Product Information Sheet for NR-19474

Francisella tularensis subsp. *tularensis*, Strain SCHU S4, Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 17

Catalog No. NR-19474

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Contributor:

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

Manufacturer:

BEI Resources

Product Description:

The *Francisella tularensis* (*F. tularensis*) subsp. *tularensis*, strain SCHU S4, Gateway® clone set consists of 19 plates which contain 1693 sequence validated clones from *F. tularensis* subsp. *tularensis*, strain SCHU S4 cloned in *Escherichia coli* (*E. coli*) DH10B-T1 cells. Each open reading frame was constructed in vector pDONR™221 (Invitrogen™) with a native start codon and no 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 Invitrogen™. Recombination was facilitated through an *att*B substrate (*att*B-PCR product or a linearized *att*B expression clone) with an *att*P substrate (pDONR™221) 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 Invitrogen™ Gateway® Technology Manual for additional details.

Material Provided:

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

Note: 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-19474 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: *Francisella tularensis* subsp. *tularensis*, Strain SCHU S4, Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 17, NR-19474."

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. Biosafety in Microbiological and Biomedical Laboratories. 5th ed. Washington, DC: U.S. Government Printing Office, 2009; see www.cdc.gov/biosafety/publications/bmbl5/index.htm.

Disclaimers:

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References:

1. Larsson, P., et. al. "The Complete Genome Sequence of *Francisella tularensis*, the Causative Agent of Tularemia." Nat. Genet. 37 (2005): 153-159. PubMed: 15640799.
2. Pandya, G. A., et. al. "Whole Genome Single Nucleotide Polymorphism Based Phylogeny of *Francisella tularensis* and its Application to the Development of a Strain Typing Assay." BMC Microbiology 9 (2009): 213. PubMed: 19811647.

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Table 1: *Francisella tularensis* subsp. *tularensis*, Strain SCHU S4, Gateway® Clone Set, Plate 17 (ZFTLA)

Clone	Well Position	Locus ID	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
8925	A01	NT06FT1162	D-alanyl-D-alanine carboxypeptidase family protein	1369	CAG45662.1	4.195763
8928	A02	NT06FT1745	glutamate/gamma-aminobutyrate anti-porter, putative	1372	CAG46153.1	4.637755
8933	A03	NT06FT0765	soluble pyridine nucleotide transhydrogenase	1375	CAG45317.1	4.223273
8936	A04	NT06FT1909	dihydroorotase	1381	CAG46293.1	4.582911
8945	A06	NT06FT1459	tRNA modification GTPase TrmE	1387	CAG45916.1	4.139149
8947	A07	NT06FT0266	UDP-N-acetylmuramate--alanine ligase	1390	CAG44872.1	4.072662
8949	A08	NT06FT0521	acetyl-CoA carboxylase, biotin carboxylase	1390	CAG45106.1	4.130935
8951	A09	NT06FT0465	UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate--D-alanyl-D-alanyl ligase, putative	1393	CAG45055.1	4.607322
8953	A10	NT06FT0528	amino acid antiporter	1396	CAG45113.1	3.944842
8955	A11	NT06FT1082	glutathione-disulfide reductase	1396	CAG45588.1	4.181232
8957	A12	NT06FT2077	Tryptophan biosynthesis protein trpCF [Includes: Indole-3-glycerolphosphate synthase (IGPS); N-(5-phospho-ribosyl)anthranilate isomerase (EC 5.3.1.24) (PRAI)]	1396	CAG46428.1	4.159742
8959	B01	NT06FT1257	choline/carnitine/betaine transporter	1399	N/A	4.231594
8961	B02	NT06FT0311	major facilitator family transporter	1402	CAG44913.1	3.199001
8963	B03	NT06FT0427	UDP-N-acetylglucosamine pyrophosphorylase	1402	CAG45020.1	4.643367
8965	B04	NT06FT0451	Glycine cleavage system P-protein	1402	CAG45042.1	4.139087
8967	B05	NT06FT0769	heat shock protein HslVU, ATPase subunit HslU	1402	CAG45320.1	4.2097
8969	B06	NT06FT0484	UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase	1405	CAG45071.1	4.584342
8971	B07	NT06FT0795	enolase	1405	CAG45342.1	3.851246

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8989	B08	NT06FT1068	O-succinylbenzoate--CoA ligase (OSB-CoA synthetase) (O-succinylbenzoyl-CoA synthetase), putative	1417	CAG45577.1	2.228652
8995	B09	NT06FT1331	DNA-methyltransferase	1420	CAG45804.1	4.026761
8997	B10	NT06FT1357	exodeoxyribonuclease VII, large subunit, putative	1420	CAG45823.1	4.356338
9000	B11	NT06FT0339	fumarate hydratase, class II	1426	CAG44939.1	4.529453
9003	B12	NT06FT0670	Uncharacterized ACR, YdiU/UPF0061 family superfamily	1429	CAG45230.1	4.114766
9007	C01	NT06FT0998	lysine-specific permease, putative	1429	CAG45514.1	4.488453
9009	C02	NT06FT1196	replicative DNA helicase	1429	CAG45692.1	4.544437
9011	C03	NT06FT1691	galactose-proton symport (galactose transporter) STY3244	1429	CAG46106.1	4.561232
9015	C04	NT06FT1857	cysteinyl-tRNA synthetase	1429	CAG46249.1	4.148355
9017	C05	NT06FT1489	ribosome-associated GTPase EngA	1432	CAG45939.1	4.093575
9019	C06	NT06FT0516	survival protein SurA, putative	1438	CAG45101.1	3.995828
9021	C07	NT06FT1175	D-alanyl-D-alanine carboxypeptidase/D-alanyl-D-alanine-endopeptidase	1438	CAG45672.1	4.015299
9023	C08	NT06FT0340	glutamyl-tRNA synthetase	1441	CAG44940.1	3.576683
9025	C09	NT06FT1494	Major Facilitator Superfamily subfamily	1441	CAG45944.1	4.15059
9027	C10	NT06FT1663	mannose-1-phosphate guanylyltransferase/mannose-6-phosphate isomerase	1441	CAG46081.1	4.081194
9029	C11	NT06FT1869	hypothetical protein	1441	CAG46259.1	4.049271
9033	C12	NT06FT0478	arginine decarboxylase, putative	1444	CAG45065.1	4.140582
9035	D01	NT06FT0612	TPR domain protein, putative	1444	CAG45183.1	4.101108
9037	D02	NT06FT1320	iron-sulfur cluster-binding protein, putative	1444	N/A	3.501385
9041	D03	NT06FT0739	DNA recombination protein rmuC	1447	CAG45292.1	4.041465
9043	D04	NT06FT1187	sulfate adenylyltransferase, subunit 1/adenylylsulfate kinase	1447	CAG45683.1	3.704216
9045	D05	NT06FT1701	dihydrolipoamide dehydrogenase	1447	CAG46116.1	3.702142
9047	D06	NT06FT0151	helicase, putative	1450	CAG44769.1	4.528966
9049	D07	NT06FT1762	pre-B cell enhancing factor	1450	N/A	4.081379
9051	D08	NT06FT1097	amino acid antiporter	1456	CAG45601.1	4.487637
9053	D09	NT06FT1891	sucrose-6-phosphate hydrolase	1459	CAG46277.1	4.008225
9055	D10	NT06FT0102	sensor histidine kinase, putative	1462	CAG44727.1	4.483584
9057	D11	NT06FT1998	Na+/H+ antiporter, probable CP0838 , putative	1462	CAG46361.1	4.049932
9059	D12	NT06FT0702	peptidyl-prolyl cis-trans isomerse D, putative	1465	CAG45261.1	4.47372
9062	E01	NT06FT1128	cardiolipin synthetase, putative	1465	CAG45630.1	4.475768
9066	E02	NT06FT1594	unnamed protein product	1465	CAG46028.1	4.435495
9069	E03	NT06FT1970	conserved hypothetical protein	1465	CAG46338.1	3.622526
9071	E04	NT06FT1562	pyruvate kinase	1471	CAG45999.1	3.71448
9073	E05	NT06FT1501	cytosol aminopeptidase	1474	CAG45951.1	4.229986
9077	E06	NT06FT0960	Deoxyribodipyrimidine photolyase-related protein superfamily	1477	CAG45480.1	3.601896
9079	E07	NT06FT1024	O-Antigen Polymerase family	1477	CAG45538.1	4.452945

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Clone	Well Position	Locus ID	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
9081	E08	NT06FT0024	glutamyl-tRNA(Gln) amidotransferase, A subunit	1480	CAG44653.1	4.236486
9083	E09	NT06FT0452	Glycine cleavage system P-protein	1480	CAG45043.1	3.468919
9085	E10	NT06FT1039	hypothetical protein	1480	CAG45552.1	4.158784
9087	E11	NT06FT1100	FeS assembly protein SufB	1480	CAG45604.1	4.356081
9089	E12	NT06FT1369	Exonuclease I	1483	CAG45833.1	2.901551
9091	F01	NT06FT0047	NADH dehydrogenase I, N subunit	1486	CAG44677.1	4.064603
9097	F02	NT06FT0463	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase(EC 6.3.2.13) (UDP-N-acetylmuramyl-tripeptide synthetase) (Meso-diaminopimelate-adding enzyme) (UDP-MurNAc-tripeptide synthetase)	1489	CAG45053.1	4.249832
9099	F03	NT06FT0639	amino acid/peptide transporter, putative	1489	CAG45205.1	4.468771
9101	F04	NT06FT1877	lysine-specific permease	1489	CAG46266.1	3.390866
9105	F05	NT06FT0461	4-alpha-glucanotransferase	1498	CAG45051.1	4.194259
9107	F06	NT06FT1338	type I site-specific deoxyribonuclease, HsdR	1501	N/A	4.407728
9109	F07	NT06FT0054	N utilization substance protein A	1504	CAG44682.1	4.118351
9111	F08	NT06FT0082	2-oxoglutarate dehydrogenase, E2 component, dihydrolipoamide succinyltransferase	1504	CAG44710.1	3.861037
9113	F09	NT06FT0198	conserved hypothetical protein	1504	CAG44811.1	3.841755
9117	F10	NT06FT1276	D-methionine ABC transporter, periplasmic D-methionine-binding protein	1507	CAG45758.1	4.436629
9120	F11	NT06FT1430	RND efflux system, outer membrane lipoprotein, NodT family, putative	1507	CAG45891.1	4.426676
9121	F12	NT06FT0248	phosphoesterase family protein	1510	CAG44854.1	3.599338
9125	G01	NT06FT0676	hypothetical protein	1513	CAG45235.1	4.389293
9128	G02	NT06FT1425	amino acid/peptide transporter	1516	CAG45886.1	4.306728
9129	G03	NT06FT1662	phosphomannomutase	1519	CAG46080.1	3.009875
9131	G04	NT06FT1669	O-antigen flippase	1522	CAG46086.1	3.339028
9133	G05	NT06FT1685	L-aspartate oxidase	1522	CAG46100.1	3.868594
9138	G06	NT06FT0601	hypothetical protein	1525	CAG45173.1	4.263607
9142	G07	NT06FT1991	amidophosphoribosyltransferase	1525	CAG46354.1	4.259672
9144	G08	NT06FT1245	related to ATP-dependent DNA helicase II, putative	1528	N/A	4.008508
9146	G09	NT06FT0615	piperideine-6-carboxylate dehydrogenase	1531	CAG45185.1	4.223383
9147	G10	NT06FT2089	ribonuclease G	1531	CAG46437.1	4.137818
9149	G11	NT06FT0959	putative deoxyribodipyrimidine photolyase	1534	CAG45479.1	4.315515
9151	G12	NT06FT0405	glutamate--cysteine ligase	1540	CAG45000.1	5.333117
9153	H01	NT06FT0144	glycerol kinase	1543	CAG44763.1	5.093973
9155	H02	NT06FT1307	amino acid permease, putative	1543	CAG45782.1	5.047959
9157	H03	NT06FT1838	hydro-lyase, Fe-S type, tartrate/fumarate family	1549	CAG46233.1	4.40736
9159	H04	NT06FT1548	intracellular growth locus protein, IglB	1555	CAG45991.1	5.036013
9161	H05	NT06FT1978	intracellular growth locus protein, IglB	1555	CAG46346.1	5.005145
9181	H07	NT06FT0067	ATP synthase F1, alpha subunit	1576	CAG44695.1	4.984772

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9183	H08	NT06FT1080	amino acid/peptide transporter	1576	CAG45586.1	5.117386
9185	H09	NT06FT0406	integral membrane protein MviN	1579	CAG45001.1	4.123496
9187	H10	NT06FT0832	carbohydrate kinase, putative	1579	CAG45371.1	4.937302
9189	H11	NT06FT1153	amino acid permease, putative	1579	CAG45653.1	5.0095
9191	H12	NT06FT1524	sulfate permease family protein	1579	CAG45972.1	5.219126

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