

Supplementary data for the article:

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1 **Supplementary data**

2 **Lysine acetylation of major *Chlamydia trachomatis* antigens**

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11

12 **Materials and methods**

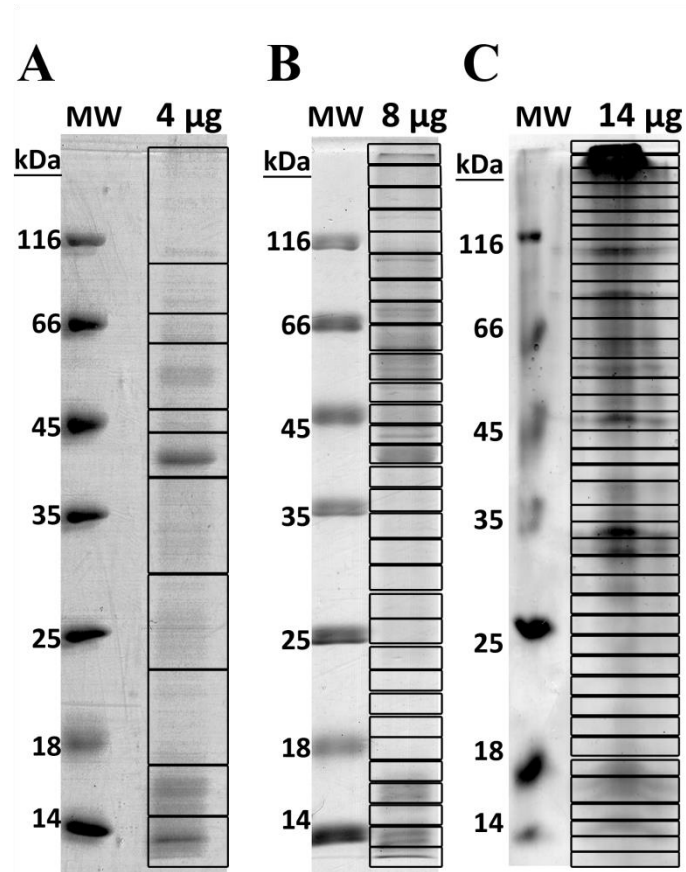
13 **Evaluation of CtB Lysine acetylation westernblot**

14 Imaging and analyses of the westernblot probed with AcK specific antibody was performed by laser
15 Typhoon 7000 series scanner and Image Quant TL 7.0 software (GE Healthcare, USA). In brief, for
16 scanning the BCIP/NBT developed immunomembranes, Typhoon's fluorescent stage and in-lab
17 designed scanning membrane program were applied according to manufacturer's general directions.
18 To quantify intensity of the immunologic responses, an un-calibrated mode of pixel inverter function
19 was chosen (linear function defined by Inverted pixel value = Bit-depth-1-pixel value, with Bit-depth
20 being 255 for 8-bit grey scale images), with 16 pixel fixed width band detection, peak slope of 150,
21 noise reduction level 7, minimal size of peak detected at 3% and rolling disc radius of 200 for
22 background subtraction.

23

24 **Figures and tables**

25 **Fig. E1.** Excision maps of heat inactivated CtB protein preparations on 4-12% PAA gel in reducing
26 conditions that were subjected to shotgun proteomics. Each preparation is assigned a label: A – 4 μg ,
27 B – 8 μg , C – 14 μg . Abbreviations: MW = molecular weight markers [Figure is single column wide,
28 dimensions 9 cm x 10.5cm, 500ppi]



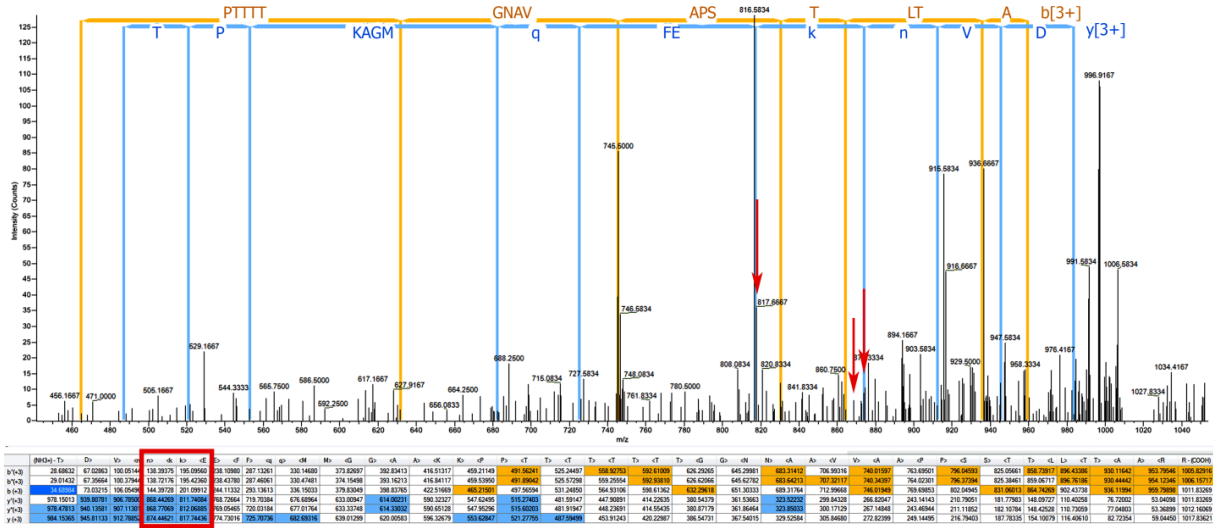
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32 **Fig. E2.** MS/MS spectrum of Major outer membrane porin (P23421) acetylated peptide
 33 TDVnK*EFqMGAKPTTTTGNVAPSTLTAR

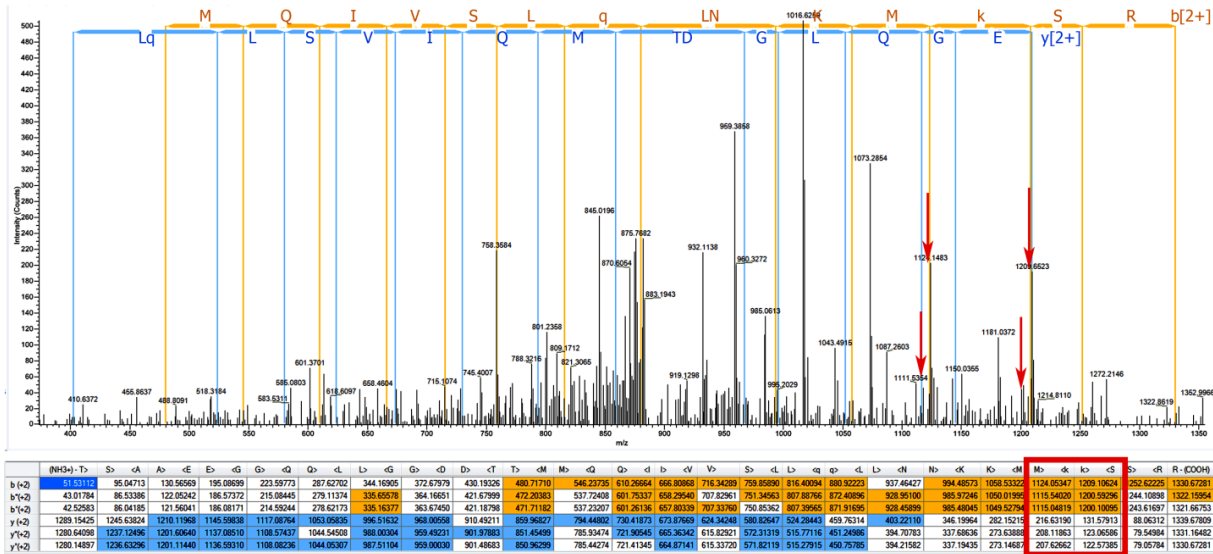
34 [Figure is double column wide, dimensions 19 cm x 9.5 cm, 500ppi]



T D V n k E F q M G A K P T T T G N A V A P S J T L T A R

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 36
 37 **Fig. E3.** MS/MS spectrum of Major outer membrane porin (P23421) acetylated peptide
 38 TSAEQLGDTMQIVSLqLNKMK*SR

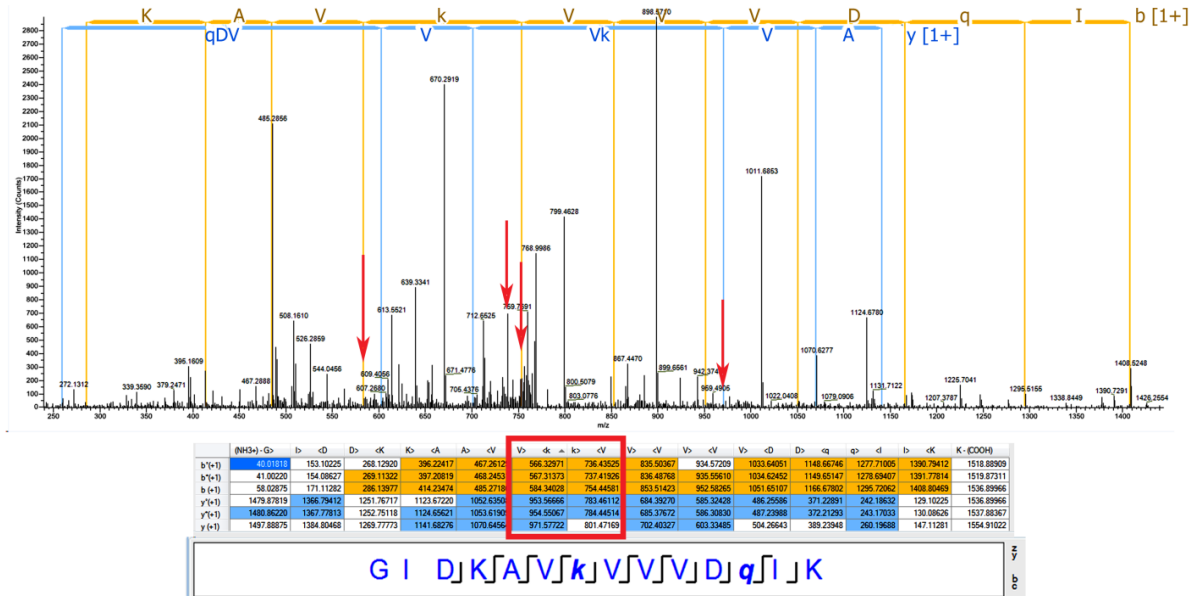
39 [Figure is double column wide, dimensions 19 cm x 10 cm, 500ppi]



T S A E Q L G D T M Q I V S L q L N K M K S R

41 **Fig. E4.** MS/MS spectrum of 60 kDa chaperonin (Q3KMQ9) acetylated peptide
 42 GIDKAVK*VVVDqIK

43 [Figure is double column wide, dimensions 19 cm x 9.1 cm, 500ppi]

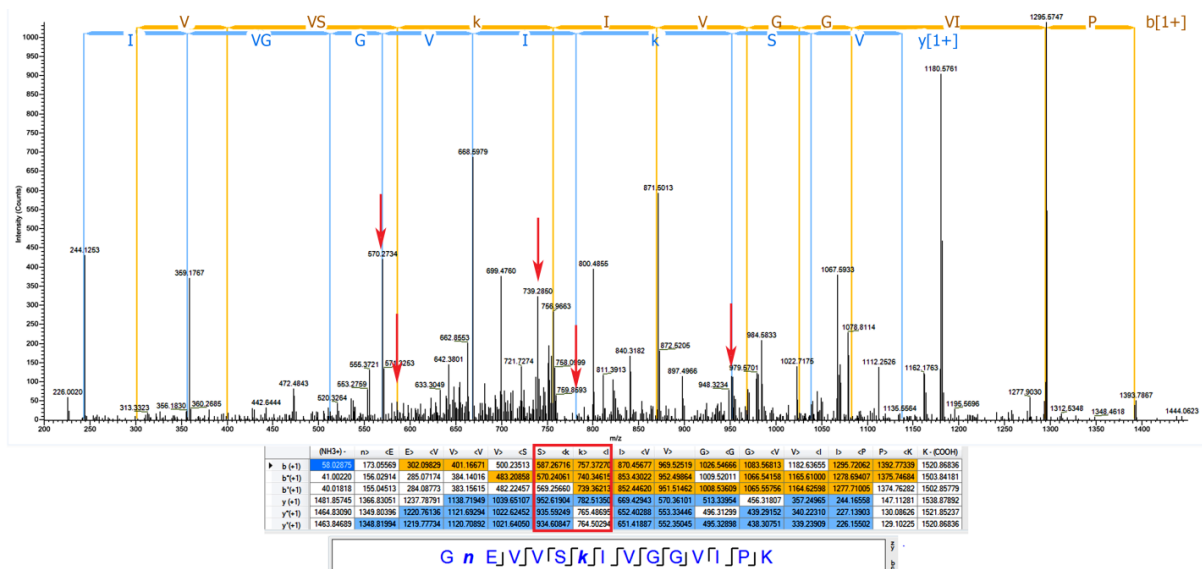


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46 **Fig. E5.** MS/MS spectrum of Elongation factor G (G4NNI1) acetylated peptide
 47 GnEVS*IVGGVIPK

48 [Figure is double column wide, dimensions 19 cm x 9 cm, 500ppi]

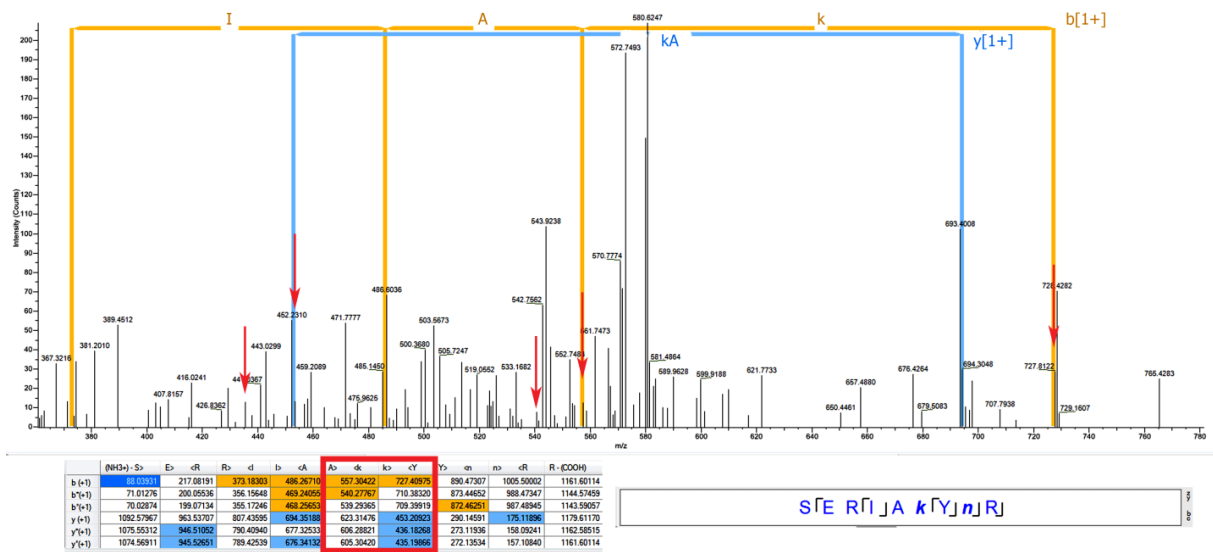


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51 **Fig. E6.** MS/MS spectrum of Enolase (O84591) acetylated peptide SERIAK*YnR

52 [Figure is double column wide, dimensions 19 cm x 9 cm, 500ppi]



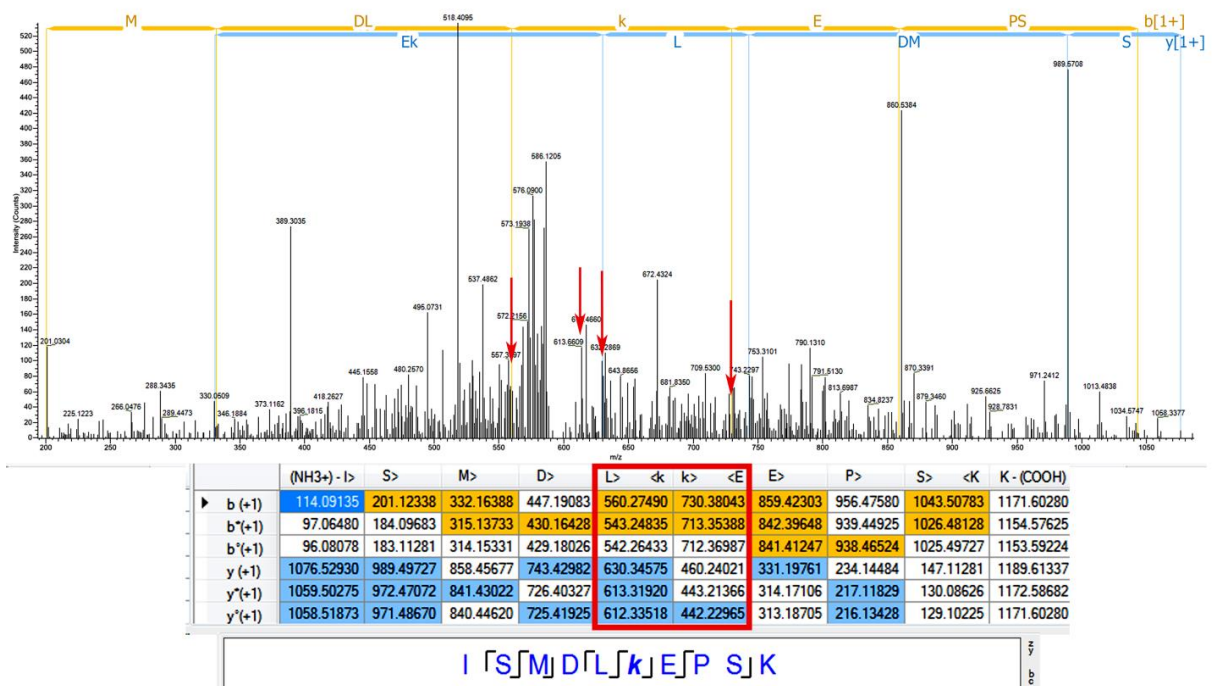
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55 **Fig. E7.** MS/MS spectrum of Polymorphic membrane protein B (Q2TGM5) acetylated peptide

56 ISMDLK*EPSK

57 [Figure is double column wide, dimensions 19 cm x 11 cm, 500ppi]

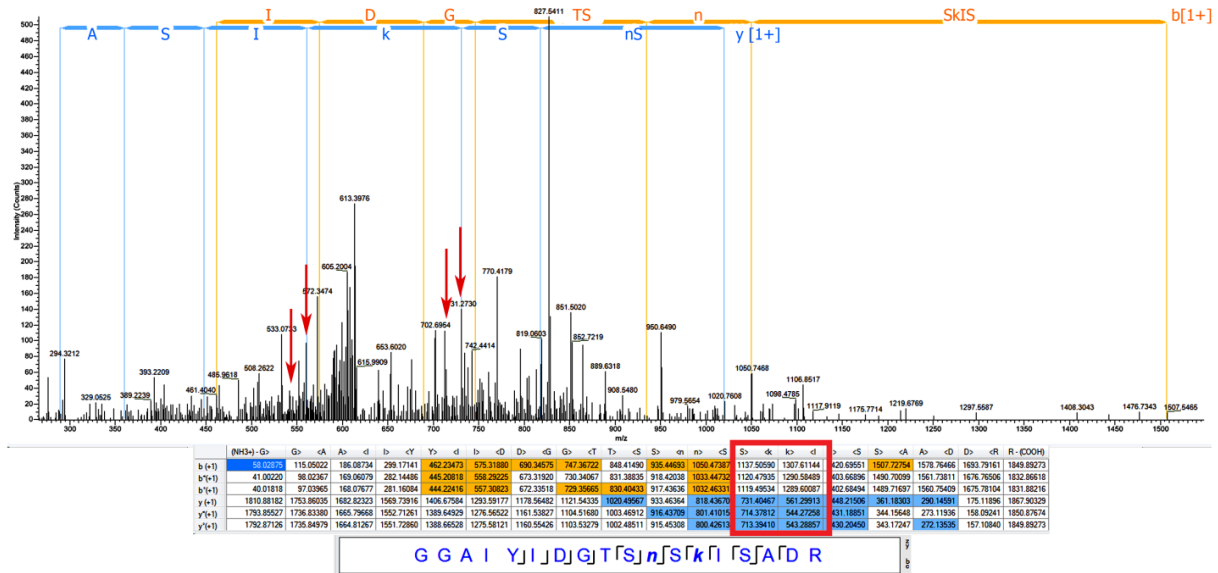


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60 **Fig. E8.** MS/MS spectrum of Polymorphic membrane protein E (Q84FV6) acetylated peptide
 61 GGAIYIDGTSnSK*ISADR

62 [Figure is double column wide, dimensions 19 cm x 9.5 cm, 500ppi]

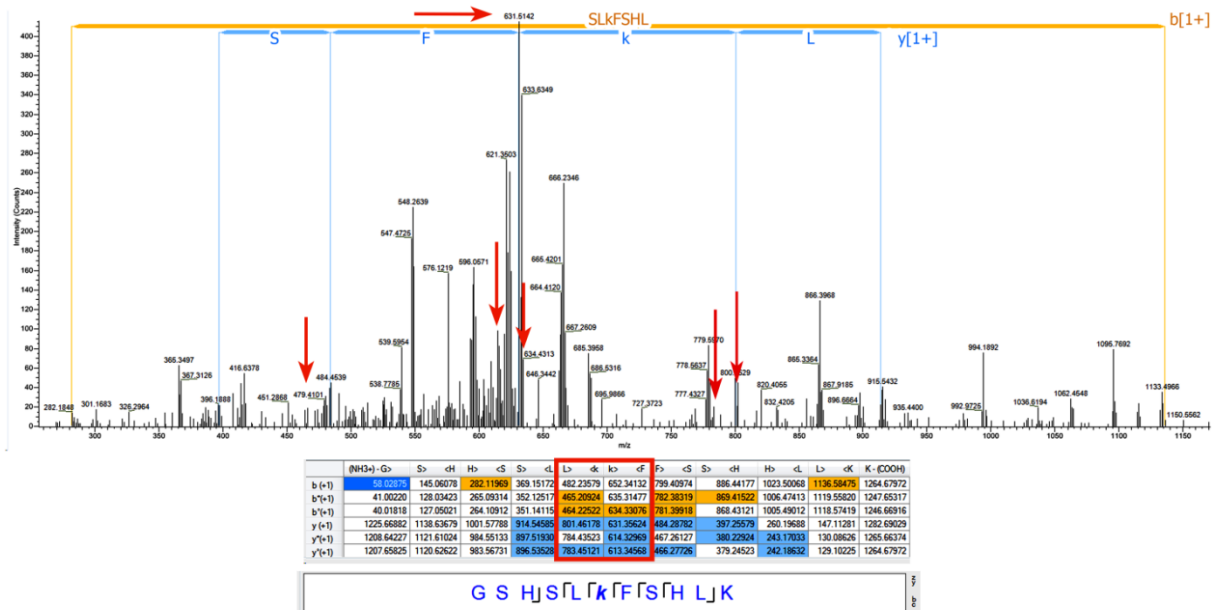


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65 **Fig. E9.** MS/MS spectrum of Polymorphic membrane protein F (Q2TGH5) acetylated peptide
 66 GSHSLK*FSLK

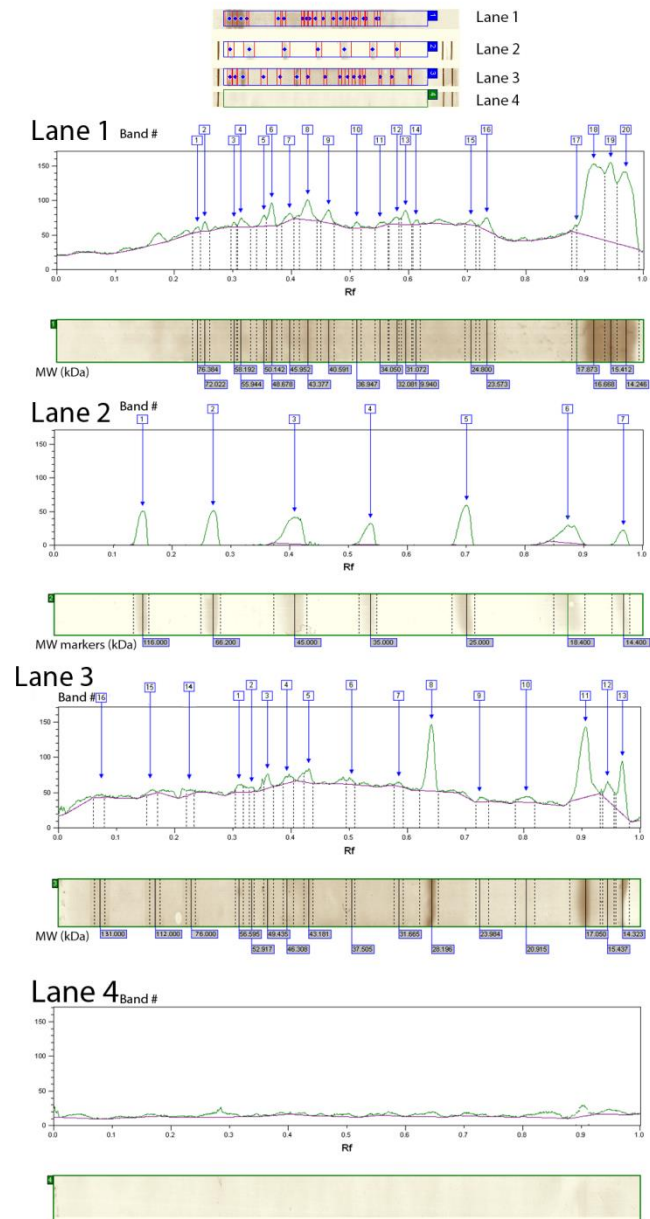
67 [Figure is double column wide, dimensions 19 cm x 10 cm, 500ppi]



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70 **Fig. E10.** Acetylated CtB band detection, estimation of band intensities and molecular weight. [Figure
 71 is single column wide, dimensions 9 cm x 17cm, 500ppi]



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74 **Table E1.** SEQUEST identification of 263 CtB protein hits with peptide FDR of 5%. Abbreviations:
75 Cov. = protein sequence coverage, # Uniq. Pep. = number of unique peptides, # PSMs = number of
76 peptide-spectrum matches

Accession	Description	Score	Cov. [%]	# Uniq. Pep.	# PSMs	MW [kDa]	calc. pI
P23421	Major outer membrane porin, serovar B OS=Chlamydia trachomatis GN=ompA PE=2 SV=1 - [MOMP_B_CHLTH]	5588.16	77.92	8	3684	42.5	5.34
Q3KMQ9	60 kDa chaperonin OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=groL PE=2 SV=3 - [CH60_CHLTA]	2448.06	86.21	30	2079	58.1	5.35
A0A0E9B231	Major outer membrane porin OS=Chlamydia trachomatis GN=ompA PE=3 SV=1 - [A0A0E9B231_CHLTH]	2156.77	45.29	1	1684	42.5	5.25
Q6U5G5	Major outer membrane porin (Fragment) OS=Chlamydia trachomatis GN=omp1 PE=3 SV=1 - [Q6U5G5_CHLTH]	2077.27	88.89	1	1706	31.2	5.10
A0A0E9GFA8	FKBP-type peptidyl-prolyl cis-trans isomerase (Trigger factor) OS=Chlamydia trachomatis GN=ERS133248_06388 PE=4 SV=1 - [A0A0E9GFA8_CHLTH]	1147.64	88.00	1	5641	25.8	9.06
Q6JBB5	Major outer membrane porin (Fragment) OS=Chlamydia trachomatis GN=ompA PE=3 SV=1 - [Q6JBB5_CHLTH]	882.47	46.69	1	847	27.5	5.00
G4NMG9	Elongation factor Tu OS=Chlamydia trachomatis serovar A (strain A2497) GN=tuf PE=3 SV=1 - [G4NMG9_CHLT4]	838.85	100.00	20	813	43.9	5.54
O84631	30S ribosomal protein S4 OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=rpsD PE=3 SV=1 - [RS4_CHLTR]	717.65	79.90	1	1114	23.7	9.99
A1X2C1	Major outer membrane porin OS=Chlamydia trachomatis GN=ompA PE=3 SV=1 - [A1X2C1_CHLTH]	564.44	22.28	1	668	42.5	5.43
G4NNI8	Outer membrane protein OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0483 PE=4 SV=1 - [G4NNI8_CHLT4]	479.85	61.84	12	447	59.3	7.21
G4NMY4	Chaperone protein DnaK OS=Chlamydia trachomatis serovar A (strain A2497) GN=dnaK PE=2 SV=1 - [G4NMY4_CHLT4]	472.07	86.12	14	781	71.2	5.14
Q2TV29	Polymorphic membrane protein D OS=Chlamydia trachomatis GN=pmpD PE=4 SV=1 - [Q2TV29_CHLTH]	397.14	58.39	9	542	160.6	4.86
A0A0E9FG31	Uncharacterized membrane-bound protein conserved in bacteria OS=Chlamydia trachomatis GN=ERS095036_13607 PE=4 SV=1 - [A0A0E9FG31_CHLTH]	393.45	65.33	1	278	25.3	9.45
A0A0E9CLT4	ATP synthase subunit beta OS=Chlamydia trachomatis GN=sctN_2 PE=3 SV=1 - [A0A0E9CLT4_CHLTH]	359.81	67.36	3	311	53.6	6.49
Q2TCJ4	Polymorphic membrane protein G OS=Chlamydia trachomatis GN=pmpG PE=4 SV=1 - [Q2TCJ4_CHLTH]	355.73	44.32	10	450	107.3	5.60
A0A0E9AUH9	Uncharacterised protein OS=Chlamydia trachomatis GN=ERS066953_01257 PE=4 SV=1 - [A0A0E9AUH9_CHLTH]	335.20	77.64	1	350	18.6	5.25
A0A0E9DIU3	Gag gene protein p24 (Core nucleocapsid protein) OS=Chlamydia trachomatis GN=ERS082929_01031 PE=4 SV=1 - [A0A0E9DIU3_CHLTH]	324.94	78.57	6	546	65.7	8.78
G4NM38	Manganese-binding protein OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0072 PE=3 SV=1 - [G4NM38_CHLT4]	320.50	92.00	9	306	39.8	5.90
G4NMM0	Uncharacterized protein OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0629 PE=4 SV=1 - [G4NMM0_CHLT4]	315.38	79.73	8	343	44.0	9.23
A0A0E9CQD9	CHLPN 76 kD protein-like OS=Chlamydia trachomatis GN=ERS075195_00406 PE=4 SV=1 - [A0A0E9CQD9_CHLTH]	283.82	85.43	11	324	50.0	8.18
A0A0E9DC36	Gag gene protein p24 (Core nucleocapsid protein) OS=Chlamydia trachomatis GN=ERS082928_02139 PE=4 SV=1 - [A0A0E9DC36_CHLTH]	282.46	82.87	1	262	31.6	8.91
A0A0E9B124	Transaldolase OS=Chlamydia trachomatis GN=talA PE=3 SV=1 - [A0A0E9B124_CHLTH]	216.87	70.95	7	307	36.1	5.03
A0A0E9GER6	Sensor histidine kinase graS OS=Chlamydia trachomatis GN=graS_2 PE=4 SV=1 - [A0A0E9GER6_CHLTH]	208.60	72.34	1	424	32.6	9.31
O84681	Probable Yop proteins translocation protein C/general secretion pathway protein OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=yscC PE=3 SV=1 - [O84681_CHLTR]	185.56	52.12	8	696	100.5	5.77
G4NP64	Outer membrane protein OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0263 PE=4 SV=1 - [G4NP64_CHLT4]	183.78	66.29	6	451	88.7	9.03
A0A0E9AZX3	Uncharacterised protein OS=Chlamydia trachomatis GN=ERS066953_00091 PE=4 SV=1 - [A0A0E9AZX3_CHLTH]	181.93	62.99	2	571	41.8	9.79
A0A0E9DHV0	Transcription termination factor Rho OS=Chlamydia trachomatis GN=rho PE=3 SV=1 - [A0A0E9DHV0_CHLTH]	180.72	76.08	7	336	51.7	7.36
A0A0E9CRR3	Putative nucleotide transport protein OS=Chlamydia trachomatis GN=tlcA_1 PE=4 SV=1 - [A0A0E9CRR3_CHLTH]	178.42	22.83	1	211	24.4	9.95
A0A0H2X3D0	DO serine protease OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=htrA PE=4 SV=1 - [A0A0H2X3D0_CHLTA]	175.01	44.67	4	269	53.3	7.02
G4NMP7	Thioredoxin peroxidase OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0654 PE=4 SV=1 - [G4NMP7_CHLT4]	173.43	90.15	7	162	22.7	5.01
A0A0E9EQQ0	Uncharacterized protein involved in outer membrane biogenesis	172.61	69.47	1	1193	165.2	6.83

	OS=Chlamydia trachomatis GN=ERS095036_05921 PE=4 SV=1 - [A0A0E9EQQ0_CHLTH]						
O84588	Protein CT_584 OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=CT_584 PE=3 SV=1 - [Y584_CHLTR]	171.18	95.63	6	215	21.1	5.87
G4NMJ8	Type III secretion cytoplasmic membrane protein SctJ OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0609 PE=4 SV=1 - [G4NMJ8_CHLT4]	170.62	66.47	5	402	37.0	6.24
A0A0H2X1M5	Phosphopeptide binding protein OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=CTA_0721 PE=4 SV=1 - [A0A0H2X1M5_CHLTA]	168.83	48.25	8	214	89.6	4.60
B0B8W9	Histone H1-like protein Hc1 OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=hctA PE=1 SV=1 - [HCT1_CHLT2]	160.66	91.20	3	512	13.7	10.70
A0A0E9CZH0	Putative membrane transport protein OS=Chlamydia trachomatis GN=invA PE=4 SV=1 - [A0A0E9CZH0_CHLTH]	159.20	62.01	3	381	77.9	8.07
G4NNI1	Elongation factor G OS=Chlamydia trachomatis serovar A (strain A2497) GN=fusA PE=3 SV=1 - [G4NNI1_CHLT4]	156.39	79.77	6	367	77.4	5.34
A0A0E9FQ09	ATP synthase subunit alpha OS=Chlamydia trachomatis GN=sctN_2 PE=3 SV=1 - [A0A0E9FQ09_CHLTH]	153.28	57.34	1	244	55.4	5.12
Q3KMX6	Probable cytosol aminopeptidase OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=pepA PE=3 SV=1 - [AMPA_CHLTA]	153.21	76.15	9	211	54.0	6.00
A0A0E9EUP2	ATP synthase subunit alpha OS=Chlamydia trachomatis GN=sctN_2 PE=3 SV=1 - [A0A0E9EUP2_CHLTH]	148.70	35.91	1	186	56.1	5.05
Q2TGM5	Polymorphic membrane protein B OS=Chlamydia trachomatis GN=pmpB PE=4 SV=1 - [Q2TGM5_CHLTH]	147.60	40.61	8	480	182.9	6.02
G4NPG0	Peptidyl-prolyl cis-trans isomerase OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0591 PE=4 SV=1 - [G4NPG0_CHLT4]	146.09	98.00	6	193	27.6	5.55
Q6JBC5	Major outer membrane porin (Fragment) OS=Chlamydia trachomatis GN=ompA PE=3 SV=1 - [Q6JBC5_CHLTH]	143.13	23.35	1	100	27.6	5.43
A0A0E9CZX7	Type III secretion system ATPase OS=Chlamydia trachomatis GN=sctN PE=4 SV=1 - [A0A0E9CZX7_CHLTH]	142.61	76.24	8	223	48.2	5.81
O84591	Enolase OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=eno PE=3 SV=1 - [ENO_CHLTR]	141.08	46.23	6	170	45.4	4.73
A0A0E9D6X4	Putative membrane associated protein OS=Chlamydia trachomatis GN=ERS075185_00609 PE=4 SV=1 - [A0A0E9D6X4_CHLTH]	140.57	87.78	1	42	9.8	8.60
Q3KMQ8	10 kDa chaperonin OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=groS PE=3 SV=1 - [CH10_CHLTA]	133.53	100.00	2	164	11.2	4.94
P0CE08	DNA-directed RNA polymerase subunit alpha OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=rpoA PE=3 SV=1 - [RPOA_CHLTR]	133.17	75.33	5	876	41.8	5.47
G4NM27	Polymorphic outer membrane protein OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0952 PE=4 SV=1 - [G4NM27_CHLT4]	132.64	49.66	7	219	108.7	6.77
O84805	50S ribosomal protein L25 OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=rplY PE=3 SV=1 - [RL25_CHLTR]	131.93	83.78	3	149	20.4	8.76
P0CE13	Glyceraldehyde-3-phosphate dehydrogenase OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=gap PE=3 SV=1 - [G3P_CHLTR]	131.45	60.48	5	160	36.3	5.90
A0A0E9D9R5	Conjugal transfer ATP-binding protein TraC OS=Chlamydia trachomatis GN=ERS082928_01152 PE=4 SV=1 - [A0A0E9D9R5_CHLTH]	130.40	100.00	1	851	18.6	9.07
A0A0E9FFW1	Sigma-54 dependent response regulator OS=Chlamydia trachomatis GN=arIR_5 PE=4 SV=1 - [A0A0E9FFW1_CHLTH]	130.19	64.98	1	128	24.9	5.24
Q2TGH5	Polymorphic membrane protein F OS=Chlamydia trachomatis GN=pmpF PE=4 SV=1 - [Q2TGH5_CHLTH]	125.11	51.55	7	342	112.7	8.43
G4NMA4	30S ribosomal protein S9 OS=Chlamydia trachomatis serovar A (strain A2497) GN=rpsI PE=3 SV=1 - [G4NMA4_CHLT4]	123.69	92.48	2	243	15.0	11.03
B0B8Q5	Elongation factor Ts OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=tsf PE=3 SV=1 - [EFTS_CHLT2]	120.65	90.78	5	188	30.9	5.90
A0A0E9GBH4	Fimbrial subunit type 1 OS=Chlamydia trachomatis GN=ERS133248_04370 PE=4 SV=1 - [A0A0E9GBH4_CHLTH]	119.62	85.60	1	1099	53.7	7.68
A0A0E9FTZ2	Plasmid recombination enzyme OS=Chlamydia trachomatis GN=ERS133249_01967 PE=4 SV=1 - [A0A0E9FTZ2_CHLTH]	118.23	85.42	1	668	56.4	8.63
G4NN42	UPF0109 protein CTO_0716 OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0716 PE=3 SV=1 - [G4NN42_CHLT4]	113.93	100.00	6	114	9.2	9.04
Q83U05	Polymorphic membrane protein E (Fragment) OS=Chlamydia trachomatis GN=pmpE PE=4 SV=1 - [Q83U05_CHLTH]	113.56	44.92	5	236	101.6	7.21
A1X5G7	30S ribosomal protein S2 OS=Chlamydia trachomatis GN=rs2 PE=3 SV=1 - [A1X5G7_CHLTH]	113.18	79.79	7	209	31.1	6.70
A0A0E9DGI7	30S ribosomal protein S3 OS=Chlamydia trachomatis GN=rpsC PE=3 SV=1 - [A0A0E9DGI7_CHLTH]	108.61	95.54	2	301	24.3	10.02
O84849	Polyribonucleotide nucleotidyltransferase OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=pnp PE=3 SV=1 - [PNP_CHLTR]	104.78	57.84	6	600	75.5	5.78
Q58HD1	Major outer membrane porin (Fragment) OS=Chlamydia trachomatis GN=omp1 PE=3 SV=1 - [Q58HD1_CHLTH]	103.49	24.60	1	65	33.9	4.88

A0A0E9FSE8	60 kDa chaperonin OS=Chlamydia trachomatis GN=groEL_2 PE=3 SV=1 - [A0A0E9FSE8_CHLTH]	100.29	81.66	1	164	24.6	5.54
A0A0E9AUP2	ATPase associated with various cellular activities family protein OS=Chlamydia trachomatis GN=clpB_3 PE=4 SV=1 - [A0A0E9AUP2_CHLTH]	99.90	78.72	1	358	21.4	7.47
B0B882	30S ribosomal protein S11 OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=rpsK PE=3 SV=1 - [RS11_CHLT2]	99.66	81.82	4	152	13.8	11.25
G4NNU8	Uncharacterized protein OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0001 PE=4 SV=1 - [G4NNU8_CHLT4]	99.24	68.08	3	655	66.0	7.34
A0A0E9G5H8	Maltodextrin-binding protein mdxE OS=Chlamydia trachomatis GN=mdxE_1 PE=4 SV=1 - [A0A0E9G5H8_CHLTH]	94.52	49.89	1	179	45.7	4.96
A0A0E9B081	ATP-dependent Clp protease%2C subunit B OS=Chlamydia trachomatis GN=clpB PE=3 SV=1 - [A0A0E9B081_CHLTH]	89.17	78.20	6	476	96.6	5.47
B0B9D5	50S ribosomal protein L19 OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=rplS PE=3 SV=1 - [RL19_CHLT2]	87.62	88.43	1	188	13.1	9.94
B2XRL5	TarP OS=Chlamydia trachomatis GN=tarP PE=4 SV=1 - [B2XRL5_CHLTH]	87.09	39.96	5	133	111.7	4.44
P38002	ATP-dependent Clp protease proteolytic subunit 1 OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=clpP1 PE=3 SV=3 - [CLPP1_CHLTR]	86.87	78.65	2	102	21.1	5.59
G4NM69	Transcription termination/antitermination protein NusA OS=Chlamydia trachomatis serovar A (strain A2497) GN=nusA PE=3 SV=1 - [G4NM69_CHLT4]	84.11	79.95	4	170	48.9	5.14
B0BCD9	Nucleoside diphosphate kinase OS=Chlamydia trachomatis serovar L2b (strain UCH-1/proctitis) GN=ndk PE=3 SV=1 - [NDK_CHLTB]	83.56	51.06	2	118	15.3	5.49
A0A0E9DPP4	Putative protease OS=Chlamydia trachomatis GN=ERS095037_01179 PE=4 SV=1 - [A0A0E9DPP4_CHLTH]	82.35	63.88	5	255	65.9	6.58
A0A0E9DN19	Putative type III secretion system membrane protein OS=Chlamydia trachomatis GN=copB PE=4 SV=1 - [A0A0E9DN19_CHLTH]	77.73	56.26	1	999	50.3	9.13
K0GGT0	Ribosome-recycling factor OS=Chlamydia trachomatis GN=frr PE=3 SV=1 - [K0GGT0_CHLTH]	74.70	90.50	3	186	20.0	8.56
O84217	Probable fructose-bisphosphate aldolase class 1 OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=fbaB PE=3 SV=1 - [ALF1_CHLTR]	73.61	63.51	5	166	38.0	6.79
A0A0E9D869	Protein disulfide isomerase OS=Chlamydia trachomatis GN=dsbH_2 PE=4 SV=1 - [A0A0E9D869_CHLTH]	73.37	84.76	3	83	18.5	8.32
Q3KM43	50S ribosomal protein L11 OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=rplK PE=3 SV=1 - [RL11_CHLTA]	72.34	100.00	3	169	15.1	9.67
Q3KLI8	30S ribosomal protein S13 OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=rpsM PE=3 SV=1 - [RS13_CHLTA]	69.99	94.26	3	202	13.9	11.02
O84100	30S ribosomal protein S1 OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=rpsA PE=3 SV=1 - [RS1_CHLTR]	69.90	62.74	5	189	63.5	5.27
A0A0E9G077	Putative UDP-N-acetylglucosamine--N-acetylmuramyl- (Pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase OS=Chlamydia trachomatis GN=murG_2 PE=4 SV=1 - [A0A0E9G077_CHLTH]	69.88	54.44	1	217	37.5	9.54
B0B895	50S ribosomal protein L16 OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=rplP PE=3 SV=1 - [RL16_CHLT2]	69.18	88.41	2	185	15.8	11.30
H6V6T8	DNA-directed RNA polymerase subunit beta OS=Chlamydia trachomatis (strain L2c) GN=rpoB PE=3 SV=1 - [H6V6T8_CHLTC]	68.86	69.73	2	403	140.0	5.91
Q6HA48	PmpC OS=Chlamydia trachomatis GN=pmpC PE=4 SV=1 - [Q6HA48_CHLTH]	68.61	38.85	4	531	187.9	4.61
Q83TT3	Major outer membrane protein OS=Chlamydia trachomatis GN=porB PE=4 SV=1 - [Q83TT3_CHLTH]	68.26	63.53	2	126	37.3	5.39
B0B930	50S ribosomal protein L9 OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=rplI PE=3 SV=1 - [RL9_CHLT2]	67.72	92.81	1	153	18.4	6.55
A0A0E9AR22	Uncharacterized protein OS=Chlamydia trachomatis GN=greA_1 PE=3 SV=1 - [A0A0E9AR22_CHLTH]	67.31	66.71	7	496	80.9	5.38
P0A4C8	30S ribosomal protein S5 OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=rpsE PE=3 SV=1 - [RS5_CHLTR]	65.70	66.06	3	244	17.8	9.85
Q3KM48	DNA-directed RNA polymerase subunit beta' OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=rpoC PE=3 SV=1 - [RPOC_CHLTA]	65.61	63.97	5	794	154.8	7.44
Q84FU2	Polymorphic membrane protein I (Fragment) OS=Chlamydia trachomatis GN=pmpI PE=4 SV=1 - [Q84FU2_CHLTH]	65.56	45.63	2	184	92.0	6.60
A4IET9	Cation efflux system protein OS=Chlamydia trachomatis GN=ERS066953_00279 PE=4 SV=1 - [A4IET9_CHLTH]	63.89	80.15	4	201	60.9	6.21
A0A0E9CC48	Enoyl-ACP reductase OS=Chlamydia trachomatis GN=fabI PE=4 SV=1 - [A0A0E9CC48_CHLTH]	63.04	42.28	3	92	31.9	5.66
B0B8T1	ATP-dependent Clp protease ATP-binding subunit ClpX OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=clpX PE=3 SV=1 - [CLPX_CHLT2]	62.51	89.50	5	193	46.2	5.72
B0B899	50S ribosomal protein L2 OS=Chlamydia trachomatis serovar L2	62.02	91.20	5	156	31.5	10.55

	(strain 434/Bu / ATCC VR-902B) GN=rplB PE=3 SV=1 - [RL2_CHLT2]						
A0A0E9CU90	ATP-dependent zinc metalloprotease FtsH OS=Chlamydia trachomatis GN=ftsH PE=3 SV=1 - [A0A0E9CU90_CHLTH]	62.01	68.89	3	441	101.6	6.19
G4NMV6	Uncharacterized protein OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0404 PE=4 SV=1 - [G4NMV6_CHLT4]	59.78	57.94	3	103	52.0	8.95
O84066	6-phosphogluconate dehydrogenase, decarboxylating OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=gnd PE=3 SV=1 - [6PGD_CHLTR]	59.62	58.54	5	97	52.6	5.44
B0B7Z0	50S ribosomal protein L21 OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=rplU PE=3 SV=1 - [RL21_CHLT2]	59.11	96.26	2	89	12.2	9.28
A0A0H2X0S9	60 kDa inner membrane protein OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=CTA_0273 PE=4 SV=1 - [A0A0H2X0S9_CHLTA]	58.71	46.89	1	347	88.0	8.81
B0B928	30S ribosomal protein S6 OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=rpsF PE=3 SV=1 - [RS6_CHLT2]	58.62	57.14	2	68	12.9	8.81
A0A0E9CT27	Integration host factor beta-subunit OS=Chlamydia trachomatis GN=hupA PE=3 SV=1 - [A0A0E9CT27_CHLTH]	58.48	93.24	1	478	17.0	10.61
A0A0E9G085	Leucine dehydrogenase OS=Chlamydia trachomatis GN=ldh PE=3 SV=1 - [A0A0E9G085_CHLTH]	58.37	61.04	5	86	33.0	5.29
A0A0E9EH39	Uncharacterised protein OS=Chlamydia trachomatis GN=ERS095036_03703 PE=4 SV=1 - [A0A0E9EH39_CHLTH]	56.73	64.52	1	189	24.3	6.38
Q3KLI3	50S ribosomal protein L6 OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=rplF PE=3 SV=1 - [RL6_CHLTA]	56.69	96.17	4	125	19.9	9.96
A0A0E9CKW5	Putative type III secretion system chaperone OS=Chlamydia trachomatis GN=ERS075193_00737 PE=4 SV=1 - [A0A0E9CKW5_CHLTH]	56.54	80.84	1	414	18.4	5.16
A0A0E9EVW0	Septal ring factor OS=Chlamydia trachomatis GN=envC_1 PE=4 SV=1 - [A0A0E9EVW0_CHLTH]	55.76	63.82	1	387	45.1	8.84
A0A0E9DFJ6	Protein of uncharacterised function%2C DUF582 OS=Chlamydia trachomatis GN=ERS082930_00129 PE=4 SV=1 - [A0A0E9DFJ6_CHLTH]	55.22	47.84	1	283	92.6	5.01
A0A0E9AS56	Uncharacterised protein OS=Chlamydia trachomatis GN=ERS066953_00847 PE=4 SV=1 - [A0A0E9AS56_CHLTH]	54.05	95.00	1	260	9.2	8.35
G4NMD9	Superoxide dismutase OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0316 PE=3 SV=1 - [G4NMD9_CHLT4]	53.49	74.31	1	101	24.9	6.73
A0A0E9GCU2	Dihydroxyacetone kinase OS=Chlamydia trachomatis GN=ERS133248_04181 PE=4 SV=1 - [A0A0E9GCU2_CHLTH]	53.06	52.44	1	339	59.8	4.64
A0A0E9CYI8	50S ribosomal protein L10 OS=Chlamydia trachomatis GN=rplJ PE=3 SV=1 - [A0A0E9CYI8_CHLTH]	52.54	75.00	3	120	18.8	6.34
A0A0E9FV45	Amino acid ABC transporter substrate-binding protein OS=Chlamydia trachomatis GN=fliY PE=4 SV=1 - [A0A0E9FV45_CHLTH]	51.14	53.26	3	74	29.0	7.37
A0A0E9E9K2	Protein translocase subunit OS=Chlamydia trachomatis GN=ERS066953_01398 PE=4 SV=1 - [A0A0E9E9K2_CHLTH]	50.57	51.75	1	140	12.8	9.20
A0A0E9DQU8	Chaperone protein DnaK OS=Chlamydia trachomatis GN=dnaK_1 PE=2 SV=1 - [A0A0E9DQU8_CHLTH]	50.42	69.86	1	358	68.3	4.92
A0A0E9FZX9	DNA strand transferase OS=Chlamydia trachomatis GN=mobA PE=4 SV=1 - [A0A0E9FZX9_CHLTH]	49.48	83.57	1	473	66.4	7.39
A0A0E9DJ74	30S ribosomal protein S16 OS=Chlamydia trachomatis GN=rpsP PE=3 SV=1 - [A0A0E9DJ74_CHLTH]	49.14	100.00	2	97	13.4	10.37
A0A0E9CB95	Alpha-1,4 glucan phosphorylase OS=Chlamydia trachomatis GN=glgP PE=3 SV=1 - [A0A0E9CB95_CHLTH]	47.59	71.38	2	254	92.8	5.96
G4NNS7	6,7-dimethyl-8-ribityllumazine synthase OS=Chlamydia trachomatis serovar A (strain A2497) GN=ribH PE=3 SV=1 - [G4NNS7_CHLT4]	47.57	53.37	3	53	17.2	7.75
A0A0E9FM37	Uncharacterised protein OS=Chlamydia trachomatis GN=ERS095036_16868 PE=4 SV=1 - [A0A0E9FM37_CHLTH]	47.18	86.36	1	77	7.5	8.34
A0A0E9DXC5	Chaperone protein HtpG OS=Chlamydia trachomatis GN=htpG PE=3 SV=1 - [A0A0E9DXC5_CHLTH]	47.02	61.24	1	153	76.4	5.07
Q3KLX6	Glucose-6-phosphate isomerase OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=pgi PE=3 SV=2 - [G6PI_CHLTA]	45.54	53.63	8	53	57.6	6.06
A0A0E9EQM9	ECM-binding protein homolog OS=Chlamydia trachomatis GN=ebh PE=4 SV=1 - [A0A0E9EQM9_CHLTH]	45.52	83.71	1	915	111.8	5.39
A0A0E9CCK9	Transcription termination/antitermination protein NusG OS=Chlamydia trachomatis GN=nusG PE=3 SV=1 - [A0A0E9CCK9_CHLTH]	43.92	100.00	6	130	20.7	5.31
A0A0E9G4T4	Uncharacterised protein OS=Chlamydia trachomatis GN=ERS133250_01363 PE=4 SV=1 - [A0A0E9G4T4_CHLTH]	43.86	93.62	1	109	5.3	9.63
A0A0E9FU79	Type III secretion chaperone OS=Chlamydia trachomatis GN=scc1 PE=4 SV=1 - [A0A0E9FU79_CHLTH]	42.74	100.00	1	62	10.4	9.11
A0A0E9EQ15	Internalin-A OS=Chlamydia trachomatis GN=inlA_3 PE=4 SV=1 - [A0A0E9EQ15_CHLTH]	42.72	74.45	1	314	50.6	5.16
B0B891	50S ribosomal protein L24 OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=rplX PE=3 SV=1 - [RL24_CHLT2]	42.14	90.09	1	308	12.6	10.43

O84357	Peptide deformylase OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=def PE=3 SV=1 - [DEF_CHLTR]	41.90	88.95	4	64	20.5	5.96
G4NNH5	Serine hydroxymethyltransferase OS=Chlamydia trachomatis serovar A (strain A2497) GN=glyA PE=3 SV=1 - [G4NNH5_CHLT4]	40.83	68.05	4	174	55.2	6.71
B0B9B0	Glutamyl-tRNA(Gln) amidotransferase subunit A OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=gatA PE=3 SV=1 - [GATA_CHLT2]	40.32	61.30	4	246	53.6	6.23
O84712	ATP-dependent Clp protease proteolytic subunit 2 OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=clpP2 PE=3 SV=1 - [CLPP2_CHLTR]	40.21	56.65	1	80	22.0	5.25
A0A0E9D2R6	MotA/TolQ/ExbB proton channel family protein OS=Chlamydia trachomatis GN=exbB PE=3 SV=1 - [A0A0E9D2R6_CHLTH]	40.19	28.88	2	54	25.9	9.17
G4NMW2	Malate dehydrogenase OS=Chlamydia trachomatis serovar A (strain A2497) GN=mdh PE=3 SV=1 - [G4NMW2_CHLT4]	39.56	61.13	1	153	37.1	7.87
G4NND8	DNA gyrase subunit A OS=Chlamydia trachomatis serovar A (strain A2497) GN=gyrA PE=3 SV=1 - [G4NND8_CHLT4]	39.08	74.64	1	373	94.1	6.68
A0A0E9GG53	Galactoside transport system permease protein mgIC OS=Chlamydia trachomatis GN=mgIC PE=4 SV=1 - [A0A0E9GG53_CHLTH]	38.80	17.54	1	60	30.1	8.85
G4NPN0	Ribonuclease E OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0880 PE=4 SV=1 - [G4NPN0_CHLT4]	37.37	63.62	2	342	60.9	7.55
A0A0E9DYC9	Uncharacterized vancomycin resistance protein OS=Chlamydia trachomatis GN=ERS133246_02510 PE=4 SV=1 - [A0A0E9DYC9_CHLTH]	37.10	60.87	1	463	64.8	8.31
K0GB74	CHLPN 76kDa-like protein OS=Chlamydia trachomatis GN=CT622 PE=4 SV=1 - [K0GB74_CHLTH]	36.94	78.98	1	317	68.5	4.92
A0A0E9C7V3	50S ribosomal protein L17 OS=Chlamydia trachomatis GN=rpIQ PE=3 SV=1 - [A0A0E9C7V3_CHLTH]	36.14	86.52	2	224	16.2	11.37
B0B8V5	Serine--tRNA ligase OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=serS PE=3 SV=1 - [SYS_CHLT2]	35.77	49.30	1	228	48.4	6.09
B0BAX0	4-hydroxy-3-methylbut-2-enyl diphosphate reductase OS=Chlamydia trachomatis serovar L2b (strain UCH-1/proctitis) GN=ispH PE=3 SV=1 - [ISPH_CHLTB]	34.62	52.44	2	106	34.2	6.37
A0A0E9AR09	Thioredoxin reductase OS=Chlamydia trachomatis GN=trxB PE=3 SV=1 - [A0A0E9AR09_CHLTH]	34.38	72.36	4	72	37.8	7.61
A0A0E9CZR0	Type III secretion system protein OS=Chlamydia trachomatis GN=sctQ PE=4 SV=1 - [A0A0E9CZR0_CHLTH]	34.20	54.69	2	48	41.1	4.64
B0B9B1	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=gatB PE=3 SV=1 - [GATB_CHLT2]	34.14	53.28	3	127	54.9	6.32
O84713	Trigger factor OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=tig PE=3 SV=1 - [TIG_CHLTR]	34.13	74.66	1	220	50.1	5.08
A0A0E9DIS5	3-oxoacyl-[acyl-carrier-protein] synthase 2 OS=Chlamydia trachomatis GN=fabF PE=3 SV=1 - [A0A0E9DIS5_CHLTH]	33.74	42.34	2	135	44.8	5.59
A0A0E9C8B1	50S ribosomal protein L13 OS=Chlamydia trachomatis GN=rpIM PE=3 SV=1 - [A0A0E9C8B1_CHLTH]	33.62	100.00	1	129	16.8	10.13
G4NMZ7	DnaK suppressor protein OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0442 PE=4 SV=1 - [G4NMZ7_CHLT4]	33.53	95.56	3	79	15.3	5.60
G4NM99	Elongation factor P OS=Chlamydia trachomatis serovar A (strain A2497) GN=efp PE=3 SV=1 - [G4NM99_CHLT4]	30.91	87.57	1	115	20.5	5.25
A0A0E9E330	Anti-sigma factor antagonist OS=Chlamydia trachomatis GN=btrV PE=3 SV=1 - [A0A0E9E330_CHLTH]	30.67	97.41	3	57	12.5	5.39
K0G9B2	Uridylate kinase OS=Chlamydia trachomatis GN=pyrH PE=3 SV=1 - [K0G9B2_CHLTH]	30.39	68.16	2	56	26.1	5.48
A0A0E9ERX5	Uncharacterised protein OS=Chlamydia trachomatis GN=ERS095036_06689 PE=4 SV=1 - [A0A0E9ERX5_CHLTH]	30.39	84.00	1	608	43.5	9.09
A0A0E9EYP0	Mevalonate kinase OS=Chlamydia trachomatis GN=ERS095036_08052 PE=4 SV=1 - [A0A0E9EYP0_CHLTH]	30.30	36.76	1	44	40.5	6.35
W8VNJ2	Major outer membrane porin (Fragment) OS=Chlamydia trachomatis GN=ompA PE=3 SV=1 - [W8VNJ2_CHLTH]	28.81	44.44	1	77	36.8	4.98
B0B7Q0	Pyruvate kinase OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=pyk PE=3 SV=1 - [KPYK_CHLT2]	28.27	78.97	2	135	53.6	6.40
G4NM39	Manganese transport system ATP-binding protein OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0073 PE=3 SV=1 - [G4NM39_CHLT4]	27.99	59.15	1	88	31.7	7.15
K0GBL9	Uncharacterized protein OS=Chlamydia trachomatis GN=CT694 PE=4 SV=1 - [K0GBL9_CHLTH]	27.77	60.99	1	113	34.6	5.17
B0B810	30S ribosomal protein S7 OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=rpsG PE=3 SV=1 - [RS7_CHLT2]	27.67	98.09	1	183	17.8	9.83
G4NN30	Protein RecA OS=Chlamydia trachomatis serovar A (strain A2497) GN=recA PE=3 SV=1 - [G4NN30_CHLT4]	27.40	63.47	3	130	41.9	9.04
B0B889	30S ribosomal protein S8 OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=rpsH PE=3 SV=1 - [RS8_CHLT2]	27.23	100.00	1	88	15.1	10.27
O84125	Biotin carboxyl carrier protein of acetyl-CoA carboxylase OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=accB PE=3 SV=1 - [BCCP_CHLTR]	26.54	68.90	3	81	18.2	5.12
A0A0E9ASB8	2-oxoglutarate dehydrogenase E1 component OS=Chlamydia	26.22	49.39	1	243	102.5	5.48

	trachomatis GN=sucA PE=4 SV=1 - [A0A0E9ASB8_CHLTH]						
A0A0E9FMW1	Putative phosphoenolpyruvate-protein phosphotransferase OS=Chlamydia trachomatis GN=ppdK PE=4 SV=1 - [A0A0E9FMW1_CHLTH]	26.18	51.37	1	233	97.4	5.11
O84757	Elongation factor P 2 OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=efp2 PE=3 SV=1 - [EFP2_CHLTR]	26.00	60.53	2	94	21.5	5.08
G4NME9	V-type sodium ATP synthase subunit K OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0326 PE=4 SV=1 - [G4NME9_CHLT4]	25.66	91.22	1	19	15.2	8.31
Q3KLH9	50S ribosomal protein L14 OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=rplN PE=3 SV=1 - [RL14_CHLTA]	25.17	82.79	1	89	13.4	9.80
A0A0E9CH94	Chaperone protein DnaJ OS=Chlamydia trachomatis GN=dnaJ PE=3 SV=1 - [A0A0E9CH94_CHLTH]	25.16	73.21	1	146	41.9	7.62
A0A0E9D3Q4	Outer membrane protein OS=Chlamydia trachomatis GN=ompH PE=4 SV=1 - [A0A0E9D3Q4_CHLTH]	23.56	63.58	1	394	19.4	4.88
A0A0E9F7I6	Sensor histidine kinase DcuS OS=Chlamydia trachomatis GN=dcuS_2 PE=4 SV=1 - [A0A0E9F7I6_CHLTH]	23.55	58.23	1	138	55.8	5.11
A0A0E9C8R9	50S ribosomal protein L18 OS=Chlamydia trachomatis GN=rplR PE=3 SV=1 - [A0A0E9C8R9_CHLTH]	23.34	90.24	1	86	13.4	10.32
O84294	Deoxyuridine 5'-triphosphate nucleotidohydrolase OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=dut PE=3 SV=1 - [DUT_CHLTR]	23.20	77.24	2	21	15.3	5.22
A0A0E9FTP1	Cation transporter E1-E2 family ATPase OS=Chlamydia trachomatis GN=zosA PE=3 SV=1 - [A0A0E9FTP1_CHLTH]	23.17	47.76	1	205	45.7	5.29
A0A0E9AYD3	Proline dipeptidase OS=Chlamydia trachomatis GN=pepP PE=4 SV=1 - [A0A0E9AYD3_CHLTH]	22.83	51.40	1	102	39.3	5.59
A0A0H2X383	Uncharacterized protein OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=CTA_0913 PE=4 SV=1 - [A0A0H2X383_CHLTA]	22.63	55.62	3	290	76.3	6.14
A0A0E9ATU0	Oligoendopeptidase F OS=Chlamydia trachomatis GN=pepF PE=4 SV=1 - [A0A0E9ATU0_CHLTH]	21.79	49.01	2	90	69.0	5.95
A0A0E9B0S2	DNA-invertase hin OS=Chlamydia trachomatis GN=hin_2 PE=4 SV=1 - [A0A0E9B0S2_CHLTH]	21.77	87.21	1	564	60.5	9.22
A0A0E9G967	Translation initiation factor IF-3 OS=Chlamydia trachomatis GN=infC_3 PE=3 SV=1 - [A0A0E9G967_CHLTH]	21.75	78.47	1	237	23.5	9.51
Q3KM44	50S ribosomal protein L1 OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=rplA PE=3 SV=1 - [RL1_CHLTA]	21.39	78.45	1	131	24.7	8.92
O84220	5'-nucleotidase SurE OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=surE PE=3 SV=2 - [SURE_CHLTR]	21.34	51.24	5	36	31.5	5.05
G4NPE4	50S ribosomal protein L4 OS=Chlamydia trachomatis serovar A (strain A2497) GN=rplD PE=3 SV=1 - [G4NPE4_CHLT4]	21.31	96.10	1	171	25.6	9.82
A0A0E9FZA9	Lon protease OS=Chlamydia trachomatis GN=lon1 PE=2 SV=1 - [A0A0E9FZA9_CHLTH]	21.07	73.50	1	475	91.9	7.39
A0A0E9DTU0	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase OS=Chlamydia trachomatis GN=gpmA_1 PE=3 SV=1 - [A0A0E9DTU0_CHLTH]	20.37	61.66	1	133	29.0	6.07
A0A0E9C3X0	Succinyl-CoA synthetase subunit alpha OS=Chlamydia trachomatis GN=sucD PE=3 SV=1 - [A0A0E9C3X0_CHLTH]	20.34	58.76	2	60	30.2	5.31
A0A0E9CWD9	Malonyl CoA-acyl carrier protein transacylase OS=Chlamydia trachomatis GN=fabD PE=3 SV=1 - [A0A0E9CWD9_CHLTH]	20.17	41.88	2	133	33.5	4.92
A0A0E9CZ71	Dihydroipoamide succinyltransferase OS=Chlamydia trachomatis GN=sucB_2 PE=3 SV=1 - [A0A0E9CZ71_CHLTH]	20.16	66.58	1	98	40.3	5.31
A0A0E9CFX5	HAD superfamily hydrolase/phosphatase OS=Chlamydia trachomatis GN=ERS075185_00712 PE=4 SV=1 - [A0A0E9CFX5_CHLTH]	19.99	64.77	3	37	34.2	5.22
A0A0E9ATY1	Putative cytosolic protein OS=Chlamydia trachomatis GN=ERS066953_00424 PE=4 SV=1 - [A0A0E9ATY1_CHLTH]	19.78	61.59	1	48	18.4	4.61
A0A0E9CKN6	MAC/perforin family protein OS=Chlamydia trachomatis GN=ERS075193_00650 PE=4 SV=1 - [A0A0E9CKN6_CHLTH]	19.72	49.14	1	209	90.8	6.47
G4NM37	Uncharacterized protein OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0071 PE=4 SV=1 - [G4NM37_CHLT4]	19.54	85.64	1	192	20.6	10.07
Q3KL01	Phosphoglycerate kinase OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=pgk PE=3 SV=1 - [PGK_CHLTA]	18.98	52.61	1	199	43.0	6.00
O84600	Thio:disulfide Interchange Protein OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=dsbD PE=4 SV=1 - [O84600_CHLTR]	18.85	37.72	1	121	76.1	6.73
A0A0E9CNE8	Anti-sigma factor antagonist OS=Chlamydia trachomatis GN=rbsV PE=3 SV=1 - [A0A0E9CNE8_CHLTH]	17.45	97.27	1	128	12.4	7.85
G4NMX4	MYG1 protein OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0421 PE=4 SV=1 - [G4NMX4_CHLT4]	17.28	43.09	1	166	34.9	6.05
A0A0E9EEQ7	Peptidoglycan associated lipoprotein OS=Chlamydia trachomatis GN=pal PE=3 SV=1 - [A0A0E9EEQ7_CHLTH]	17.19	47.03	1	54	23.1	8.65
A0A0E9FSX3	DNA polymerase I OS=Chlamydia trachomatis GN=polA PE=4 SV=1 - [A0A0E9FSX3_CHLTH]	16.59	75.36	1	145	8.0	6.28
G4NM46	DNA polymerase III subunit beta OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0080 PE=4 SV=1 - [G4NM46_CHLT4]	16.43	71.26	2	118	47.9	6.42
A0A0E9CBL1	Phosphoglucosamine mutase OS=Chlamydia trachomatis GN=glmM	16.38	74.89	1	122	49.4	6.48

	PE=3 SV=1 - [A0A0E9CBL1_CHLTH]						
A0A0E9CFY7	3-ketoacyl-ACP reductase OS=Chlamydia trachomatis GN=fabG PE=3 SV=1 - [A0A0E9CFY7_CHLTH]	16.09	71.37	2	39	26.0	7.93
A0A0E9CFX6	Protein RsbW OS=Chlamydia trachomatis GN=btrW PE=4 SV=1 - [A0A0E9CFX6_CHLTH]	16.02	69.86	1	41	16.4	6.16
G4NNY3	Methionine--tRNA ligase OS=Chlamydia trachomatis serovar A (strain A2497) GN=metG PE=3 SV=1 - [G4NNY3_CHLT4]	16.01	63.64	2	115	62.7	5.25
A0A0E9FZH4	Protein of uncharacterised function (DUF1207) OS=Chlamydia trachomatis GN=ERS066954_00213 PE=4 SV=1 - [A0A0E9FZH4_CHLTH]	15.96	30.96	2	50	46.9	5.82
Q3KKK4	50S ribosomal protein L20 OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=rplT PE=3 SV=1 - [RL20_CHLTA]	15.04	90.24	1	146	13.9	11.91
K0G1P9	Uncharacterized protein OS=Chlamydia trachomatis GN=CT214 PE=4 SV=1 - [K0G1P9_CHLTH]	15.00	44.16	1	223	60.1	8.92
K0G334	Uncharacterized protein OS=Chlamydia trachomatis GN=CT288 PE=4 SV=1 - [K0G334_CHLTH]	14.82	50.44	1	238	63.1	8.59
A0A0E9DFS3	Integrase DNA binding domain OS=Chlamydia trachomatis GN=ERS082928_02137 PE=4 SV=1 - [A0A0E9DFS3_CHLTH]	14.59	59.56	1	250	108.2	8.79
A0A0E9CCI4	Dihydrolipoyl dehydrogenase OS=Chlamydia trachomatis GN=pdhD PE=4 SV=1 - [A0A0E9CCI4_CHLTH]	14.41	62.37	1	135	49.4	6.80
A0A0E9G272	Thioredoxin OS=Chlamydia trachomatis GN=trxA PE=4 SV=1 - [A0A0E9G272_CHLTH]	14.21	100.00	1	16	7.7	6.54
A0A0E9ATV2	Putative metallo-phosphoesterase OS=Chlamydia trachomatis GN=ERS066954_00132 PE=4 SV=1 - [A0A0E9ATV2_CHLTH]	14.20	50.15	1	69	36.5	9.10
G4NND5	6-phosphogluconolactonase OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0204 PE=4 SV=1 - [G4NND5_CHLT4]	14.17	63.36	1	69	29.8	5.40
A0A0E9DPU3	Protein of uncharacterised function (DUF2709) OS=Chlamydia trachomatis GN=ERS066953_00763 PE=4 SV=1 - [A0A0E9DPU3_CHLTH]	13.96	71.43	1	112	27.5	5.39
O84820	Uncharacterized protein OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=CT_814 PE=4 SV=1 - [O84820_CHLTR]	13.95	96.24	1	100	15.6	10.80
O84640	Protein CT_635 OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=CT_635 PE=3 SV=1 - [Y635_CHLTR]	13.48	100.00	1	127	16.8	6.58
B0BBG8	Thymidylate kinase OS=Chlamydia trachomatis serovar L2b (strain UCh-1/proctitis) GN=tmk PE=3 SV=1 - [KTHY_CHLTB]	13.26	56.65	2	35	22.4	7.03
Q3KLH4	50S ribosomal protein L22 OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=rplV PE=3 SV=1 - [RL22_CHLTA]	13.04	98.20	1	113	12.4	11.34
A0A0E9D067	SH3 domain-containing protein OS=Chlamydia trachomatis GN=ERS075185_00625 PE=4 SV=1 - [A0A0E9D067_CHLTH]	12.89	71.14	1	146	48.5	7.74
A0A0E9GA42	DNA topoisomerase 1 OS=Chlamydia trachomatis GN=topA_5 PE=3 SV=1 - [A0A0E9GA42_CHLTH]	12.55	88.38	1	612	79.2	8.98
A0A0E9ASF7	Putative lipoprotein OS=Chlamydia trachomatis GN=ERS066953_00128 PE=4 SV=1 - [A0A0E9ASF7_CHLTH]	12.52	46.05	1	33	24.0	8.98
A0A0E9C683	Insulinase family metalloprotease OS=Chlamydia trachomatis GN=ERS075185_00552 PE=3 SV=1 - [A0A0E9C683_CHLTH]	12.35	53.29	2	224	109.3	5.44
B7SBR8	DppF OS=Chlamydia trachomatis GN=dppF PE=3 SV=1 - [B7SBR8_CHLTH]	12.30	63.04	1	59	31.0	9.54
A0A0H2X0H9	Uncharacterized protein OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=CTA_0012 PE=4 SV=1 - [A0A0H2X0H9_CHLTA]	12.20	70.33	1	197	48.0	7.61
G4NPB1	Protease IV OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0541 PE=4 SV=1 - [G4NPB1_CHLT4]	11.63	47.40	2	158	37.5	8.47
Q3KLQ4	Glutamate--tRNA ligase OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=gltX PE=3 SV=1 - [SYE_CHLTA]	11.44	64.82	1	164	58.5	6.57
B1Q047	Major outer membrane porin (Fragment) OS=Chlamydia trachomatis GN=omp1 PE=3 SV=1 - [B1Q047_CHLTH]	10.94	34.10	1	21	28.3	4.79
A0A0E9D018	Glycerol-3-phosphate dehydrogenase [NAD(P)+] OS=Chlamydia trachomatis GN=gpsA PE=3 SV=1 - [A0A0E9D018_CHLTH]	10.94	26.65	1	61	36.1	7.81
A0A0E9B1N6	Replicative DNA helicase OS=Chlamydia trachomatis GN=dnaB_2 PE=4 SV=1 - [A0A0E9B1N6_CHLTH]	10.84	59.17	1	133	67.2	5.31
A0A0E9DDT9	Fructose-bisphosphate aldolase OS=Chlamydia trachomatis GN=fba_1 PE=4 SV=1 - [A0A0E9DDT9_CHLTH]	10.72	100.00	1	58	10.3	8.43
A0A0E9CPU5	Putative outer membrane protein OS=Chlamydia trachomatis GN=ERS075195_00212 PE=4 SV=1 - [A0A0E9CPU5_CHLTH]	10.65	70.93	1	178	32.6	9.10
B0B7F9	UDP-3-O-acylglucosamine N-acyltransferase OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=lpxD PE=3 SV=1 - [LPXD_CHLT2]	10.55	39.55	1	93	38.4	7.69
A0A0E9C884	AMP nucleosidase OS=Chlamydia trachomatis GN=amn PE=4 SV=1 - [A0A0E9C884_CHLTH]	10.42	42.21	1	41	32.0	7.05
B0B9C6	Isoleucine--tRNA ligase OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=ileS PE=3 SV=1 - [SYI_CHLT2]	9.89	45.95	1	690	118.7	5.53
Q3KLT4	50S ribosomal protein L27 OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=rpmA PE=3 SV=1 - [RL27_CHLTA]	9.70	97.59	1	35	8.9	11.03
G4NM49	Bifunctional protein FoId OS=Chlamydia trachomatis serovar A	9.32	55.71	2	124	31.1	7.58

	(strain A2497) GN=folD PE=3 SV=1 - [G4NM49_CHLT4]						
A0A0E9B1G0	MutT/Nudix family protein OS=Chlamydia trachomatis GN=ERS066953_01175 PE=3 SV=1 - [A0A0E9B1G0_CHLTH]	9.24	57.33	1	37	17.4	5.12
A0A0E9FST2	Cysteine--tRNA ligase OS=Chlamydia trachomatis GN=cysS_1 PE=3 SV=1 - [A0A0E9FST2_CHLTH]	9.21	45.60	1	112	57.5	6.46
A0A0E9CES6	Methyltransferase OS=Chlamydia trachomatis GN=rsmD PE=4 SV=1 - [A0A0E9CES6_CHLTH]	9.02	49.47	2	63	20.9	8.44
A0A0E9G6Y0	GTPase Obg OS=Chlamydia trachomatis GN=obg_2 PE=3 SV=1 - [A0A0E9G6Y0_CHLTH]	8.80	64.90	1	225	47.8	5.27
A0A0H2X2J0	Uncharacterized protein OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=CTA_0578 PE=4 SV=1 - [A0A0H2X2J0_CHLTA]	8.71	71.48	1	135	31.0	9.04
B0B7M2	V-type ATP synthase subunit D OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=atpD PE=3 SV=1 - [VATD_CHLT2]	8.50	70.94	1	165	23.2	8.98
A0A0H2X241	Fumarate hydratase OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=fumC PE=4 SV=1 - [A0A0H2X241_CHLTA]	8.46	39.74	1	195	50.3	6.52
A0A0E9DXH9	Domain of Uncharacterised Function (DUF349) OS=Chlamydia trachomatis GN=ERS133246_02573 PE=4 SV=1 - [A0A0E9DXH9_CHLTH]	8.34	67.39	1	199	51.8	6.01
A0A0E9ATW3	Long chain fatty acid--ACP ligase OS=Chlamydia trachomatis GN=aas PE=4 SV=1 - [A0A0E9ATW3_CHLTH]	7.95	40.04	1	134	59.4	7.40
A0A0E9FIX0	Uncharacterized conserved protein OS=Chlamydia trachomatis GN=ERS095036_15907 PE=4 SV=1 - [A0A0E9FIX0_CHLTH]	7.78	60.00	1	19	8.6	6.57
A0A0E9DER9	Chlamydia protein associating with death domains OS=Chlamydia trachomatis GN=ERS075193_00154 PE=4 SV=1 - [A0A0E9DER9_CHLTH]	7.45	48.23	1	56	26.1	5.05
A0A0E9C7D8	Type III secretion system protein OS=Chlamydia trachomatis GN=flif PE=4 SV=1 - [A0A0E9C7D8_CHLTH]	7.27	49.70	1	121	37.1	6.98
A0A0E9DI70	1-deoxy-D-xylulose 5-phosphate reductoisomerase OS=Chlamydia trachomatis GN=dxr PE=3 SV=1 - [A0A0E9DI70_CHLTH]	7.19	46.97	1	314	41.7	6.06
O84463	Probable transcriptional regulatory protein CT_457 OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=CT_457 PE=3 SV=1 - [Y457_CHLTR]	7.11	70.59	1	173	26.5	5.90
A0A0E9C5V1	Aromatic amino acid aminotransferase OS=Chlamydia trachomatis GN=aspC_1 PE=3 SV=1 - [A0A0E9C5V1_CHLTH]	6.98	63.00	1	63	44.6	5.60
A0A0E9CTJ7	50S ribosomal protein L15 OS=Chlamydia trachomatis GN=rpLO PE=3 SV=1 - [A0A0E9CTJ7_CHLTH]	6.81	68.67	1	75	18.6	10.23
G4NPL7	Glycine--tRNA ligase OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0867 PE=3 SV=1 - [G4NPL7_CHLT4]	6.45	39.96	1	173	115.9	6.42
A0A0H2X242	HflX OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=hflX PE=4 SV=1 - [A0A0H2X242_CHLTA]	6.44	70.47	1	161	50.8	7.42
G4NNL4	Histidine kinase OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0511 PE=4 SV=1 - [G4NNL4_CHLT4]	6.20	76.14	1	55	39.8	5.88
A0A0E9D121	SwiB complex protein OS=Chlamydia trachomatis GN=ERS075185_00164 PE=4 SV=1 - [A0A0E9D121_CHLTH]	6.17	94.19	1	117	9.7	9.70
B0B925	Glycogen synthase OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=glgA PE=3 SV=1 - [GLGA_CHLT2]	5.31	46.62	1	75	53.4	5.94
A0A0E9GJ50	Tryptophanyl-tRNA synthetase OS=Chlamydia trachomatis GN=trpS_6 PE=4 SV=1 - [A0A0E9GJ50_CHLTH]	5.22	100.00	1	37	8.7	7.25
A0A0E9EK24	VanZ like family OS=Chlamydia trachomatis GN=ERS095036_05267 PE=4 SV=1 - [A0A0E9EK24_CHLTH]	4.90	56.40	1	25	19.8	8.92
B0RK54	Major outer membrane porin (Fragment) OS=Chlamydia trachomatis GN=omp1 PE=3 SV=1 - [B0RK54_CHLTH]	4.90	34.95	1	152	33.1	5.30
A0A0E9D3A0	Uncharacterised protein OS=Chlamydia trachomatis GN=ERS075185_00879 PE=4 SV=1 - [A0A0E9D3A0_CHLTH]	4.48	44.39	1	60	21.9	5.59
O84859	Methionine aminopeptidase OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=map PE=3 SV=1 - [MAP1_CHLTR]	4.45	54.30	1	50	32.6	6.51
K0GAB8	Uncharacterized protein OS=Chlamydia trachomatis GN=CT229 PE=4 SV=1 - [K0GAB8_CHLTH]	3.20	63.26	1	82	23.4	8.38
O84309	V-type ATP synthase beta chain OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=atpB PE=3 SV=1 - [VATB_CHLTR]	2.81	47.72	1	187	48.7	5.99

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79 **Table E2.** PEAKS DB identification of 239 CtB protein hits with FDR of 5% (on peptide level) and
80 0% (on protein level). Abbreviations: Cov. = protein sequence coverage, # Uniq. Pep. = number of
81 unique peptides # Pep. = number of peptides

Accession	Description	Score (-10lgP)	Cov [%]	# Pep.	# Uniq. Pep	MW (kDa)
G4NM84 G4NM84_CHLT4	60 kDa chaperonin OS=Chlamydia trachomatis serovar A (strain A2497) GN=groL PE=3 SV=1	361.4	82	73	4	58.1
sp Q3KMQ9 CH60_CHLTA	60 kDa chaperonin OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=groL PE=2 SV=3	361.4	82	73	4	58.1
G4NMP7 G4NMP7_CHLT4	Thioredoxin peroxidase OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0654 PE=4 SV=1	268.5	70	17	17	22.7
A0A0H2X1C0 A0A0H2X1C0_CHLTA	Thioredoxin peroxidase OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=ahpC PE=4 SV=1	268.5	70	17	17	22.7
B6EE12 B6EE12_CHLTH	Major outer membrane porin (Fragment) OS=Chlamydia trachomatis GN=omp1 PE=3 SV=1	263.8	64	59	2	39.4
sp Q3KMX6 AMPA_CHLTA	Probable cytosol aminopeptidase OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=pepA PE=3 SV=1	263.4	43	17	3	54.1
A0A0E9DIU3 A0A0E9DIU3_CHLTH	Gag gene protein p24 (Core nucleocapsid protein) OS=Chlamydia trachomatis GN=ERS082929_01031 PE=4 SV=1	260.6	34	19	4	65.7
A0A0E9CT34 A0A0E9CT34_CHLTH	Elongation factor Tu OS=Chlamydia trachomatis GN=tuf PE=3 SV=1	260.0	81	39	3	43.3
sp Q3KM40 EFTU_CHLTA	Elongation factor Tu OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=tuf PE=3 SV=1	260.0	81	39	3	43.3
Q2TV41 Q2TV41_CHLTH	Polymorphic membrane protein D OS=Chlamydia trachomatis GN=pmpD PE=4 SV=1	254.0	18	25	2	160.7
A1X3B2 A1X3B2_CHLTH	30S ribosomal protein S2 OS=Chlamydia trachomatis GN=rs2 PE=3 SV=1	243.3	53	14	2	30.9
A0A0H2X1N0 A0A0H2X1N0_CHLTA	SctN OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=sctN PE=4 SV=1	242.0	42	16	2	48.2
G4NN56 G4NN56_CHLT4	SctN OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0726 PE=4 SV=1	242.0	42	16	2	48.2
A0A0H2X2P3 A0A0H2X2P3_CHLTA	Glyceraldehyde 3-phosphate dehydrogenase OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=gapA PE=4 SV=1	221.7	45	14	2	36.3
A0A0E9AUE0 A0A0E9AUE0_CHLTH	Uncharacterised protein OS=Chlamydia trachomatis GN=ERS066953_01368 PE=4 SV=1	213.1	68	10	10	21.1
sp O84588 Y584_CHLTR	Protein CT_584 OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=CT_584 PE=3 SV=1	213.1	68	10	10	21.1
A0A0H2X1F6 A0A0H2X1F6_CHLTA	Uncharacterized protein OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=CTA_0634 PE=4 SV=1	213.1	68	10	10	21.1
M9UIQ4 M9UIQ4_CHLTH	Uncharacterized protein OS=Chlamydia trachomatis L2/434/Bu(f) GN=CTLFINAL_04420 PE=4 SV=1	213.1	68	10	10	21.1
G4NMM5 G4NMM5_CHLT4	Uncharacterized protein OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0634 PE=4 SV=1	213.1	68	10	10	21.1
A0A0H3MCR9 A0A0H3MCR9_CHLT2	Uncharacterized protein OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=CTL0847 PE=4 SV=1	213.1	68	10	10	21.1
K0GGT0 K0GGT0_CHLTH	Ribosome-recycling factor OS=Chlamydia trachomatis GN=frr PE=3 SV=1	208.6	55	10	4	20.1
G4NN64 G4NN64_CHLT4	Ribosome-recycling factor OS=Chlamydia trachomatis serovar A (strain A2497) GN=frr PE=3 SV=1	208.6	55	10	4	20.1
A0A0H2X292 A0A0H2X292_CHLTA	Anti-sigma F factor antagonist OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=rsbV PE=4 SV=1	206.6	58	6	6	12.5
M9UM43 M9UM43_CHLTH	Anti-sigma factor antagonist OS=Chlamydia trachomatis L2/434/Bu(f) GN=CTLFINAL_03560 PE=3 SV=1	206.6	58	6	6	12.5
O84431 O84431_CHLTR	Anti-sigma factor antagonist OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=rsbV_1 PE=3 SV=1	206.6	58	6	6	12.5
A0A0E9CCK9 A0A0E9CCK9_CHLTH	Transcription termination/antitermination protein NusG OS=Chlamydia trachomatis GN=nusG PE=3 SV=1	205.7	54	8	2	20.8
A0A0H3MCF1 A0A0H3MCF1_CHLT2	Uncharacterized protein OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=CTL0028 PE=4 SV=1	204.7	88	10	10	8.8
A0A0E9D2L0 A0A0E9D2L0_CHLTH	UPF0109 protein ERS066953_00249 OS=Chlamydia trachomatis GN=ERS066953_00249 PE=3 SV=1	204.7	88	10	10	8.8
M9UG13 M9UG13_CHLTH	UPF0109 protein CTLFINAL_00155 OS=Chlamydia trachomatis L2/434/Bu(f) GN=CTLFINAL_00155 PE=3 SV=1	204.7	88	10	10	8.8
A0A0H2X2Z8 A0A0H2X2Z8_CHLTA	RNA binding protein OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=CTA_0716 PE=4 SV=1	204.7	88	10	10	8.8

sp O84666 Y659_CHLTR	UPF0109 protein CT_659 OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=CT_659 PE=3 SV=1	204.7	88	10	10	8.8
Q83TT3 Q83TT3_CHLTH	Major outer membrane protein OS=Chlamydia trachomatis GN=porB PE=4 SV=1	200.2	26	8	2	37.3
sp B0B899 RL2_CHLT2	50S ribosomal protein L2 OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=rplB PE=3 SV=1	193.3	31	10	8	31.5
sp O84530 RL2_CHLTR	50S ribosomal protein L2 OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=rplB PE=3 SV=1	193.3	31	10	8	31.5
A0A0E9AXH1 A0A0E9AXH1_CHLTH	50S ribosomal protein L2 OS=Chlamydia trachomatis GN=rplB PE=3 SV=1	193.3	31	10	8	31.5
G4NNS7 G4NNS7_CHLT4	6 7-dimethyl-8-ribityllumazine synthase OS=Chlamydia trachomatis serovar A (strain A2497) GN=ribH PE=3 SV=1	191.7	41	7	7	17.2
sp O84805 RL25_CHLTR	50S ribosomal protein L25 OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=rplY PE=3 SV=1	189.7	64	10	10	20.4
sp O84217 ALF1_CHLTR	Probable fructose-bisphosphate aldolase class 1 OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=fbaB PE=3 SV=1	185.3	45	13	3	38.0
sp O84007 GATB_CHLTR	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=gatB PE=3 SV=1	181.4	17	5	5	55.0
M9UE49 M9UE49_CHLTH	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B OS=Chlamydia trachomatis L2/434/Bu(f) GN=gatB PE=3 SV=1	181.4	17	5	5	55.0
A0A0E9CFY0 A0A0E9CFY0_CHLTH	30S ribosomal protein S1 OS=Chlamydia trachomatis GN=rpsA PE=4 SV=1	177.9	20	14	14	63.6
sp O84100 RS1_CHLTR	30S ribosomal protein S1 OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=rpsA PE=3 SV=1	177.9	20	14	14	63.6
sp B0B7S2 DEF_CHLT2	Peptide deformylase OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=def PE=3 SV=1	177.1	49	8	7	20.5
sp Q3KM05 DEF_CHLTA	Peptide deformylase OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=def PE=3 SV=1	177.1	49	8	7	20.5
G4NLX2 G4NLX2_CHLT4	DegP OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0897 PE=4 SV=1	169.7	12	6	2	53.3
sp O84031 RL19_CHLTR	50S ribosomal protein L19 OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=rplS PE=3 SV=1	164.9	49	8	8	13.1
sp B0BB14 RL19_CHLTB	50S ribosomal protein L19 OS=Chlamydia trachomatis serovar L2b (strain UCH-1/proctitis) GN=rplS PE=3 SV=1	164.9	49	8	8	13.1
A0A0E9CXI8 A0A0E9CXI8_CHLTH	Malate dehydrogenase OS=Chlamydia trachomatis GN=mdh PE=3 SV=1	162.9	26	9	2	35.7
sp O84381 MDH_CHLTR	Malate dehydrogenase OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=mdh PE=3 SV=1	162.9	26	9	2	35.7
A0A0E9CQH4 A0A0E9CQH4_CHLTH	Zn binding protein OS=Chlamydia trachomatis GN=ERS075193_00385 PE=4 SV=1	157.3	24	8	2	29.6
G4NMY6 G4NMY6_CHLT4	Zn binding protein OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0433 PE=4 SV=1	157.3	24	8	2	29.6
A0A0H2X145 A0A0H2X145_CHLTA	Zn binding protein OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=CTA_0433 PE=4 SV=1	157.3	24	8	2	29.6
A0A0E9F3I9 A0A0E9F3I9_CHLTH	ATP synthase subunit beta OS=Chlamydia trachomatis GN=sctN_4 PE=3 SV=1	153.7	11	4	3	50.7
sp B0BC75 RS7_CHLTB	30S ribosomal protein S7 OS=Chlamydia trachomatis serovar L2b (strain UCH-1/proctitis) GN=rpsG PE=3 SV=1	153.2	36	6	6	17.8
G4NNI2 G4NNI2_CHLT4	30S ribosomal protein S7 OS=Chlamydia trachomatis serovar A (strain A2497) GN=rpsG PE=3 SV=1	153.2	36	6	6	17.8
A0A0H2X1S7 A0A0H2X1S7_CHLTA	HAD superfamily hydrolase/phosphatase OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=CTA_0109 PE=4 SV=1	152.9	19	4	4	34.3
A0A0E9CFX5 A0A0E9CFX5_CHLTH	HAD superfamily hydrolase/phosphatase OS=Chlamydia trachomatis GN=ERS075185_00712 PE=4 SV=1	152.9	19	4	4	34.3
A0A0H3MLD3 A0A0H3MLD3_CHLT2	SSU ribosomal protein S5P OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=rpsE PE=4 SV=1	151.5	30	7	7	17.8
sp Q3KLI5 RS5_CHLTA	30S ribosomal protein S5 OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=rpsE PE=3 SV=1	151.5	30	7	7	17.8
A0A0E9D3E4 A0A0E9D3E4_CHLTH	30S ribosomal protein S5 OS=Chlamydia trachomatis GN=rpsE PE=3 SV=1	151.5	30	7	7	17.8
M9UIB3 M9UIB3_CHLTH	30S ribosomal protein S5 OS=Chlamydia trachomatis L2/434/Bu(f) GN=rpsE PE=3 SV=1	151.5	30	7	7	17.8
G4NNG0 G4NNG0_CHLT4	50S ribosomal protein L21 OS=Chlamydia trachomatis serovar A (strain A2497) GN=rplU PE=3 SV=1	151.5	50	5	5	12.3
sp Q3KLH6 RL16_CHLTA	50S ribosomal protein L16 OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=rplP PE=3 SV=1	148.6	25	3	3	15.8
sp B0BCG0 RL16_CHLTB	50S ribosomal protein L16 OS=Chlamydia trachomatis serovar L2b (strain UCH-1/proctitis) GN=rplP PE=3 SV=1	148.6	25	3	3	15.8
A0A0E9CFD6 A0A0E9CFD6_CHLTH	50S ribosomal protein L16 OS=Chlamydia trachomatis GN=rplP_1 PE=3 SV=1	148.6	25	3	3	15.8
Q6LCD5 Q6LCD5_CHLTH	10 kDa chaperonin (Fragment) OS=Chlamydia trachomatis GN=hypA PE=3 SV=1	148.0	64	9	9	10.7

A0A0E9CAW6 A0A0E9CAW6_CHLTH	10 kDa chaperonin OS=Chlamydia trachomatis GN=groES PE=3 SV=1	148.0	61	9	9	11.2
A0A0E9G3M0 A0A0E9G3M0_CHLTH	Transporter OS=Chlamydia trachomatis GN=ERS066954_00215 PE=4 SV=1	143.0	14	7	7	77.1
A0A0H3MH86 A0A0H3MH86_CHLT2	Uncharacterized protein OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=CTL0643 PE=4 SV=1	143.0	14	7	7	77.1
M9UEF8 M9UEF8_CHLTH	Low calcium response locus protein D OS=Chlamydia trachomatis L2/434/Bu(f) GN=CTLFINAL_01820 PE=4 SV=1	143.0	19	10	10	78.0
G4NM61 G4NM61_CHLT4	Type III secretion inner membrane protein SctV OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0095 PE=4 SV=1	143.0	19	10	10	78.0
O84092 O84092_CHLTR	Low Calcium Response D OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=lcrD PE=4 SV=1	143.0	19	10	10	78.0
A0A0H3MCY4 A0A0H3MCY4_CHLT2	Low calcium response protein D (Predicted to be part of the TTSS apparatus) OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=lcrD PE=4 SV=1	143.0	19	10	10	78.0
A0A0H2X0L8 A0A0H2X0L8_CHLTA	Low calcium response protein D OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=lcrD PE=4 SV=1	143.0	19	10	10	78.0
A0A0E9DLE6 A0A0E9DLE6_CHLTH	Putative membrane transport protein OS=Chlamydia trachomatis GN=invA PE=4 SV=1	143.0	19	10	10	78.0
A0A0E9CZH0 A0A0E9CZH0_CHLTH	Putative membrane transport protein OS=Chlamydia trachomatis GN=invA PE=4 SV=1	143.0	19	10	10	78.0
A0A0H2X1D2 A0A0H2X1D2_CHLTA	Methyltransferase OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=yhhF PE=4 SV=1	140.8	26	3	3	20.9
O84494 O84494_CHLTR	Methylase OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=yhhF PE=4 SV=1	140.8	26	3	3	20.9
A0A0H3MDP4 A0A0H3MDP4_CHLT2	Methyltransferase OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=CTL0748 PE=4 SV=1	140.8	26	3	3	20.9
sp Q3KKP0 RS6_CHLTA	30S ribosomal protein S6 OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=rpsF PE=3 SV=1	139.2	35	5	4	12.9
sp B0B928 RS6_CHLT2	30S ribosomal protein S6 OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=rpsF PE=3 SV=1	139.2	35	5	4	12.9
A0A0E9DS10 A0A0E9DS10_CHLTH	ABC transporter ATPase OS=Chlamydia trachomatis GN=dppF PE=3 SV=1	134.2	21	5	3	31.0
O84412 O84412_CHLTR	DnaK Suppressor OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=dksA PE=4 SV=1	129.8	54	6	6	13.9
A0A0H3MCC6 A0A0H3MCC6_CHLT2	DnaK suppressor protein OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=dksA PE=4 SV=1	129.8	54	6	6	13.9
A0A0E9FXT1 A0A0E9FXT1_CHLTH	DnaK suppressor protein OS=Chlamydia trachomatis GN=yock PE=4 SV=1	129.8	54	6	6	13.9
M9UHY5 M9UHY5_CHLTH	Molecular chaperone DnaK OS=Chlamydia trachomatis L2/434/Bu(f) GN=CTLFINAL_03465 PE=4 SV=2	129.8	50	6	6	15.3
A0A0E9C6W0 A0A0E9C6W0_CHLTH	Trigger factor OS=Chlamydia trachomatis GN=tig PE=3 SV=1	127.8	12	4	4	50.1
sp Q3KKY7 TIG_CHLTA	Trigger factor OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=tig PE=3 SV=1	127.8	12	4	4	50.1
M9UHS2 M9UHS2_CHLTH	Deoxyuridine 5'-triphosphate nucleotidohydrolase OS=Chlamydia trachomatis L2/434/Bu(f) GN=dut PE=3 SV=1	127.5	37	3	3	15.3
A0A0E9DSY4 A0A0E9DSY4_CHLTH	Deoxyuridine 5'-triphosphate nucleotidohydrolase OS=Chlamydia trachomatis GN=dut_2 PE=3 SV=1	127.5	37	3	3	15.3
sp B0BBS3 DUT_CHLTB	Deoxyuridine 5'-triphosphate nucleotidohydrolase OS=Chlamydia trachomatis serovar L2b (strain UCH-1/proctitis) GN=dut PE=3 SV=1	127.5	37	3	3	15.3
sp O84377 AAXA_CHLTR	Porin AaxA OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=aaxA PE=3 SV=2	125.5	20	8	8	51.5
sp Q3KLY4 AAXA_CHLTA	Porin AaxA OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=aaxA PE=3 SV=2	125.5	20	8	8	51.5
A0A0E9CU42 A0A0E9CU42_CHLTH	Carbohydrate-selective porin%2C OprB family protein OS=Chlamydia trachomatis GN=aaxA PE=4 SV=1	125.5	20	8	8	51.5
G4NMV6 G4NMV6_CHLT4	Uncharacterized protein OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0404 PE=4 SV=1	125.5	20	8	8	52.0
sp B0B930 RL9_CHLT2	50S ribosomal protein L9 OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=rplI PE=3 SV=1	125.2	43	5	5	18.4
M9ULS5 M9ULS5_CHLTH	50S ribosomal protein L9 OS=Chlamydia trachomatis L2/434/Bu(f) GN=rplI PE=3 SV=1	125.2	43	5	5	18.4
G4NPM5 G4NPM5_CHLT4	50S ribosomal protein L9 OS=Chlamydia trachomatis serovar A (strain A2497) GN=rplI PE=3 SV=1	125.2	43	5	5	18.4
sp Q3KLH4 RL22_CHLTA	50S ribosomal protein L22 OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=rplV PE=3 SV=1	124.7	42	5	3	12.5
A0A0E9CJJ3 A0A0E9CJJ3_CHLTH	50S ribosomal protein L22 OS=Chlamydia trachomatis GN=rplV_1 PE=3 SV=1	124.7	42	5	3	12.5
G4NPN91 G4NPN91_CHLT4	Integration host factor beta-subunit OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0289 PE=3 SV=1	124.5	27	4	4	17.0
M9UF21 M9UF21_CHLTH	Integration host factor OS=Chlamydia trachomatis L2/434/Bu(f) GN=CTLFINAL_04880 PE=3 SV=2	124.5	27	4	4	17.0

A0A0H2X182 A0A0H2X182_CHLTA	Hypothetical membrane associated protein OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=CTA_0002 PE=4 SV=1	122.7	40	2	2	9.8
A0A0H3MCS7 A0A0H3MCS7_CHLT2	Putative membrane protein OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=CTLO256 PE=4 SV=1	122.7	40	2	2	9.8
M9UKV6 M9UKV6_CHLTH	Membrane protein OS=Chlamydia trachomatis L2/434/Bu(f) GN=CTLFINAL_01355 PE=4 SV=1	122.7	40	2	2	9.8
G4NNU9 G4NNU9_CHLT4	Putative membrane associated protein OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0002 PE=4 SV=1	122.7	40	2	2	9.8
M9UM80 M9UM80_CHLTH	Type III secretion system chaperone OS=Chlamydia trachomatis L2/434/Bu(f) GN=CTLFINAL_01575 PE=4 SV=1	121.9	38	6	6	18.4
A0A0H3MBJ5 A0A0H3MBJ5_CHLT2	Putative type III secretion system chaperone OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=CTLO299 PE=4 SV=1	121.9	38	6	6	18.4
G4NNK4 G4NNK4_CHLT4	Probable transcriptional regulatory protein CTO_0499 OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0499 PE=3 SV=1	120.0	10	2	2	26.5
sp B0B830 Y717_CHLT2	Probable transcriptional regulatory protein CTL0717 OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=CTL0717 PE=3 SV=1	120.0	10	2	2	26.5
A0A0E9EDI2 A0A0E9EDI2_CHLTH	Serine--tRNA ligase OS=Chlamydia trachomatis GN=serS_1 PE=3 SV=1	118.6	16	5	5	48.4
sp Q3KKW5 SYS_CHLTA	Serine--tRNA ligase OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=serS PE=3 SV=1	118.6	16	5	5	48.3
G4NPH1 G4NPH1_CHLT4	Elongation factor P OS=Chlamydia trachomatis serovar A (strain A2497) GN=efp PE=3 SV=1	117.5	28	5	3	21.5
sp O84757 EFP2_CHLTR	Elongation factor P 2 OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=efp2 PE=3 SV=1	117.5	28	5	3	21.5
A0A0H2X366 A0A0H2X366_CHLTA	Translation elongation factor P OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=efp_2 PE=4 SV=1	117.5	28	5	3	21.5
G4NPM8 G4NPM8_CHLT4	Insulin-degrading enzyme OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0878 PE=4 SV=1	115.3	3	3	2	108.4
O84776 O84776_CHLTR	Hydrolase/phosphatase homolog OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=CT_771 PE=3 SV=1	114.0	25	3	3	17.4
A0A0H2X385 A0A0H2X385_CHLTA	Phosphohydrolase (MutT/nudix family protein) OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=CTA_0841 PE=4 SV=1	114.0	25	3	3	17.4
G4NPJ0 G4NPJ0_CHLT4	Phosphohydrolase (MutT/nudix family protein) OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0841 PE=4 SV=1	114.0	25	3	3	17.4
A0A0E9DK93 A0A0E9DK93_CHLTH	MutT/Nudix family protein OS=Chlamydia trachomatis GN=ERS075193_00895 PE=3 SV=1	114.0	25	3	3	17.4
sp Q3KMZ0 SYM_CHLTA	Methionine--tRNA ligase OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=metG PE=3 SV=1	113.6	12	5	5	62.7
A0A0E9DB98 A0A0E9DB98_CHLTH	Methionine--tRNA ligase OS=Chlamydia trachomatis GN=metG_1 PE=3 SV=1	113.6	12	5	5	62.7
A0A0E9D4E7 A0A0E9D4E7_CHLTH	Glutamate--tRNA ligase OS=Chlamydia trachomatis GN=gltX PE=3 SV=1	112.9	7	3	3	58.6
G4NNJ1 G4NNJ1_CHLT4	Glutamate--tRNA ligase OS=Chlamydia trachomatis serovar A (strain A2497) GN=gltX PE=3 SV=1	112.9	7	3	3	58.5
M9UI50 M9UI50_CHLTH	Metallophosphoesterase OS=Chlamydia trachomatis L2/434/Bu(f) GN=CTLFINAL_03765 PE=4 SV=1	110.8	17	4	4	37.1
sp Q3KKY8 CLPP2_CHLTA	ATP-dependent Clp protease proteolytic subunit 2 OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=clpP2 PE=3 SV=1	108.1	26	4	4	22.0
M9ULH7 M9ULH7_CHLTH	ATP-dependent Clp protease proteolytic subunit OS=Chlamydia trachomatis L2/434/Bu(f) GN=clpP PE=3 SV=1	108.1	26	4	4	22.0
A0A0E9C8U7 A0A0E9C8U7_CHLTH	Ribonuclease E OS=Chlamydia trachomatis GN=rng PE=4 SV=1	108.1	14	5	5	59.4
A0A0H2X210 A0A0H2X210_CHLTA	Ribonuclease E OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=cafE PE=4 SV=1	108.1	14	5	5	59.3
M9UKL6 M9UKL6_CHLTH	Ribonuclease G OS=Chlamydia trachomatis L2/434/Bu(f) GN=CTLFINAL_00950 PE=4 SV=1	108.1	14	5	5	59.4
A0A0H3MBC8 A0A0H3MBC8_CHLT2	Ribonuclease E OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=cafE PE=4 SV=1	108.1	14	5	5	59.4
O84814 O84814_CHLTR	Axial Filament Protein OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=cafE PE=4 SV=1	108.1	14	5	5	59.3
A0A0E9DHL4 A0A0E9DHL4_CHLTH	Ribonuclease E OS=Chlamydia trachomatis GN=rng PE=4 SV=1	108.1	14	5	5	59.3
G4NPN0 G4NPN0_CHLT4	Ribonuclease E OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0880 PE=4 SV=1	108.1	14	5	5	60.9
A0A0E9CMC9 A0A0E9CMC9_CHLTH	Elongation factor P OS=Chlamydia trachomatis GN=efp-2 PE=3 SV=1	108.1	24	3	3	19.5
A0A0H2X1G3 A0A0H2X1G3_CHLTA	Translation elongation factor P OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13)	108.1	23	3	3	20.5

	GN=efp_1 PE=4 SV=1					
sp O84124 EFP1_CHLTR	Elongation factor P 1 OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=efp1 PE=3 SV=1	108.1	23	3	3	20.5
A0A0E9D1J8 A0A0E9D1J8_CHLTH	Protein RsbW OS=Chlamydia trachomatis GN=btrW PE=4 SV=1	107.7	41	5	5	16.4
O84553 O84553_CHLTR	Sigma regulatory factor-histidine kinase OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=rsbW PE=4 SV=1	107.7	41	5	5	16.4
A0A0E9CFX6 A0A0E9CFX6_CHLTH	Protein RsbW OS=Chlamydia trachomatis GN=btrW PE=4 SV=1	107.7	41	5	5	16.4
M9UMJ4 M9UMJ4_CHLTH	Histidine kinase OS=Chlamydia trachomatis L2/434/Bu(f) GN=CTLFINAL_04235 PE=4 SV=1	107.7	41	5	5	16.4
A0A0H3MLE8 A0A0H3MLE8_CHLT2	Sigma regulatory factor-histidine kinase OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=rsbW PE=4 SV=1	107.7	41	5	5	16.4
G4NPG9 G4NPG9_CHLT4	RsbW OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0599 PE=4 SV=1	107.7	39	5	5	17.3
A0A0H3MGR8 A0A0H3MGR8_CHLT2	Biotin carboxyl carrier protein of acetyl-CoA carboxylase OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=accB PE=4 SV=1	107.6	34	3	3	18.2
A0A0E9D783 A0A0E9D783_CHLTH	Acetyl-CoA carboxylase biotin carboxyl carrier protein subunit OS=Chlamydia trachomatis GN=accB PE=4 SV=1	107.6	34	3	3	18.2
A0A0E9FWY4 A0A0E9FWY4_CHLTH	MotA/TolQ/ExbB proton channel family protein OS=Chlamydia trachomatis GN=exbB PE=3 SV=1	107.2	14	2	2	25.9
M9UFX8 M9UFX8_CHLTH	Dihydrolipoyl dehydrogenase OS=Chlamydia trachomatis L2/434/Bu(f) GN=CTLFINAL_04275 PE=4 SV=1	105.3	12	5	5	49.5
A0A0H2X2R2 A0A0H2X2R2_CHLTA	Dihydrolipoamide dehydrogenase OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=lpdA PE=4 SV=1	105.3	12	5	5	49.5
A0A0E9CS98 A0A0E9CS98_CHLTH	Dihydrolipoyl dehydrogenase OS=Chlamydia trachomatis GN=pdhD PE=4 SV=1	105.3	12	5	5	49.5
A0A0H3MHJ2 A0A0H3MHJ2_CHLT2	Dihydrolipoamide dehydrogenase OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=lpdA PE=4 SV=1	105.3	12	5	5	49.5
A0A0E9CCI4 A0A0E9CCI4_CHLTH	Dihydrolipoyl dehydrogenase OS=Chlamydia trachomatis GN=pdhD PE=4 SV=1	105.3	12	5	5	49.5
M9UI72 M9UI72_CHLTH	Oxidoreductase OS=Chlamydia trachomatis L2/434/Bu(f) GN=CTLFINAL_03620 PE=4 SV=1	102.1	11	4	4	39.9
A0A0H2X2I2 A0A0H2X2I2_CHLTA	NADPH-cytochrome P450 reductase OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=cysJ PE=4 SV=1	102.1	11	4	4	39.9
G4NNH9 G4NNH9_CHLT4	NADPH-cytochrome P450 reductase OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0475 PE=4 SV=1	102.1	11	4	4	39.9
O84442 O84442_CHLTR	Sulfite Reductase OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=cysJ PE=4 SV=1	102.1	11	4	4	39.9
sp B0B916 FOLD_CHLT2	Bifunctional protein FoID OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=foID PE=3 SV=1	101.2	23	4	4	30.9
sp B0BB65 FOLD_CHLTB	Bifunctional protein FoID OS=Chlamydia trachomatis serovar L2b (strain UCH-1/proctitis) GN=foID PE=3 SV=1	101.2	23	4	4	30.9
A0A0H3MCJ3 A0A0H3MCJ3_CHLT2	Anti-sigma F factor antagonist OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=rsbV PE=4 SV=1	98.5	16	2	2	12.4
O84770 O84770_CHLTR	Anti-sigma factor antagonist OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=rsbV_2 PE=3 SV=1	98.5	16	2	2	12.4
sp O84586 PARA_CHLTR	ParA family protein CT_582 OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=CT_582 PE=3 SV=1	97.7	24	4	4	28.2
A0A0H3MDT7 A0A0H3MDT7_CHLT2	Chromosome partitioning ATPase (ParA family) OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=minD PE=4 SV=1	97.7	24	4	4	28.2
A0A0E9DFM9 A0A0E9DFM9_CHLTH	ATPase%2C ParA FAMILY OS=Chlamydia trachomatis GN=soj_1 PE=4 SV=1	97.7	24	4	4	28.2
A0A0E9D3V4 A0A0E9D3V4_CHLTH	ATPase%2C ParA FAMILY OS=Chlamydia trachomatis GN=soj_1 PE=4 SV=1	97.7	24	4	4	28.2
M9UMM8 M9UMM8_CHLTH	Chromosome partitioning protein ParA OS=Chlamydia trachomatis L2/434/Bu(f) GN=CTLFINAL_04410 PE=4 SV=1	97.7	24	4	4	28.2
G4NMM3 G4NMM3_CHLT4	ATPase ParA FAMILY OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0632 PE=4 SV=1	97.7	24	4	4	28.6
A0A0E9DV71 A0A0E9DV71_CHLTH	ATPase%2C ParA FAMILY OS=Chlamydia trachomatis GN=soj_4 PE=4 SV=1	97.7	24	4	4	28.6
sp B0B929 RS18_CHLT2	30S ribosomal protein S18 OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=rpsR PE=3 SV=1	97.2	42	4	4	9.4
sp Q3KKN9 RS18_CHLTA	30S ribosomal protein S18 OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=rpsR PE=3 SV=1	97.2	42	4	4	9.4
A0A0E9DK62 A0A0E9DK62_CHLTH	30S ribosomal protein S18 OS=Chlamydia trachomatis GN=rpsR PE=3 SV=1	97.2	42	4	4	9.4
A0A0E9DH16 A0A0E9DH16_CHLTH	GTPase HflX OS=Chlamydia trachomatis GN=hflX PE=3 SV=1	94.8	5	2	2	50.9
G4NPI2 G4NPI2_CHLT4	RNA binding protein OS=Chlamydia trachomatis serovar A	92.1	24	3	3	15.5

	(strain A2497) GN=CTO_0833 PE=3 SV=1					
A0A0E9CW55 A0A0E9CW55_CHLTH	Peptidoglycan associated lipoprotein OS=Chlamydia trachomatis GN=pal PE=3 SV=1	91.7	11	2	2	21.5
M9UNW8 M9UNW8_CHLTH	Membrane protein OS=Chlamydia trachomatis L2/434/Bu(f) GN=CTLFINAL_04505 PE=3 SV=1	91.7	11	2	2	21.5
A0A0H2X2P6 A0A0H2X2P6_CHLTA	Peptidoglycan-associated lipoprotein OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=pal PE=4 SV=1	91.7	11	2	2	21.5
A0A0H3MDU9 A0A0H3MDU9_CHLT2	Peptidoglycan-associated lipoprotein OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=pal PE=4 SV=1	91.7	11	2	2	21.5
A0A0H3MB37 A0A0H3MB37_CHLT2	Cytochrome d ubiquinol oxidase subunit I OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=cydA PE=4 SV=1	91.2	6	3	2	50.2
A0A0H2X0C7 A0A0H2X0C7_CHLTA	Cytochrome d ubiquinol oxidase subunit I OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=cydA PE=4 SV=1	91.2	6	3	2	50.2
O84016 O84016_CHLTR	Cytochrome Oxidase Subunit I OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=cydA PE=4 SV=1	91.2	6	3	2	50.2
A0A0E9CQK7 A0A0E9CQK7_CHLTH	Uncharacterized conserved protein OS=Chlamydia trachomatis GN=ERS075194_01595 PE=4 SV=1	90.9	26	3	3	18.3
sp P66123 RL27_CHLTR	50S ribosomal protein L27 OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=rpmA PE=3 SV=1	90.3	33	2	2	8.9
A0A0E9C7I7 A0A0E9C7I7_CHLTH	50S ribosomal protein L27 OS=Chlamydia trachomatis GN=rpmA PE=3 SV=1	90.3	33	2	2	8.9
A0A0E9D620 A0A0E9D620_CHLTH	Cysteine--tRNA ligase OS=Chlamydia trachomatis GN=cysS PE=3 SV=1	86.7	4	2	2	57.2
A0A0E9DWF3 A0A0E9DWF3_CHLTH	Pyruvate dehydrogenase E1 component subunit alpha OS=Chlamydia trachomatis GN=pdhA_1 PE=4 SV=1	86.2	10	3	2	37.2
G4NP68 G4NP68_CHLT4	Pyruvate dehydrogenase E1 component subunit alpha OS=Chlamydia trachomatis serovar A (strain A2497) GN=pdhA PE=4 SV=1	86.2	10	3	2	37.2
A0A0E9DI70 A0A0E9DI70_CHLTH	1-deoxy-D-xylulose 5-phosphate reductoisomerase OS=Chlamydia trachomatis GN=dxr PE=3 SV=1	85.1	6	2	2	41.8
A0A0E9CXM5 A0A0E9CXM5_CHLTH	1-deoxy-D-xylulose 5-phosphate reductoisomerase OS=Chlamydia trachomatis GN=dxr PE=3 SV=1	85.1	6	2	2	41.7
A0A0E9CJH7 A0A0E9CJH7_CHLTH	Protein of uncharacterised function (DUF2709) OS=Chlamydia trachomatis GN=ERS075193_00230 PE=4 SV=1	84.9	12	3	2	27.4
Q9S6V3 Q9S6V3_CHLTH	ADP%2C ATP carrier protein OS=Chlamydia trachomatis GN=npt1 PE=4 SV=1	84.6	6	3	3	58.1
A0A0H3MGN2 A0A0H3MGN2_CHLT2	ADP ATP carrier protein OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=CTL0321 PE=4 SV=1	84.6	6	3	3	58.1
M9UEC9 M9UEC9_CHLTH	ATPase AAA OS=Chlamydia trachomatis L2/434/Bu(f) GN=CTLFINAL_01695 PE=4 SV=1	84.6	6	3	3	58.1
sp O84068 TLC1_CHLTR	ADP ATP carrier protein 1 OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=tlcA PE=3 SV=1	84.6	6	3	3	58.1
O84248 O84248_CHLTR	Pyruvate Dehydrogenase Beta OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=pdhB PE=4 SV=1	84.4	14	4	4	36.2
A0A0E9DSX9 A0A0E9DSX9_CHLTH	Thymidylate kinase OS=Chlamydia trachomatis GN=tmk_2 PE=3 SV=1	83.9	17	2	2	22.5
sp B0B9T8 KTHY_CHLT2	Thymidylate kinase OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=tmk PE=3 SV=1	83.9	17	2	2	22.5
sp O84804 GLGA_CHLTR	Glycogen synthase OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=glgA PE=3 SV=1	82.1	5	2	2	53.4
A0A0E9CL94 A0A0E9CL94_CHLTH	Glycogen synthase OS=Chlamydia trachomatis GN=glgA2 PE=3 SV=1	82.1	5	2	2	53.4
A0A0E9DHF9 A0A0E9DHF9_CHLTH	Na(+)-translocating NADH-quinone reductase subunit A OS=Chlamydia trachomatis GN=nqrA PE=3 SV=1	82.1	12	3	3	51.8
sp O84639 NQRA_CHLTR	Na(+)-translocating NADH-quinone reductase subunit A OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=nqrA PE=3 SV=1	82.1	12	3	3	51.8
A0A0E9AS89 A0A0E9AS89_CHLTH	50S ribosomal protein L28 OS=Chlamydia trachomatis GN=rpmB PE=3 SV=1	80.2	22	3	2	10.1
sp O84088 RL28_CHLTR	50S ribosomal protein L28 OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=rpmB PE=3 SV=1	80.2	22	3	2	10.1
sp B0B9J4 RL28_CHLT2	50S ribosomal protein L28 OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=rpmB PE=3 SV=1	80.2	22	3	2	10.1
G4NP38 G4NP38_CHLT4	Putative membrane spanning protein OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0241 PE=4 SV=1	80.1	6	2	2	33.0
A0A0H3MBQ9 A0A0H3MBQ9_CHLT2	Putative exported protein OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=CTL0473 PE=4 SV=1	80.1	6	2	2	33.1
A0A0E9DL21 A0A0E9DL21_CHLTH	Putative membrane spanning protein OS=Chlamydia trachomatis GN=ERS066953_00163 PE=4 SV=1	80.1	6	2	2	33.1
A0A0E9CP53 A0A0E9CP53_CHLTH	Type III secretion chaperone OS=Chlamydia trachomatis GN=scc1 PE=4 SV=1	79.6	21	3	3	16.2
A0A0H3MHE0 A0A0H3MHE0_CHLT2	1-acyl-sn-glycerol-3-phosphate acyltransferase OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=plsC PE=4 SV=1	79.0	13	3	2	23.8

A0A0E9DER9 A0A0E9DER9_CHLTH	Chlamydia protein associating with death domains OS=Chlamydia trachomatis GN=ERS075193_00154 PE=4 SV=1	78.5	19	3	3	26.1
M9UIP8 M9UIP8_CHLTH	Dehydrogenase OS=Chlamydia trachomatis L2/434/Bu(f) GN=CTLFINAL_04565 PE=4 SV=1	78.5	18	3	3	26.8
sp O84616 PQQCL_CHLTR	PqqC-like protein OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=CT_610 PE=1 SV=1	78.5	18	3	3	26.7
G4NMQ5 G4NMQ5_CHLT4	Chlamydia protein associating with death domains OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0663 PE=4 SV=1	78.5	18	3	3	27.5
G4NPH0 G4NPH0_CHLT4	AMP nucleosidase OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0820 PE=4 SV=1	78.4	9	2	2	32.0
A0A0H2X1U4 A0A0H2X1U4_CHLTA	AMP nucleosidase OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=amn PE=4 SV=1	78.4	9	2	2	32.0
A0A0E9CTJ7 A0A0E9CTJ7_CHLTH	50S ribosomal protein L15 OS=Chlamydia trachomatis GN=rplO PE=3 SV=1	77.5	18	2	2	18.6
G4NND5 G4NND5_CHLT4	6-phosphogluconolactonase OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0204 PE=4 SV=1	76.7	8	2	2	29.8
G4NNX3 G4NNX3_CHLT4	50S ribosomal protein L31 type B OS=Chlamydia trachomatis serovar A (strain A2497) GN=rpmE2 PE=3 SV=1	76.7	39	4	4	12.2
sp Q3KN00 RL31B_CHLTA	50S ribosomal protein L31 type B OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=rpmE2 PE=3 SV=1	76.7	39	4	4	12.2
G4NPJ4 G4NPJ4_CHLT4	Acyl-acyl carrier protein synthetase OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0846 PE=4 SV=1	76.7	8	3	3	59.4
A0A0H2X0W7 A0A0H2X0W7_CHLTA	Hypothetical secreted protein OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=CTA_0275 PE=4 SV=1	74.7	12	2	2	24.0
G4NP76 G4NP76_CHLT4	Putative secreted protein OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0275 PE=4 SV=1	74.7	12	2	2	24.0
A0A0E9G4K3 A0A0E9G4K3_CHLTH	Serine hydroxymethyltransferase OS=Chlamydia trachomatis GN=glyA_2 PE=3 SV=1	74.2	4	3	2	47.1
G4NN07 G4NN07_CHLT4	CpxR OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0683 PE=4 SV=1	74.1	27	4	4	25.7
A0A0E9AYR5 A0A0E9AYR5_CHLTH	Phosphoglycerate kinase OS=Chlamydia trachomatis GN=pgk PE=3 SV=1	73.8	14	4	4	43.1
sp B0B8R9 PGK_CHLT2	Phosphoglycerate kinase OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=pgk PE=3 SV=1	73.8	14	4	4	43.1
A0A0E9FZN2 A0A0E9FZN2_CHLTH	SH3 domain-containing protein OS=Chlamydia trachomatis GN=ERS066953_00510 PE=4 SV=1	72.3	5	2	2	48.5
A0A0E9CWX0 A0A0E9CWX0_CHLTH	30S ribosomal protein S17 OS=Chlamydia trachomatis GN=rpsQ PE=3 SV=1	70.4	33	3	3	9.6
G4NPD6 G4NPD6_CHLT4	30S ribosomal protein S17 OS=Chlamydia trachomatis serovar A (strain A2497) GN=rpsQ PE=3 SV=1	70.4	33	3	3	9.6
sp B0BCF8 RS17_CHLTB	30S ribosomal protein S17 OS=Chlamydia trachomatis serovar L2b (strain UCH-1/proctitis) GN=rpsQ PE=3 SV=1	70.4	33	3	3	9.6
O84569 O84569_CHLTR	Uncharacterized protein OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=CT_565 PE=4 SV=1	67.4	12	2	2	16.0
A0A0E9CXQ1 A0A0E9CXQ1_CHLTH	Putative inner membrane protein OS=Chlamydia trachomatis GN=ERS075185_00276 PE=4 SV=1	67.4	12	2	2	16.0
A0A0H3MLF9 A0A0H3MLF9_CHLT2	Putative membrane protein OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=CTL0828 PE=4 SV=1	67.4	12	2	2	16.0
M9UIM3 M9UIM3_CHLTH	Membrane protein OS=Chlamydia trachomatis L2/434/Bu(f) GN=CTLFINAL_04320 PE=4 SV=1	67.4	12	2	2	16.0
A0A0H2X1H7 A0A0H2X1H7_CHLTA	Uncharacterized protein OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=CTA_0615 PE=4 SV=1	67.4	12	2	2	16.0
A0A0E9AW84 A0A0E9AW84_CHLTH	Putative inner membrane protein OS=Chlamydia trachomatis GN=ERS066953_01300 PE=4 SV=1	67.4	12	2	2	16.0
A0A0E9GFA7 A0A0E9GFA7_CHLTH	Chaperone protein DnaK OS=Chlamydia trachomatis GN=dnaK_4 PE=2 SV=1	65.5	2	2	2	68.5
A0A0H3MDT2 A0A0H3MDT2_CHLT2	Proline dipeptidase OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=pepP PE=4 SV=1	65.0	5	2	2	39.3
M9UII9 M9UII9_CHLTH	Aminopeptidase OS=Chlamydia trachomatis L2/434/Bu(f) GN=CTLFINAL_04365 PE=4 SV=1	65.0	5	2	2	39.3
A0A0E9AYD3 A0A0E9AYD3_CHLTH	Proline dipeptidase OS=Chlamydia trachomatis GN=pepP PE=4 SV=1	65.0	5	2	2	39.3
sp O84537 FABZ_CHLTR	3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=fabZ PE=3 SV=1	60.1	11	2	2	16.6
G4NMX4 G4NMX4_CHLT4	MYG1 protein OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0421 PE=4 SV=1	54.9	9	2	2	35.0

82

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84 **Table E3.** SEQUEST identification of 125 CtB protein hits with peptide FDR of 0.1%. Abbreviations:
 85 Cov. = protein sequence coverage, # Uniq. Pep. = number of unique peptides, # PSMs = number of
 86 peptide-spectrum matches

Accession	Description	Score	Cov. [%]	# Uniq. Pep.	# PSMs	MW [kDa]	calc. pl
P23421	Major outer membrane porin, serovar B OS=Chlamydia trachomatis GN=ompA PE=2 SV=1 -[MOMP_B_CHLTH]	1499.9	43.7	9	428	42.5	5.34
Q6U5G4	Major outer membrane porin (Fragment) OS=Chlamydia trachomatis GN=omp1 PE=3 SV=1 -[Q6U5G4_CHLTH]	652.4	25.7	1	206	31.2	5.10
B0B9L8	60 kDa chaperonin OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=groL PE=3 SV=1 - [CH60_CHLT2]	553.0	55.9	19	161	58.1	5.35
A0A0E9F3I9	ATP synthase subunit beta OS=Chlamydia trachomatis GN=sctN_4 PE=3 SV=1 - [A0A0E9F3I9_CHLTH]	138.7	3.0	1	35	50.7	4.94
P26758	Large cysteine-rich periplasmic protein OmcB, serovar C OS=Chlamydia trachomatis GN=omcB PE=2 SV=1 - [OMCBC_CHLTH]	130.1	22.1	7	37	58.6	7.21
A0A0E9CBG7	Chaperone protein DnaK OS=Chlamydia trachomatis GN=dnaK PE=2 SV=1 - [A0A0E9CBG7_CHLTH]	117.7	26.4	8	48	70.8	5.14
A0A0E9ASC3	Putative membrane associated protein OS=Chlamydia trachomatis GN=ERS066953_00494 PE=4 SV=1 - [A0A0E9ASC3_CHLTH]	92.1	25.6	1	19	9.8	8.34
A0A0E9DC36	Gag gene protein p24 (Core nucleocapsid protein) OS=Chlamydia trachomatis GN=ERS082928_02139 PE=4 SV=1 - [A0A0E9DC36_CHLTH]	91.5	21.3	1	21	31.6	8.91
A0A0E9DKJ7	Gag gene protein p24 (Core nucleocapsid protein) OS=Chlamydia trachomatis GN=ERS082931_00949 PE=4 SV=1 - [A0A0E9DKJ7_CHLTH]	84.3	18.3	2	20	42.4	8.84
G4NMM0	Uncharacterized protein OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0629 PE=4 SV=1 - [G4NMM0_CHLT4]	80.6	19.6	4	25	44	9.23
K0G3B3	CHLPN 76 kD protein-like OS=Chlamydia trachomatis GN=CT623 PE=4 SV=1 - [K0G3B3_CHLTH]	79.9	34.5	9	22	48.3	8.19
A0A0E9DYT2	Manganese-binding protein OS=Chlamydia trachomatis GN=troA_1 PE=3 SV=1 - [A0A0E9DYT2_CHLTH]	69.7	40.5	7	20	37	5.73
P0CD71	Elongation factor Tu OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=tuf PE=3 SV=1 - [EFTU_CHLTR]	61.8	33.5	8	14	43.3	5.53
O84588	Protein CT_584 OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=CT_584 PE=3 SV=1 - [Y584_CHLTR]	56.8	33.9	4	29	21.1	5.87
B0B8Q5	Elongation factor Ts OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=tsf PE=3 SV=1 - [EFTS_CHLT2]	52.7	15.6	3	14	30.9	5.90
A0A0E9CNY3	Glyceraldehyde-3-phosphate dehydrogenase OS=Chlamydia trachomatis GN=gap PE=3 SV=1 - [A0A0E9CNY3_CHLTH]	51.3	32.2	4	15	19.1	5.17
B0B9N4	30S ribosomal protein S9 OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR- 902B) GN=rpsI PE=3 SV=1 - [RS9_CHLT2]	48.7	20.9	2	14	14.5	11.0 2
A0A0E9D199	ATP-dependent Clp protease proteolytic subunit OS=Chlamydia trachomatis GN=clpP-2 PE=3 SV=1 - [A0A0E9D199_CHLTH]	46.2	19.3	2	12	21.1	5.59
A0A0E9AW79	Type III secretion structural protein OS=Chlamydia trachomatis GN=piIQ PE=3 SV=1 - [A0A0E9AW79_CHLTH]	42.9	9.7	5	10	100.2	5.76
A0A0E9CZX7	Type III secretion system ATPase OS=Chlamydia trachomatis GN=sctN PE=4 SV=1 - [A0A0E9CZX7_CHLTH]	38.9	9.5	3	10	48.2	5.81
Q1ALV0	S2 ribosomal protein (Fragment) OS=Chlamydia trachomatis GN=rs2 PE=3 SV=1 - [Q1ALV0_CHLTH]	38.3	19.7	2	9	15.4	8.88
A0A0E9AQW3	Polymorphic outer membrane protein OS=Chlamydia trachomatis GN=ERS066953_00399 PE=4 SV=1 -	36.7	5.9	5	9	160.4	4.88

	[A0A0E9AQW3_CHLTH]							
A0A0E9CNS8	Polymorphic outer membrane protein OS=Chlamydia trachomatis GN=pmpF_1 PE=4 SV=1 - [A0A0E9CNS8_CHLTH]	33.5	14.9	5	14	83.5	5.97	
A0A0E9B124	Transaldolase OS=Chlamydia trachomatis GN=talA PE=3 SV=1 - [A0A0E9B124_CHLTH]	32.2	10.4	2	8	36.1	5.03	
A0A0E9CKY8	Serine protease OS=Chlamydia trachomatis GN=htrA PE=4 SV=1 - [A0A0E9CKY8_CHLTH]	31.7	3.9	1	8	34.9	5.57	
A8KPL3	Thio-Specific Antioxidant (TSA) Peroxidase (Fragment) OS=Chlamydia trachomatis GN=ahpC PE=4 SV=1 - [A8KPL3_CHLTH]	31.3	32.8	4	8	21.7	4.86	
A0A0E9FYU5	30S ribosomal protein S11 OS=Chlamydia trachomatis GN=rpsK_1 PE=3 SV=1 - [A0A0E9FYU5_CHLTH]	28.8	16.9	1	7	9.2	10.95	
Q3KLX6	Glucose-6-phosphate isomerase OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=pgi PE=3 SV=2 - [G6PI_CHLTA]	25.8	20.2	6	6	57.6	6.06	
A0A0E9ESU7	Chaperone protein DnaK OS=Chlamydia trachomatis GN=dnaK_3 PE=2 SV=1 - [A0A0E9ESU7_CHLTH]	25.6	2.6	1	6	65.5	4.73	
A0A0E9D869	Protein disulfide isomerase OS=Chlamydia trachomatis GN=dsbH_2 PE=4 SV=1 - [A0A0E9D869_CHLTH]	25.1	29.9	3	6	18.5	8.32	
A0A0E9CZQ4	Enolase OS=Chlamydia trachomatis GN=enol PE=3 SV=1 - [A0A0E9CZQ4_CHLTH]	23.9	8.0	2	6	45.4	4.73	
B0B895	50S ribosomal protein L16 OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=rpL16 PE=3 SV=1 - [RL16_CHLT2]	22.7	12.3	1	5	15.8	11.30	
A0A0H2X245	Polymorphic outer membrane protein OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=pmpF PE=4 SV=1 - [A0A0H2X245_CHLTA]	21.6	9.3	5	5	112.7	8.34	
O84296	Superoxide dismutase [Mn] OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=sodA PE=3 SV=1 - [SODM_CHLTR]	21.3	6.3	1	5	23.5	6.33	
A0A0E9C5C6	Elongation factor G OS=Chlamydia trachomatis GN=fusA PE=3 SV=1 - [A0A0E9C5C6_CHLTH]	20.2	5.2	2	5	76.5	5.34	
A0A0E9CQA8	Fructose-bisphosphate aldolase OS=Chlamydia trachomatis GN=fbaB PE=4 SV=1 - [A0A0E9CQA8_CHLTH]	19.9	22.0	1	6	9.9	7.99	
A0A0E9AUN0	Outer membrane protein OS=Chlamydia trachomatis GN=ERS066953_00140 PE=4 SV=1 - [A0A0E9AUN0_CHLTH]	19.7	4.0	2	5	88.7	9.03	
Q83U76	Polymorphic membrane protein H (Fragment) OS=Chlamydia trachomatis GN=pmpH PE=4 SV=1 - [Q83U76_CHLTH]	19.6	4.0	2	5	104.9	6.43	
A0A0E9AZS4	Peptidyl-prolyl cis-trans isomerase OS=Chlamydia trachomatis GN=mip PE=4 SV=1 - [A0A0E9AZS4_CHLTH]	19.4	19.7	3	5	25.5	4.88	
Q2TGM2	Polymorphic membrane protein B OS=Chlamydia trachomatis GN=pmpB PE=4 SV=1 - [Q2TGM2_CHLTH]	19.0	5.1	4	4	183	5.92	
A0A0H2X1M5	Phosphopeptide binding protein OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=CTA_0721 PE=4 SV=1 - [A0A0H2X1M5_CHLTA]	18.8	8.1	4	5	89.6	4.60	
B2XRL7	Tarp protein OS=Chlamydia trachomatis PE=4 SV=1 - [B2XRL7_CHLTH]	18.8	7.7	3	5	100.5	4.46	
A0A0E9ATJ7	Probable cytosol aminopeptidase OS=Chlamydia trachomatis GN=pepA_1 PE=3 SV=1 - [A0A0E9ATJ7_CHLTH]	18.8	10.2	4	5	54.2	6.00	
B0B926	50S ribosomal protein L25 OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=rpL25 PE=3 SV=1 - [RL25_CHLT2]	18.8	28.1	3	5	20.4	8.76	
Q58HD1	Major outer membrane porin (Fragment) OS=Chlamydia trachomatis GN=omp1 PE=3 SV=1 - [Q58HD1_CHLTH]	18.5	6.1	1	5	33.9	4.88	
K0GGT0	Ribosome-recycling factor OS=Chlamydia trachomatis GN=frr PE=3 SV=1 - [K0GGT0_CHLTH]	18.0	17.9	2	6	20	8.56	
A0A0E9FYS4	Thioredoxin reductase OS=Chlamydia trachomatis GN=trxB_1 PE=3 SV=1 - [A0A0E9FYS4_CHLTH]	17.0	18.0	3	4	33.5	5.95	
POCE08	DNA-directed RNA polymerase subunit alpha OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=rpoA PE=3 SV=1 - [RPOA_CHLTR]	16.0	7.7	2	4	41.8	5.47	
A0A0E9CYI8	50S ribosomal protein L10 OS=Chlamydia trachomatis GN=rpL10 PE=3 SV=1 - [A0A0E9CYI8_CHLTH]	15.6	14.5	2	5	18.8	6.34	
Q83U05	Polymorphic membrane protein E (Fragment)	15.5	5.4	3	4	101.6	7.21	

	OS=Chlamydia trachomatis GN=pmpE PE=4 SV=1 - [Q83U05_CHLTH]						
A0A0E9E9K2	Protein translocase subunit OS=Chlamydia trachomatis GN=ERS066953_01398 PE=4 SV=1 - [A0A0E9E9K2_CHLTH]	15.1	12.3	1	4	12.8	9.20
A0A0E9CXT7	N utilization substance protein A OS=Chlamydia trachomatis GN=nusA_2 PE=4 SV=1 - [A0A0E9CXT7_CHLTH]	14.9	11.9	2	4	32.9	5.02
A0A0E9CZR5	Histone H1-like developmental protein OS=Chlamydia trachomatis GN=hctA PE=4 SV=1 - [A0A0E9CZR5_CHLTH]	13.2	11.2	1	3	13.7	10.70
A0A0E9E330	Anti-sigma factor antagonist OS=Chlamydia trachomatis GN=btrV PE=3 SV=1 - [A0A0E9E330_CHLTH]	13.0	41.4	3	3	12.5	5.39
B0B9B1	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=gatB PE=3 SV=1 - [GATB_CHLT2]	12.8	6.8	2	3	54.9	6.32
B0B8V8	6,7-dimethyl-8-ribityllumazine synthase OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=ribH PE=3 SV=1 - [RISB_CHLT2]	12.4	33.8	3	3	16.4	6.74
A0A0E9D2X3	30S ribosomal protein S3 OS=Chlamydia trachomatis GN=rpsC PE=3 SV=1 - [A0A0E9D2X3_CHLTH]	12.4	15.5	2	3	23.9	10.02
A0A0E9CSV1	MotA/TolQ/ExbB proton channel family protein OS=Chlamydia trachomatis GN=tolQ PE=3 SV=1 - [A0A0E9CSV1_CHLTH]	12.4	16.4	1	3	14.5	6.52
A0A0E9CB48	Transcription termination factor Rho OS=Chlamydia trachomatis GN=rho PE=3 SV=1 - [A0A0E9CB48_CHLTH]	12.2	6.9	2	3	51.7	7.36
A0A0E9CGP2	30S ribosomal protein S13 OS=Chlamydia trachomatis GN=rpsM PE=3 SV=1 - [A0A0E9CGP2_CHLTH]	11.9	25.4	2	3	13.8	10.71
A0A0E9CN91	Amino acid ABC transporter substrate-binding protein OS=Chlamydia trachomatis GN=ERS075194_01180 PE=4 SV=1 - [A0A0E9CN91_CHLTH]	11.7	24.3	1	3	7.6	10.26
P0CE01	50S ribosomal protein L6 OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=rplF PE=3 SV=1 - [RL6_CHLTR]	11.4	18.0	2	3	19.8	9.96
A0A0E9D403	Peptide deformylase OS=Chlamydia trachomatis GN=def PE=3 SV=1 - [A0A0E9D403_CHLTH]	9.4	24.3	2	2	20.5	5.90
A0A0E9DQ65	Leucine dehydrogenase OS=Chlamydia trachomatis GN=idh PE=4 SV=1 - [A0A0E9DQ65_CHLTH]	9.3	23.3	1	2	11.1	8.13
A0A0E9DNL0	Polymorphic outer membrane protein OS=Chlamydia trachomatis GN=pmpI PE=4 SV=1 - [A0A0E9DNL0_CHLTH]	8.5	10.0	1	2	21.2	9.19
B7SC61	PorB (Fragment) OS=Chlamydia trachomatis GN=porB PE=4 SV=1 - [B7SC61_CHLTH]	8.4	18.5	1	2	13.8	4.78
O84666	UPF0109 protein CT_659 OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=CT_659 PE=3 SV=1 - [Y659_CHLTR]	8.4	35.9	1	2	8.8	8.43
A0A0E9CPX5	30S ribosomal protein S1 OS=Chlamydia trachomatis GN=rpsA PE=4 SV=1 - [A0A0E9CPX5_CHLTH]	8.2	10.7	2	2	17.3	5.15
A0A0E9AZ23	Succinyl-CoA ligase [ADP-forming] subunit alpha OS=Chlamydia trachomatis GN=sucD PE=3 SV=1 - [A0A0E9AZ23_CHLTH]	8.1	6.2	1	2	30.2	5.48
A0A0E9C6A0	Pyruvate kinase OS=Chlamydia trachomatis GN=pykF PE=3 SV=1 - [A0A0E9C6A0_CHLTH]	8.1	3.3	1	2	53.7	6.40
A0A0E9CCK9	Transcription termination/antitermination protein NusG OS=Chlamydia trachomatis GN=nusG PE=3 SV=1 - [A0A0E9CCK9_CHLTH]	8.0	18.7	2	2	20.7	5.31
A0A0E9CM38	Polynucleotide phosphorylase/polyadenylase OS=Chlamydia trachomatis GN=pnp PE=4 SV=1 - [A0A0E9CM38_CHLTH]	7.8	11.3	2	2	27.2	6.42
A0A0E9EAX5	Putative protease OS=Chlamydia trachomatis GN=ERS133246_04554 PE=4 SV=1 - [A0A0E9EAX5_CHLTH]	7.8	4.6	1	2	42.3	6.43
A0A0E9ATU0	Oligoendopeptidase F OS=Chlamydia trachomatis GN=pepF PE=4 SV=1 - [A0A0E9ATU0_CHLTH]	7.8	5.6	2	2	69	5.95
A0A0E9AR22	Uncharacterized protein OS=Chlamydia trachomatis GN=greA_1 PE=3 SV=1 - [A0A0E9AR22_CHLTH]	7.7	4.8	2	2	80.9	5.38
A0A0E9B081	ATP-dependent Clp protease%2C subunit B OS=Chlamydia trachomatis GN=clpB PE=3 SV=1 - [A0A0E9B081_CHLTH]	7.7	1.5	1	2	96.6	5.47
B0BCD9	Nucleoside diphosphate kinase OS=Chlamydia	7.6	8.5	1	2	15.3	5.49

	trachomatis serovar L2b (strain UCH-1/proctitis) GN=ndk PE=3 SV=1 - [NDK_CHLTB]						
A0A0E9CV36	Serine hydroxymethyltransferase OS=Chlamydia trachomatis GN=glyA_2 PE=4 SV=1 - [A0A0E9CV36_CHLTH]	7.6	15.9	2	2	19.5	6.81
A0A0E9AVM4	6-phosphogluconate dehydrogenase, decarboxylating OS=Chlamydia trachomatis GN=gnd PE=3 SV=1 - [A0A0E9AVM4_CHLTH]	7.5	6.9	2	2	52.6	5.63
A0A0E9CD67	50S ribosomal protein L2 OS=Chlamydia trachomatis GN=rpB PE=3 SV=1 - [A0A0E9CD67_CHLTH]	7.5	5.3	2	2	31.4	10.4 3
P64386	Probable DNA-binding protein HU OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=hup PE=3 SV=1 - [DBH_CHLTR]	7.5	10.0	1	2	11.4	11.0 6
A0A0E9CTT3	Polymorphic outer membrane protein OS=Chlamydia trachomatis GN=pmpC PE=4 SV=1 - [A0A0E9CTT3_CHLTH]	7.3	3.2	1	2	55.1	6.62
A0A0E9CX90	5'-nucleotidase SurE OS=Chlamydia trachomatis GN=surE PE=3 SV=1 - [A0A0E9CX90_CHLTH]	7.3	10.3	2	2	31.5	4.92
A0A0E9CAZ5	30S ribosomal protein S4 OS=Chlamydia trachomatis GN=rpsD PE=3 SV=1 - [A0A0E9CAZ5_CHLTH]	4.9	11.5	1	1	23.8	10.0 5
A0A0E9CN44	Malonyl-CoA-[acyl-carrier-protein] transacylase OS=Chlamydia trachomatis GN=fabD PE=4 SV=1 - [A0A0E9CN44_CHLTH]	4.7	13.6	1	1	17.9	5.27
A0A0E9D5V8	30S ribosomal protein S16 OS=Chlamydia trachomatis GN=rpsP PE=3 SV=1 - [A0A0E9D5V8_CHLTH]	4.7	12.1	1	1	13.4	10.4 6
Q3KLT4	50S ribosomal protein L27 OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=rpmA PE=3 SV=1 - [RL27_CHLTA]	4.6	21.7	1	1	8.9	11.0 3
A0A0E9CE81	Phosphoglycerate kinase OS=Chlamydia trachomatis GN=pgk_1 PE=3 SV=1 - [A0A0E9CE81_CHLTH]	4.6	6.5	1	1	43	5.97
A0A0E9AZU9	Type III secretion cytoplasmic membrane protein SctJ OS=Chlamydia trachomatis GN=prgK PE=4 SV=1 - [A0A0E9AZU9_CHLTH]	4.4	4.9	1	1	35.5	5.72
A0A0E9CRL6	Thymidylate kinase OS=Chlamydia trachomatis GN=tmk PE=4 SV=1 - [A0A0E9CRL6_CHLTH]	4.3	23.8	1	1	9.6	8.51
A0A0E9F314	LSU ribosomal protein L1E (L4P) OS=Chlamydia trachomatis GN=ERS133246_06945 PE=4 SV=1 - [A0A0E9F314_CHLTH]	4.3	15.3	1	1	12.1	7.14
B0B9B0	Glutamyl-tRNA(Gln) amidotransferase subunit A OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=gatA PE=3 SV=1 - [GATA_CHLT2]	4.3	3.1	1	1	53.6	6.23
A0A0E9CRP3	HAD superfamily hydrolase/phosphatase OS=Chlamydia trachomatis GN=ERS075194_01797 PE=4 SV=1 - [A0A0E9CRP3_CHLTH]	4.3	8.6	1	1	17.3	4.82
A0A0E9DD28	Conjugal transfer ATP-binding protein TraC OS=Chlamydia trachomatis GN=ERS082928_01128 PE=4 SV=1 - [A0A0E9DD28_CHLTH]	4.2	27.2	1	2	16.7	8.28
A0A0E9DVP9	Uncharacterised protein OS=Chlamydia trachomatis GN=ERS133246_01556 PE=4 SV=1 - [A0A0E9DVP9_CHLTH]	4.2	11.8	1	1	20	9.26
A0A0E9B1X8	Thiol:disulfide interchange protein OS=Chlamydia trachomatis GN=ERS066955_00827 PE=4 SV=1 - [A0A0E9B1X8_CHLTH]	4.2	4.7	1	1	49.2	5.38
A0A0E9G272	Thioredoxin OS=Chlamydia trachomatis GN=trxA PE=4 SV=1 - [A0A0E9G272_CHLTH]	4.1	28.6	1	1	7.7	6.54
A0A0E9B0E1	Enoyl-ACP reductase OS=Chlamydia trachomatis GN=fabI PE=4 SV=1 - [A0A0E9B0E1_CHLTH]	4.1	5.0	1	1	32	5.35
B0B7M2	V-type ATP synthase subunit D OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=atpD PE=3 SV=1 - [VATD_CHLT2]	4.1	5.9	1	1	23.2	8.98
A0A0E9AZE6	Uncharacterised protein OS=Chlamydia trachomatis GN=ERS066955_00730 PE=4 SV=1 - [A0A0E9AZE6_CHLTH]	4.1	5.0	1	1	36.2	4.75
A0A0E9CZ22	Acetyl-CoA carboxylase biotin carboxyl carrier protein subunit OS=Chlamydia trachomatis GN=accB PE=4 SV=1 - [A0A0E9CZ22_CHLTH]	4.0	10.4	1	1	18.2	5.12
A0A0E9CQM4	Protein RecA OS=Chlamydia trachomatis GN=recA PE=3 SV=1 - [A0A0E9CQM4_CHLTH]	3.9	5.3	1	1	36.7	6.80
A0A0E9ATY1	Putative cytosolic protein OS=Chlamydia trachomatis GN=ERS066953_00424 PE=4 SV=1 - [A0A0E9ATY1_CHLTH]	3.9	11.0	1	1	18.4	4.61
W8VJ2	Major outer membrane porin (Fragment)	3.9	5.6	1	1	36.8	4.98

	OS=Chlamydia trachomatis GN=ompA PE=3 SV=1 - [W8VNJ2_CHLTH]						
Q6LCD5	10 kDa chaperonin (Fragment) OS=Chlamydia trachomatis GN=hypA PE=3 SV=1 - [Q6LCD5_CHLTH]	3.9	18.6	1	1	10.7	4.94
A0A0E9F3V8	Putative cytosolic protein OS=Chlamydia trachomatis GN=ERS095036_10045 PE=4 SV=1 - [A0A0E9F3V8_CHLTH]	3.9	8.0	1	1	22.2	4.72
A0A0E9CRR3	Putative nucleotide transport protein OS=Chlamydia trachomatis GN=tlcA_1 PE=4 SV=1 - [A0A0E9CRR3_CHLTH]	3.9	5.5	1	1	24.4	9.95
A0A0E9CUI5	Uridylate kinase OS=Chlamydia trachomatis GN=pyrH_3 PE=4 SV=1 - [A0A0E9CUI5_CHLTH]	3.8	24.0	1	1	10.5	4.96
B0B889	30S ribosomal protein S8 OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=rpsH PE=3 SV=1 - [RS8_CHLT2]	3.8	19.6	1	1	15.1	10.27
A0A0E9EK46	Outer membrane protein OS=Chlamydia trachomatis GN=ompH PE=4 SV=1 - [A0A0E9EK46_CHLTH]	3.8	15.5	1	1	14	4.60
Q3KM43	50S ribosomal protein L11 OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=rplK PE=3 SV=1 - [RL11_CHLTA]	3.7	7.1	1	1	15.1	9.67
A0A0E9CV83	Carbohydrate-selective porin%2C OprB family protein OS=Chlamydia trachomatis GN=aaxA PE=4 SV=1 - [A0A0E9CV83_CHLTH]	3.7	5.2	1	1	30.1	9.11
A0A0E9AVY3	Translation initiation factor IF-3 OS=Chlamydia trachomatis GN=infC_1 PE=4 SV=1 - [A0A0E9AVY3_CHLTH]	3.7	20.0	1	1	8.4	6.67
B0B928	30S ribosomal protein S6 OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=rpsF PE=3 SV=1 - [RS6_CHLT2]	3.7	12.5	1	1	12.9	8.81
A0A0E9DP73	Protein of uncharacterised function (DUF1207) OS=Chlamydia trachomatis GN=ERS095037_01102 PE=4 SV=1 - [A0A0E9DP73_CHLTH]	3.7	4.1	1	1	39.1	6.07
A0A0E9EUP2	ATP synthase subunit alpha OS=Chlamydia trachomatis GN=sctN_2 PE=3 SV=1 - [A0A0E9EUP2_CHLTH]	3.7	2.3	1	1	56.1	5.05
A0A0E9CRA0	Malate dehydrogenase OS=Chlamydia trachomatis GN=mdh PE=4 SV=1 - [A0A0E9CRA0_CHLTH]	3.6	11.2	1	1	11.6	5.45
A0A0E9C8R9	50S ribosomal protein L18 OS=Chlamydia trachomatis GN=rplR PE=3 SV=1 - [A0A0E9C8R9_CHLTH]	3.6	10.6	1	1	13.4	10.32
G4NNN6	Uncharacterized protein OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0755 PE=4 SV=1 - [G4NNN6_CHLT4]	3.6	7.1	1	1	34.6	5.17
A0A0E9AZP9	Cell division protein OS=Chlamydia trachomatis GN=ERS066955_00453 PE=4 SV=1 - [A0A0E9AZP9_CHLTH]	3.6	3.3	1	1	45.2	8.05
A0A0E9D2D6	Cation efflux system protein OS=Chlamydia trachomatis GN=ERS075185_00347 PE=4 SV=1 - [A0A0E9D2D6_CHLTH]	3.6	3.6	1	1	60.9	6.11
A0A0E9ERX5	Uncharacterised protein OS=Chlamydia trachomatis GN=ERS095036_06689 PE=4 SV=1 - [A0A0E9ERX5_CHLTH]	3.6	3.2	1	1	43.5	9.09
B0B9D5	50S ribosomal protein L19 OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=rplS PE=3 SV=1 - [RL19_CHLT2]	3.6	9.1	1	1	13.1	9.94
A0A0E9B1C0	Protease IV OS=Chlamydia trachomatis GN=sohB PE=4 SV=1 - [A0A0E9B1C0_CHLTH]	3.6	4.5	1	1	35.7	7.97
A0A0E9CRD3	Deoxyuridine 5'-triphosphate nucleotidohydrolase OS=Chlamydia trachomatis GN=dut PE=4 SV=1 - [A0A0E9CRD3_CHLTH]	3.5	16.5	1	1	11.6	5.39

88 **Table E4.** PEAKS DB identification of 190 CtB protein hits with FDR of 0.1% (on peptide level) and
 89 0% (on protein level). Abbreviations: Cov. = protein sequence coverage, # Uniq. Pep. = number of
 90 unique peptides # Pep. = number of peptides

Accession	Description	Score (-10lgP)	Cov. [%]	# Pep.	# Uniq. Pep.	MW [kDa]
G4NM84 G4NM84_CHLT4	60 kDa chaperonin OS=Chlamydia trachomatis serovar A (strain A2497) GN=groL PE=3 SV=1	361.4	70	46	3	58.1
sp Q3KMQ9 CH60_CHLTA	60 kDa chaperonin OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=groL PE=2 SV=3	361.4	70	46	3	58.1
A0A0E9CT34 A0A0E9CT34_CHLTH	Elongation factor Tu OS=Chlamydia trachomatis GN=tuf PE=3 SV=1	260.0	71	30	2	43.3
sp Q3KMQ4 EFTU_CHLTA	Elongation factor Tu OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=tuf PE=3 SV=1	260.0	71	30	2	43.3
Q2TV41 Q2TV41_CHLTH	Polymorphic membrane protein D OS=Chlamydia trachomatis GN=pmpD PE=4 SV=1	254.0	14	20	2	160.7
A0A0E9DIU3 A0A0E9DIU3_CHLTH	Gag gene protein p24 (Core nucleocapsid protein) OS=Chlamydia trachomatis GN=ERS082929_01031 PE=4 SV=1	260.6	29	15	3	65.7
sp Q3KMX6 AMPA_CHLTA	Probable cytosol aminopeptidase OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=pepA PE=3 SV=1	263.4	34	13	2	54.1
G4NLX2 G4NLX2_CHLT4	DegP OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0897 PE=4 SV=1	169.7	12	6	2	53.3
Q6LCD5 Q6LCD5_CHLTH	10 kDa chaperonin (Fragment) OS=Chlamydia trachomatis GN=hypA PE=3 SV=1	148.0	38	3	3	10.7
A0A0E9CAW6 A0A0E9CAW6_CHLTH	10 kDa chaperonin OS=Chlamydia trachomatis GN=groES PE=3 SV=1	148.0	36	3	3	11.2
A0A0H2X1N0 A0A0H2X1N0_CHLTA	SctN OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=sctN PE=4 SV=1	242.0	38	14	2	48.2
G4NN56 G4NN56_CHLT4	SctN OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0726 PE=4 SV=1	242.0	38	14	2	48.2
G4NMP7 G4NMP7_CHLT4	Thioredoxin peroxidase OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0654 PE=4 SV=1	268.5	67	13	13	22.7
A0A0H2X1C0 A0A0H2X1C0_CHLTA	Thioredoxin peroxidase OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=ahpC PE=4 SV=1	268.5	67	13	13	22.7
sp O84217 ALF1_CHLTR	Probable fructose-bisphosphate aldolase class 1 OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=fbaB PE=3 SV=1	185.3	37	10	3	38.0
A0A0E9F3I9 A0A0E9F3I9_CHLTH	ATP synthase subunit beta OS=Chlamydia trachomatis GN=sctN_4 PE=3 SV=1	153.7	8	3	2	50.7
sp O84031 RL19_CHLTR	50S ribosomal protein L19 OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=rplS PE=3 SV=1	164.9	49	7	7	13.1
sp B0BB14 RL19_CHLTB	50S ribosomal protein L19 OS=Chlamydia trachomatis serovar L2b (strain UCH-1/proctitis) GN=rplS PE=3 SV=1	164.9	49	7	7	13.1
sp O84805 RL25_CHLTR	50S ribosomal protein L25 OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=rplY PE=3 SV=1	189.7	46	6	6	20.4
G4NP91 G4NP91_CHLT4	Integration host factor beta-subunit OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0289 PE=3 SV=1	124.5	21	3	3	17.0
M9UF21 M9UF21_CHLTH	Integration host factor OS=Chlamydia trachomatis L2/434/Bu(f) GN=CTLFINAL_04880 PE=3 SV=2	124.5	21	3	3	17.0
A0A0E9AU0 A0A0E9AU0_CHLTH	Uncharacterized protein OS=Chlamydia trachomatis GN=ERS066953_01368 PE=4 SV=1	213.1	50	8	8	21.1
sp O84588 Y584_CHLTR	Protein CT_584 OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=CT_584 PE=3 SV=1	213.1	50	8	8	21.1
A0A0H2X1F6 A0A0H2X1F6_CHLTA	Uncharacterized protein OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=CTA_0634 PE=4 SV=1	213.1	50	8	8	21.1
M9UIQ4 M9UIQ4_CHLTH	Uncharacterized protein OS=Chlamydia trachomatis L2/434/Bu(f) GN=CTLFINAL_04420 PE=4 SV=1	213.1	50	8	8	21.1
G4NMM5 G4NMM5_CHLT4	Uncharacterized protein OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0634 PE=4 SV=1	213.1	50	8	8	21.1
A0A0H3MCR9 A0A0H3MCR9_CHLT2	Uncharacterized protein OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=CTL0847 PE=4 SV=1	213.1	50	8	8	21.1
A0A0E9CFY0 A0A0E9CFY0_CHLTH	30S ribosomal protein S1 OS=Chlamydia trachomatis GN=rpsA PE=4 SV=1	177.9	16	10	10	63.6
sp O84100 RS1_CHLTR	30S ribosomal protein S1 OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=rpsA PE=3 SV=1	177.9	16	10	10	63.6
M9UEF8 M9UEF8_CHLTH	Low calcium response locus protein D OS=Chlamydia trachomatis L2/434/Bu(f) GN=CTLFINAL_01820 PE=4	143.0	14	7	7	78.0

	SV=1					
G4NM61 G4NM61_CHLT4	Type III secretion inner membrane protein SctV OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0095 PE=4 SV=1	143.0	14	7	7	78.0
O84092 O84092_CHLTR	Low Calcium Response D OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=lcrD PE=4 SV=1	143.0	14	7	7	78.0
A0A0H3M4Y4 A0A0H3MCY4_CHLT2	Low calcium response protein D (Predicted to be part of the TTSS apparatus) OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=lcrD PE=4 SV=1	143.0	14	7	7	78.0
A0A0H2X0L8 A0A0H2X0L8_CHLTA	Low calcium response protein D OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=lcrD PE=4 SV=1	143.0	14	7	7	78.0
A0A0E9DLE6 A0A0E9DLE6_CHLTH	Putative membrane transport protein OS=Chlamydia trachomatis GN=invA PE=4 SV=1	143.0	14	7	7	78.0
A0A0E9CZH0 A0A0E9CZH0_CHLTH	Putative membrane transport protein OS=Chlamydia trachomatis GN=invA PE=4 SV=1	143.0	14	7	7	78.0
G4NNS7 G4NNS7_CHLT4	6 7-dimethyl-8-ribityllumazine synthase OS=Chlamydia trachomatis serovar A (strain A2497) GN=ribH PE=3 SV=1	191.7	41	6	6	17.2
Q83TT3 Q83TT3_CHLTH	Major outer membrane protein OS=Chlamydia trachomatis GN=porB PE=4 SV=1	200.2	25	7	2	37.3
A0A0E9CCK9 A0A0E9CCK9_CHLTH	Transcription termination/antitermination protein NusG OS=Chlamydia trachomatis GN=nusG PE=3 SV=1	205.7	37	5	2	20.8
K0GGT0 K0GGT0_CHLTH	Ribosome-recycling factor OS=Chlamydia trachomatis GN=frr PE=3 SV=1	208.6	45	8	4	20.1
G4NN64 G4NN64_CHLT4	Ribosome-recycling factor OS=Chlamydia trachomatis serovar A (strain A2497) GN=frr PE=3 SV=1	208.6	45	8	4	20.1
A0A0H3MCF1 A0A0H3MCF1_CHLT2	Uncharacterized protein OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=CTL0028 PE=4 SV=1	204.7	77	7	7	8.8
A0A0E9D2L0 A0A0E9D2L0_CHLTH	UPF0109 protein ERS066953_00249 OS=Chlamydia trachomatis GN=ERS066953_00249 PE=3 SV=1	204.7	77	7	7	8.8
M9UG13 M9UG13_CHLTH	UPF0109 protein CTLFINAL_00155 OS=Chlamydia trachomatis L2/434/Bu(f) GN=CTLFINAL_00155 PE=3 SV=1	204.7	77	7	7	8.8
A0A0H2X2Z8 A0A0H2X2Z8_CHLTA	RNA binding protein OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=CTA_0716 PE=4 SV=1	204.7	77	7	7	8.8
sp O84666 Y659_CHLTR	UPF0109 protein CT_659 OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=CT_659 PE=3 SV=1	204.7	77	7	7	8.8
sp B0B899 RL2_CHLT2	50S ribosomal protein L2 OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=rplB PE=3 SV=1	193.3	25	7	7	31.5
sp O84530 RL2_CHLTR	50S ribosomal protein L2 OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=rplB PE=3 SV=1	193.3	25	7	7	31.5
A0A0E9AXH1 A0A0E9AXH1_CHLTH	50S ribosomal protein L2 OS=Chlamydia trachomatis GN=rplB PE=3 SV=1	193.3	25	7	7	31.5
A0A0H3MLD3 A0A0H3MLD3_CHLT2	30S ribosomal protein S5P OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=rpsE PE=4 SV=1	151.5	25	5	5	17.8
sp Q3KLI5 RS5_CHLTA	30S ribosomal protein S5 OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=rpsE PE=3 SV=1	151.5	25	5	5	17.8
A0A0E9D3E4 A0A0E9D3E4_CHLTH	30S ribosomal protein S5 OS=Chlamydia trachomatis GN=rpsE PE=3 SV=1	151.5	25	5	5	17.8
M9UIB3 M9UIB3_CHLTH	30S ribosomal protein S5 OS=Chlamydia trachomatis L2/434/Bu(f) GN=rpsE PE=3 SV=1	151.5	25	5	5	17.8
A0A0E9C6W0 A0A0E9C6W0_CHLTH	Trigger factor OS=Chlamydia trachomatis GN=tig PE=3 SV=1	127.8	10	3	3	50.1
sp Q3KKY7 TIG_CHLTA	Trigger factor OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=tig PE=3 SV=1	127.8	10	3	3	50.1
sp B0B930 RL9_CHLT2	50S ribosomal protein L9 OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=rplI PE=3 SV=1	125.2	23	3	3	18.4
M9ULS5 M9ULS5_CHLTH	50S ribosomal protein L9 OS=Chlamydia trachomatis L2/434/Bu(f) GN=rplI PE=3 SV=1	125.2	23	3	3	18.4
G4NPM5 G4NPM5_CHLT4	50S ribosomal protein L9 OS=Chlamydia trachomatis serovar A (strain A2497) GN=rplI PE=3 SV=1	125.2	23	3	3	18.4
A0A0E9CXI8 A0A0E9CXI8_CHLTH	Malate dehydrogenase OS=Chlamydia trachomatis GN=mdh PE=3 SV=1	162.9	21	7	2	35.7
sp O84381 MDH_CHLTR	Malate dehydrogenase OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=mdh PE=3 SV=1	162.9	21	7	2	35.7
sp Q3KKP0 RS6_CHLTA	30S ribosomal protein S6 OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=rpsF PE=3 SV=1	139.2	29	4	4	12.9
sp B0B928 RS6_CHLT2	30S ribosomal protein S6 OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=rpsF PE=3 SV=1	139.2	29	4	4	12.9

M9UGM4 M9UGM4_CHLTH	30S ribosomal protein S6 OS=Chlamydia trachomatis L2/434/Bu(f) GN=rpsF PE=3 SV=1	139.2	29	4	4	12.9
sp O84377 AAXA_CHLTR	Porin AaxA OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=aaxA PE=3 SV=2	125.5	10	3	3	51.5
A0A0E9CU42 A0A0E9CU42_CHLTH	Carbohydrate-selective porin%2C OprB family protein OS=Chlamydia trachomatis GN=aaxA PE=4 SV=1	125.5	10	3	3	51.5
G4NMV6 G4NMV6_CHLT4	Uncharacterized protein OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0404 PE=4 SV=1	125.5	10	3	3	52.0
sp B0BC75 RS7_CHLTB	30S ribosomal protein S7 OS=Chlamydia trachomatis serovar L2b (strain UCH-1/proctitis) GN=rpsG PE=3 SV=1	153.2	17	2	2	17.8
G4NNI2 G4NNI2_CHLT4	30S ribosomal protein S7 OS=Chlamydia trachomatis serovar A (strain A2497) GN=rpsG PE=3 SV=1	153.2	17	2	2	17.8
A0A0E9G3M0 A0A0E9G3M0_CHLTH	Transporter OS=Chlamydia trachomatis GN=ERS066954_00215 PE=4 SV=1	143.0	9	4	4	77.1
A0A0H3MH86 A0A0H3MH86_CHLT2	Uncharacterized protein OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=CTL0643 PE=4 SV=1	143.0	9	4	4	77.1
G4NNG0 G4NNG0_CHLT4	50S ribosomal protein L21 OS=Chlamydia trachomatis serovar A (strain A2497) GN=rplU PE=3 SV=1	151.5	45	4	4	12.3
A0A0H3MB37 A0A0H3MB37_CHLT2	Cytochrome d ubiquinol oxidase subunit I OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=cydA PE=4 SV=1	91.2	4	2	2	50.2
A0A0H2X0C7 A0A0H2X0C7_CHLTA	Cytochrome d ubiquinol oxidase subunit I OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=cydA PE=4 SV=1	91.2	4	2	2	50.2
O84016 O84016_CHLTR	Cytochrome Oxidase Subunit I OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=cydA PE=4 SV=1	91.2	4	2	2	50.2
M9UM80 M9UM80_CHLTH	Type III secretion system chaperone OS=Chlamydia trachomatis L2/434/Bu(f) GN=CTLFINAL_01575 PE=4 SV=1	121.9	20	2	2	18.4
A0A0H3MBJ5 A0A0H3MBJ5_CHLT2	Putative type III secretion system chaperone OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=CTL0299 PE=4 SV=1	121.9	20	2	2	18.4
A0A0H2X292 A0A0H2X292_CHLTA	Anti-sigma F factor antagonist OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=rsbV PE=4 SV=1	206.6	51	5	5	12.5
M9UM43 M9UM43_CHLTH	Anti-sigma factor antagonist OS=Chlamydia trachomatis L2/434/Bu(f) GN=CTLFINAL_03560 PE=3 SV=1	206.6	51	5	5	12.5
O84431 O84431_CHLTR	Anti-sigma factor antagonist OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=rsbV_1 PE=3 SV=1	206.6	51	5	5	12.5
A0A0H2X182 A0A0H2X182_CHLTA	Hypothetical membrane associated protein OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=CTA_0002 PE=4 SV=1	122.7	40	2	2	9.8
A0A0E9D6X4 A0A0E9D6X4_CHLTH	Putative membrane associated protein OS=Chlamydia trachomatis GN=ERS075185_00609 PE=4 SV=1	122.7	40	2	2	9.8
M9UKV6 M9UKV6_CHLTH	Membrane protein OS=Chlamydia trachomatis L2/434/Bu(f) GN=CTLFINAL_01355 PE=4 SV=1	122.7	40	2	2	9.8
G4NNU9 G4NNU9_CHLT4	Putative membrane associated protein OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0002 PE=4 SV=1	122.7	40	2	2	9.8
sp O84007 GATB_CHLTR	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=gatB PE=3 SV=1	181.4	17	5	5	55.0
M9UE49 M9UE49_CHLTH	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B OS=Chlamydia trachomatis L2/434/Bu(f) GN=gatB PE=3 SV=1	181.4	17	5	5	55.0
A0A0E9C8U7 A0A0E9C8U7_CHLTH	Ribonuclease E OS=Chlamydia trachomatis GN=rng PE=4 SV=1	108.1	8	2	2	59.4
A0A0H2X210 A0A0H2X210_CHLTA	Ribonuclease E OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=cafE PE=4 SV=1	108.1	8	2	2	59.3
M9UKL6 M9UKL6_CHLTH	Ribonuclease G OS=Chlamydia trachomatis L2/434/Bu(f) GN=CTLFINAL_00950 PE=4 SV=1	108.1	8	2	2	59.4
A0A0H3MBC8 A0A0H3MBC8_CHLT2	Ribonuclease E OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=cafE PE=4 SV=1	108.1	8	2	2	59.4
O84814 O84814_CHLTR	Axial Filament Protein OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=cafE PE=4 SV=1	108.1	8	2	2	59.3
A0A0E9DHL4 A0A0E9DHL4_CHLTH	Ribonuclease E OS=Chlamydia trachomatis GN=rng PE=4 SV=1	108.1	8	2	2	59.3
G4NPN0 G4NPN0_CHLT4	Ribonuclease E OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0880 PE=4 SV=1	108.1	7	2	2	60.9
sp B0B7S2 DEF_CHLT2	Peptide deformylase OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=def PE=3 SV=1	177.1	30	5	5	20.5
sp Q3KM05 DEF_CHLTA	Peptide deformylase OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=def PE=3 SV=1	177.1	30	5	5	20.5
A0A0E9DI70 A0A0E9DI70_CHLTH	1-deoxy-D-xylulose 5-phosphate reductoisomerase OS=Chlamydia trachomatis GN=dxr PE=3 SV=1	85.1	6	2	2	41.8

A0A0E9CXM5 A0A0E9CX M5_CHLTH	1-deoxy-D-xylulose 5-phosphate reductoisomerase OS=Chlamydia trachomatis GN=dxr PE=3 SV=1	85.1	6	2	2	41.7
A0A0E9EDI2 A0A0E9EDI2 _CHLTH	Serine--tRNA ligase OS=Chlamydia trachomatis GN=serS_1 PE=3 SV=1	118.6	13	4	4	48.4
sp Q3KKW5 SYS_CHLTA	Serine--tRNA ligase OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=serS PE=3 SV=1	118.6	13	4	4	48.3
sp Q3KLH6 RL16_CHLTA	50S ribosomal protein L16 OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=rpL16 PE=3 SV=1	148.6	20	2	2	15.8
sp B0BCG0 RL16_CHLTB	50S ribosomal protein L16 OS=Chlamydia trachomatis serovar L2b (strain UCH-1/proctitis) GN=rpL16 PE=3 SV=1	148.6	20	2	2	15.8
A0A0E9CFD6 A0A0E9CFD 6_CHLTH	50S ribosomal protein L16 OS=Chlamydia trachomatis GN=rpL16 PE=3 SV=1	148.6	20	2	2	15.8
A0A0E9DS10 A0A0E9DS1 0_CHLTH	ABC transporter ATPase OS=Chlamydia trachomatis GN=dppF PE=3 SV=1	134.2	19	4	2	31.0
A0A0E9CMC9 A0A0E9CM C9_CHLTH	Elongation factor P OS=Chlamydia trachomatis GN=efp-2 PE=3 SV=1	108.1	24	3	3	19.5
A0A0E9DDN6 A0A0E9DD N6_CHLTH	Elongation factor P OS=Chlamydia trachomatis GN=efp-2 PE=3 SV=1	108.1	23	3	3	20.5
sp O84804 GLGA_CHLTR	Glycogen synthase OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=glgA PE=3 SV=1	82.1	5	2	2	53.4
A0A0E9CL94 A0A0E9CL9 4_CHLTH	Glycogen synthase OS=Chlamydia trachomatis GN=glgA2 PE=3 SV=1	82.1	5	2	2	53.4
O84412 O84412_CHLTR	DnaK Suppressor OS=Chlamydia trachomatis (strain D/UW- 3/Cx) GN=dksA PE=4 SV=1	129.8	43	4	4	13.9
A0A0H3MCC6 A0A0H3MC C6_CHLT2	DnaK suppressor protein OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=dksA PE=4 SV=1	129.8	43	4	4	13.9
A0A0E9FXT1 A0A0E9FXT 1_CHLTH	DnaK suppressor protein OS=Chlamydia trachomatis GN=yocK PE=4 SV=1	129.8	43	4	4	13.9
M9UHY5 M9UHY5_CHLTH	Molecular chaperone DnaK OS=Chlamydia trachomatis L2/434/Bu(f) GN=CTLFINAL_03465 PE=4 SV=2	129.8	39	4	4	15.3
M9UFX8 M9UFX8_CHLTH	Dihydrolipooyl dehydrogenase OS=Chlamydia trachomatis L2/434/Bu(f) GN=CTLFINAL_04275 PE=4 SV=1	105.3	5	2	2	49.5
A0A0H2X2R2 A0A0H2X2R 2_CHLTA	Dihydrolipoamide dehydrogenase OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=lpdA PE=4 SV=1	105.3	5	2	2	49.5
A0A0E9CS98 A0A0E9CS9 8_CHLTH	Dihydrolipooyl dehydrogenase OS=Chlamydia trachomatis GN=pdhD PE=4 SV=1	105.3	5	2	2	49.5
A0A0H3MHJ2 A0A0H3MH J2_CHLT2	Dihydrolipoamide dehydrogenase OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=lpdA PE=4 SV=1	105.3	5	2	2	49.5
A0A0E9CCI4 A0A0E9CCI4 _CHLTH	Dihydrolipooyl dehydrogenase OS=Chlamydia trachomatis GN=pdhD PE=4 SV=1	105.3	5	2	2	49.5
A0A0E9DGP2 A0A0E9DG P2_CHLTH	Pyruvate dehydrogenase%2C E1 component%2C beta subunit OS=Chlamydia trachomatis GN=pdhB PE=4 SV=1	84.4	8	2	2	36.2
A0A0H3MBQ9 A0A0H3MB Q9_CHLT2	Putative exported protein OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=CTL0473 PE=4 SV=1	80.1	6	2	2	33.1
A0A0E9DL21 A0A0E9DL2 1_CHLTH	Putative membrane spanning protein OS=Chlamydia trachomatis GN=ERS066953_00163 PE=4 SV=1	80.1	6	2	2	33.1
sp Q3KKY8 CLPP2_CHLT A	ATP-dependent Clp protease proteolytic subunit 2 OS=Chlamydia trachomatis serovar A (strain ATCC VR- 571B / DSM 19440 / HAR-13) GN=clpP2 PE=3 SV=1	108.1	26	4	4	22.0
M9ULH7 M9ULH7_CHLTH	ATP-dependent Clp protease proteolytic subunit OS=Chlamydia trachomatis L2/434/Bu(f) GN=clpP PE=3 SV=1	108.1	26	4	4	22.0
A0A0E9FWY4 A0A0E9FW Y4_CHLTH	MotA/TolQ/ExbB proton channel family protein OS=Chlamydia trachomatis GN=exbB PE=3 SV=1	107.2	14	2	2	25.9
M9UI72 M9UI72_CHLTH	Oxidoreductase OS=Chlamydia trachomatis L2/434/Bu(f) GN=CTLFINAL_03620 PE=4 SV=1	102.1	5	2	2	39.9
A0A0H2X2I2 A0A0H2X2I 2_CHLTA	NADPH-cytochrome P450 reductase OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=cysJ PE=4 SV=1	102.1	5	2	2	39.9
G4NNH9 G4NNH9_CHLT4	NADPH-cytochrome P450 reductase OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0475 PE=4 SV=1	102.1	5	2	2	39.9
O84442 O84442_CHLTR	Sulfite Reductase OS=Chlamydia trachomatis (strain D/UW- 3/Cx) GN=cysJ PE=4 SV=1	102.1	5	2	2	39.9
A0A0E9DWF3 A0A0E9DW F3_CHLTH	Pyruvate dehydrogenase E1 component subunit alpha OS=Chlamydia trachomatis GN=pdhA_1 PE=4 SV=1	86.2	8	2	2	37.2
G4NP68 G4NP68_CHLT4	Pyruvate dehydrogenase E1 component subunit alpha OS=Chlamydia trachomatis serovar A (strain A2497) GN=pdhA PE=4 SV=1	86.2	8	2	2	37.2
A0A0H3MGN2 A0A0H3MG N2_CHLT2	ADP ATP carrier protein OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=CTL0321 PE=4 SV=1	84.6	4	2	2	58.1

M9UEC9 M9UEC9_CHLTH	ATPase AAA OS=Chlamydia trachomatis L2/434/Bu(f) GN=CTLFINAL_01695 PE=4 SV=1	84.6	4	2	2	58.1
sp O84068 TLC1_CHLTR	ADP ATP carrier protein 1 OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=tlcA PE=3 SV=1	84.6	4	2	2	58.1
A0A0E9DLH1 A0A0E9DLH1_CHLTH	ADP%2C ATP carrier protein OS=Chlamydia trachomatis GN=tlc-1 PE=4 SV=1	84.6	4	2	2	58.1
sp P66123 RL27_CHLTR	50S ribosomal protein L27 OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=rpmA PE=3 SV=1	90.3	33	2	2	8.9
A0A0E9C7I7 A0A0E9C7I7_CHLTH	50S ribosomal protein L27 OS=Chlamydia trachomatis GN=rpmA PE=3 SV=1	90.3	33	2	2	8.9
G4NNF9 G4NNF9_CHLT4	50S ribosomal protein L27 OS=Chlamydia trachomatis serovar A (strain A2497) GN=rpmA PE=3 SV=1	90.3	33	2	2	8.9
sp Q3KLT4 RL27_CHLTA	50S ribosomal protein L27 OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=rpmA PE=3 SV=1	90.3	33	2	2	8.9
A0A0E9D620 A0A0E9D620_CHLTH	Cysteine--tRNA ligase OS=Chlamydia trachomatis GN=cysS PE=3 SV=1	86.7	4	2	2	57.2
A0A0H2X1S7 A0A0H2X1S7_CHLTA	HAD superfamily hydrolase/phosphatase OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=CTA_0109 PE=4 SV=1	152.9	19	4	4	34.3
A0A0E9CFX5 A0A0E9CFX5_CHLTH	HAD superfamily hydrolase/phosphatase OS=Chlamydia trachomatis GN=ERS075185_00712 PE=4 SV=1	152.9	19	4	4	34.3
M9UHS2 M9UHS2_CHLTH	Deoxyuridine 5'-triphosphate nucleotidohydrolase OS=Chlamydia trachomatis L2/434/Bu(f) GN=dut PE=3 SV=1	127.5	37	3	3	15.3
A0A0E9DSY4 A0A0E9DSY4_CHLTH	Deoxyuridine 5'-triphosphate nucleotidohydrolase OS=Chlamydia trachomatis GN=dut_2 PE=3 SV=1	127.5	37	3	3	15.3
sp B0BBS3 DUT_CHLTH	Deoxyuridine 5'-triphosphate nucleotidohydrolase OS=Chlamydia trachomatis serovar L2b (strain UCH-1/proctitis) GN=dut PE=3 SV=1	127.5	37	3	3	15.3
O84776 O84776_CHLTR	Hydrolase/phosphatase homolog OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=CT_771 PE=3 SV=1	114.0	25	3	3	17.4
A0A0H2X385 A0A0H2X385_CHLTA	Phosphohydrolase (MutT/nudix family protein) OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=CTA_0841 PE=4 SV=1	114.0	25	3	3	17.4
G4NPJ0 G4NPJ0_CHLT4	Phosphohydrolase (MutT/nudix family protein) OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0841 PE=4 SV=1	114.0	25	3	3	17.4
A0A0E9DK93 A0A0E9DK93_CHLTH	MutT/Nudix family protein OS=Chlamydia trachomatis GN=ERS075193_00895 PE=3 SV=1	114.0	25	3	3	17.4
sp B0B9I6 FOLD_CHLT2	Bifunctional protein FoLD OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=foLD PE=3 SV=1	101.2	11	2	2	30.9
sp B0BB65 FOLD_CHLTH	Bifunctional protein FoLD OS=Chlamydia trachomatis serovar L2b (strain UCH-1/proctitis) GN=foLD PE=3 SV=1	101.2	11	2	2	30.9
M9UI50 M9UI50_CHLTH	Metallophosphoesterase OS=Chlamydia trachomatis L2/434/Bu(f) GN=CTLFINAL_03765 PE=4 SV=1	110.8	14	3	3	37.1
sp Q3KMZ0 SYM_CHLTA	Methionine--tRNA ligase OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=metG PE=3 SV=1	113.6	6	3	3	62.7
A0A0E9DB98 A0A0E9DB98_CHLTH	Methionine--tRNA ligase OS=Chlamydia trachomatis GN=metG_1 PE=3 SV=1	113.6	6	3	3	62.7
A0A0E9CW55 A0A0E9CW55_CHLTH	Peptidoglycan associated lipoprotein OS=Chlamydia trachomatis GN=pal PE=3 SV=1	91.7	11	2	2	21.5
M9UNW8 M9UNW8_CHLTH	Membrane protein OS=Chlamydia trachomatis L2/434/Bu(f) GN=CTLFINAL_04505 PE=3 SV=1	91.7	11	2	2	21.5
A0A0H2X2P6 A0A0H2X2P6_CHLTA	Peptidoglycan-associated lipoprotein OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=pal PE=4 SV=1	91.7	11	2	2	21.5
A0A0H3MDU9 A0A0H3MDU9_CHLT2	Peptidoglycan-associated lipoprotein OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=pal PE=4 SV=1	91.7	11	2	2	21.5
sp O84586 PARA_CHLTR	ParA family protein CT_582 OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=CT_582 PE=3 SV=1	97.7	24	4	4	28.2
A0A0H3MDT7 A0A0H3MDT7_CHLT2	Chromosome partitioning ATPase (ParA family) OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=minD PE=4 SV=1	97.7	24	4	4	28.2
A0A0E9DFM9 A0A0E9DFM9_CHLTH	ATPase%2C ParA FAMILY OS=Chlamydia trachomatis GN=soj_1 PE=4 SV=1	97.7	24	4	4	28.2
A0A0E9D3V4 A0A0E9D3V4_CHLTH	ATPase%2C ParA FAMILY OS=Chlamydia trachomatis GN=soj_1 PE=4 SV=1	97.7	24	4	4	28.2
M9UMM8 M9UMM8_CHLTH	Chromosome partitioning protein ParA OS=Chlamydia trachomatis L2/434/Bu(f) GN=CTLFINAL_04410 PE=4 SV=1	97.7	24	4	4	28.2
G4NMM3 G4NMM3_CHLT4	ATPase ParA FAMILY OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0632 PE=4 SV=1	97.7	24	4	4	28.6
A0A0E9DV71 A0A0E9DV71_CHLTH	ATPase%2C ParA FAMILY OS=Chlamydia trachomatis GN=soj_4 PE=4 SV=1	97.7	24	4	4	28.6

G4NPH0 G4NPH0_CHLTH	AMP nucleosidase OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0820 PE=4 SV=1	78.4	9	2	2	32.0
A0A0H2X1U4 A0A0H2X1U4_CHLTA	AMP nucleosidase OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=amn PE=4 SV=1	78.4	9	2	2	32.0
A0A0E9D1J8 A0A0E9D1J8_CHLTH	Protein RsbW OS=Chlamydia trachomatis GN=btrW PE=4 SV=1	107.7	23	3	3	16.4
O84553 O84553_CHLTR	Sigma regulatory factor-histidine kinase OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=rsbW PE=4 SV=1	107.7	23	3	3	16.4
A0A0E9CFX6 A0A0E9CFX6_CHLTH	Protein RsbW OS=Chlamydia trachomatis GN=btrW PE=4 SV=1	107.7	23	3	3	16.4
M9UMJ4 M9UMJ4_CHLTH	Histidine kinase OS=Chlamydia trachomatis L2/434/Bu(f) GN=CTLFINAL_04235 PE=4 SV=1	107.7	23	3	3	16.4
A0A0H3MLE8 A0A0H3MLE8_CHLT2	Sigma regulatory factor-histidine kinase OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=rsbW PE=4 SV=1	107.7	23	3	3	16.4
G4NPG9 G4NPG9_CHLTH	RsbW OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0599 PE=4 SV=1	107.7	22	3	3	17.3
A0A0E9D4E7 A0A0E9D4E7_CHLTH	Glutamate--tRNA ligase OS=Chlamydia trachomatis GN=gltX PE=3 SV=1	112.9	4	2	2	58.6
G4NNJ1 G4NNJ1_CHLTH	Glutamate--tRNA ligase OS=Chlamydia trachomatis serovar A (strain A2497) GN=gltX PE=3 SV=1	112.9	4	2	2	58.5
A0A0H3MGR8 A0A0H3MGR8_CHLT2	Biotin carboxyl carrier protein of acetyl-CoA carboxylase OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=accB PE=4 SV=1	107.6	20	2	2	18.2
A0A0E9D783 A0A0E9D783_CHLTH	Acetyl-CoA carboxylase biotin carboxyl carrier protein subunit OS=Chlamydia trachomatis GN=accB PE=4 SV=1	107.6	20	2	2	18.2
G4NPJ4 G4NPJ4_CHLTH	Acyl-acyl carrier protein synthetase OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0846 PE=4 SV=1	76.7	6	2	2	59.4
A0A0H2X0W7 A0A0H2X0W7_CHLTA	Hypothetical secreted protein OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=CTA_0275 PE=4 SV=1	74.7	12	2	2	24.0
G4NP76 G4NP76_CHLTH	Putative secreted protein OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0275 PE=4 SV=1	74.7	12	2	2	24.0
A0A0E9CQK7 A0A0E9CQK7_CHLTH	Uncharacterized conserved protein OS=Chlamydia trachomatis GN=ERS075194_01595 PE=4 SV=1	90.9	26	3	3	18.3
sp B0B929 RS18_CHLT2	30S ribosomal protein S18 OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=rpsR PE=3 SV=1	97.2	27	3	3	9.4
sp Q3KKN9 RS18_CHLTA	30S ribosomal protein S18 OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=rpsR PE=3 SV=1	97.2	27	3	3	9.4
A0A0E9DK62 A0A0E9DK62_CHLTH	30S ribosomal protein S18 OS=Chlamydia trachomatis GN=rpsR PE=3 SV=1	97.2	27	3	3	9.4
A0A0E9DSX9 A0A0E9DSX9_CHLTH	Thymidylate kinase OS=Chlamydia trachomatis GN=tmk_2 PE=3 SV=1	83.9	17	2	2	22.5
sp B0B9T8 KTHY_CHLTH	Thymidylate kinase OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=tmk PE=3 SV=1	83.9	17	2	2	22.5
A0A0H2X1D2 A0A0H2X1D2_CHLTA	Methyltransferase OS=Chlamydia trachomatis serovar A (strain ATCC VR-571B / DSM 19440 / HAR-13) GN=yhhF PE=4 SV=1	140.8	18	2	2	20.9
O84494 O84494_CHLTR	Methylase OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=yhhF PE=4 SV=1	140.8	18	2	2	20.9
A0A0H3MDP4 A0A0H3MDP4_CHLT2	Methyltransferase OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) GN=CTL0748 PE=4 SV=1	140.8	18	2	2	20.9
G4NPI2 G4NPI2_CHLTH	RNA binding protein OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0833 PE=3 SV=1	92.1	24	3	3	15.5
A0A0E9DER9 A0A0E9DER9_CHLTH	Chlamydia protein associating with death domains OS=Chlamydia trachomatis GN=ERS075193_00154 PE=4 SV=1	78.5	15	2	2	26.1
M9UIP8 M9UIP8_CHLTH	Dehydrogenase OS=Chlamydia trachomatis L2/434/Bu(f) GN=CTLFINAL_04565 PE=4 SV=1	78.5	15	2	2	26.8
sp O84616 PQQCL_CHLTH	PqqC-like protein OS=Chlamydia trachomatis (strain D/UW-3/Cx) GN=CT_610 PE=1 SV=1	78.5	15	2	2	26.7
G4NMQ5 G4NMQ5_CHLTH	Chlamydia protein associating with death domains OS=Chlamydia trachomatis serovar A (strain A2497) GN=CTO_0663 PE=4 SV=1	78.5	14	2	2	27.5