

The nucleotide sequence of the 60kDa cysteine rich outer membrane protein of *Chlamydia psittaci* strain EAE/A22/M

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Chlamydia are Gram negative bacteria which have an oligate intracellular life cycle. There are three species within the genus *Chlamydia*; *Chlamydia trachomatis*, *Chlamydia psittaci* and *Chlamydia pneumoniae*.

C. psittaci shows a diverse host specificity causing latent and acute gastrointestinal infections in avian species, also conjunctivitis and pneumonitis in many feral and domesticated mammals. Human infection by *C. psittaci* is rare.

The chlamydial life cycle involves two morphological forms the intracellular reticulate bodies (RBs) and the spore-like elementary bodies (EBs). One major factor known to retard infectious EB formation is cysteine deprivation (1). This may be related to inhibition of the synthesis of the 60 kDa cysteine rich outer membrane protein (CrP). This protein is involved in cross linking in the EB cell wall where it may serve to maintain the structural integrity of the organism.

The complete nucleotide sequence for the 60 kDa cysteine rich outer membrane protein (CrP) of *C. psittaci* was determined using dideoxy chain termination sequencing on double stranded plasmid DNA. The sequence shows 70% and 71% homology to the serovars L1 and B 60 kDa CrP genes respectively (2). The

structural gene consists of an open reading frame of 1671 base pairs starting with ATG at 190 bp and ending with a TAA termination codon (Fig. 1).

Structural analysis of the *C. psittaci* DNA sequence revealed a single hairpin loop 32 bp downstream of the termination codon with a predicted free energy of $-33 \text{ kcal mol}^{-1}$. This hairpin loop was characteristic of a Rho-independent RNA-polymerase transcription terminator with a run of four thymine residues downstream of the hairpin loop structure (3).

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1 CTAGACGGTAGATGCAACAATAGTAAACAGTCTTATCTGTTTAAATTTGGTTAGGAGTTAGGAGGTAATATTTCCCTGCTAACTGCCTTTATGAAAAATAACTTA
115 AATGTTGAGGGTAAGAGTTCACAACTTCTACCCGATGGCAGAAGAAAAATACACACGCGATAGGAGAATCTGTCACAACTCATCAGACGAGTAGTACGGCTCTCGCG
M S K L I R R V V T V L A
229 CTAACAGTAGTGGCGAGTTCATTTGCCAGCGGAAGATAGAGCCGCTGCTGCAGAGTCTCTTGTCTACAAGATTCATTTGCCAGTACTGAAAACGAGATGACAAATGTTTTTCAA
L T S M A S S F A S G K I E A A A A E S L A T R F I A S T E N A D D N V F Q
343 GCACAGCCCAAGAAGTTAGATTTGGTCGTAAACAAAATCAAGACAAAGAAAACATACTGAAGCTTCTCTGTGATAAAGAATTTATCTCTGTGAAGGTGCCAGTGCCAA
A T A K K V R F G R N K N Q R Q E Q K H T E A F C D K E F Y P C E G G Q C Q
457 CCAGTAGACGCTACACAAGATCTGCTACGGCAAAATGATTTGTGTCGGTGTAAACGATGACTGTAACGTTGAAATCAGCCAACTCTGACCTGAATATGCAACGATGAGTCT
P V D A T Q E S C Y G K M Y C V R V N D D C N V E I S Q S V P E Y A T V G S
571 CCTATCTTATGAAATCTCGCTGAGGTAAAGAAATGCGTTAATGTTGTGATTACTCAACAGCTTCTTGGCAAGTTGAGTTTGTGAGCAGTGTATCTGCGACCAACCA
P Y P I E I L A V G K K D C V N V V I T Q Q L P C E V E F V S S D P A T T P
685 ACCTCGGATAGCAAAATTAATCTGGACAATGATCGCTTAGGTCAGGTTGAAAAATGCAAAATACCGTTTGGGTAAACCTCTAAAGAAGTTGTTGCTTCCCGCCGCTACT
T S D S K L I W T I D R L G Q G E K C K I T V W V V K P L K E G C C F T A A T
799 GTATGCTTGGCCAACTGCTCTTATACCAATGCGGACACAGCTATTTGTATTAAGCAAGAAGTCTGAAATGCGCTTACGTTAGCTTGGCCAGTTGTTACAAAATC
V C A C P E L R S Y T K C G Q P A I C I K Q E G P E C A C L R C P V C Y K I
913 GAAGTTTGCACACAGGTTCTGCTATAGCCCGTAATGTTGTCGCGATAACCCAGTTCGCCGATGGCTATACTATGCTTCAGGACACCGCTTCTTCTTAACTTAGGAGAT
E V C N T G S A I A R N V V D N P V P D G Y T H A S G Q R V L S F N L G D
1027 ATGCGCTCTGGGATCTCAATTTAAAGTCTGTTGTTGAGTTTGGCCACAAAAGAGGAAAAAGTTACTAACGTGGCTACTGTATCTTACTCGGAGGACATAAATGTTCTGCTAAC
M R P G D S K C F C V E F C P Q K R G K V T N V A T V S Y C G G H C C S A N
1141 GTAACCTAGTGTAAAGCAACCTACGTAACAAATATCTCTGGAGCTGACTGGTCTTATGATGTAAGCCTGAGAATACACTATCGTTGATCTACCCAGGAGACTCT
V T T V V N E P C V Q V H I S G A D W S Y V C K P V E Y T I V V S N P G D L
1255 AAATTTACGATGATGATAGAAATACCCACCTTCAGGACCAAAATTTAGAAAGTCTGCTGGAGCTGAAATCTGCTGTAAACAAAGCTGTATGGTGCATCAAGAAATGTC
K L Y D V V I E D T A P S G A T I L E A A G A E I C C N K A V W C I K E M C
1369 CCAGGAGAGACTCTCAATTTAAAGTCTGTTGTTGAGTAAAGCAAAAGCCAGGTAATTTACAAAATCAAGTTGTTGTCAAAATCACTCCGATTTGGAACTGACTCTCTGGCA
P G E T L Q F K V V A K A Q S P G K F T N Q V V V K T N S D C G T C T S C A
1483 GAAGTTACAAACATGGAAGGCTTGCAGCTACGCATATGTCGTAATCGATACCAATGATCTTATGCTAGGAGAAAATACTGTATACCGTATTTGTTGAACCAACCGT
E V T T H W K G L A A T H M C V I D T N D P I C V G E N T V Y R I C V T N R
1597 GGTCTGCAAGATACGAAGCTCTGTTAATCTTAAAGTTTCTAAGGAACTACAACCCGTTCTCTTCCAGTCCAACAAAAGAACCTACAGGGAATACAGTAGTATT
G S A E D T N V S L I L K F S K E L Q P V S S S G P T K G T I T G N T V V F
1711 GATGCTCTACATAAATAGTCTAAGGAATCTAGAGATTTTCTGTAACTTAAAGGAATTCCTCCAGGAGTCTCCAGGAGAGGCTATCTTCTTCTCAGACACTCAAGC
D A L P K L G S K E S V E F S V T L K G I A P G D A R G E A I L S S D T L T
1825 GTACCTGTGCTGATACAGAAAACACACTGTTATTAATCTCTTAAATTTCTTAACTTTGAAAGATTTGTAACGAAAAGCCCTGCTAGAAATTTCTCAGGACGCTTTTGTG
V P V A D T E N T H V Y *
1939 TCTCTTCTATGCTCAGGATTTCTCGGATCCCTCTAGGAAATGTCACAAAATTAATTAATAATTTAATTAAGTTGAGTGGTTAAACTCTTTGTCTTAAAGTATTT
2053 AGAAGGAGTTTTCGATGCTGTTGAGAAC

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Figure 1. Nucleotide sequence and deduced amino acid sequence of the 60 kDa Cysteine Rich Outer Membrane Protein of *Chlamydia psittaci*. The start and stop codons are underlined and the putative ribosome binding site is doubly underlined. Potential stem loop structures are shown by facing arrows.