100 nucleotides before being hybridized onto the chip. After washing as described, for example, by D.J. Lockhart et al. (1996) and application of different electric fields (Sosnowsky et al., 1997), the labelled compounds are detected and quantified, the hybridizations being carried out at least in duplicate. Comparative analyses of the signal intensities obtained with respect to the same probe for different samples and/or for different probes with the same sample, determine the differential expression of RNA or of DNA derived from the sample.

The nucleotide sequences according to the invention may, in addition, be used in DNA chips where other nucleotide probes specific for other microorganisms are also present, and may allow the carrying out of a serial test allowing rapid identification of the presence of a microorganism in a sample.

Accordingly, the subject of the invention is also the nucleotide sequences according to the invention, characterized in that they are immobilized on a support of a DNA chip.

The DNA chips, characterized in that they contain at least one nucleotide sequence according to the invention, immobilized on the support of the said chip, also form part of the invention.

The said chips will preferably contain several probes or nucleotide sequences of the invention of different length and/or corresponding to different genes so as to identify, with greater certainty, the specificity of the target sequences or the desired mutation in the sample to be analysed.

Accordingly, the analyses carried out by means of primers and/or probes according to the invention, immobilized on supports such as DNA chips, will make it possible, for example, to identify, in samples, mutations linked to variations such as intraspecies variations. These variations may be correlated or associated with pathologies specific to the variant identified and will make it possible to select the appropriate treatment.

The invention thus comprises a DNA chip according to the invention, characterized in that it contains, in addition, at least one nucleotide sequence of a microorganism different from *Chlamydia pneumoniae,* immobilized on the support of the said chip; preferably, the different microorganism will be chosen from an associated microorganism, a bacterium of the *Chlamydia* family, and a variant of the species *Chlamydia pneumoniae*.

Another subject of the present invention is a vector for the cloning and/or the expression of a sequence, characterized in that it contains a nucleotide sequence according to the invention. Among the said vectors according to the invention, the vectors containing a nucleotide sequence encoding a polypeptide of the cellular, preferably outer, envelope of *Chlamydia pneumoniae* or one of its representative fragments, are preferred. In a specific embodiment, the vectors contain a nucleotide sequence encoding a *Chlamydia pneumoniae* secreted polypeptide or one of its representative fragments or encoding a transport polypeptide, a surface exposed polypeptide, a lipoprotein or one of its representative fragments, a polypeptide involved in lipopolysaccharide (LPS) biosynthesis, a Type III and non-Type III secreted polypeptide, a polypeptide containing RGD attachment sites, a cell wall anchored surface polypeptide, a polypeptide not found in *Chlamydia trachomatis*, a ribosomal polypeptide or a polypeptide involved in secretion, transcription, translation, maturation of proteins, a polypeptide involved in the synthesis of the wall, a polypeptide involved in the virulence, a polypeptide involved in the intermediate metabolism, in particular in the metabolism of sugars and/or of cofactors, a polypeptide involved in the metabolism of nucleotides, of amino acids, of nucleic acids or of fatty acids of *Chlamydia pneumoniae* or one of their representative fragments, or a polypeptide specific to *Chlamydia pneumoniae*.

According to the invention, the vectors comprise the elements necessary to allow the expression and/or the secretion of the said nucleotide sequences in a given host cell, and form part of the invention. The vector should, in this case, comprise a promoter, signals for initiation and for termination of translation, as well as appropriate regions for regulation of transcription. It should be capable of being stably maintained in the host cell and may optionally possess particular signals specifying the secretion of the translated protein. These different elements are chosen according to the host cell used. To this effect, the nucleotide sequences according to the invention may be inserted into autonomously-replicating vectors within the chosen host, or integrative vectors in the chosen host.

Any of the standard methods known to those skilled in the art for the insertion of DNA fragments into a vector may be used to construct expression vectors containing a chimeric gene consisting of appropriate transcriptional/translational control signals and the protein coding sequences. These methods may include *in vitro* recombinant DNA and synthetic techniques and *in vivo* recombinants (genetic recombination).

Expression of a polypeptide, peptide or derivative, or analogs thereof encoded by a polynucleotide sequence in SEQ ID No. 1 or ORFs contained within SEQ ID No. 1 may be regulated by a second nucleic acid sequence so that the protein or peptide is expressed in a host transformed with the recombinant DNA molecule. For example, expression of a protein or peptide may be controlled by any promoter/enhancer element known in the art. Promoters which may be used to control expression include, but are not limited to, the CMV promoter, the SV40 early promoter region (Bernoist and Chambon, 1981, Nature 290:304-310), the promoter contained in the 3' long terminal repeat of Rous sarcoma virus (Yamamoto, *et al.*, 1980, Cell 22:787-797), the herpes thymidine kinase promoter (Wagner *et al.*, 1981, Proc. Natl. Acad. Sci. U.S.A. 78:1441-1445), the regulatory sequences of the metallothionein gene (Brinster *et al.*, 1982, Nature 296:39-42); prokaryotic expression vectors such as the ∃-lactamase promoter (Villa-Kamaroff, *et al.*, 1978, Proc. Natl. Acad. Sci. U.S.A. 75:3727-3731), or the *tac* promoter (DeBoer, *et al.*, 1983, Proc. Natl. Acad. Sci. U.S.A. 80:21-25); see also "Useful proteins from recombinant bacteria" in Scientific American, 1980, 242:74-94; plant expression vectors comprising the nopaline synthetase promoter region (Herrera-Estrella *et al.*, 1983, Nature 303:209-213) or the cauliflower mosaic virus 35S RNA promoter (Gardner, *et al.*, 1981, Nucl. Acids Res. 9:2871), and the promoter of the photosynthetic enzyme ribulose biphosphate carboxylase (Herrera-Estrella *et al.*, 1984, Nature 310:115-120); promoter elements from yeast or other fungi such as the Gal 4 promoter, the ADC (alcohol dehydrogenase) promoter, PGK (phosphoglycerol kinase) promoter, alkaline phosphatase promoter, and the following animal transcriptional control regions, which exhibit tissue specificity and have been utilized in transgenic animals: elastase I gene control region which is active in pancreatic acinar cells (Swift *et al.*, 1984, Cell 38:639-646; Ornitz *et al.*, 1986, Cold Spring Harbor Symp. Quant. Biol. 50:399-409; MacDonald, 1987, Hepatology 7:425-515); insulin gene control region which is active in pancreatic beta cells (Hanahan, 1985, Nature 315:115-122), immunoglobulin gene control region which is active in lymphoid cells (Grosschedl *et al.*, 1984, Cell 38:647-658; Adames *et al.*, 1985, Nature 318:533-538; Alexander *et al.*, 1987, Mol. Cell. Biol. 7:1436-1444), mouse mammary tumor virus control region which is active in testicular, breast, lymphoid and mast cells (Leder *et al.*, 1986, Cell 45:485-495), albumin gene control region which is active in liver (Pinkert *et al.*, 1987, Genes and Devel. 1:268-276), alpha-fetoprotein gene control region which is active in liver (Krumlauf *et al.*, 1985, Mol. Cell. Biol. 5:1639-1648; Hammer *et al.*, 1987, Science 235:53-58; alpha 1-antitrypsin gene control region which is active in the liver (Kelsey *et al.*, 1987, Genes and Devel. 1:161-171), beta-globin gene control region which is active in myeloid cells (Mogram *et al.*, 1985, Nature 315:338-340; Kollias *et al.*, 1986, Cell 46:89-94; myelin basic protein gene control region which is active in oligodendrocyte cells in the brain (Readhead *et al.*, 1987, Cell 48:703-712); myosin light chain-2 gene control region which is active in skeletal muscle (Sani, 1985, Nature 314:283-286), and gonadotropic releasing hormone gene control region which is active in the hypothalamus (Mason *et al.*, 1986, Science 234:1372-1378).

The vectors according to the invention are, for example, vectors of plasmid or viral origin. In a specific embodiment, a vector is used that comprises a promoter operably linked to a protein or peptide-encoding a nucleic acid sequence in SEQ ID No. 1, or ORFs contained within SEQ ID No. 1, one or more origins of replication, and, optionally, one or more selectable markers (*e.g.*, an antibiotic resistance gene). Expression vectors comprise regulatory sequences that control gene expression, including gene expression in a desired host cell. Preferred vectors for the expression of the polypeptides of the invention include the pET-type plasmid vectors (Promega) or pBAD plasmid vectors (Invitrogen). Furthermore, the vectors according to the invention are useful for transforming host cells so as to clone or express the nucleotide sequences of the invention.

Expression can also be achieved using targeted homologous recombination to activate *Chlamydia pneumoniae* genes present in the cloned genomic DNA. A heterologous regulatory element may be inserted into a stable cell line or cloned microorganism, such that it is operatively linked with an endogenous *Chlamydia pneumoniae* gene present in the cloned genome, using techniques, such as targeted homologous recombination, which are well known to those of skill in the art (*See, e.g.*, Chappel, U.S. Patent No. 4,215,051 and Skoultchi, WO 91/06667 each of which is incorporated herein in its entirety).

Expression vector/host cell systems containing inserts of polynucleotide sequences in SEQ ID No. 1 or ORFs within SEQ ID No. 1, which encode polypeptides, peptides or derivatives, or analogs thereof, can be identified by three general approaches: (a) nucleic acid hybridization, (b) presence or absence of "marker" gene functions, and (c) expression of inserted sequences. In the first approach, the presence of a polynucleotide sequence inserted in an expression vector can be detected by nucleic acid hybridization using probes comprising sequences that are homologous to an inserted polynucleotide sequence. In the second approach, the recombinant vector/host system can be identified and selected based upon the presence or absence of certain "marker" gene functions (*e.g.*, thymidine kinase activity, resistance to antibiotics, transformation phenotype, occlusion body formation in baculovirus, etc.) caused by the insertion of a polynucleotide sequence in the vector. For example, if the polynucleotide sequence in SEQ ID No. 1 or ORFs within SEQ ID No. 1 is inserted within the marker gene sequence of the vector, recombinants containing the insert can be identified by the absence of the marker gene function. In the third approach, recombinant expression vectors can be identified by assaying the product of the polynucleotide sequence expressed by the recombinant. Such assays can be based, for example, on the physical or functional properties of the expressed polypeptide in *in vitro* assay systems, *e.g.*, binding with antibody, promotion of cell proliferation.

Once a particular recombinant DNA molecule is identified and isolated, several methods known in the art may be used to propagate it. The clones identified may be introduced into an appropriate host cell by standard methods, such as for example lipofection, electroporation, and heat shock. Once a suitable host system and growth conditions are established, recombinant expression vectors can be propagated and prepared in quantity.

The invention also encompasses the host cells transformed by a vector according to the invention. These cells may be obtained by introducing into host cells a nucleotide sequence inserted into a vector as defined above, and then culturing the said cells under conditions allowing the replication and/or the expression of the transfected nucleotide sequence.

The host cell may be chosen from eukaryotic or prokaryotic systems, such as for example bacterial cells (Olins and Lee, 1993), but also yeast cells (Buckholz, 1993), as well as animal cells, in particular cultures of mammalian cells (Edwards and Aruffo, 1993), and in particular Chinese hamster ovary (CHO) cells, but also insect cells in which methods using baculoviruses for example may be used (Luckow, 1993).

Furthermore, a host cell strain may be chosen which modulates the expression of the inserted sequences, or modifies and processes the gene product in the specific fashion desired. Expression from certain promoters can be elevated in the presence of certain inducers; thus, expression of the genetically engineered polypeptide may be controlled. Furthermore, different host cells have characteristic and specific mechanisms for the translational and post-translational processing and modification (*e.g.*, glycosylation, phosphorylation) of proteins. Appropriate cell lines or host systems can be chosen to ensure the desired modification and processing of the foreign protein expressed. For example, expression in a bacterial system can be used to produce an unglycosylated core protein product. Expression in yeast will produce a glycosylated product. Expression in mammalian cells can be used to ensure "native" glycosylation of a heterologous protein. Furthermore, different vector/host expression systems may effect processing reactions to different extents.

A preferred host cell for the expression of the proteins of the invention consists of prokaryotic cells, such as Gram$^-$ bacteria. A further preferred host cell according to the invention is a bacterium belonging to the *Chlamydia* family, more preferably belonging to the species *Chlamydia pneumoniae* or chosen from a microorganism associated with the species *Chlamydia pneumoniae.*

In other specific embodiments, the polypeptides, peptides or derivatives, or analogs thereof may be expressed as a fusion, or chimeric protein product (comprising the protein, fragment, analog, or derivative joined via a peptide bond to a heterologous protein sequence (of a different protein)). Such a chimeric product can be made by ligating the appropriate nucleic acid sequences encoding the desired amino acid sequences to each other by methods known in the art, in the proper coding frame, and expressing the chimeric product by methods commonly known in the art. Alternatively, such a chimeric product may be made by protein synthetic techniques, *e.g.*, by use of a peptide synthesizer.

Genomic sequences can be cloned and expressed as translational gene products (*i.e.*, peptides, polypeptides, and proteins) or transcriptional gene products (*i.e.*, antisense and ribozymes).

The invention further relates to the intracellular production of an antisense nucleic acid sequence of SEQ ID No. 1 by transcription from an exogenous sequence. For example, a vector can be introduced *in vivo* such that it is taken up by a cell, within which cell the vector or a portion thereof is transcribed, producing an antisense nucleic acid (RNA) of the invention. Such a vector would contain a sequence encoding an antisense nucleic acid. Such a vector can remain episomal or become chromosomally integrated, as long as it can be transcribed to produce the desired antisense RNA. Such vectors can be constructed by recombinant DNA technology methods standard in the art.

Vectors can be plasmid, viral, or others known in the art, used for replication and expression in mammalian cells. Expression of the sequence encoding the an antisense RNA can be by any promoter known in the art to act in mammalian, preferably human, cells. Such promoters can be inducible or constitutive. Such promoters include but are not limited to: the CMV promoter, the SV40 early promoter region (Bernoist and Chambon, 1981, Nature 290:304-310), the promoter contained in the 3N long terminal repeat of Rous sarcoma virus (Yamamoto *et al.*, 1980, Cell 22:787-797), the herpes thymidine kinase promoter (Wagner *et al.*, 1981, Proc. Natl. Acad. Sci. U.S.A. 78:1441-1445), the regulatory sequences of the metallothionein gene (Brinster *et al.*, 1982, Nature 296:39-42), etc.

In a specific embodiment, the antisense oligonucleotide comprises catalytic RNA, or a ribozyme (see, *e.g.*, PCT International Publication WO 90/11364, published October 4, 1990; Sarver *et al.*, 1990, Science 247:1222-1225). In another embodiment, the oligonucleotide is a 2N-0-methylribonucleotide (Inoue *et al.*, 1987, Nucl. Acids Res. 15:6131-6148), or a chimeric RNA-DNA analog (Inoue *et al.*, 1987, FEBS Lett. 215:327-330).

In another embodiment, the antisense nucleic acids of the invention comprise a sequence complementary to at least a portion of an RNA transcript of a polynucleotide sequence in SEQ ID No. 1. However, absolute complementarity, although preferred, is not required. A sequence "complementary to at least a portion of an RNA," as referred to herein, means a sequence having sufficient complementarity to be able to hybridize with the RNA, forming a stable duplex; in the case of double-stranded antisense nucleic acid sequence, a single strand of the duplex DNA may thus be tested, or triplex formation may be assayed. The ability to hybridize will depend on both the degree of complementarity and the length of the antisense nucleic acid. Generally, the longer the hybridizing nucleic acid, the more base mismatches with an RNA transcribed from SEQ ID No. 1 may contain and still form a stable duplex (or triplex, as the case may be). One skilled in the art can ascertain a tolerable degree of mismatch by use of standard procedures to determine the melting point of the hybridized complex.

The invention also relates to the animals, except humans, comprising one of the above-described transformed cells according to the invention.

The production of transgenic animals according to the invention overexpressing one or more of the *Chlamydia pneumoniae* genes will be preferably carried out on rats, mice or rabbits according to methods well known to persons skilled in the art such as viral or nonviral transfections. The transgenic animals overexpressing one or more of the said genes may be obtained by transfection of multiple copies of the said genes under the control of a powerful promoter of a ubiquitous nature, or which.is selective for one type of tissue. The transgenic animals may also be obtained by homologous recombination on embryonic stem cells, transfer of these stem cells to embryos, selection of the chimeras affected at the level of the reproductive lines, and growth of the said chimeras.

The transformed cells as well as the transgenic animals according to the invention can be used in methods of preparing the recombinant polypeptide.

It is now possible to produce recombinant polypeptides in a relatively large quantity by genetic engineering using the cells transformed with expression vectors according to the invention or using transgenic animals according to the invention.

The methods of preparing a polypeptide of the invention in recombinant form, characterized in that they use a vector and/or a cell transformed with a vector according to the invention and/or a transgenic animal comprising one of the said transformed cells according to the invention, are themselves included in the present invention.

Among the said methods of preparing a polypeptide of the invention in recombinant form, the methods of preparation using a vector, and/or a cell transformed with the said vector and/or a transgenic animal comprising one of the said transformed cells, containing a nucleotide sequence encoding a polypeptide of the cellular envelope of *Chlamydia pneumoniae* or one of its representative fragments, more preferably encoding a polypeptide of the outer cellular envelope of *Chlamydia pneumoniae* or one of its fragment, are preferred.

Among the said methods of preparing a polypeptide of the invention in recombinant form, the methods of preparation using a vector, and/or a cell transformed with the said vector and/or a transgenic animal comprising one of the said transformed cells, containing a nucleotide sequence encoding a *Chlamydia pneumoniae* secreted polypeptide or one of its representative fragments or encoding a transport polypeptide, a surface exposed polypeptide, a lipoprotein or one of its representative fragments, a polypeptide involved in lipopolysaccharide biosynthesis, a Type III or other secreted polypeptide, a polypeptide containing RGD attachment sites, a cell wall anchored surface polypeptide, a polypeptide not found in *Chlamydia trachomatis*, a ribosomal polypeptide or a polypeptide involved in secretion, transcription, translation, maturation of proteins, a polypeptide involved in the synthesis of the wall, a polypeptide involved in the virulence, a polypeptide involved in the intermediate metabolism, in particular in the metabolism of sugars and/or of cofactors, a polypeptide involved in the metabolism of nucleotides, of amino acids, of nucleic acids or of fatty acids of *Chlamydia pneumoniae* or one of their representative fragments, or a polypeptide specific to *Chlamydia pneumoniae*, are also preferred.

The recombinant polypeptides obtained as indicated above may be provided either in glycosylated or non-glycosylated form and may or may not have the natural tertiary structure.

A preferred variant consists in producing a recombinant polypeptide fused to a "carrier" protein (chimeric protein). The advantage of this system is that it allows a stabilization and a reduction in proteolysis of the recombinant product, an increase in solubility during renaturation in vitro and/or a simplification of purification when the fusion partner has affinity for a specific ligand.

More particularly, the invention relates to a method of preparing a polypeptide of the invention comprising the following steps:

a) culture of the transformed cells under conditions allowing the expression of a recombinant polypeptide having a nucleic acid sequence according to the invention;

b) where appropriate, recovery of the said recombinant polypeptide.

When the method of preparing a polypeptide of the invention uses a transgenic animal according to the invention, the recombinant polypeptide is then extracted from the said animal.

The subject of the invention is also a polypeptide capable of being obtained by a method of the invention as described above.

The invention also comprises a method of preparing a synthetic polypeptide, characterized in that it uses an amino acid sequence of polypeptides according to the invention.

The invention also relates to a synthetic polypeptide obtained by a method according to the invention.

Polypeptides according to the invention may also be prepared by conventional techniques in the field of peptide synthesis under conditions suitable to produce the polypeptides encoded by the polynucleotide of the invention. This synthesis may be carried out in and recovered from a homogeneous solution or on a solid phase.

For example, the synthesis technique in a homogeneous solution described by Houbenweyl in 1974 may be used.

This method of synthesis consists in successively condensing, in pairs, the successive amino acids in the required order, or in condensing amino acids and fragments previously formed and already containing several amino acids in the appropriate order, or alternatively several fragments thus previously prepared, it being understood that care will have been taken to protect beforehand all the reactive functional groups carried by these amino acids or fragments, with the exception of the amine functional groups of one and the carboxyl functional groups of the other or vice versa, which should normally take part in the formation of the peptide bonds, in particular after activation of the carboxyl functional group, according to methods well known in peptide synthesis.

According to another preferred technique of the invention, the one described by Merrifield is used.

To manufacture a peptide chain according to the Merrifield method, a highly porous polymer resin is used, onto which the first C-terminal amino acid of the chain is attached. This amino acid is attached onto a resin via its carboxyl group and its amine functional group is protected. The amino acids which will constitute the peptide chain are thus attached, one after another, onto the amine group, each time deprotected beforehand, of the portion of the peptide chain already formed, and which is attached to the resin. When the entire peptide chain desired is formed, the protecting groups are removed from the various amino acids constituting the peptide chain and the peptide is detached from the resin with the aid of an acid.

The invention relates, in addition, to hybrid (fusion) polypeptides having at least one polypeptide or one of its representative fragments according to the invention, and a sequence of a polypeptide capable of eliciting an immune response in humans or animals.

Advantageously, the antigenic determinant is such that it is capable of eliciting a humoral and/or cellular response. An antigenic determinant may be identified by screening expression libraries of the *Chlamydia pneumoniae* genome with antibodies contained in the serum of patients infected with a bacterium belonging to the species *Chlamydia pneumoniae*. An antigenic determinant may comprise a polypeptide or one of its representative fragments according to the invention, in glycosylated form, used in order to obtain immunogenic compositions capable of inducing the synthesis of antibodies directed against multiple epitopes. The said polypeptides or their glycosylated fragments also form part of the invention.

These hybrid molecules may consist, in part, of a carrier molecule for polypeptides or for their representative fragments according to the invention, combined with a portion which may be immunogenic, in particular an epitope of the diphtheria toxin, the tetanus toxin, a hepatitis B virus surface antigen (patent FR 79 21811), the poliomyelitis virus VP1 antigen or any other viral or bacterial toxin or antigen.

The methods of synthesizing the hybrid molecules include the methods used in genetic engineering to construct hybrid nucleotide sequences encoding the desired polypeptide sequences. Reference may be advantageously made, for example, to the technique for producing genes encoding fusion proteins described by Minton in 1984.

The said hybrid nucleotide sequences encoding a hybrid polypeptide as well as the hybrid polypeptides according to the invention, characterized in that they are recombinant polypeptides obtained by the expression of the said hybrid nucleotide sequences, also form part of the invention.

The invention also comprises the vectors characterized in that they contain one of the said hybrid nucleotide sequences. The host cells transformed by the said vectors, the transgenic animals comprising one of the said transformed cells as well as the methods of preparing recombinant polypeptides using the said vectors, the said transformed cells and/or the said transgenic animals of course also form part of the invention.

The polypeptides according to the invention, the antibodies according to the invention described below and the nucleotide sequences according to the invention may advantageously be used in *in vitro* and/or *in vivo* methods for the detection and/or the identification of bacteria belonging to the species *Chlamydia pneumoniae*, in a biological sample (biological tissue or fluid) which is likely to contain them. These methods, depending on the specificity of the polypeptides, of the antibodies and of the nucleotide sequences according to the invention which will be used, may in particular detect and/or identify the bacterial variants belonging to the species *Chlamydia pneumoniae* as well as the associated microorganisms capable of being detected by the polypeptides, the antibodies and the nucleotide sequences according to the invention which will be chosen. It may, for example, be advantageous to choose a polypeptide, an antibody or a nucleotide sequence according to the invention, which is capable of detecting any bacterium of the Chlamydia family by choosing a polypeptide, an antibody and/or a nucleotide sequence according to the invention which is specific to the family or, on the contrary, it will be most particularly advantageous to target a variant of the species *Chlamydia pneumoniae*, which is responsible, for example, for the induction or the worsening of pathologies specific to the targeted variant, by choosing a polypeptide, an antibody and/or a nucleotide sequence according to the invention which is specific to the said variant.

The polypeptides according to the invention may advantageously be used in a method for the detection and/or the identification of bacteria belonging to the species *Chlamydia pneumoniae* or to an associated microorganism, in a biological sample (biological tissue or fluid) which is likely to contain them, characterized in that it comprises the following steps:

a) bringing this biological sample into contact with a polypeptide or one of its representative fragments according to the invention (under conditions allowing an immunological reaction between the said polypeptide and the antibodies which may be present in the biological sample);

b) detecting the antigen-antibody complexes which may be formed.

Preferably, the biological sample consists of a fluid, for example a human or animal serum, blood or biopsies.

Any conventional procedure may be used to carry out such a detection of the antigen-antibody complexes which may be formed.

By way of example, a preferred method uses immunoenzymatic procedures based on the ELISA technique, immunofluorescence procedures or radioimmunological procedures (RIA), and the like.

Accordingly, the invention also relates to the polypeptides according to the invention, labelled with the aid of a suitable label such as a label of the enzymatic, fluorescent or radioactive type.

Such methods comprise, for example, the following steps:

- deposition of defined quantities of a polypeptide composition according to the invention into the wells of a microtitre plate,
- introduction, into the said wells, of increasing dilutions of serum, or of a different biological sample as defined above, which has to be analysed,
- incubation of the microplate,
- introduction, into the wells of the microtitre plate, of labelled antibodies directed against human or animal immunoglobulins, these antibodies having been labelled with the aid of an enzyme selected from those which are capable of hydrolyzing a substrate, thereby modifying the absorption of the radiation of the latter, at least at a defined wavelength, for example at 550 nm,
- detection, by comparison with a control, of the quantity of substrate hydrolyzed.

The invention also relates to a kit or set for the detection and/or the identification of bacteria belonging to the species *Chlamydia pneumoniae* or to an associated microorganism, characterized in that it comprises the following components:

- a polypeptide according to the invention,

- where appropriate, the reagents for constituting the medium appropriate for the immunological or specific reaction,
- the reagents allowing the detection of the antigen-antibody complexes produced by the immunological reaction between the polypeptide(s) of the invention and the antibodies which may be present in the biological sample, it being possible for these reagents also to carry a label, or to be capable of being recognized in turn by a labelled reagent, more particularly in the case where the polypeptide according to the invention is not labelled,
- where appropriate, a reference biological sample (negative control) free of antibodies recognized by a polypeptide according to the invention,
- where appropriate, a reference biological sample (positive control) containing a predetermined quantity of antibodies recognized by a polypeptide according to the invention.

According to the invention, the polypeptides, peptides, fusion proteins or other derivatives, or analogs thereof encoded by a polynucleotide sequence in SEQ ID No. 1, may be used as an immunogen to generate antibodies which immunospecifically bind such an immunogen. Such antibodies may include, but are not limited to, polyclonal and monoclonal antibodies, humanized or chimeric antibodies, single chain antibodies, Fab fragments, $F(ab')_2$ fragments, fragments produced by a Fab expression library, anti-idiotypic (anti-Id) antibodies, and epitope-binding fragments of any of the above. In a specific embodiment, the antibody to a polypeptide, peptide or other derivative, or analog thereof encoded by a polynucleotide sequence in SEQ ID No. 1 is a bispecific antibody (see generally, *e.g.* Fanger and Drakeman, 1995, *Drug News and Perspectives* 8: 133-137). Such a bispecific antibody is genetically engineered to recognize both (1) an epitope and (2) one of a variety of "trigger" molecules, *e.g.* Fc receptors on myeloid cells, and CD3 and CD2 on T cells, that have been identified as being able to cause a cytotoxic T-cell to destroy a particular target. Such bispecific antibodies can be prepared either by chemical conjugation, hybridoma, or recombinant molecular biology techniques known to the skilled artisan.

Various procedures known in the art may be used for the production of polyclonal antibodies to a polypeptide, peptide or other derivative, or analog thereof encoded by a polynucleotide sequence in SEQ ID No. 1. For the production of antibody, various host animals can be immunized by injection with a polypeptide, or peptide or other derivative, or analog thereof, including but not limited to rabbits, mice, rats, etc. Various adjuvants, depending on the host species, may be used to increase the immunological response, including but not limited to Stimulon™ QS-21 (Aquila Biopharmaceuticals, Inc., Framingham, MA), MPL™ (3-O-deacylated monophosphoryl lipid A; RIBI ImmunoChem Research, Inc., Hamilton, MT), aluminum phosphate, IL-12 (Genetics Institute, Cambridge, MA), Freund's (complete and incomplete), mineral gels such as aluminum hydroxide, surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanins, dinitrophenol, BCG (bacille Calmette-Guerin), and corynebacterium parvum. Alternatively, polyclonal antibodies may be prepared by purifying, on an affinity column onto which a polypeptide according to the invention has been previously attached, the antibodies contained in the serum of patients infected with a bacterium belonging to the species *Chlamydia pneumoniae.*

For preparation of monoclonal antibodies directed toward a polypeptide, peptide or other derivative, or analog, any technique which provides for the production of antibody molecules by continuous cell lines in culture may be used. For example, the hybridoma technique originally developed by Kohler and Milstein (1975, Nature 256:495-497), as well as the trioma technique, the human B-cell hybridoma technique (Kozbor *et al.*, 1983, Immunology Today 4:72), and the EBV-hybridoma technique to produce human monoclonal antibodies (Cole *et al.*, 1985, in Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, Inc., pp. 77-96). In an additional embodiment of the invention, monoclonal antibodies can be produced in germ-free animals utilizing technology described in PCT/US90/02545. In another embodiment of the invention, transgenic non-human animals can be used for the production of human antibodies utilizing technology described in WO 98/24893 and WO 96/33735. According to the invention, human antibodies may be used and can be obtained by using human hybridomas (Cote *et al.*, 1983, Proc. Natl. Acad. Sci. U.S.A. 80:2026-2030) or by transforming human B cells with EBV virus *in vitro* (Cole *et al.*, 1985, in Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, pp. 77-96). In fact, according to the invention, techniques developed for the production of "chimeric antibodies" (Morrison *et al.*, 1984, PROC. NATL. ACAD. SCI. U.S.A. 81:6851-6855; Neuberger *et al.*, 1984, Nature 312:604-608; Takeda *et al.*, 1985, Nature 314:452-454) by splicing the genes from a mouse antibody molecule specific for a polypeptide, peptide or other derivative, or analog together with genes from a human antibody molecule of appropriate biological activity can be used; such antibodies are within the scope of this invention.

According to the invention, techniques described for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce polypeptide or peptide-specific single chain antibodies. An additional embodiment of the invention utilizes the techniques described for the construction of Fab expression libraries (Huse *et al.*, 1989, Science 246:1275-1281) to allow rapid and easy identification of monoclonal Fab fragments with the desired specificity for polypeptides, derivatives, or analogs.

Antibody fragments which contain the idiotype of the molecule can be generated by known techniques. For example, such fragments include but are not limited to: the $F(ab')_2$ fragment which can be produced by pepsin digestion of the antibody molecule; the Fab' fragments which can be generated by reducing the disulfide bridges of the $F(ab')_2$ fragment, the Fab fragments which can be generated by treating the antibody molecule with papain and a reducing agent, and Fv fragments.

In addition, techniques have been developed for the production of chimerized (*See*, e.g., Boss, M. et al., U.S. Patent No. 4,816,397; and Cabilly, S. et al., U.S. Patent No. 5,585,089 each of which is incorporated herein by reference in its entirety) humanized antibodies (*See*, e.g., Queen, U.S. Patent No. 5,585,089, which is incorporated herein by reference in its entirety.) An immunoglobulin light or heavy chain variable region consists of a "framework" region interrupted by three hypervariable regions, referred to as complementarily determining regions (CDRs). The extent of the framework region and CDRs have been precisely defined (See, "Sequences of Proteins of Immunological Interest", Kabat, E. et al., U.S. Department of Health and Human Services (1983). Briefly, humanized antibodies are antibody molecules from non-human species having one or more CDRs from the non-human species and a framework from a human immunoglobulin molecule.

The antibodies of the invention may also be labelled in the same manner as described above for the nucleic probes of the invention such as an enzymatic, fluorescent or radioactive type labelling.

The invention relates, in addition, to a method for the detection and/or the identification of bacteria belonging to the species *Chlamydia pneumoniae* or to an associated microorganism in a biological sample, characterized in that it comprises the following steps:

a) bringing the biological sample (biological tissue or fluid) into contact with a mono- or polyclonal antibody according to the invention (under conditions allowing an immunological reaction between the said antibodies and the polypeptides of the bacterium belonging to the species *Chlamydia pneumoniae* or to an associated microorganism which may be present in the biological sample, that is, under conditions suitable for the formation of immune complexes);

b) detecting the antigen-antibody complex which may be formed.

Also falling within the scope of the invention is a kit or set for the detection and/or the identification of bacteria belonging to the species *Chlamydia pneumoniae* or to an associated microorganism, characterized in that it comprises the following components:

- a polyclonal or monoclonal antibody according to the invention, labeled where appropriate;
- where appropriate, a reagent for constituting the medium appropriate for carrying out the immunological reaction;
- a reagent allowing the detection of the antigen-antibody complexes produced by the immunological reaction, it being possible for this reagent also to carry a label, or to be capable of being recognized in turn by a labelled reagent, more particularly in the case where the said monoclonal or polyclonal antibody is not labelled;
- where appropriate, reagents for carrying out the lysis of the cells in the sample tested.

The principle of the DNA chip which was explained above may also be used to produce protein "chips" on which the support has been coated with a polypeptide or an antibody according to the invention, or arrays thereof, in place of the DNA. These protein "chips" make it possible, for example, to analyze the biomolecular interactions (BIA) induced by the affinity capture of target analytes onto a support coated, for example, with proteins, by surface plasma resonance (SPR). Reference may be made, for example, to the techniques for coupling proteins onto a solid support which are described in EP 524 800 or to the methods describing the use of biosensor-type protein chips such as the BIAcore-type technique (Pharmacia) (Arlinghaus et al., 1997, Krone et al., 1997, Chatelier et al., 1995). These polypeptides or antibodies according to the invention, capable of specifically binding antibodies or polypeptides derived from the sample to be analysed, may thus be used in protein chips for the detection and/or the identification of proteins in samples. The said protein chips may in particular be used for infectious diagnosis and may preferably contain, per chip, several polypeptides and/or antibodies of the invention of different specificity, and/or polypeptides and/or antibodies capable of recognizing microorganisms different from *Chlamydia pneumoniae*.

Accordingly, the subject of the present invention is also the polypeptides and the antibodies according to the invention, characterized in that they are immobilized on a support, in particular of a protein chip.

The protein chips, characterized in that they contain at least one polypeptide or one antibody according to the invention immobilized on the support of the said chip, also form part of the invention.

The invention comprises, in addition, a protein chip according to the invention, characterized in that it contains, in addition, at least one polypeptide of a microorganism different from *Chlamydia pneumoniae* or at least one antibody directed against a compound of a microorganism different from *Chlamydia pneumoniae,* immobilized on the support of the said chip.

The invention also relates to a kit or set for the detection and/or the identification of bacteria belonging to the species *Chlamydia pneumoniae* or to an associated microorganism, or for the detection and/or the identification of a microorganism characterized in that it comprises a protein chip according to the invention.

The subject of the present invention is also a method for the detection and/or the identification of bacteria belonging to the species *Chlamydia pneumoniae* or to an associated microorganism in a biological sample, characterized in that it uses a nucleotide sequence according to the invention.

More particularly, the invention relates to a method for the detection and/or the identification of bacteria belonging to the species *Chlamydia pneumoniae* or to an associated microorganism in a biological sample, characterized in that it comprises the following steps:

a) where appropriate, isolation of the DNA from the biological sample to be analysed, or optionally production of a cDNA from the RNA in the biological sample;

b) specific amplification of the DNA of bacteria belonging to the species *Chlamydia pneumoniae* or to an associated microorganism with the aid of at least one primer according to the invention;

c) detection of the amplification products.

These may be detected, for example, by the molecular hybridization technique using a nucleic probe according to the invention. This probe will be advantageously labelled with a nonradioactive (cold probe) or radioactive element.

For the purposes of the present invention, "DNA in the biological sample" or "DNA contained in the biological sample" will be understood to mean either the DNA present in the biological sample considered, or optionally the cDNA obtained after the action of a reverse transcriptase-type enzyme on the RNA present in the said biological sample.

Another aim of the present invention consists in a method according to the invention, characterized in that it comprises the following steps:

a) bringing a nucleotide probe according to the invention into contact with a biological sample, the DNA contained in the biological sample having, where appropriate, been previously made accessible to hybridization, under conditions allowing the hybridization of the probe to complementary base pairs of the DNA of a bacterium belonging to the species *Chlamydia pneumoniae* or to an associated microorganism;

b) detecting the hybridization complex formed between the nucleotide probe and the DNA in the biological sample.

The present invention also relates to a method according to the invention, characterized in that it comprises the following steps:

a) bringing a nucleotide probe immobilized on a support according to the invention into contact with a biological sample, the DNA in the sample having, where appropriate, been previously made accessible to hybridization, under conditions allowing the hybridization of the probe to the DNA of a bacterium belonging to the species *Chlamydia pneumoniae* or to an associated microorganism;

b) bringing the hybrid formed between the nucleotide probe immobilized on a support and the DNA contained in the biological sample, where appropriate after removal of the DNA in the biological sample which has not hybridized with the probe, into contact with a labelled nucleotide probe according to the invention;

c) detecting the new hybrid formed in step b).

According to an advantageous embodiment of the method for the detection and/or the identification defined above, it is characterized in that, prior to step a), the DNA in the biological sample is primer-extended and/or amplified beforehand with the aid of at least one primer according to the invention.

The invention relates, in addition, to a kit or set for the detection and/or the identification of bacteria belonging to the species *Chlamydia pneumoniae* or to an associated microorganism, characterized in that it comprises the following components:

a) a nucleotide probe according to the invention;

b) where appropriate, the reagents necessary for carrying out a hybridization reaction;

c) where appropriate, at least one primer according to the invention as well as the reagents (e.g., polymerase and/or deoxynucleotide triphosphates) necessary for a DNA amplification reaction.

The invention also relates to a kit or set for the detection and/or the identification of bacteria belonging to the species *Chlamydia pneumoniae* or to an associated microorganism, characterized in that it comprises the following components:

a) a nucleotide probe, called capture probe, according to the invention;

b) an oligonucleotide probe, called detection probe, according to the invention;

c) where appropriate, at least one primer according to the invention as well as the reagents (e.g., polymerase and/or deoxynucleotide triphosphates) necessary for a DNA amplification reaction.

The invention also relates to a kit or set for the detection and/or the identification of bacteria belonging to the species *Chlamydia pneumoniae* or to an associated microorganism, characterized in that it comprises the following components:

a) at least one primer according to the invention;

b) where appropriate, the reagents necessary for carrying out a DNA amplification reaction;

c) where appropriate, a component which makes it possible to check the sequence of the amplified fragment, more particularly an oligonucleotide probe according to the invention.

The invention relates, in addition, to a kit or set for the detection and/or the identification of bacteria belonging to the species *Chlamydia pneumoniae* or to an associated microorganism, or for the detection and/or the identification of a microorganism characterized in that it comprises a DNA chip according to the invention.

The invention also relates to a method or to a kit or set according to the invention for the detection and/or the identification of bacteria belonging to the species *Chlamydia pneumoniae*, characterized in that the said primer and/or the said probe according to the invention are chosen from the nucleotide sequences specific to the species *Chlamydia pneumoniae*, in that the said polypeptides according to the invention are chosen from the polypeptides specific to the species *Chlamydia pneumoniae* and in that the said antibodies according to the invention are chosen from the antibodies directed against the polypeptides according to the invention chosen from the polypeptides specific to the species *Chlamydia pneumoniae*.

Preferably, the said method or the said kit or set above according to the invention, for the detection and/or the identification of bacteria belonging to the species *Chlamydia pneumoniae* is characterized in that the said primer and/or the said probe or the said polypeptides are chosen from the nucleotide sequences or polypeptides according to the invention which have been identified as being specific to the species *Chlamydia pneumoniae* and in that the said antibodies according to the invention are chosen from the antibodies directed against the polypeptides according to the invention chosen from the polypeptides identified as being specific to the species *Chlamydia pneumoniae*.

The invention relates, in addition, to a method or a kit or set according to the invention for the diagnosis of predispositions to, or of a condition caused by, cardiovascular diseases, preferably linked to the presence of atheroma, which are induced or worsened by a *Chlamydia pneumoniae* infection.

The invention also relates to a method or a kit or set according to the invention for the diagnosis of predispositions to, or of conditions caused by, respiratory diseases induced or worsened by a *Chlamydia pneumoniae* infection; preferably, the said respiratory disease is asthma.

According to another aspect, the subject of the invention is the use of polypeptides according to the invention, of cells transformed with a vector according to the invention and/or of transformed animals according to the invention, for the biosynthesis or the biodegradation of organic or inorganic compounds.

As has been mentioned above, the nucleotide sequences of the invention were identified by homology with sequences known to encode, for example, polypeptides or fragments of enzymatic polypeptides involved in the biosynthesis or the biodegradation of organic or inorganic molecules.

It is thus possible to use the said polypeptides of the invention in a similar manner for the biosynthesis or the biodegradation of organic or inorganic compounds of industrial or therapeutic interest (called compounds of interest).

Among these polypeptides, there may be mentioned in particular the enzymes involved in metabolism, such as the proteolytic enzymes, amino transferases, glucose metabolism, or the enzymes which may be used in the biosynthesis of sugars, amino acids, fatty acids, polypeptides, nucleotides, nucleic acids or any other organic or inorganic compound or in the biodegradation of organic or inorganic compounds.

Among these polypeptides, there may be mentioned, in addition, the mutated or modified enzymes corresponding to mutated or modified polypeptides according to the invention which may also be used for the biosynthesis or the biodegradation of organic or inorganic compounds at the industrial level, such as, for example, the production of compounds of interest, the reprocessing of manufacturing residues applied to the food industries, to the papermaking industry or to the chemical and pharmaceutical industries.

The methods of biosynthesis or biodegradation of organic or inorganic compounds, characterized in that they use a polypeptide or one of its representative fragments according to the invention, transformed cells according to the invention and/or a transformed animal according to the invention, also form part of the invention.

The invention relates, in addition, to the use of a nucleotide sequence according to the invention, of a polypeptide according to the invention, of an antibody according to the invention, of a cell according to the invention, and/or of a transformed animal according to the invention, for the selection of an organic or inorganic compound capable of modulating, regulating, inducing or inhibiting the expression of genes, and/or of modifying the cellular replication of eukaryotic or prokaryotic cells or capable of inducing, inhibiting or worsening the pathologies linked to an infection by *Chlamydia pneumoniae* or one of its associated microorganisms.

The invention also comprises screening assays that comprise methods of selecting compounds capable of binding to a polypeptide, fusion polypeptide or one of its representative fragments according to the invention, capable of binding to a nucleotide sequence according to the invention, or capable of recognizing an antibody according to the invention, and/or capable of modulating, regulating, inducing or inhibiting the expression of genes, and/or of modifying the growth or the cellular replication of eukaryotic or prokaryotic cells, or capable of inducing, inhibiting or worsening, in an animal or human organism, the pathologies linked to an infection by *Chlamydia pneumoniae* or one of its associated microorganisms, characterized in that it comprises the following steps:

a) bringing the said compound into contact with the said polypeptide, the said nucleotide sequence, with a transformed cell according to the invention and/or administering the said compound to a transformed animal according to the invention;

b) determining the capacity of the said compound to bind with the said polypeptide or the said nucleotide sequence, or to modulate, regulate, induce or inhibit the expression of genes, or to modulate growth or cellular replication, or to induce, inhibit or worsen in the said transformed animal, the pathologies linked to an infection by *Chlamydia pneumoniae* or one of its associated microorganisms.

The transformed cells and/or animals according to the invention may advantageously serve as a model and may be used in methods for studying, identifying and/or selecting compounds capable of being responsible for pathologies induced or worsened by *Chlamydia pneumoniae,* or capable of preventing and/or of treating these pathologies such as, for example, cardiovascular or respiratory diseases. In particular, the transformed host cells, in particular bacteria of the *Chlamydia* family whose transformation with a vector according to the invention may, for example, increase or inhibit its infectivity, or modulate the pathologies usually induced or worsened by the infection, may be used to infect animals in which the onset of pathologies will be monitored. These nontransformed animals, infected for example with transformed *Chlamydia* bacteria, may serve as a study model. In the same manner, the transformed animals according to the invention may, for example, exhibit predispositions to cardiovascular and/or respiratory diseases and thus be used in methods for selecting compounds capable of preventing and/or of treating the said diseases. The said methods using the said transformed cells and/or transformed animals form part of the invention.

The compounds capable of being selected may be organic compounds such as polypeptides or carbohydrates or any other organic or inorganic compounds already known, or new organic compounds produced using molecular modeling techniques and obtained by chemical or biochemical synthesis, these techniques being known to persons skilled in the art.

The said selected compounds may be used to modulate the growth and/or the cellular replication of *Chlamydia pneumoniae* or any other associated microorganism and thus to control infection by these microorganisms. The said compounds according to the invention may also be used to modulate the growth and/or the cellular replication of all eukaryotic or prokaryotic cells, in particular tumour cells and infectious microorganisms, for which the said compounds will prove active, the methods which make it possible to determine the said modulations being well known to persons skilled in the art.

Compound capable of modulating the growth of a microorganism is understood to designate any compound which makes it possible to act, to modify, to limit and/or to reduce the development, the growth, the rate of proliferation and/or the viability of the said microorganism.

This modulation may be achieved, for example, by an agent capable of binding to a protein and thus of inhibiting or of potentiating its biological activity, or capable of binding to a membrane protein of the outer surface of a microorganism and of blocking the penetration of the said microorganism into the host cell or of promoting the action of the immune system of the infected organism directed against the said microorganism. This modulation may also be achieved by an agent capable of binding to a nucleotide sequence of a DNA or RNA of a microorganism and of blocking, for example, the expression of a polypeptide whose biological or structural activity is necessary for the growth or for the reproduction of the said microorganism.

Associated microorganism is understood to designate in the present invention any microorganism whose gene expression may be modulated, regulated, induced or inhibited, or whose growth or cellular replication may also be modulated by a compound of the invention. Associated microorganism is also understood to designate in the present invention any microorganism containing nucleotide sequences or polypeptides according to the invention. These microorganisms may, in some cases, contain polypeptides or nucleotide sequences identical or homologous to those of the invention may also be detected and/or identified by the detection and/or identification methods or kit according to the invention and may also serve as a target for the compounds of the invention.

The invention relates to the compounds capable of being selected by a method of selection according to the invention.

The invention also relates to a pharmaceutical composition comprising a compound chosen from the following compounds:

a nucleotide sequence according to the invention;

a polypeptide according to the invention;

a vector according to the invention;

an antibody according to the invention; and

a compound capable of being selected by a method of selection according to the invention, optionally in combination with a pharmaceutically acceptable vehicle.

An effective quantity is understood to designate a sufficient quantity of the said compound or antibody, or of a polypeptide of the invention, which makes it possible to modulate the growth of *Chlamydia pneumoniae* or of an associated microorganism.

The invention also relates to a pharmaceutical composition comprising one or more polypeptides according to the invention and/or one or more fusion polypeptides according to the invention. Such compositions further comprise a pharmaceutically acceptable carrier or vehicle. Pharmaceutical compositions include compositions that comprise a polypeptide or fusion polypeptide that immunoreacts with seropositive serum of an individual infected with *Chlamydia pneumoniae.* In one embodiment, a pharmaceutical composition according to the invention can be utilized for the prevention or the treatment of an infection by a bacterium belonging to the species *Chlamydia pneumoniae* or by an associated microorganism.

The invention relates, in addition, to an immunogenic composition or a vaccine composition, characterized in that it comprises one or more polypeptides according to the invention and/or one or more hybrid (fusion) polypeptides according to the invention. Such compositions further comprise a pharmaceutically acceptable carrier or vehicle. Immunogenic compositions or fusion polypeptide include compositions that comprise a polypeptide that immunoreacts with seropositive serum of an individual infected with *Chlamydia pneumoniae*.

Immunogenic or vaccine compositions can also comprise DNA immunogenic or vaccine compositions comprising polynucleotide sequences of the invention operatively associated with a regulatory sequence that controls gene expression. Such compositions can include compositions that direct expression of a neutralizing epitope of *Chlamydia pneumoniae*.

The invention also comprises the use of a transformed cell according to the invention, for the preparation of a vaccine composition.

The invention also relates to a vaccine composition, characterized in that it contains a nucleotide sequence according to the invention, a vector according to the invention and/or a transformed cell according to the invention.

The invention also relates to the vaccine compositions according to the invention, for the prevention or the treatment of an infection by a bacterium belonging to the species *Chlamydia pneumoniae* or by an associated microorganism.

The invention also relates to the use of DNA encoding polypeptides of *Chlamydia pneumoniae*, in particular antigenic determinants, to be formulated as vaccine compositions. In accordance with this aspect of the invention, the DNA of interest is engineered into an expression vector under the control of regulatory elements, which will promote expression of the DNA, *i.e.*, promoter or enhancer elements. In one preferred embodiment, the promoter element may be cell-specific and permit substantial transcription of the DNA only in predetermined cells. The DNA may be introduced directly into the host either as naked DNA (U.S. Patent No. 5,679,647 incorporated herein by reference in their entirety) or formulated in compositions with other agents which may facilitate uptake of the DNA including viral vectors, *i.e.*, adenovirus vectors, or agents which facilitate immunization, such as bupivicaine and other local anesthetics (U.S. Patent 5,593,972 incorporated herein by reference in their entirety), saponins (U.S. Patent 5,739,118 incorporated herein by reference in their entirety) and cationic polyamines (published international application WO 96/10038 incorporated herein by reference in their entirety).

The DNA sequence encoding the antigenic polypeptide and regulatory element may be inserted into a stable cell line or cloned microorganism, using techniques, such as targeted homologous recombination, which are well known to those of skill in the art, and described *e.g.*, in Chappel, U.S. Patent No. 4,215,051; Skoultchi, WO 91/06667 each of which is incorporated herein by reference in its entirety.

Such cell lines and microorganisms may be formulated for vaccine purposes. In yet another embodiment, the DNA sequence encoding the antigenic polypeptide and regulatory element may be delivered to a mammalian host and introduced into the host genome via homologous recombination (*See*, Chappel, U.S. Patent No. 4,215,051; Skoultchi, WO 91/06667 each of which is incorporated herein by reference in its entirety.

Preferably, the immunogenic and/or vaccine compositions according to the invention intended for the prevention and/or the treatment of an infection by *Chlamydia pneumoniae* or by an associated microorganism will be chosen from the immunogenic and/or vaccine compositions comprising a polypeptide or one of its representative fragments corresponding to a protein, or one of its representative fragments, of the cellular envelope of *Chlamydia pneumoniae*. The vaccine compositions comprising nucleotide sequences will also preferably comprise nucleotide sequences encoding a polypeptide or one of its representative fragments corresponding to a protein, or one of its representative fragments, of the cellular envelope of *Chlamydia pneumoniae*.

Among these preferred immunogenic and/or vaccine compositions, the most preferred are those comprising a polypeptide or one of its representative fragments, or a nucleotide sequence or one of its representative fragments whose sequences are chosen from the nucleotide or amino acid sequences identified in this functional group and listed above.

The polypeptides of the invention or their representative fragments entering into the immunogenic compositions according to the invention may be selected by techniques known to persons skilled in the art, such as for example on the capacity of the said polypeptides to stimulate T cells, which results, for example, in their proliferation or the secretion of interleukins, and which leads to the production of antibodies directed against the said polypeptides.

In mice, in which a weight dose of the vaccine composition comparable to the dose used in humans is administered, the antibody reaction is tested by collecting serum followed by a study of the formation of a complex between the antibodies present in the serum and the antigen of the vaccine composition, according to the customary techniques.

According to the invention, the said vaccine compositions will be preferably in combination with a pharmaceutically acceptable vehicle and, where appropriate, with one or more appropriate immunity adjuvants.

Various types of vaccines are currently available for protecting humans against infectious diseases: attenuated live microorganisms (*M. bovis* - BCG for tuberculosis), inactivated microorganisms (influenza virus), acellular extracts (*Bordetella pertussis* for whooping cough), recombinant proteins (hepatitis B virus surface antigen), polysaccharides (pneumococci). Experiments are underway on vaccines prepared from synthetic peptides or from genetically modified microorganisms expressing heterologous antigens. Even more recently, recombinant plasmid DNAs carrying genes encoding protective antigens were proposed as an alternative vaccine strategy. This type of vaccination is carried out with a particular plasmid derived from an *E. coli* plasmid which does not replicate *in vivo* and which encodes only the vaccinal protein. Animals were immunized by simply injecting the naked plasmid DNA into the muscle. This technique leads to the expression of the vaccine protein *in situ* and to a cell-type (CTL) and a humoral type (antibody) immune response. This double induction of the immune response is one of the main advantages of the technique of vaccination with naked DNA.

The vaccine compositions of the present invention can be evaluated in *in vitro* and *in vivo* animal models prior to host, e.g., human, administration. For example, *in vitro* neutralization assays such as those described by Peterson et al. (1988) can be utilized. The assay described by Peterson et al. (1988) is suitable for testing vaccine compositions directed toward either *Chlamydia pneumoniae* or *Chlamydia trachomatis*.

Briefly, hyper-immune antisera is diluted in PBS containing 5% guinea pig serum, as a complement source. *Chlamydiae* (10^4 IFU; infectious units) are added to the antisera dilutions. The antigen-antibody mixtures are incubated at 37EC for 45 minutes and inoculated into duplicate confluent Hep-2 or HeLa cell monolayers contained in glass vials (e.g., 15 by 45 mm), which have been washed twice with PBS prior to inoculation. The monolayer cells are infected by centrifugation at 1000X g for 1 hour followed by stationary incubation at 37E for 1 hour. Infected monolayers are incubated for 48 or 72 hours, fixed and stained with a *Chlamydiae* specific antibody, such as anti-MOMP for *C.trachomatis, etc.* IFUs are counted in ten fields at a magnification of 200X. Neutralization titer is assigned based on the dilution that gives 50% inhibition as compared to control monolayers/IFU.

The efficacy of vaccine compositions can be determined *in vivo* by challenging animal models of *Chlamydia pneumoniae* infection, e.g., mice or rabbits, with the vaccine compositions. For example, *in vivo* vaccine composition challenge studies can be performed in the murine model of *Chlamydia pneumonia* infection described by Moazed et al. (1997). Briefly, male homozygous apoE deficient and/or C57 BL/6J mice are immunized with vaccine compositions. Post-vaccination, the mice are mildly sedated by subcutaneous injection of a mixture of ketamine and xylazine, and inoculated intranasally with a total volume of 0.03-0.05 ml of organisms suspended in SPG medium or with SPG alone. The inoculations of *Chlamydia pneumoniae* are approximately $3x10^7$ IFU/mouse. The mice are inoculated with *Chlamydia pneumoniae* at 8, 10, and 12 weeks of age. Tissues are then collected from the lung, spleen, heart, etc. at 1-20 weeks after the first inoculation. The presence of organisms is scored using PCR, histology and immunocytochemistry, or by quantitative culture/IFU after tissue homogenization.

Alternatively, *in vivo* vaccine composition challenge studies can be performed in the rabbit model of *Chlamydia pneumoniae* described by Laitinen et al. (1997). Briefly, New Zealand white rabbits (5 months old) are immunized with the vaccine compositions. Post-vaccination, the rabbits are sedated with Hypnorm, 0.3 ml/Kg of body weight, intramuscularly, and inoculated intranasally with a total of 0.5 ml of *Chlamydia pneumoniae* suspended in SPG medium or with SPG alone. The inoculations of *Chlamydia pneumoniae* are approximately $3x10^7$ IFU/rabbit. The rabbits are reinfected in the same manner and with the same dose 3 weeks after the primary inoculation. Tissues are then collected 2 weeks after the primary infection and 1, 2, and 4 weeks after the reinfection. The presence of *Chlamydia pneumoniae* is scored using PCR, histology and immunocytochemistry, or by quantitative culture/IFU after tissue homogenization.

The vaccine compositions comprising nucleotide sequences or vectors into which the said sequences are inserted are in particular described in International Application No. WO 90/11092 and also in International Application No. WO 95/11307.

The nucleotide sequence constituting the vaccine composition according to the invention may be injected into the host after having been coupled to compounds which promote the penetration of this polynucleotide inside the cell or its transport up to the cell nucleus. The resulting conjugates may be encapsulated into polymeric microparticles, as described in International Application No. WO 94/27238 (Medisorb Technologies International).

According to another embodiment of the vaccine composition according to the invention, the nucleotide sequence, preferably a DNA, is complexed with the DEAE-dextran (Pagano et al., 1967) or with nuclear proteins (Kaneda et al., 1989), with lipids (Felgner et al., 1987) or encapsulated into liposomes (Fraley et al., 1980) or alternatively introduced in the form of a gel facilitating its transfection into the cells (Midoux et al., 1993, Pastore et al., 1994). The polynucleotide or the vector according to the invention may also be in suspension in a buffer solution or may be combined with liposomes.

Advantageously, such a vaccine will be prepared in accordance with the technique described by Tacson et al. or Huygen et al. in 1996 or alternatively in accordance with the technique described by Davis et al. in International Application No. WO 95/11307.

Such a vaccine may also be prepared in the form of a composition containing a vector according to the invention, placed under the control of regulatory elements allowing its expression in humans or animals. It is possible, for example, to use, as vector for the *in vivo* expression of the polypeptide antigen of interest, the plasmid pcDNA3 or the plasmid pcDNA1/neo, both marketed by Invitrogen ® & D Systems, Abingdon, United Kingdom). It is also possible to use the plasmid V1Jns.tPA, described by Shiver et al. in 1995. Such a vaccine will advantageously comprise, in addition to the recombinant vector, a saline solution, for example a sodium chloride solution.

The immunogenic compositions of the invention can also be utilized as part of methods for immunization, wherein such methods comprise administering to a host, e.g., a human host, an immunizing amount of the immunogenic compositions of the invention. In a preferred embodiment, the method of immunizing is a method of immunizing against *Chlamydia pneumoniae*.

A pharmaceutically acceptable vehicle is understood to designate a compound or a combination of compounds entering into a pharmaceutical or vaccine composition which does not cause side effects and which makes it possible, for example, to facilitate the administration of the active compound, to increase its life and/or its efficacy in the body, to increase its solubility in solution or alternatively to enhance its preservation. These pharmaceutically acceptable vehicles are well known and will be adapted by persons skilled in the art according to the nature and the mode of administration of the active compound chosen.

As regards the vaccine formulations, these may comprise appropriate immunity adjuvants which are known to persons skilled in the art, such as, for example, aluminum hydroxide, a representative of the family of muramyl peptides such as one of the peptide derivatives of N-acetyl-muramyl, a bacterial lysate, or alternatively incomplete Freund's adjuvant, Stimulon™ QS-21 (Aquila Biopharmaceuticals, Inc., Framingham, MA), MPL™ (3-O-deacylated monophosphoryl lipid A; RIBI ImmunoChem Research, Inc., Hamilton, MT), aluminum phosphate, IL-12 (Genetics Institute, Cambridge, MA).

Preferably, these compounds will be administered by the systemic route, in particular by the intravenous route, by the intranasal, intramuscular, intradermal or subcutaneous route, or by the oral route. More preferably, the vaccine composition comprising polypeptides according to the invention will be administered several times, spread out over time, by the intradermal or subcutaneous route.

Their optimum modes of administration, dosages and galenic forms may be determined according to criteria which are generally taken into account in establishing a treatment adapted to a patient, such as for example the patient's age or body weight, the seriousness of his general condition, tolerance of the treatment and the side effects observed.

The invention comprises the use of a composition according to the invention for the treatment or the prevention of cardiovascular diseases, preferably linked to the presence of atheroma, which are induced or worsened by *Chlamydia pneumoniae*.

Finally, the invention comprises the use of a composition according to the invention for the treatment or the prevention of respiratory diseases which are induced or worsened by the presence of *Chlamydia pneumoniae*, preferably asthma.

Other characteristics and advantages of the invention appear in the following examples and figures:

<u>Legend to the figures :</u>

Figure 1 : Line for the production of *Chlamydia pneumoniae* sequences

Figure 2 : Analysis of the sequences and assembling

Figure 3 : Finishing techniques

Figure 3a) : Assembly map

Figure 3b) : Determination and use of the orphan ends of the contigs

EXAMPLES

Experimental procedures

Cells

The *Chlamydia pneumoniae* strain (CM1) used by the inventors is obtained from ATCC (American Culture Type Collection) where it has the reference number ATCC 1360-VR.

It is cultured on HeLa 229 cells, obtained from the American Type Culture Collection, under the reference ATCC CCL-2.1.

Culture of the cells

The HeLa ATCC CCL-2.1 cells are cultured in 75-ml cell culture flasks (Corning). The culture medium is Dulbecco's modified cell culture medium (Gibco BRL No. 04101965) supplemented with MEM amino acids (Gibco BRL - No. 04301140) L (5 ml per 500 ml of medium) and 5% foetal calf serum (Gibco BRL No. 10270 batch 40G8260K) without antibiotics or antifungals.

The cell culture stock is maintained in the following manner. The cell cultures are examined under an inverted microscope. 24 hours after confluence, each cellular lawn is washed with PBS (Gibco BRL No. 04114190), rinsed and then placed for 5 min in an oven in the presence of 3 ml of trypsine (Gibco BRL No. 25200056). The cellular lawn is then detached and then resuspended in 120 ml of culture medium, the whole is stirred in order to make the cellular suspension homogeneous. 30 ml of this suspension are then distributed per cell culture flask. The flasks are kept in a CO_2 oven (5%) for 48 hours at a temperature of 37°C. The cell stock is maintained so as to have available daily 16 flasks of subconfluent cells. It is these subconfluent cells which will be used so as to be infected with Chlamydia. 25-ml cell culture flasks are also used, these flasks are prepared in a similar manner but the volumes used for maintaining the cells are the following: 1 ml of trypsine, 28 ml of culture medium to resuspend the cells, 7 ml of culture medium are used per 25-ml flask.

Infection of the cells with Chlamydia

Initially, the Chlamydiae are obtained frozen from ATCC (-70°C), in suspension in a volume of 1 ml. This preparation is slowly thawed, 500 µl are collected and brought into contact with subconfluent cells, which are obtained as indicated above, in a 25-ml cell culture flask, containing 1 ml of medium, so as to cover the cells. The flask is then centrifuged at 2000 rpm in a "swing" rotor for microtitre plates, the centrifuge being maintained at a temperature of 35°C. After centrifugation, the two flasks are placed in an oven at 35°C for three hours. 6 ml of culture medium containing cycloheximide (1 μg/ml) are then added and the flask is stored at 35°C. After 72 hours, the level of infection is evaluated by direct immunofluorescence and by the cytopathogenic effect caused to the cells.

Direct immunofluorescence

Starting with infected cells, which were obtained as indicated above, a cellular smear is deposited with a Pasteur pipette on a microscope slide. The cellular smear is fixed with acetone for 10 minutes; after draining the acetone, the smear is covered with 30 μl of murine monoclonal antibodies directed against MOMP (major outer membrane protein) of Chlamydia (Syva, Biomérieux) labelled with fluorescein isothiocyanate. The whole is then incubated in a humid chamber at a temperature of 37°C. The slides are then rinsed with water, slightly dried, and then after depositing a drop of mounting medium, a coverslip is mounted before reading. The reading is carried out with the aid of a fluorescence microscope equipped with the required filters (excitation at 490 nm, emission at 520 nm).

Harvesting of the *Chlamydia pneumoniae*

After checking the infection by direct immunofluorescence, carried out as indicated above, the culture flasks are opened under a sterile cabinet, sterile glass beads with a diameter of the order of a millimeter are placed in the flask. The flask is closed and then vigorously stirred while being maintained horizontally, the cellular lawn at the bottom, so that the glass beads can have a mechanical action on the cellular lawn. Most of the cells are thus detached or broken; the effect of the stirring is observed under an optical microscope so as to ensure proper release of Chlamydiae.

Large-scale infection of the cell cultures

The product of the Chlamydiae harvest (culture medium and cellular debris) is collected with a pipette, and distributed into three cell culture flasks containing subconfluent HeLa ATCC CCL-2.1 cells, obtained as indicated above. The cells thus inoculated are placed under gentle stirring (swing) in an oven at 35°C. After one hour, the flasks are kept horizontally in an oven so that the culture medium covers the cells for 3 hours. 30 ml of culture medium containing actydione (1 μg/ml) are then added to each of the flasks. The culture flasks are then stored at 35°C for 72 hours. The cells thus infected are examined under an optical microscope after 24 hours, the cytopathogenic effect is evaluated by the appearance of cytoplasmic inclusions which are visible under an inverted optical microscope. After 72 hours, the vacuoles containing the Chlamydiae occupy the cytoplasm of the cell and push the cell nucleus sideways. At this stage, numerous cells are spontaneously destroyed and have left free elementary bodies in the culture medium. The Chlamydiae are harvested as described above and are either frozen at –80°C or used for another propagation.

Purification of the Chlamydiae

The product of the Chlamydia harvests is stored at -80°C and thawed on a water bath at room temperature. After thawing, each tube is vigorously stirred for one minute and immersed for one minute in an ultrasound tank (BRANSON 1200); the tubes are then stirred by inverting before being centrifuged for 5 min at 2000 rpm. The supernatant is carefully removed and kept at cold temperature (ice). The supernatant is vigorously stirred and then filtered on nylon filters having pores of 5 microns in diameter on a support (Nalgene) allowing a delicate vacuum to be established under the nylon filter. For each filtration, three nylon filters are superposed; these filters are replaced after every 40 ml of filtrate. Two hundred milliliters of filtration product are kept at cold temperature, and then after stirring by inverting, are centrifuged at 10,000 rpm for 90 min, the supernatant is removed and the pellet is taken up in 10 ml of 10 mM Tris, vigorously vortexed and then centrifuged at 10,000 rpm for 90 min. The supernatant is removed and the pellet is taken up in a buffer (20 mM Tris pH 8.0, 50 mM KCl, 5 mM $MgCl_2$) to which 800 units of DNAse I (Boehringer) are added. The whole is kept at 37°C for one hour. One ml of 0.5 M EDTA is then added, the whole is vortexed and frozen at –20°C.

Preparation of the DNA

The Chlamydiae purified above are thawed and subjected to a proteinase K (Boehringer) digestion in a final volume of 10 ml. The digestion conditions are the following: 0.1 mg/ml proteinase K, 0.1 × SDS at 55EC, stirring every 10 min. The product of digestion is then subjected to a double extraction with phenol-chloroform, two volumes of ethanol are added and the DNA is directly recovered with a Pasteur pipette having one end in the form of a hook. The DNA is dried on the edge of the tube and then resuspended in 500 µl of 2 mM Tris pH 7.5. The DNA is stored at 4°C for at least 24 hours before being used for the cloning.

Cloning of the DNA

After precipitation, the DNA is quantified by measuring the optical density at 260 nm. Thirty µg of Chlamydia DNA are distributed into 10 tubes of 1.5 ml and diluted in 300 µl of water. Each of the tubes is subjected to 10 applications of ultrasound lasting for 0.5 sec in a sonicator (unisonix XL2020). The contents of the 10 tubes are then grouped and concentrated by successive extractions with butanol (Sigma B1888) in the following manner: two volumes of butanol are added to the dilute DNA mixture. After stirring, the whole is centrifuged for five minutes at 2500 rpm and the butanol is removed. This operation is repeated until the volume of the aqueous phase is less than 1 ml. The DNA is then precipitated in the presence of ethanol and of 0.5 M sodium acetate pH 5.4, and then centrifuged for thirty minutes at 15,000 rpm at cold temperature (4°C). The pellet is washed with 75% ethanol, centrifuged for five minutes at 15,000 rpm and dried at room temperature. A tenth of the preparation is analysed on a 0.8% agarose gel. Typically, the size of the DNA fragments thus prepared is between 200 and 8000 base pairs.

To allow the cloning of the DNA obtained, the ends are repaired. The DNA is distributed in an amount of 10 µg/tube, in the following reaction medium: 100 µl final volume, 1 × buffer

(Biolabs 201L), 0.5 µl BSA 0.05 mg/ml, 0.1 mM dATP, 0.1 mM each of dGTP, dCTP or dTTP, 60,000 IU T4 DNA polymerase. The reaction is incubated for thirty minutes at 16°C. The contents of each of the tubes are then grouped before carrying out an extraction with phenol-chloroform and then precipitating the aqueous phase as described above. After this step, the DNA thus prepared is phosphorylated. For that, the DNA is distributed into tubes in an amount of 10 µg per tube, and then in a final volume of 50 µl, the reaction is prepared in the following manner: 1 mM ATP, 1 × kinase buffer, 10 IU T4 polynucleotide kinase (Biolabs 201L). The preparation is incubated for thirty minutes at 37°C. The contents of the tubes are combined and a phenol-chloroform extraction and then a precipitation are carried out in order to precipitate the DNA. The latter is then suspended in 1 µl of water and then the DNA fragments are separated according to their size on a 0.8% agarose gel (1 × TAE). The DNA is subjected to an electric field of 5 V/cm and then visualized on a UV table. The fragments whose size varies between 1200 and 2000 base pairs are selected by cutting out the gel. The gel fragment thus isolated is placed in a tube and then the DNA is purified with the Qiaex kit (20021 Qiagen), according to the procedure provided by the manufacturer.

<u>Preparation of the vector</u>

14 µg of the cloning vector pGEM-5Zf (Proméga P2241) are diluted in a final volume of 150 µl and are subjected to digestion with the restriction enzyme EcoRV 300 IU (Biolabs 195S) according to the protocol and with the reagents provided by the manufacturer. The whole is placed at 37°C for 150 min and then distributed in the wells of a 0.8% agarose gel subjected to an electric field of 5 V/cm. The linearized vector is visualized on a UV table, isolated by cutting out the gel and then purified by the Qiaex kit (Qiagen 20021) according to the manufacturer's recommendations. The purification products are grouped in a tube, the volume is measured and then half the volume of phenol is added and the whole is vigorously stirred for 1 min. Half the volume of chloroform-isoamyl alcohol 24:1 is added and vigorously stirred for 1 min. The whole is centrifuged at 15,000 rpm for 5 min at 4°C, the aqueous phase is recovered and transferred into a tube. The DNA is precipitated in the presence of 0.3 M sodium acetate, pH 5.4 and 3 volumes of ethanol and placed at -20°C for 1 hour. The DNA is then centrifuged at 15,000 rpm for 30 min at 4°C, the supernatant is removed while preserving the pellet, washed twice with 70% ethanol. After drying at room temperature, the DNA is suspended in 25 µl of water.

<u>Phosphorylation of the vector</u>

25 µl of the vector prepared in the preceding step are diluted in a final volume of 500 µl of the following reaction mixture:

After repair, the DNA is subjected to a phenol-chloroform extraction and a precipitation, the pellet is then taken up in 10 µl of water, the DNA is quantified by measuring the optical density at 260 nm. The quantified DNA is ligated into the vector PGEm-5Zf(+) prepared by the restriction enzyme EcoRV and dephosphorylated (see preparation of the vector). The ligation is carried out under three conditions which vary in the ratio between the number of vector molecules and the number of insert molecules. Typically, an equimolar ratio, a ratio of 1:3 and a ratio of 3:1 are used for the ligations which are, moreover, carried out under the following conditions: vector PGEm-5Zf(+) 25 ng, cut DNA, ligation buffer in a final volume of 20 μl with T4 DNA ligase (Amersham E70042X); the whole is then placed in a refrigerator overnight and then a phenol-chloroform extraction and a precipitation are carried out in a conventional manner. The pellet is taken up in 5 μl of water.

Transformation of the bacteria

Plating of the bacteria

Petri dishes containing LB Agar medium containing ampicillin (50 μg/ml), Xgal (280 μg/ml) [5-bromo-4-chloro-indolyl-beta-D-galactopyranoside (Sigma B-4252)], IPTG (140 μg/ml) [isopropyl-beta-D-thiogalactoside (Sigma I-6758)] are used, 50 and 100 μl of bacteria are plated for each of the ligations. The Petri dishes are placed upside down at 37°C for 15 to 16 hours in an oven. The number of "recombinant" positive clones is evaluated by counting the white colonies and the blue colonies which are thought to contain the vector alone.

Evaluation of the "recombinant" positive clones

Ninety-four white colonies and two blue colonies are collected with the aid of sterile cones and are deposited at the bottom of the wells of plates designed for carrying out the amplification techniques. 30 μl of the following reaction mixture are added to each well: 1.7 mM $MgCl_2$, 0.2 mM each of dATP, dCTP, dGTP and dTTP, two synthetic oligonucleotides corresponding to sequences flanking the cloning site on either side and orienting the synthesis of the DNA in a convergent manner (0.5 μM RP and PU primers, 1 U TAQ polymerase (GibcoBRL 18038-026)).

The colonies thus prepared are subjected to a temperature of 94°C for 5 min and then to 30 thermal cycles composed of the following steps: 94°C for 40 s, 50°C for 30 s, 72°C for 180 s. The reaction is then kept for 7 min at 72°C and then kept at 4°C.

The amplification products are deposited on an agarose gel (0.8%), stained with ethidium bromide, subjected to electrophoresis, and then analysed on an ultraviolet table. The presence of an amplification fragment having a size greater than 500 base pairs indicates the presence of an insert. The bacterial clones are then prepared so as to study the sequence of their insert.

Sequencing

To sequence the inserts of the clones obtained as above, these were amplified by PCR on bacteria cultures carried out overnight using the primers for the vectors flanking the inserts. The sequence of the ends of these inserts (on average 500 bases on each side) was determined by automated fluorescent sequencing on an ABI 377 sequencer, equipped with the ABI Prism DNA Sequencing Analysis software (version 2.1.2).

Analysis of the sequences

The sequences obtained by sequencing in a high-yield line (Figure 1) are stored in a database; this part of the production is independent of any treatment of the sequences. The sequences are extracted from the database, avoiding all the regions of inadequate quality, that is to say the regions for which uncertainties are observed on the sequence at more than 95%. After extraction, the sequences are introduced into a processing line, the diagram of which is described in Figure 2. In a first path of this processing line, the sequences are assembled by the Gap4 software from R. Staden (Bonfield et al., 1995) (OS UNIX/SUN Solaris); the results obtained by this software are kept in the form of two files which will be used for a subsequent processing. The first of these files provides information on the sequence of each of the contigs obtained. The second file represents all the clones participating in the composition of all the contigs as well as their positions on the respective contigs.

The second processing path uses a sequence assembler (TIGR-Asmg assembler UNIX/SUN Solaris); the results of this second processing path are kept in the form of a file in the TIGR-Asmg format which provides information on the relationship existing between the sequences selected for the assembly. This assembler is sometimes incapable of linking contigs whose ends overlap over several hundreds of base pairs.

The results obtained from these two assemblers are compared with the aid of the BLAST program, each of the contigs derived from one assembly path being compared with the contigs derived from the other path.

For the two processing paths, the strict assembly parameters are fixed (95% homology, 30 superposition nucleotides). These parameters avoid 3 to 5% of the clones derived from eukaryotic cells being confused with sequences obtained from the clones derived from *Chlamydia pneumoniae*. The eukaryotic sequences are however preserved during the course of this project; the strategy introduced, which is described below, will be designed, inter alia, not to be impeded by these sequences derived from contaminating clones.

The results of these two assemblers are processed in a software developed for this project. This software operates on a Windows NT platform and receives, as data, the results derived from the STADEN software and/or the results derived from the TIGR-Asmg assembler, the software, results, after processing of the data, in the determination of an assembly map which gives the proximity relationship and the orientation of the contigs in relation to one another (Figure 3a). Using this assembly map, the software determines all the primers necessary for finishing the project. This treatment, which will be detailed below, has the advantage of distinguishing the isolated sequences derived from the contaminations, by the DNA eukaryotic cells, of the small-sized sequences clearly integrated into the project by the relationships which they establish with contigs. In order to allow, without any risk of error, the arrangement and the orientation of the contigs in relation to one another, a statistical evaluation of the accuracy of the names (naming) "naming" of sequence is made from the results of "contigation". This evaluation makes it possible to give each of the clone plates, as well as each of the subsets of plates, a weight which is inversely proportional to probable error rate existing in the "naming" of the sequences obtained from this plate or from a subset of this plate. In spite of a low error rate, errors may occur throughout the steps of production of the clones and of the sequences. These steps are numerous, repetitive and although most of them are automated, others, like the deposition in the sequencers, are manual; it is then possible for the operator to make mistakes such as the inversion of two sequences. This type of error has a repercussion on the subsequent processing of the data, by resulting in relationships (between the contigs) which do not exist in reality, then in attempts at directed sequencing between the contigs which will end in failure. It is because of this that the evaluation of the naming errors is of particular importance since it allows the establishment of a probabilistic assembly map from which it becomes possible to determine all the clones which will serve as template to obtain sequences separating two adjacent contigs. Table 2 of parent U.S. application serial No. 60/107078 filed November 4, 1998 and French application 97-14673 filed November 21, 1997, each of which is incorporated by reference herein in its entirety, gives the clones and the sequences of the primers initially used during the initial operations.

To avoid the step which consists in ordering and then preparing the clones by conventional microbiological means, outer and inner primers oriented towards the regions not yet sequenced are defined by the software. The primers thus determined make it possible to prepare, by PCR, a template covering the nonsequenced region. It is the so-called outer primers (the ones most distant from the region to be sequenced) which are used to prepare this template. The template is then purified and a sequence is obtained on each of the two strands during 2 sequencing reactions which each use one of the 2 inner primers. In order to facilitate the use of this approach, the two outer primers and the two inner primers are prepared and then stored on the same position of 4 different 96-well plates. The two plates containing the outer primers are used to perform the PCRs which will serve to prepare the templates. These templates will be purified on purification columns preserving the topography of the plates. Each of the sequences will be obtained using primers situated on one and then on the other of the plates containing the inner primers. This distribution allows a very extensive automation of the process and results in a method which is simple to use for finishing the regions not yet sequenced. Table 3 of parent U.S. application serial No. 60/107078 filed November 4, 1998 and French application 97-14673 filed November 21, 1997, each of which is incorporated by reference herein in its entirety, gives the names and the sequences of the primers used for finishing *Chlamydia pneumoniae*.

Finally, a number of contigs exist in a configuration where one of their ends is not linked to any other contig end (Figure 3b) by a connecting clone relationship (a connecting clone is defined as a clone having one sequence end on a contig and the other end of its sequence on another contig; furthermore, this clone must be derived from a plate or a subset of plates with adequate naming quality). For the *Chlamydia pneumoniae* project, this particular case occurred 24 times. Two adjacent PCR primers orienting the synthesis of the DNA towards the end of the consensus sequence are defined for each of the orphan ends of the consensus sequence. The primer which is closest to the end of the sequence is called the inner primer whereas the primer which is more distant from the end of the sequence is called the outer primer. The outer primers are used to explore the mutual relationship between the orphan ends of the different contigs. The presence of a single PCR product and the possibility of amplifying this product unambiguously using the inner primers evokes the probable relationship between the contigs on which the primers which allowed the amplification are situated. This relationship will be confirmed by sequencing and will allow the connection between the orphan ends of the consensus sequences. This strategy has made it possible to obtain a complete map of the *Chlamydia pneumoniae* chromosome and then to finish the project.

Quality control

All the bases not determined with certainty in the chromosomal sequence were noted and the density of uncertainties was measured on the entire chromosome. The regions with a high density of uncertainties were noted and the PCR primers spanning these regions were drawn and are represented in Table 4 of parent U.S. application serial No. 60/107078 filed November 4, 1998 and French application 97-14673 filed November 21, 1997 each of which is incorporated by reference herein in its entirety.

The sequence of each of the PCR products was obtained with two operational primers different from the amplification primers. The sequences were obtained in both directions for all the PCRs (100% success).

Data banks

Local reorganizations of major public banks were used. The protein bank used consists of the nonredundant fusion of the Genpept bank (automated translation of GenBank, NCBI; Benson et al., 1996).

The entire BLAST software (public domain, Altschul et al., 1990) for searching for homologies between a sequence and protein or nucleic data banks was used. The significance levels used depend on the length and the complexity of the region tested as well as the size of the reference bank. They were adjusted and adapted to each analysis.

The results of the search for homologies between a sequence according to the invention and protein or nucleic data banks are presented and summarized in Table 1 below.

Table 1: List of coding chromosome regions and homologies between these regions and the sequence banks.

Legend to Table 1: Open reading frames are identified with the GenMark software version 2.3A (GenePro), the template used is *Chlamydia pneumoniae* of order 4 on a length of 196 nucleotides with a window of 12 nucleotides and a minimum signal of 0.5. The reading frames ORF2 to ORF 1137 are numbered in order of appearance on the chromosome, starting with ORF2 (ORF column). The positions of the beginning and of the end are then given in column 2 (position). When the position of the beginning is greater than the position of the end, this means that the region is encoded by the strand complementary to the sequence which was given in the sequence SEQ ID No. 1.

All the putative products were subjected to a search for homology on GENPEPT (release 102 for SEQ ID No. 2 to SEQ ID No. 1137, and release 108 for SEQ ID No. 1138 to SEQ ID No. 1291 and SEQ ID No. 6844 to SEQ ID No. 6849) with the BLASTP software (Altschul et al. 1990). With, as parameters, the default parameters with the exception of the expected value E set at 10^{-5} (for SEQ ID No. 2 to SEQ ID No. 1137) and P value set at e^{-10} (for SEQ ID No. 1138 to SEQ ID No. 1291 and SEQ ID No. 6844 to SEQ ID No. 6849). Subsequently, only the identities greater than 30% (I% column) were taken into account. The description of the most homologous sequence is given in the Homology column; the identifier for the latter sequence is given in the ID column and the animal species to which this sequence belongs is given in the Species column. The Homology score is evaluated by the sum of the blast scores for each region of homology and reported in the Score column.

Materials and Methods for transmembrane domains:

The DAS software was used as recommended by the authors (Cserzo et al., 1997).

This method uses, to predict the transmembrane domains, templates derived from a sampling of selected proteins. All the regions for which a "Cutoff" greater than 1.5 was found by the program were taken into account.

Additional ORF Finder Programs

For this analysis, two additional ORF finder programs were used to predict potential open reading frames of a minimum length of 74 amino acids; Glimmer (Salzberg, S.L., Delcher, A., Kasif, S., and W. White. 1998. Microbial gene identification using interpolated Markov models. Nucleic Acids Res. 26:544-548.), and an in-house written program. The in-house program used a very simple search algorithm. The analysis required the that the genomic DNA sequence text be in the 5' to 3' direction, the genome is circular, and that TAA, TAG, and TGA are stop codons. The search parameters were as follows:

(1) A search for an ORF that started with a GTG codon was performed. If no GTG codons were found, then a search for an ATG codon was performed. However, if a GTG codon was found, then a search downstream for a ATG codon was performed. All start and stop nucleotide positions were recorded.

(2) A search for an ORF that started with a TTG codon was performed. If no TTG codons were found, then a search for a ATG codon was performed. However, if a TTG codon was found, then a search downstream for a ATG codon was performed. All start and stop nucleotide positions were recorded.

(3) The analysis described in steps 1 and 2 were repeated for the opposite strand of DNA sequence.

(4) A search for ORFs that determined all ORF lengths using start and stop positions in the same reading frames was performed.

(5) All ORFs whose DNA length was less than 225 nucleotides were eliminated from the search.

Surface Exposed Protein Search Criteria

Potential cell surface vaccine targets are outer membrane proteins such as porins, lipoproteins, adhesions and other non-integral proteins. In *Chlamydia psittaci*, the major immunogens is a group of putative outer membrane proteins (POMPs) and no homologs have been found in *Chlamydia pneumoniae* and *Chlamydia trachomatis* by traditional analysis (Longbottom, D., Russell, M., Dunbar, S.M., Jones, G.E., and A.J. Herring. 1998. Molecular Cloning and Characterization of the Genes Coding for the Highly Immunogenic Cluster of 90-Kilodalton Envelope Proteins from *Chlamydia psittaci* Subtype That Causes Abortion in Sheep. Infect Immun 66:1317-1324.) Several putative outer membrane proteins have been identified in *Chlamydia pneumoniae,* all of which may represent vaccine candidates. The major outer membrane protein (MOMP) gene (omp1) has been found in various isolates of *Chlamydia pneumoniae* (Jantos, CA., Heck, S., Roggendorf, R., Sen-Gupta, M., and Hegemann, JH. 1997. Antigenic and molecular analyses of different chlamydia pneumoniae strains. J. Clin Microbiology 35(3):620-623.) Various criteria, as listed below, were used to identify putative surface exposed ORFs from the genomic DNA sequence of *Chlamydia pneumoniae* (French application 97-14673 filed 21 November 1997). Any ORF which met any one or more of the individual criteria were listed in this category.

Protein homology searches were done using the Blastp 2.0 tool (Altschul, S.F., Madden, T.L., Schaffer, A.A., Zhang, J., Zhang, Z., Miller, W., and D.J. Lipman. 1997. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402.) An ORF product was labeled surface exposed if there was homology to a known, or hypothetical, or putative surface exposed protein with a P score better than e^{-10}.

Most, if not all, proteins that are localized to the membrane of bacteria, via a secretory pathway, contain a signal peptide. A software program, SignalP, analyzes the amino acid sequence of an ORF for such a signal peptide (Nielsen, H., Engelbrecht. J., Brunak, S., and G. von Heijne. 1997. Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites. Protein Engineering 10:1-6.) The first 60 N-terminal amino acids of each ORF were analyzed by SignalP using the Gram-Negative software database. The output generates four separate values, maximum C, maximum Y, maximum S, and mean S. The S-score, or signal region, is the probability of the position belonging to the signal peptide. The C-score, or cleavage site, is the probability of the position being the first in the mature protein. The Y-score is the geometric average of the C-score and a smoothed derivative of the S-score. A conclusion of either a Yes or No is given next to each score. If all four conclusions are Yes and the C-terminal amino acid is either a phenylalanine (F) or a tyrosine (Y), the ORF product was labelled outer membrane (Struyve, M., Moons, M., and J. Tommassen.

1991. Carboxy-terminal Phenylalanine is Essential for the Correct Assembly of a Bacterial Outer Membrane Protein. J. Mol. Biol. 218:141-148.)

The program called Psort, determines the localization of a protein based on its signal sequence, recognition of transmembrane segments, and analysis of its amino acid composition (Nakai, K., and M. Kanehisa. 1991. Expert system for predicting protein localization sites in gram-negative bacteria. Proteins 11:95-110.) An ORF product is considered to be an outer membrane protein if the output data predicts the protein as outer membrane with a certainty value of 0.5 or better and whose value is at least twice as large as the next predicted localized certainty value.

Finally, ORF products that were not predicted to be outer membrane or surface exposed, based on the above criteria, were further analyzed. The blastp output data for these ORFs were searched using various general and specific keywords, suggestive of known cell surface exposed proteins. An ORF was labeled surface exposed if the keywords matched had a Blastp hit, had a P score better than e^{-10}, and that there was no better data indicating otherwise. The following is a list of the searched keywords:

Adhesion	Adhesin	Invasin	Invasion	Extensin	
Omp	Outer Surface	Porin	Outer Membrane		
Cell Surface	Cell Wall	Pilus	Pilin	Flagellar sheath	BtuB
Cir	ChuA	CopB	ExeD	FadL	FecA
FepA	FhuA	FmdC	FomA	FrpB	GspD
HemR	HgbA	Hgp	HmbR	HmuR	HMW
HrcC	Hrp	InvG	LamB	LbpA	LcrQ
Lmp1	MxiD	MOMP	PilE	HpaA	NolW
NspA	OpcP	OpnP	Opr	OspA	PhoE
PldA	Por	PscC	PulD	PupA	QuiX
RafY	ScrY	SepC	ShuA	SomA	SpiA
Tbp1	Yop	YscC	mip	Tol	

Those ORFs that did not meet the minimum requirement for being an outer membrane protein based on the above search criteria but which were homologous to identified outer membrane ORFs in *Chlamydia trachomatis* were included. The *Chlamydia trachomatis* genome (French patent applications FR97-15041, filed 28 November 1997 and 97-16034 filed 17 December 1997) was analyzed using the above search criteria and a number of outer membrane ORFs were identified. These *Chlamydia trachomatis* ORFs were then tested against the *Chlamydia pneumoniae* genome using Blastp. Any *Chlamydia pneumoniae* ORF with a Blastp P value better than e^{-10} against a *Chlamydia trachomatis* outer membrane was included in this section, if there was no better data indicating otherwise. A list of ORFs in the *Chlamydia pneumoniae* genome encoding putative surface exposed proteins is set forth above in the specification.

Identification of Putative Lipoproteins in the Genome of *Chlamydia pneumoniae*

Lipoproteins are the most abundant post-translationally modified bacterial secretory proteins (Pugsley, A. P.. 1993. The complete general secretory pathway in Gram-negative bacteria. Microbiol. Rev. 57:50-108). The characteristic features of lipoproteins are a thiol-linked diacylglyceride and an amine-linked monoacyl group on the cysteine that becomes the amino-terminal residue after signal peptide cleavage by Signal Peptidase II. (Pugsley, A. P.. 1993. The complete general secretory pathway in Gram-negative bacteria. Microbiol. Rev. 57:50-108). The identification of putative lipoproteins from the genomic sequencing of *Chlamydia pneumoniae* was done by examining the deduced amino acid sequence of identified ORFs for the presence of a signal peptide with a Signal Peptidase II cleavage site analogous to the consensus sequence for prolipoprotein modification and processing reactions (Hayashi, S., and H. C. Wu. 1992. Identification and characterization of lipid-modified proteins in bacteria, p. 261-285. *In* N. M. Hooper and A. J. Turner (ed.) Lipid modification of proteins: A practical approach. Oxford University Press, New York; Sutcliffe, I. C. and R. R. B. Russell. 1995. Lipoproteins of Gram-positive bacteria. J. Bacteriol. 177:1123-1128.).

Chlamydia pneumoniae ORFs were initially screened for the most basic of lipoprotein characteristics, a cysteine in the first 30 amino acids of the deduced protein. ORFs with a standard start codon (ATG, GTG, or TTG) and having one or more of the following characteristics were selected for direct analysis of their first 30 amino acids:

(a) Significant Signal P value (at least two out of the four values are Yes)

(b) PSORT value indicating membrane passage (IM-inner membrane, Peri-periplasm, or OM-outer membrane)

(c) Identification of the word lipoprotein among the ORF blastp data set.

(d) A Blastp value of $<e^{-10}$ with a putative lipoprotein from *Chlamydia trachomatis* (French applications 97-15041 filed 28 November 1997 and 97-16034 filed 17 December 1997).

The first 30 amino acids of each ORF in this set were analyzed for the characteristics commonly found in lipoprotein signal peptides (Pugsley, A. P.. 1993. The complete general secretory pathway in Gram-negative bacteria. Microbiol. Rev. 57:50-108; Hayashi, S., and H. C. Wu. 1992.

Identification and characterization of lipid- modified proteins in bacteria, p. 261-285. *In* N. M. Hooper and A. J. Turner (ed.) Lipid modification of proteins: A practical approach. Oxford University Press, New York; Sutcliffe, I. C. and R. R. B. Russell. 1995. Lipoproteins of Gram-positive bacteria. J. Bacteriol. 177:1123-1128.) Putative lipoprotein signal peptides were required to have a cysteine between amino acid 10 and 30 and reach a minimum score of three based on the following criteria for lipoprotein signal peptides:

(a) Identification of specific amino acids in specific positions around the cysteine which are part of the consensus Signal Peptidase II cleavage site (Hayashi, S., and H. C. Wu. 1992. Identification and characterization of lipid-modified proteins in bacteria, p. 261-285. *In* N. M. Hooper and A. J. Turner (ed.) Lipid modification of proteins: A practical approach. Oxford University Press, New York); Sutcliffe, I. C. and R. R. B. Russell. 1995. Lipoproteins of Gram-positive bacteria. J. Bacteriol. 177:1123-1128). Since the identification of the cleavage site is the most important factor in identifying putative lipoproteins, each correctly positioned amino acid contributed toward reaching the minimum score of three. (b) A hydrophobic region rich in alanine and leucine prior to the cleavage site (Pugsley, A. P.. 1993. The complete general secretory pathway in Gram-negative bacteria. Microbiol. Rev. 57:50-108) contributed toward reaching the minimum score of three.

(c) A short stretch of hydrophilic amino acids greater than or equal to 1 usually lysine or arginine following the N-terminal methionine (Pugsley, A. P.. 1993. The complete general secretory pathway in Gram-negative bacteria. Microbiol. Rev. 57:50-108) contributed toward reaching the minimum score of three.

A list of ORFs in the *Chlamydia pneumoniae* genome encoding putative lipoproteins is set forth above in the specification.

LPS-Related ORFs of *Chlamydia pneumoniae*

Lipopolysaccharide (LPS) is an important major surface antigen of Chlamydia cells. Monoclonal antibodies (Mab) directed against LPS of *Chlamydia pneumoniae* have been identified that can neutralize the infectivity of *Chlamydia pneumoniae* both in vitro and in vivo (Peterson, E.M., de la Maza, L.M., Brade, L., Brade, H. 1998. Characterization of a Neutralizing Monoclonal Antibody Directed at the Lipopolysaccharide of *Chlamydia pneumonia*. Infect. Immun. Aug. 66(8):3848-3855.) Chlamydial LPS is composed of lipid A and a core oligosaccharide portion and is phenotypically of the rough type (R-LPS) (Lukacova, M., Baumann, M., Brade, L., Mamat, U., Brade, H. 1994. Lipopolysaccharide Smooth-Rough Phase Variation in Bacteria of the Genus *Chlamydia*. Infect. Immun. June 62(6):2270-2276.) The lipid A component is composed of fatty acids which serve to anchor LPS in the outer membrane. The core component contains sugars and sugar derivatives such as a trisaccharide of 3-deoxy-D-manno-octulosonic acid (KDO) (Reeves, P.R., Hobbs, M., Valvano, M.A., Skurnik, M., Whitfield, C., Coplin, D., Kido, N., Klena, J., Maskell, D., Raetz, C.R.H., Rick, P.D. 1996. *Bacterial Polysaccharide Synthesis and Gene Nomenclature* pp. 10071-10078, Elsevier Science Ltd.). The KDO gene product is a multifunctional glycosyltransferase and represents a shared epitope among the Chlamydia. For a review of LPS biosynthesis see, e.g., Schnaitman, C.A., Klena, J.D. 1993. Genetics of Lipopolysaccharide Biosynthesis in Enteric Bacteria. Microbiol. Rev. 57:655-682.

A text search of the ORF blastp results identified several genes that are involved in Chlamydial LPS production with a P score better than e^{-10}. The following key-terms were used in the text search: KDO, CPS (Capsular Polysaccharide Biosynthesis), capsule, LPS, rfa, rfb, rfc, rfe, rha, rhl, core, epimerase, isomerase, transferase, pyrophosphorylase, phosphatase, aldolase, heptose, manno, glucose, lpxB, fibronectin, fibrinogen, fucosyltransferase , lic, lgt, pgm, tolC, rol, ChoP, phosphorylcholine, waaF, PGL-Tb1. A list of ORFs in the *Chlamydia pneumoniae* genome encoding putative polypeptides involved in LPS biosynthesis is set forth above in the specification.

Type III And Other Secreted Products

Type III secretion enables gram-negative bacteria to secrete and inject pathogenicity proteins into the cytosol of eukaryotic host cells (Hueck, C. J., 1998. Type III Protein Secretion Systems in Bacterial Pathogens of Animals and Plants. In Microbiology and Molecular Biology Reviews. 62:379-433.) These secreted factors often resemble eukaryotic signal transduction factors, thus enabling the bacterium to redirect host cell functions (Lee, C.A., 1997. Type III secretion systems: machines to deliver bacterial proteins into eukaryotic cells? Trends Microbiol. 5:148-156.) In an attempt to corrupt normal cellular functions, Chlamydial pathogenicity factors injected into the host cytosol will nonetheless, as cytoplasmic constituents be processed and presented in the context of the Major Histocompatibility Complex (MHC class I). As such, these pathogenicity proteins represent MHC class I antigens and will play an important role in cellular immunity. Also included in this set are secreted non-type III products that may play a role as vaccine components.

A text search of the ORF blastp results identified genes that are involved in *Chlamydia pneumoniae* protein secretion with a P score better than e^{-10}. The following key-terms were used in the text search in an effort to identify surface localized or secreted products: Yop, Lcr, Ypk, Exo, Pcr, Pop, Ipa, Vir, Ssp, Spt, Esp, Tir, Hrp, Mxi, hemolysin, toxin, IgA protease, cytolysin, tox, hap, secreted and Mip.

Chlamydia pneumoniae ORFs that did not meet the above keyword search criteria, but have homologs *in Chlamydia trachomatis* that do meet the search criteria are included herein. The *Chlamydia trachomatis* genome (French patent applications FR97-15041, filed 28 November 1997 and 97-16034 filed 17 December 1997) was analyzed using the above search criteria and a number of ORFs were identified. These *Chlamydia trachomatis* ORFs were tested against the *Chlamydia pneumoniae* genome using Blastp. Any *Chlamydia pneumoniae* ORF with a Blastp P value < e^{-10} against a *Chlamydia trachomatis* homolog, identified using the above search criteria, was included. A list of ORFs in the *Chlamydia pneumoniae* genome encoding putative secreted proteins is in the specification.

Chlamydia pneumoniae: RGD Recognition Sequence

Proteins that contain Arg-Gly-Asp (RGD) attachment site, together with integrins that serve as their receptor constitute a major recognition system for cell adhesion. The RGD sequence is the cell attachment site of a large number of adhesive extracellular matrix, blood, and cell surface proteins and nearly half of the known integrins recognize this sequence in their adhesion protein ligands. There are many RGD containing microbial proteins such as the penton protein of adenovirus, the coxsackie virus, the foot and mouth virus and pertactin, a 69 kDa (kilodalton) surface protein of *Bordetella pertussis,* that serve as ligands through which these microbes bind to integrins on the cell surfaces and gain entry into the cell. The following provides evidence supporting the importance of RGD in microbial adhesion:

a) The adenovirus penton base protein has a cell rounding activity and when penton base was expressed in E. coli, it caused cell rounding and cells adhered to polystyrene wells coated with the protein. Mutant analysis showed that both these properties required an RGD sequence. Virus mutants with amino acid substitutions in the RGD sequence, showed much less adherence to HeLa S3 cells, and also were delayed in virus reproduction (Bai, M., Harfe, B., and Freimuth, P. 1993. Mutations That Alter an RGD Sequence in the Adenovirus Type 2 Penton Base Protein Abolish Its Cell-Rounding Activity and Delay Virus Reproduction in Flat Cells. J. Virol. 67:5198-5205).

b) It has been shown that attachment and entry of coxsackie virus A9 to GMK cells were dependent on an RGD motif in the capsid protein VP1. VP1 has also been shown to bind $\alpha_v\beta_3$ integrin, which is a vitronectin receptor (Roivainen, M., Piirainen, L., Hovi, T., Virtanen, I., Riikonen, T., Heino, J., and Hyypia, T. 1994. Entry of Coxsackievirus A9 into Host Cells: Specific Interactions with a_vb_3 Integrin, the Vitronectin Receptor Virology, 203:357-65).

c) During the course of whooping cough, *Bordetella pertussis* interacts with alveolar macrophages and other leukocytes on the respiratory epithelium. Whole bacteria adheres by means of two proteins, filamentous hemagglutinin (FHA) and pertussis toxin. FHA interacts with two classes of molecules on macrophages, galactose containing glycoconjugates and the integrin CR3. The interaction between CR3 and FHA involves recognition of RGD sequence at the positions 1097-1099 in FHA (Relman, D., Tuomanen, E., Falkow, S., Golenbock, D. T., Saukkonen, K., and Wright, S. D. "Recognitition of a Bacterial Adhesin by an Integrin: Macrophage CR3 Binds Filamentous Hemagglutinin of Bordetella Pertussis." Cell, 61:1375-1382 (1990)).

d) Pertactin, a 69 kDa outer membrane protein of *Bordetella pertussis,* has been shown to promote attachment of Chinese hamster ovary cells (CHO). This attachment is mediated by recognition of RGD sequence in pertactin by integrins on CHO cells and can be inhibited by synthetic RGD containing peptide homologous to the one present in pertactin (Leininger, E., Roberts, M., Kenimer, J. G., Charles, I. G., Fairweather, N., Novotny, P., and Brennan, M. J. 1991. Pertactin, an Arg-Gly-Asp containing *Bordetella pertussis* surface protein that promotes adherence of mammalian cells Proc. Natl. Acad. Sci. USA, 88:345-349).

e) The RGD sequence is highly conserved in the VP1 protein of foot and mouth disease virus (FMDV). Attachment of FMDV to baby hamster kidney cells (BHK) has been shown to be mediated by VP1 protein via the RGD sequence. Antibodies against the RGD sequence of VP1 blocked attachment of virus to BHK cells (Fox, G., Parry, N. R., Barnett, P. V., McGinn, B., Rowland, D. J., and Brown, F. 1989. The Cell Attachment Site on Foot-and-Mouth Disease Virus Includes the Amino Acid Sequence RGD (Arginine-Glycine-Aspartic Acid) J. Gen. Virol., 70:625-637).

It has been demonstrated that bacterial adherence can be based on interaction of a bacterial adhesin RGD sequence with an integrin and that bacterial adhesins can have multiple binding site characteristic of eukaryotic extracellular matrix proteins. RGD recognition is one of the important mechanisms used by microbes to gain entry into eukaryotic cells.

The complete deduced protein sequence of the *Chlamydia pneumoniae* genome was searched for the presence of RGD sequence. There were a total of 54 ORFs that had one or more RGD sequences. Not all RGD containing proteins mediate cell attachment. It has been shown that RGD containing peptides that have proline immediately following the RGD sequence are inactive in cell attachment assays (Pierschbacher & Ruoslahti. 1987. Influence of stereochemistry of the sequence Arg-Gly-Asp-Xaa on binding specificity in cell adhesion. J. Biol. Chem. *262*:17294-98). ORFs that had RGD, with proline as the amino acid following the RGD sequence were excluded from the list. Also, RGD sequence may not be available at the surface of the protein or may be present in a context that is not compatible with integrin binding. Since not all RGD- containing proteins are involved in cell attachment, several other criteria were used to refine the list of RGD- containing proteins. A list of ORFs in the *Chlamydia pneumoniae* genome encoding polypeptides with RGD recognition sequence(s) is in the specification.

Non-*Chlamydia trachomatis* ORFs

Chlamydia pneumoniae ORFs were compared to the ORFs in the *Chlamydia trachomatis* genome (French patent applications FR97-15041, filed 28 November 1997 and 97-16034 filed 17 December 1997) using Blastp. Any *Chlamydia pneumoniae* ORF with a Blastp P value worse than e·

10 (i.e. >e^{-10}) against *Chlamydia trachomatis* ORFs are included in this section. A list of ORFs in the *Chlamydia pneumoniae* genome which are not found in *Chlamydia trachomatis* is set forth above in the specification.

Cell Wall Anchor Surface ORFs

Many surface proteins are anchored to the cell wall of Gram-positive bacteria via the conserved LPXTG motif (Schneewind, O., Fowler, A., and Faull, K.F. 1995. Structure of the Cell Wall Anchor of Surface Proteins in *Staphylococcus aureus*. Science 268:103-106). A search of the *Chlamydia pneumoniae* ORFs was done using the motif LPXTG. A list of ORFs in the *Chlamydia pneumoniae* genome encoding polypeptides anchored to the cell wall is in the specification.

ATCC Deposits

Samples of *Chlamydia pneumoniae* were deposited with the American Type Culture Collection (ATCC), Rockville, Maryland, on November 19, 1998 and assigned the accession number ---. Cells can be grown, harvested and purified, and DNA can be prepared as discussed above. In order to enable recovery of specific fragments of the chromosome, one can run targeted PCR reactions, whose amplification products can then be sequenced and/or cloned into any suitable vector, according to standard procedures known to those skilled in the art.

In addition, a sample of three pools of clones covering chromosomal regions of interest were deposited with the American Type Culture Collection (ATCC), Rockville, Maryland, on November 19, 1998 and assigned the indicated accession number: — . Each pool of clones contains a series of clones. When taken together, the three pools in the sample cover a portion of the chromosome, with a redundancy of slightly more than two. The total number of clones in the sample is 196.

The clones cover the following three regions of interest:

(i) position 30,000 to 40,000 of SEQ ID No. 1, referred to as region A;

(ii) position 501,500 to 557,000 of SEQ ID No. 1, referred to as region B; and

(iii) position 815,000 to 830,000 of SEQ ID No. 1, referred to as region C.

Table 4 lists groups of oligonucleotides to be used to amplify each of ORFs 2-1291 according to standard procedures known to those skilled in the art. Such oligonucleotides are listed as SEQ ID Nos. 1292 to 6451. For each ORF, the following is listed: one forward primer positioned 2,000 bp upstream of the beginning of the ORF; one forward primer positioned 200 bp upstream of the beginning of the ORF; one reverse primer positioned 2,000 bp downstream at the end of ORF, which is 2,000 bp upstream of the end site of the ORF on the complementary strand; and one reverse primer 200 bp downstream at the end of ORF, which is 200 bp upstream of the end site of the ORF on the complementary strand. The corresponding SEQ ID Nos. for the primers are listed in Table 4, where Fp is the proximal forward primer; Fd is the distal forward primer; Bp is the proximal reverse primer; and Bd is the distal reverse primer. The positions of the 5' ends of each of these primers on the nucleotide sequence of SEQ ID No. 1 are shown in Table 5.

Table 6 lists oligonucleotides (SEQ ID Nos. 6452-6843) to be used to amplify the inserts of each of the 196 clones present in the pooled sample according to standard procedures well known to those of skill in the art. These primers can also be utilized to amplify the chromosomal region corresponding to the region A, B or C within which the particular insert lies. Their positions are indicated in Table 7.

The present invention is not to be limited in scope by the specific embodiments described herein, which are intended as single illustrations of individual aspects of the invention, and functionally equivalent methods and components are within the scope of the invention. Indeed, various modifications of the invention, in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and accompanying drawings. Such modifications are intended to fall within the scope of the appended claims.

All publications and patent applications mentioned in this specification are herein incorporated by reference to the same extent as if each individual publication or patent application was specifically and individually indicated to be incorporated by reference.

TABLE 1

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF2	42	794	triosephosphate isomerase	L27492	*Thermotoga maritima*	567	54
ORF3	1258	1614	putative				
ORF4	1807	2418	polypeptide deformylase	D90906	*Synechocystis sp.*	316	40
ORF5	3393	2491	hypothetical protein	Z75208	*Bacillus subtilis*	338	42
ORF6	3639	4067	unknown	U87792	*Bacillus subtilis*	117	38
ORF7	5649	4270	putative				
ORF8	7463	6012	putative				
ORF9	8051	8962	putative				
ORF10	9129	9959	putative				
ORF11	10687	10361	putative				
ORF12	10927	11232	putative				
ORF13	11246	12727	amidase	U49269	*Moraxella catarrhalis*	1108	42
ORF14	12691	14190	PET112	D90913	*Synechocystis sp.*	1044	46
ORF15	14484	17249	POMP91A	U65942	*Chlamydia psittaci*	1074	43
ORF16	16039	15770	putative				
ORF17	17845	20853	putative				
ORF18	21137	22042	putative				
ORF19	22046	23476	putative				
ORF20	23681	26110	putative				
ORF21	26109	25861	putative				
ORF22	26241	26978	putative				
ORF23	26960	27754	putative				
ORF24	27747	28577	putative				
ORF25	28887	29492	POMP91A	U65942	*Chlamydia psittaci*	180	39
ORF26	29432	30028	POMP91A	U65942	*Chlamydia psittaci*	361	51
ORF27	30024	31472	POMP91A	U65942	*Chlamydia psittaci*	879	54
ORF28	31758	32288	putative 98 kDa outer membrane protein	U72499	*Chlamydia psittaci*	144	43
ORF29	32201	33991	putative 98 kDa outer membrane protein	U72499	*Chlamydia psittaci*	1126	48
ORF30	33852	34541	putative 98 kDa outer membrane protein	U72499	*Chlamydia psittaci*	589	62
ORF31	34783	36063	POMP91B precursor	U65943	*Chlamydia psittaci*	469	46
ORF32	36009	37529	putative 98 kDa outer membrane protein	U72499	*Chlamydia psittaci*	1338	51
ORF33	37881	39362	putative 98 kDa outer membrane protein	U72499	*Chlamydia psittaci*	671	40

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF34	39418	39161	putative				
ORF35	39366	40715	POMP90A precursor	U65942	*Chlamydia psittaci*	904	47
ORF36	43076	41094	putative				
ORF37	43800	43066	putative				
ORF38	44828	43785	putative				
ORF39	45340	44753	homologous to unidentified E. coli protein	M96343	*Bacillus subtilis*	136	44
ORF40	45752	45372	o530; This 530 aa orf is 33 pct identical (14 gaps) to 525 residues of an approx. 640 aa protein YHES_HAEIN SW: P44808	AE000184	*Escherichia coli*	269	43
ORF41	46996	45701	ABC transporter, ATP-binding protein (yheS)	AE000596	*Helicobacter pylori*	878	39
ORF42	47961	47569	putative				
ORF43	48960	48040	hypothetical protein	D64001	*Synechocystis sp.*	404	37
ORF44	51452	50133	Lon protease-like protein	X74215	*Homo sapiens*	1232	54
ORF45	52606	51335	unknown	Z54285	*Schizosaccharomyces pombe*	781	47
ORF46	53684	53319	putative				
ORF47	54195	53746	putative				
ORF48	55278	56453	heat-shock protein	U15010	*Legionella pneumophila*	975	45
ORF49	56493	57266	branched chain alpha-keto acid dehydrogenase E1-alpha	M97391	*Bacillus subtilis*	329	36
ORF50	57297	58526	branched chain alpha-keto acid dehydrogenase E1-beta	M97391	*Bacillus subtilis*	707	50
ORF51	59851	58565	putative				
ORF52	61495	59924	ComE	D90903	*Synechocystis sp.*	134	55
ORF53	61324	62151	putative				
ORF54	62132	62470	Hpr protein	X12832	*Bacillus subtilis*	136	36
ORF55	62474	63733	enzyme I (ptsI)	U32844	*Haemophilus influenzae*	381	35
ORF56	63881	64186	f831; This 831 aa orf is 46 pct identical (11 gaps) to 709 residues of an approx. 712 aa protein PT1A_ECOLI SW: P32670	AE000326	*Escherichia coli*	123	34
ORF57	64611	64318	ORF107	X17014	*Bacillus subtilis*	128	33
ORF58	65485	64673	putative				
ORF59	65999	65301	dnaZX-like ORF put. DNA polymerase III	X06803	*Bacillus subtilis*	596	52

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF60	66244	67281	putative				
ORF61	67265	67699	putative				
ORF62	67703	68539	putative				
ORF63	68805	70736	putative				
ORF64	69172	68831	putative				
ORF65	70642	71142	putative				
ORF66	71325	72029	putative				
ORF67	72060	73637	putative				
ORF68	74061	76175	YqfF	D84432	*Bacillus subtilis*	542	44
ORF69	78351	77680	porphobilinogen deaminase	D28503	*Clostridium josui*	262	42
ORF70	79356	78355	sms protein	D90914	*Synechocystis sp.*	736	52
ORF71	79983	79693	ribonuclease III (rnc)	AE000579	*Helicobacter pylori*	98	33
ORF72	80441	79938	ORF3	D64116	*Bacillus subtilis*	268	44
ORF73	80475	80969	putative				
ORF74	81296	83080	hypothetical protein	Y14079	*Bacillus subtilis*	893	38
ORF75	83291	83932	manganese superoxide dismutase	X77021	*Caenorhabditis elegans*	622	58
ORF76	84005	84769	acetyl-CoA carboxylase beta subunit (accD)	AE000604	*Helicobacter pylori*	602	50
ORF77	84975	85244	deoxyuridinetriphosphatase (dut)	U32776	*Haemophilus influenzae*	110	41
ORF78	85123	85425	deoxyuridine 5'-triphosphate nucleotidohydrolase (dut)	AE000596	*Helicobacter pylori*	265	68
ORF79	85397	85903	ORF2	L26916	*Pseudomonas aeruginosa*	173	34
ORF80	85909	86583	enzyme IIANtr	U18997	*Escherichia coli*	170	42
ORF81	86626	88065	putative				
ORF82	89257	91026	putative				
ORF83	91291	93030	putative				
ORF84	93295	94086	putative				
ORF85	95285	94707	putative				
ORF86	95667	96557	putative				
ORF87	96317	97456	putative				
ORF88	98435	97968	putative				
ORF89	99460	98426	putative				
ORF90	100144	101325	elongation factor Tu	L22216	*Chlamydia trachomatis*	1917	95

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF91	101457	101720	putative				
ORF92	101704	102273	transcription factor	L10348	*Thermus aquaticus thermophilus*	376	49
ORF93	102356	102805	ribosomal protein L11	D13303	*Bacillus subtilis*	458	63
ORF94	102835	103530	ribosomal protein L1	Z11839	*Thermotoga maritima*	642	51
ORF95	103549	104058	ribosomal protein L10	M89911	*Streptomyces antibioticus*	82	31
ORF96	104096	104491	rpl12 (AA 1-128)	X53178	*Synechocystis PCC6803*	325	47
ORF97	104601	108386	DNA-directed RNA polymerase beta chain	X64172	*Staphylococcus aureus*	2740	52
ORF98	108401	112054	rpoC	V00339	*Escherichia coli*	2947	54
ORF99	112033	112590	acetylornithine deacetylase (EC 5.1.1.16)	M22622	*Leptospira biflexa*	514	62
ORF100	112672	113682	transaldolase	L19437	*Homo sapiens*	755	49
ORF101	113726	114121	putative				
ORF102	114711	114136	putative				
ORF103	115267	115755	putative				
ORF104	115911	116543	putative				
ORF105	116736	118055	ATPase alpha-subunit	X63855	*Thermus aquaticus thermophilus*	934	50
ORF106	117968	118522	adenosine triphosphatase A subunit	D50528	*Acetabularia acetabulum*	147	32
ORF107	118530	119843	V-ATPase B subunit	U96487	*Desulfurococcus sp. SY*	751	48
ORF108	119816	120457	putative				
ORF109	120451	122430	v-type Na-ATPase	X76913	*Enterococcus hirae*	264	35
ORF110	122504	122950	ATP synthase, subunit K	U67478	*Methanococcus jannaschii*	184	31
ORF111	123528	126347	valyl-tRNA synthetase	X05891	*Escherichia coli*	1679	49
ORF112	126332	129166	protein kinase-like protein	U19250	*Streptomyces coelicolor*	427	37
ORF113	134690	129213	UvrA	D49911	*Thermus thermophilus*	3107	41
ORF114	134925	136382	pyruvate kinase	U83196	*Chlamydia trachomatis*	1748	71
ORF115	137870	136482	HtrB protein	X61000	*Escherichia coli*	147	38
ORF116	137899	138240	putative				
ORF117	138239	137928	putative				
ORF118	139558	138257	putative				
ORF119	140352	139516	YbbP	AB002150	*Bacillus subtilis*	231	46
ORF120	140498	141841	cyanide insensitive terminal oxidase	Y10528	*Pseudomonas aeruginosa*	538	50
ORF121	141855	142658	cyanide insensitive terminal oxidase	Y10528	*Pseudomonas aeruginosa*	310	40
ORF122	144258	143050	putative				
ORF123	145258	144494	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF124	145454	146749	product similar to E. coli PhoH protein	Z97025	*Bacillus subtilis*	836	47
ORF125	147318	146767	putative				
ORF126	148261	147677	putative				
ORF127	149029	152157	isoleucyl-tRNA synthetase	U04953	*Homo sapiens*	2361	52
ORF128	154108	152201	leader peptidase I	D90904	*Synechocystis sp.*	225	47
ORF129	155135	154308	putative				
ORF130	155141	155467	YtiA	AF008220	*Bacillus subtilis*	201	43
ORF131	155703	156779	orf 361; ranslated orf similarity to SW: RF1_SALTY peptide chain release factor 1 of Salmonella typhimurium	X78969	*Coxiella burnetii*	863	59
ORF132	156748	157635	product similar to E.coli PRFA2 protein	Z49782	*Bacillus subtilis*	144	37
ORF133	157653	158996	Ffh	U82109	*Thermus aquaticus*	797	45
ORF134	159363	159986	tRNA (guanine-N1)-methyltransferase (trmD)	U32705	*Haemophilus influenzae*	545	49
ORF135	159880	160446	putative				
ORF136	160477	160839	ribosomal protein L19	X72627	*Synechocystis sp.*	319	50
ORF137	160898	161539	putative protein highly homologous to E. coli RNase HII .	D32253	*Magnetospirillum sp.*	427	49
ORF138	161527	162153	5'guanylate kinase (gmk)	U32848	*Haemophilus influenzae*	385	43
ORF139	162144	162443	putative				
ORF140	162437	164098	methionyl-tRNA synthetase	AB004537	*Schizosaccharomyces pombe*	861	54
ORF141	165451	164228	exodeoxyribonuclease V (recD)	U32811	*Haemophilus influenzae*	432	32
ORF142	166349	165411	putative				
ORF143	166949	168442	putative				
ORF144	169416	171029	putative				
ORF145	170857	171459	putative				
ORF146	172652	173428	putative biotin-protein ligase	Z97992	*Schizosaccharomyces pombe*	292	44
ORF147	174626	173439	putative				
ORF148	174816	175613	putative				
ORF149	175598	175954	putative				
ORF150	175958	176935	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF151	177708	176938	orf 3'of chaperonin homolog hypB [Chlamydia psittaci, pigeon strain P-1041, Peptide Partial, 98 aa]	S40172	*Chlamydia psittaci*	376	74
ORF152	177128	177376	putative				
ORF153	179472	177841	putative	M69217	*Chlamydia pneumoniae*	2678	100
ORF154	179822	179517	putative	M69217	*Chlamydia pneumoniae*	498	99
ORF155	181793	179943	Pz-peptidase	D88209	*Bacillus licheniformis*	1088	38
ORF156	182628	181876	o247; This 247 aa orf is 51 pct identical (0 gaps) to 117 residues of an approx. 160 aa protein YPH7_CHRVI SW: P45371	AE000174	*Escherichia coli*	401	42
ORF157	184420	183074	glutamate-1-semialdehyde 2,1-aminomutase	X53696	*Escherichia coli*	823	41
ORF158	184988	184467	ORF o211	U28377	*Escherichia coli*	87	54
ORF159	185483	185112	hypothetical protein	D90906	*Synechocystis sp.*	91	33
ORF160	185902	185483	ribose 5-phosphate isomerase	U28377	*Escherichia coli*	111	41
ORF161	186174	185839	ribose 5-phosphate isomerase A (SP:P27252)	U32729	*Haemophilus influenzae*	190	46
ORF162	187720	186587	hypothetical	D83026	*Bacillus subtilis*	536	42
ORF163	188318	190933	ATP-dependent protease binding subunit	M29364	*Escherichia coli*	2010	53
ORF164	191090	191635	putative				
ORF165	191547	192743	putative				
ORF166	192969	193469	putative				
ORF167	194044	193610	putative				
ORF168	194196	195809	unknown	Z84395	*Mycobacterium tuberculosis*	242	52
ORF169	196088	198073	DNA ligase (EC 6.5.1.2)	M24278	*Escherichia coli*	1317	46
ORF170	198132	199454	putative				
ORF171	199351	202818	putative				
ORF172	204552	202999	PcpB	U60175	*Sphingomonas chlorophenolica*	80	41
ORF173	205648	204692	putative				
ORF174	205807	207327	leucine tRNA synthetase	AF008220	*Bacillus subtilis*	1595	57
ORF175	207182	207775	leucyl-tRNA synthetase	X06331	*Escherichia coli*	363	51
ORF176	207779	208267	transfer RNA-Leu synthetase	M88581	*Bacillus subtilis*	285	43
ORF177	208267	209577	KDO transferase	Z31593	*Chlamydia pneumoniae*	2262	100

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF178	211807	211271	KDO-transferase	X80061	*Chlamydia psittaci*	105	38
ORF179	212188	211844	putative				
ORF180	214079	212448	pyrophosphate-dependent phosphofructokinase beta subunit	Z32850	*Ricinus communis*	1003	45
ORF181	214907	214083	CinI	U44893	*Butyrivibrio fibrisolvens*	111	41
ORF182	216154	215429	putative				
ORF183	216115	216678	putative				
ORF184	216728	217282	putative				
ORF185	217267	217866	putative				
ORF186	218593	218261	putative				
ORF187	219821	218994	putative				
ORF188	221382	220309	putative				
ORF189	222719	221433	GMP synthetase	M10101	*Escherichia coli*	1151	48
ORF190	223521	222724	IMP dehydrogenase	X66859	*Acinetobacter calcoaceticus*	778	58
ORF191	224499	225008	putative				
ORF192	225140	225559	putative				
ORF193	225555	226802	putative				
ORF194	227800	226892	putative				
ORF195	228335	228072	putative				
ORF196	229251	228643	putative				
ORF197	230983	229622	YqhX	D84432	*Bacillus subtilis*	1386	56
ORF198	231483	230983	acetyl-CoA carboxylase biotin carboxyl carrier protein	U38804	*Porphyra purpurea*	199	52
ORF199	232063	231509	elongation factor P	D64001	*Synechocystis sp.*	282	32
ORF200	232739	232053	pentose-5-phosphate-3-epimerase	D90911	*Synechocystis sp.*	463	43
ORF201	233166	234356	putative				
ORF202	233518	233165	putative				
ORF203	234536	235186	ORF2	L35036	*Chlamydia psittaci*	570	60
ORF204	235379	236689	putative				
ORF205	236680	237618	putative				
ORF206	237521	238345	putative				
ORF207	238281	238973	putative				
ORF208	238871	240115	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF209	240191	241564	putative				
ORF210	242281	241604	YqiZ	D84432	*Bacillus subtilis*	379	39
ORF211	242933	242274	f222; This 222 aa orf is 48 pct identical (0 gaps) to 208 residues of an approx. 232 aa protein YCKA_BACSU SW: P42399	AE000284	*Escherichia coli*	382	45
ORF212	243416	242976	arginine repressor protein (argR)	U32800	*Haemophilus influenzae*	229	46
ORF213	243500	244531	sialoglycoprotease	U15958	*Pasteurella haemolytica*	565	53
ORF214	244480	246021	oligopeptide permease homolog AII	AF000366	*Borrelia burgdorferi*	457	34
ORF215	246330	247811	OppAIV	AF000948	*Borrelia burgdorferi*	453	35
ORF216	247831	249174	OppA gene product	X56347	*Bacillus subtilis*	255	37
ORF217	249437	251038	dciAE	X56678	*Bacillus subtilis*	469	37
ORF218	251325	252212	OppB gene product	X56347	*Bacillus subtilis*	652	42
ORF219	253156	254007	oligopeptidepermease	X89237	*Streptococcus pyogenes*	574	48
ORF220	253974	254852	ATP binding protein	L18760	*Lactococcus lactis*	433	40
ORF221	255258	256094	KDO-transferase	X80061	*Chlamydia psittaci*	106	46
ORF222	256640	257455	putative				
ORF223	257502	258239	2-OXOGLUTARAT	A47930	*Spinacia oleracea*	636	52
ORF224	257869	257501	putative				
ORF225	259248	260897	pyrophosphate-fructose 6-phosphate 1-phosphotransferase beta-subunit	M55191	*Solanum tuberosum*	1055	44
ORF226	262753	261788	putative				
ORF227	263059	262757	putative				
ORF228	264375	263182	putative				
ORF229	265985	264747	putative				
ORF230	266637	266059	putative				
ORF231	267338	266538	putative				
ORF232	267922	267473	putative				
ORF233	269647	270771	tRNA guanine transglycosylase	L33777	*Zymomonas mobilis*	628	44
ORF234	272777	273145	ORF 4	D00624	*Bacteriophage chp1*	100	41
ORF235	273253	273636	putative				
ORF236	273705	273977	putative				
ORF237	276016	275717	putative				
ORF238	276439	276020	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF239	276792	277253	putative				
ORF240	277318	277599	putative				
ORF241	278578	277877	putative				
ORF242	279258	278554	FbpC	U33937	*Neisseria gonorrhoeae*	312	39
ORF243	280435	279533	putative				
ORF244	281547	280849	putative				
ORF245	281696	282325	CMP-2-keto-3-deoxyoctulosonic acid synthetase	U15192	*Chlamydia trachomatis*	637	63
ORF246	282459	284069	CTP synthetase	U15192	*Chlamydia trachomatis*	2000	68
ORF247	284056	284517	ORF3	U15192	*Chlamydia trachomatis*	453	65
ORF248	284606	285775	glucose 6-phosphate dehydrogenase	U83195	*Chlamydia trachomatis*	1263	77
ORF249	285592	285987	glucose 6-phosphate dehydrogenase	U83195	*Chlamydia trachomatis*	519	79
ORF250	286179	286976	glucose-6-phosphate dehydrogenase isozyme	D88189	*Actinobacillus actinomycetemcomitans*	216	40
ORF251	287583	287002	putative				
ORF252	287951	287451	putative				
ORF253	288499	288816	putative				
ORF254	289674	288505	putative				
ORF255	288839	289213	putative				
ORF256	289970	290254	putative				
ORF257	291931	292803	gamma-D-glutamyl-L-diamino acid endopeptidase II	X64809	*Bacillus sphaericus*	95	39
ORF258	293258	292755	ScoS9	U43429	*Streptomyces coelicolor*	233	45
ORF259	293718	293272	ribosomal protein L13 (rpL13)	U32823	*Haemophilus influenzae*	364	47
ORF260	294630	293953	glutamine transport ATP-binding protein Q	U67524	*Methanococcus jannaschii*	387	46
ORF261	296153	294636	putative				
ORF262	294817	295068	putative				
ORF263	296354	297862	conserved hypothetical protein	AE000586	*Helicobacter pylori*	641	46
ORF264	298415	297879	putative				
ORF265	298777	298253	putative				
ORF266	299572	298781	putative				
ORF267	300487	299633	putative				
ORF268	301586	300702	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF269	302440	301571	putative				
ORF270	302838	302437	putative				
ORF271	303335	302745	putative				
ORF272	304394	303852	putative				
ORF273	304606	305223	f311; This 311 aa orf is 22 pct identical (13 gaps) to 186 residues of an approx. 488 aa protein YACA_BACSU SW: P37563; pyul of D21139	AE000232	*Escherichia coli*	250	38
ORF274	305394	306236	survival protein surE	U81296	*Sinorhizobium meliloti*	156	42
ORF275	306501	307439	YqfU	D84432	*Bacillus subtilis*	547	42
ORF276	308033	307458	3-octaprenyl-4-hydroxybenzoate carboxy-lyase	U61168	*Bacillus firmus*	403	42
ORF277	308924	308037	4-hydroxybenzoate octaprenyltransferase	U61168	*Bacillus firmus*	152	40
ORF278	309485	310180	putative				
ORF279	310426	311214	putative				
ORF280	311597	311253	putative				
ORF281	312772	311780	putative				
ORF282	313425	312772	putative				
ORF283	313646	313377	putative				
ORF284	313937	314665	lysophospholipase homolog	AF006678	*Schistosoma mansoni*	141	44
ORF285	315576	314755	dnaZX	X17014	*Bacillus subtilis*	154	39
ORF286	316157	315531	unknown	D26185	*Bacillus subtilis*	284	31
ORF287	318657	316156	DNA gyrase	L47978	*Aeromonas salmonicida*	1785	48
ORF288	321042	318676	DNA gyrase subunit B	U35453	*Clostridium acetobutylicum*	1838	59
ORF289	321445	321098	putative				
ORF290	322309	321710	putative				
ORF291	323190	322366	outer membrane protein	AE000654	*Helicobacter pylori*	376	43
ORF292	323843	323181	hypothetical	U70214	*Escherichia coli*	356	37
ORF293	324878	323856	ATP-binding protein (abc)	U32744	*Haemophilus influenzae*	545	44
ORF294	325340	326410	f374; This 374 aa orf is 30 pct identical (9 gaps) to 102 residues of an approx. 512 aa protein FLIC_SALMU SW: P06177	AE000299	*Escherichia coli*	1194	62
ORF295	326433	327836	Xas A	AE000246	*Escherichia coli*	479	33

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF296	328465	327839	putative				
ORF297	329360	328857	putative				
ORF298	330907	329357	putative				
ORF299	332455	330956	MgtE	U18744	*Bacillus firmus*	203	36
ORF300	334536	332395	putative				
ORF301	336091	334877	putative				
ORF302	336103	337302	putative				
ORF303	338129	338830	putative				
ORF304	338965	339501	putative				
ORF305	339508	340143	putative				
ORF306	340247	342967	putative				
ORF307	343385	343810	cAMP-dependent protein kinase type I regulatory subunit	U75932	*Rattus norvegicus*	102	37
ORF308	344171	343935	acyl carrier protein (acpP)	AE000570	*Helicobacter pylori*	198	55
ORF309	345082	344330	3-ketoacyl-ACP reductase	U39441	*Vibrio harveyi*	598	48
ORF310	346005	345082	malonyl-CoA:Acyl carrier protein transacylase	U59433	*Bacillus subtilis*	538	45
ORF311	346784	346437	beta-ketoacyl-acyl carrier protein synthase III (fabH)	AE000540	*Helicobacter pylori*	273	50
ORF312	347029	346715	beta-ketoacyl-acyl carrier protein synthase III	M77744	*Escherichia coli*	265	63
ORF313	347034	347723	recombination protein	D90916	*Synechocystis sp.*	363	42
ORF314	348075	350459	putative				
ORF315	350598	351071	putative				
ORF316	351075	352175	rifampicin resistance protein	L22690	*Rickettsia rickettsii*	495	46
ORF317	353291	352230	putative				
ORF318	353442	354467	pyruvate dehydrogenase E1 component, alpha subunit	D90915	*Synechocystis sp.*	571	44
ORF319	354451	354933	pyruvate dehydrogenase E1 beta subunit	U09137	*Arabidopsis thaliana*	495	59
ORF320	355000	355449	pyruvate dehydrogenase E1 component, beta subunit	U38804	*Porphyra purpurea*	336	47
ORF321	355448	356743	F23B12.5	Z77659	*Caenorhabditis elegans*	759	46
ORF322	355953	355642	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF323	359310	356827	glycogen phosphorylase B	U47025	*Homo sapiens*	2193	57
ORF324	359120	359377	putative				
ORF325	359525	359908	putative				
ORF326	361290	359947	DnaA	D89066	*Staphylococcus aureus*	375	46
ORF327	363785	361362	hypothetical	U32781	*Haemophilus influenzae*	394	44
ORF328	364496	363888	putative				
ORF329	364832	365290	putative				
ORF330	365304	365669	dpj	M76470	*Escherichia coli*	160	45
ORF331	366599	365667	NADPH thioredoxin reductase	AC002329	*Arabidopsis thaliana*	975	60
ORF332	367291	369030	ribosomal protein S1 (rpS1)	U32801	*Haemophilus influenzae*	1209	41
ORF333	369134	369808	NusA	U74759	*Chlamydia trachomatis*	995	87
ORF334	369917	370438	NusA	U74759	*Chlamydia trachomatis*	760	87
ORF335	370365	372647		U74759	*Chlamydia trachomatis*	2173	61
ORF336	372557	373066	initiation factor IF2-beta (infB; gtg start codon)	X00513	*Escherichia coli*	333	39
ORF337	373020	373442	ORF6 gene product	Z18631	*Bacillus subtilis*	192	34
ORF338	373467	374195	tRNA pseudouridine 55 synthase	D90917	*Synechocystis sp.*	358	47
ORF339	374176	375099	hypothetical 34.6 kD protein in rpsT-ileS intergenic region	AE000113	*Escherichia coli*	395	39
ORF340	375676	375083	hypothetical GTP-binding protein in pth 3' region	AE000219	*Escherichia coli*	507	53
ORF341	376173	375634	hypothetical	U32723	*Haemophilus influenzae*	480	59
ORF342	376564	377643	YscU	U08019	*Yersinia enterocolitica*	538	37
ORF343	377956	379773	lcrD gene product	X67771	*Yersinia enterocolitica*	1302	47
ORF344	379781	380425	putative				
ORF345	380281	381000	putative				
ORF346	381008	381460	putative				
ORF347	381460	383037	4-alpha-glucanotransferase	L37874	*Clostridium butyricum*	302	38
ORF348	383257	383523	ribosomal protein L28 (rpL28)	U32776	*Haemophilus influenzae*	175	55
ORF349	383553	385304	hypothetical protein	D90901	*Synechocystis sp.*	565	38
ORF350	385397	386458	comE ORF1	D64002	*Synechocystis sp.*	187	10
ORF351	387242	386514	putative				
ORF352	388764	387013	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF353	390120	390932	methylenetetrahydrofolate dehydrogenase	D64000	*Synechocystis sp.*	588	53
ORF354	390919	391818	f351; Residues 1-121 are 100 pct identical to YOJL_ECOLI SW: P33944 (122 aa) and aa 152-351 are 100 pct identical to YOJK_ECOLI SW: P33943	AE000310	*Escherichia coli*	186	39
ORF355	392379	391885	small protein	D90914	*Synechocystis sp.*	387	46
ORF356	392582	392986	putative				
ORF357	392776	393684	putative				
ORF358	394151	394804	RecF protein	D90907	*Synechocystis sp.*	232	34
ORF359	394928	395308	putative				
ORF360	395259	395990	putative				
ORF361	397815	395953	hypothetical	U32773	*Haemophilus influenzae*	391	36
ORF362	398850	397831	H. influenzae predicted coding region HI0807	U32763	*Haemophilus influenzae*	580	39
ORF363	400085	399099	putative				
ORF364	401245	400073	YtgC	AF008220	*Bacillus subtilis*	244	30
ORF365	401474	401136	putative				
ORF366	402199	401423	unknown	U52850	*Erysipelothrix rhusiopathiae*	534	46
ORF367	403193	402186	putative				
ORF368	403650	404165	putative				
ORF369	404343	405914	adenine nucleotide translocase	Z49227	*Arabidopsis thaliana*	1280	55
ORF370	405984	407327	putative				
ORF371	407712	408806	putative				
ORF372	410439	409075	putative				
ORF373	411826	410954	putative				
ORF374	412482	414302	lepA gene product	X91655	*Bacillus subtilis*	1827	59
ORF375	415402	414407	6-phosphogluconate dehydrogenase, decarboxylating (gnd)	U32737	*Haemophilus influenzae*	687	51
ORF376	415848	415237	6-phosphogluconate dehydrogenase, 6PGD [Ceratitis capitata=medflies, Peptide, 481 aa]	S67873	*Ceratitis capitata*	695	64
ORF377	417131	415866	tyrosyl-tRNA synthetase (tyrS)	J01719	*Escherichia coli*	821	45
ORF378	417258	417566	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF379	418326	417454	whiG-Stv gene product	X68709	*Streptoverticillium griseocarneum*	464	41
ORF380	420057	418426	FLHA gene product	X63698	*Bacillus subtilis*	455	49
ORF381	420448	420720	ferredoxin IV	M59855	*Rhodobacter capsulatus*	174	63
ORF382	420980	421552	putative				
ORF383	421556	422029	putative				
ORF384	422461	422925	putative				
ORF385	423562	424320	putative				
ORF386	424250	424591	putative				
ORF387	424830	426047	putative				
ORF388	426240	427397	putative				
ORF389	428841	430703	GcpE	D90908	*Synechocystis sp.*	877	47
ORF390	430694	431446	YfiH	U50134	*Escherichia coli*	136	35
ORF391	431597	432100	putative				
ORF392	432165	432779	putative				
ORF393	433272	432832	dihydrolipoamide succinyltransferase (sucB)	U32839	*Haemophilus influenzae*	475	64
ORF394	433925	433227	dihydrolipoamide succinyltransferase (sucB)	U32839	*Haemophilus influenzae*	332	45
ORF395	436678	433934	alpha-ketoglutarate dehydrogenase	U41762	*Rhodobacter capsulatus*	1530	44
ORF396	437176	438357	oxygen-independent coproporphyrinogen III oxidase (hemN)	AE000628	*Helicobacter pylori*	442	42
ORF397	440317	438518	putative				
ORF398	440001	440345	putative				
ORF399	441233	440517	ORF f286	U18997	*Escherichia coli*	168	45
ORF400	440719	441012	putative				
ORF401	442192	441230	putative				
ORF402	442888	442343	putative				
ORF403	442371	442961	putative				
ORF404	443578	443003	[karp] gene products	M86605	*Chlamydia trachomatis*	505	78
ORF405	444500	443526	aminopeptidase	D17450	*Mycoplasma salivarium*	273	39
ORF406	444842	444528	putative				
ORF407	445009	444743	putative	L39923	*Mycobacterium leprae*	133	33

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF408	445718	445182	putative				
ORF409	445807	447804	Sulp	U18908	*Zea mays*	1307	52
ORF410	448738	447803	putative				
ORF411	449628	448618	RuvB protein	U38840	*Thermotoga maritima*	845	53
ORF412	450298	450867	deoxycytidine triphosphate deaminase (dcd)	AE000554	*Helicobacter pylori*	573	58
ORF413	450713	451207	putative				
ORF414	451211	452452	hemolysin	D90914	*Synechocystis sp.*	227	39
ORF415	452448	453659	similar to [SwissProt Accession Number P37908]	D90888	*Escherichia coli*	96	33
ORF416	454843	453725	NifS gene product	L34879	*Anabaena azollae*	533	38
ORF417	455608	454865	hypothetical protein	D90908	*Synechocystis sp.*	371	36
ORF418	456243	457007	putative				
ORF419	457016	457708	putative				
ORF420	458368	457979	unknown	D26185	*Bacillus subtilis*	152	36
ORF421	459496	458372	mutY homolog	U63329	*Homo sapiens*	466	46
ORF422	459493	460194	hypothetical protein	D90914	*Synechocystis sp.*	98	38
ORF423	461446	460355	putative				
ORF424	462298	461450	putative				
ORF425	462444	463349	enoyl-ACP reductase	Y13861	*Nicotiana tabacum*	1008	69
ORF426	464241	463342	putative				
ORF427	464574	465065	putative				
ORF428	465129	465611	putative				
ORF429	465571	466317	putative				
ORF430	466317	467093	H. pylori predicted coding region HP0152	AE000536	*Helicobacter pylori*	246	36
ORF431	466999	467502	putative				
ORF432	469691	467715	unidentified transporter-ATP binding	Z82044	*Bacillus subtilis*	496	45
ORF433	470691	469660	acetyl-CoA carboxylase subunit	AF008220	*Bacillus subtilis*	781	52
ORF434	472010	470709	putative				
ORF435	471545	471799	putative				
ORF436	472359	472045	putative				
ORF437	473523	472732	orf1	X75413	*Escherichia coli*	313	42
ORF438	474889	473441	murE gene product	Z15056	*Bacillus subtilis*	679	37
ORF439	477323	475365	penicillin-binding protein 2	X59630	*Neisseria meningitidis*	451	42

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF440	478496	477597	hypothetical protein	D90906	*Synechocystis sp.*	534	52
ORF441	478722	479273	putative				
ORF442	479277	479705	putative				
ORF443	480050	481450	chromosomal replication initiator protein DnaA	D90909	*Synechocystis sp.*	793	40
ORF444	481469	482053	OrfH	U35673	*Borrelia burgdorferi*	157	37
ORF445	482600	482025	putative				
ORF446	482654	484204	NADH:ubiquinone oxidoreductase subunit B	Z37111	*Vibrio alginolyticus*	801	49
ORF447	484211	485170	NADH:ubiquinone oxidoreductase (GP:Z37111_4)	U32702	*Haemophilus influenzae*	258	48
ORF448	485170	485838	NADH:uniquinone oxidoreductase	Z37111	*Vibrio alginolyticus*	543	55
ORF449	485813	486580	unidentified protein of Na+-translocating NADH-quinone reductase	D49364	*Vibrio alginolyticus*	488	48
ORF450	486976	486638	putative				
ORF451	489071	487764	putative				
ORF452	489341	489090	putative				
ORF453	489958	489152	putative				
ORF454	490549	489962	putative				
ORF455	491163	490522	putative				
ORF456	491396	491112	putative				
ORF457	492121	491390	putative				
ORF458	492304	494838	ClpC adenosine triphosphatase	U02604	*Bacillus subtilis*	2370	46
ORF459	495943	494822	hypothetical protein in purB 5' region	AE000213	*Escherichia coli*	927	53
ORF460	496011	496565	putative				
ORF461	496569	497228	putative				
ORF462	497358	497834	putative				
ORF463	497770	498327	putative				
ORF464	499209	499589	putative				
ORF465	499520	499792	putative				
ORF466	500774	504169	putative 98 kDa outer membrane protein	U72499	*Chlamydia psittaci*	1215	45
ORF467	504139	504600	putative 98 kDa outer membrane protein	U72499	*Chlamydia psittaci*	319	47
ORF468	504865	506877	putative 98 kDa outer membrane protein	U72499	*Chlamydia psittaci*	992	42

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF469	506790	507671	putative 98 kDa outer membrane protein	U72499	*Chlamydia psittaci*	739	46
ORF470	507718	510507	putative 98 kDa outer membrane protein	U72499	*Chlamydia psittaci*	1813	42
ORF471	508325	507912	putative				
ORF472	510660	513440	POMP90A precursor	U65942	*Chlamydia psittaci*	1830	46
ORF473	514965	513787	hypothetical	D83026	*Bacillus subtilis*	482	48
ORF474	517347	515419	putative 98 kDa outer membrane protein	U72499	*Chlamydia psittaci*	1554	51
ORF475	517058	517363	putative				
ORF476	517798	517277	putative 98 kDa outer membrane protein	U72499	*Chlamydia psittaci*	222	41
ORF477	518200	517847	POMP91B precursor	U65943	*Chlamydia psittaci*	162	42
ORF478	518300	521146	putative 98 kDa outer membrane protein	U72499	*Chlamydia psittaci*	1900	45
ORF479	521392	522948	POMP91A	U65942	*Chlamydia psittaci*	490	39
ORF480	523244	524809	putative 98 kDa outer membrane protein	U72499	*Chlamydia psittaci*	507	35
ORF481	524379	524125	putative				
ORF482	524649	526238	putative 98 kDa outer membrane protein	U72499	*Chlamydia psittaci*	969	41
ORF483	526265	527104	putative				
ORF484	526947	526702	putative				
ORF485	526975	528450	putative 98 kDa outer membrane protein	U72499	*Chlamydia psittaci*	197	48
ORF486	528408	529199	putative outer membrane protein	U72499	*Chlamydia psittaci*	154	37
ORF487	530612	529542	putative				
ORF488	531656	530616	putative				
ORF489	533974	532067	putative				
ORF490	536432	534324	putative				
ORF491	537150	536707	putative				
ORF492	537928	537080	putative				
ORF493	538438	537932	putative				
ORF494	538737	538333	putative				
ORF495	539594	539127	putative				
ORF496	541215	539590	putative				
ORF497	542571	541282	putative				
ORF498	543014	542457	putative				
ORF499	543369	542962	putative				
ORF500	543809	546628	putative 98 kDa outer membrane protein	U72499	*Chlamydia psittaci*	506	89
ORF501	546619	549525	POMP91A	U65942	*Chlamydia psittaci*	128	50

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF502	547293	546994	putative				
ORF503	549699	550523	putative 98 kDa outer membrane protein	U72499	*Chlamydia psittaci*	96	32
ORF504	550490	551551	putative 98 kDa outer membrane protein	U72499	*Chlamydia psittaci*	223	33
ORF505	551448	552623	putative 98 kDa outer membrane protein	U72499	*Chlamydia psittaci*	139	46
ORF506	552652	555117	putative 98 kDa outer membrane protein	U72499	*Chlamydia psittaci*	487	48
ORF507	555029	555493	putative				
ORF508	558006	555673	putative				
ORF509	559694	558162	putative				
ORF510	558208	558573	putative				
ORF511	561692	559899	putative				
ORF512	561412	561708	putative				
ORF513	563942	561777	1,4-alpha-glucan branching enzyme	X73903	*Streptomyces coelicolor*	1743	45
ORF514	564969	563950	putative				
ORF515	566204	564936	YqeV	D84432	*Bacillus subtilis*	639	38
ORF516	567717	566302	putative GTPase required for high frequency lysogenization by bacteriophage lambda	U00005	*Escherichia coli*	686	41
ORF517	568526	567708	putative				
ORF518	569467	568742	putative				
ORF519	571065	569431	putative				
ORF520	571828	571118	arginine-binding periplasmic protein 1 precursor	AE000188	*Escherichia coli*	197	45
ORF521	572202	573308	putative				
ORF522	573146	575056	putative				
ORF523	575023	575916	carboxysome formation protein	D90901	*Synechocystis sp.*	557	59
ORF524	577891	576497	putative				
ORF525	578914	578204	putative				
ORF526	579924	578857	putative				
ORF527	580187	579858	protein kinase C inhibitor	D90906	*Synechocystis sp.*	260	49
ORF528	580017	580406	putative				
ORF529	581086	580187	Yer156cp	U18917	*Saccharomyces cerevisiae*	176	34
ORF530	581367	581828	putative				
ORF531	581678	582367	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF532	582361	583428	putative				
ORF533	584690	583431	putative				
ORF534	585237	584950	putative				
ORF535	585626	586888	hypothetical protein	D64004	*Synechocystis sp.*	805	45
ORF536	586846	587907	putative				
ORF537	589049	588180	putative				
ORF538	590500	589301	putative				
ORF539	590755	592458	aminoacyl-tRNA synthetase	L25105	*Chlamydia trachomatis*	2125	71
ORF540	592526	592903	has homology to putative heat shock proteins of Bacillus subtilis and Clostridium acetobutylicum; ORFA; putative	L25105	*Chlamydia trachomatis*	324	59
ORF541	592836	593747	Possible negative regulator of CIRCE element; Homologs in B. subtilis and Clostridia spp. referred to as hrcA or orfA	U52216	*Chlamydia trachomatis*	960	65
ORF542	593747	594298	grpE	M62819	*Chlamydia trachomatis*	661	71
ORF543	594331	595947	DnaK protein homolog; 71,550 Da; putative	M69227	*Chlamydia pneumoniae*	2619	100
ORF544	595905	596309	DnaK protein homolog; 71,550 Da; putative	M69227	*Chlamydia pneumoniae*	674	100
ORF545	596514	597215	putative				
ORF546	597184	597957	vacB gene product	U14003	*Escherichia coli*	306	48
ORF547	597755	598612	ORF-2	D11024	*Shigella flexneri*	168	46
ORF548	598602	599204	homologous to DNA glycosylases; hypothetical	D83026	*Bacillus subtilis*	374	47
ORF549	599373	599939	putative				
ORF550	600903	602072	hemolysin	X73141	*Serpulina hyodysenteriae*	362	36
ORF551	602240	602587	hypothetical protein	D90908	*Synechocystis sp.*	182	35
ORF552	602637	603272	putative				
ORF553	603142	604512	putative				
ORF554	604627	605853	conserved hypothetical protein	AE000579	*Helicobacter pylori*	423	40
ORF555	605790	606620	putative				
ORF556	606571	607281	putative	L14679	*Lactococcus lactis*	384	45
ORF557	609004	607355	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF558	610906	609932	putative				
ORF559	611786	611004	diaminopimelate epimerase	D90917	*Synechocystis sp.*	207	55
ORF560	612333	611746	ATP-dependent Clp protease proteolytic subunit	D90915	*Synechocystis sp.*	389	44
ORF561	613897	612341	serine hydroxymethyltransferase	D90903	*Synechocystis sp.*	909	52
ORF562	615179	616279	putative				
ORF563	616610	617383	putative				
ORF564	618796	617810	ORF o328	U18997	*Escherichia coli*	413	45
ORF565	620004	618826	branched chain alpha-keto acid dehydrogenase E2	M97391	*Bacillus subtilis*	688	41
ORF566	619649	619918	putative				
ORF567	621265	620021	Hypothetical protein	Y14083	*Bacillus subtilis*	727	37
ORF568	622359	621265	hypothetical	U32691	*Haemophilus influenzae*	294	52
ORF569	623420	622560	rRNA methylase	D90913	*Synechocystis sp.*	244	38
ORF570	624297	623335	hypothetical protein (SP:P39587)	U67605	*Methanococcus jannaschii*	147	35
ORF571	624773	624174	riboflavin synthase alpha chain	AE000261	*Escherichia coli*	424	50
ORF572	625029	625484	ORF 168	D28752	*Synechococcus sp.*	323	43
ORF573	625488	625883	YteA	AF008220	*Bacillus subtilis*	172	35
ORF574	625892	626395	signalpeptidase II	X78084	*Staphylococcus carnosus*	204	38
ORF575	626444	627790	D-alanine permease (dagA)	U32770	*Haemophilus influenzae*	566	33
ORF576	627912	628607	putative				
ORF577	628774	629697	putative				
ORF578	629660	631639	POMP91A	U65942	*Chlamydia psittaci*	579	44
ORF579	631725	633551	putative				
ORF580	633520	636957	putative 98 kDa outer membrane protein	U72499	*Chlamydia psittaci*	266	45
ORF581	637232	638098	adhesion protein	D90903	*Synechocystis sp.*	267	38
ORF582	640648	639593	GTP-binding protein	D90901	*Synechocystis sp.*	759	45
ORF583	640979	640728	50S ribosomal protein L27	U38804	*Porphyra purpurea*	265	65
ORF584	641327	641007	50S ribosomal subunit protein L21	U18997	*Escherichia coli*	210	41
ORF585	641687	642283	hypothetical protein	D90906	*Synechocystis sp.*	76	39
ORF586	643023	642286	assimilatory sulfite reductase	L26503	*Saccharomyces cerevisiae*	284	42
ORF587	643330	643076	putative				
ORF588	643704	643351	ribosomal protein S10 (rpS10)	U32761	*Haemophilus influenzae*	349	69

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF589	645628	643676	translation elongation factor EF-G (fusA)	AE000625	*Helicobacter pylori*	1991	58
ORF590	645783	645538	elongation factor G (AA 1-691)	X16278	*Thermus aquaticus thermophilus*	170	80
ORF591	646269	645793	ribosomal protein S7	Z11567	*Chlamydia trachomatis*	730	88
ORF592	646751	646314	ribosomal protein S12 (AA 1-123)	X52912	*Cryptomonas phi*	485	67
ORF593	647848	647045	putative				
ORF594	648393	650336	ORF of prc gene (alt.)	D00674	*Escherichia coli*	554	42
ORF595	651016	650420	hypothetical sulfur-rich protein	U41759	*Chlamydia psittaci*	301	50
ORF596	652956	651289	60kDa CrP	X53511	*Chlamydia pneumoniae*	2951	100
ORF597	653395	653126	9kDa CrP	X53511	*Chlamydia pneumoniae*	502	99
ORF598	655740	654193	glutamyl-tRNA synthetase homolog	U41759	*Chlamydia psittaci*	2259	82
ORF599	656508	655966	early stage-specific transcription experimentally demonstrated; early upstream open reading frame (EUO)	L13598	*Chlamydia psittaci*	666	62
ORF600	658140	657022	unknown	U41759	*Chlamydia psittaci*	950	44
ORF601	660216	658525	RecJ recombination protein	U41759	*Chlamydia psittaci*	807	73
ORF602	663238	660248	protein-export membrane protein SecD	D64000	*Synechocystis sp.*	413	41
ORF603	664461	663157	putative				
ORF604	665735	664635	putative				
ORF605	666212	666994	hypothetical protein	D64006	*Synechocystis sp.*	538	58
ORF606	666998	667921	o298; This 298 aa orf is 33 pct identical (24 gaps) to 248 residues of an approx. 256 aa protein CDSA_ECOLI SW: P06466	AE000238	*Escherichia coli*	253	45
ORF607	667909	668568	cytidylate kinase	AE000193	*Escherichia coli*	400	48
ORF608	668502	669203	hypothetical protein	D90915	*Synechocystis sp.*	225	33
ORF609	669154	670893	arginyl-tRNA-synthetase	D64006	*Synechocystis sp.*	1365	49
ORF610	672226	670853	UDP-N-acetylglucosamine enolpyruvyl transferase (murZ)	U32788	*Haemophilus influenzae*	642	40
ORF611	671137	671424	putative				
ORF612	672453	673001	putative				
ORF613	673072	674721	putative				
ORF614	674549	674262	putative				
ORF615	675518	674796	ORF246 gene product	X59551	*Escherichia coli*	520	43
ORF616	676083	675499	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF617	676630	676067	putative				
ORF618	677016	676600	ORF3	D10279	*Bacillus subtilis*	361	63
ORF619	677647	677015	peptide release factor 2	X99401	*Bacillus firmus*	427	43
ORF620	677990	678259	unknown	Z49939	*Saccharomyces cerevisiae*	175	48
ORF621	679444	680097	unknown	D26185	*Bacillus subtilis*	263	38
ORF622	680097	680897	unknown	D64126	*Bacillus subtilis*	506	45
ORF623	681637	680849	putative				
ORF624	681409	682281	putative				
ORF625	682453	682821	putative				
ORF626	682763	683902	sensor protein	L39904	*Myxococcus xanthus*	190	48
ORF627	684616	683969	putative				
ORF628	685169	684534	putative				
ORF629	685986	685117	putative				
ORF630	686278	687288	NtrC/NifA-like protein regulator	U17902	*Escherichia coli*	820	45
ORF631	687483	688151	putative				
ORF632	688740	689501	putative				
ORF633	690242	689622	putative				
ORF634	690470	691126	unknown	Z48008	*Saccharomyces cerevisiae*	380	46
ORF635	692600	691497	putative				
ORF636	692674	695064	phenylalanyl-tRNA synthetase beta-subunit (pheT)	U32810	*Haemophilus influenzae*	593	45
ORF637	695049	696032	putative				
ORF638	697964	696585	OppC-like protein	D85103	*Synechococcus sp.*	371	37
ORF639	699803	698274	OppB gene product	X56347	*Bacillus subtilis*	197	40
ORF640	701926	699788	AppA	U20909	*Bacillus subtilis*	324	43
ORF641	703196	702567	putative				
ORF642	704221	703208	putative				
ORF643	704240	705289	ferrochelatase	X73417	*Arabidopsis thaliana*	266	42
ORF644	706070	705300	histidine periplasmic binding protein P29	U58045	*Campylobacter jejuni*	128	31
ORF645	706841	706254	conserved hypothetical protein	AE000592	*Helicobacter pylori*	155	37
ORF646	707596	706811	putative				
ORF647	708666	707677	ADP-glucose pyrophosphorylase	X55650	*Solanum tuberosum*	595	43
ORF648	709793	709119	pyrE-F gene product	X71842	*Arabidopsis thaliana*	400	44

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF649	711523	710132	transcription termination factor	J01673	*Escherichia coli*	1251	60
ORF650	712236	711523	putative				
ORF651	714734	712125	DNA polymerase I	J04479	*Streptococcus pneumoniae*	1334	43
ORF652	715759	714761	protease IV	U67512	*Methanococcus jannaschii*	101	55
ORF653	717538	715886	adenine nucleotide translocase	Z49227	*Arabidopsis thaliana*	832	39
ORF654	719113	720243	replicative DNA helicase	D26185	*Bacillus subtilis*	776	44
ORF655	720590	722422	homologous to E.coli gidA	X62540	*Pseudomonas putida*	1575	52
ORF656	722406	723056	putative				
ORF657	723551	723120	nucleoside 5'-diphosphate phosphotransferase (EC 2.7.4.6)	J05207	*Myxococcus xanthus*	451	62
ORF658	724246	723626	Holliday junction DNA helicase (ruvA)	U32716	*Haemophilus influenzae*	293	43
ORF659	724754	724251	crossover junction endodeoxyribonuclease (ruvC)	U32717	*Haemophilus influenzae*	296	53
ORF660	725868	724900	putative				
ORF661	727115	726270	putative				
ORF662	728126	727119	glyceraldehyde-3-phosphate dehydrogenase	U83198	*Chlamydia trachomatis*	1340	75
ORF663	728594	728208	ribosomal protein L17	L33834	*Chlamydia trachomatis*	439	82
ORF664	729614	728604	RNA polymerase alpha-subunit	L33834	*Chlamydia trachomatis*	1356	89
ORF665	729778	729533	RNA polymerase alpha-subunit	L33834	*Chlamydia trachomatis*	273	82
ORF666	730149	729751	ribosomal protein S11	L33834	*Chlamydia trachomatis*	562	90
ORF667	730539	730174	ribosomal protein S13	L33834	*Chlamydia trachomatis*	544	89
ORF668	731983	730598	homolog	L25077	*Chlamydia trachomatis*	1956	83
ORF669	732427	731996	ribosomal protein CtrL15e	M80325	*Chlamydia trachomatis*	563	77
ORF670	732917	732423	ribosomal protein CtrS5e	M80325	*Chlamydia trachomatis*	702	84
ORF671	733598	733320	ribosomal protein L6	M60652	*Chlamydia trachomatis*	316	87
ORF672	733869	733492	ribosomal protein L6	M60652	*Chlamydia trachomatis*	469	77
ORF673	734298	733900	ribosomal protein CtrS8e	M80325	*Chlamydia trachomatis*	572	82
ORF674	734858	734319	ribosomal protein CtrL5e	M80325	*Chlamydia trachomatis*	730	90
ORF675	735195	734863	ribosomal protein CtrL24e	M80325	*Chlamydia trachomatis*	420	70
ORF676	735578	735342	ribosomal protein CtrL14e	M80325	*Chlamydia trachomatis*	270	95
ORF677	735861	735604	ribosomal protein S17e	M80325	*Chlamydia trachomatis*	322	77
ORF678	736492	736079	50S ribosomal protein L16	D90905	*Synechocystis sp.*	439	60

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF679	737192	736524	ribosomal protein S3	D64071	*Actinobacillus actinomycetemcomitans*	612	58
ORF680	737555	737211	ribosomal protein L22	Z21677	*Thermotoga maritima*	228	48
ORF681	738688	737837	50S ribosomal subunit protein L2	U18997	*Escherichia coli*	769	62
ORF682	739048	738713	putative				
ORF683	739736	739065	ribosomal protein L4	X67014	*Bacillus stearothermophilus*	308	46
ORF684	740477	739773	ribosomal protein L3	Z46265	*Thermus aquaticus thermophilus*	463	50
ORF685	740659	740958	putative				
ORF686	741722	740721	putative				
ORF687	742789	741827	methionyl-tRNA formyltransferase	D64001	*Synechocystis sp.*	511	48
ORF688	743618	742782	UDP-N-acetylglucosamine acyltransferase	L22690	*Rickettsia rickettsii*	542	43
ORF689	744092	743634	(3R)-hydroxymyristol acyl carrier protein dehydrase	D90910	*Synechocystis sp.*	339	55
ORF690	744604	744107	UDP-3-0-acyl N-acetylglcosamine deacetylase	D90902	*Synechocystis sp.*	287	45
ORF691	744953	744498	UDP-3-O-acyl-GlcNAc deacetylase	U67855	*Pseudomonas aeruginosa*	262	51
ORF692	746608	744986	apolipoprotein N-acyltransferase (cute)	U32716	*Haemophilus influenzae*	194	50
ORF693	747085	746621	low homology to P14 protein of Heamophilus influenzar and 14.2 kDa protein of Escherichia coli	D78189	*Bacillus subtilis*	235	37
ORF694	747974	747219	polymerase III	M22996	*Bacillus subtilis*	180	34
ORF695	748594	748169	hypothetical protein	D90914	*Synechocystis sp.*	160	43
ORF696	749145	748573	putative				
ORF697	749652	749957	trxA	L39892	*Chlamydia psittaci*	393	72
ORF698	750446	749979	spoU	L39892	*Chlamydia psittaci*	559	72
ORF699	751219	750446	mip	L39892	*Chlamydia psittaci*	948	60
ORF700	753042	751291	aspartyl-tRNA synthetase	D90910	*Synechocystis sp.*	1347	47
ORF701	754309	753020	histidine--tRNA ligase	Z17214	*Streptococcus equisimilis*	757	44
ORF702	755120	756175	hexosephosphate transport protein	M89480	*Salmonella typhimurium*	870	49
ORF703	756120	756485	hexosephosphate transport protein	M89479	*Escherichia coli*	321	45
ORF704	756499	760227	DNA polymerase III alpha-subunit (dnaE)	AE000646	*Helicobacter pylori*	1977	42
ORF705	761217	760297	putative				
ORF706	761297	761809	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF707	761782	762282	putative				
ORF708	762260	762895	putative				
ORF709	762867	763316	hypothetical protein	D90908	*Synechocystis sp.*	177	43
ORF710	763780	763325	putative				
ORF711	763861	765168	DD-carboxypeptidase	M85047	*Bacillus subtilis*	292	37
ORF712	766809	765697	fmu and fmv protein	D90902	*Synechocystis sp.*	130	36
ORF713	768051	766888	putative				
ORF714	768566	768321	putative				
ORF715	769342	768551	putative				
ORF716	770532	769378	putative				
ORF717	771451	770804	putative				
ORF718	773058	771847	3-phosphoglycerate kinase	U83197	*Chlamydia trachomatis*	1540	72
ORF719	773094	773456	putative				
ORF720	774376	773093	putative phosphate permease	U84890	*Mesembryanthemum crystallinum*	870	45
ORF721	775123	774380	putative				
ORF722	775398	774916	putative				
ORF723	775046	776077	sporulation protein	M57689	*Bacillus subtilis*	698	43
ORF724	776070	777041	was dppE	U00039	*Escherichia coli*	565	56
ORF725	777964	777536	orf288; translated orf similarity to SWISS-PROT: YGI2_PSEPU hypothetical 32.4 kDa protein of Pseudomomas putida	Y10436	*Coxiella burnetii*	256	46
ORF726	778176	777904	B.subtilis genes rpmH, rnpA, 50kd, gidA and gidB	X62539	*Bacillus subtilis*	112	37
ORF727	778621	779334	putative				
ORF728	781173	780307	f406; This 406 aa orf is 28 pct identical (12 gaps) to 264 residues of an approx. 440 aa protein YAOA_SCHPO SW: Q10089	AE000263	*Escherichia coli*	603	40
ORF729	781526	781116	f406; This 406 aa orf is 28 pct identical (12 gaps) to 264 residues of an approx. 440 aa protein YAOA_SCHPO SW: Q10089	AE000263	*Escherichia coli*	258	45
ORF730	782784	781555	f423; This 423 aa orf is 29 pct identical (1 gaps) to 172 residues of an approx. 488 aa protein YC24_CYAPA SW: P48260	AE000263	*Escherichia coli*	197	44

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF731	783572	782805	hypothetical chloroplast ORF 16	U38804	*Porphyra purpurea*	597	52
ORF732	785032	783581	ABC transporter subunit	D64004	*Synechocystis sp.*	1720	62
ORF733	786412	785360	putative				
ORF734	788429	786450	pbp	Y14206	*Streptomyces coelicolor*	148	55
ORF735	788944	788528	penicillin-binding protein 3	X84053	*Pseudomonas aeruginosa*	148	38
ORF736	789758	788901	putative				
ORF737	790332	791504	major outer membrane protein	M64064	*Chlamydia pneumoniae*	2028	99
ORF738	791846	792721	ribosomal protein S2	U60196	*Chlamydia trachomatis*	904	70
ORF739	792724	793569	elongation factor Ts	U60196	*Chlamydia trachomatis*	1023	71
ORF740	793580	794323	UMP kinase	U60196	*Chlamydia trachomatis*	891	72
ORF741	794304	794843	ribosome-releasing factor	U60196	*Chlamydia trachomatis*	673	73
ORF742	795217	795732	unknown	D26185	*Bacillus subtilis*	105	42
ORF743	795722	796795	unknown	D26185	*Bacillus subtilis*	208	33
ORF744	798735	797053	putative	L33796	*Vibrio cholerae*	386	34
ORF745	799823	798681	putative				
ORF746	799297	799578	putative				
ORF747	801313	799808	Pkn5	U40656	*Myxococcus xanthus*	345	33
ORF748	802453	801332	putative				
ORF749	803299	802457	putative				
ORF750	803811	803290	putative				
ORF751	805151	803826	YscN	U02499	*Yersinia enterocolitica*	1185	53
ORF752	805860	805156	putative				
ORF753	806604	806332	putative				
ORF754	806913	806608	putative				
ORF755	808222	806903	putative				
ORF756	808751	808146	putative				
ORF757	809437	808673	putative				
ORF758	809939	809454	putative				
ORF759	811235	810213	delta-aminolevulinate synthase (EC 2.3.1.37)	M30785	*Escherichia coli*	172	40
ORF760	811779	813056	DNA gyrase subunit B	U35453	*Clostridium acetobutylicum*	584	38
ORF761	812890	812516	putative				
ORF762	812954	813583	DNA gyrase subunit B	Z19108	*Spiroplasma citri*	371	39

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF763	813587	815023	gyrA	X92503	*Mycobacterium smegmatis*	414	55
ORF764	815420	815746	putative				
ORF765	816036	817010	orf-X; hypothetical protein; Method: conceptual translation supplied by author	U48870	*Bacillus subtilis*	569	47
ORF766	817111	817356	unknown	Z74024	*Mycobacterium tuberculosis*	114	34
ORF767	817791	818609	3-deoxy-d-manno-octulosonic acid 8-phosphate synthetase	Z50747	*Chlamydia psittaci*	1112	78
ORF768	818609	819094	protein of unknown function	Z50747	*Chlamydia psittaci*	545	65
ORF769	819104	819823	ATP binding protein	U72493	*Chlamydia trachomatis*	1099	88
ORF770	820722	819826	putative				
ORF771	822313	821000	putative				
ORF772	823503	822238	putative				
ORF773	823678	825612	putative				
ORF774	825461	826312	putative				
ORF775	827280	826645	putative				
ORF776	828604	827171	76 kDa protein	L23921	*Chlamydia pneumoniae*	2179	100
ORF777	830026	828713	76 kDa protein	L23921	*Chlamydia pneumoniae*	1162	100
ORF778	831047	830085	mviB homolog	U50732	*Chlamydia trachomatis*	982	58
ORF779	831725	831051	mviB homolog	U50732	*Chlamydia trachomatis*	740	65
ORF780	832220	833098	T05H10.2	Z47812	*Caenorhabditis elegans*	407	34
ORF781	833851	833396	ribosomal protein S4 (rps4)	AE000633	*Helicobacter pylori*	372	53
ORF782	834068	835039	This ORF is homologous to a 40.0 kd hypothetical protein in the htrB 3' region from E. coli. Accession Number X61000	L22217	*Mycoplasma-like organism*	377	49
ORF783	835792	835127	uridine kinase	L31783	*Mus musculus*	436	43
ORF784	837624	836116	ORF f397	U29581	*Escherichia coli*	92	38
ORF785	838951	840882	putative				
ORF786	840869	842185	exodeoxyribonuclease V (recB)	U32811	*Haemophilus influenzae*	409	40
ORF787	841989	843455	DNA helicase II	U39703	*Mycoplasma genitalium*	110	46
ORF788	843242	844021	exodeoxyribonuclease V (recB)	U32811	*Haemophilus influenzae*	196	40
ORF789	845018	843987	MreC protein	M31792	*Escherichia coli*	76	53
ORF790	846174	844990	aspartate aminotransferase (aspC)	X03629	*Escherichia coli*	754	40
ORF791	848509	846311	GreA	U02878	*Rickettsia prowazekii*	190	35

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF792	848568	849014	putative				
ORF793	849082	850488	NADH:ubiquinone oxidoreducatase subunit A (GP:Z37111 2)	U32702	*Haemophilus influenzae*	445	37
ORF794	851512	850574	porphobilinogen synthase	U38348	*Chlorobium vibrioforme*	769	45
ORF795	852064	852447	putative				
ORF796	852398	853690	putative				
ORF797	855118	854243	geranylgeranyl pyrophosphate synthase	D85029	*Arabidopsis thaliana*	408	41
ORF798	855751	855128	f147; This 147 aa orf is 26 pct identical (1 gaps) to 99 residues of an approx. 728 aa protein E2BE RABIT SW: P47823	AE000143	*Escherichia coli*	187	36
ORF799	856551	855829	membrane associated regulatory protein	M28368	*Salmonella typhimurium*	172	36
ORF800	856730	858556	unknown function	Z32530	*Chlamydia trachomatis*	842	35
ORF801	858717	859601	exodeoxyribonuclease V (recD)	U32811	*Haemophilus influenzae*	182	51
ORF802	859591	860205	exonuclease V alpha subunit (AA 1-608)	X04582	*Escherichia coli*	235	45
ORF803	861132	860284	putative				
ORF804	861426	861163	30S ribosomal protein S20	Z67753	*Odontella sinensis*	153	41
ORF805	861701	862921	putative				
ORF806	863026	864798	major sigma factor	U04442	*Chlamydia psittaci*	2661	94
ORF807	864831	865256	putative				
ORF808	865226	866581	dihydropterin pyrophosphokinase /dihydropteroate synthase	Y08611	*Pisum sativum*	455	48
ORF809	866562	867119	dehydrofolate reductase, type I (folA)	U32772	*Haemophilus influenzae*	213	49
ORF810	867025	867816	M. jannaschii predicted coding region MJ0768	U67522	*Methanococcus jannaschii*	207	36
ORF811	867820	868497	putative				
ORF812	869743	868661	RecA	U16739	*Chlamydia trachomatis*	1512	87
ORF813	870633	870094	unknown function	Z32530	*Chlamydia trachomatis*	308	45
ORF814	871929	870646	unknown function	Z32530	*Chlamydia trachomatis*	1410	63
ORF815	872538	872086	putative				
ORF816	873908	872517	putative				
ORF817	874281	874670	nifR3-like gene product	Z37984	*Azospirillum brasilense*	181	32
ORF818	874582	875286	ORF1 gene product	X62399	*Escherichia coli*	307	42
ORF819	877857	875377	DNA topoisomerase I	L27797	*Bacillus subtilis*	1488	50

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF820	878446	879255	putative				
ORF821	880635	879268	sigma factor (ntrA) (AA 1-502)	X05888	*Azotobacter vinelandii*	257	47
ORF822	882524	880593	DNA helicase II	D90906	*Synechocystis sp.*	1140	50
ORF823	882612	883319	ipa-57d gene product	X73124	*Bacillus subtilis*	601	51
ORF824	884155	883538	hypothetical protein	D90915	*Synechocystis sp.*	344	39
ORF825	884340	885611	19/20 residue stretch (32-51) identical to N-terminal putative signal sequence of unknown, partly cloned B. subtilis gene.; putative	L19954	*Bacillus subtilis*	456	37
ORF826	885722	887302	heat shock protein	L12004	*Chlamydia trachomatis*	915	39
ORF827	887587	888153	bas1 protein	Z34917	*Hordeum vulgare*	474	50
ORF828	888627	888220	putative				
ORF829	889330	888716	hypothetical protein	Y14079	*Bacillus subtilis*	223	55
ORF830	889898	889323	peptidoglycan-associated lipoprotein	X65796	*Escherichia coli*	222	50
ORF831	891190	889898	TolB	U32470	*Haemophilus influenzae*	280	35
ORF832	891828	891247	putative				
ORF833	892421	892017	exbD peptide	M28819	*Escherichia coli*	77	48
ORF834	893116	892421	inner membrane protein (tolQ)	U32722	*Haemophilus influenzae*	157	54
ORF835	892521	892925	putative				
ORF836	893392	895419	inner membrane copper tolerance protein	Z36905	*Escherichia coli*	120	35
ORF837	895745	896527	unknown	D26185	*Bacillus subtilis*	381	41
ORF838	896668	897558	succinate dehydrogenase subunit C	Y08563	*Paenibacillus macerans*	253	40
ORF839	897565	899442	succinate dehydrogenase subunit A	Y08563	*Paenibacillus macerans*	1667	57
ORF840	899420	900229	succinate dehydrogenase subunit B	Y08563	*Paenibacillus macerans*	656	54
ORF841	903230	900237	putative				
ORF842	905081	903234	putative				
ORF843	906931	905045	sigma factor SibG regulation protein RsbU	D90905	*Synechocystis sp.*	117	35
ORF844	907248	907832	putative				
ORF845	907784	908128	putative				
ORF846	908132	908677	putative				
ORF847	908589	909320	putative				
ORF848	909405	911465	putative				
ORF849	911677	912360	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF850	912303	912821	putative				
ORF851	912937	913983	putative				
ORF852	915128	914067	putative				
ORF853	916658	915303	enolase	L29475	*Bacillus subtilis*	1036	60
ORF854	915627	915376	enolase	U43738	*Mycoplasma pneumoniae*	226	65
ORF855	917707	916853	excinuclease ABC subunit B (uvrB)	U32804	*Haemophilus influenzae*	724	46
ORF856	918837	917722	excinuclease ABC subunit B (uvrB)	U32804	*Haemophilus influenzae*	1029	54
ORF857	919868	918837	tryptophanyl-tRNA synthetase (trpS)	U32746	*Haemophilus influenzae*	376	40
ORF858	920434	919880	putative				
ORF859	921187	920438	ORF8	X82078	*Chlamydia sp.*	164	50
ORF860	921959	921195	hypothetical protein	X62475	*Chlamydia psittaci*	511	44
ORF861	923773	921995	Threonyl tRNA Synthetase	Z80360	*Bacillus subtilis*	1476	44
ORF862	922146	922415	putative				
ORF863	923943	923674	putative				
ORF864	924077	925006	putative				
ORF865	925436	925083	putative				
ORF866	926524	925349	putative				
ORF867	927920	926433	putative				
ORF868	928319	927951	putative				
ORF869	928963	928334	putative				
ORF870	929248	930987	DNA mismatch repair protein (mutL)	U32692	*Haemophilus influenzae*	585	40
ORF871	930995	932059	YqhT	D84432	*Bacillus subtilis*	445	39
ORF872	932121	933515	putative				
ORF873	932881	932513	putative				
ORF874	933485	935746	pulD (ttg start codon)	M32613	*Klebsiella pneumoniae*	210	33
ORF875	935724	937082	epsE	M96172	*Vibrio cholerae*	890	55
ORF876	937229	938410	PilG	U32588	*Neisseria gonorrhoeae*	280	38
ORF877	938281	938805	putative				
ORF878	938809	939255	putative				
ORF879	939165	939782	putative				
ORF880	939760	940791	putative				
ORF881	940822	941106	putative				
ORF882	940977	941351	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF883	942537	941623	yscT	L25667	*Yersinia pseudotuberculosis*	169	44
ORF884	942784	942500	yscS	L25667	*Yersinia pseudotuberculosis*	173	42
ORF885	943149	942799	HrcR	AE000107	*Rhizobium sp. NGR234*	265	52
ORF886	943799	943029	pathogenicity protein	M64094	*Xanthomonas campestris*	252	41
ORF887	944055	943732	putative	M74011	*Yersinia enterocolitica*	112	33
ORF888	944413	943994	putative				
ORF889	945395	944556	putative				
ORF890	945853	945389	putative				
ORF891	946392	945751	HrcJ	U56662	*Erwinia amylovora*	229	44
ORF892	947410	948081	putative				
ORF893	949871	948915	ORF YOR196c	Z75104	*Saccharomyces cerevisiae*	702	44
ORF894	951058	949868	dihydrolipoamide dehydrogenase E3 subunit	M57435	*Bacillus subtilis*	745	39
ORF895	951249	950959	dihydrolipoamide acetyltransferase E3 subunit	M73535	*Staphylococcus aureus*	166	49
ORF896	951664	952134	putative				
ORF897	952674	952165	SNF	X98455	*Bacillus cereus*	229	47
ORF898	953491	952589	helicase	U39680	*Mycoplasma genitalium*	307	42
ORF899	955324	953495	F01G4.1	Z68341	*Caenorhabditis elegans*	133	57
ORF900	955823	955281	putative				
ORF901	957082	955847	branched-chain amino acid carrier	Z48676	*Lactobacillus delbrueckii*	297	40
ORF902	957902	957270	endonuclease III	U11289	*Bacillus subtilis*	317	37
ORF903	959231	957906	homologous to E.coli 50K	X62539	*Bacillus subtilis*	805	45
ORF904	959376	960284	phosphatidylserine decarboxylase	U72715	*Chlamydia trachomatis*	776	51
ORF905	960266	961669	putative				
ORF906	961856	964765	secretory component	U06928	*Caulobacter crescentus*	1812	55
ORF907	966855	965395	28.2% of identity to the Escherichia coli GTP-binding protein Era; putative	L47648	*Bacillus subtilis*	778	41
ORF908	968204	966975	poly(A) polymerase	L47709	*Bacillus subtilis*	383	41
ORF909	968791	968237	ClpX-like protein	U18229	*Bacillus subtilis*	340	39
ORF910	969498	968731	ATP-dependent protease ATPase subunit	D64006	*Synechocystis sp.*	846	66
ORF911	969858	969511	ClpP	U16135	*Synechococcus sp.*	257	54

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF912	970118	969762	ATP-dependent clp protease proteolytic component (clpP)	AE000591	*Helicobacter pylori*	362	63
ORF913	970593	970300	putative				
ORF914	971261	970542	putative				
ORF915	971680	971123	putative				
ORF916	971876	975100	SNF	X98455	*Bacillus cereus*	778	49
ORF917	975419	976516	MreB protein	M96343	*Bacillus subtilis*	960	55
ORF918	976584	978320	phospho enol pyruvate carboxykinase	S56812	*Chlorobium limicola*	1667	64
ORF919	977680	977231	putative				
ORF920	978399	980738	putative				
ORF921	980756	981928	putative				
ORF922	982974	981931	precursor protein (AA -22 to 371)	X52557	*Chlamydia trachomatis*	97	50
ORF923	984120	983119	NAD+ dependent glycerol-3-phosphate dehydrogenase	L47648	*Bacillus subtilis*	618	43
ORF924	985502	984120	AgX-1 antigen [human, infertile patient, testis, Peptide, 505 aa]	S73498	*Homo sapiens*	254	34
ORF925	987180	985882	ORF 4	M72718	*Bacillus subtilis*	697	38
ORF926	987172	987444	putative				
ORF927	989846	989049	nifU-like protein	AE000542	*Helicobacter pylori*	302	31
ORF928	991048	989846	putative				
ORF929	991638	990955	phosphoglyceromutase	L09651	*Zymomonas mobilis*	471	53
ORF930	991794	992498	ORFX13	L09228	*Bacillus subtilis*	403	39
ORF931	993619	993041	biotin [acetyl-CoA-carboxylase] ligase	L47709	*Bacillus subtilis*	136	38
ORF932	993530	994792	rod-shape-determining protein	M22857	*Escherichia coli*	312	44
ORF933	995970	994795	cadmium-transporting ATPase	D64005	*Synechocystis sp.*	358	47
ORF934	996857	995739	ATPase	L28104	*Transposon Tn5422*	449	39
ORF935	997603	996782	putative				
ORF936	998969	997572	seryl-trna synthetase	Y09924	*Staphylococcus aureus*	851	42
ORF937	998896	1000023	orf2, homologue to B.subtilis ribG	X64395	*Escherichia coli*	596	40
ORF938	1000087	1001340	GTP cyclohydrolase II	D90912	*Synechocystis sp.*	1078	52
ORF939	1001357	1001818	riboflavin synthase beta subunit	U27202	*Actinobacillus pleuropneumoniae*	278	36
ORF940	1003288	1001873	putative				
ORF941	1003487	1004146	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF942	1004485	1005639	D-alanine glycine permease (dagA)	AE000603	*Helicobacter pylori*	394	33
ORF943	1005643	1005972	hypothetical protein MTCY180.08	Z97193	*Mycobacterium tuberculosis*	274	58
ORF944	1006784	1006116	similar to trithorax protein in final three exons	U13875	*Caenorhabditis elegans*	155	46
ORF945	1007563	1006769	yycJ	D78193	*Bacillus subtilis*	406	38
ORF946	1009226	1007568	YtpT	AF008220	*Bacillus subtilis*	992	47
ORF947	1009989	1009336	putative				
ORF948	1015852	1016337	putative				
ORF949	1016561	1016181	putative				
ORF950	1016297	1017532	putative				
ORF951	1016802	1016452	putative				
ORF952	1018993	1017701	phenolhydroxylase component	U32702	*Haemophilus influenzae*	909	47
ORF953	1019454	1019137	ORF	M63939	*Escherichia coli*	96	45
ORF954	1020764	1019562	pCTHom1 gene product	M94254	*Chlamydia trachomatis*	1185	65
ORF955	1021405	1021037	histone H1-like protein	M80324	*Chlamydia psittaci*	319	62
ORF956	1021821	1024286	phosphoprotein	L25078	*Chlamydia trachomatis*	739	41
ORF957	1024697	1024248	putative				
ORF958	1025569	1024508	protoporphyrinogen oxidase	U25114	*Mus musculus*	86	38
ORF959	1026969	1025590	oxygen independent coprophorphyrinogen III oxidase	D90912	*Synechocystis sp.*	880	42
ORF960	1027789	1026947	uroporphyrinogen decarboxylase	M97208	*Bacillus subtilis*	372	38
ORF961	1031199	1027945	transcription-repair coupling factor (trcF) (mfd)	U32805	*Haemophilus influenzae*	1584	42
ORF962	1031717	1031172	alanyl-tRNA synthetase	X95571	*Thiobacillus ferrooxidans*	76	31
ORF963	1033057	1031612	alanyl-tRNA synthetase	AE000353	*Escherichia coli*	889	40
ORF964	1033425	1033039	alanyl-tRNA synthetase (alaS)	AE000629	*Helicobacter pylori*	327	51
ORF965	1033784	1033200	alanyl-tRNA synthetase	X59956	*Rhizobium leguminosarum*	416	47
ORF966	1033963	1036038	transketolase	Z73234	*Bacillus subtilis*	1398	44
ORF967	1036945	1036010	AMP nucleosidase	AE000290	*Escherichia coli*	265	42
ORF968	1037110	1037679	elongation factor P	U14003	*Escherichia coli*	458	51
ORF969	1037696	1037944	putative				
ORF970	1038916	1037975	putative				
ORF971	1040582	1039026	HSP60 chaperonin	X62914	*Clostridium perfringens*	284	31

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF972	1040997	1042337	PROBABLE UDP-N-ACETYLMURAMOYLALANYL-D-GLUTAMYL-2, 6-DIAMINOLIGASE (EC 6.3.2.15).	AB001488	*Bacillus subtilis*	446	39
ORF973	1042357	1043403	ORF-Y (AA 1-360)	X51584	*Escherichia coli*	582	45
ORF974	1043367	1044623	UDP-N-acetylmuramoylalanine-D-glutamate ligase (murD)	U32793	*Haemophilus influenzae*	348	42
ORF975	1044607	1045362	hypothetical protein	Y14079	*Bacillus subtilis*	115	38
ORF976	1045384	1046538	spoVE gene product (AA 1-366)	X51419	*Bacillus subtilis*	479	35
ORF977	1046447	1047517	mur	Y13922	*Enterococcus hirae*	256	45
ORF978	1047521	1049956	UDP-N-acetylmuramate-alanine ligase (murC)	U32794	*Haemophilus influenzae*	756	38
ORF979	1050611	1050036	unknown	Z74024	*Mycobacterium tuberculosis*	78	44
ORF980	1050925	1050566	cycY gene product	U14003	*Escherichia coli*	179	34
ORF981	1051728	1051090	putative				
ORF982	1051743	1052063	hypothetical protein	D90908	*Synechocystis sp.*	135	33
ORF983	1052101	1053126	trna delta(2)-isopentenylpyrophosphate transferase	Z98209	*Mycobacterium tuberculosis*	441	37
ORF984	1054201	1053107	conserved hypothetical protein	AE000579	*Helicobacter pylori*	826	44
ORF985	1054242	1055555	putative				
ORF986	1055483	1055908	putative				
ORF987	1056609	1056965	YqeL	D84432	*Bacillus subtilis*	202	38
ORF988	1056961	1058232	beta-ketoacyl-ACP synthase	L13242	*Ricinus communis*	1266	55
ORF989	1058238	1058687	diadenosine tetraphosphatase	U30313	*Homo sapiens*	122	42
ORF990	1059371	1058727	inorganic pyrophosphatase (ppa)	AE000576	*Helicobacter pylori*	209	39
ORF991	1059526	1060578	leucine dehydrogenase LeuDH	U51099	*Bacillus cereus*	680	45
ORF992	1061553	1060579	3'(2'),5'-bisphosphate nucleotidase	U40433	*Arabidopsis thaliana*	335	43
ORF993	1061674	1062411	putative				
ORF994	1062377	1064077	2-acylglycerophosphoethanolamine acyl transferase/acyl carrier protein synthetase	U29581	*Escherichia coli*	383	44
ORF995	1064116	1065243	7-keto-8-aminopelargonic acid synthetase (bioF)	M29291	*Bacillus sphaericus*	200	35
ORF996	1067451	1065178	priA	Y10304	*Bacillus subtilis*	1009	43

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF997	1068065	1067376	putative				
ORF998	1068209	1068706	putative				
ORF999	1069958	1068819	unknown	U41759	*Chlamydia psittaci*	777	41
ORF1000	1071163	1070033	unknown	U41759	*Chlamydia psittaci*	381	36
ORF1001	1072438	1071332	unknown	U41759	*Chlamydia psittaci*	254	37
ORF1002	1072997	1073476	putative				
ORF1003	1074239	1075864	lysyl-tRNA synthetase	D90906	*Synechocystis sp.*	1007	48
ORF1004	1076790	1075867	cysteinyl-tRNA synthetase	L14580	*Bacillus subtilis*	395	52
ORF1005	1077268	1076573	cys-tRNA synthetase (cysS)	U32693	*Haemophilus influenzae*	431	56
ORF1006	1077999	1078724	putative				
ORF1007	1079088	1078672	ribonuclease P protein component (gtg start codon)	M11056	*Escherichia coli*	78	46
ORF1008	1079642	1079944	30S ribosomal subunit protein S14	U18997	*Escherichia coli*	260	50
ORF1009	1080501	1079995	F18C12.2	Z75536	*Caenorhabditis elegans*	118	38
ORF1010	1080775	1081341	putative				
ORF1011	1083158	1081350	deoxyribodipyrimidine photolyase	J03294	*Bacillus subtilis*	687	44
ORF1012	1084677	1083235	DNA mismatch repair protein	U71154	*Aquifex pyrophilus*	735	48
ORF1013	1085648	1084632	DNA mismatch repair protein	D90909	*Synechocystis sp.*	565	39
ORF1014	1086117	1086737	DNA primase (dnaG)	U32735	*Haemophilus influenzae*	303	40
ORF1015	1086692	1087897	DnaG	Z83860	*Mycobacterium tuberculosis*	222	37
ORF1016	1088646	1089005	putative				
ORF1017	1089146	1089805	putative				
ORF1018	1092931	1089890	glycyl-tRNA synthetase	U20547	*Chlamydia trachomatis*	2569	48
ORF1019	1093179	1092889	putative				
ORF1020	1093584	1094204	phosphatidylglycerophosphate synthase	U87792	*Bacillus subtilis*	163	55
ORF1021	1095619	1094192	glycogen (starch) synthase	D90899	*Synechocystis sp.*	574	40
ORF1022	1096074	1096628	partial ctc gene product (AA 1-186)	X16518	*Bacillus subtilis*	86	37
ORF1023	1096633	1097082	peptidyl-tRNA hydrolase	U31570	*Chlamydia trachomatis*	378	53
ORF1024	1097266	1097601	ribosomal protein S6 (rps6)	AE000630	*Helicobacter pylori*	179	39
ORF1025	1097622	1097867	ribosomal protein S18 homolog; putative	M62820	*Chlamydia trachomatis*	324	86
ORF1026	1097886	1098392	putative heat shock protein ORF; putative	M62820	*Chlamydia trachomatis*	190	79
ORF1027	1099521	1099279	putative				
ORF1028	1099689	1101053	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF1029	1102192	1101107	putative				
ORF1030	1104950	1102116	glycerol-3-phosphate acyltransferase	M80571	*Cucumis sativus*	574	43
ORF1031	1106508	1104946	ORF_f495; orfF of ECMRED, uses 2nd start	U18997	*Escherichia coli*	855	38
ORF1032	1106722	1107249	putative				
ORF1033	1107463	1108101	PlsX	U59433	*Bacillus subtilis*	282	45
ORF1034	1108041	1108421	fatty acid/phospholipid synthesis protein (plsX)	AE000540	*Helicobacter pylori*	205	35
ORF1035	1108520	1113370	putative 98 kDa outer membrane protein	U72499	*Chlamydia psittaci*	352	44
ORF1036	1114958	1113447	putative				
ORF1037	1116915	1115071	lipid A disaccharide synthetase (lpxB)	U32786	*Haemophilus influenzae*	477	42
ORF1038	1118183	1116894	poly(A) polymerase	AE000123	*Escherichia coli*	555	46
ORF1039	1118846	1120030	putative	L12968	*Escherichia coli*	880	50
ORF1040	1120040	1120522	glucosamine fructose-6-phosphate aminotransferase (isomerizing) (glmS)	AE000651	*Helicobacter pylori*	396	52
ORF1041	1120510	1121430	glutamine amidotransferase; glucosamine--fructose-6-phosphate aminotransferase	AE000450	*Escherichia coli*	494	44
ORF1042	1121321	1121866	L-glutamine:D-fructose-6-P amidotransferase precursor	U17352	*Thermus aquaticus thermophilus*	374	50
ORF1043	1122123	1122899	tyrosine-specific transport protein	AE000284	*Escherichia coli*	281	41
ORF1044	1124842	1125564	putative				
ORF1045	1126526	1125579	cell division protein (ftsY)	U32760	*Haemophilus influenzae*	497	41
ORF1046	1126519	1127676	succinyl-CoA synthetase beta-subunit	J01619	*Escherichia coli*	784	43
ORF1047	1127672	1128571	succinyl coenzyme A synthetase alpha subunit	U23408	*Dictyostelium discoideum*	978	63
ORF1048	1130230	1131336	putative				
ORF1049	1131480	1132553	putative				
ORF1050	1132830	1133843	putative				
ORF1051	1134121	1134855	serine protease HtrA	D90905	*Synechocystis sp.*	307	51
ORF1052	1134642	1135592	GsrA protein	D78376	*Yersinia enterocolitica*	497	41
ORF1053	1135964	1135653	putative				
ORF1054	1137132	1135954	R11H6.1	Z93386	*Caenorhabditis elegans*	445	37
ORF1055	1137169	1140102	Ydr430cp; CAI: 0.15	U33007	*Saccharomyces cerevisiae*	559	40

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF1056	1141365	1140112	hypothetical 54.7 kD protein in udp 3' region precursor (o475)	AE000459	*Escherichia coli*	222	34
ORF1057	1142150	1141356	phosphatidylserine synthase (pssA)	AE000614	*Helicobacter pylori*	307	41
ORF1058	1142520	1145660	ribonucleotide reductase subunit M1	K02927	*Mus musculus*	1433	45
ORF1059	1145627	1146721	ribonucleoside diphosphate reductase, beta subunit (nrdB)	AE000553	*Helicobacter pylori*	443	32
ORF1060	1146862	1147545	unknown	Z95398	*Mycobacterium leprae*	191	35
ORF1061	1147666	1148190	YtqB	AF008220	*Bacillus subtilis*	262	44
ORF1062	1148514	1148224	ORF2	U01958	*Bacillus licheniformis*	135	54
ORF1063	1149136	1148348	ORF2	M31827	*Bacillus subtilis*	268	40
ORF1064	1149702	1149166	putative				
ORF1065	1150031	1150591	unknown	Z85982	*Mycobacterium tuberculosis*	445	49
ORF1066	1150785	1151147	ribosomal protein L20 (AA 1-119)	X16188	*Bacillus stearothermophilus*	273	44
ORF1067	1151165	1152181	phenylalany-tRNA synthetase beta subunit	Z75208	*Bacillus subtilis*	777	40
ORF1068	1152522	1154591	putative				
ORF1069	1155666	1154566	putative				
ORF1070	1156743	1155670	putative				
ORF1071	1156859	1157815	hypothetical	U32723	*Haemophilus influenzae*	252	42
ORF1072	1157982	1160735	ATP-binding protein	U01376	*Escherichia coli*	1314	56
ORF1073	1162620	1160917	polynucleotide phosphorylase	AF010578	*Pisum sativum*	1416	52
ORF1074	1162970	1162590	polyribonucleotide phophorylase	U52048	*Spinacia oleracea*	312	53
ORF1075	1163532	1164020	orf150 gene product	X95938	*Porphyromonas gingivalis*	335	43
ORF1076	1163995	1164294	putative				
ORF1077	1165569	1165030	putative				
ORF1078	1166108	1165566	putative				
ORF1079	1166644	1166141	putative				
ORF1080	1167055	1168374	putative				
ORF1081	1169218	1168337	methionine aminopeptidase	D64003	*Synechocystis sp.*	488	54
ORF1082	1169823	1169218	ORF o197	U18997	*Escherichia coli*	281	30
ORF1083	1171324	1170572	putative				
ORF1084	1172085	1171177	hypothetical	U32720	*Haemophilus influenzae*	162	44
ORF1085	1172394	1173773	fumarase	D64000	*Synechocystis sp.*	1292	57
ORF1086	1175209	1173881	prs-associated putative membrane protein	U02424	*Escherichia coli*	570	39

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF1087	1175555	1175127	hypothetical protein in pth-prs intergenic region	AE000219	*Escherichia coli*	278	46
ORF1088	1175778	1177043	hypothetical protein	Z96072	*Mycobacterium tuberculosis*	109	43
ORF1089	1177177	1179048	putative				
ORF1090	1179156	1180085	penicillin tolerance protein (lytB)	U32781	*Haemophilus influenzae*	731	54
ORF1091	1180045	1180779	putative				
ORF1092	1181942	1180788	putative				
ORF1093	1182296	1181961	putative				
ORF1094	1183844	1182300	putative				
ORF1095	1184420	1183848	putative				
ORF1096	1185382	1184366	putative				
ORF1097	1185858	1185226	putative				
ORF1098	1186164	1186481	putative				
ORF1099	1187386	1186484	site-specific recombinase	U92524	*Salmonella typhimurium*	401	48
ORF1100	1187370	1189028	phophoglucoisomerase-like protein	L40822	*Chlamydia trachomatis*	1154	63
ORF1101	1189321	1190889	putative				
ORF1102	1191142	1192146	NADP-malate dehydrogenase	L40958	*Flaveria bidentis*	775	46
ORF1103	1191974	1191729	putative				
ORF1104	1193815	1192991	putative				
ORF1105	1195702	1194248	o460; This 460 aa orf is 46 pct identical (26 gaps) to 458 residues of an approx. 488 aa protein ARCD_PSEAE SW: P18275	AE000256	*Escherichia coli*	1022	44
ORF1106	1196303	1195716	putative				
ORF1107	1196831	1196337	putative				
ORF1108	1197807	1196746	putative				
ORF1109	1198740	1197883	putative				
ORF1110	1200232	1198721	shikimate 5-dehydrogenase	U67551	*Methanococcus jannaschii*	245	37
ORF1111	1201286	1200135	3-dehydroquinate synthase (aroB)	U32705	*Haemophilus influenzae*	478	45
ORF1112	1202386	1201259	2,3-dihydroxybenzoic acid	L29562	*Vibrio anguillarum*	780	50
ORF1113	1202901	1202350	putative				
ORF1114	1204162	1202816	5-enolpyruvylshikimate 3-phosphate synthase	U67500	*Methanococcus jannaschii*	520	40
ORF1115	1203177	1203464	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF1116	1205028	1204180	putative				
ORF1117	1206392	1204878	bioA gene product	A02587	*unidentified*	834	48
ORF1118	1206742	1206086	dethiobiotin synthase (bioD)	U32830	*Haemophilus influenzae*	243	37
ORF1119	1207872	1206724	L-alanine - pimelyl CoA ligase	U51868	*Bacillus subtilis*	601	41
ORF1120	1208852	1207851	biotin sythase	U24147	*Arabidopsis thaliana*	892	52
ORF1121	1210518	1209742	tryptophan hydroxylase	U26428	*Gallus gallus*	237	34
ORF1122	1210703	1211494	dihydrodipicolinate reductase	U47017	*Pseudomonas syringae pv. tabaci*	345	37
ORF1123	1211870	1212754	aspartate-semialdehyde dehydrogenase	U67476	*Methanococcus jannaschii*	444	43
ORF1124	1212742	1214064	aspartokinase III	U00006	*Escherichia coli*	473	47
ORF1125	1214046	1214858	dihydrodipicolinate synthase	D64006	*Synechocystis sp.*	238	40
ORF1126	1215551	1216318	putative				
ORF1127	1216493	1216849	putative				
ORF1128	1217183	1219612	putative				
ORF1129	1220068	1219673	putative				
ORF1130	1219710	1220669	putative				
ORF1131	1220630	1221376	putative				
ORF1132	1221645	1223681	unknown	D26185	*Bacillus subtilis*	621	43
ORF1133	1223894	1224988	putative				
ORF1134	1225000	1225830	high level kasgamycin resistance	D26185	*Bacillus subtilis*	422	41
ORF1135	1227810	1225879	hypothetical protein	D90903	*Synechocystis sp.*	1129	43
ORF1136	1226528	1226908	putative				
ORF1137	1229972	1228311	exonuclease VII, large subunit (xseA)	U32723	*Haemophilus influenzae*	666	46
ORF1138	47569	47018	Integrase/recombinase	AE001308	*Chlamydia trachomatis*	716	72
ORF1139	49980	49117	putative				
ORF1140	53356	52898	putative				
ORF1141	54477	54884	O-Sialoglycoprotein Endopeptidase	AE001307	*Chlamydia trachomatis*	311	51
ORF1142	63753	63998	PTS PEP Phosphotransferase	AE001306	*Chlamydia trachomatis*	198	61
ORF1143	77164	77487	putative				
ORF1144	79724	79302	Sms Protein	AE001302	*Chlamydia trachomatis*	458	57
ORF1145	88721	88951	putative				
ORF1146	94067	94429	putative				
ORF1147	122832	123341	hypothetical protein	AE001303	*Chlamydia trachomatis*	398	61
ORF1148	147536	147234	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF1149	158990	159346	S16 Ribosomal Protein	AE001277	*Chlamydia trachomatis*	467	78
ORF1150	168470	168979	putative				
ORF1151	169183	169452	putative				
ORF1152	171785	171504	Cationic Amino Acid Transporter	AE001278	*Chlamydia trachomatis*	262	68
ORF1153	172518	171775	Cationic Amino Acid Transporter	AE001278	*Chlamydia trachomatis*	533	48
ORF1154	193599	194045	putative				
ORF1155	195704	196075	S/T Protein Kinase	AE001288	*Chlamydia trachomatis*	536	82
ORF1156	210687	210145	KDO-transferase	X80061	*Chlamydia pneumoniae*	856	96
ORF1157	211100	210708	putative				
ORF1158	215420	215088	putative				
ORF1159	217914	218246	putative				
ORF1160	218925	218701	putative				
ORF1161	223785	223525	IMP dehydrogenase	U13372	*Borrelia burgdorferi*	270	63
ORF1162	224271	223999	putative				
ORF1163	228691	228407	putative				
ORF1164	235050	235334	(Methylase)	AE001287	*Chlamydia trachomatis*	331	66
ORF1165	252308	253021	Oligopeptide Permease	AE001293	*Chlamydia trachomatis*	838	72
ORF1166	258280	258912	Dicarboxylate Translocator	AE001294	*Chlamydia trachomatis*	909	80
ORF1167	261325	261567	putative				
ORF1168	268195	268878	hypothetical protein	AE001287	*Chlamydia trachomatis*	556	52
ORF1169	269447	268881	putative				
ORF1170	271263	271538	putative				
ORF1171	271957	272346	putative				
ORF1172	274176	274550	putative				
ORF1173	275736	275314	Disulfide bond Oxidoreductase	AE001291	*Chlamydia trachomatis*	519	73
ORF1174	276490	276927	hypothetical protein	AE001291	*Chlamydia trachomatis*	249	53
ORF1175	277577	277861	hypothetical protein	AE001291	*Chlamydia trachomatis*	256	52
ORF1176	288163	287909	putative				
ORF1177	290130	289789	putative				
ORF1178	290989	291225	putative				
ORF1179	291372	291860	adenylate cyclase	AE001286	*Chlamydia trachomatis*	388	48
ORF1180	311239	311622	putative				
ORF1181	328665	328384	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF1182	337348	338289	sodium-dependent transporter	AF017105	*Chlamydia psittaci*	1112	72
ORF1183	364764	364369	Prolipoprotein Diacylglycerol Transferase	AE001298	*Chlamydia trachomatis*	300	54
ORF1184	389623	390135	hypothetical protein	AE001282	*Chlamydia trachomatis*	75	33
ORF1185	393729	394343	ABC superfamily ATPase	AE001282	*Chlamydia trachomatis*	473	52
ORF1186	407379	407621	putative				
ORF1187	410944	410708	putative				
ORF1188	427632	427988	putative				
ORF1189	428172	428486	putative				
ORF1190	436761	437246	hypothetical protein	AE001279	*Chlamydia trachomatis*	661	81
ORF1191	460911	461159	putative				
ORF1192	477597	477313	hypothetical protein	AE001300	*Chlamydia trachomatis*	309	62
ORF1193	487303	487001	putative				
ORF1194	487764	487534	Glycine Cleavage System H Protein	AE001300	*Chlamydia trachomatis*	221	67
ORF1195	498502	499017	hypothetical protein	AE001275	*Chlamydia trachomatis*	206	32
ORF1196	499795	500466	putative				
ORF1197	571928	572344	putative				
ORF1198	572367	572131	putative				
ORF1199	588184	587915	hypothetical protein	AE001312	*Chlamydia trachomatis*	256	62
ORF1200	600587	600907	(Metalloenzyme)	AE001316	*Chlamydia trachomatis*	314	61
ORF1201	609731	608895	putative				
ORF1202	614039	614755	hypothetical protein	AE001317	*Chlamydia trachomatis*	475	46
ORF1203	614823	615152	putative				
ORF1204	638244	638831	ABC Transporter ATPase	AE001315	*Chlamydia trachomatis*	614	61
ORF1205	638819	639094	(Metal Transport Protein)	AE001315	*Chlamydia trachomatis*	265	63
ORF1206	639073	639636	(Metal Transport Protein)	AE001315	*Chlamydia trachomatis*	687	69
ORF1207	647901	648236	hypothetical protein	AE001317	*Chlamydia trachomatis*	139	38
ORF1208	678510	679469	phosphohydrolase	AE001320	*Chlamydia trachomatis*	995	63
ORF1209	688178	688732	hypothetical protein	AE001320	*Chlamydia trachomatis*	366	43
ORF1210	696045	696563	methyltransferase	AE001321	*Chlamydia trachomatis*	369	49
ORF1211	708998	708588	Glucose-1-P Adenyltransferase	AE001322	*Chlamydia trachomatis*	507	83
ORF1212	709808	710089	putative				
ORF1213	718240	717737	Glycerol-3-P Phosphatidyltransferase	AE001323	*Chlamydia trachomatis*	573	66
ORF1214	737828	737565	S19 Ribosomal Protein	AE001323	*Chlamydia trachomatis*	439	94

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF1215	779502	780257	hypothetical protein	AE001322	*Chlamydia trachomatis*	476	48
ORF1216	806310	805864	hypothetical protein	AE001337	*Chlamydia trachomatis*	512	67
ORF1217	820931	820707	putative				
ORF1218	837696	839096	Exodeoxyribonuclease V, Gamma	AE001334	*Chlamydia trachomatis*	967	49
ORF1219	883307	883549	putative				
ORF1220	892010	891726	putative				
ORF1221	893277	893564	putative				
ORF1222	936998	937225	Gen. Secretion Protein E	AE001327	*Chlamydia trachomatis*	256	67
ORF1223	946865	947419	putative				
ORF1224	975187	975411	SWF/SNF family helicase	AE001341	*Chlamydia trachomatis*	363	96
ORF1225	985882	985517	hypothetical protein	AE001342	*Chlamydia trachomatis*	166	33
ORF1226	987713	987180	hypothetical protein	AE001342	*Chlamydia trachomatis*	447	59
ORF1227	988215	987733	Flagellar M-Ring Protein	AE001342	*Chlamydia trachomatis*	304	44
ORF1228	988754	988530	Flagellar M-Ring Protein	AE001342	*Chlamydia trachomatis*	92	36
ORF1229	992542	992841	hypothetical protein	AE001343	*Chlamydia trachomatis*	112	39
ORF1230	992759	993067	hypothetical protein	AE001343	*Chlamydia trachomatis*	100	32
ORF1231	1004247	1004528	D-Ala/Gly Permease	AE001344	*Chlamydia trachomatis*	283	64
ORF1232	1015013	1014294	235aa long hypothetical protein	AB009472	*Pyrococcus horikoshii*	104	54
ORF1233	1056147	1056545	putative				
ORF1234	1077682	1078035	predicted disulfide bond isomerase	AE001351	*Chlamydia trachomatis*	233	46
ORF1235	1088121	1088381	putative				
ORF1236	1098430	1098852	Predicted Kinase	AE001352	*Chlamydia trachomatis*	384	59
ORF1237	1098798	1099319	Predicted Kinase	AE001352	*Chlamydia trachomatis*	322	45
ORF1238	1123198	1123515	Transport Permease	AE001354	*Chlamydia trachomatis*	313	72
ORF1239	1123606	1124256	Tyrosine Transport	AE001354	*Chlamydia trachomatis*	577	58
ORF1240	1124453	1124797	Tyrosine Transport	AE001354	*Chlamydia trachomatis*	323	50
ORF1241	1129253	1129567	putative				
ORF1242	1164947	1164474	hypothetical protein	AE001357	*Chlamydia trachomatis*	412	56
ORF1243	1170457	1170053	hypothetical protein	AE001358	*Chlamydia trachomatis*	283	59
ORF1244	1172342	1171863	ABC transporter permease	AE001358	*Chlamydia trachomatis*	457	55
ORF1245	1192155	1192835	putative				
ORF1246	1192759	1192992	putative				
ORF1247	1193861	1194142	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF1248	1194036	1193779	(D-Amino Acid Dehydrogenase)	AE001311	*Chlamydia trachomatis*	269	79
ORF1249	1209748	1209053	conserved hypothetical protein	AE000958	*Archaeoglobus fulgidus*	121	38
ORF1250	1215111	1215419	putative				
ORF1251	1216302	1216538	putative				
ORF1252	1228072	1227818	hypothetical protein	AE001306	*Chlamydia trachomatis*	134	39
ORF1253	1228304	1228080	xseB	AL021897	*Mycobacterium tuberculosis*	89	33
ORF1254	26599	26222	putative				
ORF1255	27609	27367	putative				
ORF1256	67206	66967	putative				
ORF1257	70612	70352	putative				
ORF1258	132703	132945	putative				
ORF1259	178073	178393	putative				
ORF1260	208576	208349	putative				
ORF1261	209156	208929	putative				
ORF1262	209263	209024	putative				
ORF1263	210304	210639	putative				
ORF1264	299009	299452	putative				
ORF1265	352106	351717	putative				
ORF1266	420182	419949	Flagellar Secretion Protein	AE001280	*Chlamydia trachomatis*	115	43
ORF1267	553602	553381	putative				
ORF1268	556538	556807	putative				
ORF1269	594348	593797	putative				
ORF1270	595169	594876	putative				
ORF1271	662148	662381	putative				
ORF1272	706528	706893	putative				
ORF1273	803315	803650	putative				
ORF1274	849551	849306	putative				
ORF1275	913676	913275	putative				
ORF1276	927087	926836	putative				
ORF1277	930587	930360	putative				
ORF1278	986531	986764	ORF 12	M72718	*Bacillus subtilis*	106	48
ORF1279	996229	996486	putative				
ORF1280	1000373	1000002	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF1281	1010291	1010037	putative				
ORF1282	1011128	1010793	106aa long hypothetical protein	AB009472	*Pyrococcus horikoshii*	159	50
ORF1283	1012924	1012694	putative				
ORF1284	1028659	1028913	putative				
ORF1285	1086481	1086762	putative				
ORF1286	1118658	1118879	Phosphoglucomutase	AE001354	*Chlamydia trachomatis*	291	84
ORF1287	1170098	1169835	hypothetical protein	AE001358	*Chlamydia trachomatis*	187	53
ORF1288	1180828	1181184	putative				
ORF1289	1182658	1183035	putative				
ORF1290	1195076	1194795	putative				
ORF1291	1195890	1196183	putative				

Table 2

ORF Nos	begin	end	potential start
2	42	794	42
3	1258	1614	1261
4	1807	2418	1807
5	3393	2491	3393
6	3639	4067	3639
7	5649	4270	5649
8	7463	6012	7463
9	8051	8962	8051
10	9129	9959	9138
11	10687	10361	10639
12	10927	11232	10927
13	11246	12727	11246
14	12691	14190	12691
15	14484	17249	14484
16	16039	15770	16036
17	17845	20853	17845
18	21137	22042	21137
19	22046	23476	22046
20	23681	26110	23681
21	26109	25861	26109
22	26241	26978	26241
23	26960	27754	26960
24	27747	28577	27747
25	28887	29492	28950
26	29432	30028	29432
27	30024	31472	30024
28	31758	32288	31758
29	32201	33991	32201
30	33852	34541	33852
31	34783	36063	34783
32	36009	37529	36009
33	37881	39362	37881
34	39418	39161	39418

ORF Nos	begin	end	potential start
35	39366	40715	39366
36	43076	41094	43076
37	43800	43066	43800
38	44828	43785	44768
39	45340	44753	45340
40	45752	45372	45752
41	46996	45701	46996
42	47961	47569	47961
43	48960	48040	48960
44	51452	50133	51452
45	52606	51335	52606
46	53684	53319	53684
47	54195	53746	54195
48	55278	56453	55278
49	56493	57266	56493
50	57297	58526	57297
51	59851	58565	59851
52	61495	59924	61495
53	61324	62151	61324
54	62132	62470	62132
55	62474	63733	62474
56	63881	64186	63881
57	64611	64318	64611
58	65485	64673	65485
59	65999	65301	65999
60	66244	67281	66244
61	67265	67699	67265
62	67703	68539	67760
63	68805	70736	68805
64	69172	68831	69172
65	70642	71142	70642
66	71325	72029	71325
67	72060	73637	72060
68	74061	76175	74061

ORF Nos	begin	end	potential start
69	78351	77680	78351
70	79356	78355	79356
71	79983	79693	79983
72	80441	79938	80441
73	80475	80969	80475
74	81296	83080	81332
75	83291	83932	83291
76	84005	84769	84005
77	84975	85244	84975
78	85123	85425	85123
79	85397	85903	85397
80	85909	86583	85909
81	86626	88065	86626
82	89257	91026	89257
83	91291	93030	91291
84	93295	94086	93295
85	95285	94707	95279
86	95667	96557	95667
87	96317	97456	96317
88	98435	97968	98435
89	99460	98426	99460
90	100144	101325	100144
91	101457	101720	101457
92	101704	102273	101704
93	102356	102805	102356
94	102835	103530	102835
95	103549	104058	103549
96	104096	104491	104096
97	104601	108386	104601
98	108401	112054	108401
99	112033	112590	112033
100	112672	113682	112672
101	113726	114121	113726
102	114711	114136	114711

ORF Nos	begin	end	potential start
103	115267	115755	115267
104	115911	116543	115911
105	116736	118055	116778
106	117968	118522	117968
107	118530	119843	118530
108	119816	120457	119816
109	120451	122430	120451
110	122504	122950	122504
111	123528	126347	123528
112	126332	129166	126332
113	134690	129213	134690
114	134925	136382	134931
115	137870	136482	137867
116	137899	138240	137899
117	138239	137928	138239
118	139558	138257	139558
119	140352	139516	140352
120	140498	141841	140498
121	141855	142658	141855
122	144258	143050	144258
123	145258	144494	145258
124	145454	146749	145454
125	147318	146767	147318
126	148261	147677	148261
127	149029	152157	149029
128	154108	152201	154108
129	155135	154308	155135
130	155141	155467	155141
131	155703	156779	155703
132	156748	157635	156748
133	157653	158996	157653
134	159363	159986	159363
135	159880	160446	159880
136	160477	160839	160477

ORF Nos	begin	end	potential start
137	160898	161539	160898
138	161527	162153	161527
139	162144	162443	162144
140	162437	164098	162437
141	165451	164228	165451
142	166349	165411	166349
143	166949	168442	166949
144	169416	171029	169416
145	170857	171459	170857
146	172652	173428	172652
147	174626	173439	174626
148	174816	175613	174816
149	175598	175954	175598
150	175958	176935	175958
151	177708	176938	177708
152	177128	177376	177128
153	179472	177841	179472
154	179822	179517	179822
155	181793	179943	181793
156	182628	181876	182628
157	184420	183074	184420
158	184988	184467	184988
159	185483	185112	185483
160	185902	185483	185902
161	186174	185839	186174
162	187720	186587	187720
163	188318	190933	188318
164	191090	191635	191090
165	191547	192743	191547
166	192969	193469	192969
167	194044	193610	194044
168	194196	195809	194196
169	196088	198073	196088
170	198132	199454	198132

ORF Nos	begin	end	potential start
171	199351	202818	199351
172	204552	202999	204552
173	205648	204692	205639
174	205807	207327	205807
175	207182	207775	207182
176	207779	208267	207779
177	208267	209577	208267
178	211807	211271	211807
179	212188	211844	212188
180	214079	212448	214079
181	214907	214083	214907
182	216154	215429	216154
183	216115	216678	216115
184	216728	217282	216728
185	217267	217866	217267
186	218593	218261	218590
187	219821	218994	219821
188	221382	220309	221382
189	222719	221433	222719
190	223521	222724	223521
191	224499	225008	224499
192	225140	225559	225140
193	225555	226802	225555
194	227800	226892	227743
195	228335	228072	228335
196	229251	228643	229251
197	230983	229622	230983
198	231483	230983	231483
199	232063	231509	232063
200	232739	232053	232739
201	233166	234356	233166
202	233518	233165	233518
203	234536	235186	234536
204	235379	236689	235379

ORF Nos	begin	end	potential start
205	236680	237618	236689
206	237521	238345	237521
207	238281	238973	238281
208	238871	240115	238871
209	240191	241564	240191
210	242281	241604	242281
211	242933	242274	242933
212	243416	242976	243416
213	243500	244531	243500
214	244480	246021	244480
215	246330	247811	246330
216	247831	249174	247870
217	249437	251038	249455
218	251325	252212	251325
219	253156	254007	253156
220	253974	254852	253974
221	255258	256094	255258
222	256640	257455	256640
223	257502	258239	257502
224	257869	257501	257869
225	259248	260897	259248
226	262753	261788	262753
227	263059	262757	263059
228	264375	263182	264375
229	265985	264747	265985
230	266637	266059	266637
231	267338	266538	267338
232	267922	267473	267922
233	269647	270771	269647
234	272777	273145	272777
235	273253	273636	273253
236	273705	273977	273705
237	276016	275717	276016
238	276439	276020	276418

ORF Nos	begin	end	potential start
239	276792	277253	276792
240	277318	277599	277318
241	278578	277877	278578
242	279258	278554	279258
243	280435	279533	280435
244	281547	280849	281547
245	281696	282325	281717
246	282459	284069	282459
247	284056	284517	284056
248	284606	285775	284606
249	285592	285987	285592
250	286179	286976	286179
251	287583	287002	287583
252	287951	287451	287951
253	288499	288816	288499
254	289674	288505	289674
255	288839	289213	288839
256	289970	290254	289970
257	291931	292803	291931
258	293258	292755	293258
259	293718	293272	293718
260	294630	293953	294630
261	296153	294636	296153
262	294817	295068	294817
263	296354	297862	296354
264	298415	297879	298415
265	298777	298253	298777
266	299572	298781	299572
267	300487	299633	300487
268	301586	300702	301568
269	302440	301571	302440
270	302838	302437	302838
271	303335	302745	303335
272	304394	303852	304394

ORF Nos	begin	end	potential start
273	304606	305223	304606
274	305394	306236	305394
275	306501	307439	306501
276	308033	307458	308033
277	308924	308037	308924
278	309485	310180	309485
279	310426	311214	310426
280	311597	311253	311504
281	312772	311780	312772
282	313425	312772	313425
283	313646	313377	313646
284	313937	314665	313937
285	315576	314755	315576
286	316157	315531	316157
287	318657	316156	318657
288	321042	318676	321042
289	321445	321098	321445
290	322309	321710	322309
291	323190	322366	323181
292	323843	323181	323843
293	324878	323856	324878
294	325340	326410	325340
295	326433	327836	326433
296	328465	327839	328465
297	329360	328857	329360
298	330907	329357	330907
299	332455	330956	332455
300	334536	332395	334536
301	336091	334877	336091
302	336103	337302	336103
303	338129	338830	338129
304	338965	339501	338965
305	339508	340143	339508
306	340247	342967	340247

ORF Nos	begin	end	potential start
307	343385	343810	343385
308	344171	343935	344171
309	345082	344330	345073
310	346005	345082	346005
311	346784	346437	346784
312	347029	346715	347029
313	347034	347723	347034
314	348075	350459	348075
315	350598	351071	350598
316	351075	352175	351096
317	353291	352230	353267
318	353442	354467	353442
319	354451	354933	354451
320	355000	355449	355000
321	355448	356743	355448
322	355953	355642	355953
323	359310	356827	359310
324	359120	359377	359120
325	359525	359908	359525
326	361290	359947	361290
327	363785	361362	363746
328	364496	363888	364496
329	364832	365290	364832
330	365304	365669	365304
331	366599	365667	366599
332	367291	369030	367291
333	369134	369808	369134
334	369917	370438	369917
335	370365	372647	370365
336	372557	373066	372557
337	373020	373442	373020
338	373467	374195	373467
339	374176	375099	374176
340	375676	375083	375676

ORF Nos	begin	end	potential start
341	376173	375634	376173
342	376564	377643	376564
343	377956	379773	377956
344	379781	380425	379805
345	380281	381000	380281
346	381008	381460	381008
347	381460	383037	381460
348	383257	383523	383257
349	383553	385304	383553
350	385397	386458	385400
351	387242	386514	387242
352	388764	387013	388764
353	390120	390932	390120
354	390919	391818	390961
355	392379	391885	392379
356	392582	392986	392582
357	392776	393684	392776
358	394151	394804	394151
359	394928	395308	394928
360	395259	395990	395259
361	397815	395953	397815
362	398850	397831	398850
363	400085	399099	400085
364	401245	400073	401236
365	401474	401136	401474
366	402199	401423	402199
367	403193	402186	403166
368	403650	404165	403650
369	404343	405914	404343
370	405984	407327	405984
371	407712	408806	407712
372	410439	409075	410439
373	411826	410954	411826
374	412482	414302	412482

ORF Nos	begin	end	potential start
375	415402	414407	415402
376	415848	415237	415848
377	417131	415866	417131
378	417258	417566	417258
379	418326	417454	418326
380	420057	418426	420057
381	420448	420720	420448
382	420980	421552	420980
383	421556	422029	421556
384	422461	422925	422461
385	423562	424320	423562
386	424250	424591	424250
387	424830	426047	424830
388	426240	427397	426240
389	428841	430703	428841
390	430694	431446	430694
391	431597	432100	431597
392	432165	432779	432165
393	433272	432832	433272
394	433925	433227	433922
395	436678	433934	436678
396	437176	438357	437176
397	440317	438518	440317
398	440001	440345	440001
399	441233	440517	441233
400	440719	441012	440719
401	442192	441230	442192
402	442888	442343	442888
403	442371	442961	442371
404	443578	443003	443578
405	444500	443526	444500
406	444842	444528	444842
407	445009	444743	445009
408	445718	445182	445718

ORF Nos	begin	end	potential start
409	445807	447804	445807
410	448738	447803	448738
411	449628	448618	449628
412	450298	450867	450298
413	450713	451207	450713
414	451211	452452	451211
415	452448	453659	452448
416	454843	453725	454843
417	455608	454865	455608
418	456243	457007	456243
419	457016	457708	457016
420	458368	457979	458368
421	459496	458372	459496
422	459493	460194	459493
423	461446	460355	461446
424	462298	461450	462298
425	462444	463349	462444
426	464241	463342	464241
427	464574	465065	464574
428	465129	465611	465129
429	465571	466317	465571
430	466317	467093	466317
431	466999	467502	466999
432	469691	467715	469691
433	470691	469660	470691
434	472010	470709	472010
435	471545	471799	471545
436	472359	472045	472359
437	473523	472732	473523
438	474889	473441	474889
439	477323	475365	477323
440	478496	477597	478496
441	478722	479273	478722
442	479277	479705	479277

ORF Nos	begin	end	potential start
443	480050	481450	480050
444	481469	482053	481469
445	482600	482025	482600
446	482654	484204	482654
447	484211	485170	484211
448	485170	485838	485170
449	485813	486580	485813
450	486976	486638	486976
451	489071	487764	489071
452	489341	489090	489341
453	489958	489152	489958
454	490549	489962	490549
455	491163	490522	491163
456	491396	491112	491396
457	492121	491390	492121
458	492304	494838	492304
459	495943	494822	495943
460	496011	496565	496170
461	496569	497228	496569
462	497358	497834	497358
463	497770	498327	497770
464	499209	499589	499209
465	499520	499792	499520
466	500774	504169	500774
467	504139	504600	504139
468	504865	506877	504865
469	506790	507671	506790
470	507718	510507	507718
471	508325	507912	508325
472	510660	513440	510660
473	514965	513787	514920
474	517347	515419	517347
475	517058	517363	517058
476	517798	517277	517798

ORF Nos	begin	end	potential start
477	518200	517847	518200
478	518300	521146	518363
479	521392	522948	521407
480	523244	524809	523322
481	524379	524125	524379
482	524649	526238	524649
483	526265	527104	526268
484	526947	526702	526947
485	526975	528450	526975
486	528408	529199	528408
487	530612	529542	530612
488	531656	530616	531656
489	533974	532067	533974
490	536432	534324	536432
491	537150	536707	537150
492	537928	537080	537928
493	538438	537932	538438
494	538737	538333	538737
495	539594	539127	539594
496	541215	539590	541215
497	542571	541282	542571
498	543014	542457	543014
499	543369	542962	543369
500	543809	546628	543815
501	546619	549525	546619
502	547293	546994	547293
503	549699	550523	549699
504	550490	551551	550490
505	551448	552623	551448
506	552652	555117	552652
507	555029	555493	555029
508	558006	555673	558006
509	559694	558162	559694
510	558208	558573	558208

ORF Nos	begin	end	potential start
511	561692	559899	561692
512	561412	561708	561412
513	563942	561777	563942
514	564969	563950	564969
515	566204	564936	566198
516	567717	566302	567717
517	568526	567708	568526
518	569467	568742	569467
519	571065	569431	571065
520	571828	571118	571783
521	572202	573308	572202
522	573146	575056	573146
523	575023	575916	575023
524	577891	576497	577891
525	578914	578204	578914
526	579924	578857	579924
527	580187	579858	580187
528	580017	580406	580017
529	581086	580187	581086
530	581367	581828	581367
531	581678	582367	581678
532	582361	583428	582361
533	584690	583431	584690
534	585237	584950	585237
535	585626	586888	585626
536	586846	587907	586888
537	589049	588180	589049
538	590500	589301	590455
539	590755	592458	590755
540	592526	592903	592526
541	592836	593747	592836
542	593747	594298	593747
543	594331	595947	594331
544	595905	596309	595905

ORF Nos	begin	end	potential start
545	596514	597215	596514
546	597184	597957	597184
547	597755	598612	597755
548	598602	599204	598602
549	599373	599939	599373
550	600903	602072	600903
551	602240	602587	602240
552	602637	603272	602637
553	603142	604512	603142
554	604627	605853	604627
555	605790	606620	605790
556	606571	607281	606571
557	609004	607355	609004
558	610906	609932	610906
559	611786	611004	611786
560	612333	611746	612333
561	613897	612341	613897
562	615179	616279	615179
563	616610	617383	616610
564	618796	617810	618796
565	620004	618826	620004
566	619649	619918	619649
567	621265	620021	621265
568	622359	621265	622359
569	623420	622560	623420
570	624297	623335	624297
571	624773	624174	624773
572	625029	625484	625029
573	625488	625883	625488
574	625892	626395	625892
575	626444	627790	626444
576	627912	628607	627930
577	628774	629697	628774
578	629660	631639	629660

ORF Nos	begin	end	potential start
579	631725	633551	631725
580	633520	636957	633520
581	637232	638098	637232
582	640648	639593	640648
583	640979	640728	640979
584	641327	641007	641327
585	641687	642283	641687
586	643023	642286	643023
587	643330	643076	643330
588	643704	643351	643704
589	645628	643676	645628
590	645783	645538	645756
591	646269	645793	646269
592	646751	646314	646751
593	647848	647045	647848
594	648393	650336	648393
595	651016	650420	651007
596	652956	651289	652956
597	653395	653126	653395
598	655740	654193	655740
599	656508	655966	656508
600	658140	657022	658140
601	660216	658525	660216
602	663238	660248	663238
603	664461	663157	664452
604	665735	664635	665735
605	666212	666994	666212
606	666998	667921	666998
607	667909	668568	667909
608	668502	669203	668502
609	669154	670893	669175
610	672226	670853	672226
611	671137	671424	671137
612	672453	673001	672453

ORF Nos	begin	end	potential start
613	673072	674721	673072
614	674549	674262	674549
615	675518	674796	675518
616	676083	675499	676083
617	676630	676067	676630
618	677016	676600	677016
619	677647	677015	677647
620	677990	678259	677990
621	679444	680097	679444
622	680097	680897	680097
623	681637	680849	681637
624	681409	682281	681409
625	682453	682821	682453
626	682763	683902	682763
627	684616	683969	684616
628	685169	684534	685169
629	685986	685117	685986
630	686278	687288	686278
631	687483	688151	687483
632	688740	689501	688740
633	690242	689622	690242
634	690470	691126	690470
635	692600	691497	692600
636	692674	695064	692674
637	695049	696032	695064
638	697964	696585	697964
639	699803	698274	699803
640	701926	699788	701926
641	703196	702567	703196
642	704221	703208	704221
643	704240	705289	704240
644	706070	705300	706070
645	706841	706254	706838
646	707596	706811	707596

ORF Nos	begin	end	potential start
647	708666	707677	708666
648	709793	709119	709793
649	711523	710132	711523
650	712236	711523	712236
651	714734	712125	714734
652	715759	714761	715759
653	717538	715886	717538
654	719113	720243	719113
655	720590	722422	720590
656	722406	723056	722406
657	723551	723120	723551
658	724246	723626	724246
659	724754	724251	724754
660	725868	724900	725868
661	727115	726270	727115
662	728126	727119	728126
663	728594	728208	728594
664	729614	728604	729614
665	729778	729533	729778
666	730149	729751	730149
667	730539	730174	730539
668	731983	730598	731983
669	732427	731996	732427
670	732917	732423	732917
671	733598	733320	733598
672	733869	733492	733869
673	734298	733900	734298
674	734858	734319	734858
675	735195	734863	735195
676	735578	735342	735578
677	735861	735604	735861
678	736492	736079	736492
679	737192	736524	737192
680	737555	737211	737555

ORF Nos	begin	end	potential start
681	738688	737837	738688
682	739048	738713	739048
683	739736	739065	739736
684	740477	739773	740477
685	740659	740958	740659
686	741722	740721	741722
687	742789	741827	742789
688	743618	742782	743618
689	744092	743634	744092
690	744604	744107	744604
691	744953	744498	744953
692	746608	744986	746608
693	747085	746621	747085
694	747974	747219	747974
695	748594	748169	748594
696	749145	748573	749145
697	749652	749957	749652
698	750446	749979	750446
699	751219	750446	751219
700	753042	751291	753042
701	754309	753020	754309
702	755120	756175	755120
703	756120	756485	756120
704	756499	760227	756499
705	761217	760297	761178
706	761297	761809	761330
707	761782	762282	761782
708	762260	762895	762299
709	762867	763316	762867
710	763780	763325	763780
711	763861	765168	763861
712	766809	765697	766809
713	768051	766888	768051
714	768566	768321	768566

ORF Nos	begin	end	potential start
715	769342	768551	769342
716	770532	769378	770532
717	771451	770804	771451
718	773058	771847	773058
719	773094	773456	773094
720	774376	773093	774376
721	775123	774380	775123
722	775398	774916	775398
723	775046	776077	775046
724	776070	777041	776070
725	777964	777536	777964
726	778176	777904	778176
727	778621	779334	778684
728	781173	780307	781173
729	781526	781116	781526
730	782784	781555	782784
731	783572	782805	783572
732	785032	783581	785032
733	786412	785360	786412
734	788429	786450	788429
735	788944	788528	788944
736	789758	788901	789758
737	790332	791504	790338
738	791846	792721	791846
739	792724	793569	792724
740	793580	794323	793580
741	794304	794843	794304
742	795217	795732	795217
743	795722	796795	795722
744	798735	797053	798735
745	799823	798681	799823
746	799297	799578	799297
747	801313	799808	801313
748	802453	801332	802453

ORF Nos	begin	end	potential start
749	803299	802457	803299
750	803811	803290	803811
751	805151	803826	805151
752	805860	805156	805860
753	806604	806332	806604
754	806913	806608	806913
755	808222	806903	808222
756	808751	808146	808751
757	809437	808673	809437
758	809939	809454	809939
759	811235	810213	811235
760	811779	813056	811779
761	812890	812516	812890
762	812954	813583	812954
763	813587	815023	813587
764	815420	815746	815420
765	816036	817010	816036
766	817111	817356	817111
767	817791	818609	817797
768	818609	819094	818609
769	819104	819823	819104
770	820722	819826	820722
771	822313	821000	822313
772	823503	822238	823503
773	823678	825612	823678
774	825461	826312	825461
775	827280	826645	827280
776	828604	827171	828604
777	830026	828713	830026
778	831047	830085	831047
779	831725	831051	831725
780	832220	833098	832220
781	833851	833396	833851
782	834068	835039	834068

ORF Nos	begin	end	potential start
783	835792	835127	835792
784	837624	836116	837624
785	838951	840882	838951
786	840869	842185	840869
787	841989	843455	841989
788	843242	844021	843242
789	845018	843987	844997
790	846174	844990	846174
791	848509	846311	848509
792	848568	849014	848568
793	849082	850488	849088
794	851512	850574	851512
795	852064	852447	852064
796	852398	853690	852398
797	855118	854243	855118
798	855751	855128	855751
799	856551	855829	856551
800	856730	858556	856730
801	858717	859601	858717
802	859591	860205	859591
803	861132	860284	861132
804	861426	861163	861426
805	861701	862921	861701
806	863026	864798	863026
807	864831	865256	864831
808	865226	866581	865226
809	866562	867119	866562
810	867025	867816	867025
811	867820	868497	867820
812	869743	868661	869743
813	870633	870094	870633
814	871929	870646	871929
815	872538	872086	872538
816	873908	872517	873908

ORF Nos	begin	end	potential start
817	874281	874670	874281
818	874582	875286	874582
819	877857	875377	877857
820	878446	879255	878446
821	880635	879268	880635
822	882524	880593	882524
823	882612	883319	882612
824	884155	883538	884155
825	884340	885611	884343
826	885722	887302	885722
827	887587	888153	887587
828	888627	888220	888627
829	889330	888716	889330
830	889898	889323	889898
831	891190	889898	891190
832	891828	891247	891828
833	892421	892017	892421
834	893116	892421	893116
835	892521	892925	892521
836	893392	895419	893392
837	895745	896527	895745
838	896668	897558	896668
839	897565	899442	897565
840	899420	900229	899420
841	903230	900237	903230
842	905081	903234	905081
843	906931	905045	906931
844	907248	907832	907299
845	907784	908128	907784
846	908132	908677	908132
847	908589	909320	908589
848	909405	911465	909405
849	911677	912360	911725
850	912303	912821	912303

ORF Nos	begin	end	potential start
851	912937	913983	912937
852	915128	914067	915128
853	916658	915303	916658
854	915627	915376	915627
855	917707	916853	917707
856	918837	917722	918837
857	919868	918837	919868
858	920434	919880	920434
859	921187	920438	921187
860	921959	921195	921959
861	923773	921995	923773
862	922146	922415	922146
863	923943	923674	923943
864	924077	925006	924077
865	925436	925083	925436
866	926524	925349	926524
867	927920	926433	927920
868	928319	927951	928319
869	928963	928334	928963
870	929248	930987	929248
871	930995	932059	930995
872	932121	933515	932175
873	932881	932513	932881
874	933485	935746	933485
875	935724	937082	935724
876	937229	938410	937229
877	938281	938805	938281
878	938809	939255	938824
879	939165	939782	939165
880	939760	940791	939790
881	940822	941106	940822
882	940977	941351	940977
883	942537	941623	942429
884	942784	942500	942763

ORF Nos	begin	end	potential start
885	943149	942799	943149
886	943799	943029	943799
887	944055	943732	944055
888	944413	943994	944404
889	945395	944556	945395
890	945853	945389	945853
891	946392	945751	946392
892	947410	948081	947431
893	949871	948915	949871
894	951058	949868	951058
895	951249	950959	951249
896	951664	952134	951664
897	952674	952165	952674
898	953491	952589	953491
899	955324	953495	955324
900	955823	955281	955823
901	957082	955847	957082
902	957902	957270	957902
903	959231	957906	959231
904	959376	960284	959376
905	960266	961669	960347
906	961856	964765	961856
907	966855	965395	966855
908	968204	966975	968204
909	968791	968237	968791
910	969498	968731	969498
911	969858	969511	969858
912	970118	969762	970118
913	970593	970300	970593
914	971261	970542	971261
915	971680	971123	971680
916	971876	975100	971876
917	975419	976516	975419
918	976584	978320	976584

ORF Nos	begin	end	potential start
919	977680	977231	977680
920	978399	980738	978399
921	980756	981928	980756
922	982974	981931	982962
923	984120	983119	984120
924	985502	984120	985502
925	987180	985882	987180
926	987172	987444	987172
927	989846	989049	989846
928	991048	989846	991048
929	991638	990955	991638
930	991794	992498	991794
931	993619	993041	993619
932	993530	994792	993548
933	995970	994795	995970
934	996857	995739	996857
935	997603	996782	997603
936	998969	997572	998969
937	998896	1000023	998896
938	1000087	1001340	1000087
939	1001357	1001818	1001357
940	1003288	1001873	1003288
941	1003487	1004146	1003496
942	1004485	1005639	1004689
943	1005643	1005972	1005643
944	1006784	1006116	1006784
945	1007563	1006769	1007563
946	1009226	1007568	1009226
947	1009989	1009336	1009989
948	1015852	1016337	1015852
949	1016561	1016181	1016561
950	1016297	1017532	1016297
951	1016802	1016452	1016802
952	1018993	1017701	1018993

ORF Nos	begin	end	potential start
953	1019454	1019137	1019454
954	1020764	1019562	1020764
955	1021405	1021037	1021405
956	1021821	1024286	1021821
957	1024697	1024248	1024697
958	1025569	1024508	1025551
959	1026969	1025590	1026969
960	1027789	1026947	1027789
961	1031199	1027945	1031199
962	1031717	1031172	1031717
963	1033057	1031612	1033057
964	1033425	1033039	1033425
965	1033784	1033200	1033784
966	1033963	1036038	1033963
967	1036945	1036010	1036945
968	1037110	1037679	1037110
969	1037696	1037944	1037696
970	1038916	1037975	1038916
971	1040582	1039026	1040582
972	1040997	1042337	1040997
973	1042357	1043403	1042357
974	1043367	1044623	1043367
975	1044607	1045362	1044607
976	1045384	1046538	1045384
977	1046447	1047517	1046447
978	1047521	1049956	1047521
979	1050611	1050036	1050611
980	1050925	1050566	1050925
981	1051728	1051090	1051728
982	1051743	1052063	1051743
983	1052101	1053126	1052101
984	1054201	1053107	1054201
985	1054242	1055555	1054242
986	1055483	1055908	1055483

ORF Nos	begin	end	potential start
987	1056609	1056965	1056609
988	1056961	1058232	1056985
989	1058238	1058687	1058238
990	1059371	1058727	1059371
991	1059526	1060578	1059526
992	1061553	1060579	1061553
993	1061674	1062411	1061674
994	1062377	1064077	1062377
995	1064116	1065243	1064116
996	1067451	1065178	1067451
997	1068065	1067376	1068065
998	1068209	1068706	1068230
999	1069958	1068819	1069958
1000	1071163	1070033	1071163
1001	1072438	1071332	1072438
1002	1072997	1073476	1072997
1003	1074239	1075864	1074239
1004	1076790	1075867	1076790
1005	1077268	1076573	1077268
1006	1077999	1078724	1077999
1007	1079088	1078672	1079088
1008	1079642	1079944	1079642
1009	1080501	1079995	1080468
1010	1080775	1081341	1080775
1011	1083158	1081350	1083158
1012	1084677	1083235	1084677
1013	1085648	1084632	1085648
1014	1086117	1086737	1086117
1015	1086692	1087897	1086692
1016	1088646	1089005	1088646
1017	1089146	1089805	1089146
1018	1092931	1089890	1092931
1019	1093179	1092889	1093179
1020	1093584	1094204	1093584

ORF Nos	begin	end	potential start
1021	1095619	1094192	1095619
1022	1096074	1096628	1096074
1023	1096633	1097082	1096633
1024	1097266	1097601	1097266
1025	1097622	1097867	1097622
1026	1097886	1098392	1097886
1027	1099521	1099279	1099521
1028	1099689	1101053	1099704
1029	1102192	1101107	1102192
1030	1104950	1102116	1104950
1031	1106508	1104946	1106508
1032	1106722	1107249	1106722
1033	1107463	1108101	1107463
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1035	1108520	1113370	1108520
1036	1114958	1113447	1114958
1037	1116915	1115071	1116915
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1040	1120040	1120522	1120040
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1045	1126526	1125579	1126526
1046	1126519	1127676	1126519
1047	1127672	1128571	1127672
1048	1130230	1131336	1130230
1049	1131480	1132553	1131480
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1051	1134121	1134855	1134121
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1053	1135964	1135653	1135964
1054	1137132	1135954	1137132

ORF Nos	begin	end	potential start
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1056	1141365	1140112	1141344
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1058	1142520	1145660	1142520
1059	1145627	1146721	1145627
1060	1146862	1147545	1146862
1061	1147666	1148190	1147666
1062	1148514	1148224	1148514
1063	1149136	1148348	1149136
1064	1149702	1149166	1149702
1065	1150031	1150591	1150031
1066	1150785	1151147	1150785
1067	1151165	1152181	1151165
1068	1152522	1154591	1152522
1069	1155666	1154566	1155666
1070	1156743	1155670	1156740
1071	1156859	1157815	1156859
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1073	1162620	1160917	1162620
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1075	1163532	1164020	1163532
1076	1163995	1164294	1163995
1077	1165569	1165030	1165569
1078	1166108	1165566	1166108
1079	1166644	1166141	1166644
1080	1167055	1168374	1167055
1081	1169218	1168337	1169218
1082	1169823	1169218	1169823
1083	1171324	1170572	1171324
1084	1172085	1171177	1172085
1085	1172394	1173773	1172394
1086	1175209	1173881	1175209
1087	1175555	1175127	1175360
1088	1175778	1177043	1175778

ORF Nos	begin	end	potential start
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1090	1179156	1180085	1179156
1091	1180045	1180779	1180045
1092	1181942	1180788	1181942
1093	1182296	1181961	1182296
1094	1183844	1182300	1183844
1095	1184420	1183848	1184420
1096	1185382	1184366	1185382
1097	1185858	1185226	1185858
1098	1186164	1186481	1186185
1099	1187386	1186484	1187386
1100	1187370	1189028	1187370
1101	1189321	1190889	1189321
1102	1191142	1192146	1191142
1103	1191974	1191729	1191974
1104	1193815	1192991	1193815
1105	1195702	1194248	1195702
1106	1196303	1195716	1196303
1107	1196831	1196337	1196831
1108	1197807	1196746	1197651
1109	1198740	1197883	1198668
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1111	1201286	1200135	1201286
1112	1202386	1201259	1202350
1113	1202901	1202350	1202901
1114	1204162	1202816	1204162
1115	1203177	1203464	1203177
1116	1205028	1204180	1205028
1117	1206392	1204878	1206392
1118	1206742	1206086	1206742
1119	1207872	1206724	1207872
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1122	1210703	1211494	1210703

ORF Nos	begin	end	potential start
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1124	1212742	1214064	1212742
1125	1214046	1214858	1214046
1126	1215551	1216318	1215551
1127	1216493	1216849	1216493
1128	1217183	1219612	1217183
1129	1220068	1219673	1220068
1130	1219710	1220669	1219710
1131	1220630	1221376	1220630
1132	1221645	1223681	1221645
1133	1223894	1224988	1223900
1134	1225000	1225830	1225000
1135	1227810	1225879	1227810
1136	1226528	1226908	1226528
1137	1229972	1228311	1229972
1138	47569	47018	47569
1139	49980	49117	49980
1140	53356	52898	53356
1141	54477	54884	54477
1142	63753	63998	63753
1143	77164	77487	77164
1144	79724	79302	79724
1145	88721	88951	88721
1146	94067	94429	94067
1147	122832	123341	122832
1148	147536	147234	147536
1149	158990	159346	158990
1150	168470	168979	168470
1151	169183	169452	169204
1152	171785	171504	171785
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1155	195704	196075	195704
1156	210687	210145	210684

ORF Nos	begin	end	potential start
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1160	218925	218701	218925
1161	223785	223525	223785
1162	224271	223999	224271
1163	228691	228407	228691
1164	235050	235334	235050
1165	252308	253021	252308
1166	258280	258912	258280
1167	261325	261567	261325
1168	268195	268878	268195
1169	269447	268881	269447
1170	271263	271538	271263
1171	271957	272346	271957
1172	274176	274550	274176
1173	275736	275314	275736
1174	276490	276927	276490
1175	277577	277861	277577
1176	288163	287909	288163
1177	290130	289789	290130
1178	290989	291225	290989
1179	291372	291860	291372
1180	311239	311622	311239
1181	328665	328384	328665
1182	337348	338289	337348
1183	364764	364369	364764
1184	389623	390135	389623
1185	393729	394343	393729
1186	407379	407621	407379
1187	410944	410708	410944
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1189	428172	428486	428172
1190	436761	437246	436761

ORF Nos	begin	end	potential start
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1192	477597	477313	477597
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1194	487764	487534	487764
1195	498502	499017	498502
1196	499795	500466	499795
1197	571928	572344	571928
1198	572367	572131	572367
1199	588184	587915	588184
1200	600587	600907	600587
1201	609731	608895	609731
1202	614039	614755	614039
1203	614823	615152	614823
1204	638244	638831	638244
1205	638819	639094	638819
1206	639073	639636	639073
1207	647901	648236	647901
1208	678510	679469	678510
1209	688178	688732	688178
1210	696045	696563	696045
1211	708998	708588	708998
1212	709808	710089	709808
1213	718240	717737	718240
1214	737828	737565	737828
1215	779502	780257	779502
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1217	820931	820707	820931
1218	837696	839096	837696
1219	883307	883549	883307
1220	892010	891726	892010
1221	893277	893564	893277
1222	936998	937225	936998
1223	946865	947419	946865
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ORF Nos	begin	end	potential start
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1230	992759	993067	992759
1231	1004247	1004528	1004268
1232	1015013	1014294	1015013
1233	1056147	1056545	1056147
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1235	1088121	1088381	1088121
1236	1098430	1098852	1098430
1237	1098798	1099319	1098798
1238	1123198	1123515	1123198
1239	1123606	1124256	1123606
1240	1124453	1124797	1124453
1241	1129253	1129567	1129253
1242	1164947	1164474	1164947
1243	1170457	1170053	1170457
1244	1172342	1171863	1172342
1245	1192155	1192835	1192155
1246	1192759	1192992	1192759
1247	1193861	1194142	1193861
1248	1194036	1193779	1194036
1249	1209748	1209053	1209748
1250	1215111	1215419	1215111
1251	1216302	1216538	1216302
1252	1228072	1227818	1228072
1253	1228304	1228080	1228304
1254	26599	26222	26599
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1256	67206	66967	67197
1257	70612	70352	70588
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ORF Nos	begin	end	potential start
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1262	209263	209024	209263
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1264	299009	299452	299030
1265	352106	351717	352061
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1267	553602	553381	553602
1268	556538	556807	556538
1269	594348	593797	594342
1270	595169	594876	595160
1271	662148	662381	662160
1272	706528	706893	706528
1273	803315	803650	803339
1274	849551	849306	849551
1275	913676	913275	913676
1276	927087	926836	927087
1277	930587	930360	930587
1278	986531	986764	986531
1279	996229	996486	996229
1280	1000373	1000002	1000334
1281	1010291	1010037	1010273
1282	1011128	1010793	1011128
1283	1012924	1012694	1012924
1284	1028659	1028913	1028659
1285	1086481	1086762	1086481
1286	1118658	1118879	1118658
1287	1170098	1169835	1170098
1288	1180828	1181184	1180828
1289	1182658	1183035	1182658
1290	1195076	1194795	1195055
1291	1195890	1196183	1195890
1292	189042	188809	189030

ORF Nos	begin	end	potential start
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Table 4

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39	1366	1367	3870	3871
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TABLE 5

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1295	F	1229162	3015	F	832943	4735	B	459146
1296	F	1588	3016	F	835834	4736	B	458008
1297	F	1229711	3017	F	833938	4737	B	459836
1298	F	2253	3018	F	837457	4738	B	458598
1299	F	369	3019	F	835536	4739	B	460488
1300	F	3381	3020	F	838723	4740	B	459717
1301	F	1508	3021	F	836826	4741	B	461652
1302	F	4042	3022	F	840649	4742	B	460417
1303	F	2126	3023	F	838723	4743	B	462365
1304	F	5735	3024	F	841751	4744	B	461391
1305	F	3843	3025	F	839825	4745	B	463286
1306	F	7832	3026	F	842960	4746	B	461680
1307	F	5909	3027	F	841123	4747	B	463584
1308	F	8887	3028	F	843765	4748	B	462520
1309	F	7010	3029	F	841844	4749	B	464418
1310	F	10139	3030	F	844768	4750	B	463584
1311	F	8175	3031	F	842852	4751	B	465539
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1313	F	8799	3033	F	844175	4753	B	466398
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1901	F	295757	3621	F	1146086	5341	B	752086
1902	F	298027	3622	F	1148126	5342	B	750667
1903	F	296092	3623	F	1146211	5343	B	752569
1904	F	298555	3624	F	1148913	5344	B	751458
1905	F	296582	3625	F	1147044	5345	B	753343
1906	F	299403	3626	F	1149702	5346	B	753262
1907	F	297511	3627	F	1147890	5347	B	755162
1908	F	300409	3628	F	1150561	5348	B	754535
1909	F	298579	3629	F	1148660	5349	B	756429
1910	F	301332	3630	F	1150946	5350	B	756398
1911	F	299433	3631	F	1149046	5351	B	758298
1912	F	302215	3632	F	1152302	5352	B	756708
1913	F	300282	3633	F	1150392	5353	B	758611
1914	F	302492	3634	F	1154344	5354	B	760465
1915	F	300618	3635	F	1152371	5355	B	762358
1916	F	303627	3636	F	1155448	5356	B	761441
1917	F	301730	3637	F	1153548	5357	B	763356
1918	F	304350	3638	F	1156630	5358	B	762077
1919	F	302487	3639	F	1154729	5359	B	763945

1920	F	305173	3640	F	1157756	5360	B	762528
1921	F	303226	3641	F	1155862	5361	B	764410
1922	F	306244	3642	F	1160695	5362	B	763118
1923	F	304350	3643	F	1158788	5363	B	765018
1924	F	307232	3644	F	1162326	5364	B	763539
1925	F	305310	3645	F	1160468	5365	B	765504
1926	F	307799	3646	F	1163300	5366	B	764000
1927	F	305877	3647	F	1161413	5367	B	765907
1928	F	309173	3648	F	1163763	5368	B	765391
1929	F	307301	3649	F	1161842	5369	B	767328
1930	F	310158	3650	F	1164224	5370	B	767041
1931	F	308306	3651	F	1162283	5371	B	768951
1932	F	311020	3652	F	1164800	5372	B	768271
1933	F	309118	3653	F	1162908	5373	B	770171
1934	F	311031	3654	F	1165312	5374	B	768799
1935	F	309126	3655	F	1163427	5375	B	770686
1936	F	311552	3656	F	1165877	5376	B	769562
1937	F	309658	3657	F	1163960	5377	B	771608
1938	F	312510	3658	F	1166827	5378	B	770752
1939	F	310614	3659	F	1164936	5379	B	772652
1940	F	313134	3660	F	1168099	5380	B	771701
1941	F	311255	3661	F	1166212	5381	B	773620
1942	F	313674	3662	F	1168991	5382	B	773316
1943	F	311717	3663	F	1167093	5383	B	775178
1944	F	314490	3664	F	1169769	5384	B	773690
1945	F	312633	3665	F	1167907	5385	B	775579
1946	F	315306	3666	F	1170349	5386	B	774596
1947	F	313355	3667	F	1168446	5387	B	776522
1948	F	315932	3668	F	1170953	5388	B	776300
1949	F	314033	3669	F	1169031	5389	B	778224
1950	F	318434	3670	F	1171641	5390	B	775346
1951	F	316516	3671	F	1169703	5391	B	777266
1952	F	320876	3672	F	1172172	5392	B	775618
1953	F	318949	3673	F	1170256	5393	B	777518
1954	F	321403	3674	F	1173649	5394	B	777266

1955	F	319547	3675	F	1171759	5395	B	779200
1956	F	322084	3676	F	1174885	5396	B	778224
1957	F	320217	3677	F	1172999	5397	B	780087
1958	F	322911	3678	F	1175559	5398	B	778396
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1960	F	323634	3680	F	1176927	5400	B	779557
1961	F	321726	3681	F	1175025	5401	B	781481
1962	F	325117	3682	F	1178912	5402	B	780503
1963	F	323211	3683	F	1176985	5403	B	782380
1964	F	326213	3684	F	1179826	5404	B	781419
1965	F	324254	3685	F	1177910	5405	B	783311
1966	F	327607	3686	F	1180498	5406	B	781747
1967	F	325695	3687	F	1178666	5407	B	783680
1968	F	328162	3688	F	1181716	5408	B	783004
1969	F	326262	3689	F	1179839	5409	B	784912
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1971	F	326723	3691	F	1180140	5411	B	785752
1972	F	329134	3692	F	1183626	5412	B	785255
1973	F	327178	3693	F	1181716	5413	B	787155
1974	F	330734	3694	F	1184128	5414	B	786655
1975	F	328810	3695	F	1182244	5415	B	788572
1976	F	332123	3696	F	1185004	5416	B	788671
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1981	F	333980	3701	F	1185251	5421	B	791900
1982	F	337129	3702	F	1186262	5422	B	791734
1983	F	335202	3703	F	1184361	5423	B	793679
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1985	F	335955	3705	F	1187160	5425	B	794875
1986	F	338746	3706	F	1190885	5426	B	793809
1987	F	336795	3707	F	1188990	5427	B	795692
1988	F	339217	3708	F	1191507	5428	B	794580
1989	F	337362	3709	F	1189579	5429	B	796450

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1991	F	338083	3711	F	1190008	5431	B	796966
1992	F	343144	3712	F	1192524	5432	B	795956
1993	F	341266	3713	F	1190640	5433	B	797855
1994	F	343699	3714	F	1192759	5434	B	797018
1995	F	341813	3715	F	1190869	5435	B	798918
1996	F	344108	3716	F	1193642	5436	B	798989
1997	F	342204	3717	F	1191742	5437	B	800875
1998	F	344851	3718	F	1193557	5438	B	800069
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2000	F	346148	3720	F	1194015	5440	B	799840
2001	F	344219	3721	F	1192120	5441	B	801701
2002	F	346493	3722	F	1195490	5442	B	801533
2003	F	344590	3723	F	1193560	5443	B	803445
2004	F	346815	3724	F	1196093	5444	B	802717
2005	F	344907	3725	F	1194215	5445	B	804581
2006	F	347836	3726	F	1196474	5446	B	803559
2007	F	345956	3727	F	1194592	5447	B	805419
2008	F	350379	3728	F	1197659	5448	B	804032
2009	F	348432	3729	F	1195724	5449	B	805931
2010	F	350856	3730	F	1198499	5450	B	805383
2011	F	348951	3731	F	1196578	5451	B	807291
2012	F	352008	3732	F	1199912	5452	B	806107
2013	F	350106	3733	F	1197986	5453	B	807988
2014	F	353209	3734	F	1200969	5454	B	806533
2015	F	351305	3735	F	1199133	5455	B	808430
2016	F	354224	3736	F	1202121	5456	B	806954
2017	F	352312	3737	F	1200227	5457	B	808724
2018	F	354781	3738	F	1202957	5458	B	807133
2019	F	352871	3739	F	1201058	5459	B	809033
2020	F	355223	3740	F	1202590	5460	B	808442
2021	F	353261	3741	F	1200694	5461	B	810357
2022	F	355393	3742	F	1203923	5462	B	808972
2023	F	353519	3743	F	1202049	5463	B	810896
2024	F	358901	3744	F	1204631	5464	B	809674

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2026	F	356594
2027	F	354692
2028	F	359240
2029	F	357374
2030	F	359721
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2032	F	361071
2033	F	359240
2034	F	363605
2035	F	361731
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2038	F	364567
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2056	F	373223
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2058	F	373939
2059	F	372017

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3771	F	1214374
3772	F	1216927
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3774	F	1219490
3775	F	1217534
3776	F	1219431
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3778	F	1220403
3779	F	1218475

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5468	B	811472
5469	B	813357
5470	B	813325
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5474	B	813808
5475	B	815737
5476	B	815246
5477	B	817168
5478	B	815995
5479	B	817892
5480	B	817264
5481	B	819164
5482	B	817579
5483	B	819491
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2062	F	375351	3782	F	1223653	5502	B	827511
2063	F	373487	3783	F	1221767	5503	B	829428
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2066	F	377737	3786	F	1226308	5506	B	830262
2067	F	375828	3787	F	1224409	5507	B	832158
2068	F	379537	3788	F	1225625	5508	B	831286
2069	F	377660	3789	F	1223654	5509	B	833182
2070	F	380033	3790	F	1227566	5510	B	831946
2071	F	378160	3791	F	1225677	5511	B	833848
2072	F	380789	3792	F	1227858	5512	B	833372
2073	F	378889	3793	F	1225937	5513	B	835267
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2075	F	379279	3795	F	1226189	5515	B	835992
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2081	F	383278	3801	B	4545	5521	B	839751
2082	F	386271	3802	B	3694	5522	B	839381
2083	F	384392	3803	B	5513	5523	B	841221
2084	F	386780	3804	B	4290	5524	B	841127
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2087	F	387504	3807	B	7846	5527	B	844323
2088	F	389901	3808	B	7687	5528	B	843691
2089	F	388001	3809	B	9583	5529	B	845602
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2092	F	391612	3812	B	10261	5532	B	845319
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2103	F	392782	3823	B	19400	5543	B	853690
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2108	F	397607	3828	B	22265	5548	B	855338
2109	F	395705	3829	B	24185	5549	B	857240
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2115	F	399008	3835	B	28258	5555	B	860735
2116	F	401183	3836	B	27241	5556	B	859824
2117	F	399301	3837	B	29113	5557	B	861787
2118	F	401964	3838	B	27977	5558	B	860442
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2173	F	428558	3893	B	56326	5613	B	890775
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2188	F	439741	3908	B	62699	5628	B	893347
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2190	F	438296	3910	B	63981	5630	B	893787
2191	F	436377	3911	B	65858	5631	B	895711
2192	F	440475	3912	B	64268	5632	B	895642
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2194	F	440281	3914	B	64423	5634	B	896759
2195	F	438394	3915	B	66309	5635	B	898650
2196	F	440989	3916	B	64834	5636	B	897802
2197	F	439080	3917	B	66756	5637	B	899694
2198	F	442121	3918	B	65705	5638	B	899665
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2522	F	604391	4242	B	232306	5962	B	1058919
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DEMANDES OU BREVETS VOLUMINEUX

LA PRÉSENTE PARTIE DE CETTE DEMANDE OU CE BREVET COMPREND PLUS D'UN TOME.

CECI EST LE TOME 1 DE 7

NOTE: Pour les tomes additionels, veuillez contacter le Bureau canadien des brevets

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JUMBO APPLICATIONS/PATENTS

THIS SECTION OF THE APPLICATION/PATENT CONTAINS MORE THAN ONE VOLUME

THIS IS VOLUME 1 OF 7

NOTE: For additional volumes please contact the Canadian Patent Office

WHAT IS CLAIMED IS:

1- An isolated polynucleotide having a nucleotide sequence of a *Chlamydia pneumoniae* genome, comprising

(a) the a nucleotide sequence of SEQ ID No. 1;

(b) the nucleotide sequence contained within the *Chlamydia pneumoniae* genomic DNA in ATCC Deposit No. _______;

(c) the nucleotide sequence contained in a clone insert in ATCC Deposit No. ________;

(d) a nucleotide sequence exhibiting at least 99.9% identity with the sequence of SEQ ID No. 1; or

(e) a nucleotide sequence exhibiting at least 80% homology to SEQ ID No. 1.

2- An isolated polynucleotide which hybridizes to SEQ ID No. 1 or to the *Chlamydia pneumoniae* genomic DNA contained in ATCC deposit No. _______ or to a clone insert in ATCC Deposit No. _______ under conditions of high stringency.

3- An isolated polynucleotide which hybridizes to SEQ ID No. 1 or to the *Chlamydia pneumoniae* genomic DNA contained in ATCC deposit No. _____ under conditions of intermediate stringency.

4- An isolated polynucleotide having a nucleotide sequence of an open reading frame (ORF) of a *Chlamydia pneumoniae* genome, comprising:

(a) a nucleotide sequence chosen from one of ORF2 to ORF 1297;

(b) a nucleotide sequence exhibiting at least 99.9% identity with one of ORF2 to ORF 1297; or

(c) a nucleotide sequence exhibiting at least 80% homology to one of ORF2 to ORF 1297.

5- An isolated polynucleotide which hybridizes to one of ORF2 to ORF 1297 under conditions of high stringency.

6- An isolated polynucleotide which hybridizes to one of ORF2 to ORF 1297 under conditions of intermediate stringency.

7- The polynucleotide of Claims 2, 3, 4, 5, or 6 which encodes the following polypeptides or fragments thereof:

(a) a *Chlamydia pneumoniae* transmembrane polypeptide having between 1 and 3 transmembrane domains;

(b) a *Chlamydia pneumoniae* transmembrane polypeptide having between 4 and 6 transmembrane domains;

(c) a *Chlamydia pneumoniae* transmembrane polypeptide having at least 7 transmembrane domains;

(d) a *Chlamydia pneumoniae* polypeptide involved in intermediate metabolism of sugars and/or cofactors;

(e) a *Chlamydia pneumoniae* polypeptide involved in intermediate metabolism of nucleotides or nucleic acids;

(f) a *Chlamydia pneumoniae* polypeptide involved in metabolism of amino acids or polypeptides;

(g) a *Chlamydia pneumoniae* polypeptide having involved in metabolism of fatty acids;

(h) a *Chlamydia pneumoniae* polypeptide involved in the synthesis of the cell wall;

(i) a *Chlamydia pneumoniae* polypeptide involved in transcription, translation, and/or maturation process;

(j) a *Chlamydia pneumoniae* transport polypeptide;

(k) a *Chlamydia pneumoniae* polypeptide involved in the virulence process;

(l) a *Chlamydia pneumoniae* polypeptide involved in the secretory system and/or which is secreted;

(m) a *Chlamydia pneumoniae* polypeptide of the cellular envelope or outer cellular envelope of *Chlamydia pneumoniae*.

(n) a *Chlamydia pneumoniae* surface exposed polypeptide;

(o) a *Chlamydia pneumoniae* lipoprotein;

(p) a *Chlamydia pneumoniae* polypeptide involved in lipopolysaccharide biosynthesis;

(q) a *Chlamydia pneumoniae* KDO-related polypeptide;

(r) a *Chlamydia pneumoniae* phosphomannomutase-related polypeptide;

(s) a *Chlamydia pneumoniae* lipid A component-related polypeptide;

(t) a *Chlamydia pneumoniae* phosphoglucomutase-related polypeptide;

(u) a *Chlamydia pneumoniae* polypeptide that contains an RGD sequence;

(v) a *Chlamydia pneumoniae* Type III secreted polypeptide;

(w) a *Chlamydia pneumoniae* cell wall anchored surface polypeptide; or

(x) a *Chlamydia pneumoniae* polypeptide that is not found in *Chlamydia trachomatis*.

8- A polynucleotide encoding a fusion protein, comprising one of ORF2 to ORF1297 of Claim 4, 5, or 6 ligated in frame to a polynucleotide encoding a heterologous polypeptide.

9- A recombinant vector that contains the polynucleotide of Claim 1, 2, 3, 4, 5 or 6.

10- A recombinant vector that contains the polynucleotide of Claim 8.

11- A recombinant vector that contains the polynucleotide of Claim 4, 5 or 6, operatively associated with a regulatory sequence that controls gene expression.

12- A recombinant vector that contains the polynucleotide of Claim 8 operatively associated with a regulatory sequence that controls gene expression.

13- A genetically engineered host cell that contains the polynucleotide of Claim 1, 2, 3, 4, 5 or 6.

14- A genetically engineered host cell that contains the polynucleotide of Claim 8.

15- A genetically engineered host cell that contains the polynucleotide of Claim 4, 5 or 6 operatively associated with a regulatory sequence that controls gene expression in the host cell.

16- A genetically engineered host cell that contains the polynucleotide of Claim 8 operatively associated with a regulatory sequence that controls gene expression in the host cell.

17- A method for producing a polypeptide, comprising:

(a) culturing the genetically engineered host cell of Claim 15 under conditions suitable to produce the polypeptide encoded by the polynucleotide; and

(b) recovering the polypeptide from the culture.

18- A method for producing a fusion protein, comprising:

(a) culturing the genetically engineered host cell of Claim 16 under conditions suitable to produce the fusion protein encoded by the polynucleotide; and

(b) recovering the fusion protein from the culture.

19- A polypeptide encoded by the polynucleotide of Claim 4, 5 or 6.

20- The polypeptide of Claim 19 which immunoreacts with seropositive serum of an individual infected with *Chlamydia pneumoniae.*

21- The polypeptide of Claim 19 which comprises the following polypeptides or fragments thereof:

(a) a *Chlamydia pneumoniae* transmembrane polypeptide having between 1 and 3 transmembrane domains;

(b) a *Chlamydia pneumoniae* transmembrane polypeptide having between 4 and 6 transmembrane domains;

(c) a *Chlamydia pneumoniae* transmembrane polypeptide having at least 7 transmembrane domains;

(d) a *Chlamydia pneumoniae* polypeptide involved in intermediate metabolism of sugars and/or cofactors;

(e) a *Chlamydia pneumoniae* polypeptide involved in intermediate metabolism of nucleotides or nucleic acids;

(f) a *Chlamydia pneumoniae* polypeptide involved in metabolism of amino acids or polypeptides;

(g) a *Chlamydia pneumoniae* polypeptide involved in metabolism of fatty acids;

(h) a *Chlamydia pneumoniae* polypeptide involved in the synthesis of the cell wall;

(i) a *Chlamydia pneumoniae* polypeptide involved in transcription, translation, and/or maturation process;

(j) a *Chlamydia pneumoniae* transport polypeptide;

(k) a *Chlamydia pneumoniae* polypeptide involved in the virulence process;

(l) a *Chlamydia pneumoniae* polypeptide involved in the secretory system and/or which is secreted;

(m) a *Chlamydia pneumoniae* polypeptide of the cellular envelope or outer cellular envelope of *Chlamydia pneumoniae.*

(n) a *Chlamydia pneumoniae* surface exposed polypeptide;

(o) a *Chlamydia pneumoniae* lipoprotein;

(p) a *Chlamydia pneumoniae* polypeptide involved in lipopolysaccharide biosynthesis;

(q) a *Chlamydia pneumoniae* KDO-related polypeptide;

(r) a *Chlamydia pneumoniae* phosphomannomutase-related polypeptide;

(s) a *Chlamydia pneumoniae* phosphoglucomutase-related polypeptide;

(t) a *Chlamydia pneumoniae* lipid A component-related polypeptide;

(u) a *Chlamydia pneumoniae* polypeptide that contains an RGD sequence;

(v) a *Chlamydia pneumoniae* Type III secreted polypeptide;

(w) a *Chlamydia pneumoniae* cell wall anchored surface polypeptide; or

(x) a *Chlamydia pneumoniae* polypeptide that is not found in *Chlamydia trachomatis*.

22- A fusion protein encoded by the polynucleotide of Claim 8.

23- The fusion protein of Claim 22 which immunoreacts with seropositive serum of an individual infected with *Chlamydia pneumoniae*.

24- An antibody that immunospecifically binds to the polypeptide of Claim 19.

25- An antibody that immunospecifically binds to the fusion protein of Claim 22.

26- A method for the detection and/or identification of *Chlamydia pneumoniae* in a biological sample, comprising:

(a) contacting the sample with a polynucleotide primer of Claim 1, 2, 3, 4, 5, or 6 in the presence of a polymerase enzyme and nucleotides under conditions which permit primer extension; and

(b) detecting the presence of primer extension products in the sample in which the detection of primer extension products indicates the presence of *Chlamydia pneumoniae* in the sample.

27- A method for the detection and/or identification of *Chlamydia pneumoniae* in a biological sample, comprising:

(a) contacting the sample with a polynucleotide probe of Claim 1, 2, 3, 4, 5, or 6 under conditions which permit hybridization of complementary base pairs; and

(b) detecting the presence of hybridization complexes in the sample in which the detection of hybridization complexes indicates the presence of *Chlamydia pneumoniae* in the sample.

28- A method for the detection and/or identification of *Chlamydia pneumoniae* in a biological sample, comprising:

(a) contacting the sample with the antibody of Claim 24 under conditions suitable for the formation of immune complexes; and

(b) detecting the presence of immune complexes in the sample, in which the detection of immune complexes indicates the presence of *Chlamydia pneumoniae* in the sample.

29- A method for the detection and/or identification of antibodies to *Chlamydia pneumoniae* in a biological sample, comprising:

(a) contacting the sample with a polypeptide of Claim 19 under conditions suitable for the formation of immune complexes; and

(b) detecting the presence of immune complexes in the sample, in which the detection of immune complexes indicates the presence of *Chlamydia pneumoniae* in the sample.

30- A DNA chip containing an array of polynucleotides comprising at least one of the polynucleotides of Claim 1, 2, 3, 4, 5, or 6.

31- A protein chip containing an array of polypeptides comprising at least one of the polypeptides of Claim 19.

32- An immunogenic composition comprising the polypeptide of Claim 19 and a pharmaceutically acceptable carrier.

33- An immunogeneic composition comprising the polypeptide of Claim 20 and a pharmaceutically acceptable carrier.

34- An immunogenic composition comprising the fusion protein of Claim 22 and a pharmaceutically acceptable carrier.

35- An immunogenic composition comprising the fusion protein of Claim 23 and a pharmaceutically acceptable carrier.

36- A pharmaceutical composition comprising the polypeptide of Claim 19 and a pharmaceutically acceptable carrier.

37- A pharmaceutical composition comprising the polypeptide of Claim 20 and a pharmaceutically acceptable carrier.

38- A pharmaceutical composition comprising the polypeptide of Claim 22 and a pharmaceutically acceptable carrier.

39- A pharmaceutical composition comprising the polypeptide of Claim 23 and a pharmaceutically acceptable carrier.

40- A method of immunizing against *Chlamydia pneumoniae*, comprising: administering to a host an immunizing amount of the immunogenic composition of Claim 32.

41- A method of immunizing against *Chlamydia pneumoniae*, comprising: administering to a host an immunizing amount of the immunogenic composition of Claim 33.

42- A method of immunizing against *Chlamydia pneumoniae*, comprising administering to a host an immunizing amount of the immunogenic composition of Claim 34.

43- A method of immunizing against *Chlamydia pneumoniae*, comprising: administering to a host an immunizing amount of the immunogenic composition of Claim 35.

44- A DNA immunogenic composition comprising the expression vector of Claim 11.

45- The DNA composition of Claim 44, wherein the DNA composition directs the expression of a neutralizing epitope of *Chlamydia pneumoniae.*

46- A DNA immunogenic composition comprising the expression vector of Claim 12.

47- The DNA composition of Claim 46, wherein the DNA composition directs the expression of a neutralizing epitope of *Chlamydia pneumoniae.*

48- A screening assay, comprising:

(a) contacting a test compound with an isolated polynucleotide of Claim 1, 2, 3, 4, 5 or 6; and

(b) detecting whether binding occurs.

49- A screening assay, comprising:

(a) contacting a test compound with the polypeptide of Claim19; and

(b) detecting whether binding occurs.

50- A screening assay, comprising:

(a) contacting a test compound with the polypeptide of Claim 22; and

(b) detecting whether binding occurs.

51- A kit comprising a container containing an isolated polynucleotide of Claim 1, 2, 3, 4, 5 or 6.

52- The kit of Claim 51 wherein the polynucleotide is a primer or a probe.

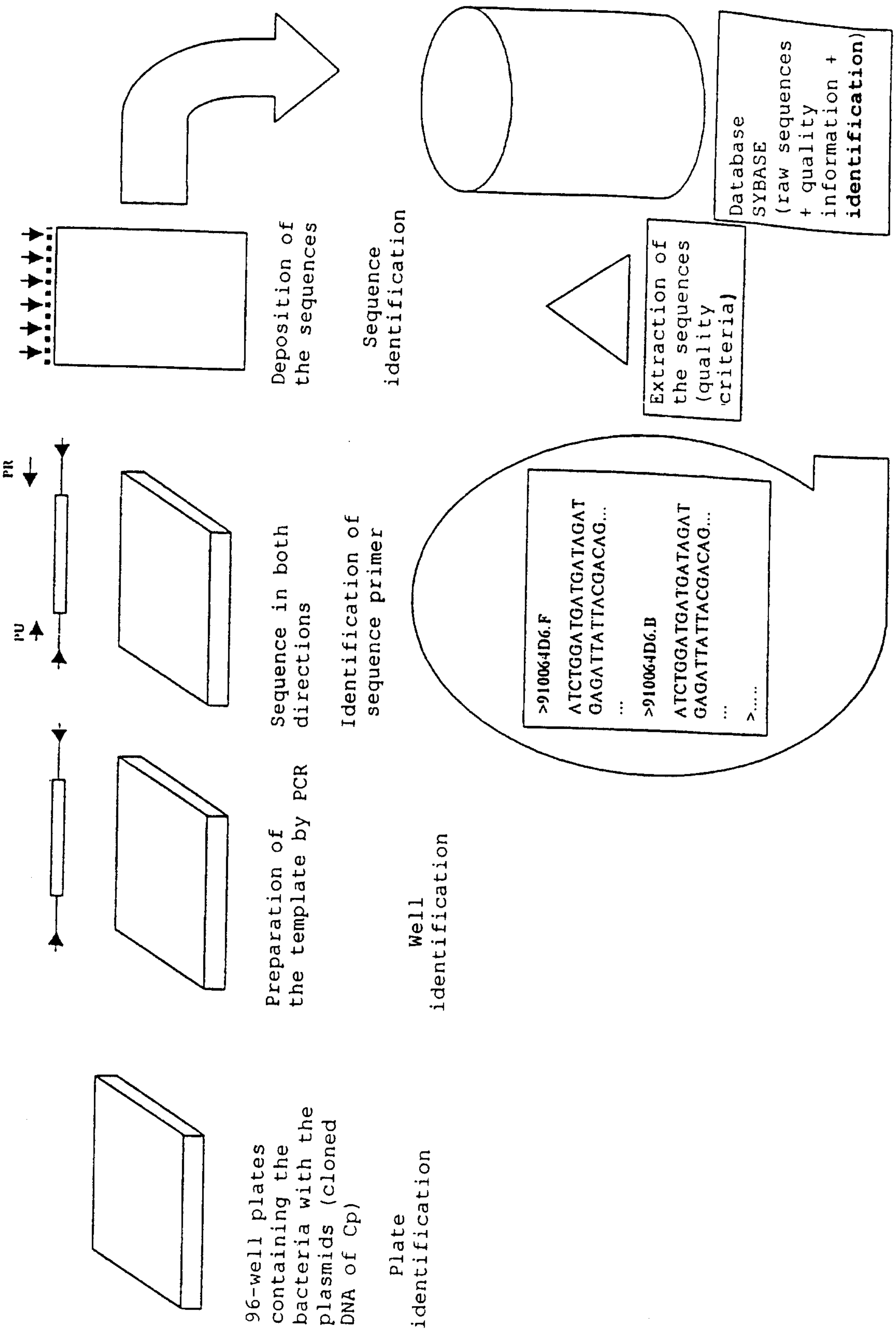
53- The kit of Claim 51 wherein the polynucleotide is a primer and the kit further comprises a container containing a polymerase.

54- The kit of Claim 51 which further comprises a container containing deoxynucleotide triphosphates.

55- A kit comprising a container containing an antibody that immunospecifically binds to the polypeptide of Claim 19.

56- A kit comprising a container containing an antibody that immunospecifically binds to the fusion protein of Claim 22.

Figure 1.


96-well plates containing the bacteria with the plasmids (cloned DNA of Cp)
Plate identification
Preparation of the template by PCR
Well identification
PU
PR
Sequence in both directions
Identification of sequence primer
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ATCTGGATGATGATAGAT
GAGATTATTACGACAG...
>910064D6.B
ATCTGGATGATGATAGAT
GAGATTATTACGACAG...
Deposition of the sequences
Sequence identification
Extraction of the sequences (quality criteria)
Database SYBASE (raw sequences + quality information + identification)

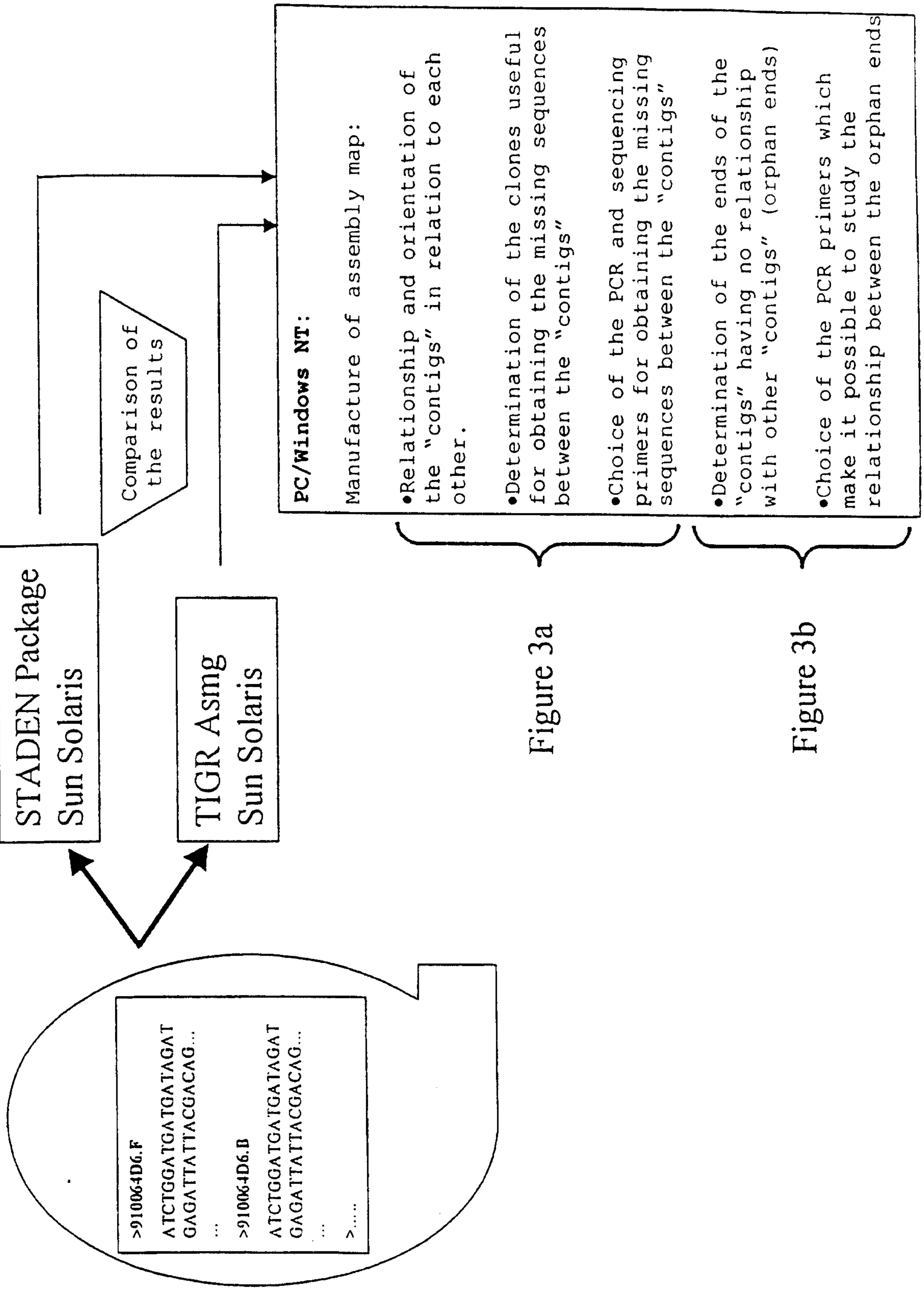
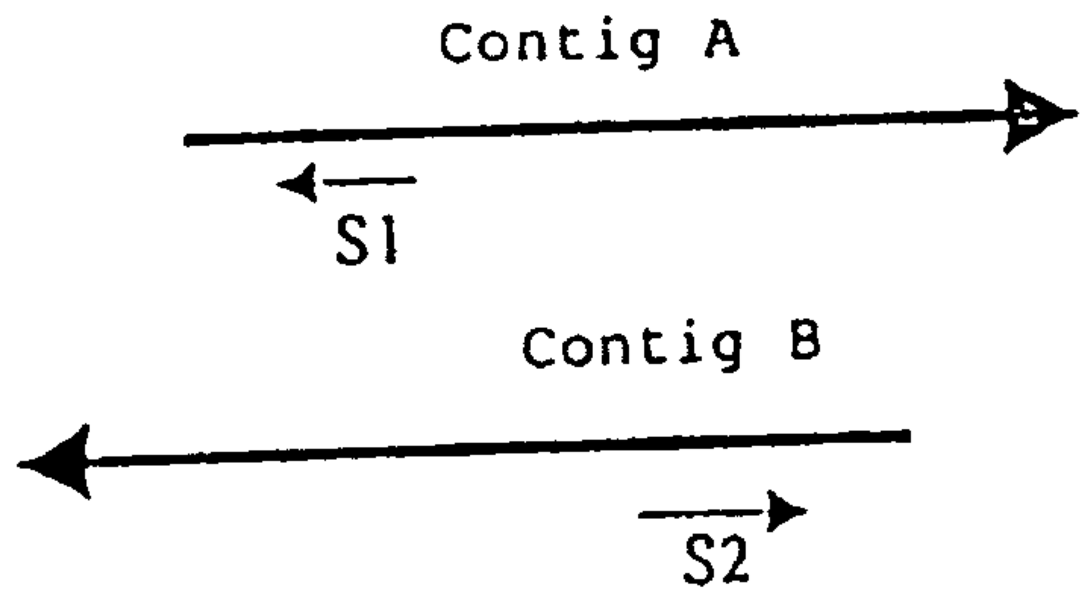


Figure 2.

Figure 3a

Figure 3b

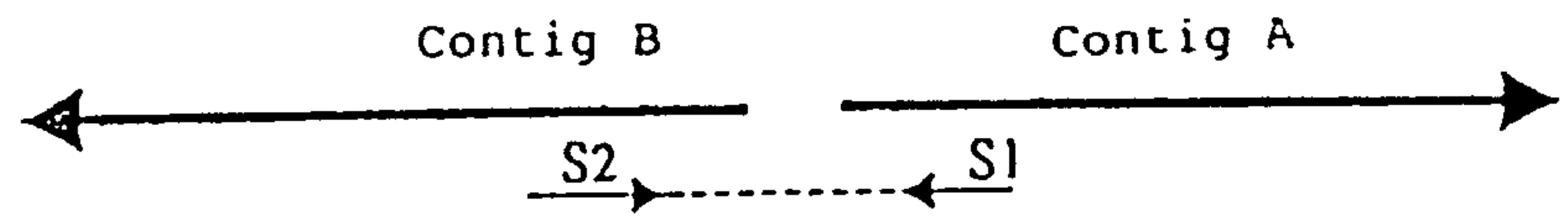
FIGURE 3A



Statistical determination of the sequences:

1- Belonging to the same clone

2- Situated on two different contigs

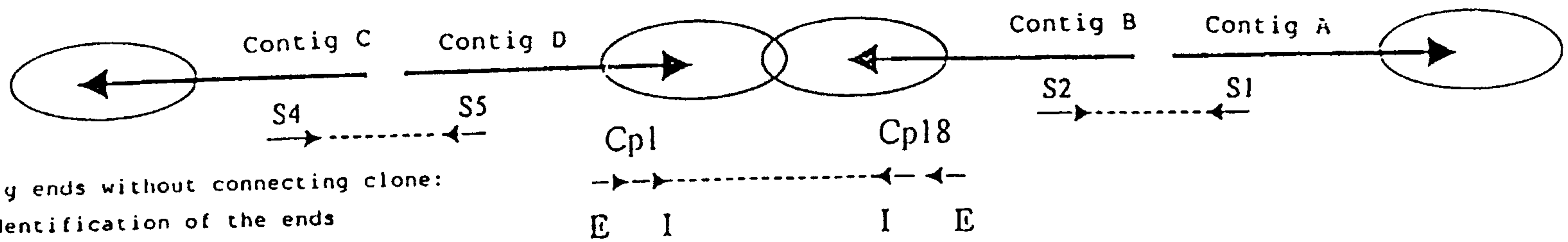


Distribution and position of the sequences on the contigs:

1- Define the arrangement of the contigs in relation to each other

2- Define the PCR primers which make it possible to fill the sequence

FIGURE 3B



Contig ends without connecting clone:

1- Identification of the ends

2- Determination of outer and inner PCR primers for studying the relationships between the contigs

E: outer primers

I: inner primers