

Table S1. Bacterial strains, plasmids and primers used in this study.

| Strain name | Genotype | Reference |
|----------------------------------|--|------------------|
| <i>C. jejuni</i> | | |
| JHH1 | - | (49) |
| NCTC 11168 O | - | (34) |
| JHH1 <i>ΔpglB</i> | <i>cj1126c::kan</i> | This study |
| JHH1 <i>ΔeptC</i> | <i>cj0256c::kan</i> | This study |
| NCTC 11168 (NRC) | - | (22) |
| NCTC 11168 (NRC) <i>ΔpglB</i> | <i>cj1126c::kan</i> | (22) |
| <i>E. coli</i> | | |
| DH5α | F ⁻ <i>ΔendA1 hsdR17 supE44 thi-1 recA1 Δ(argF-lacZYA)U169 (80d lacZ ΔM15) gyrA96λ-</i> | Invitrogen |
| CLM24 | w3110, <i>ΔwaaL</i> | (44) |
| Plasmid List | Genotype | Reference |
| pMLBAD | Arabinose-inducible vector, Tmp ^R | (66) |
| pCj-pglB | pCj- <i>pglB</i> PglB cloned in pCE111-28, Cm ^R | (23) |
| PCRscript | High copy <i>E. coli</i> vector, Amp ^R | Stratagene |
| pGEM-T | High copy <i>E. coli</i> vector, Amp ^R | Promega |
| pACYC(<i>pgl</i>) | pACYC184 containing <i>C. jejuni</i> <i>pgl</i> cluster, Cm ^R | (50) |
| pWA2 | pBR322 containing hexa-His-tagged AcrA under control of Tet promoter, Amp ^R | (44) |
| PWM10 | Mob+ <i>repB lacZ oriV</i> plasmid containing Kan ^R | (67) |
| PCRscript- <i>cj0256up/down</i> | PCRscript containing <i>cj0256up/down</i> , Amp ^R | This study |
| pNS1 | pGEM-T containing <i>pglB::kan</i> derived from NCTC11168 <i>ΔpglB</i> , Amp ^R , Kan ^R | This study |
| pNS2 | PCRscript containing <i>cj0256 up-Kan</i> cassette derived from PWM-Cj0256 down, Amp ^R , Kan ^R | This study |
| pNS3 | pMLBAD containing C-terminal HA-tagged <i>cj0256</i> , Tmp ^R | This study |
| Primer list | Sequence (5' ⇒ 3') | |
| PglBF | GAAGACGATAAATTAAGAAAAGCG | |
| PglBR | TCATCTTGCG GCACTATAAC | |
| 0256-1- <i>Pst</i> I-F | ACCTCTGCGAGTTGAGTTTAAATCTTGCGTATAAGC | |
| 0256-2- <i>Hinc</i> II-R | AAAAAAGTCGACAGTAAACTGAAACCAAGTTAATCTAAGC | |
| 0256-3- <i>Hinc</i> II-F | TATTAAGTCGACATCCTAAACTTAAGGCAAATCCATGAAGC | |
| 0256-4- <i>Xho</i> I-R | TTACTCGAGAAATTTAATCATCAAATTTGGACGC | |
| Cj0256 <i>Pst</i> I-HA-R | ATCTGCGAGTCAAGCGTAATCTGGAACATCGTATGGGTATGGATTTGCCTTAAGTT TAGG | |
| Cj0256 <i>Eco</i> RI-HA-F | ATAGAATTCACCATGCTTAGATTAAGTTGTTTCAGTTTAC | |

Table S2. Glycopeptides identified in *C. jejuni* JHH1

| Cj No. | Gene Name | Protein Name/ accession number | Precursor mass (charge) | RT [min] | Sequence | MT score | Pepsin | Thermolysin | Trypsin |
|---------|----------------|---|----------------------------|-------------|---|-----------------|--------|-------------|---------|
| Cj0011c | <i>Cj0011c</i> | Putative non-specific DNA binding protein | 929.42622 (+3) | 85.11 | ⁴⁹ EANFTSIDDLK ⁶⁰ | 35 ^c | | | X |
| Cj0011c | | | 1214.54342 (+2) | 60.39 | ⁴⁴ LEYRKEAN ⁵¹ | 20 ^b | | X | |
| Cj0011c | | | 1093.48165 (+2) | 48.00 | ⁴⁶ YRKEAN ⁵¹ | 20 ^b | | X | |
| Cj0011c | | | 1217.54684 (+2) | 59.39 | ⁴⁶ YRKEANFT ⁵³ | 29 ^a | X | | |
| Cj0081 | <i>cydA</i> | Cytochrome bd oxidase subunit I | 922.05849 (+3) | 67.96 | ³⁵¹ EN(+1)NDTIAMANHK ³⁶² | 33 ^c | | | X |
| Cj0081 | | | 1390.08981 (+2) | 76.97 | ³⁵¹ ENNDTIAM(+16)ANHK ³⁶² | 56 ^c | | | X |
| Cj0081 | | | 922.06197 (+3) | 65.69 | ³⁵¹ ENNDTIAMAN(+1)HK ³⁶² | 53 ^c | | | X |
| Cj0081 | | | 1382.08932 (+2) | 65.78 | ³⁵¹ ENNDTIAMANHK ³⁶² | 50 ^c | | | X |
| Cj0081 | | | 1155.50314 (+2) | 78.20 | ³⁵⁰ KENNDTIA ³⁵⁷ | 23 ^c | | | X |
| Cj0081 | | | 1155.50143 (+2) | 53.77 | ³⁴⁸ LAKENNDT ³⁵⁵ | 44 ^b | | X | |
| Cj0081 | | | 922.09315 (+3) | 58.42 | ²⁷⁷ NPKKTIDNNEV ²⁸⁸ | 60 ^a | X | | |
| Cj0089 | <i>Cj0089</i> | Putative lipoprotein | 1130.45700 (+2) | 59.88 | ⁷⁰ NCGDFNK ⁷⁶ | 50 ^c | | | X |
| Cj0114 | <i>Cj0114</i> | Putative periplasmic protein | 1089.48042 (+3) | 54.78 | ¹⁷⁶ IENNNTQNTQDDKAKQ ¹⁹¹ | 28 ^b | | X | |
| Cj0114 | | | 1127.17671 (+3) | 64.80 | ¹⁷⁶ IENNNTQNTQDDKAKQI ¹⁹² | 40 ^b | | X | |
| Cj0114 | | | 917.42903 (+3) | 74.48 | ¹⁴⁸ KNELNDANLSVK ¹⁵⁹ | 27 ^c | | | X |
| Cj0114 | | | 1133.50900 (+2) | 85.61 | ¹⁵² NDANLSVK ¹⁵⁹ | 35 ^c | | | X |
| Cj0114 | | | 1311.59225 (+2) | 80.39 | ¹⁴⁹ NELNDANLSVK ¹⁵⁹ | 73 ^c | | | X |
| Cj0114 | | | 946.76863 (+3) | 102.71 | ¹⁴⁷ SKNELN(+1)DANLSVK ¹⁵⁹ | 20 ^c | | | X |
| Cj0114 | | | 946.43959 (+3) | 74.47 | ¹⁴⁷ SKNELNDANLSVK ¹⁵⁹ | 65 ^c | | | X |
| Cj0114 | | | 979.74525 (+3) | 69.76 | ⁸⁹ SQVEENNQNIENN ¹⁰¹ | 57 ^b | | X | |

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|---------|----------------|--|-----------------|--------|--|-----------------|---|---|---|
| Cj0131 | <i>Cj0131</i> | Putative peptidase M23 family protein | 1407.59701 (+2) | 82.07 | ⁷³ DDNTSAMVIADEK ⁸⁵ | 81 ^c | | | X |
| Cj0131 | | | 1146.98324 (+2) | 42.77 | ⁷¹ HKDDNTSA ⁷⁸ | 60 ^a | X | | |
| Cj0131 | | | 1212.50497 (+2) | 50.22 | ⁷¹ HKDDNTSAM ⁷⁹ | 70 ^a | X | | |
| Cj0131 | | | 779.00215 (+3) | 47.35 | ⁷⁰ LHKDDNTS ⁷⁷ | 45 ^b | | X | |
| Cj0131 | | | 802.68733 (+3) | 46.49 | ⁷⁰ LHKDDNTSA ⁷⁸ | 37 ^b | | X | |
| Cj0131 | | | 846.36287 (+3) | 56.75 | ⁷⁰ LHKDDNTSAM ⁷⁹ | 54 ^b | | X | |
| Cj0131 | | | 1277.04330 (+2) | 47.11 | ⁷⁰ LHKDDNTSAM(+16) ⁷⁹ | 60 ^b | | X | |
| Cj0143c | <i>Cj0143c</i> | Putative periplasmic solute binding protein for ABC transport system | 1455.64987 (+2) | 66.41 | ²¹ KNLEQEQNTSSNL ³³ | 55 ^a | X | | |
| Cj0152c | <i>Cj0152c</i> | Putative membrane protein | 1326.93465 (+3) | 92.07 | ¹⁶¹ AQETNQTESVLP SQNISLQENDK ¹⁸³ | 87 ^c | | | X |
| Cj0152c | | | 1331.05441 (+2) | 63.37 | ¹²³ FKDEQNN(+1)TSAT ¹³³ | 72 ^b | | X | |
| Cj0152c | | | 1201.00790 (+2) | 54.75 | ¹²³ FKDEQNN ¹³⁰ | 27 ^b | | X | |
| Cj0152c | | | 1244.52328 (+2) | 54.44 | ¹²³ FKDEQNNTS ¹³¹ | 63 ^b | | X | |
| Cj0152c | | | 1280.04440 (+2) | 55.61 | ¹²³ FKDEQNNTSA ¹³² | 32 ^a | X | | |
| Cj0152c | | | 1330.56698 (+2) | 55.77 | ¹²³ FKDEQNNTSAT ¹³³ | 43 ^a | X | | |
| Cj0152c | | | 1361.30623 (+3) | 118.53 | ¹²³ FKDEQNNTSATVIDIIGQAQENLK ¹⁴⁶ | 54 ^c | | | X |
| Cj0152c | | | 970.75838 (+3) | 53.72 | ¹⁵⁶ IDNNKAQETNQTE ¹⁶⁸ | 38 ^a | X | | |
| Cj0152c | | | 1391.60200 (+3) | 76.07 | ¹⁸⁷ IENNISENNTTL ¹⁹⁸ | 30 ^a | X | | |
| Cj0152c | | | 1227.53256 (+2) | 47.66 | ¹⁶⁰ KAQETNQTE ¹⁶⁸ | 43 ^a | X | | |
| Cj0152c | | | 1257.03378 (+2) | 48.61 | ¹²⁴ KDEQNNTSAT ¹³³ | 47 ^a | X | | |
| Cj0152c | | | 1306.56759 (+2) | 56.67 | ¹²⁴ KDEQNNTSATV ¹³⁴ | 63 ^a | X | | |
| Cj0152c | | | 1150.02291 (+2) | 68.19 | ²⁴⁷ KEKDFNI ²⁵³ | 30 ^a | X | | |
| Cj0152c | | | 1133.48874 (+2) | 53.23 | ¹⁷⁸ LQENDKN ¹⁸⁴ | 35 ^b | | X | |
| Cj0152c | | | 1468.66183 (+2) | 68.19 | ¹⁷⁸ LQENDKNISIENN ¹⁹⁰⁺ | 60 ^b | | X | |

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|---------|----------------|-----------------------------------|-----------------|--------|--|-----------------|---|---|---|
| Cj0152c | | | 1283.56356 (+2) | 63.60 | ¹⁸¹ NDKNISIENN ¹⁹⁰⁺ | 69 ^a | X | | |
| Cj0152c | | | 1412.11581 (+2) | 64.71 | ¹⁷⁹ QENDKNISIENN ¹⁹⁰⁺ | 45 ^a | X | | |
| Cj0152c | | | 1444.01460 (+3) | 123.85 | ¹²¹ TFFKDEQNNTSATVIDIIGQAQENLK ¹⁴⁶ | 61 ^c | | | X |
| Cj0152c | | | 1032.78658 (+3) | 62.05 | ¹⁵⁵ VIDNNKAQETNQTES ¹⁶⁹ | 68 ^b | | X | |
| Cj0152c | | | 762.34755 (+3) | 54.61 | ²⁴⁶ VKEKDFN ²⁵² | 30 ^a | X | | |
| Cj0152c | | | 800.03987 (+3) | 74.19 | ²⁴⁶ VKEKDFNI ²⁵³ | 30 ^b | | X | |
| Cj0152c | | | 1098.83980 (+3) | 64.83 | ¹⁵³ VVIDNNKAQETNQTES ¹⁶⁹ | 66 ^b | | X | |
| Cj0158c | <i>Cj0158c</i> | Putative haem-binding lipoprotein | 1213.55501 (+3) | 119.43 | ¹²¹ NHSFLSDEIQNLADFINK ¹³⁹ | 79 ^c | | | X |
| Cj0168c | <i>Cj0168c</i> | Putative periplasmic protein | 1111.96762 (+2) | 80.57 | ²¹ ANTPSDVN ²⁸ | 20 ^c | | | X |
| Cj0168c | | | 1226.52755 (+2) | 59.80 | ²¹ ANTPSDVNQ ³⁰ | 28 ^a | X | | |
| Cj0168c | | | 1295.04965 (+2) | 61.34 | ²¹ ANTPSDVNQTH ³¹ | 48 ^b | | X | |
| Cj0168c | | | 1345.57467 (+2) | 57.73 | ²¹ ANTPSDVNQHT ³² | 61 ^b | | X | |
| Cj0168c | | | 1359.57284 (+2) | 60.22 | ²¹ (+28)ANTPSDVNQHT ³² | 46 ^b | | X | |
| Cj0168c | | | 1409.61959 (+2) | 55.91 | ²¹ ANTPSDVNQHTK ³³ | 53 ^c | | | X |
| Cj0168c | | | 1445.14202 (+2) | 55.43 | ²¹ ANTPSDVNQHTKA ³⁴ | 49 ^b | | X | |
| Cj0168c | | | 963.76131 (+3) | 56.95 | ²⁰ AANTPSDVNQHTK ³³ | 30 ^c | | | X |
| Cj0168c | | | 1110.46957 (+2) | 68.86 | ²⁶ DVNQHT ³² | 40 ^c | | | X |
| Cj0168c | | | 1174.51596 (+2) | 48.51 | ²⁶ DVNQHTK ³³ | 53 ^c | | | X |
| Cj0168c | | | 1210.03158 (+2) | 52.67 | ²⁶ DVNQHTKA ³⁴ | 41 ^b | | X | |
| Cj0168c | | | 1310.54855 (+2) | 83.71 | ²² N(+1)TPSDVNQHT ³² | 45 ^c | | | X |
| Cj0168c | | | 1003.42269 (+2) | 53.37 | ²⁸ NQHT ³² | 28 ^c | | | X |
| Cj0168c | | | 1102.98656 (+2) | 45.13 | ²⁸ NQHTKA ³⁴ | 44 ^b | | X | |
| Cj0168c | | | 1310.05636 (+2) | 56.94 | ²² NTPSDVNQHT ³² | 50 ^b | | X | |
| Cj0168c | | | 1374.10373 (+2) | 69.29 | ²² NTPSDVNQHTK ³³ | 47 ^b | | X | |
| Cj0168c | | | 1201.52755 (+2) | 70.45 | ²⁴ PSDVNQHT ³² | 30 ^c | | | X |
| Cj0168c | | | 1272.56344 (+2) | 54.55 | ²⁴ PSDVNQHTK ³³ | 56 ^c | | | X |
| Cj0168c | | | 1153.98568 (+2) | 67.94 | ²⁵ SDVNQHT ³² | 47 ^c | | | X |
| Cj0168c | | | 812.35817 (+3) | 48.90 | ²⁵ SDVNQHTK ³³ | 29 ^c | | | X |

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|---------|----------------|-------------------------------------|-----------------|--------|--|-----------------|---|---|---|
| Cj0168c | | | 1133.98214 (+2) | 79.18 | ²³ TPSDV N QT ³⁰ | 39 ^c | | | X |
| Cj0168c | | | 1253.02963 (+2) | 60.06 | ²³ TPSDV N QTHT ³² | 63 ^b | | X | X |
| Cj0168c | | | 1317.08212 (+2) | 54.36 | ²³ TPSDV N QTHTK ³³ | 46 ^b | | X | |
| Cj0168c | | | 1052.95480 (+2) | 50.10 | ²⁷ V N QTHT ³² | 34 ^b | | X | |
| Cj0168c | | | 1117.00180 (+2) | 44.65 | ²⁷ V N QTHTK ³³ | 27 ^b | | X | |
| Cj0176c | <i>Cj0176c</i> | Putative lipoprotein | 1208.54586 (+2) | 57.86 | ²⁸ KDL N KTEY ³⁵ | 38 ^a | X | | |
| Cj0176c | | | 1251.54989 (+2) | 57.63 | ³⁰ L N KTEYNSQ ³⁸ | 45 ^b | | X | |
| Cj0176c | | | 998.44143 (+2) | 69.33 | ²⁹ DL N KT ³³ | 27 ^c | | | X |
| Cj0182 | <i>Cj0182</i> | Putative transporter | 1092.96225 (+2) | 54.33 | ⁵⁸ DS N STQK ⁶⁴ | 41 ^c | | | X |
| Cj0182 | | | 1168.86885 (+3) | 92.92 | ⁶⁵ IEENLENN N ATLIQEANQR ⁸² | 20 ^c | | | X |
| Cj0182 | | | 1327.10763 (+2) | 113.06 | ⁵⁴ IELLDS N STQK ⁶⁴ | 59 ^c | | | X |
| Cj0182 | | | 1392.10556 (+2) | 67.81 | ⁵⁷ LDS N STQKIEEN ⁶⁸ | 52 ^b | | X | |
| Cj0200c | <i>Cj0200c</i> | Putative periplasmic protein | 1186.51046 (+2) | 84.48 | ²⁹ AQIYDN(+1) N K ³⁶ | 36 ^c | | | X |
| Cj0200c | | | 1186.01962 (+2) | 81.26 | ²⁹ AQIYDN N K ³⁶ | 41 ^c | | | X |
| Cj0200c | | | 1029.93002 (+2) | 58.12 | ³² YDN N K ³⁶ | 25 ^c | | | X |
| Cj0200c | | | 1080.45394 (+2) | 62.31 | ³² YDN N KT ³⁷ | 26 ^c | | | X |
| Cj0235c | <i>secG</i> | Preprotein translocase SecG subunit | 1045.49963 (+3) | 70.75 | ⁸¹ AEKIKVEN N NTTIPSA ⁹⁶ | 72 ^a | X | | |
| Cj0235c | | | 1380.67500 (+3) | 83.08 | ⁸¹ AEKIKVEN N NTTIPSAPIVPATPN(+1)TN ¹⁰⁴ | 26 ^a | X | | |
| Cj0235c | | | 1342.32918 (+3) | 82.66 | ⁸¹ AEKIKVEN N NTTIPSAPIVPATPNT ¹⁰⁵ | 36 ^a | X | | |
| Cj0235c | | | 1380.34456 (+3) | 80.97 | ⁸¹ AEKIKVEN N NTTIPSAPIVPATPNTN ¹⁰⁶ | 22 ^a | X | | |
| Cj0235c | | | 1409.35530 (+3) | 81.19 | ⁸¹ AEKIKVEN N NTTIPSAPIVPATPNTNS ¹⁰⁷ | 26 ^a | X | | |
| Cj0235c | | | 1027.94271 (+2) | 58.71 | ¹¹⁸ DV N SSK ¹²³ | 41 ^c | | | X |
| Cj0235c | | | 1275.63533 (+3) | 80.54 | ⁸³ KIKVEN N NTTIPSAPIVPATPNT ¹⁰⁵ | 24 ^a | X | | |
| Cj0235c | | | 1313.65034 (+3) | 82.19 | ⁸³ KIKVEN N NTTIPSAPIVPATPNTN ¹⁰⁶ | 27 ^a | X | | |
| Cj0235c | | | 1119.98861 (+2) | 47.54 | ¹¹⁶ PSDV N SSK ¹²³ | 45 ^a | X | | |
| Cj0235c | | | 1552.21957 (+2) | 123.22 | ¹⁰⁷ SIAPSAPQLPSDV N SSK ¹²³ | 47 ^c | | | X |

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|---------|----------------|--|-----------------|--------|---|-----------------|---|---|---|
| Cj0238 | <i>Cj0238</i> | Putative mechanosensitive ion channel family protein | 886.05067 (+3) | 54.86 | ⁵⁰ EFKKNNDE NS ST ⁶¹ | 43 ^b | | X | |
| Cj0238 | | | 1345.57028 (+2) | 53.73 | ⁵¹ FKKNN(+1)DE NS ST ⁶¹ | 28 ^b | | X | |
| Cj0238 | | | 1345.08468 (+2) | 47.28 | ⁵¹ FKKNNDE NS ST ⁶¹ | 81 ^b | | X | |
| Cj0238 | | | 1418.61898 (+2) | 59.38 | ⁵¹ FKKNNDE NS STF ⁶² | 99 ^a | X | | |
| Cj0238 | | | 1504.15011 (+2) | 57.70 | ⁵¹ FKKNNDE NS STFNG ⁶³ | 76 ^a | X | | |
| Cj0256 | <i>Cj0256</i> | Putative sulfatase family protein | 1074.45968 (+2) | 32.14 | ²¹³ EN N HTK ²¹⁸ | 26 ^c | | | X |
| Cj0256 | | | 1354.63717 (+2) | 47.07 | ²¹¹ YRE NN HTK ^{KL} ²²⁰ | 25 ^a | X | | |
| Cj0268c | <i>Cj0268c</i> | Putative transmembrane protein | 1468.19345 (+2) | 123.37 | ²⁶⁸ AALAEGEAN N ATIISAK ²⁸³ | 45 ^c | | | X |
| Cj0268c | | | 955.45235 (+3) | 84.34 | ²⁶⁹ ALAEGEAN N ATIISAK ²⁸³ | 24 ^c | | | X |
| Cj0277 | <i>MreC</i> | Rod shape-determining protein MreC | 1113.96652 (+2) | 54.81 | ⁹⁰ EDQ N STK ⁹⁶ | 43 ^c | | | X |
| Cj0277 | | | 1227.04953 (+2) | 79.97 | ⁸⁸ I LE DQ N STK ⁹⁶ | 21 ^c | | | X |
| Cj0289c | <i>peb3</i> | Major antigenic peptide Peb3 | 1057.95846 (+2) | 67.79 | ⁸⁸ D F N V SK ⁹³ | 40 ^c | | | X |
| Cj0289c | | | 929.11555 (+3) | 86.37 | ⁸⁵ FGKDF N VSKIKP ⁹⁶ | 45 ^b | | X | |
| Cj0289c | | | 972.14442 (+3) | 81.94 | ⁸⁶ GKDF N VSKIKPLY ⁹⁸ | 60 ^a | X | | |
| Cj0365c | <i>cmeC</i> | Outer membrane channel protein CmeC (multidrug efflux system CmeABC) | 1149.50290 (+2) | 55.24 | ⁴⁷ EN N SSITK ⁵⁴ | 33 ^c | | | X |
| Cj0365c | | | 1149.99423 (+2) | 74.42 | ⁴⁷ EN(+1) N SSITK ⁵⁴ | 48 ^c | | | X |
| Cj0365c | | | 1300.05734 (+2) | 70.10 | ⁴² LSWEKEN N SS ⁵¹ | 57 ^b | | X | |
| Cj0365c | | | 1199.99423 (+2) | 59.25 | ⁴⁴ WEKEN N SS ⁵ | 53 ^b | | X | |

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|---------|----------------|--|-----------------|--------|--|-----------------|---|---|---|
| Cj0366c | <i>cmeB</i> | Inner membrane efflux transporter CmeB | 1042.80232 (+3) | 93.96 | ⁶³⁴ DRN V SADEIAM(+16)ELNK ⁶⁴⁸ | 20 ^c | | | X |
| Cj0366c | | | 1555.69247 (+2) | 93.06 | ⁶³⁴ DRN V SADEIAMELNK ⁶⁴⁸ | 27 ^c | | | X |
| Cj0366c | | | 1080.16780 (+3) | 91.20 | ⁶³⁴ DRN V SADEIAMELNKK ⁶⁴⁹ | 37 ^c | | | X |
| Cj0366c | | | 1139.02768 (+2) | 62.00 | ⁶²⁹ LKD W KDRN ⁶³⁶ | 21 ^b | | X | |
| Cj0367c | <i>cmeA</i> | protein CmeA (multidrug efflux | 1392.32832 (+3) | 132.56 | ²⁶⁸ AIFDN N NSTLLPGAFATITSEGF I QK ²⁹³ | 29 ^c | | | X |
| Cj0367c | | | 1020.45456 (+2) | 56.45 | ¹²¹ DF N RSKA ¹²⁷ | 20 ^b | | X | |
| Cj0371 | <i>Cj0371</i> | Hypothetical protein | 1105.47592 (+2) | 59.97 | ⁷⁵ DL N GTER ⁸¹ | 23 ^c | | | X |
| Cj0376 | <i>Cj0376</i> | Putative periplasmic protein | 1113.48556 (+2) | 55.17 | ⁴⁷ FDRDK N QT ⁵⁴ | 27 ^b | | X | |
| Cj0397c | <i>Cj0397c</i> | Hypothetical protein | 1094.82735 (+3) | 144.12 | ¹⁰¹ ENINDL N NTAFQNELK ¹¹⁶ | 40 ^c | | | X |
| Cj0397c | | | 1326.08871 (+2) | 96.87 | ¹⁰⁰ KENINDL N NTA ¹¹⁰ | 66 ^c | | | X |
| Cj0399 | <i>Cj0399</i> | Colicin V production protein homolog | 1119.49166 (+2) | 69.74 | ¹⁷⁹ DL N NTQK ¹⁸⁵ | 28 ^c | | | X |
| Cj0399 | | | 1155.00924 (+2) | 51.99 | ¹⁸⁰ L N NTQKGE ¹⁸⁷ | 58 ^b | | X | |
| Cj0399 | | | 1447.17062 (+2) | 127.81 | ¹⁷³ LQDIVSDL N NTQK ¹⁸⁵ | 76 ^c | | | X |
| Cj0399 | | | 1256.04489 (+2) | 53.89 | ¹⁷⁸ SDL N NTQKGE ¹⁸⁷ | 52 ^a | X | | |
| Cj0404 | <i>Cj0404</i> | Putative transmembrane protein | 1366.07186 (+2) | 60.28 | ⁹⁸ FQDEQ N TTQNT ¹⁰⁸ | 62 ^b | | X | |
| Cj0404 | | | 1036.43074 (+3) | 68.36 | ⁹⁸ FQDEQ N TTQNTTSS ¹¹² | 68 ^b | | X | |
| Cj0404 | | | 1242.00521 (+2) | 52.91 | ⁹⁸ QDEQ N TTQN ¹⁰⁷ | 36 ^b | | X | |
| Cj0404 | | | 1292.52865 (+2) | 56.07 | ⁹⁸ QDEQ N TTQNT ¹⁰⁸ | 30 ^b | | X | |
| Cj0404 | | | 958.39644 (+3) | 58.99 | ⁹⁸ QDEQ N TTQNTTSS ¹¹¹ | 45 ^b | | X | X |

| | | | | | | | | | |
|---------|----------------|---------------------------------------|-----------------|--------|--|-----------------|---|---|---|
| Cj0404 | | | 987.40755 (+3) | 58.90 | ⁹⁸ QDEQNTTQNTTSS ¹¹² | 65 ^b | | X | |
| Cj0404 | | | 976.77113 (+3) | 55.57 | ⁹⁵ RKQFQDEQNTTQ ¹⁰⁷ | 54 ^a | X | | |
| Cj0404 | | | 1048.46761 (+3) | 56.15 | ⁹⁵ RKQFQDEQNTTQNT ¹⁰⁸ | 22 ^a | X | | |
| Cj0404 | | | 1115.83235 (+3) | 57.32 | ⁹⁵ RKQFQDEQNTTQNTT ¹¹⁰ | 28 ^a | X | | |
| Cj0454c | <i>Cj0454c</i> | Hypothetical protein | 1075.49020 (+2) | 47.64 | ⁸⁸ LRSENKKS ⁹⁵ | 35 ^b | | X | |
| Cj0454c | | | 1305.58822 (+2) | 51.84 | ⁸⁹ RSENKKSLEQ ⁹⁸ | 27 ^a | X | | |
| Cj0454c | | | 998.92215 (+2) | 31.91 | ⁹⁰ SENK ⁹⁴ | 20 ^c | | | X |
| Cj0494 | <i>Cj0494</i> | Putative exporting protein | 1184.99813 (+2) | 78.48 | ²⁵ EDN(+1)NITKE ³² | 56 ^c | | | X |
| Cj0494 | | | 1119.98397 (+2) | 70.74 | ²⁵ EDNNITK ³¹ | 27 ^c | | | X |
| Cj0494 | | | 1184.50680 (+2) | 76.88 | ²⁵ EDNITKE ³² | 32 ^c | | | X |
| Cj0494 | | | 1143.47189 (+2) | 59.16 | ²² NFKEDNN ²⁸ | 46 ^b | | X | |
| Cj0508 | <i>Cj0508</i> | Penicillin-binding protein 1A | 1232.59005 (+2) | 32.62 | ³⁰⁶ IVKRDKDAN ³¹⁴ | 23 ^b | | X | |
| Cj0511 | <i>Cj0511</i> | Putative secreted protease | 1333.58688 (+2) | 119.63 | ⁶⁶ DDQNIISNLVDK ⁷⁶ | 24 ^c | | | X |
| Cj0511 | | | 1282.60188 (+3) | 120.94 | ⁵⁶ TLAIVEQYYVDDQNIISNLVDK ⁷⁶ | 59 ^c | | | X |
| Cj0540 | <i>Cj0540</i> | Putative exporting protein | 1263.54464 (+2) | 51.17 | ¹⁶⁹ LTSKENNNSN ¹⁷⁸ | 49 ^b | | X | |
| Cj0592c | <i>Cj0592c</i> | Putative periplasmic protein | 1311.54854 (+3) | 54.37 | ⁹⁸ INQSSENNES ¹⁰⁷ | 37 ^b | | X | |
| Cj0592c | | | 959.08388 (+3) | 65.41 | ¹²⁰ IYPSKTTEN(+1)NQSS ¹³² | 23 ^b | | X | |
| Cj0592c | | | 1437.63766 (+2) | 56.70 | ¹²⁰ IYPSKTTENNQSS ¹³² | 23 ^b | | X | |
| Cj0592c | | | 1237.18770 (+3) | 85.74 | ¹²⁵ TTENNQSSIFSDDVNM(+16)TQEK ¹⁴⁴⁺ | 66 ^c | | | X |
| Cj0592c | | | 1231.85640 (+3) | 93.84 | ¹²⁵ TTENNQSSIFSDDVNM TQEK ¹⁴⁴⁺ | 77 ^c | | | X |
| Cj0592c | | | 1232.18355 (+3) | 95.09 | ¹²⁵ TTENNQSSIFSDDVN(+1)MTQEK ¹⁴⁴ | 70 ^c | | | X |
| Cj0599 | <i>Cj0599</i> | Putative OmpA family membrane protein | 1213.03402 (+2) | 104.07 | ¹⁰⁹ DLNSTLDNK ¹¹⁷ | 63 ^c | | | X |

| | | | | | | | | | |
|---------|----------------|-------------------------------------|-----------------|--------|---|-----------------|---|---|---|
| Cj0599 | | | 903.42220 (+3) | 102.35 | ¹⁶⁶ KLDNNITIDEK ¹⁷⁶ | 20 ^c | | | X |
| Cj0599 | | | 884.76253 (+3) | 70.91 | ¹⁰⁴ KQLSKDLNSTL ¹¹⁴ | 33 ^a | X | | |
| Cj0599 | | | 1084.84554 (+3) | 79.50 | ¹⁶⁰ SKELQSKLDNNITIDE ¹⁷⁵ | 49 ^a | X | | |
| Cj0610c | <i>Cj0610c</i> | Putative periplasmic protein | 1041.93844 (+2) | 53.17 | ³³¹ EENASK ³³⁶ | 38 ^c | | | X |
| Cj0610c | | | 1089.49362 (+2) | 45.38 | ²⁹³ IKDENNRS ³⁰⁰ | 21 ^b | | X | |
| Cj0610c | | | 1162.52938 (+2) | 61.68 | ³²⁹ LKEENASK ³³⁶ | 45 ^c | | X | X |
| Cj0610c | | | 1156.01181 (+2) | 89.59 | ⁸⁰ SIDENLSK ⁸⁷ | 45 ^c | | | X |
| Cj0610c | | | 1007.12184 (+3) | 70.22 | ⁹¹ VLNTLENDENTSHK ¹⁰⁴ | 59 ^c | | | X |
| Cj0633 | <i>Cj0633</i> | Putative periplasmic protein | 1173.49861 (+3) | 155.51 | ⁶⁰ DHYEIGIFQENEFDN(+1)NK ⁷⁶ | 43 ^c | | | X |
| Cj0633 | | | 1173.17488 (+3) | 105.99 | ⁶⁰ DHYEIGIFQENEFDNK ⁷⁶ | 86 ^c | | | X |
| Cj0633 | | | 1358.57613 (+3) | 112.67 | ¹²³ DTNLTQDQNTL ¹³³ | 28 ^c | | | X |
| Cj0652 | <i>pbpC</i> | Penicillin-binding protein | 1067.11092 (+3) | 74.43 | ⁴⁶⁷ ENNNTTIENQMDENK ⁴⁸¹ | 23 ^c | | | X |
| Cj0652 | | | 1109.81111 (+3) | 93.98 | ⁴⁶⁷ ENNNTTIENQMDENK ⁴⁸² | 28 ^c | | | X |
| Cj0652 | | | 1133.81709 (+3) | 112.51 | ⁴⁶⁵ SIENNNTTIENQMDENK ⁴⁸¹ | 68 ^c | | | X |
| Cj0694 | <i>Cj0694</i> | Putative periplasmic protein | 1352.07052 (+2) | 118.96 | ¹²⁵ EFQDPTGDFNK ¹³⁵ | 36 ^c | | | X |
| Cj0694 | | | 1092.97445 (+2) | 48.75 | ³⁰³ FQKDQN ³⁰⁸ | 24 ^b | | X | |
| Cj0694 | | | 1358.57809 (+2) | 62.74 | ³⁰³ FQKDQNIISED ³¹³ | 72 ^b | | X | |
| Cj0694 | | | 1039.45552 (+3) | 108.29 | ⁴²⁴ NTDQNSSYVWINDNK ⁴³⁸ | 42 ^c | | | X |
| Cj0694 | | | 1092.47067 (+2) | 78.24 | ¹²⁹ PTGDFNK ¹³⁵ | 24 ^c | | | X |
| Cj0694 | | | 1184.01754 (+2) | 54.71 | ³⁰⁴ QKDQNIISE ³¹¹ | 29 ^a | X | | |
| Cj0694 | | | 1285.05026 (+2) | 53.85 | ³⁰⁴ QKDQNIISED ³¹³ | 44 ^a | X | | |
| Cj0734c | <i>hisJ</i> | Histidine-binding protein precursor | 1191.53646 (+2) | 68.59 | ²⁷ ESNASVELK ³⁵ | 74 ^c | | | X |
| Cj0734c | | | 1312.60153 (+2) | 81.49 | ²⁵ NKESNASVELK ³⁵ | 56 ^c | | | X |
| Cj0734c | | | 1060.83638 (+3) | 87.09 | ²⁸ SNASVELKVG TAPNYKP ⁴⁴ | 32 ^b | | X | |
| Cj0776c | <i>Cj0776c</i> | Hypothetical protein | 1017.12202 (+3) | 68.57 | ⁷⁷ IQKQETNPLDENQS ⁹⁰ | 31 ^b | | X | |

| | | | | | | | | | |
|---------|----------------|--|-----------------|--------|--|-----------------|---|---|---|
| Cj0776c | | | 1098.95980 (+2) | 57.78 | ¹⁰¹ ISENNQS ¹⁰⁷ | 20 ^b | | X | |
| Cj0776c | | | 1461.15255 (+2) | 76.73 | ⁷⁹ KQETNPLDENQSL ⁹¹ | 33 ^a | X | | |
| Cj0776c | | | 1122.49300 (+3) | 74.63 | ⁷⁹ KQETNPLDENQSLNNDT ⁹⁵ | 74 ^a | X | | |
| Cj0776c | | | 1256.51791 (+2) | 56.39 | ¹⁰⁸ LNNDTNTSNN ¹¹⁷ | 48 ^b | | X | |
| Cj0776c | | | 1152.16841 (+3) | 59.29 | ¹⁰⁸ LNNDTNTSNNINTNENKQ ¹²⁵ | 76 ^b | | X | |
| Cj0776c | | | 1033.43965 (+3) | 60.36 | ¹¹⁰ NDTNTSNNINTNENK ¹²⁴ | 24 ^c | | | X |
| Cj0780 | <i>napA</i> | Periplasmic nitrate reductase | 1299.52975 (+2) | 65.64 | ³⁸² AKGDDNESLED ³⁹² | 36 ^b | | X | |
| Cj0780 | | | 934.73238 (+3) | 104.60 | ³⁸⁴ GDDNESLEDFKK ³⁹⁵ | 48 ^c | | | X |
| Cj0780 | | | 1264.01290 (+2) | 65.50 | ³⁸³ KGDDNESLED ³⁹² | 57 ^b | | X | |
| Cj0843c | <i>Cj0843c</i> | Putative secreted transglycosylase | 1083.01937 (+2) | 53.36 | ³⁷² IKDYNKTRQ ³⁸⁰ | 23 ^b | | X | |
| Cj0843c | | | 1140.50167 (+2) | 54.69 | ³²⁵ IRDANASQ ³³² | 27 ^b | | X | |
| Cj0843c | | | 1036.95492 (+2) | 56.29 | ³⁷³ KDYNK ³⁷⁷ | 27 ^c | | | X |
| Cj0843c | | | 1464.69040 (+2) | 136.94 | ¹⁶⁹ KYDLDLNTSLVNK ¹⁸¹ | 33 ^c | | | X |
| Cj0846 | <i>Cj0846</i> | Putative metallophosphoesterase | 808.39253 (+3) | 72.35 | ²⁷⁷ IKVDLNTSK ²⁸⁵ | 21 ^c | | | X |
| Cj0944c | <i>Cj0944c</i> | Putative periplasmic protein | 1034.44137 (+2) | 49.59 | ²¹⁹ ENNASK ²²⁴ | 44 ^c | | | X |
| Cj0944c | | | 1163.99032 (+2) | 78.17 | ²¹⁹ ENNASKPY ²²⁶ | 31 ^c | | | X |
| Cj0944c | | | 1034.93222 (+2) | 52.27 | ²¹⁹ EN(de)NASK ²²⁴ | 47 ^c | | | X |
| Cj0944c | | | 1284.07345 (+2) | 64.78 | ²³⁵ IKLDENSTQN ²⁴⁴ | 62 ^b | | X | |
| Cj0944c | | | 1227.52890 (+2) | 56.49 | ²³⁶ KLDENSTQN ²⁴⁴ | 37 ^b | | X | |
| Cj0982c | <i>cjaA</i> | Putative amino-acid transporter periplasmic solute-binding protein | 876.05824 (+3) | 79.56 | ¹³⁷ DSNITSVEDLK ¹⁴⁷ | 38 ^c | | | X |
| Cj0982c | | | 957.09956 (+3) | 113.86 | ¹³⁷ DSNITSVEDLKDK ¹⁴⁹ | 30 ^c | | | X |
| Cj0982c | | | 990.78157 (+3) | 86.28 | ¹³⁷ DSNITSVEDLKDKT ¹⁵⁰ | 21 ^b | | X | |
| Cj0982c | | | 952.43965 (+3) | 82.76 | ¹³⁸ SNITSVEDLKDKT ¹⁵⁰ | 54 ^b | | X | |

| | | | | | | | | | |
|---------|----------------|---|-----------------|--------|---|-----------------|---|---|---|
| Cj0982c | | | 1118.01071 (+2) | 57.31 | ¹³² VAVPKDSN ¹³⁹ | 27 ^b | | X | |
| Cj0982c | | | 1440.15597 (+2) | 83.68 | ¹³² VAVPKDSNITSVED ¹⁴⁵ | 26 ^b | | X | |
| Cj0982c | | | 1732.82956 (+2) | 87.72 | ¹³² VAVPKDSNITSVEDLKDKT ¹⁵⁰ | 56 ^b | | X | |
| Cj0982c | | | 1183.53805 (+2) | 58.03 | ¹³⁴ VPKDSNITS ¹⁴² | 54 ^a | X | | |
| Cj0982c | | | 1297.59372 (+2) | 67.49 | ¹³⁴ VPKDSNITSVE ¹⁴⁴ | 30 ^a | X | | |
| Cj0983 | <i>JlpA</i> | Surface-exposed lipoprotein | 1198.04757 (+2) | 99.83 | ¹⁰⁴ GEANASISIK ¹¹³ | 51 ^c | | | X |
| Cj0983 | | | 1179.51718 (+2) | 60.34 | ¹⁰¹ IYKGEANAS ¹⁰⁹ | 50 ^b | | X | |
| Cj0983 | | | 1043.82027 (+3) | 117.40 | ⁹⁸ SNEIYKGEANASISIK ¹¹³ | 26 ^c | | | X |
| Cj0983 | | | 1022.80800 (+3) | 97.61 | ¹⁴¹ VVSDINASLFQQDPK ¹⁵⁵ | 57 ^c | | | X |
| Cj1013c | <i>Cj1013c</i> | Putative cytochrome C biogenesis protein | 958.08015 (+3) | 77.68 | ⁷²⁸ AFKDGNWTRADEG ⁷⁴⁰ | 21 ^b | | X | |
| Cj1013c | | | 1077.45053 (+2) | 66.03 | ⁷³¹ DGNWTR ⁷³⁶ | 25 ^c | | | X |
| Cj1013c | | | 1113.49459 (+2) | 71.74 | ⁷²⁹ FKDGNWTR ⁷³⁶ | 25 ^b | | X | |
| Cj1013c | | | 1100.15535 (+3) | 77.24 | ¹⁷¹ NAHYTYKENNNSDPLL ¹⁸⁶ | 52 ^a | X | | |
| Cj1013c | | | 1245.51706 (+2) | 49.70 | ¹⁷⁵ TYKENNNSD ¹⁸³ | 25 ^b | | X | |
| Cj1013c | | | 1294.03524 (+2) | 59.55 | ¹⁷⁵ TYKENNNSDP ¹⁸⁴ | 51 ^b | | X | |
| Cj1013c | | | 1350.58639 (+2) | 66.15 | ¹⁷⁵ TYKENNNSDPL ¹⁸⁵ | 55 ^b | | X | |
| Cj1013c | | | 1061.97946 (+2) | 57.12 | ²²⁷ VKIDEN ²³² | 41 ^b | | X | |
| Cj1013c | | | 1300.05429 (+2) | 73.83 | ¹⁷⁶ YKENNNSDPL ¹⁸⁵ | 48 ^b | | X | |
| Cj1013c | | | 1432.11898 (+2) | 72.23 | ¹⁷⁴ YTYKENNNSDPL ¹⁸⁵ | 27 ^b | | X | |
| Cj1032 | <i>Cj1032</i> | Membrane fusion component of efflux system (mutlidrug efflux system CmeDEF) | 1212.04403 (+2) | 86.27 | ¹⁹⁸ IDQNGTELK ²⁰⁶ | 48 ^c | | | X |
| Cj1053c | <i>Cj1053c</i> | Putative integral membrane protein | 1040.96725 (+2) | 61.82 | ⁷⁵ DINVSK ⁸⁰ | 51 ^c | | | X |
| Cj1053c | | | 1156.00241 (+2) | 48.07 | ⁹³ ISKDNNQS ¹⁰⁰ | 45 ^b | | X | |

| | | | | | | | | | |
|---------|----------------|---|-----------------|--------|---|-----------------|---|---|---|
| Cj1126c | <i>pglB</i> | Oligosaccharide transferase to <i>N</i> -glycosylate proteins | 1202.99154 (+2) | 60.27 | ⁵³⁰ MKDYNQSN ⁵³⁷ | 56 ^b | | X | |
| Cj1126c | | | 1310.03952 (+2) | 67.53 | ⁵³⁰ MKDYNQSNVD ⁵³⁹ | 76 ^b | | X | |
| Cj1126c | | | 1268.52230 (+2) | 57.98 | ⁵²⁹ MMKDYNQSN ⁵³⁷ | 45 ^b | | X | |
| Cj1126c | | | 1375.56906 (+2) | 63.57 | ⁵²⁹ MMKDYNQSNVD ⁵³⁹ | 55 ^b | | X | |
| Cj1345c | <i>Cj1345c</i> | Putative periplasmic protein | 1079.97250 (+2) | 90.01 | ⁵⁹ DYNITK ⁶⁴ | 36 ^c | | | X |
| Cj1345c | | | 1077.47848 (+2) | 68.80 | ¹⁵⁴ SEINASK ¹⁶⁰ | 38 ^c | | | X |
| Cj1373 | <i>Cj1373</i> | Putative ntegral membrane protein | 1208.24190 (+3) | 84.62 | ⁴⁸⁵ LEVIIRFPNNKNDQNTSNT ⁵⁰³ | 24 ^b | | X | |
| Cj1444c | <i>kpsD</i> | Capsule polysaccharide export system periplasmic protein | 1630.74800 (+3) | 113.93 | ¹⁷ AVDVSQIISAEDQGSTTTSIDQNLSSNYDIA | 57 ^c | | | X |
| Cj1444c | | | 1062.47116 (+2) | 68.30 | ⁵⁰ ENNLTK ⁵⁵ | 32 ^c | | | X |
| Cj1444c | | | 1062.96286 (+2) | 71.27 | ⁵⁰ EN(de)NLTK ⁵⁵ | 41 ^c | | | X |
| Cj1444c | | | 1015.14918 (+3) | 65.06 | ⁴⁵ DIANKENNLTKIHQ ⁵⁸ | 45 ^a | X | | |
| Cj1444c | | | 1104.48568 (+2) | 48.95 | ⁴⁶ IANKENN ⁵² | 23 ^b | | X | |
| Cj1444c | | | 976.80745 (+3) | 59.30 | ⁴⁶ IANKENNLTKIHQ ⁵⁸ | 49 ^a | X | | |
| Cj1496c | <i>Cj1496c</i> | Putative periplasmic protein | 1226.06112 (+2) | 95.95 | ⁶⁹ EAEVNATLAK ⁷⁸ | 61 ^c | | | X |
| Cj1496c | | | 879.74599 (+3) | 65.00 | ⁶⁶ EKKEAEVNATL ⁷⁶ | 20 ^a | X | | |
| Cj1496c | | | 903.42628 (+3) | 64.44 | ⁶⁶ EKKEAEVNATLA ⁷⁷ | 21 ^a | X | | |
| Cj1496c | | | 960.77022 (+3) | 68.19 | ⁶⁶ ENLEKKEAEVNAT ⁷⁵ | 36 ^b | | X | |
| Cj1496c | | | 1133.99911 (+2) | 70.62 | ⁶⁸ KEAEVNAT ⁷⁵ | 61 ^c | | | X |
| Cj1496c | | | 1290.10617 (+2) | 65.05 | ⁶⁸ KEAEVNATLAK ⁷⁸ | 83 ^c | | | X |
| Cj1496c | | | 1198.02121 (+2) | 50.15 | ¹⁶⁴ KNLDNNASN ¹⁷² | 37 ^a | X | | |
| Cj1496c | | | 1076.94491 (+2) | 55.06 | ¹⁶⁶ LDNNASN ¹⁷² | 34 ^b | | X | |
| Cj1496c | | | 879.74507 (+3) | 56.47 | ⁶⁵ LEKKEAEVNAT ⁷⁵ | 46 ^b | | X | |
| Cj1496c | | | 1133.96859 (+2) | 76.06 | ¹⁶⁵ NLDNNASN ¹⁷² | 34 ^c | | | X |

| | | | | | | | | | |
|---------|----------------|--|-----------------|--------|---|-----------------|--|---|---|
| Cj1565c | <i>PfIA</i> | Paralyzed flagella protein PfIA | 1215.21126 (+3) | 168.27 | ⁴⁴⁶ ASDEVFFALGDNNASFLHQR ⁴⁶⁵ | 21 ^c | | | X |
| Cj1565c | | | 1008.43106 (+2) | 48.55 | ⁴⁹³ YKEGN ⁴⁹⁷ | 26 ^b | | X | |
| Cj1621 | <i>Cj1621</i> | Putative periplasmic protein | 1180.03183 (+2) | 117.20 | ¹⁹³ TYSLDLNK ²⁰⁰ | 43 ^c | | | X |
| Cj1661 | <i>Cj1661</i> | Possible ABC transport system permease | 1091.46261 (+2) | 52.77 | ¹⁸⁷ GENNQSK ¹⁹³ | 27 ^c | | | X |
| Cj1661 | | | 1212.52951 (+2) | 50.74 | ¹⁸⁶ IGENNQSKE ¹⁹⁴ | 33 ^b | | X | |
| Cj1670c | <i>cgpA</i> | Putative periplasmic protein | 1054.96542 (+2) | 84.91 | ⁶⁹ DLDV ⁷⁴ NK ⁷⁴ | 39 ^c | | | X |
| Cj1670c | | | 1111.50705 (+2) | 107.33 | ⁶⁸ IDL ⁷⁴ DV ⁷⁴ NK ⁷⁴ | 39 ^c | | | X |
| Cj1670c | | | 1018.46144 (+3) | 84.36 | ⁶¹ LDGSEDKIDL ⁷⁵ DV ⁷⁵ NK ⁷⁵ | 68 ^b | | X | |
| Cj1670c | | | 1027.46455 (+3) | 119.50 | ⁶⁰ NLDGSEDKIDL ⁷⁴ DV ⁷⁴ NK ⁷⁴ | 33 ^c | | | X |
| Cj1670c | | | 1055.80476 (+3) | 78.82 | ⁶⁰ NLDGSEDKIDL ⁷⁵ DV ⁷⁵ NK ⁷⁵ | 45 ^b | | X | |
| Cj1670c | | | 879.41450 (+3) | 63.13 | ¹⁰⁰ V ¹¹⁰ TIPEK ¹¹⁰ NSSKQ ¹¹⁰ | 20 ^b | | X | |
| CJE1384 | <i>CJE1384</i> | Hypothetical protein | 1083.97506 (+2) | 61.04 | ²⁶ EQ ³² NGSVK ³² | 20 ^c | | | X |
| CJE1384 | | | 1539.16561 (+2) | 103.98 | ¹⁸ GNPQYTSYE ³² Q ³² NGSVK ³² | 45 ^c | | | X |
| CJE1384 | | | 1310.07040 (+2) | 61.42 | ²³ TSYE ³³ Q ³³ NGSVK ³³ | 38 ^b | | X | |

Total 49 (29) 100 (54) 117 (65)

Table S2. Glycopeptides identified in *C. jejuni* JHH1. Identifications are grouped according to the corresponding Cj#. For each identification the precursor mass, charge and retention time [RT] are given for the highest Mascot (MT) ion score. The number of unique glycopeptides and corresponding glycosylation sites shown within () for each protease digestion is provided (Total).

X' denotes protease treatment providing identification of that peptide.

a,b,c correspond to identifications from pepsin, thermolysin and trypsin, respectively.

Table S3. Identified glycoprotein glycosylation sites in *C. jejuni* JHH1

| Cj No | Gene name | Protein name / Accession number | Functional classification | Sequon peptide sequence | Number of sites | Reference |
|---------|----------------|---|---------------------------|--|-----------------|--------------|
| Cj0011c | <i>cj0011c</i> | Putative non-specific DNA binding protein / GI:218561704 | DNA binding and uptake | ⁴⁹ EANFT ⁵³ | 1 | 27 |
| Cj0081 | <i>cydA</i> | Cytochrome bd oxidase subunit I / GI:218561764 | Redox pathways | ³⁵¹ ENNDT ³⁵⁵ | 2 | 29 |
| Cj0081 | | | | ²⁸³ DNNES ²⁸⁷ | | This study |
| Cj0089 | <i>cj0089</i> | Putative lipoprotein / GI:218561770 | Function unknown | ⁷³ DFNKS ⁷⁷ | 1 | 27 |
| Cj0114 | <i>cj0114</i> | Putative periplasmic protein / GI:57237121 | Function unknown | ¹⁷⁷ ENNNT ¹⁸¹ | 3 | 32 |
| Cj0114 | | | | ¹⁵³ DANLS ¹⁵⁷ | | 27 |
| Cj0114 | | | | ⁹⁹ ENNFT ¹⁰³ | | 22 |
| Cj0131 | <i>cj0131</i> | Putative peptidase M23 family protein / GI:218561812 | Protease | ⁷³ DDNTS ⁷⁷ | 1 | This study |
| Cj0143c | <i>cj0143c</i> | Putative periplasmic solute binding protein for ABC transport system / GI:218561824 | Small molecule transport | ¹⁶³ EQNTS ¹⁶⁷ | 1 | 68 |
| Cj0152c | <i>cj0152c</i> | Putative membrane protein / GI:86153908 | Function unknown | ¹⁶³ ETNQT ¹⁶⁷ | 6 | 27 |
| Cj0152c | | | | ¹²⁶ EQNNT ¹³⁰ | | 29 |
| Cj0152c | | | | ¹⁸⁸ ENNISENNTT ¹⁹⁷ | | This study * |
| Cj0152c | | | | ²⁵⁰ DFNIS ²⁵⁴ | | 29 |
| Cj0152c | | | | ¹⁸² DKNIS ¹⁸⁶ | | This study |
| Cj0158c | <i>cj0158c</i> | Putative haem-binding lipoprotein / GI:218561839 | Iron uptake | ¹¹⁹ DKNHS ¹²³ | 1 | This study |
| Cj0168c | <i>cj0168c</i> | Putative periplasmic protein / GI:218561848 | Function unknown | ²⁶ DVNQT ³⁰ | 1 | 32 |
| Cj0176c | <i>cj0176c</i> | Putative lipoprotein / GI:218561855 | Iron uptake | ²⁹ DLNKT ³³ | 1 | This study |
| Cj0182 | <i>cj0182</i> | Putative transporter / GI:218561861 | Membrane transport | ⁵⁸ DSNST ⁶² | 2 | This study |

| | | | | | | |
|---------|----------------|---|--|--|---|------------|
| Cj0182 | | | | ⁷⁰ ENNAT ⁷⁴ | | This study |
| Cj0200c | <i>cj0200c</i> | Putative periplasmic protein / GI:218561879 | Function unknown | ³³ DN ³⁷ NKT | 1 | 22 |
| Cj0235c | <i>secG</i> | Preprotein translocase SecG subunit / GI:57237295 | Protein exportation | ⁸⁷ ENNNT ⁹¹ | 2 | This study |
| Cj0235c | | | | ¹¹⁸ DVN ¹²² SS | | 32 |
| Cj0238 | <i>cj0238</i> | Putative mechanosensitive ion channel family protein / GI:218561902 | Membrane transport; osmotic homeostasis | ⁵⁶ DEN ⁶⁰ SS | 1 | 27 |
| Cj0256 | <i>cj0256</i> | EptC phosphoethanolamine transferase / GI:218561919 | Carbohydrate modification | ²¹³ ENN ²¹⁷ HT | 1 | 27 |
| Cj0268c | <i>cj0268c</i> | Putative transmembrane protein / GI:218561931 | Function unknown | ²⁷⁷ EAN ²⁸¹ AT | 1 | This study |
| Cj0277 | <i>mreC</i> | Rod shape-determining protein MreC / GI:218561940 | Cell wall maintenance | ⁹¹ DQN ⁹⁵ ST | 1 | 27 |
| Cj0289c | <i>peb3</i> | Major antigenic peptide PEB3 / GI:218561951 | Small molecule transport | ⁸⁸ DF ⁹² NVS | 1 | 22 |
| Cj0365c | <i>cmeC</i> | (multidrug efflux system CmeABC) / GI:218562023 | Membrane transport; cellular exportation | ⁴⁷ EN ⁵¹ SS | 1 | 29 |
| Cj0366c | <i>cmeB</i> | Inner membrane efflux transporter CmeB / GI:218562024 | Membrane transport; cellular exportation | ⁶³⁴ DR ⁶³⁸ NVS | 1 | 27 |
| Cj0367c | <i>cmeA</i> | Periplasmic fusion protein CmeA (multidrug efflux system CmeABC) | Membrane transport; cellular exportation | ²⁷¹ DN ²⁷⁵ NNS | 2 | 69 |
| Cj0367c | | | | ¹²¹ DF ¹²⁵ NRS | | 69 |
| Cj0371 | <i>cj0371</i> | Hypothetical protein / GI:218562029 | Function unknown | ⁷⁵ DL ⁷⁹ NGT | 1 | 27 |
| Cj0376 | <i>cj0376</i> | Putative periplasmic protein / GI:218562034 | Cell wall maintenance | ⁵⁰ DK ⁵⁴ NQT | 1 | This study |
| Cj0397c | <i>cj0397c</i> | Hypothetical protein / GI:57237452 | Function unknown | ¹⁰⁵ DL ¹⁰⁹ NNT | 1 | 29 |
| Cj0399 | <i>cj0399</i> | Colicin V production protein homolog / GI:218562057 | Bacteriocin production | ¹⁷⁹ DL ¹⁸³ NNT | 1 | 29 |
| Cj0404 | <i>cj0404</i> | Putative transmembrane protein / GI:218562062 | Membrane protein | ¹⁰⁰ EQ ¹⁰⁴ N ¹⁰⁴ TT | 1 | This study |
| Cj0454c | <i>cj0454c</i> | Hypothetical protein / GI:218562109 | Function unknown | ⁹¹ EN ⁹⁵ NKS | 1 | 27 |
| Cj0494 | <i>cj0494</i> | Putative exporting protein / GI:218562149 | Membrane transport; cellular exportation | ²⁶ DN ³⁰ NIT | 1 | 27 |

| | | | | | | |
|---------|----------------|--|--|--|---|--------------|
| Cj0508 | <i>cj0508</i> | Penicillin-binding protein 1A / GI:218562161 | Cell wall maintenance | ³¹² DANLS ³¹⁶ | 1 | This study |
| Cj0511 | <i>cj0511</i> | Putative secreted protease / GI:205355370 | Protease | ⁶⁷ DQNIS ⁷¹ | 1 | 27 |
| Cj0540 | <i>cj0540</i> | Putative exporting protein / GI:218562192 | Membrane transport; cellular exportation | ¹⁷³ ENNS ¹⁷⁷ | 1 | This study |
| Cj0592c | <i>cj0592c</i> | Putative periplasmic protein / GI:218562243 | Function unknown | ⁹⁶ DINQSSENNES ¹⁰⁷ | 3 | This study * |
| Cj0592c | | | | ¹²⁷ ENNQS ¹³¹ | | This study |
| Cj0599 | <i>cj0599</i> | Putative OmpA family membrane protein / GI:218562250 | Membrane transport; cellular exportation | ¹⁰⁹ DLNST ¹¹³ | 2 | 29 |
| Cj0599 | | | | ¹⁶⁸ DNNIT ¹⁷² | | 29 |
| Cj0610c | <i>cj0610c</i> | Putative periplasmic protein / GI:218562261 | Function unknown; hydrolase domain | ³³¹ EENAS ³³⁵ | 4 | 27 |
| Cj0610c | | | | ²⁹⁶ ENNRS ³⁰⁰ | | This study |
| Cj0610c | | | | ⁸² DENLS ⁸⁶ | | 27 |
| Cj0610c | | | | ⁹⁸ DENTS ¹⁰² | | This study |
| Cj0633 | <i>cj0633</i> | Putative periplasmic protein / GI:218562283 | Polysaccharide modification | ⁷³ DNKS ⁷⁷ | 3 | This study |
| Cj0633 | | | | ¹²³ DTNLTQDQNL ¹³³ | | This study * |
| Cj0652 | <i>pbpC</i> | Penicillin-binding protein / GI:218562302 | Cell wall maintenance | ⁴⁶⁷ ENNNT ⁴⁷¹ | 1 | 27 |
| Cj0694 | <i>cj0694</i> | Putative periplasmic protein / GI:218562333 | Protein folding | ¹³² DFNKT ¹³⁶ | 3 | 27 |
| Cj0694 | | | | ³⁰⁶ DQNIS ³¹⁰ | | 27 |
| Cj0694 | | | | ⁴²⁶ DQNSS ⁴³⁰ | | This study |
| Cj0734c | <i>hisJ</i> | Histidine-binding protein precursor / GI:218562373 | Periplasmic small molecule transport | ²⁷ ESNAS ³¹ | 1 | 69 |
| Cj0776c | <i>cj0776c</i> | Hypothetical protein / GI:121612758 | Function unknown | ⁸⁶ DENQS ⁹⁰ | 3 | This study |
| Cj0776c | | | | ¹⁰³ ENNQS ¹⁰⁷ | | This study |

| | | | | | | |
|---------|----------------|---|--|-------------------------------------|---|------------|
| Cj0776c | | | | ¹¹¹ DTNTS ¹¹⁵ | | This study |
| Cj0780 | <i>napA</i> | Periplasmic nitrate reductase / GI:112360114 | Nitrogen metabolism | ³⁸⁵ DDNES ³⁸⁹ | 1 | This study |
| Cj0843c | <i>cj0843c</i> | Putative secreted transglycosylase / GI:218562471 | Cell wall maintenance | ³⁷⁴ DYNKT ³⁷⁸ | 3 | 27 |
| Cj0843c | | | | ³²⁷ DANAS ³³¹ | | 26 |
| Cj0843c | | | | ¹⁷³ DLNTS ¹⁷⁷ | | 27 |
| Cj0846 | <i>cj0846</i> | Putative metallophosphoesterase / GI:218562474 | Metallophosphoesterase | ²⁸⁰ DLNTS ²⁸⁴ | 1 | 27 |
| Cj0944c | <i>cj0944c</i> | Putative periplasmic protein / GI:218562563 | Function unknown | ²¹⁹ ENNAS ²²³ | 2 | This study |
| Cj0944c | | | | ²³⁸ DENST ²⁴² | | This study |
| Cj0982c | <i>cjaA</i> | Putative amino-acid transporter periplasmic solute-binding protein / GI:112360304 | Periplasmic small molecule transport | ¹³⁷ DSNIT ¹⁴¹ | 1 | 29 |
| Cj0983 | <i>jlpA</i> | Surface-exposed lipoprotein / GI:157415242 | Adherence factor | ¹⁰⁵ EANAS ¹⁰⁹ | 2 | 47 |
| Cj0983 | | | | ¹⁴⁴ DINAS ¹⁴⁸ | | 47 |
| Cj1013c | <i>cj1013c</i> | Putative cytochrome C biogenesis protein / GI:218562629 | Energy metabolism | ⁷³¹ DGNWT ⁷³⁵ | 3 | 27 |
| Cj1013c | | | | ¹⁷⁸ ENNNS ¹⁸² | | 27 |
| Cj1013c | | | | ²³⁰ DENLT ²³⁴ | | 27 |
| Cj1032 | <i>cj1032</i> | (mutlidrug efflux system CmeDEF) / GI:218562648 | Membrane transport; cellular exportation | ¹⁹⁹ DQNGT ²⁰³ | 1 | 27 |
| Cj1053c | <i>cj1053c</i> | Putative integral membrane protein / GI:218562669 | Membrane protein | ⁷⁵ DINVS ⁷⁹ | 2 | 27 |
| Cj1053c | | | | ⁹⁶ DNNQS ¹⁰⁰ | | This study |
| Cj1126c | <i>pglB</i> | Oligosaccharide transferase to <i>N</i> -glycosylate proteins / GI:218562740 | <i>N</i> -linked glycosylation | ⁵³² DYNQS ⁵³⁶ | 1 | 29 |
| Cj1345c | <i>cj1345c</i> | Putative periplasmic protein / GI:218562954 | Function unknown | ⁵⁹ DYNIT ⁶³ | 2 | 27 |
| Cj1345c | | | | ¹⁵⁴ EINAS ¹⁵⁸ | | 27 |

| | | | | | | |
|---------|----------------|---|--|-------------------------------------|---|------------|
| Cj1373 | <i>cj1373</i> | Putative integral membrane protein / GI:57238417 | Membrane transport; cellular exportation | ⁴⁹⁷ DQNTS ⁵⁰¹ | 1 | This study |
| Cj1444c | <i>kpsD</i> | Capsule polysaccharide export system periplasmic protein / GI:121613488 | Capsule polysaccharide export system | ³⁷ DQNLS ⁴¹ | 2 | This study |
| Cj1444c | | | | ⁵⁰ ENNLT ⁵⁴ | | 27 |
| Cj1496c | <i>cj1496c</i> | Putative periplasmic protein / GI:112360803 | Function unknown | ⁷¹ EVNAT ⁷⁵ | 2 | 70 |
| Cj1496c | | | | ¹⁶⁷ DNNAS ¹⁷¹ | | 70 |
| Cj1565c | <i>pflA</i> | Paralyzed flagella protein PflA / GI:157415781 | Flagellar motility | ⁴⁵⁵ DNNAS ⁴⁶⁰ | 2 | 27 |
| Cj1565c | | | | ⁴⁹⁵ EGNFS ⁴⁹⁹ | | 27 |
| Cj1621 | <i>cj1621</i> | Putative periplasmic protein / GI:218563210 | Function unknown | ¹⁹⁷ DLNKT ²⁰¹ | 1 | 29 |
| Cj1661 | <i>cj1661</i> | Possible ABC transport system permease / GI:218563249 | Membrane transport; cellular exportation | ¹⁸⁸ ENNQS ¹⁹² | 1 | 27 |
| Cj1670c | <i>cgpA</i> | Putative periplasmic protein / GI:57238681 | Function unknown | ⁷¹ DVNKS ⁷⁵ | 2 | 27 |
| Cj1670c | | | | ¹⁰⁴ EKNSS ¹⁰⁸ | | 22 |
| CJE1384 | <i>cje1384</i> | Hypothetical protein / GI:57238121 | Function unknown | ²⁶ EQNGS ³⁰ | 1 | This study |

* Peptide contains 2 confirmed *N*-glycosylation sites

| | |
|--|-----------|
| Total glycosylation sites | 93 |
| Total proteins | 58 |
| Novel proteins within dataset | 15 |
| Novel sites within dataset | 34 |
| Previously seen protein absent in this dataset+ | 10 |

Supplemental Tables References

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