

>Icl|NC_002695.2_cds_NP_308028.1_1 [gene=thrL] [locus_tag=ECs_0001] [db_xref=GeneID:913387] [protein=thr operon leader peptide] [protein_id=NP_308028.1] [location=190..273] [gbkey=CDS]
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GCCCGCCGGATTCCGCTGGCGATTGAAAACCTTCGTCGACCAAGGAATTGCCAAATAAACATGTCCTGCATGG
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TCAGTAA>Icl|NC_002695.2_cds_NP_308032.1_5 [gene=yaax] [locus_tag=ECs_0005] [db_xref=GeneID:913394] [protein=hypothetical protein] [protein_id=NP_308032.1] [location=5251..5547] [gbkey=CDS]
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[gene=yaax] [locus_tag=ECs_0006] [db_xref=GeneID:913395] [protein=peroxide resistance protein] [protein_id=NP_308033.1] [location=complement(5700..6476)] [gbkey=CDS]

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incorporating molybdenum into molybdopterin] [protein_id=NP_308036.1] [location=9323..9910] [gbkey=CDS]
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[gene=fhuA] [locus_tag=ECs_0154] [db_xref=GeneID:913783] [protein=ferrichrome outer membrane transporter]
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CTAA >cl|NC_002695.2_cds_NP_308182.1_149 [gene=fhuC] [locus_tag=ECs_0155] [db_xref=GeneID:913784] [protein=iron(3+)-
hydroxamate import ABC transporter ATPase] [protein_id=NP_308182.1] [location=174101..174898] [gbkey=CDS]
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>|c|NC_002695.2_cds_NP_308183.1_150 [gene=fhuD] [locus_tag=ECs_0156] [db_xref=GeneID:913786] [protein=iron(3+)-hydroxamate import ABC transporter periplasmic binding protein] [protein_id=NP_308183.1] [location=174898..175788] [gbkey=CDS]

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>|c|NC_002695.2_cds_NP_308186.1_153 [gene=clca] [locus_tag=ECs_0159] [db_xref=GeneID:913789] [protein=H(+)/Cl(-) exchange transporter] [protein_id=NP_308186.1] [location=179307..180728] [gbkey=CDS]

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CACCGCGCCTTTGGTAA >Icl|NC_002695.2_cds_NP_308280.1_243 [gene=dinJ] [locus_tag=ECs_0253]
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[location=289892..290185] [gbkey=CDS]
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[gene=yafO] [locus_tag=ECs_0260] [db_xref=GeneID:914353] [protein=mRNA interferase toxin of the YafO-YafN toxin-antitoxin
system] [protein_id=NP_308287.1] [location=290188..290586] [gbkey=CDS]

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CCTGAAGGGCGGGAGGGGTTGACGTTGCGTCCGTTATTACGCAATGCTGGTGCAGCTGGCAATAACACC
CTGAAATTGCCGGGATTATGTTGATGATGCCGCTGAGTGGCTGACCCATGATGGTCTGATTGCCAG
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[protein_id=NP_308330.1] [location=319559..321892] [gbkey=CDS] ATGTCAGGAATGAAAGTTAGCCAGGCTGAGAAAGCAGCTCGGGGTCACTGGTCAAGAATTTCCTGCCGTTGGCGTAA TGACTGAAAATCGGCACCAGCCCTGCCGCTGTGCCGGGAAAGACCGCTTCGATTGATGACAGGAAGGGCGGG GAACGTGGTTCTGTAACCGTGCAGGGCAGGTGATGCCCTGCCGTTGTAAGTAAAGTACTGGATGTAAGGCTTAA AGAGGACAGACAGAATAAACGGCATTATGCCAACCTGCTGCCAGTATCTCAGGGATGCTGAATCTGTTCTCTGAAAA AGAGGACAGGGAGAAAAGCTCAGCAGTGCTGGCTGCCGTTGTTGATAAGTCCGCCAGACCACTGGCAATGCCCTA TGACGAGTAAAGGGTTCTGCACTGCCTGCCGGAAATTACCGCTATGCATAAAGTCGGTGGTGTGCCATTCCGCG GGAGATCTGTCGTTCCATTGTATGCAGATGGAGAGCTGGTAAATCTCAGGTTAATCAACGCTAATGGGGCAATGCTT CTTAAAGGCCGTCAGGTTAAGATGCCCTTACCTGGTGAAGGTTACTGCCAAAGCAGCCAAACGGCTCTGGATAGCGG AAGGATATGCCACCGCACTTACTATCAACTATCTGACTGGCGATGCTGATGGTGGCTTTCGTCGTCATTTCCCTT TCCCTGGCGAGCATTGCCCTGCACTGAGTACCAACGCCAACAGATAATTATTGCTGCTGCCGATCTCACCGTGGGG GCAAAACAAGGGGCGAGCTTACCGGGGCTGCAATTGCAACATGGCCTCCGCTGTGTTGGTACTGGAACGATG CATTCACGAAAACGGCGAAGAAGCCACCCGGCATGCAATTGAGTAATAAAACAGCTGTTGCCAGCCCTTCGAC ACAATGAGCGAAGCTGAAATTACCGCGCTGAGCGTCAGCGAAAAGCGCAGAGGGTAGTGGATCACTATAAAATTCACT GGCAGTAGACCGCAACGGGAGCTCCTTCACGCTATGAGCGGGGCTGGAAAGTTATCTATTACGCCATTGGGCC GTGATGTCGCTGCCCTGTTAGCGCCTCGACGACCTTTTACATCCGCAAAATTGCGTCTCTCGTGAAACCCCTCAA CTGATCGTCCGAAACAGCAGAATCCGGCGCGCAACTTATGGATTTCGCAACGGTGTGCTGATACCGGACAGGATT GTTCAGCCCGCACGATAAGAAGCACTGGTACGCTGCGAGGTGGATTACCGCAGCCGTTGACGGTAGTCAC TGGAAACCCATGCCCGCATTCTGGCGCTGGATCGCCGAGGTTTAACTCTGAAAACGGGACATTATTCTG GCTGCGATTGTTATGGTGTGGTAACCGTTATGACTGGCAGCTGTTCTGGAGGTCACTGCCCTGGGGAAAGTGG GAGTATTCTGCTGAAATAGCAACCATGCTGGGGTGAAGATAACCGCACCTCGCAACCCATTGAAATGCTGAGTCG CAAGAGAACGAGCTGCCATTAGGTTTCACTGATTGACCTCCCGACAGGAAAAGTGGAGGGTGAACGGGGCGGA CTAAAGGCATACTGCCGGATGCCGTTACCGGATCCAAATATGAGACCGCTTCAACCCACATCCGGCGGT CATCCTGGCTGTGAAACAATAATCCGATGCGCTTACGATCGTAGTGGTGGAGTTCACGCCGAAGGGTGTACCTGCATT TCCCCGACCAAGATAGCCCCGGAGGAACCGCATACCCAGCTCAAAGAGAAAATTGCCAGTGAAGCTAGCGGTGATTGTCG CAGCTTATGAGCGTTACGCCAGGACATTGCTTACGAGCAGAATTGCTTACGAGCACTCCGATGAGCGCTCAC CATCAAACGTGATGCTGATTGAGCTTTCGGCTACCTGAGGTCTTACCTGACACCACGGGATGTTATGG GGAACGCTAATATTGTCACGTCAGCCCTGCAACTTACCTTACCATGCTTACATGGCTGAGTTACATGGAGGCTAACGGCTAT AAAAATACGCTCAGTGTGACCATGTTGGCAAGGGGCTACCGTTAATGCTCAAGGAATATGGGCTGAGTATGAGAAAACG ACGGACCAATCAAGGAATGCAAGACTAATCTGCCCTAACAGAGAGGAAAGCAATGCTGACTGGTGCACGGGAAATGCGATGAGT TTGCAAGCGAAATAA >|cl|NC_002695.2_cds_NP_308331.1_285 [locus_tag=ECs_0304] [db_xref=GeneID:914403] [protein=hypothetical protein] [protein_id=NP_308331.1] [location=complement(322025..322981)] [gbkey=CDS] GTGACTAGTTATTCAAACCTTCCAATCAAATAAAAGAAACCATCAATAATAATTGATCATGAAATTGATGATTGGGA CATTATAAAAAAACTCAATCACAACTTAAATAAAATATCCATGGTGCAGGTAGAAATATCGTTGATTGTTAGATT TAGGTAACGGGATTTTATTCACAAACTTCCCTTGATGACTCTACAAGAAGACTGAAATTAGAGTGGCACCCCAATGAT AAATTCCATATATATTGAGTCCGTTGTTGCTGAGTTAATGACACTATATGCTTTCTAAAGGGATACTATCA CAATCAGTTATCTCAAATAGAAATATAACAAATGCTCTCATGTTCATTTGAAAACCTAGGTTCTTATGTTAG ACGTTTATAGAACCGGTTAAAGAGTAAATGAGACAACTCCAGACCCCCAAATATAAAATTGCTATACATGTTATTTAAC AAGGCCCAATGGCATGTTACATCACAGGCTCTCACGAAACCTCATGGATGCCATAAATTTCTTACAGAGAGCA CAAAATAGCCTTACATGAGTACAGGCTCTCACGAAACCTCATGGATGCCATAAAGAGAGGAAACTG CCAGGAGATTTAGAATATTCTCATGCTGTTAATATTGCTATAATGCAATTAAACGCTTCAATACCAAGAGCAA ATGCTAGGTAGTTAGTTCTGTTATTGAGGCTCTGGACTATGACCTTAAACGCTTAAATGAGTTGAAATTACAAAGGA CATCCTTAACTGCTGCCAGGCCAACACGGGGGTTAGAATTGAAAAGAAGATGTTATTTCTTGGAGGTTATTGAAA ACTTAATTAAAGCCATAAAGAAAACCGACATAAATAAAATTACAACCTGAGTGGATGTTAAATCAATTCAAATAA >|cl|NC_002695.2_cds_NP_308332.2_286 [gene=yagP] [locus_tag=ECs_0305] [db_xref=GeneID:914404] [protein=LysR family transcriptional regulator] [protein_id=NP_308332.2] [location=complement(323657..324556)] [gbkey=CDS] ATGAAAATCGATCTTAACTTACCCATTTCATGGTGCAGGTAGCAGAAGAGAGTAATTGAGCTGTTAAATCAATTCAAATAA CGCGCTCAGTTAATTGACAGAAGCGGGAGAACGGCTGCATAATCGCTGTCATTACCTTATCCGGTATTGAGGCAGCG TTCGAAGAGATGGTTCTGACCATGTCGCCACGCCGACTTCTCAGAATCGCGTGCAGCTCAATAGCTGAGAAGATTCTTC AGGTCCGCTAATCGCTCGTTGAGCAGCCAATCCAGCCGTTACGCTGAGTATTGAGGATGAGGAATTTCGATA 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CGCAGGACGACGGTGTGATGGATGAAACCAACGCCCTCGCTGACCCATCAGGAAGTGCAGGGTTATTACAGGTG GTGCATCAATTGCCGTAACGCCGGGATCTGCCGTTCTGCTGAGCTGCTGAGTGGAGAAGTGAAGGAGATCAAGCCTGGAT TATTCACTGCTGAAAGATGGTGAAGCTGGCTGGACTTTCCGGCTGCCAGAGATGACCACAAACTCGGTTCTGA

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[gene=psiF] [locus_tag=ECs_0434] [db_xref=GeneID:914536] [protein=phosphate starvation-inducible protein PsiF]
[protein_id=NP_308461.2] [location=463061..463381] [gbkey=CDS]
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[locus_tag=ECs_0442] [db_xref=GeneID:914544] [protein=hypothetical protein] [protein_id=NP_308469.2]
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>Ic|NC_002695.2_cds_NP_308635.1_569 [gene=cusS] [locus_tag=ECs_0608] [db_xref=GenoID:916966] [protein=copper-sensing histidine kinase in two-component regulatory system with CusR] [protein_id=NP_308635.1]
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[protein=two-component regulatory system response regulator CusR] [protein_id=NP_308636.1]
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[db_xref=GenoID:916969] [protein=Cu(I)/Ag(I) efflux system periplasmic protein CusF] [protein_id=NP_308638.1]
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[protein=membrane fusion protein of copper/silver efflux system] [protein_id=NP_308639.1] [location=680015..681238]
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[db_xref=GeneID:916972] [protein=copper/silver efflux system] [protein_id=NP_308640.1] [location=681250..684387]
[gbkey=CDS]

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CATCAGCCTGA >|c|NC_002695.2_cds_NP_308661.1_596 [gene=entB] [locus_tag=ECs_0634] [db_xref=GeneID:916993]
[protein=isochorismatase] [protein_id=NP_308661.1] [location=709165..710022] [gbkey=CDS]
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AAAGAGCAGAGCGATGAAGATCGGGCGCTGTTGAATGATATGTTGGGGCGGGCTGACCCGTCGGCGAACAGCAAA
GGTGGTGGATCGACTGACGCCAGATGCCGACGACACGGTCTGGTGAAGTGGCGCTACAGCGCTTCTCGTGGCGAACAGCAAA
TGGAGCAAATGCTCAAAGAGAGTGGACGTAACCGCTGATTATTACCGGGTATATGCCACATTGGCTGATGACCA
GCAACCGACGCATTATGCGCGATATTAAACCGTTATGGTGGCGGATGCGCTGGCGATTACCGTGTGACGAGCATT
GATGTCGCTGAAATATGTCGGGACGTTCTGGCCGGTGGTGAATGACCGAAGAATTACTGCCAGCACCTATCCCCGCA
GCAAAGCGCGCTGCGTGGAGGTGATCCTGCGCTGGACGAGTCCGATGAACCGTTCGATGACGACAACCTGATCGAC
TACGGTCTGGATTGGTGCATGATGGCGCTGGCGCTGGCGCAAAGTCGATGGCGATATCGACTTGTGATGTT
GGCGAAAAACCCGACCATCGACGCCGGTGGAAAGCTACTCTCCGCGAGGTGAATAA
>|c|NC_002695.2_cds_NP_308662.1_597 [gene=entA] [locus_tag=ECs_0635] [db_xref=GeneID:916994] [protein=2,3-dihydro-
2,3-dihydroxybenzoate dehydrogenase] [protein_id=NP_308662.1] [location=710022..710768] [gbkey=CDS]
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GTTAACCTGTTCCAGCAAACCATGAACCAAGCTTCCGCGTCAAGCGGGGGCGATTGTCAGTGTGGCGTCCGACGCC
CACACACGCCCGTATTGGTATGAGTGCCTATGGCGCATCGAAAGCGGGCCTGAAAAGCCTGGCGTTAGCGTCCGGCTG
GAACTGGCGGGTAGCGCGTGCCTGTAATGTTGGTTCGCCGGTCCACCGATACCGATATGCAACGCACGCTGTTGGT
GAGCGATGACGCCAGAACAGCGTATTGCGGCTTGGCGAGCAGTTAAACTGGCATTCCGCTGGGGAAAATCGCCC
GTCCACAAGAGATCGCAACACGATTGTTCTCGCCTGACCTCGCCAGCCATACCCCTACAGGATATTGTTG
GATGGCGGCTAACGCTGGGGCATAA >|c|NC_002695.2_cds_NP_308663.1_598 [gene=entH] [locus_tag=ECs_0636]
[db_xref=GeneID:916995] [protein=enterobactin synthesis proofreading thioesterase] [protein_id=NP_308663.1]
[location=710771..711184] [gbkey=CDS]
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GTGGGCACGGAACCTAACGCCACACATCATGCCCGGTGTCAGGCAAGGTACCGCGCTGCCAGCCGCTGC
TGGCGGCAAATACAGAGCTGGAAATCGTGTGTTGATGACAGGGCGGCTGACTGCACTTGTGCGTGGTACGG
CAGTTTGGGATGA >|c|NC_002695.2_cds_NP_308664.1_599 [gene=cstA] [locus_tag=ECs_0637] [db_xref=GeneID:916996]
[protein=carbon starvation protein involved in peptide utilization] [protein_id=NP_308664.1] [location=711365..713470]
[gbkey=CDS]
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GGCGCGCAAATGGTACCTGCCAGGGATGATGGCTACTGCCGGGGTGGTCTGCCGGTGCAGGATTCA
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TCATAGCCGCTGGGGAAACGTATACCGTGTGCTACCATTCCGCTGGCGTGTTCATGGGATCTACCGTGC
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GAAAGTCGACCTGGCACCGTACTTGAATTACCGCGTGCAGCTGACCTGGATGCTGGGGTTACGGTTGG
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GCTCAACCAAGATTGCCAGCGAAGTGGAGAACAGTCGATCATTCGGCGTGGCGGTTGC
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CTGTTATTCTGACGGCGGTGGATGCAAGGTACGGCGTGTGCGCGCTTATGTTGCAAGGATCTGCTGGGCGTGG
GGCGCTGAAACGGACCGATTACTGCCGCTAACCTGCTGGCAACGGCGCTGCGTGGCGTGGGGCTACTCCTG
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TGGTGCAGGCAAAAGGCCGCACTAA >|c|NC_002695.2_cds_NP_009502593.1_600 [gene=ybdD] [locus_tag=ECs_5382]
[db_xref=GeneID:62676059] [protein=hypothetical protein] [protein_id=NP_009502593.1] [location=713652..713849] [gbkey=CDS]
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CGCGCTACGGTGGAAAAGGCCGCGCGCTGCTGCTAA >|c|NC_002695.2_cds_NP_308665.1_601 [gene=ybdH]
[locus_tag=ECs_0638] [db_xref=GeneID:916997] [protein=oxidoreductase] [protein_id=NP_308665.1]
[location=complement(713859..714947)] [gbkey=CDS]
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GCTGAGTCCGGTGACGATCGCAGCGTGGTATTGGCGTGGCGCACTACTCGACACCAGCAAAGCCCTCGCCCG
CCGTCGGCTGCCATTGTCGCGCAACGATGCCGCCACCTGCCGCTGGACACCCGCTCCGTGGTATA
ACGATGCCGACAGCGCTGCATTAGAGATTTGACGACGCCAATTGAGTGGCTGGGAAACGGAGATTATCCTC
AATGCGCCGCAACAATATCTGCTGGCGGGATCGGTGATACGCTGGCAAATGGTATGAAGCGGTGGCTGGCTCCGCA
ACCAAGAACGTTGCCCTAACCGTGCAGCTGGGATCAATAATGCTCAGGCCATTGCGACGTCTGTTAAACAGTAGCG
AACAGGCCTGCCATCAGCAAATCAGCAGTTAACGCAATCATTGCGATGTGGGGATGCCATTGCTGGGT
GGGATGGTGGTGGCTGGGATCGTTTACGCGTAGCGGCCATGCCGTACATAACGGCTGACTGTCTGCC
ACAAACCGAGAAGTTCTCCACGGCACCAAAGTCGCTACGGAATTCTGGTCAAAGCGCCTGCTGGGTAGGATGATG
TGCTGGCGCAATTAAACCGGGCGTATCAGCGTTTCATCTGCCACTACGCTGGCGAGCTGGAAAGTGGATATCAATAAT
CAGGCAGAGATCGATAAAAGTGGATTGCCACACCTTGCAGCCGGTGGAGTCCATTACCTGCCAGTCACGCTGACACC
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[gene=ybdI] [locus_tag=ECs_0639] [db_xref=GeneID:916998] [protein=methionine aminotransferase] [protein_id=NP_308666.11] [location=715056..716216] [gbkey=CDS]

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ACACAGTGGCCAGGGGGCAACCAAATACGCCCATGACGGCGTGCAGGCCCTTGCAGGGCATTGCTCAGAAAACG
GAACGTTGTGGCTATCAACCAAGATGCCGATAGCGATATCACCGTAACGGCAGGGCGACGGAAGCGTTACCGCGC
GATTACCGCACTGGTGCAGTGGCGATGAAGTGGATTGTTGATCCCAGCTATGACAGTTACGCCCGCCATCGCGC
TTTCTGGGGAAATAGTGAAGCGTATGGCACTGCAACCACCGCATTTCGCGTTGACTGGCAGGAATTGCCGATTGTTA
AGCGAGCGCACCAAGACTGGTATCCTCAACACTCCGATAATCCCAGTGCAACTGTCTGGCAGCAGGCTGATTGCGCGC
TTTGTGGCAGGCGATGCCGGCACAGAGATTGTCATTAGCGATGAAGTCTACGAGCACATCAACTTTCACACAGG
GCCATGCCAGTGTGCTGGCGATCCGAGCTGCGTGGAGCGGGGGTGGCGGTGTCATGTTGGCAAGACCTATCATATG
ACCGGCTGGAAAGTGGTTATTGTTGCGCCAGCGCCATCAGGCCAAATTGCAAGGTACATCAGTATCTGACCTT
TTCGGTGAATACCCGGCACAGCTGGCAATTGCCGATATGCTACGTGCAAGACCTGAGCATTCTGCGTTACCGGACT
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TTTTGCTGGTGGATTACAGCGGTTTCTACCCCTGGATGATGTTGAGTTGCAAGTGGCTGACGCCGGAGCACGGCGT
GGCGGCGATTCCGCTATGGTGGTTTGCAGCCATCCCTCCACATAACTGATTGCTCTGTTGCCAAGAAGGAAT
CGACGTTGCTGGCAGCTGAACGACTGCCAGCTGTAG >|NC_002695.2_cds_NP_308667.1_603 [gene=ybdM]

[locus_tag=ECs_0640] [db_xref=GeneID:916999] [protein=chromosome partitioning protein ParB] [protein_id=NP_308667.1] [location=complement(716217..716846)] [gbkey=CDS]

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CGCGATTAATGAAATCCGATGGCAGTCATCAGGTTAGGCCCTTCTGTAAGAGGCCAGTGGATTGCGTTCTGTTGTTA
AAAACAGCCAACCTATGCTTAATGATAACACCAAAACAGTGGCACCCACCCGAAAAAAACTGCTGAAAAAAATCATT
GAAATAGATGGTTTACCCAAACCAATTGTTGTCACGGCATACGGATAAAAATGCCCTGAAATCGGGATGTTTACCG
CCATGAAATTGGTAAGGCTCATCATTAATACGCTAAAGGTTATTGCGGGTACCTGTCTGGAAGGTACGC
GTAATCAACGCATGCCGAGCTATTGCTCATATCGCCTGGAGCCATCAATACGCCATGTCGGAAATCGC
CGTGAACTCAGTCAGTGGGATGGGACGATAATGAAAGAGCTGGGAGCTGGGAAATGGCAGCGACGAAGTGTGCGCCT
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>|NC_002695.2_cds_NP_308668.1_604 [gene=ybdN] [locus_tag=ECs_0641] [db_xref=GeneID:917000]

[protein=phosphoadenosine phosphosulfate reductase] [protein_id=NP_308668.1] [location=complement(716819..718039)] [gbkey=CDS]

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ACCGAATGGCAGTGTGGAACCTGATGTCGAATGGTACGTCAAGCCCCGCAAGATGCGATAACCGATCCTGACTTT
TCTGCTTTACCGCAGGCATGACCTTCGAACAATTGTCAGTGAGTTGCCAATGGTTTACAAAAACGTCGGCG
GCGATGATGATGGCATCCGTGGATGAGTCTACAACCGTTTGTGCCATGCCAGTTAAATAACACGTTTGC
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CGTCATATGCAATTGCGAACCTTTGGCCGGAGCAACGACAAGGATTATGGCTCTACGTTATCGAACCGGATCG
CTGGGCTGATGTCGAGCTGGGGTAAAGTGGCGCATTACGCCGAGCTGATAATCATTCTATGGGC
ATCGGAAAATCTCAAGCCAGAACATTAGTACTGGCAAGAATATGCAATTGCTGCTCAATAGCATGCCGGAAAAAC
GCTGAGCATACCGCAATTGCGCATTATGGCACTGGTATCAGAAAAAGGAGCATGAGGTTCCACAAACCCAGCA
AGGGGACATTGGCGCGAAAGATATCCCTCTGGCGGGATGCAAAAGTTACTCAATAACGATTACTGGTGTGG
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ATACTATGCAACAACGATTAA >|NC_002695.2_cds_NP_308669.1_605 [gene=ybdO] [locus_tag=ECs_0642]

[db_xref=GeneID:917001] [protein=transcriptional regulator] [protein_id=NP_308669.1] [location=complement(718186..719088)] [gbkey=CDS]

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CTCAGAGGCCATTGACAAACAAATTATAGTCATAAGTCCGCTGCCACGCCAGATTCCCTGTCAGGATCTGGTACCC
CATTTCTGCTTAATAATAGTATGCTGATCCGCTGCCACGCCAGATTCCCTGTCAGGATCTGGTACCC
TCATGTCAGCAGAGAATGCTGAAGAACCTGTTGGTACCGCAAAGCCGATCTGGTACCC
CGTCCGTCATTGCACTGCCATTGCAACGATTGCTAATCTAATTGAGTAAAGCATCCACGAATTACTGACAA
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ACAGATTACTGGGAATAGTCCCTATGAACTTATAACTCCACCGTGAATTCTTAAATTAAAAGAGATAAAACTAGA
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ACCGTCAAATGAGTGTGGGG >|NC_002695.2_cds_NP_308670.3_606 [gene=dsbG] [locus_tag=ECs_0643]

[db_xref=GeneID:917002] [protein=thiol:disulfide interchange protein] [protein_id=NP_308670.3] [location=complement(719298..720044)] [gbkey=CDS]

ATGTTAAAAAGATACTTTACTGGCTCTGCTGCCATGCCGAGAGGAACCTCCTGCTCCAGTAAAGCGAT
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TGGGCGTCACCATCACCTGACTCCAGATGGTAAGCAGCCTATCTGGTTACATGTACAACGAGAAAGGTGAAAACCTG
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CCTCGACGGTAAAAAAGATGCGCCGGTATTGTCAGTCTCGCCGATCCGTTCTGCCATATTGTAACAGTTCTGGC
AGCAGGGCGGCCGTGGTAGATTCTGGCAAAGTACAGTTGAGAACATTGTTGGTTGGGGTATCAAACCAGAAAGTCCG
GCGACAGCCGCCAATTCTGCCCTCAAAGATCCGCAAAAACCTGGCAAGAATATGAAGCCTCTGGGGCAAGCTAA
GCTAAACGTGCCTGCAAACGTAAGTACAGAGCAAATGAAAGTGTAAAGCGACAACGAGAAACTCATGGACGATCTGGGG
CAAATGTCACCCGGCTATCTATTACATGAGTAAGGAAAATACGCTGCAACAGGCCGTGGGGTGGCCGATCAGAAAAGC
CTTAATATCATTGGGAAATAATAA >Icl|NC_002695.2_cds_NP_308671.1_607 [gene=ahpC] [locus_tag=ECs_0644]
[db_xref=GeneID:917003] [protein=alkyl hydroperoxide reductase] [protein_id=NP_308671.1] [location=720416..720979]
[gbkey=CDS]

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CTTCGACAACATGCGTAGAGATGAAGGCTGGCTGACCGTGCACCTCGTGTGCGTAAATCAAAGCAGCACAGTAGCT
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CTAA >Icl|NC_002695.2_cds_NP_308672.1_608 [gene=ahpF] [locus_tag=ECs_0645] [db_xref=GeneID:917004] [protein=alkyl hydroperoxide reductase] [protein_id=NP_308672.1] [location=721078..722673] [gbkey=CDS]

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CGGTGGTATCCGTCGAAAGAAGCGCAGTCTCTGCTGGAGACGATTCGCCATTGACGGTGTATTGAATTGAAACCT
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CACACTGCAATTGACGGCGCACCTCCAGAACGAGATCACTGATGTAACGTGATGGCGTCCGGCAGTGGTGTGAA
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CAGAAGAGCTGAACAAGCGTATGCTTACGTTGATGGCGAACGTTTGGTGTGAGTCTCGATACCCTGATATCGAAAA
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CATCATGCCACTGGCGAGGTGCCAAAGCCTCTGAGTGTGTTGACTACCTGATTCGCCACCAAATGCGATA
>Icl|NC_002695.2_cds_NP_308673.1_609 [gene=uspG] [locus_tag=ECs_0646] [db_xref=GeneID:917005] [protein=universal stress protein UP12] [protein_id=NP_308673.1] [location=complement(722794..723222)] [gbkey=CDS]

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CCAATCTGCTGTACTGGTCGTTGCTAA >Icl|NC_002695.2_cds_NP_308674.1_610 [gene=ybdR] [locus_tag=ECs_0647]
[db_xref=GeneID:917006] [protein=Zn-dependent NAD(P)-binding oxidoreductase] [protein_id=NP_308674.1]
[location=723443..724681] [gbkey=CDS]

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CAATGCGGGTAAAGGCGCTGCGCTAAATAAAAACAGATACCGAGTCCCGCGCATTGTTGGTATAGTCACCTGTATG
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TGACAATGAAACAGCCGGTTAAATTCCGCAATTAGCGATGGCGAAGTGCCTGCGACGCTGGTGTATCCGGCAAA
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TCACTGGGAACCTCCGGCGCGTGCACCCACCTGAAAGTGTGCGTAAAGTCAACGAGCAGAAGCTGCTGGCGACT
ACCTGCTTAA >Icl|NC_002695.2_cds_NP_308677.1_612 [gene=rna] [locus_tag=ECs_0650] [db_xref=GeneID:917009]
[protein=ribonuclease II] [protein_id=NP_308677.1] [location=complement(725552..726358)] [gbkey=CDS]
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[db_xref=GeneID:917018] [protein=sensory histidine kinase in two-component regulatory system with CitB]
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GCGTCGCCGGTAA>|c|NC_002695.2_cds_NP_308810.1_735 [gene=gpmA] [locus_tag=ECs_0783] [db_xref=GeneID:917517] [protein=phosphoglyceromutase 1] [protein_id=NP_308810.1] [location=complement(870716..871468)] [gbkey=CDS] ATGGCTGTAACTAAGCTGGTTCTGGTCTGCTATGCCGAAAGTCAGTGGAAACAAAGAAAACCGTTACCGGGTGGTACGA CGTGGATCTGCTGAGAAAGCGTAAGCGAACAAAGCAGCAGGTAGCTGCTGAAAGAGGAAAGTTACAGCTTGACT TTGCTTACACCTCTGCTGAAACGCCATCCATACCTGTTGGAATGTCGTCGGACGAACTGATCAGGATGCCGCC GTTGAGAAATCCTGAAACTGAAACAGTCACGCGTCACTACGGTGCCTGCAGGGTCTGAAACAAAGCGGAAACTGCTGAAAATA TGGCGACGAGCAGGTGAAACAGTCAGTGGCGTGTGGTTGCAGTGACTCCGCCGAACTGACTAAAGATGATGAGCGTTATC CGGGTCACGATCCCGTACCGGAAACTGAGCGAGAAAGAAGTGCCTGACGGAAAGCCTGGCGTACCGATTGCCGC GTGATCCCTACTGGAATGAAACATTGCGCGTATGAAAGAGCGGTAGCGCGTAATCATCGCTGACACGGTAACCT GTTACGTGCGCTGGTGAATATCTGATAACATGAGCGAAGAAGAGATTCTTGAGCTGAATATCCGACCGCGTGC CG TGGTTATGAGTTGACGAGAACTTCAAACCGCTGAAACGCTATTATCTGGTAATGCTGACGAGATCGCGCGAAAGCA GCAGCCGTTGCGAACCGGGTAAAGCGAAGTAA>|c|NC_002695.2_cds_NP_308811.1_736 [gene=galM] 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[db_xref=GeneID:917534] [protein=6-phosphogluconolactonase] [protein_id=NP_308822.1] [location=882460..883455]

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[location=complement(883496..884449)] [gbkey=CDS]

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CCGATGGAAAATGCGTCTAAACGGCGTCTGGTATTCTGTGAGGAATTATCGGTATGCCGTAAGCTTATCGACTG CCAGGTCTTAACGATCACACAGCATCGCTTGGTGCAGAAATTCCCCGCCGAATTACCTTAATTATCTCAATCAA TGCGCCTCGGACGATTGCCGAATAATTCTGGGTACACGATGCTGTTTACCCACAAGAATGA >Icl|NC_002695.2_cds_NP_308998.1_912 [gene=cydC] [locus_tag=ECs_0971] [db_xref=GeneID:917716] [protein=glutathione ABC transporter ATP-binding protein] [protein_id=NP_308998.1] [location=complement(1058552..1060273)] [gbkey=CDS] ATGCCTGGTCTACCTATCTGGCACTGTATAAACGTCATAAAATGGATGTTAGCTTGTGTTATGTGCTGGCAATTGT GACGCTGCTGCCAGTATCGTGTGACACTTCCGGCTGGTCTCGGCCCTCAGCGGTGCGGGGGTTGCCGGAC TGTACAGCTTCAACTATGCTACCCGCTGCCGGTGTGCGTGTGAGCAATCACCCTGACTGCCGGCGTTATTTGAA CGTCTGGTAAGTCAGCACGCCACTTCCCGCTGTGAGCATCTGCCATTACACCTTCAAGCAAATTGTTGCCCTCTC CCCTGCCGGACTGCCGCTATCGTCAGGGCGAATTGCTCAACCGCGTGGTGGCGGATGTTGACATCGCTCGATCATCTT ACCTGCGCTTATCTGCCGCTGGTGGCGCTTTGTGGTATTATGGTGGTACAATCGGGTTAAGTTCTTGTGATTCC CCCCTGCCCTTACGCTGGCGGCTTATGTTACTGACGCTTCTGATGCCACCGCTGTTTATCTGTGCGGGAAAAG 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GCGGACTCTCTCGTCCAAACAAATAATGTGATGACAACGGGAAATTATTGAGCAAGGTACTCACGCAAGACTGCT GCCAGACAGGGCGTTATTACGCTAACGAGGGTTGTAA >Icl|NC_002695.2_cds_NP_308999.1_913 [gene=cydD] [locus_tag=ECs_0972] [db_xref=GeneID:917714] [protein=amino acid ABC transporter permease] [protein_id=NP_308999.1] [location=complement(1060274..1062040)] [gbkey=CDS] ATGAAATAATCTGCTAAAAAGAGTTAACCCCGCTGGTAAACACGCAAAGCGTACCTCCCAACGTTGGCTGAATATTTC TCCTGCTGCTGGCTTGTGAGCGGCAATTGATCATTGCCAGGCATGGTCTGCGCAATTCTGCAACATATGATTA TGGAGAATATTCCCGTGAAGCCCTGCTGCTTCCCTTACGTTACTGGTCTGACCTTGTACTGCCGCGATGGTGGT TGGTACCGCAACGGGTGGTTATCACGCCGGCAGCATATCGCTTCTGCCATCCGCGTCAAGGTTCTGACCGTCTGCA ACAAGCAGGGCCAGCGTGGATTCAAGGTAACCTGCCGGAGCTGGCGACGCGTGGTACTCGAGCAAATTGACGATATGC ATGATTACTATGCACTGCCGCAATTGGCGCTGGCAGTGTGCGTGGCTGCTGATTTGTTGCGATCTCCCTC TCTAACTGGGCTGCCGCTCATTCTGCTGGGACTGACCCGTTAATTCCGTTGTTATGGCGCTGGTGGGATGGGGC TGCGATGCTAACCGACGTAACCTCTCGCTTGTGCTGCTTAAGTGGCATTCTCGATGCCCTGCCGGCATGGAAA 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[location=1170992..1171738] [gbkey=CDS]

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regulator] [protein_id=NP_309114.1] [location=1178803..1179390] [gbkey=CDS]
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TGGCAGCCTGA >Icl|NC_002695.2_cds_NP_309118.1_1024 [gene=pchA] [locus_tag=ECs_1091] [db_xref=GeneID:62675966] [protein=transcriptional regulator PchA] [protein_id=NP_309118.1] [location=complement(1183365..1183679)] [gbkey=CDS] ATGCTACATGATCACGTGGCAGAACATGTCGGAGAAAAAAGGACTGTACCGGAGAGCAGCTAACGATGGCAAAAGTGAT GGTACAGCTAAGTGTGACCAAGAAAAGAAAAGTGGCGGCACAGAAACAGCAGAGTGTGGCTAACAGACTACATTGAGTTGGGAATGGGATTGAAAGAG CGGTTTACCGGTAAACCTGACCGAAATAAAACAAGCGGTAAACAGACTACATTGAGTTGGGAATGGGATTGAAAGAG >Icl|NC_002695.2_cds_NP_309120.2_1025 [locus_tag=ECs_1092] [db_xref=GeneID:915166] [protein=endopeptidase] [protein_id=NP_309120.2] [location=complement(1184145..1184669)] [gbkey=CDS] TTGCCATTCTGATTGTGGCCATTGCTGTTCTGGCTGGCAATCGTTGGTATGAACCGTGTCTGTGTGGT TATCATTGCTCTGCTGGCTGTGGCGCTTAGTCTGGGCTGAATCATTACCGTATCACGCCATCATCTACAAAG AGCAGCGCATAAAAAGCCAGTGAGCTGGAGCTGGCGAACGCGACAATTACTGATATGCAGATACGCCAGCGTGTGTC GCTGCACTTGATGCCAGATACTCGAGGGATTAGCCGATGCGAGAGCTGAAATGAAACTCTGCGTGTGATGTGCCG 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system] [protein_id=NP_309432.1] [location=1454277..1454651] [gbkey=CDS]
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[db_xref=GeneID:912372] [protein=flagella synthesis protein FlgN] [protein_id=NP_309475.1]
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[gene=flgA] [locus_tag=ECs_1450] [db_xref=GeneID:913008] [protein=assembly protein for flagellar basal-body periplasmic P ring]
[protein_id=NP_309477.1] [location=complement(1489489..1490148)] [gbkey=CDS]
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[db_xref=GeneID:913983] [protein=flagellar component of cell-proximal portion of basal-body rod] [protein_id=NP_309478.1]
[location=1490303..1490719] [gbkey=CDS]

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[db_xref=GeneID:913368] [protein=flagellar component of cell-proximal portion of basal-body rod] [protein_id=NP_309479.1]
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>Icl|NC_002695.2_cds_NP_309481.1_1344 [gene=flgE] [locus_tag=ECs_1454] [db_xref=GeneID:914188] [protein=flagellar hook
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CGCTAA >Icl|NC_002695.2_cds_NP_309482.1_1345 [gene=flgF] [locus_tag=ECs_1455] [db_xref=GeneID:912868]
[protein=flagellar component of cell-proximal portion of basal-body rod] [protein_id=NP_309482.1] [location=1493084..1493839]
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[locus_tag=ECs_1456] [db_xref=GeneID:912784] [protein=flagellar component of cell-distal portion of basal-body rod]
[protein_id=NP_309483.1] [location=1493977..1494759] [gbkey=CDS]
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>Icl|NC_002695.2_cds_NP_309484.1_1347 [gene=flgH] [locus_tag=ECs_1457] [db_xref=GeneID:912879] [protein=flagellar
protein of basal-body outer-membrane L ring] [protein_id=NP_309484.1] [location=1494812..1495510] [gbkey=CDS]
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CAGCATCGTTAA >Icl|NC_002695.2_cds_NP_309662.1_1515 [locus_tag=ECs_1635] [db_xref=GeneID:913244] [protein=phage major capsid protein] [protein_id=NP_309662.1] [location=1636165..1637190] [gbkey=CDS]
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CCGGAAACACGAAGCTGGGGAGTTCCGGCATTACGGTAACGACTGGCAGACGCTGGAGCTGGTTCACCG
GCCACGGTTACTCCGAAACTGAATGGAGTGGCTGCCCGGCATTCCAGGTTATAAGACAGTCTGACACTGG
ACTGAA

TGCGCTACGCTACGGATTTACAAAAAATGCAGCGTATGGCGTTGAGATAGAAAGTCTGGTGTGGAGATAATGCAC CGGCATCATCATAA >|c|NC_002695.2_cds_NP_309809.1_1657 [locus_tag=ECs_1782] [db_xref=GeneID:913047] [protein=S lysis protein] [protein_id=NP_309809.1] [location=1776838..1777053] [gbkey=CDS]
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>|c|NC_002695.2_cds_NP_309810.1_1658 [locus_tag=ECs_1783] [db_xref=GeneID:913045] [protein=hypothetical protein] [protein_id=NP_309810.1] [location=1777058..1777402] [gbkey=CDS]
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ATGAATATGATGGCCGTGCCGTTACGGCAACTCTCTTATGAGTTAACATAATGGCGAACCATACGTTCCATGAA ACCTGTCGTTGCCGGGATGGGGCTGGCCTGGCAATCACAGTTGGCTAAGTTAACAGCAGCTTTGCGTCAACTATAACGG AAATCGTTATGGTTGCTGAGGATGGGAAACACGCAATATGGTGTCCATGCCACTTCGAAAACCTGCCGGCTGGCTACAA ACCATTAATCCAACAAAGTAAAACCGAAATCCCGATAAGGTATCCGGTACAGGAAGAGTGCAGCGATGTTCTTA CGAGTACTGGACGAAGGGTTTGTGTTAATCCCCGTTAAGGAGCTGATGGAAGAAACTCAACCAGGCTGTGCTGACA TGAAACGGGATAAAAACATTGCCAGTGTGTTGCTACCGGGCTGAATGAGTGGAAACAGGTTAAAGCCCGCATGTATCA AAAATCCGTACGCTGGTAAATGAAGCGAATATGCTGATTGATTGTCCTGGCTGATACAGGCAAAGGGAAAATAACAA GGCAGGATTGA >|c|NC_002695.2_cds_NP_309813.1_1661 [locus_tag=ECs_5722] [db_xref=GeneID:62675887] [protein=hypothetical protein] [protein_id=NP_309813.1] [location=1778826..1778972] [gbkey=CDS]
ATGGGGTGGCTAATGATATCAGATAAAACTCATAACCGCTGGTAAGAGAGCCTGCTGTACTTGTGCGCATTTCATTAGT CATGCTGGTGCCTACCTTCTTCCACCGCCTGGCGAGTCCTGACGTTATCGGGACTGGTGGGGTGA >|c|NC_002695.2_cds_NP_309813.1_1662 [locus_tag=ECs_1786] [db_xref=GeneID:913037] [protein=phage endopeptidase] [protein_id=NP_309813.1] [location=1778980..1779447] [gbkey=CDS]
ATGAACCGTGTCTGTGTTGATTATTGTCCTGGCGTTGGCTATGGTCGCGTGTGGCTGGCAACAAACCATACCG TGACAACCGCCTCACCTAACAGCGCAGCGCATAAAAAGCCAGAGCTGGAACAGGCGAATGCCACCATCTGACA TGCAGGTGCGCCAGCGTGTGTTGCTGCCGTGGCTGATGCAAATACTCGAGGGAGTTAGCCGATGCGAGAGCTGAAATGAA ACTCTGCGTGCTGATGTTGCCGTGGCTGTAAGGCCCTGCCGATCAACGCCACCTGCTCCGGTACCGTGTGAGGCCAC CGGCACCTCCGGCGTGGATAATGCAACCGGCCCCGACTGGCAGACACCGCTGAACGGGATTATTCATCCTCAGAGAAC GGTTGATGACAATGCGAAGCAGCTGGAAAGGGGACAGGACTATATCCGACTCAGTGCCTGAACCTAA >|c|NC_002695.2_cds_NP_309814.1_1663 [locus_tag=ECs_1787] [db_xref=GeneID:913034] [protein=lipoprotein precursor] [protein_id=NP_309814.1] [location=1779200..1779385] [gbkey=CDS]
ATGCGAGAGCTGAAAATGAAACTCTGCGTGTGATGTTGCCGCTGGTCGTAAGGCCCTGCCGATCAACGCCACCTGCTCC GGTACCGTGCCTGAAAGCCACCGCACCTCCGGCGTGGATAATGCAACCGGCCCCGACTGGCAGACACCGCTGAACGGGA TTATTCATCCTCAGAGAACGGTTGA >|c|NC_002695.2_cds_NP_309815.1_1664 [locus_tag=ECs_1788] [db_xref=GeneID:913028] [protein=hypothetical protein] [protein_id=NP_309815.1] [location=complement(1779810..1780037)] [gbkey=CDS]
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GTGCTGACAACGCAAAACGAAAATTGCGCTGGCGCTCATGTCGGGAAAAACAAAACAGCGTCAGCCCTGCCCGG TTATTGCGCGAAGACAGCCAGGGTTAAAGGCTCGCAGCTGGCAAAAGATCCGGAGGTGCTTGCCTTATGCCGTAAC AGTGCAGAGACGGTGGAGGTGGATGAGGTTCTGTTATCGGCAGAAAAAAATCAGAGCCGGAGGATAACCCCGTCGCCGT GAGGCAGGCTGCAATACCACAGCCGAGAACAAATCCGGAGATGCCACCGCCCGTGGTATCTCTGGTATTGAGTA TATGGAGGACGGTCTCCGATCCGGTAAAGCGATGGGGCTTCTGGTGGAGAACATTAATACGACCCCAGGCTGG CGCTGGATGCCGTTATAAGCTGGCGAGTTACCGCACCATAAAAAGGGGATGCCGGAAAAATCGCAAAAGGTGAC GCGCGAAAAAAAGCGGTAACCGTTGCCACCACCCCGCTGGTGGTAATAATGATAATGAGGGAACCG ATGA >|c|NC_002695.2_cds_NP_309819.1_1667 [locus_tag=ECs_1792] [db_xref=GeneID:912990] [protein=phage terminase large subunit] [protein_id=NP_309819.1] [location=1781294..1782955] [gbkey=CDS]
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GGCGGGATGCAGGAGGCTGA >Icl|NC_002695.2_cds_NP_309823.1_1671 [locus_tag=ECs_1796] [db_xref=GeneID:912943]
[protein=phage DNA packaging protein] [protein_id=NP_309823.1] [location=1787750..1788076] [gbkey=CDS]
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GTTATGA >Icl|NC_002695.2_cds_NP_309824.1_1672 [locus_tag=ECs_1797] [db_xref=GeneID:912938] [protein=phage head-tail
adaptor] [protein_id=NP_309824.1] [location=1788086..1788436] [gbkey=CDS]
ATGGCAATATCTGCAGGTCGCTGACACAGATGATAAGTGTCTGAACCCGGTTAACCGTAACGCTGCCGGAGAAAT
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[db_xref=GeneID:912937] [protein=phage minor tail protein] [protein_id=NP_309825.1] [location=1788433..1788879] [gbkey=CDS]
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[locus_tag=ECs_1799] [db_xref=GeneID:912932] [protein=phage minor tail protein] [protein_id=NP_309826.1]
[location=1788876..1789220] [gbkey=CDS]
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[db_xref=GeneID:912931] [protein=phage major tail protein] [protein_id=NP_309827.2] [location=1789279..1789995] [gbkey=CDS]
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>Icl|NC_002695.2_cds_NP_309828.1_1676 [locus_tag=ECs_1801] [db_xref=GeneID:912930] [protein=phage tail assembly
protein] [protein_id=NP_309828.1] [location=1790001..1790375] [gbkey=CDS]
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[locus_tag=ECs_1803] [db_xref=GeneID:912925] [protein=phage tail length tape measure protein] [protein_id=NP_309830.1]
[location=1790733..1793813] [gbkey=CDS]
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[locus_tag=ECs_1804] [db_xref=GeneID:912922] [protein=phage minor tail protein] [protein_id=NP_309831.1]
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GAGGTTTCTGTTATCCACGAAGCCCTGGCAGCGTGTGAGCTGACTTGGCAGTGGCGAATTACGCCAACGTTGCTG
GCGTACAGCAACGGCGCAGGTTACACCATGCCAGCGTGTGAGCTGACTTGGCAGCAGGCCACTGCCCTATTGCGCTGG
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[db_xref=GeneID:912522] [protein=beta-phosphoglucomutase] [protein_id=NP_309923.1] [location=1888099..1888758]
[gbkey=CDS]
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CTTTACGTCCACTCACTGCGCGAGCTGACGGTTAATGCTGTGCTGCCCGTATTGCAATTGCTGGCAGAGCTCCGC
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CCTTCTGGAAAACGTATAG >|cl|NC_002695.2_cds_NP_309924.1_1762 [gene=ycjV] [locus_tag=ECs_1897]
[db_xref=GeneID:912514] [protein=sugar transporter subunit] [protein_id=NP_309924.1] [location=1888772..1889854]
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ATGTCATTCTTGTGAGCAAAACGGAAATAGCAATTGCTAA >|cl|NC_002695.2_cds_NP_309925.1_1763 [gene=ompG]
[locus_tag=ECs_1898] [db_xref=GeneID:912504] [protein=outer membrane porin G] [protein_id=NP_309925.1]
[location=1889899..1890804] [gbkey=CDS]

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CCTGACCCGGCGTTCCGTAATTATGGTTACACTACGTTGATGAACCGGGTAAGACACGCCAATATCAGCGCTGGA
AAATCGGCCAGACTGGATGACTGACGATTACGTTAACGGTTGGTGTGATGTATAAATTGCCAAC
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GTGTCGGCGTAAATTACTCGTCTGA >|cl|NC_002695.2_cds_NP_309926.1_1764 [gene=ycjW] [locus_tag=ECs_1899]
[db_xref=GeneID:912493] [protein=LacI family transcriptional repressor] [protein_id=NP_309926.1]
[location=complement(1890915..1891913)] [gbkey=CDS]

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[locus_tag=ECs_1900] [db_xref=GeneID:912488] [protein=hypothetical protein] [protein_id=NP_309927.1]
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CCCGCGTGGAAATTAAATAGGAGATAATTGCGATGA >|cl|NC_002695.2_cds_NP_309928.1_1766 [gene=ycjF]
[locus_tag=ECs_1901] [db_xref=GeneID:912484] [protein=inner membrane protein] [protein_id=NP_309928.1]
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GCTG

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CAGGCCGGTATTGATCAGTCTCATCCAGCGCTCAACGCTGGTATGCCCAATCCATGAAACGCAAGCGATCGAAGT
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CAAACGCCAGCGAAAATAA >Icl|NC_002695.2_cds_NP_309929.1_1767 [gene=tyrR] [locus_tag=ECs_1902]
[db_xref=GeneID:912481] [protein=aromatic amino acid biosynthesis and transport regulon transcriptional regulator]
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CACTTCCGTAACGCTGAATTCTGCAAGCCTACGGTGTGCGATTGCGCAATTGCTGATGGCCACTGAAAGGCTGG
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GCAGCTGGCTGACTGAAAGCTAA >Icl|NC_002695.2_cds_NP_309931.2_1769 [gene=ycjG] [locus_tag=ECs_1904]
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[protein=NAD-dependent epimerase/dehydratase] [protein_id=NP_309933.3] [location=complement(1898840..1899478)]
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[db_xref=GeneID:912407] [protein=murein tripeptide (L-ala-gamma-D-glutamyl-meso-DAP) transporter subunit]
[protein_id=NP_309938.2] [location=1902722..1904335] [gbkey=CDS]
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>|c|NC_002695.2_cds_NP_310832.1_2609 [gene=cbeA] [locus_tag=ECs_2805] [db_xref=GenelD:912732] [protein=antitoxin of toxin-antitoxin system] [protein_id=NP_310832.1] [location=2749755..2750123] [gbkey=CDS]
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GCCCT GTT CGGGC ACGT CTGGT GCAGGAGGGTAACCGGTTGCATTACCTTGCACCGCCGGTATCAGAGGCCTGT
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TGGTTACGTTATCTGGCTTTATCCGACGCCGAAATGAAAATTAA >|c|NC_002695.2_cds_NP_310833.1_2610
[gene=yeeV] [locus_tag=ECs_2806] [db_xref=GenelD:912310] [protein=toxin of the YeeV-YeeU toxin-antitoxin system]
[protein_id=NP_310833.1] [location=2750212..2750475] [gbkey=CDS]
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GCGCCTGTACCCGCTCTCAGTTAA >|c|NC_002695.2_cds_NP_310834.2_2611 [gene=yeeW] [locus_tag=ECs_2807]
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GCGCTGGCGCTCTGGATGAACGGGAAAGAAACCAACGCAATACATCAAACGCCGACCAGGAGAACGAGGAGATTGCGCT
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[protein=hypothetical protein] [protein_id=NP_311036.1] [location=2941106..2941462] [gbkey=CDS]
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GTAGTGCCTGATAAGTTGCCGCGTGAATACAGAAACGGTTGCCCTTGCCTAGTGAAGGCTGGAAACGA
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[location=2941909..2942151] [gbkey=CDS]
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TGA >|NC_002695.2_cds_NP_311038.1_2801 [locus_tag=ECs_5743] [db_xref=GeneID:62675797] [protein=hypothetical
protein] [protein_id=YP_009502644.1] [location=2942155..2942289] [gbkey=CDS]
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[protein_id=NP_311039.1] [location=2942308..2942562] [gbkey=CDS]
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GCAAGTCCGGTTAA >|NC_002695.2_cds_NP_311040.1_2803 [locus_tag=ECs_3013] [db_xref=GeneID:916717]
[protein=integrase] [protein_id=NP_311040.1] [location=2942596..2943882] [gbkey=CDS]
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[protein=transcriptional activator of csgD and csgBA] [protein_id=NP_311041.1] [location=2943957..2944604] [gbkey=CDS]
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TCAATCCGTGACCGTGCTGACCGGGATTAAAATGCCGTCGGTGAACCGTAAAGTGCTGTATGCCAAAGGGGCGAACG TTACCACTGACAAAGGCATTATCGATTCCTGAATCAGTATGAAGAAGCGGTCAAAGTCGATCCGCGTCGCCGCAAGAG ATGATTGATGAAGCGGTGCAAGACGGCGAAACAATCTGATGGTGGCTGAGTCGGTAAGGCACAGGGGATGGCGCA CGAGGCCCTCCAGCGTACCGATATTACTATTCTGCAAAGCCAGCGTATTGATTGCCGCCCTGAAAGCCACCGGCAAAC CGCTGGTCTGGTCTGATGAACGGCGTCCGCTGGCGCTGGTAAAGAAGATCAGCAGGCTGATGCAGTTCTGGAAACC TGGTTGCCGGGACTGAAGCGGTAAATGCAATTGCCGATGTTGTTGGCATTACAACCGTCCGGTAAGCTGCCGAT GTCTCCCGCGTCTGTCGGCAGATCCCGGTACTACAGCATCTGAAACACCGTCGTCCTGATAATGCCGACAAGC CGAACAAATACTTCGCGTTATTTGATGAAGCTAACGGGCCTTATCCGTTCCGCTATGGTCTGAGCTATACCACT TTCACCGTCTGATGTGAAACCTTCTGCGCCGACCATGAAGCGTACGGCAAAGTGACGGCAGCGTGCAGGTGACGAA CACCGTAAACGCGAAGGGCACGGTAGTGCAGATGACTTGCAGGATGTGACGGCTTCATGAGCGTCCAGTGAAGC AGCTGAAAGGCTTGAGAAATCACCCCTGAAGCCGGCGAAACCCAGACCGTCAGCTCCGATTGATATCGAGGCGCTG AAGTTCTGGAATCAACAGATGAAATATGACGCCGAGCCTGGCAAGTTCAATGTTATGGCACTGATCCGCACCGT TAAGAAAGGCGAGTTGAGTTGCTGAA >|cl|NC_002695.2_cds_NP_311047.1_2810 [gene=ldl] [locus_tag=ECs_3020] [db_xref=GeneID:916724] [protein=D-lactate dehydrogenase] [protein_id=NP_311047.1] [location=2951233..2952948] [gbkey=CDS]

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ATGAGCCATGCTGGGACTGTTTCCATCCGATCGTGAATGCAAGGTGATTAATCGCGAAAACGAAACGATTTCTCA CCATTACACCCACCGCTTGTGATGGCGCGATTCCGGTAGTTGCGCCTTCATTGGCACTACACAGATTGGCTGGA ATTGCGGGTGGCGACTATCTGGAAGTTATCCTGGTTACCGGACTGGCGCTGGCTGCTGTTATGGCGTTATGCTC GCTGGGGTGGCGTAGGGCGGGTACCGTTGCAACTCCGCTGTTTAAGTGGTCTGGCGCTTATCGCTGGTCTGGTTGTGCGC TGGTGGCAGGGTGGCACTGTTTACACCGGTTACCTACTTACCTGGTATTCCGAGCTTCTGGAATATCAACAAAGAG GAAGGCCCTAGCTTCCAGTCGACGCTGGCGATTGGCGTGGTAGTGGAAAGTGCTGCTGCCCTTACGTTAACT ATGGGGCTACGGTTATCGTTGTTCTAG >|cl|NC_002695.2_cds_NP_311050.2_2813 [gene=yohD] [locus_tag=ECs_3023] [db_xref=GeneID:916727] [protein=DedA family inner membrane protein] [protein_id=NP_311050.2] [location=2954849..2955427] [gbkey=CDS]

ATGGATCTCAATACACTCATCACAATATGGTTATGCCGCGCTGGTATCGGTAGCCTGGCGGAAGGTGAAACCGTGAC TTTGCTGGAGGCCCTGCCGACATCAGGGCTATTAAAGTCCGCTGGTACTTCTGAGCGCTTGGCGCATGA TTGGCGACCGAGGTGCTCTATGTGCGGGCGGGTTGGCGTAAGCTGTTACGCCGTTCTCTAAACATCAGGATAAA ATTGAGCGGGCGCAGAAACTGATCCAACGCCATCCGATCTGTTGTCATTGGTACCGCCTTATGTTATGGCTTCCGGT GATTGGCCCGACGCTGATTGGTGCAGGCCAGCTGCCCGAAAATCTTCTGCCGTTAATATTCTGCCGCACTTGCCT GGGCGTTGATTGGTACCGTGGTAGTGGCGCTGGTGGTAGGCGCTGGTGGCTGAAACGACGCCGGAAAGAAAAA GCCGGATAATCAGCGTAA >|cl|NC_002695.2_cds_NP_311051.1_2814 [gene=yohF] [locus_tag=ECs_3024] [db_xref=GeneID:916728] [protein=oxidoreductase] [protein_id=NP_311051.1] [location=complement(2955557..2956318)] [gbkey=CDS]

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CGCATGAGATTGCCAGCCTGGTGGCTTCTGGAGGGCGAAATTACACCACCGGGCAGTCGTTGATAGTGAT
GGCGGCTTATGTTGGCGAACCCAGAATAG >Icl|NC_002695.2_cds_NP_311052.3_2815 [gene=mdtQ]
[locus_tag=ECs_3025] [db_xref=GeneID:916729] [protein=channel/filament proteins] [protein_id=NP_311052.3]
[location=complement(2956371..2957897)] [gbkey=CDS]

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ACGCTGA >Icl|NC_002695.2_cds_NP_311053.1_2816 [gene=dusC] [locus_tag=ECs_3026] [db_xref=GeneID:916730]
[protein=tRNA-dihydrouridine synthase C] [protein_id=NP_311053.1] [location=complement(2958502..2959452)] [gbkey=CDS]
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[protein_id=NP_311055.2] [location=complement(2960820..2961464)] [gbkey=CDS]

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AGAGCGTAA>Icl|NC_002695.2_cds_NP_311225.2_2986 [gene=dedD] [locus_tag=ECs_3198] [db_xref=GeneID:916906] [protein=membrane-anchored periplasmic protein involved in septation] [protein_id=NP_311225.2] [location=complement(3157509..3158171)] [gbkey=CDS]
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[protein=phosphohistidinoprotein-hexose phosphotransferase component of PTS system] [protein_id=NP_311314.1]
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TTAA >|cl|NC_002695.2_cds_NP_311427.2_3184 [gene=yfhR] [locus_tag=ECs_3400] [db_xref=GenelD:915154]

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[locus_tag=ECs_3406] [db_xref=GeneID:914928] [protein=3-phenylpropionate dioxygenase ferredoxin subunit]
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>I|NC_002695.2_cds_NP_311434.1_3191 [gene=hcaB] [locus_tag=ECs_3407] [db_xref=GeneID:914919] [protein=2,3-dihydroxy-2,3-dihydrophenylpropionate dehydrogenase] [protein_id=NP_311434.1] [location=3391861..3392673] [gbkey=CDS]
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>|NC_002695.2_cds_NP_311631.1_3380 [gene=cysC] [locus_tag=ECs_3604] [db_xref=GeneID:914674] [protein=adenosine 5'-phosphosulfate kinase] [protein_id=NP_311631.1] [location=complement(3594037..3594642)] [gbkey=CDS]
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CGAACATAATGAAACGGCTACTGCGGGTGGAGAAGCCAGGGTACTGGAAGTGGCCACCGCCGAGAATGTCGGCGA AATGGAGCGCGGCTGGTATGACACTGGCGATATTGCGTTGACGAGCAGGGCTTGTGAGATTCAAGGCGCAGA AACGCTTGCCTAAATTGCAAGCGAAATGGTGCCTGGAAATGGTGGAAACACTGGCACTGGTGTGTTGCCAGATAAA GTCCATGCCACTGCGATTAAAGAGCGATGCCAGCAAAGGCGAGGCAGTGGTCTTTCACACAGATAACGAACGCG CGATAAGTTGCAACAGTATGCCCGTGAGCACGGCGTCCGGAGCTGCTGTCGCTGATATTGCTATTGAAACAGA TGCCATTACTTGGCAGCGGCAAACCTGACTTGTGACGGTAAAGGCTGGTAGACGAAAGTGGAAACACGATGAGTGA >cl|NC_002695.2_cds_NP_311721.1_3464 [gene=galR] [locus_tag=ECs_3694] [db_xref=GeneID:916490] [protein=galactose-inducible d-galactose regulon transcriptional repressor] [protein_id=NP_311721.1] [location=3699127..3700158] [gbkey=CDS] ATGGCGACCATAAAGGATGTTAGCCCGACTGGCAGCGCTTCACTGCGCCACCGTTCACCGCTGCTGATTAATAATTACCCAA AGCCAGCGAAGCTCCCGCTGGCTGTCATAGTCGCAATGGAGTCTCTAGCTATACCCGAACGCCAACGCCGTGCGC TGGCGCAGACCAACTGAAACGGTGGCTGCGTTATCACACCGTAATTCTTATTGATGGCAATGTTACCAACGAAACAAAAGAGCGTCAAGGC GTCGAACAGGTGGCTTATCACACCGTAATTCTTATTGATGGCAATGTTACCAACGAAACAAAAGAGCGTCAAGGC CATTGAGCAACTGATCCGCCATCGCTGCTGCGTTGGCTGCGTCCATGCCAAAATGATCCCGATGCCGATTAGCCTCAT TATTGAAACAAATGCCGGTATGGTGTGATCAACCGTATCTGCCCTGGCTTGAACCGTTGATTGCTCTGGACGAT CGTTACGGTGCCTGGCTGGCTACGCGTCATTAACTCAGCAAGGTACACCGCATTGGTTATCTGCTCTAACCACTC TATTCTGACGCCGAAGATGCTGCAAGGGTATTACGATGCCCTGCTGAAAGTGGTATTGCGGCAATGACCGGCTGG TGACATTGGCAACCAGACGAAAGCGCGGGGAAACAGGCAATGACCGAGCTTGGGAGCGAGAAGAAATTCACTGCG GTAGCCTGTTATAACGATTCAATGGCGGGGGTGCATGGCGTTCTCAATGATAATGGTATTGATGACCGGGTGAGAT TTCGTTAATTGGCTTGTGATGCTGGTGTACGCTATGTCGCTCCGCGCTGACCACCGTGCCTACCAATCGTA CGATGGCGACCCAGGCTGCCGAACCTGGCTGGCGCTGGCGATAATGCCCTCTCCGGAAATCAACTATGCTTTAGT CCGACGCTGGTACGTCGTCATTCACTGTCACCTCCGTCGCTGGAGGCAAGTCATGCAACCAGCGACTAA >cl|NC_002695.2_cds_NP_311722.1_3465 [gene=lysA] [locus_tag=ECs_3695] [db_xref=GeneID:916478] [protein=diaminopimelate decarboxylase] [protein_id=NP_311722.1] [location=complement(3700165..3701427)] [gbkey=CDS] 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TAACTTGGAACACCATGCCGTGCACACCCACAGCGCCGGATGGAAGTTTCTATTCAATATGGATGATGACG
CCTGCGTTTCCACATGATGGGCAGCGCAAGAACCGTCACATTGTGATGCATAACGAGCAGGCGGTGATCTCCCCG
AGCTGGTCGATTCTCGCGCTGGAAACCAAGCTTACCTTATCTGGGGCATGGCGGGTAAAACCAGGTCTTGA

TGATATGGACCATGTGGCGTTAAAGATTGCGCTAG >|c|NC_002695.2_cds_NP_311728.2_3471 [gene=yqeF]

[locus_tag=ECs_3701] [db_xref=GeneID:916487] [protein=short chain acyltransferase] [protein_id=NP_311728.2]

[location=complement(3706939..3708120)] [gbkey=CDS]

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GTCAGGTGTTGACTGCAGGGCAGGGCAGAATCCGGCAAGGCAATCGGCTATTAAAGGTGGTCTGCCTAATAGCGTTCT
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TTGGCAATAGCCAGCTGGTGAAGTCTGTGATGGTTATGGGATGCCTCAATGATTATCATATTGGTGTACC
GCCGAAAATCTGGCTCGGAATATGGCATCAGCCGTCATTGCAAGGATGCTTACGCACTTAGCTCGCAACAAAAAGCGCG
AGCGGGGATTGACGCCGGACATTAAAGATGAGATCGTCCCGTAATGACCCAAAGTAACGGTCAAGACGTTGGGTTG
ATACCGATGAACAGCCCACACACTGACGCCAGTGCAGAAGGTTAGCCGTTAAACCTTCATTGATAGTCTCGGTTCT
GTGACAGCGGGTAATGCATCCATAAACGATGGCGCAGCTCGGTAAATGATGAGCGAAGGCAAAGCACAGAGCGTT
GAATTACCGTGCCTGGCGCATCGCGCATTTGCCAGCGTGGTGAATGGGATCCGGCATTGATGGGAATTGCGCCGGTGT
ATGCGACCCGGCTTGCCTGGCGTGAAGCTGGCAGTGGCTGATGTTGATCTATGAGGCTAATGCAATGGTGGCGATCGCACTCG
GCACAGGCCTTCGGTGAAGATGCTTGAGTGGGATGAGCGTCGGGCAATGCAATGGTGGCGATCGCACTCG
TCACCCGATAGGCCTTCCGGTTGCCAATCCTGGTTCTGGTTCATGAAATGGTGAACAGTAATGCCGAAAGGAC
TGGCAACGTTGTATCGGGGGGCCAGGGTGTGGCATTGACCAATTGACGTACGAATAG

>|c|NC_002695.2_cds_NP_311729.1_3472 [locus_tag=ECs_3702] [db_xref=GeneID:916486] [protein=transporter protein]

[protein_id=NP_311729.1] [location=3708375..3709604] [gbkey=CDS]

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CACATAAAAGCTTATGCCAGTTCATCCTCATCAGAAAACATCAGCAGGTGAAGGGATAACGGGCGCGTAACACACTAC
TATGGCAAGAAGATTGTAATCTGATTACACGCTGACTTCATGCCCTTTTGTGTCGTGTTGATATATGCACTGGC
AATTACCAACTCACTTACGGAACAGCTGGCAAAGCATATGGTTATTGATCTCGCATCCGTATGTTGGTGAAGTCTGGGTG
TTGTTATTCTGAATCTCATTCTGATGGACGTATGCCACTATTGGTAATGGGATTGGTATTCCATTG
ATTGCCATTCTATTCTTCCATTACCTGTAGTAGGTTGCAACCTGATCTATTAAACAACCCAGGTAGAGTTCAA
TCAGAATACCCCTCACCAGATATGGATATCGATTCCCGTGTGGTTCCGCTTAGCCATACGCCATTATTCTACGT
TTGCCATAGACAGACGTAAAAATGGCGAACACGCTATGGATAATGCAAAAAAATTGAAAGTCGCTTATCTCATC
ATCTGCATAAGTGTACTGTTCTTGCTTCTAGCTGCCGAACGCCAGCATGGTGTCAATTCCGGGTTATTGCA
AGGGGTGACCTTATCGGCCTTCTATGCTGCCGAACGCCAGCATGGTGTCAATTCCGGGATTATTGCGCAG
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CAGCAGGGTGGTGAAGAAAAGCTGTGCAATTACCGCGCAGTCAATTGTTGATCGTGTATTGCGCATGATCTTCTATTG
TTGTCGATTAACCCGAACCGCATTCTGATGTTATGCGATCAGCGGCCGCTTACGCCATGATACTTCTCATG
CTACGCTATCAACATATCTCATCCGGCCTTAAACCCCTGGCGCTTACGCCATGGAAATCTGATTACGCTGATCGTGGGTATC
CTGCGTATCGGTATGTTCTTAGCTAA >|c|NC_002695.2_cds_NP_311730.2_3473 [gene=yqeH] [locus_tag=ECs_3703]

[db_xref=GeneID:916484] [protein=LuxR family transcriptional regulator] [protein_id=NP_311730.2] [location=3710064..3710696]

[gbkey=CDS]

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GTATCTAACAAAAACACAATGCGAGGATAAGCGGATATATTGTCGATTTTCAGTAAGTTTACGTCATT
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AGATCAGACAACATTATTGGTCGTTATTGTCATTACAGAGGTAACACATTAACGATGGAATTCAACCCATAATG
GGGTATATGGTTCTGGTTATAATCCATATCAGATTGCTGAAGTTCTGGATATGGATATCGTAGCATCTACCGTACAA
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>|c|NC_002695.2_cds_NP_311731.1_3474 [gene=yqeI] [locus_tag=ECs_3704] [db_xref=GeneID:916483] [protein=transcriptional regulator]

[protein_id=NP_311731.1] [location=3711030..3711839] [gbkey=CDS]

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GACTGTTGCGGAAATTAAATGGCTGCCATTAAATGTAACAGAAGATAACATTGATGGGTTGAAAGAGTTGATAAATA
AAACACGGATACTGGATTGGGGATTACTGCAAAAAATATCGTGGTTACTTCCTTGTGAAAATCTCACCGGG
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TCGTGGTTGA >|c|NC_002695.2_cds_NP_311732.1_3475 [gene=yqeJ] [locus_tag=ECs_3705] [db_xref=GeneID:916481]
[protein=hypothetical protein] [protein_id=NP_311732.1] [location=3711836..3712315] [gbkey=CDS]

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TCAATACGGCAGAATATTGAATACACATGGGTTAAAACATGACACAGCCCATTAAACATCAAAGAAAAGTTAATAAGTT
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GCTATAATACTAAAGCAAGGTAAGCATGCTTTATTGAGCATTGGTAACAGAGCAATAATGCATTGTGCAAGGTA
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[protein_id=NP_311733.2] [location=complement(3712464..3712889)] [gbkey=CDS]

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[db_xref=GeneID:916473] [protein=hypothetical protein] [protein_id=NP_311734.1] [location=3713319..3713810] [gbkey=CDS]
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CATGTACATTAA >Icl|NC_002695.2_cds_NP_311735.1_3478 [gene=ygeG] [locus_tag=ECs_3708] [db_xref=GeneID:916472]
[protein=SycD-like chaperone family TPR-repeat-containing protein] [protein_id=NP_311735.1] [location=3714036..3714527]
[gbkey=CDS]
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GATAATGGCTAA >Icl|NC_002695.2_cds_NP_311736.1_3479 [gene=ygeH] [locus_tag=ECs_3709] [db_xref=GeneID:916471]
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[protein=type III secretion apparatus protein OrgA/MxiK] [protein_id=NP_311742.1] [location=complement(3718734..3719315)]
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[db_xref=GeneID:916464] [protein=type III secretion system lipoprotein precursor EprK] [protein_id=NP_311743.1]
[location=complement(3719331..3720065)] [gbkey=CDS]
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AACGTACCGCGAAGAAACTGGCTCGCAACCGCACGCCGACTCGTGTACTAA >Icl|NC_002695.2_cds_NP_311976.1_3692 [gene=dnaG] [locus_tag=ECs_3949] [db_xref=GeneID:916216] [protein=DNA
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[gene=ygjJ] [locus_tag=ECs_3960] [db_xref=GeneID:916209] [protein=transporter] [protein_id=NP_311987.1]
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TGGGGCGCTGCGTAA >Icl|NC_002695.2_cds_NP_311994.2_3710 [gene=ygjP] [locus_tag=ECs_3967]
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>cl|NC_002695.2_cds_NP_312026.1_3742 [gene=tdcR] [locus_tag=ECs_3999] [db_xref=GeneID:916156] [protein=threonine dehydratase operon activator protein] [protein_id=NP_312026.1] [location=4007011..4007355] [gbkey=CDS]
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[protein=alpha-dehydro-beta-deoxy-D-glucarate aldolase] [protein_id=NP_312031.1] [location=complement(4012150..4012920)]
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[db_xref=GeneID:916158] [protein=toxin of the SohB(PrfF)-YhaV toxin-antitoxin system] [protein_id=NP_312035.1]
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[protein=transcriptional repressor of the aga regulon] [protein_id=NP_312036.1] [location=complement(4017219..4018028)]
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[gbkey=CDS]

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[gbkey=CDS]

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[locus_tag=ECs_4015] [db_xref=GenelD:916151] [protein=N-acetylgalactosamine-6-phosphate deacetylase]
[protein_id=NP_312042.2] [location=4022160..4023293] [gbkey=CDS]

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[protein=alternate ribosome-rescue factor A] [protein_id=YP_009502653.1] [location=complement(4173571..4173789)]
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>Icl|NC_002695.2_cds_NP_312184.1_3895 [gene=zntR] [locus_tag=ECs_4157] [db_xref=GeneID:915990] [protein=zntA gene
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[gene=rplQ] [locus_tag=ECs_4159] [db_xref=GeneID:915985] [protein=50S ribosomal subunit protein L17]
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>|c|NC_002695.2_cds_NP_312202.1_3913 [gene=rplN] [locus_tag=ECs_4175] [db_xref=GeneID:915973] [protein=50S ribosomal subunit protein L14] [protein_id=NP_312202.1] [location=complement(4182918..4183289)] [gbkey=CDS]
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