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SUPPORTING INFECTIOUS DISEASE RESEARCH

Yersinia pestis, Strain KIM, Gateway[®] Clone Set, Recombinant in *Escherichia coli*, Plate 27

Catalog No. NR-19623

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For research use only. Not for human use.

Contributor:

Pathogen Functional Genomics Resource Center at the J. Craig Venter Institute

Manufacturer:

BEI Resources

Product Description:

The Yersinia pestis (Y. pestis), strain KIM, Gateway[®] clone set consists of 43 plates (plate 2 of this clone set has been discontinued) which contain more than 3600 sequence validated clones from Y. pestis, strain KIM cloned in *Escherichia coli* (*E. coli*) DH10B-T1 cells. Each open reading frame was constructed in vector <u>pDONRTM221</u> (InvitrogenTM) with an ATG start codon and a TAG stop codon. The sequence was validated by full length sequencing of each clone with greater than 1X coverage and a mutation rate of less than 0.2%. Detailed information about each clone is shown in Table 1.

Information related to the use of Gateway[®] Clones can be obtained from <u>Invitrogen</u>TM. Recombination was facilitated through an *att*B substrate (*att*B-PCR product or a linearized *att*B expression clone) with an *att*P substrate (pDONRTM221) to create an *att*L-containing entry clone. The entry clone contains recombinational cloning sites, *att*L1 and *att*L2 to facilitate gene transfer into a destination vector, M13 forward and reverse priming sites for sequencing and a kanamycin resistance gene for selection. Please refer to the InvitrogenTM Gateway[®] Technology Manual for additional details.

Material Provided:

Each inoculated well of the 96-well plate contains approximately 60 μ L of *E. coli* culture (strain DH10B-T1) in Luria Bertani (LB) Broth containing 50 μ g/mL kanamycin supplemented with 15% glycerol.

<u>Note:</u> Production in the 96-well format has increased risk of cross-contamination between adjacent wells. Individual clones should be purified (e.g. single colony isolation and purification using good microbiological practices) and sequence-verified prior to use. BEI Resources cannot confirm or validate any clone not identified on the plate information table.

Packaging/Storage:

NR-19623 was packaged aseptically in a 96-well plate. The

product is provided frozen and should be stored at -80°C or colder immediately upon arrival. For long-term storage, the vapor phase of a liquid nitrogen freezer is recommended. Freeze-thaw cycles should be avoided.

Growth Conditions:

Media:

LB Broth or Agar containing 50 µg/mL kanamycin.

Incubation:

Temperature: *E. coli*, strain DH10B-T1 clones should be grown at 37°C.

Atmosphere: Aerobic

Propagation:

- 1. Scrape top of frozen well with a pipette tip and streak onto agar plate.
- 2. Incubate the plates at 37°C for 18 to 24 hours.

Citation:

Acknowledgment for publications should read "The following reagent was obtained through BEI Resources, NIAID, NIH: *Yersinia pestis*, Strain KIM, Gateway[®] Clone Set, Recombinant in *Escherichia coli*, Plate 27, NR-19623."

Biosafety Level: 1

Appropriate safety procedures should always be used with this material. Laboratory safety is discussed in the following publication: U.S. Department of Health and Human Services, Public Health Service, Centers for Disease Control and Prevention, and National Institutes of Health. <u>Biosafety in</u> <u>Microbiological and Biomedical Laboratories</u>. 5th ed. Washington, DC: U.S. Government Printing Office, 2009; see <u>www.cdc.gov/biosafety/publications/bmbl5/index.htm</u>.

Disclaimers:

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Use of this product is subject to the terms and conditions of the BEI Resources Material Transfer Agreement (MTA). The MTA is available on our Web site at <u>www.beiresources.org</u>.

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References:

- Deng, W., et al. "Genome Sequence of Yersinia pestis KIM." <u>J. Bacteriol.</u> 184 (2002): 4601-4611. PubMed: 12142430.
- Lindler, L. E., et al. "Complete DNA Sequence and Detailed Analysis of the *Yersinia pestis* KIM5 Plasmid Encoding Murine Toxin and Capsular Antigen." <u>Infect.</u> <u>Immun.</u> 66 (1998): 5731-5742. PubMed: 9826348.

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Clone	Well			OPE	Accession	
Cione	Position	Locus ID	Description (Gene name)		Number	Average Depth of
	1 USILIUII			Lengui	TAUNDER	Coverage
36850	A01	NTL02YP3701	DNA polymerase III, psi subunit	438	AAM87297.1	5
36924	A02	NTL02YP0420	hypothetical protein	462	AAM84016.1	5.591633
38587	A04	NTL02YP2617	inner membrane permease of galactoside ABC transporter	1026	AAM86213.1	3.572233
38603	A05	NTL02YP1508	hypothetical protein	1032	AAM85104.1	3.558769
38624	A06	NTL02YP2593	putative inner membrane permease of ABC transporter	1041	AAM86189.1	3.53469
38635	A07	NTL02YP3702	putative enzyme	1044	AAM87298.1	3.458487
38669	A08	NTL02YP1511	hypothetical protein	1062	AAM85106.1	2.553539
38691	A09	NTL02YP1509	hypothetical protein	1071	AAM85105.1	3.420342
38745	A10	NTL02YP2608	putative ABC transporter binding protein	1092	AAM86204.1	3.469965
38773	A11	NTL02YP0421	hypothetical protein	1107	AAM84017.1	3.4551
38790	A12	NTL02YP2604	putative ATPase	<u>11</u> 13	AAM86200.1	3.450997
37029	B01	NTL02YP0426	hypothetical protein	492	AAM84022.1	3.983083
37075	B02	NTL02YP3683	putative outer membrane protein	507	AAM87279.1	1.985375
37110	B04	NTL02YP0422	hypothetical protein	519	AAM84018.1	2.813953
37191	B05	NTL02YP1519	hypothetical protein	546	AAM85115.1	2.8157
37260	B06	NTL02YP1521	hypothetical protein	570	AAM85117.1	2
37301	B07	NTL02YP2596	putative siderophore biosynthetic protein	582	AAM86192.1	2.811897
37354	B08	NTL02YP1522	hypothetical protein	600	AAM85118.1	2.814063
37366	B09	NTL02YP1503	hypothetical protein	603	AAM85099.1	2.793157
38920	B11	NTL02YP2610	putative transport protein	1182	AAM86206.1	3.310147
39043	C01	NTL02YP2609	hypothetical protein	<u>12</u> 57	AAM86205.1	4.046261
39068	C02	NTL02YP3695	hypothetical protein	1272	AAM87291.1	3.395579
39076	C03	NTL02YP3682	hypothetical protein	1278	AAM87278.1	3.820182
39116	C04	NTL02YP2597	putative siderophore biosynthetic protein	1299	AAM86193.1	3.342793
39135	C05	NTL02YP3693	putative transport system permease protein	1308	AAM87289.1	3.96365
39159	C06	NTL02YP0427	periplasmic binding protein	1320	AAM84023.1	3.458824
37381	C07	NTL02YP2602	2-deoxycytidine 5-triphosphate deaminase	609	AAM86198.1	2.802773
37396	C08	NTL02YP3697	hyperosmotically inducible periplasmic protein	615	AAM87293.1	2.789313
37435	C09	NTL02YP3681	hypothetical protein	624	AAM87277.1	2.793675
37556	C10	NTL02YP2607	hypothetical protein	663	AAM86203.1	2.853485
37545	C11	NTL02YP0423	hypothetical protein	663	AAM84019.1	2.802276

 Table 1: Yersinia pestis, Strain KIM, Gateway[®] Clone Set, Recombinant in Escherichia coli, Plate 27 (UYPWA)

 Clone
 Well

 Clone
 Description (Cone name)

 OPE
 Accession

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Product Information Sheet for NR-19623

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Image: space in the state in the s	Clone	Well Position	Locus ID ¹	Description (Gene name)	ORF Length	Accession Number	Average Depth of
37601 C12 NTL02YP2612 putaliave membrane protein 681 AAM86199.1 2.790569 37639 D01 NTL02YP3612 putaliave membrane protein 696 AAM87285.1 4.101078 37732 D03 NTL02YP3690 putaliave membrane protein 702 AAM87285.1 4.101078 37741 D04 NTL02YP3690 putne-nucleoside phosphorylase 722 AAM87286.1 2.250653 39431 D05 NTL02YP5190 conserved hypothetical protein 1524 AAM87294.1 3.0704908 39443 D07 NTL02YP5151 hypothetical protein 1690 AAM86191.1 3.30702 39643 D08 NTL02YP5152 putative siderophore biosynthetic protein 1890 AAM86191.1 3.304909 37865 D10 NTL02YP5152 putative siderophore biosynthetic protein 768 AAM86191.1 3.63361 37864 D10 NTL02YP5154 phypothetical protein 753 AAM86191.1 2.2 37868 E04 NTL02YP0475 urbothetical protein					J		Coverage
37632 D01 NTL02YP2612 putative membrane protein 696 AAM82206.1 7.153333 37762 D02 NTL02YP569 pytohetical protein 702 AAM87286.1 2.250653 37741 D04 NTL02YP569 pytohetical protein 1524 AAM87286.1 2.250653 39431 D05 NTL02YP502 conserved hypothetical protein 1524 AAM87281.1 3.310702 39482 D07 NTL02YP3698 peptde chain release factor RF-3 1590 AAM86211.1 3.310702 39443 D08 NTL02YP2555 pupthetical protein 1880 AAM8610.1 6.167718 39560 D10 NTL02YP2555 phypothetical protein 753 AAM8610.1 2.52327 37661 D10 NTL02YP1516 probable plin chaperone 780 AAM8510.2.1 3.632927 37662 E03 NTL02YP0418 Trobable plin chaperone 780 AAM8720.1 2.52327 37663 E04 NTL02YP0437 urdine phosphypothetical protein 813 AAM872	37601	C12	NTL02YP2603	uridine/cytidine kinase	681	AAM86199.1	2.790569
37662 D02 NTL02YP5899 hypothetical protein 702 AAM87285.1 2.250653 37741 D04 NTL02YP0419 ATP-binding component of leucine mansport 726 AAM87286.1 2.250653 37741 D04 NTL02YP1502 conserved hypothetical protein 1524 AAM87294.1 3.658568 39482 D07 NTL02YP1502 conserved hypothetical protein 1698 AAM857294.1 3.0704908 39660 D08 NTL02YP2515 hypothetical protein 1881 AAM85108.1 3.695992 39643 D09 NTL02YP2505 putatws siderophore biosynthetic protein 1881 AAM86108.1 3.695992 39644 D10 NTL02YP5056 putatws siderophore biosynthetic protein 1881 AAM8101.1 2 37605 D11 NTL02YP1512 hypothetical protein 768 AAM84014.1 2 37864 D12 NTL02YP6369 putatws siderophorabes 807 AAM85128.1 6.74443 37087 E03 NTL02YP6439 inore membrane permease	37639	D01	NTL02YP2612	putative membrane protein	696	AAM86208.1	7.153533
37732 D03 NTL02YP5800 purine-nucleoside phosphorylase 726 AAM87286.1 2.250653 37741 D04 NTL02YP0419 ATP-binding component of leucine transport 732 AAM84015.1 7.160622 39431 D05 NTL02YP3698 peptide chain release factor RF-3 1590 AAM87294.1 3.704908 39560 D08 NTL02YP2515 NAD-linked malate dehydrogenase (malic anyme) 1688 AAM8611.1 3.365922 39643 D09 NTL02YP1510 hypothetical protein 1880 AAM86108.1 3.655992 39646 D10 NTL02YP506 hypothetical protein 758 AAM85102.1 6.167718 3780 E01 NTL02YP5041 ATP-binding component of high-affmity branched-chain amino acid 768 AAM84012.1 3.632927 37808 E03 NTL02YP3694 Probable plin chaperone 780 AAM84033.1 4.032419 37808 E04 NTL02YP4392 inder thaperone 813 AAM8202.1 3.24072 37841 E05 NTL02YP4392	37662	D02	NTL02YP3689	hypothetical protein	702	AAM87285.1	4.101078
37741 Do4 NTL02YP0419 ATP-binding component of leucine mansport 732 AAM84015.1 7.160622 39431 D05 NTL02YP1520 conserved hypothetical protein 1524 AAM857116.1 3.658568 39462 D07 NTL02YP1530 peptide chain release factor RF-3 1590 AAM8729.11 3.704908 39560 D08 NTL02YP2515 hypothetical protein 1698 AAM86101.1 3.630702 39646 D10 NTL02YP2555 putative siderophore biosynthetic protein 1890 AAM85102.1 6.167718 37605 D11 NTL02YP4506 putative siderophore biosynthetic protein 1890 AAM85102.1 6.167718 37805 D01 NTL02YP450 ATP-binding component of high-affinity 768 AAM85102.1 6.361227 37808 E04 NTL02YP439 ATP-binding component of high-affinity 768 AAM8212.1 2.6249X/10sc-5-phosphate aldolase 813 AAM87290.1 6.811254 37807 E05 NTL02YP4394 hypothetical protein 813 AAM8205.1 <td< td=""><td>37732</td><td>D03</td><td>NTL02YP3690</td><td>purine-nucleoside phosphorylase</td><td>726</td><td>AAM87286.1</td><td>2.250653</td></td<>	37732	D03	NTL02YP3690	purine-nucleoside phosphorylase	726	AAM87286.1	2.250653
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39643 DO9 NTL02YP1512 hypothetical protein 1881 AAM85108.1 3.659592 39646 D10 NTL02YP2595 putative siderophore biosynthetic protein 1890 AAM85102.1 6.167718 37805 D11 NTL02YP1506 hypothetical protein 753 AAM85102.1 6.167718 37841 D12 NTL02YP0418 ATP-binding component of high-affinity branched-chain amino acid 768 AAM84014.1 2 37863 E04 NTL02YP0494 hypothetical protein 813 AAM84021.1 3.632927 37983 E04 NTL02YP0392 uidine phosphorylase 807 AAM84021.1 2.352927 38061 E06 NTL02YP0392 2-dexyribose-5-phosphate aldolase 813 AAM8728.1 6.57443 38061 E06 NTL02YP0495 hypothetical protein 849 AAM84006.1 2.4072 38104 E08 NTL02YP1496 hypothetical protein 848 AAM84062.1 2 38114 E09 NTL02YP1496 hypothetical protein 129 </td <td>39560</td> <td>D08</td> <td>NTL02YP2615</td> <td>NAD-linked malate dehydrogenase (malic enzyme)</td> <td>1698</td> <td>AAM86211.1</td> <td>3.310702</td>	39560	D08	NTL02YP2615	NAD-linked malate dehydrogenase (malic enzyme)	1698	AAM86211.1	3.310702
39646 D10 NTL02YP2595 putative siderophore biosynthetic protein 1753 AAM86191.1 3.633161 37805 D11 NTL02YP1506 hypothetical protein 7753 AAM85102.1 6.167718 37841 D12 NTL02YP1506 hypothetical protein 7763 AAM84014.1 2 37860 E01 NTL02YP1516 probable pills chaperone 780 AAM85112.1 3.632927 37963 E03 NTL02YP0437 uridine phosphorylase 807 AAM87201.1 6.811254 37987 E05 NTL02YP3692 2-deoxythose-5-phosphate aldolase 813 AAM87208.1 6.247443 38087 E06 NTL02YP1494 hypothetical protein 849 AAM8508.1 3.24072 38110 E08 NTL02YP0429 inner membrane phospholipase A 858 AAM8408.1 2.14984 38117 E10 NTL02YP1036 putative CDP-partose synthetical 858 AAM8308.1 2.34072 38613 E12 NTL02YP1484 hypothetical protein 153	39643	D09	NTL02YP1512	hypothetical protein	1881	AAM85108.1	3.695992
37805 D11 NTL02YP1506 hypothetical protein 753 AAM85102.1 6.167718 37841 D12 NTL02YP0418 ATP-binding component of high-affinity 768 AAM84014.1 2 37860 E01 NTL02YP0418 probable pilin chaperone 780 AAM84013.1 4.035419 37963 E03 NTL02YP0364 hypothetical protein 813 AAM87290.1 6.811254 37987 E05 NTL02YP0429 inner membrane permease 846 AAM87290.1 2.2 38081 E06 NTL02YP0429 inner membrane permease 846 AAM8202.1 2.2 38081 E06 NTL02YP0429 inner membrane permease 846 AAM84005.1 2 38110 E08 NTL02YP0429 Normerse symthatese 858 AAM84002.1 2 38110 E08 NTL02YP0439 outer membrane phospholipase A 879 AAM83682.1 2 38177 E10 NTL02YP0444 hypothetical protein 129 AAM84001.1 5.349495	39646	D10	NTL02YP2595	putative siderophore biosynthetic protein	1890	AAM86191.1	3.633161
37841 D12 NTL02YP0418 ATP-binding component of high-affinity branched-chain amino acid 768 AAM84014.1 2 37880 E01 NTL02YP0437 uridine phosphorylase 780 AAM84033.1 4.035419 37988 E04 NTL02YP0437 uridine phosphorylase 807 AAM87209.1 6.811254 37987 E05 NTL02YP3692 2-deoxyribose-5-phosphate aldolase 813 AAM87288.1 6.574443 38087 E06 NTL02YP0429 inner membrane permease 846 AAM84002.1 3.24072 38114 E08 NTL02YP0412 RNA polymerase, sigma(32) factor 858 AAM84008.1 6.14588 38114 E09 NTL02YP0438 outer membrane phospholipase A 879 AAM8508.1 2 38117 E10 NTL02YP143 hypothetical protein 153 AAM8508.1 2.917098 36401 F01 NTL02YP143 hypothetical protein 153 AAM8407.1 4.852308 36498 F02 NTL02YP0402 hypothetical protein 396	37805	D11	NTL02YP1506	hypothetical protein	753	AAM85102.1	6.167718
37860 E01 NTL02YP1516 probable pilin chaperone 780 AAM85112.1 3.632927 37963 E03 NTL02YP0437 uridine phosphorylase 807 AAM84033.1 4.035419 37988 E04 NTL02YP3692 2.deoxyribose-5.phosphate aldolase 813 AAM87281.1 6.5124443 38081 E06 NTL02YP3692 2.deoxyribose-5.phosphate aldolase 813 AAM84025.1 2 38081 E07 NTL02YP1496 hypothetical protein 849 AAM84002.1 6.14588 38114 E09 NTL02YP105 putative CDP-paratose synthetase 858 AAM84652.1 2 38177 E10 NTL02YP1039 outer membrane phospholipase A 879 AAM85081.1 2.917098 35965 E11 NTL02YP1484 hypothetical protein 123 AAM85081.1 2.917098 36401 F01 NTL02YP1484 hypothetical protein 324 AAM84001.1 5.54303 36704 F03 NTL02YP1402 hypothetical protein 326 AAM8400	37841	D12	NTL02YP0418	ATP-binding component of high-affinity branched-chain amino acid	768	AAM84014.1	2
37963 E03 NTL02YP0437 uridine phosphorylase 807 AAM84033.1 4.035419 37988 E04 NTL02YP3694 hypothetical protein 813 AAM87288.1 6.574443 37987 E05 NTL02YP3692 2-deoxyribose-5-phosphate aldolase 813 AAM87288.1 2.7 38087 E07 NTL02YP1046 hypothetical protein 846 AAM8008.1 2.7 38087 E07 NTL02YP1056 putative CDP-paratose synthetase 858 AAM84008.1 6.14588 38117 E10 NTL02YP1489 outer membrane phospholipase A 879 AAM85080.1 2 36013 E12 NTL02YP1483 hypothetical protein 153 AAM8667.1 4.822308 36401 F01 NTL02YP0405 hypothetical protein 321 AAM84067.1 5.349393 36735 F04 NTL02YP0405 hypothetical protein 326 AAM84002.1 5.21739 36789 F06 NTL02YP0406 hypothetical protein 420 AAM84002.1 5.	37880	E01	NTL02YP1516	probable pilin chaperone	780	AAM85112.1	3.632927
37988 E04 NTL02YP3694 hypothetical protein 813 AAM87280.1 6.811254 37987 E05 NTL02YP3692 2-deoxyribose-5-phosphate aldolase 813 AAM87288.1 6.574443 38081 E06 NTL02YP0429 inner membrane permease 846 AAM84025.1 2 38081 E07 NTL02YP0429 Inner membrane permease 846 AAM84008.1 6.14588 38114 E09 NTL02YP1056 putative CDP-paratose synthetase 858 AAM84085.1 2 38013 E12 NTL02YP1483 hypothetical protein 129 AAM85080.1 2 36013 E12 NTL02YP1484 hypothetical protein 123 AAM84001.1 5.34903 36704 F03 NTL02YP1484 hypothetical protein 321 AAM84001.1 5.34903 36788 F06 NTL02YP1484 hypothetical protein 420 AAM84021.1 4.293478 36789 F06 NTL02YP0402 hypothetical protein 420 AAM84010.1 6.307531 </td <td>37963</td> <td>E03</td> <td>NTL02YP0437</td> <td>uridine phosphorylase</td> <td>807</td> <td>AAM84033.1</td> <td>4.035419</td>	37963	E03	NTL02YP0437	uridine phosphorylase	807	AAM84033.1	4.035419
37987 E05 NTL02YP3692 2-deoxyribose-5-phosphate aldolase 813 AAMB7288.1 6.574443 38081 E06 NTL02YP0429 inner membrane permease 846 AAM85092.1 2 38087 E07 NTL02YP0428 hypothetical protein 849 AAM85092.1 3.24072 38110 E08 NTL02YP1426 RNA polymerase, sigma(32) factor 858 AAM85092.1 2 38117 E10 NTL02YP1038 outer membrane phospholipase A 879 AAM85081.1 2 38013 E12 NTL02YP1484 hypothetical protein 153 AAM85081.1 2.917088 36401 F01 NTL02YP1444 hypothetical protein 324 AAM85081.1 2.917088 36438 F02 NTL02YP0405 hypothetical protein 396 AAM83084.1 5.753394 36735 F04 NTL02YP0406 hypothetical protein 402 AAM84002.1 4.283478 36789 F06 NTL02YP0406 hypothetical protein 438 AAM8401.1 6.	37988	E04	NTL02YP3694	hypothetical protein	813	AAM87290.1	6.811254
38081 E06 NTL02YP0429 inner membrane permease 846 AAM84025.1 2 38087 E07 NTL02YP0412 RNA polymerase, sigma(32) factor 889 AAM84005.1 6.14588 38110 E08 NTL02YP0412 RNA polymerase, sigma(32) factor 858 AAM84005.1 2.24072 38177 E10 NTL02YP0389 outer membrane phospholipase A 879 AAM83080.1 2 38003 E11 NTL02YP1483 hypothetical protein 129 AAM85081.1 2.917098 36401 F01 NTL02YP1484 hypothetical protein 321 AAM84067.1 4.852308 36498 F02 NTL02YP0405 hypothetical protein 321 AAM84001.1 5.34903 36704 F03 NTL02YP0406 hypothetical protein 402 AAM8400.1 5.753394 36788 F06 NTL02YP0406 hypothetical protein 420 AAM8400.1 6.307531 38438 F08 NTL02YP1480 glucokinase 975 AAM84001.1 6.307531<	37987	E05	NTL02YP3692	2-deoxyribose-5-phosphate aldolase	813	AAM87288.1	6.574443
38087 EO7 NTL02YP1496 hypothetical protein 849 AAM85092.1 3.24072 38110 E08 NTL02YP012 RNA polymerase, sigma(32) factor 858 AAM84652.1 2 38177 E10 NTL02YP0369 outer membrane phospholipase A 879 AAM83985.1 6.394995 38663 E11 NTL02YP1484 hypothetical protein 153 AAM85080.1 2 36013 E12 NTL02YP1484 hypothetical protein 325 AAM84667.1 4.852308 36401 F01 NTL02YP1484 hypothetical protein 321 AAM8398.1 2 36735 F04 NTL02YP402 hypothetical protein 396 AAM8400.1 5.753394 36788 F05 NTL02YP0402 hypothetical protein 420 AAM8401.1 5.32473 36843 F07 NTL02YP0406 hypothetical protein 420 AAM8401.1 6.307531 38438 F08 NTL02YP0446 hypothetical protein 438 AAM8401.1 6.307531	38081	E06	NTL02YP0429	inner membrane permease	846	AAM84025.1	2
38110 E08 NTL02YP0412 RNA polymerase, sigma(32) factor 858 AAM84008.1 6.14588 38114 E09 NTL02YP1036 putative CDP-paratose synthetase 858 AAM84652.1 2 38177 E10 NTL02YP1389 outer membrane phospholipase A 879 AAM83985.1 6.394995 35965 E11 NTL02YP1484 hypothetical protein 129 AAM85081.1 2.917098 36401 F01 NTL02YP1484 hypothetical protein 321 AAM840667.1 4.852308 36498 F02 NTL02YP0405 hypothetical protein 321 AAM84001.1 5.34903 36735 F04 NTL02YP0406 hypothetical protein 402 AAM8398.1 2 36735 F04 NTL02YP1488 hypothetical protein 420 AAM84001.1 5.34903 36788 F06 NTL02YP1480 glucokinase 975 AAM8401.01 6.307531 38438 F08 NTL02YP1480 glucokinase 975 AAM85076.1 5.854187 <	38087	E07	NTL02YP1496	hypothetical protein	849	AAM85092.1	3.24072
38114 E09 NTL02YP1056 putative CDP-paratose synthetase 858 AAM84652.1 2 38177 E10 NTL02YP1039 outer membrane phospholipase A 879 AAM83985.1 6.394995 35965 E11 NTL02YP1433 hypothetical protein 129 AAM85080.1 2 36013 E12 NTL02YP1484 hypothetical protein 153 AAM84001.1 5.34903 36404 F01 NTL02YP0405 hypothetical protein 321 AAM84001.1 5.34903 36704 F03 NTL02YP0402 hypothetical protein 402 AAM84001.1 5.573394 36735 F04 NTL02YP1488 hypothetical protein 420 AAM8401.1 5.521739 36789 F06 NTL02YP0406 hypothetical protein 438 AAM8401.1 6.307531 38438 F07 NTL02YP0414 hypothetical protein 438 AAM8401.1 6.307531 38448 F10 NTL02YP1490 glucokinase 975 AAM85082.1 2.87788	38110	E08	NTL02YP0412	RNA polymerase, sigma(32) factor	858	AAM84008.1	6.14588
38177 E10 NTL02YP0389 outer membrane phospholipase A 879 AAM83985.1 6.394995 35965 E11 NTL02YP1483 hypothetical protein 129 AAM85080.1 2 36013 E12 NTL02YP1484 hypothetical protein 153 AAM85081.1 2.917098 36401 F01 NTL02YP1071 hypothetical protein 321 AAM84001.1 5.34903 36735 F04 NTL02YP0402 hypothetical protein 306 AAM83998.1 2 36735 F04 NTL02YP0406 hypothetical protein 402 AAM85084.1 5.753394 36788 F05 NTL02YP1488 hypothetical protein 420 AAM84002.1 4.293478 36789 F06 NTL02YP1480 glucokinase 975 AAM85076.1 5.854187 38509 F09 NTL02YP1480 glucokinase 975 AAM85095.1 3.182569 38648 F10 NTL02YP1499 ATP-binding protein of iron ABC 1050 AAM86077.1 2.778881 <	38114	E09	NTL02YP1056	putative CDP-paratose synthetase	858	AAM84652.1	2
35965 E11 NTL02YP1483 hypothetical protein 129 AAM85080.1 2 36013 E12 NTL02YP1484 hypothetical protein 153 AAM85081.1 2.917098 36401 F01 NTL02YP1071 hypothetical protein 285 AAM84667.1 4.852308 36498 F02 NTL02YP0405 hypothetical protein 321 AAM83081.1 2.917098 36735 F04 NTL02YP0402 hypothetical protein 396 AAM83081.1 5.753394 36789 F06 NTL02YP0406 hypothetical protein 420 AAM84002.1 4.293478 36789 F06 NTL02YP0414 hypothetical protein 438 AAM8401.1 6.307531 38438 F07 NTL02YP0414 hypothetical protein of iron ABC 975 AAM85076.1 5.854187 38509 F09 NTL02YP1480 glucokinase 975 AAM85081.1 2.778881 38686 F11 NTL02YP1486 hypothetical protein of iron ABC 1050 AAM86177.1 2.778881 </td <td>38177</td> <td>E10</td> <td>NTL02YP0389</td> <td>outer membrane phospholipase A</td> <td>879</td> <td>AAM83985.1</td> <td>6.394995</td>	38177	E10	NTL02YP0389	outer membrane phospholipase A	879	AAM83985.1	6.394995
36013 E12 NTL02YP1484 hypothetical protein 153 AAM85081.1 2.917098 36401 F01 NTL02YP1071 hypothetical protein 321 AAM84067.1 4.852308 36498 F02 NTL02YP0405 hypothetical protein 321 AAM84001.1 5.34903 36704 F03 NTL02YP0402 hypothetical protein 396 AAM8402.1 5.753394 36735 F04 NTL02YP1076 hypothetical protein 420 AAM8402.1 5.521739 36785 F05 NTL02YP1076 putative transcriptional regulator 420 AAM85076.1 5.854187 36789 F06 NTL02YP0414 hypothetical protein of iron ABC 975 AAM85076.1 5.854187 38438 F08 NTL02YP1480 glucokinase 975 AAM85076.1 5.854187 38646 F11 NTL02YP1499 ATP-binding protein of iron ABC 1050 AAM85082.1 2.778881 36855 F12 NTL02YP1495 imidazoleglycerolphosphatedhydratase 1068 AAM	35965	E11	NTL02YP1483	hypothetical protein	129	AAM85080.1	2
36401 F01 NTL02YP1071 hypothetical protein 285 AAM84667.1 4.852308 36498 F02 NTL02YP0405 hypothetical protein 321 AAM84001.1 5.34903 36704 F03 NTL02YP0402 hypothetical protein 396 AAM8308.1 2 36735 F04 NTL02YP0406 hypothetical protein 402 AAM84002.1 4.293478 36789 F06 NTL02YP1476 putative transcriptional regulator 420 AAM8401.1 6.307531 36845 F07 NTL02YP1480 glucokinase 975 AAM85076.1 5.854187 38509 F09 NTL02YP1480 glucokinase 975 AAM85076.1 5.854187 38648 F10 NTL02YP1499 ATP-binding protein of iron ABC transporter 1050 AAM85082.1 2.778881 38686 F11 NTL02YP1486 hypothetical protein 441 AAM85082.1 2 38686 G01 NTL02YP1486 hypothetical protein 471 AAM85082.1 2 <td>36013</td> <td>E12</td> <td>NTL02YP1484</td> <td>hypothetical protein</td> <td>153</td> <td>AAM85081.1</td> <td>2.917098</td>	36013	E12	NTL02YP1484	hypothetical protein	153	AAM85081.1	2.917098
36498 F02 NTL02YP0405 hypothetical protein 321 AAM84001.1 5.34903 36704 F03 NTL02YP0402 hypothetical protein 396 AAM8398.1 2 36735 F04 NTL02YP1488 hypothetical protein 402 AAM85084.1 5.753394 36788 F05 NTL02YP0406 hypothetical protein 420 AAM84002.1 4.293478 36789 F06 NTL02YP0406 hypothetical protein 420 AAM8401.1 6.307531 36438 F07 NTL02YP0480 glucokinase 975 AAM85076.1 5.854187 38648 F08 NTL02YP0386 magnesium and cobalt permease 999 AAM85082.1 4.662175 38648 F10 NTL02YP1480 fursporter 1050 AAM85095.1 3.182569 38686 F11 NTL02YP1486 hypothetical protein 441 AAM86473.1 2.778881 36855 F12 NTL02YP1486 hypothetical protein 450 AAM84673.1 1.987755	36401	F01	NTL02YP1071	hypothetical protein	285	AAM84667.1	4.852308
36704 F03 NTL02YP0402 hypothetical protein 396 AAM83998.1 2 36735 F04 NTL02YP1488 hypothetical protein 402 AAM85084.1 5.753394 36788 F05 NTL02YP1076 putative transcriptional regulator 420 AAM84002.1 4.293478 36789 F06 NTL02YP1076 putative transcriptional regulator 420 AAM8401.1 6.307531 36845 F07 NTL02YP0414 hypothetical protein 438 AAM85076.1 5.854187 38609 F09 NTL02YP1480 glucokinase 975 AAM85095.1 3.182569 38648 F10 NTL02YP1499 ATP-binding protein of iron ABC transporter 1050 AAM86095.1 3.182569 38686 F11 NTL02YP12581 imidazoleglycerolphosphate dehydratase histidinol-phosphate phosphatase 1068 AAM86177.1 2.778881 36855 F12 NTL02YP1494 hypothetical protein 450 AAM8468.1 1.987755 36955 G02 NTL02YP1077 hypothetical prote	36498	F02	NTL02YP0405	hypothetical protein	321	AAM84001.1	5.34903
36735 F04 NTL02YP1488 hypothetical protein 402 AAM85084.1 5.753394 36788 F05 NTL02YP0406 hypothetical protein 420 AAM84002.1 4.293478 36789 F06 NTL02YP0406 hypothetical protein 420 AAM84010.1 6.307531 36845 F07 NTL02YP0414 hypothetical protein 438 AAM84010.1 6.307531 38438 F08 NTL02YP0386 magnesium and cobalt permease 999 AAM83982.1 4.662175 38648 F10 NTL02YP0386 magnesium and cobalt permease 999 AAM85095.1 3.182569 38686 F11 NTL02YP1499 ATP-binding protein of iron ABC transporter 1050 AAM86177.1 2.778881 36855 F12 NTL02YP1486 hypothetical protein 441 AAM85082.1 2 36866 G01 NTL02YP1486 hypothetical protein 4471 AAM84673.1 1.987755 36955 G02 NTL02YP1072 hypothetical protein 471 AAM84668.1	36704	F03	NTL02YP0402	hypothetical protein	396	AAM83998.1	2
36788 F05 NTL02YP0406 hypothetical protein 420 AAM84002.1 4.293478 36789 F06 NTL02YP1076 putative transcriptional regulator 420 AAM84010.1 5.521739 36845 F07 NTL02YP0414 hypothetical protein 438 AAM85076.1 5.521739 38438 F08 NTL02YP0486 magnesium and cobalt permease 999 AAM85076.1 5.854187 38509 F09 NTL02YP0386 magnesium and cobalt permease 999 AAM85095.1 3.182569 38648 F10 NTL02YP1499 ATP-binding protein of iron ABC transporter 1050 AAM86177.1 2.778881 36855 F12 NTL02YP1486 hypothetical protein 441 AAM85082.1 2 36886 G01 NTL02YP1077 hypothetical protein 450 AAM86177.1 2.778881 36955 G02 NTL02YP1072 hypothetical protein 450 AAM84673.1 1.987755 36955 G02 NTL02YP1072 hypothetical protein 525 <	36735	F04	NTL02YP1488	hypothetical protein	402	AAM85084.1	5.753394
36789 F06 NTL02YP1076 putative transcriptional regulator 420 AAM84512.1 5.521739 36845 F07 NTL02YP0414 hypothetical protein 438 AAM84010.1 6.307531 38438 F08 NTL02YP1480 glucokinase 975 AAM85076.1 5.854187 38509 F09 NTL02YP0386 magnesium and cobalt permease 999 AAM83982.1 4.662175 38648 F10 NTL02YP1499 ATP-binding protein of iron ABC transporter 1050 AAM85095.1 3.182569 38686 F11 NTL02YP1486 hypothetical protein 441 AAM85082.1 2.778881 36855 F12 NTL02YP1777 hypothetical protein 450 AAM84673.1 1.987755 36955 G02 NTL02YP1077 hypothetical protein 471 AAM83984.1 1.994329 37125 G03 NTL02YP1498 hypothetical protein 525 AAM84668.1 1.994329 37130 G06 NTL02YP1499 hypothetical protein 528 AAM83996	36788	F05	NTL02YP0406	hypothetical protein	420	AAM84002.1	4.293478
36845 F07 NTL02YP0414 hypothetical protein 438 AAM84010.1 6.307531 38438 F08 NTL02YP1480 glucokinase 975 AAM85076.1 5.854187 38509 F09 NTL02YP0386 magnesium and cobalt permease 999 AAM83982.1 4.662175 38648 F10 NTL02YP1499 ATP-binding protein of iron ABC transporter 1050 AAM85095.1 3.182569 38686 F11 NTL02YP2581 imidazoleglycerolphosphate dehydratase histidinol-phosphate phosphatase 1068 AAM86177.1 2.778881 36855 F12 NTL02YP1486 hypothetical protein 441 AAM85082.1 2 36866 G01 NTL02YP1077 hypothetical protein 450 AAM84673.1 1.987755 36955 G02 NTL02YP1072 hypothetical protein 471 AAM84068.1 1.994329 37125 G05 NTL02YP1498 hypothetical protein 525 AAM85095.1 2 37130 G06 NTL02YP1498 hypothetical protein 528 </td <td>36789</td> <td>F06</td> <td>NTL02YP1076</td> <td>putative transcriptional regulator</td> <td>420</td> <td>AAM84512.1</td> <td>5.521739</td>	36789	F06	NTL02YP1076	putative transcriptional regulator	420	AAM84512.1	5.521739
38438 F08 NIL02YP1480 glucokinase 975 AAM85076.1 5.854187 38509 F09 NTL02YP0386 magnesium and cobalt permease 999 AAM83982.1 4.662175 38648 F10 NTL02YP1499 ATP-binding protein of iron ABC transporter 1050 AAM85095.1 3.182569 38686 F11 NTL02YP2581 imidazoleglycerolphosphate dehydratase histidinol-phosphate phosphatase 1068 AAM86177.1 2.778881 36855 F12 NTL02YP1486 hypothetical protein 441 AAM85082.1 2 36866 G01 NTL02YP1077 hypothetical protein 450 AAM84673.1 1.987755 36955 G02 NTL02YP1072 hypothetical protein 471 AAM83984.1 1.927593 37025 G03 NTL02YP1498 hypothetical protein 525 AAM85094.1 2 37130 G06 NTL02YP1498 hypothetical protein 528 AAM85075.1 2 37353 G08 NTL02YP1485 putative cytochrome 600	36845	F07	NTL02YP0414	hypothetical protein	438	AAM84010.1	6.307531
38509F09NTL02YP0386magnesium and cobalt permease999AAM83982.14.66217538648F10NTL02YP1499ATP-binding protein of iron ABC transporter1050AAM85095.13.18256938686F11NTL02YP2581imidazoleglycerolphosphate dehydratase histidinol-phosphate phosphatase1068AAM86177.12.77888136855F12NTL02YP1486hypothetical protein441AAM85082.1236886G01NTL02YP1077hypothetical protein450AAM84673.11.98775536955G02NTL02YP1072hypothetical protein471AAM83984.11.92759337025G03NTL02YP1498hypothetical protein525AAM85094.1237130G06NTL02YP1498hypothetical protein528AAM85094.1237133G07NTL02YP1479hypothetical protein528AAM85075.1237353G08NTL02YP1485putative cytochrome600AAM85079.1238847G09NTL02YP1067putative O-antigen chain length determinant1152AAM84663.13.39010138982G12NTL02YP0395.5bypothetical protein11212AAM84663.13.126997	38438	F08	NTL02YP1480	glucokinase	975	AAM85076.1	5.854187
38648F10NTL02YP1499ATP-binding protein of iron ABC transporter1050AAM85095.13.18256938686F11NTL02YP2581imidazoleglycerolphosphate dehydratase histidinol-phosphate phosphatase1068AAM86177.12.77888136855F12NTL02YP1486hypothetical protein441AAM85082.1236886G01NTL02YP1077hypothetical protein450AAM84673.11.98775536955G02NTL02YP1072hypothetical protein471AAM83984.11.92759337025G03NTL02YP1072hypothetical protein489AAM84668.11.99432937125G05NTL02YP1498hypothetical protein525AAM85094.1237130G06NTL02YP1479hypothetical protein528AAM83996.12.79753537133G07NTL02YP1479hypothetical protein528AAM85075.1237353G08NTL02YP1061putative cytochrome600AAM85079.1238862G11NTL02YP1067putative O-antigen chain length determinant1152AAM84663.13.39010138982G12NTL02YP0395hypothetical protein11212AAM84663.13.126997	38509	F09	NTL02YP0386	magnesium and cobalt permease	999	AAM83982.1	4.662175
38686F11NTL02YP2581imidazoleglycerolphosphate dehydratase histidinol-phosphate phosphatase1068AAM86177.12.77888136855F12NTL02YP1486hypothetical protein441AAM85082.1236886G01NTL02YP1077hypothetical protein450AAM84673.11.98775536955G02NTL02YP0388hypothetical protein471AAM83984.11.92759337025G03NTL02YP1072hypothetical protein489AAM84688.11.99432937125G05NTL02YP1498hypothetical protein525AAM85094.1237130G06NTL02YP1499hypothetical protein528AAM85094.1237133G07NTL02YP1479hypothetical protein528AAM85075.1237853G08NTL02YP161putative cytochrome600AAM84500.13.39306838862G11NTL02YP1067putative O-antigen chain length determinant1152AAM84663.13.39010138982G12NTL02YP0395hypothetical protein1212AAM83991.13.126997	38648	F10	NTL02YP1499	transporter	1050	AAM85095.1	3.182569
36855 F12 NTL02YP1486 hypothetical protein 441 AAM85082.1 2 36886 G01 NTL02YP1077 hypothetical protein 450 AAM84673.1 1.987755 36955 G02 NTL02YP0388 hypothetical protein 471 AAM83984.1 1.927593 37025 G03 NTL02YP1072 hypothetical protein 489 AAM84668.1 1.994329 37125 G05 NTL02YP1498 hypothetical protein 525 AAM85094.1 2 37130 G06 NTL02YP1498 hypothetical protein 528 AAM83996.1 2.797535 37133 G07 NTL02YP1479 hypothetical protein 528 AAM85075.1 2 37353 G08 NTL02YP1485 putative cytochrome 600 AAM8500.1 3.393068 38862 G11 NTL02YP1067 putative O-antigen chain length determinant 1152 AAM84663.1 3.390101 38982 G12 NTL02YP0395 bypothetical protein 1212 AAM83991.1 3.126997	38686	F11	NTL02YP2581	imidazoleglycerolphosphate dehydratase histidinol-phosphate phosphatase	1068	AAM86177.1	2.778881
36886 G01 NTL02YP1077 hypothetical protein 450 AAM84673.1 1.987755 36955 G02 NTL02YP0388 hypothetical protein 471 AAM83984.1 1.927593 37025 G03 NTL02YP1072 hypothetical protein 489 AAM84668.1 1.994329 37125 G05 NTL02YP1498 hypothetical protein 525 AAM85094.1 2 37130 G06 NTL02YP1498 hypothetical protein 528 AAM83996.1 2.797535 37133 G07 NTL02YP1479 hypothetical protein 528 AAM85075.1 2 37353 G08 NTL02YP1479 putative cytochrome 600 AAM85079.1 2 38847 G09 NTL02YP1061 putative mannosyltransferase protein 1143 AAM84500.1 3.393068 38862 G11 NTL02YP1067 putative O-antigen chain length determinant 1152 AAM84663.1 3.390101 38982 G12 NTL02YP0395 bypothetical protein 1212 AAM83991.1 <t< td=""><td>36855</td><td>F12</td><td>NTL02YP1486</td><td>hypothetical protein</td><td>441</td><td>AAM85082.1</td><td>2</td></t<>	36855	F12	NTL02YP1486	hypothetical protein	441	AAM85082.1	2
36955 G02 NTL02YP0388 hypothetical protein 471 AAM83984.1 1.927593 37025 G03 NTL02YP1072 hypothetical protein 489 AAM84668.1 1.994329 37125 G05 NTL02YP1498 hypothetical protein 525 AAM85094.1 2 37130 G06 NTL02YP1498 hypothetical protein 528 AAM83996.1 2.797535 37133 G07 NTL02YP1479 hypothetical protein 528 AAM85075.1 2 37353 G08 NTL02YP1485 putative cytochrome 600 AAM85079.1 2 38847 G09 NTL02YP1061 putative mannosyltransferase protein 1143 AAM84500.1 3.393068 38862 G11 NTL02YP1067 putative O-antigen chain length determinant 1152 AAM84663.1 3.390101 38982 G12 NTL02YP0395 bypothetical protein 1212 AAM83991.1 3.126997	36886	G01	NTL02YP1077	hypothetical protein	450	AAM84673.1	1.987755
37025 G03 NTL02YP1072 hypothetical protein 489 AAM84668.1 1.994329 37125 G05 NTL02YP1498 hypothetical protein 525 AAM85094.1 2 37130 G06 NTL02YP0400 hypothetical protein 528 AAM83996.1 2.797535 37133 G07 NTL02YP1479 hypothetical protein 528 AAM85075.1 2 37353 G08 NTL02YP1485 putative cytochrome 600 AAM85079.1 2 38847 G09 NTL02YP1061 putative mannosyltransferase protein 1143 AAM84500.1 3.393068 38862 G11 NTL02YP1067 putative O-antigen chain length determinant 1152 AAM84663.1 3.390101 38982 G12 NTL02YP0395 bypothetical protein 1212 AAM83991.1 3.126997	36955	G02	NTL02YP0388	hypothetical protein	471	AAM83984.1	1.927593
37125 G05 NTL02YP1498 hypothetical protein 525 AAM85094.1 2 37130 G06 NTL02YP0400 hypothetical protein 528 AAM83996.1 2.797535 37133 G07 NTL02YP1479 hypothetical protein 528 AAM85075.1 2 37353 G08 NTL02YP1485 putative cytochrome 600 AAM85079.1 2 38847 G09 NTL02YP1061 putative mannosyltransferase protein 1143 AAM84500.1 3.393068 38862 G11 NTL02YP1067 putative O-antigen chain length determinant 1152 AAM84663.1 3.390101 38982 G12 NTL02YP0395 bypothetical protein 1212 AAM83991.1 3.126997	37025	G03	NTL02YP1072	hypothetical protein	489	AAM84668.1	1.994329
37130 G06 NTL02YP0400 hypothetical protein 528 AAM83996.1 2.797535 37133 G07 NTL02YP1479 hypothetical protein 528 AAM85075.1 2 37353 G08 NTL02YP1485 putative cytochrome 600 AAM85079.1 2 38847 G09 NTL02YP1061 putative mannosyltransferase protein 1143 AAM84500.1 3.393068 38862 G11 NTL02YP1067 putative O-antigen chain length determinant 1152 AAM84663.1 3.390101 38982 G12 NTL02YP0395 bypothetical protein 1212 AAM83991.1 3.126997	37125	G05	NTL02YP1498	hypothetical protein	525	AAM85094.1	2
3/133 G0/ N1L02YP1479 hypothetical protein 528 AAM85075.1 2 37353 G08 NTL02YP1485 putative cytochrome 600 AAM85079.1 2 38847 G09 NTL02YP1061 putative mannosyltransferase protein 1143 AAM84500.1 3.393068 38862 G11 NTL02YP1067 putative O-antigen chain length determinant 1152 AAM84663.1 3.390101 38982 G12 NTL02YP0395 bypothetical protein 1212 AAM83991.1 3.126997	37130	G06	NIL02YP0400	hypothetical protein	528	AAM83996.1	2.797535
37353 GU8 NTL02YP1485 putative cytochrome 600 AAM85079.1 2 38847 G09 NTL02YP1061 putative mannosyltransferase protein 1143 AAM84500.1 3.393068 38862 G11 NTL02YP1067 putative O-antigen chain length determinant 1152 AAM84663.1 3.390101 38982 G12 NTL02YP0395 bypothetical protein 1212 AAM83991.1 3.126997	3/133	G07	NIL02YP1479	nypotnetical protein	528	AAM85075.1	2
38862 G11 NTL02YP1067 putative mannosyltransferase protein 1143 AAM84500.1 3.393068 38862 G11 NTL02YP1067 putative O-antigen chain length determinant 1152 AAM84663.1 3.390101 38982 G12 NTL02YP0395 bypothetical protein 1212 AAM83991.1 3.126997	37353	G08	NILU2YP1485	putative cytochrome	600	AAM85079.1	2
38982 G12 NTL02YP0395 bypothetical protein 1212 AAM83991.1 3.126997	38847 38862	G09 G11	NTL02YP1061 NTL02YP1067	putative mannosyltransferase protein putative O-antigen chain length	1143 1152	AAM84500.1 AAM84663.1	3.393068 3.390101
	38082	G12	NTI 02700305	hypothetical protein	1212	AAM83001 1	3 126997

biei resources

Product Information Sheet for NR-19623

SUPPORTING INFECTIOUS DISEASE RESEARCH

Clone	Well Position	Locus ID ¹	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
38985	H01	NTL02YP1070	putative drug efflux protein	1215	AAM84666.1	1.633466
38987	H02	NTL02YP0384	hypothetical protein	1218	AAM83980.1	3.251987
39034	H03	NTL02YP1481	hypothetical protein	1248	AAM85077.1	3.195652
39082	H04	NTL02YP1057	putative O-antigen synthesis protein, WbyH	1284	AAM84653.1	3.889728
39087	H05	NTL02YP0417	inner membrane permease of high-affinity branched-chain amino	1287	AAM84013.1	6.182366
39100	H06	NTL02YP0398	sn-glycerol-3-phosphate dehydrogenase (anaerobic), membrane anchor subunit	1293	AAM83994.1	3.770443
39122	H07	NTL02YP1068	inosine-guanosine kinase	1305	AAM84664.1	3.976208
37394	H08	NTL02YP2586	phosphoribosyl-amp cyclohydrolase	615	AAM86182.1	2.79542
37404	H09	NTL02YP2582	hypothetical protein	618	AAM86178.1	2.574468
37411	H10	NTL02YP0392	putative homoserine/homoserine lactone efflux protein	621	AAM83988.1	2.783661
37410	H11	NTL02YP0391	threonine efflux protein	621	AAM83987.1	2.789713
37438	H12	NTL02YP0404	putative enzyme	627	AAM84000.1	2.794603

¹The locus ID numbers given in this table were obtained from JCVI at the time of deposition. Please note that the locus tags have since been updated by JCVI and the corrected locus ID numbers can be obtained from the <u>JCVI-CMR</u> webpage using the locus search option and inputting the above locus IDs.