

***Francisella tularensis* subsp. *tularensis*, Strain SCHU S4, Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 15**

Catalog No. NR-19472

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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-19472 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 15, NR-19472."

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 15 (ZFTKY)

Clone	Well Position	Locus ID	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
8457	A01	NT06FT0902	glycosyl transferase, family 2 SP1365, putative	1087	CAG45431.1	3.971481
8460	A02	NT06FT1275	D-methionine transport ATP-binding protein	1087	CAG45757.1	5.074517
8461	A03	NT06FT1903	membrane protein, putative	1087	CAG46288.1	4.703772
8465	A04	NT06FT1527	glutamate-gated chloride channel alpha3B subunit, putative	1090	CAG45975.1	4.678899
8468	A05	NT06FT0415	hypothetical protein	1093	CAG45009.1	3.473925
8469	A06	NT06FT0523	small mechanosensitive ion channel, MscS family, putative	1093	CAG45108.1	4.671546
8471	A07	NT06FT0993	chorismate synthase	1093	CAG45509.1	3.642269
8473	A08	NT06FT1340	hypothetical protein	1093	CAG45810.1	4.721866
8475	A09	NT06FT0407	hypothetical protein	1096	CAG45002.1	4.156934
8477	A10	NT06FT0818	daunorubicin resistance transmembrane protein	1096	CAG45362.1	4.034672
8479	A11	NT06FT1503	membrane protein, putative	1096	CAG45953.1	3.603102
8484	A12	NT06FT0685	DNA/RNA endonuclease G	1099	CAG45243.1	4.8899
8486	B01	NT06FT1073	oxidoreductase, aldo/keto reductase family	1099	CAG45581.1	4.514104
8487	B02	NT06FT1406	Lipopolysaccharide core biosynthesis mannosyltransferase lpcc	1099	CAG45868.1	3.614195
8489	B03	NT06FT1561	fructose-bisphosphate aldolase, class II, Calvin cycle subtype	1099	CAG45998.1	4.140127
8495	B04	NT06FT1923	riboflavin biosynthesis protein RibD	1102	CAG46304.1	4.819419
8498	B05	NT06FT0022	RND efflux membrane fusion protein	1105	CAG44651.1	5.093213
8500	B06	NT06FT0977	heat shock protein, putative	1108	CAG45495.1	3.221119
8501	B07	NT06FT0449	glycine cleavage system T protein	1111	CAG45040.1	4.390639
8504	B08	NT06FT1312	3-dehydroquinate synthase	1114	CAG45787.1	5.057451
8505	B09	NT06FT1929	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase	1114	CAG46310.1	4.491921
8507	B10	NT06FT2024	recA protein	1114	CAG46383.1	4.350987
8511	B11	NT06FT0582	Type I restriction modification DNA specificity domain protein	1117	CAG45156.1	2.967771
8514	B12	NT06FT1373	membrane protein, putative	1117	CAG45837.1	3.951656
8516	C01	NT06FT1502	Predicted permease YjgP/YjgQ family superfamily	1117	CAG45952.1	3.837959

Clone	Well Position	Locus ID	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
8521	C02	NT06FT0336	L-lactate dehydrogenase	1120	CAG44936.1	3.608036
8523	C03	NT06FT1611	hypothetical protein	1120	CAG46040.1	3.663393
8525	C04	NT06FT1810	Carbohydrate binding domain protein	1120	CAG46210.1	4.578571
8527	C05	NT06FT1407	hypothetical protein	1123	CAG45869.1	3.26358
8529	C06	NT06FT0760	GTP-binding protein YchF	1126	CAG45312.1	4.011545
8531	C07	NT06FT1677	glycosyl transferase, group 1 family protein, putative	1126	CAG46094.1	4.735346
8535	C08	NT06FT0100	ubiquinol oxidase family protein	1129	N/A	3.648361
8537	C09	NT06FT0468	aspartate-semialdehyde dehydrogenase	1129	CAG45058.1	4.682019
8540	C10	NT06FT0879	Ribonuclease D (RNase D), putative	1129	CAG45409.1	4.735164
8541	C11	NT06FT0498	phospho-N-acetylmuramoyl-pentapeptide-transferase	1132	CAG45083.1	4.733216
8543	C12	NT06FT0640	alanine racemase	1132	CAG45206.1	4.615724
8545	D01	NT06FT1016	phosphoribosylaminoimidazole carboxylase, ATPase subunit	1132	CAG45530.1	3.448763
8547	D02	NT06FT1252	probable exported protein STY0033 , putative	1132	CAG45736.1	4.050353
8549	D03	NT06FT1419	ABC transporter permease	1135	CAG45880.1	3.664317
8551	D04	NT06FT1827	lipoprotein VacJ	1135	CAG46224.1	2.835242
8555	D06	NT06FT1271	queuine tRNA-ribosyltransferase	1138	CAG45753.1	4.448155
8557	D07	NT06FT0527	membrane protein, PerM family	1141	CAG45112.1	4.233129
8559	D08	NT06FT0905	ribokinase, putative	1141	CAG45434.1	4.703769
8565	D09	NT06FT1195	radical SAM enzyme, Cfr family	1147	CAG45691.1	3.668701
8568	D10	NT06FT0920	undecaprenyldiphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase	1150	CAG45444.1	4.415652
8570	D11	NT06FT1169	-	1150	N/A	4.962609
8571	D12	NT06FT0439	BNR/Asp-box repeat protein, putative	1153	CAG45032.1	4.393755
8573	E01	NT06FT0627	putrescine ABC transporter, ATP-binding protein	1156	CAG45195.1	3.728374
8576	E02	NT06FT1060	8-amino-7-oxononanoate synthase	1162	CAG45569.1	4.683305
8577	E03	NT06FT0133	oligopeptide ABC transporter, periplasmic oligopeptide-binding protein, putative	1165	N/A	3.419742
8579	E04	NT06FT1277	probable tyrosine-specific transport protein, putative	1165	CAG45759.1	2.33133
8583	E05	NT06FT0537	major facilitator family transporter, putative	1168	CAG45121.1	4.137842
8585	E06	NT06FT1328	N-acetylglucosamine-6-phosphate deacetylase	1168	CAG45801.1	4.357021
8590	E07	NT06FT0806	metabolite-proton symporter, putative	1171	CAG45352.1	4.247652
8591	E08	NT06FT1704	DUF185	1171	CAG46119.1	4.587532
8594	E09	NT06FT0184	lipoprotein, putative	1174	CAG44798.1	4.807496
8595	E10	NT06FT0457	glucose-1-phosphate adenyltransferase	1174	N/A	3.149063
8598	E11	NT06FT0551	proton/peptide symporter family protein, putative	1174	N/A	4.632879
8599	E12	NT06FT0855	cation efflux family protein	1174	CAG45389.1	4.183986
8603	F01	NT06FT0091	oxygen-independent coproporphyrinogen III oxidase, putative	1177	CAG44717.1	3.929482
8607	F02	NT06FT1801	lipid-A-disaccharide synthase	1177	CAG46201.1	4.124894

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8609	F03	NT06FT0209	cell division protein FtsZ	1180	CAG44821.1	4.617797
8611	F04	NT06FT1102	sufB/sufD domain protein	1180	CAG45606.1	3.822034
8614	F05	NT06FT1405	chologylglycine hydrolase	1180	CAG45867.1	4.952542
8618	F06	NT06FT0409	folylpolyglutamate synthase/dihydrofolate synthase	1186	CAG45004.1	4.174536
8621	F08	NT06FT1938	drug resistance transporter, Bcr/CflA family, putative	1186	CAG46316.1	4.406408
8623	F09	NT06FT1972	conserved hypothetical protein	1186	CAG46340.1	4.712479
8625	F10	NT06FT2027	acetate kinase	1189	CAG46386.1	4.277544
8628	F11	NT06FT1610	hypothetical protein	1192	CAG46039.1	4.919463
8629	F12	NT06FT1807	1-deoxy-D-xylulose 5-phosphate reductoisomerase	1192	CAG46207.1	4.665268
8631	G01	NT06FT0168	S-adenosylmethionine synthetase	1195	CAG44782.1	4.653556
8633	G02	NT06FT1358	hippurate hydrolase	1195	CAG45824.1	4.61841
8635	G03	NT06FT2045	phosphoribosylglycinamide formyltransferase 2	1195	CAG46400.1	4.072803
8638	G04	NT06FT0075	AmpG-related permease	1198	CAG44703.1	4.889816
8639	G05	NT06FT0558	Succinyl-CoA synthetase beta chain (SCS-beta)	1198	CAG45137.1	4.63606
8642	G06	NT06FT1002	aspartate transaminase (EC 2.6.1.1) , putative	1198	CAG45517.1	4.864775
8643	G07	NT06FT1363	u1937b; B1937_F1_4	1198	N/A	3.983306
8645	G08	NT06FT1828	chitinase BH0916 , putative	1198	N/A	4.579299
8649	G09	NT06FT0491	ABC transporter ATP-binding protein	1204	N/A	4.647841
8651	G10	NT06FT0682	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	1204	CAG45240.1	4.371262
8654	G11	NT06FT1725	tyrosine-specific transport protein, putative	1207	CAG46135.1	4.283347
8655	G12	NT06FT0749	glutathione-regulated potassium-efflux system protein	1210	CAG45302.1	4.61405
8659	H01	NT06FT1396	cysteine desulfurase	1210	CAG45859.1	4.195041
8662	H02	NT06FT0652	outer membrane protein	1213	CAG45216.1	3.82028
8663	H03	NT06FT0661	3-phosphoshikimate 1-carboxyvinyltransferase	1213	CAG45221.1	4.604287
8666	H04	NT06FT0673	metabolite transport protein homolog ywtG, putative	1213	N/A	4.884584
8669	H05	NT06FT0183	putative bicyclomycin/multidrug transport protein (MFS superfamily)	1216	CAG44797.1	4.620888
8671	H06	NT06FT0529	putrescine ABC transporter, periplasmic putrescine-binding protein	1216	CAG45114.1	4.614309
8673	H07	NT06FT0985	cadmium-translocating P-type ATPase	1216	N/A	4.320724
8675	H08	NT06FT1997	drug resistance transporter, Bcr/CflA family	1216	CAG46360.1	4.322368
8677	H09	NT06FT2012	K ⁺ -transporting ATPase, A subunit	1216	N/A	4.616776
8681	H10	NT06FT1306	Major Facilitator Superfamily subfamily	1219	CAG45781.1	4.277276
8687	H11	NT06FT0913	major facilitator family transporter	1222	CAG45437.1	4.350245
8691	H12	NT06FT1757	thiolase family protein	1222	CAG46164.1	4.832242