

***Francisella tularensis* subsp. *tularensis*, Strain SCHU S4, Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 18**

Catalog No. NR-19475

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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 *attB* substrate (*attB*-PCR product or a linearized *attB* expression clone) with an *attP* substrate (pDONR™221) to create an *attL*-containing entry clone. The entry clone contains recombinational cloning sites, *attL1* and *attL2* 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-19475 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 18, NR-19475."

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/bmb15/index.htm.

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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 18 (ZFTLB)

Clone	Well Position	Locus ID	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
9195	A01	NT06FT0226	bifunctional purine biosynthesis protein PurH	1582	CAG44836.1	5.035398
9197	A02	NT06FT1152	GMP synthase	1585	CAG45652.1	5.038486
9201	A03	NT06FT0730	amino acid/peptide transporter, putative	1603	CAG45284.1	5.092327
9203	A04	NT06FT0129	peptide chain release factor 3	1612	CAG44751.1	4.522953
9205	A05	NT06FT0497	phosphoenolpyruvate carboxykinase	1621	CAG45082.1	4.924738
9209	A07	NT06FT0046	NADH dehydrogenase I, M subunit	1624	CAG44676.1	4.909483
9211	A08	NT06FT0261	inner membrane protein, 60 kDa	1642	CAG44866.1	4.80268
9213	A09	NT06FT1498	glucose-6-phosphate isomerase	1657	CAG45948.1	4.896801
9217	A10	NT06FT0327	conserved hypothetical protein	1660	CAG44928.1	5.15241
9221	A11	NT06FT1606	hypothetical protein	1669	CAG46035.1	4.837627
9223	A12	NT06FT1955	chaperonin GroEL	1669	CAG46329.1	4.343319
9225	B01	NT06FT0211	DNA polymerase III, subunits gamma and tau, programmed	1675	CAG44823.1	4.899104
9227	B02	NT06FT0412	CTP synthase	1675	CAG45007.1	4.848955
9229	B03	NT06FT0496	glutamyl-tRNA synthetase	1681	CAG45081.1	4.779298
9231	B04	NT06FT1004	DNA repair protein RecN	1684	CAG45519.1	4.803444
9233	B05	NT06FT1521	transport ATP-binding protein CydC VC1180	1684	CAG45969.1	5.026722
9235	B06	NT06FT1480	2-polyprenylphenol 6-hydroxylase	1693	CAG45931.1	4.489073
9237	B07	NT06FT1050	beta-hexosamidase A precursor BH0675	1702	CAG45561.1	4.965335
9241	B08	NT06FT1038	lipoprotein, putative	1708	CAG45551.1	4.772248
9243	B09	NT06FT1873	probable glucosyltransferase, putative	1714	CAG46262.1	4.331972
9245	B10	NT06FT2062	ABC transporter, ATP-binding protein	1714	CAG46415.1	4.764877
9247	B11	NT06FT0213	lysyl-tRNA synthetase	1717	CAG44825.1	4.750146
9249	B12	NT06FT0897	ABC transporter, ATP-binding protein, MsbA family, putative	1717	CAG45426.1	4.987187
9251	C01	NT06FT1280	cyanophycin synthetase	1720	CAG45762.1	4.784302
9253	C02	NT06FT1754	long-chain-fatty-acid--CoA ligase	1723	CAG46161.1	4.738247
9255	C03	NT06FT1426	long-chain fatty-acid-CoA ligase	1726	CAG45887.1	5.012746
9257	C04	NT06FT1635	NADH oxidase	1726	CAG46058.1	4.708575
9259	C05	NT06FT0781	penicillin-binding protein 3	1729	CAG45330.1	4.914401

Clone	Well Position	Locus ID	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
9261	C06	NT06FT2018	indolepyruvate decarboxylase, putative	1732	CAG46377.1	7.154734
9263	C07	NT06FT2002	membrane protein, putative	1735	CAG46363.1	6.935447
9265	C08	NT06FT1689	ATP-dependent RNA helicase DeaD	1744	CAG46104.1	6.834862
9267	C09	NT06FT0939	aspartate:alanine antiporter	1750	CAG45462.1	3.721143
9269	C10	NT06FT1538	conserved hypothetical protein	1765	CAG45981.1	6.74221
9271	C11	NT06FT1968	conserved hypothetical protein	1765	CAG46336.1	6.877054
9273	C12	NT06FT1171	RNA polymerase sigma factor rpoD (Sigma-70)	1768	CAG45668.1	3.712104
9275	D01	NT06FT1680	sugar dehydratase	1771	CAG46097.1	6.596838
9277	D02	NT06FT0526	single-stranded-DNA-specific exonuclease RecJ	1777	CAG45111.1	7.016882
9279	D03	NT06FT0514	arginyl-tRNA synthetase	1780	CAG45099.1	7.120225
9282	D04	NT06FT1330	conserved hypothetical protein	1783	CAG45803.1	4.632081
9283	D05	NT06FT0310	cytochrome d ubiquinol oxidase, subunit I	1789	CAG44912.1	4.970933
9285	D06	NT06FT0503	dolichyl-phosphate-mannose-protein mannosyltransferase family protein	1798	CAG45088.1	4.89099
9287	D07	NT06FT1069	chorismate binding enzyme	1798	CAG45578.1	4.82703
9290	D08	NT06FT0120	lipid A export ATP-binding/permease protein MsbA	1801	CAG44742.1	4.776791
9292	D09	NT06FT0007	aspartyl-tRNA synthetase	1807	CAG44640.1	4.685667
9298	D10	NT06FT1520	cydD	1816	CAG45968.1	4.71641
9299	D11	NT06FT1314	pilQ protein, putative	1819	CAG45789.1	3.011545
9304	D12	NT06FT0079	succinate dehydrogenase, flavoprotein subunit	1828	CAG44707.1	4.778993
9309	E01	NT06FT0534	mismatch repair protein MutL	1837	CAG45119.1	2.195427
9314	E02	NT06FT0182	DNA topoisomerase IV, B subunit	1849	CAG44796.1	3.671714
9319	E03	NT06FT1342	GTP-binding protein TypA	1852	CAG45812.1	4.839093
9322	E04	NT06FT2046	endochitinase ChiA precursor, putative	1855	CAG46401.1	2.842588
9326	E05	NT06FT0428	glucosamine--fructose-6-phosphate aminotransferase, isomerizing	1873	CAG45021.1	4.658836
9334	E06	NT06FT1415	FAD linked oxidase, N-terminal	1888	CAG45876.1	4.5
9338	E07	NT06FT0296	NhaP-type Na ⁺ /H ⁺ and K ⁺ /H ⁺ antiporter	1909	CAG44901.1	4.480356
9339	E08	NT06FT1374	glucose-inhibited division protein A	1918	CAG45838.1	1.91658
9341	E09	NT06FT0391	Chaperone protein htpG (Heat shock protein htpG) (High temperatureprotein G)	1921	CAG44989.1	4.609058
9345	E10	NT06FT0838	hypothetical protein	1924	CAG45375.1	4.654366
9349	E11	NT06FT1702	pyruvate dehydrogenase complex dihydrolipoamide acetyltransferase	1930	CAG46117.1	4.045596
9358	E12	NT06FT0455	1,4-alpha-glucan branching enzyme	1957	CAG45046.1	2.725089
9360	F01	NT06FT1445	chaperone protein DnaK	1963	CAG45902.1	2.728477
9361	F02	NT06FT1266	protein-export membrane protein SecD	1972	CAG45748.1	4.614097
9364	F03	NT06FT1731	GTP pyrophosphokinase	1978	CAG46141.1	2.623862
9365	F04	NT06FT1493	cell division protein FtsH	1981	CAG45943.1	4.410399
9371	F05	NT06FT1378	peptidase, M13 family	2017	N/A	4.492315

Clone	Well Position	Locus ID	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
9382	F06	NT06FT0783	polyribonucleotide nucleotidyltransferase	2053	CAG45332.1	5.206527
9393	F07	NT06FT1840	ATP-dependent DNA helicase RecG	2074	CAG46234.1	5.190935
9395	F08	NT06FT2011	K ⁺ -transporting ATPase, B subunit	2074	CAG46371.1	5.225651
9397	F09	NT06FT0863	glycyl-tRNA synthetase, beta subunit	2119	CAG45397.1	5.184993
9399	F10	NT06FT2028	phosphate acetyltransferase	2131	CAG46387.1	5.122008
9405	F11	NT06FT0917	guanosine-3,5-bis(diphosphate) 3-pyrophosphohydrolase	2158	CAG45441.1	5.177016
9407	F12	NT06FT0240	primosomal replication factor Y VC2678 [similarity]	2188	CAG44848.1	4.501828
9409	G01	NT06FT1045	predicted N6-adenine-specific DNA methylase	2188	CAG45556.1	5.1266
9416	G02	NT06FT1752	isocitrate dehydrogenase, NADP-dependent	2251	CAG46159.1	4.830298
9418	G03	NT06FT0132	DNA helicase II	2257	CAG44754.1	4.535667
9419	G04	NT06FT0436	DNA topoisomerase IV, A subunit	2260	CAG45029.1	4.950885
9421	G05	NT06FT0808	catalase/peroxidase HPI	2260	CAG45354.1	4.900885
9423	G06	NT06FT1755	oxidoreductase, acyl-CoA dehydrogenase family	2275	CAG46162.1	4.837363
9425	G07	NT06FT0277	ferrous iron transport protein B	2278	CAG44882.1	4.90957
9430	G08	NT06FT0801	42 kDa endochitinase	2317	CAG45348.1	4.742339
9432	G09	NT06FT1026	DNA topoisomerase I	2329	CAG45539.1	2.726492
9433	G10	NT06FT1784	ribonuclease R	2332	CAG46186.1	4.801029
9436	G11	NT06FT1896	transglutaminase domain protein	2344	N/A	2.711604
9439	G12	NT06FT0040	NADH dehydrogenase I, G subunit	2401	CAG44670.1	4.751354
9443	H01	NT06FT1806	outer membrane protein, OMP85 family, putative	2413	CAG46206.1	4.708247
9447	H02	NT06FT1120	leucyl-tRNA synthetase	2476	CAG45623.1	4.600565
9453	H03	NT06FT1879	DNA translocase ftsK	2536	CAG46268.1	3.577287
9455	H04	NT06FT0055	Translation initiation factor IF-2	2575	CAG44683.1	5.130485
9457	H05	NT06FT2009	sensor histidine kinase KdpD, putative	2596	CAG46369.1	3.001926
9463	H06	NT06FT2075	aminopeptidase N	2611	CAG46426.1	5.027959
9467	H07	NT06FT1243	alanyl-tRNA synthetase	2632	CAG45729.1	5.117401
9469	H08	NT06FT1808	DNA gyrase, A subunit	2641	CAG46208.1	2.634987
9472	H09	NT06FT0278	pyruvate, phosphate dikinase	2668	CAG44883.1	4.856822
9476	H10	NT06FT1703	pyruvate dehydrogenase, E1 component	2716	CAG46118.1	4.814433
9477	H11	NT06FT0122	DNA polymerase I	2728	CAG44744.1	4.870601
9479	H12	NT06FT1756	3-hydroxyacyl-CoA dehydrogenase/enoyl-CoA hydratase/isomerase family protein	2731	CAG46163.1	4.89015