SUPPLEMENTARY MATERIAL

Figure Legends

Fig. S1. Growth phenotypes of the *F. tularensis ssrA* and *smpB* mutants in chemically defined Chamberlain medium (CDM). The *smpB* and *ssrA* mutants, the complemented mutants, and the WT were inoculated in CDM from overnight cultures. To monitor their growth, OD_{600} measurements were taken at the indicated time points and plotted.

Fig. S2. *F. tularensis smpB* mutant strain is sensitive to heat. The *smpB* and *ssrA* mutants, the complemented mutants, and the WT were grown to saturation in liquid culture, brought to the same optical density, serially diluted, and equal aliquots spotted on chocolate agar plates. Plates were incubated at 37°C or 40°C, as indicated.

Fig. S3. *F. tularensis smpB* mutant is defective in Intracellular replication. The *smpB* mutant and WT were transformed with a plasmid encoding green fluorescent protein under the control of constitutively active *F. tularensis groEL* promoter. The transformed cells were used to infect a nearly confluent culture of mouse bone marrow derived macrophages at the equivalent multiplicity of infection. Fluorescence was detected 16 h later using epifluorescent and phase-contrast microscopy, and photographed using a digital camera. Merged phase-contrast and fluorescence images obtained at the same magnification (at 200X) are shown.

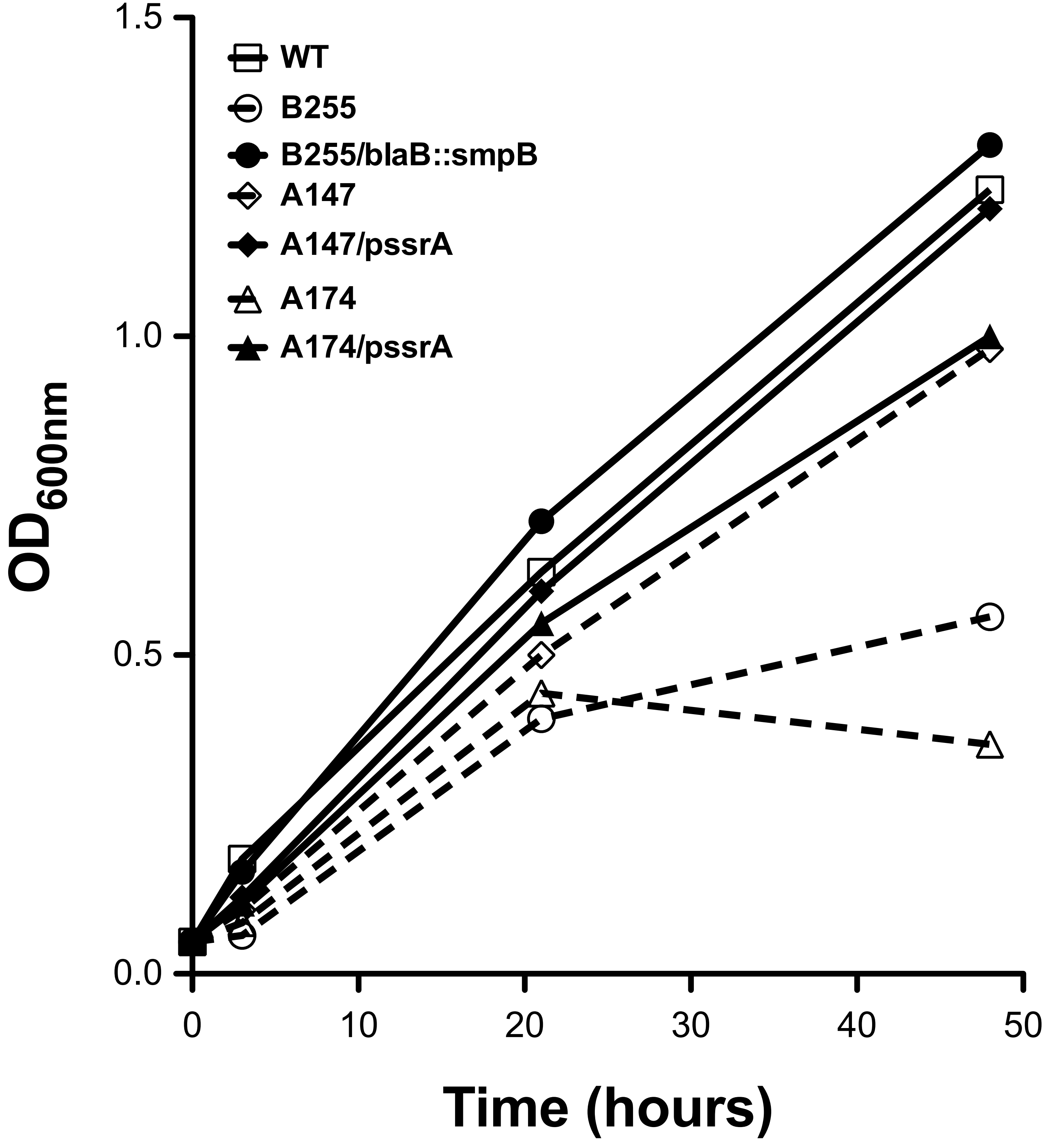
1.5
1.0
0.5
0.0
OD$_{600nm}$
0
10
20
30
40
50
Time (hours)
WT
B255
B255/blaB::smpB
A147
A147/pssrA
A174
A174/pssrA

Fig. S1

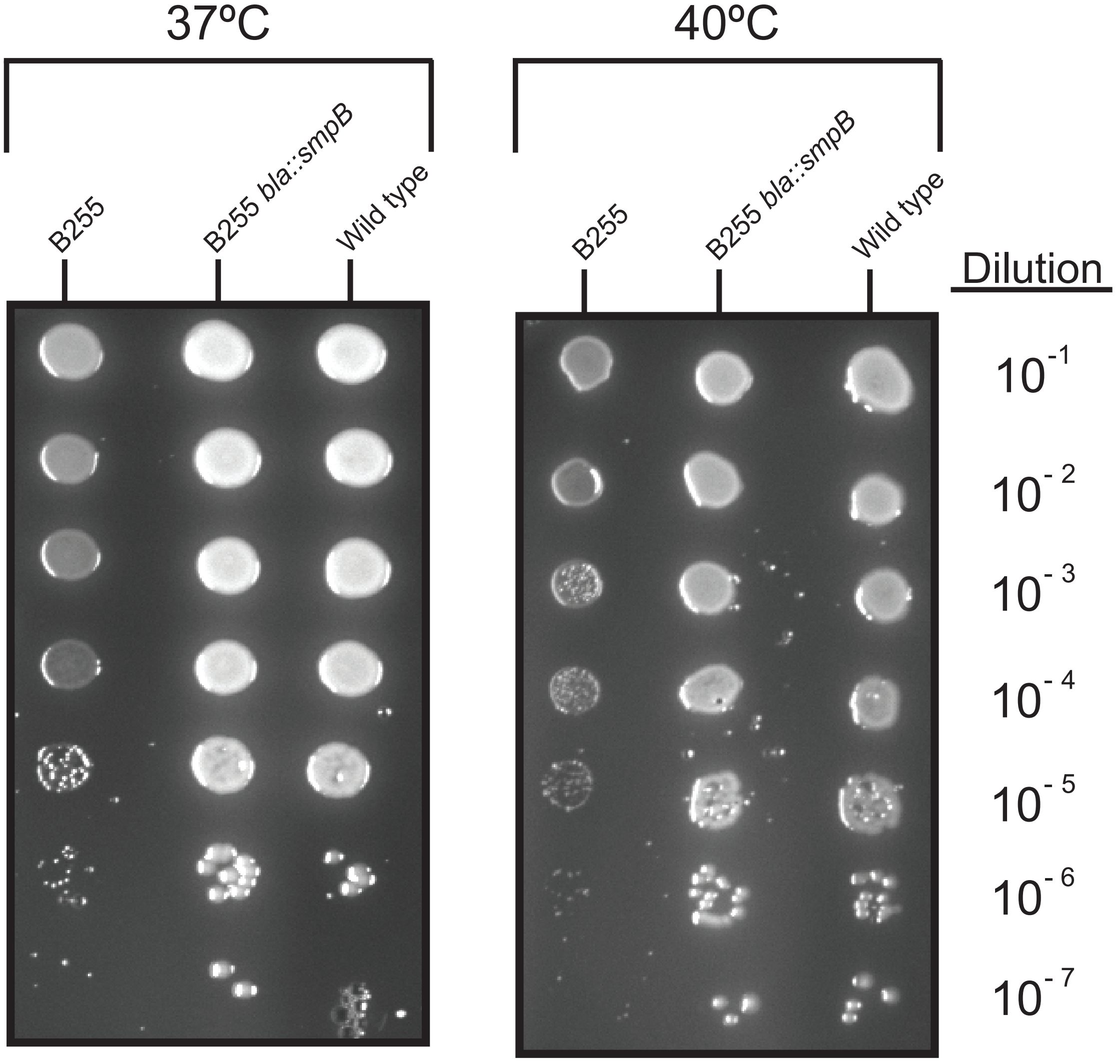
37ºC
40ºC
B255
B255 *bla::smpB*
Wild type
B255
B255 *bla::smpB*
Wild type
Dilution
10^{-1}
10^{-2}
10^{-3}
10^{-4}
10^{-5}
10^{-6}
10^{-7}

Fig. S2

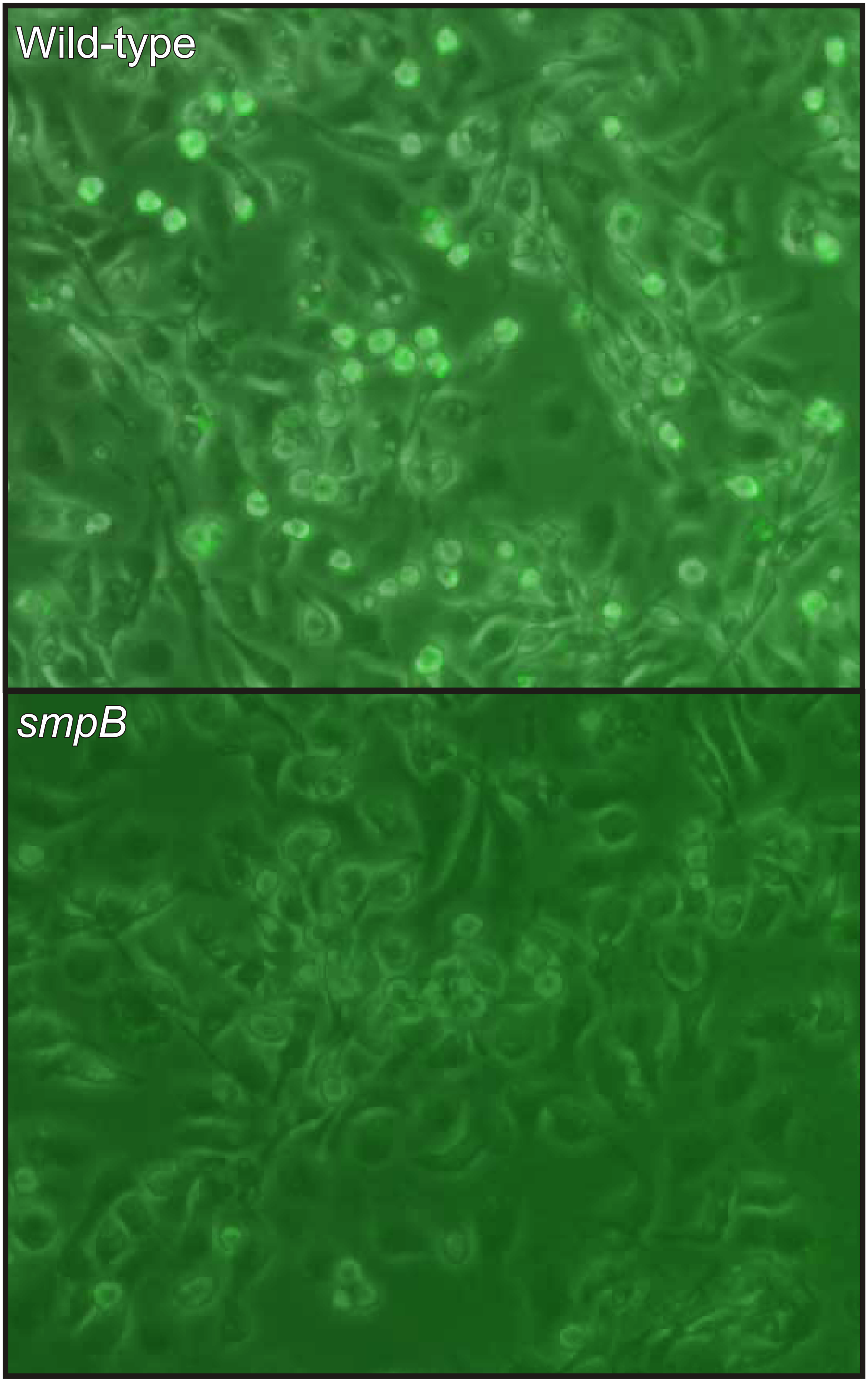

Fig. S3

Table S1. Proteins tagged by the *F. tularensis* tmRNA system. All tagged substrates were assigned to functional categories according to *F. tularensis* genome database.

UniProt ID	Protein Description
	Amino acid transport and metabolism
Q2A193|Q2A193_FRATH	Glutamine synthetase FTL_1899
Q2A2Q0|Q2A2Q0_FRATH	Prephenate dehydratase FTL_1336
Q2A3Q1|Q2A3Q1_FRATH	Histidine decarboxylase FTL_0938
Q2A419|AROK_FRATH	Shikimate kinase aroK
Q2A441|Q2A441_FRATH	Gamma-glutamyltranspeptidase FTL_0766
Q2A490|Q2A490_FRATH	Proton-dependent oligopeptide transport (POT) family protein FTL_0711
Q2A4T3|Q2A4T3_FRATH	Spermidine synthase FTL_0500
Q2A4U9|Q2A4U9_FRATH	Shikimate 5-dehydrogenase FTL_0481
Q2A4V1|GCSPA_FRATH	Probable glycine dehydrogenase [decarboxylating] subunit 1 gcvPA
Q2A4V2|Q2A4V2_FRATH	Glycine cleavage system H protein FTL_0478
Q2A510|Q2A510_FRATH	Oligopeptidase A FTL_0419
Q2A544|Q2A544_FRATH	Amino acid permease FTL_0382
Q2A5D8|Q2A5D8_FRATH	NAD(P)-specific glutamate dehydrogenase FTL_0269
Q2A5V4|TRPA_FRATH	Tryptophan synthase alpha chain trpA
	Carbohydrate transport and metabolism
Q2A278|ENO_FRATH	Enolase eno
Q2A284|Q2A284_FRATH	Chitinase family 18 protein FTL_1521
Q2A2B1|GPMI_FRATH	2,3-bisphosphoglycerate-independent phosphoglycerate mutase gpmI
Q2A2G7|Q2A2G7_FRATH	UDP-glucose 4-epimerase FTL_1430
Q2A368|Q2A368_FRATH	Pyruvate kinase FTL_1148
Q2A383|Q2A383_FRATH	Inositol-1-monophosphatase FTL_1132
Q2A4U2|Q2A4U2_FRATH	4-alpha-glucanotransferase FTL_0488
Q2A543|Q2A543_FRATH	Mannose-6-phosphate isomerase, FTL_0383
Q2A5V7|Q2A5V7_FRATH	Chitinase FTL_0093
Q2A369|PGK_FRATH	Phosphoglycerate kinase pgk
	Fatty acids and lipids metabolism
Q2A1E1|Q2A1E1_FRATH	Lipase/acyltransferase FTL_1839
Q2A221|Q2A221_FRATH	Acetyl-CoA carboxylase, biotin carboxyl carrier protein subunit FTL_1592
Q2A2F5|Q2A2F5_FRATH	Enoyl-[acyl-carrier-protein] reductase (NADH) FTL_1442
Q2A377|Q2A377_FRATH	3-oxoacyl-(Acyl-carrier-protein) reductase FTL_1139
Q2A378|Q2A378_FRATH	Acyl carrier protein FTL_1138
Q2A4K6|Q2A4K6_FRATH	Long chain fatty acid CoA ligase FTL_0586
Q2A4K8|Q2A4K8_FRATH	Fusion product of 3-hydroxacyl-CoA dehydrogenase and acyl-CoA-binding protein FTL_0584
Q2A4M9|Q2A4M9_FRATH	Delta 9 acyl-lipid fatty acid desaturase FTL_0557
Q2A4Y0|PSD_FRATH	Phosphatidylserine decarboxylase proenzyme psd
Q2A5B4|ACCA_FRATH	Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha accA
Q2A5H7|Q2A5H7_FRATH	Phosphatidate cytidylyltransferase FTL_0229
Q2A5L0|LPXD1_FRATH	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase 1

	lpxD1
	Energy metabolism
Q2A1F6|Q2A1F6_FRATH	NADH-quinone oxidoreductase FTL_1824
Q2A1I8|Q2A1I8_FRATH	Citrate synthase FTL_1789
Q2A1J2|Q2A1J2_FRATH	Succinate dehydrogenase iron-sulfur protein FTL_1785
Q2A1J4|Q2A1J4_FRATH	Dihydrolipoamide succinyltransferase component of 2-oxoglutarate dehydrogenase complex FTL_1783
Q2A1S0|Q2A1S0_FRATH	GlpX protein FTL_1701
Q2A2X4|Q2A2X4_FRATH	Pyruvate/2-oxoglutarate dehydrogenase complex,dihydrolipoamide dehydrogenase component FTL_1248
Q2A370|Q2A370_FRATH	Glyceraldehyde-3-phosphate dehydrogenase FTL_1146
Q2A3E4|Q2A3E4_FRATH	Inorganic pyrophosphatase FTL_1061
Q2A4K4|Q2A4K4_FRATH	Isocitrate dehydrogenase FTL_0588
Q2A598|Q2A598_FRATH	Dihydrolipoyl dehydrogenase FTL_0311
Q2A599|Q2A599_FRATH	Pyruvate dehydrogenase, E2 component FTL_0310
Q2A5L5|Q2A5L5_FRATH	Cytochrome O ubiquinol oxidase subunit II FTL_0191
Q2A5L7|Q2A5L7_FRATH	Cytochrome d terminal oxidase, polypeptide subunit I FTL_0189
Q2A1K3|ACON_FRATH	Aconitate hydratase acn
	Cofactors, prosthetic groups, electron carriers metabolism
Q2A260|PDXS_FRATH	Pyridoxal biosynthesis lyase pdxS
Q2A2C4|Q2A2C4_FRATH	Thiamine pyrophosphokinase FTL_1477
Q2A2W3|Q2A2W3_FRATH	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase/dihydropteroate synthase FTL_1265
Q2A319|Q2A319_FRATH	Cobalamin (Vitamin B12) synthesis protein/P47K family protein FTL_1200
Q2A3K0|Q2A3K0_FRATH	AhpC/Tsa family protein FTL_0996
Q2A3N1|Q2A3N1_FRATH	Soluble pyridine nucleotide transhydrogenase FTL_0960
Q2A4C6|PANB_FRATH	3-methyl-2-oxobutanoate hydroxymethyltransferase panB
Q2A4C7|PANC_FRATH	Pantothenate synthetase panC
Q2A563|Q2A563_FRATH	Putative uncharacterized protein FTL_0356
	Nucleotides and nucleosides metabolism
Q2A1C4|Q2A1C4_FRATH	Amidophosphoribosyltransferase FTL_1861
Q2A2C3|Q2A2C3_FRATH	Inosine-5-monophosphate dehydrogenase FTL_1478
Q2A2X0|Q2A2X0_FRATH	ATP-dependent RNA helicase RhlE FTL_1252
Q2A311|DCD_FRATH	Deoxycytidine triphosphate deaminase dcd
Q2A3L0|Q2A3L0_FRATH	Biofunctional protein, glutaredoxin 3 protein/Ribonucleoside-diphosphate reductase, beta subunit FTL_0984
Q2A3P2|Q2A3P2_FRATH	Ribose-phosphate pyrophosphokinase FTL_0949
Q2A5H6|DUT_FRATH	Deoxyuridine 5'-triphosphate nucleotidohydrolase dut
	Other metabolism - biosynthesis
Q2A2J0|SYT_FRATH	Threonyl-tRNA synthetase thrS
Q2A3M3|Q2A3M3_FRATH	Tyrosyl-tRNA synthetase FTL_0968
Q2A4U1|SYGA_FRATH	Glycyl-tRNA synthetase alpha subunit glyQ
Q2A5I8|SYE_FRATH	Glutamyl-tRNA synthetase gltX
Q2A298|KATG_FRATH	Catalase-peroxidase katG
Q2A2B3|Q2A2B3_FRATH	Cytidine deaminase FTL_1488
Q2A3V3|Q2A3V3_FRATH	Beta-lactamase FTL_0879
Q2A460|Q2A460_FRATH	Oxidoreductase, short-chain dehydrogenase family protein FTL_0743
	Putative enzymes
Q2A2T7|Q2A2T7_FRATH	Short-chain dehydrogenase/reductase FTL_1294

Q2A612|Q2A612_FRATH	Acid phosphatase FTL_0031
	Secondary metabolites biosynthesis, transport, and catabolism
Q2A3R1|Q2A3R1_FRATH	DJ-1/PfpI family protein FTL_0928
Q2A3Y4|Q2A3Y4_FRATH	Isochorismatase hydrolase family protein FTL_0846
	Translation, ribosomal structure and biogenesis
Q2A1M0|EFTU_FRATH	Elongation factor Tu tuf
Q2A1M3|RL11_FRATH	50S ribosomal protein L11 rplK
Q2A269|PNP_FRATH	Polyribonucleotide nucleotidyltransferase pnp
Q2A2A3|Q2A2A3_FRATH	Translation initiation inhibitor FTL_1498
Q2A2E4|RL21_FRATH	50S ribosomal protein L21 rplU
Q2A2J2|RL35_FRATH	50S ribosomal protein L35 rpmI
Q2A332|RL13_FRATH	50S ribosomal protein L13 rplM
Q2A3H5|RL9_FRATH	50S ribosomal protein L9 rplI
Q2A484|Q2A484_FRATH	Ribonuclease E FTL_0717
Q2A4R2|RL33_FRATH	50S ribosomal protein L33 rpmG
Q2A4X1|Q2A4X1_FRATH	Methionine aminopeptidase FTL_0459
Q2A5F4|RL18_FRATH	50S ribosomal protein L18 rplR
Q2A5H2|EFG_FRATH	Elongation factor G fusA
Q2A5I1|EFTS_FRATH	Elongation factor Ts tsf
Q2A5I2|RS2_FRATH	30S ribosomal protein S2 rpsB
Q2A5X7|RS20_FRATH	30S ribosomal protein S20 rpsT
	Post-translational modification, protein turnover, chaperones
P94797|CH10_FRATH	10 kDa chaperonin groS
Q2A144|Q2A144_FRATH	Peptide methionine sulfoxide reductase msrA FTL_1960
Q2A1U2|Q2A1U2_FRATH	Putative uncharacterized protein FTL_1678
Q2A2K4|Q2A2K4_FRATH	Peptidyl-prolyl cis-trans isomerase FTL_1393
Q2A2L3|Q2A2L3_FRATH	Glutathione peroxidase FTL_1383
Q2A327|DNAJ_FRATH	Chaperone protein dnaJ
Q2A328|DNAK_FRATH	Chaperone protein dnaK
Q2A3B3|Q2A3B3_FRATH	Macrophage infectivity potentiator, FTL_1097
Q2A3B5|Q2A3B5_FRATH	Peptide methionine sulfoxide reductase FTL_1093
Q2A3M7|HSLU_FRATH	ATP-dependent hsl protease ATP-binding subunit hslU hslU
Q2A3T9|Q2A3T9_FRATH	ATP-dependent protease La FTL_0894
Q2A3U2|TIG_FRATH	Trigger factor tig
Q2A5E0|HTPG_FRATH	Chaperone protein htpG
Q2A5J9|Q2A5J9_FRATH	Pyrrolidone-carboxylate peptidase FTL_0207
Q2A5V6|Q2A5V6_FRATH	ClpB protein FTL_0094
	Motility, attachment and secretion structure (Intracellular trafficking and secretion)
Q2A1V9|Q2A1V9_FRATH	Hypothetical membrane protein FTL_1658
Q2A2Y3|Q2A2Y3_FRATH	Signal recognition particle protein, Ffh FTL_1239
Q2A3Y2|Q2A3Y2_FRATH	Preprotein translocase, subunit D, membrane protein FTL_0848
Q2A420|Q2A420_FRATH	Type IV pilin multimeric outer membrane protein FTL_0800
Q2A422|Q2A422_FRATH	Type IV pili glycosylation protein FTL_0798
Q2A5B6|SECB2_FRATH	Protein-export protein secB 2
	Transport
Q2A1C0|Q2A1C0_FRATH	Outer membrane protein tolC FTL_1865
Q2A3P4|Q2A3P4_FRATH	Major facilitator superfamily (MFS) transport protein FTL_0946
Q2A2E7|Q2A2E7_FRATH	Major facilitator superfamily (MFS) transport protein FTL_1450

Q2A205|FETP_FRATH	Probable Fe(2+)-trafficking protein FTL_1608
Q2A3R3|Q2A3R3_FRATH	Ferritin-like protein FTL_0926
Q2A4H6|Q2A4H6_FRATH	Putative uncharacterized protein FTL_0617
	Cell envelope biogenesis, outer membrane
Q2A1R5|LOLA_FRATH	Outer-membrane lipoprotein carrier protein lolA
Q2A292|Q2A292_FRATH	Glycerophosphoryl diester phosphodiesterase family protein FTL_1511
Q2A294|Q2A294_FRATH	D-alanyl-D-alanine carboxypeptidase/D-alanyl-D-alanine-endopeptidase FTL_1509
Q2A2Q8|Q2A2Q8_FRATH	Outer membrane associated protein FTL_1328
Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carboxypeptidase (Penicillin binding protein) family protein FTL_1060
Q2A3F6|Q2A3F6_FRATH	D-alanyl-D-alanine carboxypeptidase (Penicillin binding protein) family protein FTL_1046
Q2A4L9|Q2A4L9_FRATH	Putative uncharacterized protein FTL_0573
Q2A516|Q2A516_FRATH	UDP-N-acetylglucosamine 1-carboxyvinyltransferase FTL_0413
Q2A5M6|Q2A5M6_FRATH	Acyltransferase FTL_0180
	Cell cycle
Q2A4R5|MINE_FRATH	Cell division topological specificity factor minE
Q9ZAW3|FTSZ_FRATH	Cell division protein ftsZ ftsZ
	DNA replication, recombination, and repair
Q2A237|Q2A237_FRATH	DNA mismatch repair protein FTL_1576
Q2A259|Q2A259_FRATH	DNA gyrase subunit B FTL_1547
Q2A2C8|Q2A2C8_FRATH	DNA excision repair enzyme, subunit A FTL_1473
Q2A2K5|Q2A2K5_FRATH	Cold-shock DEAD-box protein A FTL_1392
Q2A3T8|Q2A3T8_FRATH	Histone-like protein HU form B FTL_0895
Q2A4K2|Q2A4K2_FRATH	ATp-dependent helicase FTL_0590
Q2A4Q7|Q2A4Q7_FRATH	Transposase isftu1
Q2A4Q9|Q2A4Q9_FRATH	ATP-dependent DNA helicase RecG FTL_0524
Q2A4W8|Q2A4W8_FRATH	DNA topoisomerase IV subunit A FTL_0462
Q2A504|Q2A504_FRATH	DNA topoisomerase I FTL_0426
Q2A627|Q2A627_FRATH	Single-stranded DNA-binding protein FTL_0014
Q2A639|Q2A639_FRATH	DNA polymerase III, beta chain FTL_0002
	Regulation of gene expression, RNA-binding
Q2A3T5|HFQ_FRATH	Protein hfq
	Signal transduction and regulation
Q2A207|Q2A207_FRATH	Stringent starvation protein A, regulator of transcription FTL_1606
Q2A2Z0|Q2A2Z0_FRATH	Putative uncharacterized protein FTL_1231
Q2A4N4|Q2A4N4_FRATH	Two-component response regulator FTL_0552
Q2A4X3|Q2A4X3_FRATH	Cold shock protein FTL_0457
	Transcription
Q2A1M8|RPOC_FRATH	DNA-directed RNA polymerase subunit beta' rpoC
Q2A3F2|Q2A3F2_FRATH	RNA polymerase sigma factor FTL_1050
Q2A4I2|Q2A4I2_FRATH	Transcription termination factor Rho FTL_0610
Q2A5E5|RPOA1_FRATH	DNA-directed RNA polymerase subunit alpha 1 rpoA1
	Unknown function - conserved
Q2A2G0|Q2A2G0_FRATH	Putative uncharacterized protein FTL_1437
Q2A2S5|Q2A2S5_FRATH	Putative uncharacterized protein FTL_1306
Q2A2W1|Q2A2W1_FRAT	Putative uncharacterized protein FTL_1267

H	
Q2A347|Q2A347_FRATH	Putative uncharacterized protein FTL_0125
Q2A372|Q2A372_FRATH	Putative uncharacterized protein FTL_1144
Q2A3E6|Q2A3E6_FRATH	Putative uncharacterized protein FTL_1059
Q2A3L6|Q2A3L6_FRATH	Putative uncharacterized protein FTL_0977
Q2A3P8|Q2A3P8_FRATH	Putative uncharacterized protein FTL_0941
Q2A3R0|Y929_FRATH	UPF0082 protein FTL_0929 FTL_0929
Q2A4P7|Q2A4P7_FRATH	Outer membrane protein OmpH FTL_0536
Q2A565|Q2A565_FRATH	Putative uncharacterized protein FTL_0354
Q2A632|Q2A632_FRATH	Outer membrane protein FTL_0009
	Unknown function - novel
P18149|MP17_FRATH	17 kDa major membrane protein FTL_0421
Q2A1C8|Q2A1C8_FRATH	Putative uncharacterized protein FTL_1852
Q2A1I4|Q2A1I4_FRATH	Putative uncharacterized protein FTL_1793
Q2A234|Q2A234_FRATH	Putative uncharacterized protein FTL_1579
Q2A254|Q2A254_FRATH	Hypothetical membrane protein FTL_1552
Q2A274|Q2A274_FRATH	Putative uncharacterized protein FTL_1532
Q2A2A7|Q2A2A7_FRATH	Putative uncharacterized protein FTL_1494
Q2A2M0|Q2A2M0_FRATH	Putative uncharacterized protein FTL_1371
Q2A2Z4|Q2A2Z4_FRATH	Putative uncharacterized protein FTL_1225
Q2A355|Q2A355_FRATH	Putative uncharacterized protein FTL_0117
Q2A358|Q2A358_FRATH	Intracellular growth locus, subunit D FTL_0114
Q2A358|Q2A358_FRATH	Intracellular growth locus, subunit D FTL_0114
Q2A3A5|Q2A3A5_FRATH	Putative uncharacterized protein FTL_1110
Q2A3B8|Q2A3B8_FRATH	Putative uncharacterized protein FTL_1088
Q2A3D0|Q2A3D0_FRATH	Putative uncharacterized protein FTL_1075
Q2A3G5|Q2A3G5_FRATH	Putative uncharacterized protein FTL_1037
Q2A3J9|Q2A3J9_FRATH	Putative uncharacterized protein FTL_0997
Q2A3K2|Q2A3K2_FRATH	Putative uncharacterized protein FTL_0994
Q2A3V2|Q2A3V2_FRATH	Putative uncharacterized protein FTL_0880
Q2A3W0|Q2A3W0_FRATH	Putative uncharacterized protein FTL_0870
Q2A404|Q2A404_FRATH	Hypothetical lipoprotein FTL_0823
Q2A405|Q2A405_FRATH	Putative uncharacterized protein FTL_0822
Q2A4A7|Q2A4A7_FRATH	Putative uncharacterized protein FTL_0694
Q2A4D9|Q2A4D9_FRATH	Putative uncharacterized protein FTL_0661
Q2A4E4|Q2A4E4_FRATH	Hypothetical membrane protein FTL_0655
Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized protein FTL_0572
Q2A4M3|Q2A4M3_FRATH	Outer membrane protein FTL_0569
Q2A4Z1|Q2A4Z1_FRATH	Putative uncharacterized protein FTL_0439
Q2A518|Q2A518_FRATH	Putative uncharacterized protein FTL_0411
Q2A5N2|Q2A5N2_FRATH	Putative uncharacterized protein FTL_0174
Q2A5V5|Q2A5V5_FRATH	Putative uncharacterized protein FTL_0097

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

UniProt ID	**Protein Description**	**Junction peptide**	**Tagged peptide**	**Protein length**	**Tagged site**	**MQScore**	**pValue**
sp|P18149|MP17_FRATH	17 kDa major membrane	K.DTAAAQTATTEQAAAVSKPAGNK.K	DTAAAQTATTEQAAAVSKP	149	55	2.413	0.006
sp|P94797|CH10_FRATH	10 kDa chaperonin groS	K.VGDETLLAGNK.K	VGDETLL	95	83	3.589	0.004
sp|P94797|CH10_FRATH	10 kDa chaperonin groS	E.TLLMMREEDIMGIAGNKK.E	TLLMMREEDIMGI	95	93	2.88	0.001
sp|P94797|CH10_FRATH	10 kDa chaperonin groS	K.VGDETLLMMREEDIMGIAGNKK.E	VGDETLLMMREEDIMGI	95	93	3.439	0.001
sp|P94797|CH10_FRATH	10 kDa chaperonin groS	E.DIMGIIAGNKKE.N	DIMGII	95	94	3.759	0.002
sp|P94797|CH10_FRATH	10 kDa chaperonin groS	R.EEDIMGIIAGNKKENR.V	EEDIMGII	95	94	3.684	0.009
sp|P94797|CH10_FRATH	10 kDa chaperonin groS	R.EEDIMGIIAGNKK.E	EEDIMGII	95	94	3.419	0.000
sp|P94797|CH10_FRATH	10 kDa chaperonin groS	D.IMGIIAGNKKE.N	IMGII	95	94	3.071	0.002
sp|P94797|CH10_FRATH	10 kDa chaperonin groS	E.TLLMMREEDIMGIIAGNKK.E	TLLMMREEDIMGII	95	94	3.751	0.000
sp|P94797|CH10_FRATH	10 kDa chaperonin groS	E.TLLMMREEDIMGIIAGNKKE.N	TLLMMREEDIMGII	95	94	3.595	0.001
sp|P94797|CH10_FRATH	10 kDa chaperonin groS	E.TLLMM+16REEDIMGIIAGNKK.E	TLLMMREEDIMGII	95	94	2.805	0.006
sp|P94797|CH10_FRATH	10 kDa chaperonin groS	E.TLLMMREEDIM+16GIIAGNKKE.N	TLLMMREEDIMGII	95	94	2.786	0.002
sp|P94797|CH10_FRATH	10 kDa chaperonin groS	E.TLLMM+16REEDIMGIIAGNKKE.N	TLLMMREEDIMGII	95	94	2.735	0.000
sp|P94797|CH10_FRATH	10 kDa chaperonin groS	K.VGDETLLMMREEDIMGIIAGNK.K	VGDETLLMMREEDIMGII	95	94	4.507	0.000
sp|P94797|CH10_FRATH	10 kDa chaperonin groS	K.VGDETLLMMREEDIMGIIAGNKK.E	VGDETLLMMREEDIMGII	95	94	4.303	0.000
sp|P94797|CH10_FRATH	10 kDa chaperonin groS	K.VGDETLLMM+16REEDIMGIIAGNKK.E	VGDETLLMMREEDIMGII	95	94	3.233	0.000
sp|P94797|CH10_FRATH	10 kDa chaperonin groS	K.VGDETLLM+16M+16REEDIMGIIAGNK.K	VGDETLLMMREEDIMGII	95	94	2.895	0.001
sp|P94797|CH10_FRATH	10 kDa chaperonin groS	E.DIMGIIAAGNKKE.N	DIMGIIA	95	95	3.948	0.000
sp|P94797|CH10_FRATH	10 kDa chaperonin groS	E.EDIMGIIAAGNKKE.N	EDIMGIIA	95	95	2.878	0.001
sp|P94797|CH10_FRATH	10 kDa chaperonin groS	R.EEDIMGIIAAGNKK.E	EEDIMGIIA	95	95	3.638	0.000
sp|P94797|CH10_FRATH	10 kDa chaperonin groS	E.TLLMMREEDIMGIIAAGNKKE.N	TLLMMREEDIMGIIA	95	95	3.674	0.000
sp|P94797|CH10_FRATH	10 kDa chaperonin groS	E.TLLMMREEDIMGIIAAGNKK.E	TLLMMREEDIMGIIA	95	95	3.606	0.000
sp|P94797|CH10_FRATH	10 kDa chaperonin groS	K.VGDETLLMMREEDIMGIIAAGNKK.E	VGDETLLMMREEDIMGIIA	95	95	3.79	0.000
sp|P94797|CH10_FRATH	10 kDa chaperonin groS	K.VGDETLLMMREEDIMGIIAAGNK.K	VGDETLLMMREEDIMGIIA	95	95	3.168	0.000
sp|P94797|CH10_FRATH	10 kDa chaperonin groS	K.VGDETLLMM+16REEDIMGIIAAGNKK.E	VGDETLLMMREEDIMGIIA	95	95	2.936	0.000
sp|P94797|CH10_FRATH	10 kDa chaperonin groS	K.VGDETLLMMREEDIM+16GIIAAGNKK.E	VGDETLLMMREEDIMGIIA	95	95	2.604	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	E.GLKAVTAGMNPMDLKRGIDKATAAGNKKE.N	GLKAVTAGMNPMDLKRGIDKATA	544	125	3.038	0.010
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	E.GIVAGGGVAAGNKKE.N	GIVAGGGVA	544	418	4.1	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	R.KAIEAPLAGNK.K	KAIEAPL	544	451	3.104	0.003
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	E.SSVVVNQVKAAGNKKE.N	SSVVVNQVKA	544	471	3.972	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	E.SSVVVNQVKANAGNKKE.N	SSVVVNQVKAN	544	472	3.233	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	E.SSVVVNQVKANQAGNKKE.N	SSVVVNQVKANQ	544	473	3.231	0.000

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

sp|P94798|CH60_FRATH	60 kDa chaperonin groL	E.SSVVVNQVKANQGAGNKKE.N	SSVVVNQVKANQG	544	474	2.632	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	E.SSVVVNQVKANQGNYGAGNKKE.N	SSVVVNQVKANQGNYG	544	477	3.405	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	E.SSVVVNQVKANQGNYGYNAAGNKKE.N	SSVVVNQVKANQGNYGYNA	544	480	3.018	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	E.SSVVVNQVKANQGNYGYNAANAGNKKE.N	SSVVVNQVKANQGNYGYNAAN	544	482	2.835	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	R.SALQHAASIAGNK.K	SALQHAASI	544	510	3.702	0.001
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	R.SALQHAASIAAGNK.K	SALQHAASIA	544	511	4.346	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	R.SALQHAASIAGLAGNK.K	SALQHAASIAGL	544	513	4.381	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	R.SALQHAASIAGLAGNKK.E	SALQHAASIAGL	544	513	3.34	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	R.SALQHAASIAGLMAGNK.K	SALQHAASIAGLM	544	514	4.425	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	R.SALQHAASIAGLMAGNKK.E	SALQHAASIAGLM	544	514	3.86	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	R.SALQHAASIAGLM+16AGNK.K	SALQHAASIAGLM	544	514	3.75	0.003
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	R.SALQHAASIAGLMIAGNK.K	SALQHAASIAGLMI	544	515	4.362	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	R.SALQHAASIAGLMIAGNKK.E	SALQHAASIAGLMI	544	515	4.232	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	R.SALQHAASIAGLM+16IAGNK.K	SALQHAASIAGLMI	544	515	4.025	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	R.SALQHAASIAGLMITAGNK.K	SALQHAASIAGLMIT	544	516	4.241	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	R.SALQHAASIAGLMITAGNKK.E	SALQHAASIAGLMIT	544	516	4.202	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	R.SALQHAASIAGLM+16ITAGNK.K	SALQHAASIAGLMIT	544	516	3.979	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	R.SALQHAASIAGLMITAGNKKE.N	SALQHAASIAGLMIT	544	516	3.291	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	R.SALQHAASIAGLMITTAGNK.K	SALQHAASIAGLMITT	544	517	4.503	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	R.SALQHAASIAGLMITTAGNKK.E	SALQHAASIAGLMITT	544	517	3.777	0.001
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	R.SALQHAASIAGLM+16ITTAGNK.K	SALQHAASIAGLMITT	544	517	3.501	0.001
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	R.SALQHAASIAGLMITTEAGNK.K	SALQHAASIAGLMITTE	544	518	4.248	0.002
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	R.SALQHAASIAGLMITTEAAGNK.K	SALQHAASIAGLMITTEA	544	519	4.259	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	R.SALQHAASIAGLMITTEAAGNKK.E	SALQHAASIAGLMITTEA	544	519	3.736	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	R.SALQHAASIAGLM+16ITTEAAGNKK.E	SALQHAASIAGLMITTEA	544	519	2.127	0.001
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	R.SALQHAASIAGLMITTEAMAGNK.K	SALQHAASIAGLMITTEAM	544	520	2.956	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	R.SALQHAASIAGLMITTEAM+16AGNK.K	SALQHAASIAGLMITTEAM	544	520	2.046	0.006
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	R.SALQHAASIAGLMITTEAM+16IAGNK.K	SALQHAASIAGLMITTEAMI	544	521	2.064	0.007
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	R.SALQHAASIAGLMITTEAMIAGNK.K	SALQHAASIAGLMITTEAMI	544	521	2.056	0.006
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	R.SALQHAASIAGLMITTEAMIGEIKAGNK.K	SALQHAASIAGLMITTEAMIGEIK	544	525	3.719	0.001
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	R.SALQHAASIAGLMITTEAMIGEIKEAAAGNK.K	SALQHAASIAGLMITTEAMIGEIKEAA	544	528	3.673	0.001
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	E.AAPAAGNKKENR.V	AAPA	544	530	4.225	0.009
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	E.AAPAAGNKKE.N	AAPA	544	530	3.475	0.000

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

splP94798lCH60_FRATH	60 kDa chaperonin groL	R.SALQHAASIAGLMITTEAMIGEIKEAAPAAGNK.K	SALQHAASIAGLMITTEAMIGEIKEAAPA	544	530	3.868	0.000
splP94798lCH60_FRATH	60 kDa chaperonin groL	E.AAPAMPAGNKKE.N	AAPAMP	544	532	4.124	0.000
splP94798lCH60_FRATH	60 kDa chaperonin groL	E.AAPAMPAGNKK.E	AAPAMP	544	532	3.333	0.000
splP94798lCH60_FRATH	60 kDa chaperonin groL	E.AAPAM+16PAGNKKE.N	AAPAMP	544	532	2.84	0.000
splP94798lCH60_FRATH	60 kDa chaperonin groL	E.AAPAMPAGNK.K	AAPAMP	544	532	2.022	0.005
splP94798lCH60_FRATH	60 kDa chaperonin groL	K.EAAPAMPAGNKK.E	EAAPAMP	544	532	3.85	0.001
splP94798lCH60_FRATH	60 kDa chaperonin groL	E.AAPAMPMAGNKKE.N	AAPAMPM	544	533	4.227	0.000
splP94798lCH60_FRATH	60 kDa chaperonin groL	E.AAPAMPMAGNKK.E	AAPAMPM	544	533	3.632	0.000
splP94798lCH60_FRATH	60 kDa chaperonin groL	E.AAPAM+16PMAGNKKE.N	AAPAMPM	544	533	3.594	0.001
splP94798lCH60_FRATH	60 kDa chaperonin groL	E.AAPAMPM+16AGNKKE.N	AAPAMPM	544	533	3.594	0.000
splP94798lCH60_FRATH	60 kDa chaperonin groL	E.AAPAMPM+16AGNK.K	AAPAMPM	544	533	2.749	0.002
splP94798lCH60_FRATH	60 kDa chaperonin groL	*.EAAPAMPMAGNKK.E	EAAPAMPM	544	533	4.052	0.000
splP94798lCH60_FRATH	60 kDa chaperonin groL	*.EAAPAM+16PM+16AGNK.K	EAAPAMPM	544	533	3.268	0.000
splP94798lCH60_FRATH	60 kDa chaperonin groL	E.AAPAMPMGAGNKKE.N	AAPAMPMG	544	534	4.229	0.000
splP94798lCH60_FRATH	60 kDa chaperonin groL	E.AAPAMPMGAGNKK.E	AAPAMPMG	544	534	4.026	0.000
splP94798lCH60_FRATH	60 kDa chaperonin groL	E.AAPAMPM+16GAGNKKE.N	AAPAMPMG	544	534	3.658	0.000
splP94798lCH60_FRATH	60 kDa chaperonin groL	E.AAPAM+16PM+16GAGNK.K	AAPAMPMG	544	534	3.48	0.000
splP94798lCH60_FRATH	60 kDa chaperonin groL	E.AAPAM+16PMGAGNKKE.N	AAPAMPMG	544	534	3.48	0.000
splP94798lCH60_FRATH	60 kDa chaperonin groL	E.AAPAMPMGAGNK.K	AAPAMPMG	544	534	3.355	0.000
splP94798lCH60_FRATH	60 kDa chaperonin groL	E.AAPAMPM+16GAGNK.K	AAPAMPMG	544	534	2.941	0.001
splP94798lCH60_FRATH	60 kDa chaperonin groL	E.AAPAM+16PM+16GAGNKKE.N	AAPAMPMG	544	534	2.282	0.000
splP94798lCH60_FRATH	60 kDa chaperonin groL	*.EAAPAMPMGAGNKK.E	EAAPAMPMG	544	534	4.019	0.000
splP94798lCH60_FRATH	60 kDa chaperonin groL	*.EAAPAM+16PM+16GAGNK.K	EAAPAMPMG	544	534	3.523	0.004
splP94798lCH60_FRATH	60 kDa chaperonin groL	*.EAAPAMPM+16GAGNK.K	EAAPAMPMG	544	534	2.554	0.001
splP94798lCH60_FRATH	60 kDa chaperonin groL	*.EAAPAMPM+16GAGNKK.E	EAAPAMPMG	544	534	2.272	0.000
splP94798lCH60_FRATH	60 kDa chaperonin groL	*.EAAPAM+16PM+16GAGNKK.E	EAAPAMPMG	544	534	2.27	0.000
splP94798lCH60_FRATH	60 kDa chaperonin groL	E.AAPAMPMGGAGNKKE.N	AAPAMPMGG	544	535	4.398	0.001
splP94798lCH60_FRATH	60 kDa chaperonin groL	E.AAPAMPMGGAGNKK.E	AAPAMPMGG	544	535	4.313	0.000
splP94798lCH60_FRATH	60 kDa chaperonin groL	E.AAPAMPM+16GGAGNK.K	AAPAMPMGG	544	535	3.88	0.000
splP94798lCH60_FRATH	60 kDa chaperonin groL	E.AAPAMPM+16GGAGNKKE.N	AAPAMPMGG	544	535	3.616	0.001
splP94798lCH60_FRATH	60 kDa chaperonin groL	E.AAPAM+16PMGGAGNK.K	AAPAMPMGG	544	535	3.601	0.000
splP94798lCH60_FRATH	60 kDa chaperonin groL	E.AAPAM+16PM+16GGAGNK.K	AAPAMPMGG	544	535	3.55	0.000
splP94798lCH60_FRATH	60 kDa chaperonin groL	E.AAPAM+16PMGGAGNKKE.N	AAPAMPMGG	544	535	3.477	0.001

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

sp|P94798|CH60_FRATH	60 kDa chaperonin groL	E.AAPAM+16PMGGAGNKK.E	AAPAMPMGG	544	535	2.651	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	E.AAPAM+16PM+16GGAGNKKE.N	AAPAMPMGG	544	535	2.238	0.003
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	*.EAAPAMPM+16GGAGNK.K	EAAPAMPMGG	544	535	3.753	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	*.EAAPAMPMGGAGNKK.E	EAAPAMPMGG	544	535	3.75	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	*.EAAPAMPMGGAGNK.K	EAAPAMPMGG	544	535	3.615	0.005
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	*.EAAPAM+16PMGGAGNKK.E	EAAPAMPMGG	544	535	2.673	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	*.EAAPAM+16PM+16GGAGNK.K	EAAPAMPMGG	544	535	2.596	0.002
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	*.EAAPAMPM+16GGAGNKK.E	EAAPAMPMGG	544	535	2.513	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	E.AAPAMPMGGGAGNKK.E	AAPAMPMGGG	544	536	4.339	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	E.AAPAMPMGGGAGNKKE.N	AAPAMPMGGG	544	536	4.264	0.009
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	E.AAPAM+16PMGGGAGNK.K	AAPAMPMGGG	544	536	3.977	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	E.AAPAMPM+16GGGAGNK.K	AAPAMPMGGG	544	536	3.855	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	E.AAPAM+16PMGGGAGNKKE.N	AAPAMPMGGG	544	536	3.453	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	E.AAPAMPM+16GGGAGNKKE.N	AAPAMPMGGG	544	536	3.368	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	E.AAPAM+16PM+16GGGAGNK.K	AAPAMPMGGG	544	536	3.248	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	E.AAPAMPM+16GGGAGNKK.E	AAPAMPMGGG	544	536	2.99	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	*.EAAPAMPMGGGAGNKK.E	EAAPAMPMGGG	544	536	4.083	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	*.EAAPAM+16PM+16GGGAGNK.K	EAAPAMPMGGG	544	536	3.608	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	*.EAAPAMPM+16GGGAGNKK.E	EAAPAMPMGGG	544	536	2.289	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	E.AAPAMPMGGGMAGNKKE.N	AAPAMPMGGGM	544	537	4.539	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	E.AAPAMPMGGGMAGNKK.E	AAPAMPMGGGM	544	537	3.961	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	E.AAPAMPMGGGM+16AGNKKE.N	AAPAMPMGGGM	544	537	3.814	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	E.AAPAMPM+16GGGMAGNK.K	AAPAMPMGGGM	544	537	3.332	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	E.AAPAMPMGGGMAGNK.K	AAPAMPMGGGM	544	537	3.327	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	E.AAPAM+16PM+16GGGMAGNK.K	AAPAMPMGGGM	544	537	2.777	0.003
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	E.AAPAMPM+16GGGM+16AGNK.K	AAPAMPMGGGM	544	537	2.741	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	E.AAPAM+16PMGGGMAGNK.K	AAPAMPMGGGM	544	537	2.616	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	E.AAPAMPMGGGM+16AGNK.K	AAPAMPMGGGM	544	537	2.499	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	E.AAPAMPMGGGM+16AGNKK.E	AAPAMPMGGGM	544	537	2.368	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	*.EAAPAMPMGGGMAGNKK.E	EAAPAMPMGGGM	544	537	3.399	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	E.AAPAMPMGGGMGAGNKKE.N	AAPAMPMGGGMG	544	538	4.552	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	E.AAPAMPMGGGMGAGNKK.E	AAPAMPMGGGMG	544	538	4.361	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	E.AAPAMPMGGGMGAGNK.K	AAPAMPMGGGMG	544	538	4.139	0.000

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

splP94798lCH60_FRATH	60 kDa chaperonin groL	E.AAPAM+16PMGGGMGAGNKKE.N	AAPAMPMGGGMG	544	538	3.504	0.000
splP94798lCH60_FRATH	60 kDa chaperonin groL	E.AAPAMPM+16GGGMGAGNKKE.N	AAPAMPMGGGMG	544	538	3.367	0.000
splP94798lCH60_FRATH	60 kDa chaperonin groL	E.AAPAM+16PM+16GGGMGAGNK.K	AAPAMPMGGGMG	544	538	3.291	0.000
splP94798lCH60_FRATH	60 kDa chaperonin groL	E.AAPAMPM+16GGGMGAGNKK.E	AAPAMPMGGGMG	544	538	3.137	0.000
splP94798lCH60_FRATH	60 kDa chaperonin groL	E.AAPAMPM+16GGGMGAGNK.K	AAPAMPMGGGMG	544	538	2.711	0.000
splP94798lCH60_FRATH	60 kDa chaperonin groL	E.AAPAMPMGGGM+16GAGNK.K	AAPAMPMGGGMG	544	538	2.63	0.000
splP94798lCH60_FRATH	60 kDa chaperonin groL	E.AAPAMPMGGGM+16GAGNKKE.N	AAPAMPMGGGMG	544	538	2.415	0.000
splP94798lCH60_FRATH	60 kDa chaperonin groL	E.AAPAM+16PMGGGMGAGNK.K	AAPAMPMGGGMG	544	538	2.19	0.009
splP94798lCH60_FRATH	60 kDa chaperonin groL	E.AAPAM+16PMGGGMGAGNKK.E	AAPAMPMGGGMG	544	538	2.049	0.003
splP94798lCH60_FRATH	60 kDa chaperonin groL	*.EAAPAMPMGGGMGAGNKK.E	EAAPAMPMGGGMG	544	538	4.027	0.000
splP94798lCH60_FRATH	60 kDa chaperonin groL	*.EAAPAM+16PMGGGMGAGNK.K	EAAPAMPMGGGMG	544	538	3.908	0.000
splP94798lCH60_FRATH	60 kDa chaperonin groL	*.EAAPAM+16PM+16GGGMGAGNK.K	EAAPAMPMGGGMG	544	538	3.57	0.000
splP94798lCH60_FRATH	60 kDa chaperonin groL	*.EAAPAMPMGGGMGAGNK.K	EAAPAMPMGGGMG	544	538	3.56	0.000
splP94798lCH60_FRATH	60 kDa chaperonin groL	*.EAAPAMPM+16GGGM+16GAGNK.K	EAAPAMPMGGGMG	544	538	2.499	0.002
splP94798lCH60_FRATH	60 kDa chaperonin groL	E.AAPAMPMGGGMGGAGNKKE.N	AAPAMPMGGGMGG	544	539	4.527	0.004
splP94798lCH60_FRATH	60 kDa chaperonin groL	E.AAPAMPMGGGMGGAGNKK.E	AAPAMPMGGGMGG	544	539	4.346	0.000
splP94798lCH60_FRATH	60 kDa chaperonin groL	E.AAPAMPMGGGMGGAGNK.K	AAPAMPMGGGMGG	544	539	4.208	0.000
splP94798lCH60_FRATH	60 kDa chaperonin groL	E.AAPAMPMGGGM+16GGAGNKKE.N	AAPAMPMGGGMGG	544	539	4.148	0.000
splP94798lCH60_FRATH	60 kDa chaperonin groL	E.AAPAM+16PM+16GGGMGGAGNK.K	AAPAMPMGGGMGG	544	539	3.946	0.000
splP94798lCH60_FRATH	60 kDa chaperonin groL	E.AAPAMPMGGGM+16GGAGNK.K	AAPAMPMGGGMGG	544	539	3.694	0.000
splP94798lCH60_FRATH	60 kDa chaperonin groL	E.AAPAM+16PMGGGM+16GGAGNK.K	AAPAMPMGGGMGG	544	539	3.663	0.000
splP94798lCH60_FRATH	60 kDa chaperonin groL	E.AAPAM+16PMGGGMGGAGNK.K	AAPAMPMGGGMGG	544	539	3.623	0.000
splP94798lCH60_FRATH	60 kDa chaperonin groL	E.AAPAM+16PMGGGMGGAGNKK.E	AAPAMPMGGGMGG	544	539	2.793	0.000
splP94798lCH60_FRATH	60 kDa chaperonin groL	E.AAPAMPM+16GGGMGGAGNK.K	AAPAMPMGGGMGG	544	539	2.707	0.000
splP94798lCH60_FRATH	60 kDa chaperonin groL	E.AAPAMPMGGGM+16GGAGNKK.E	AAPAMPMGGGMGG	544	539	2.704	0.000
splP94798lCH60_FRATH	60 kDa chaperonin groL	E.AAPAMPM+16GGGM+16GGAGNK.K	AAPAMPMGGGMGG	544	539	2.349	0.000
splP94798lCH60_FRATH	60 kDa chaperonin groL	E.AAPAM+16PMGGGM+16GGAGNKKE.N	AAPAMPMGGGMGG	544	539	2.238	0.001
splP94798lCH60_FRATH	60 kDa chaperonin groL	*.EAAPAMPMGGGMGGAGNKK.E	EAAPAMPMGGGMGG	544	539	4.386	0.000
splP94798lCH60_FRATH	60 kDa chaperonin groL	*.EAAPAMPM+16GGGMGGAGNK.K	EAAPAMPMGGGMGG	544	539	4.003	0.000
splP94798lCH60_FRATH	60 kDa chaperonin groL	*.EAAPAM+16PM+16GGGMGGAGNK.K	EAAPAMPMGGGMGG	544	539	3.901	0.000
splP94798lCH60_FRATH	60 kDa chaperonin groL	*.EAAPAMPM+16GGGM+16GGAGNK.K	EAAPAMPMGGGMGG	544	539	3.829	0.000
splP94798lCH60_FRATH	60 kDa chaperonin groL	E.AAPAMPMGGGMGGMAGNKK.E	AAPAMPMGGGMGGM	544	540	4.597	0.000
splP94798lCH60_FRATH	60 kDa chaperonin groL	E.AAPAMPMGGGMGGMAGNKKE.N	AAPAMPMGGGMGGM	544	540	4.571	0.000

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

sp|P94798|CH60_FRATH	60 kDa chaperonin groL	E.AAPAMPMGGGM+16GGMAGNKK.E	AAPAMPMGGGMGGM	544	540	3.898	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	E.AAPAMPMGGGMGGMAGNK.K	AAPAMPMGGGMGGM	544	540	3.553	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	E.AAPAMPMGGGMGGM+16AGNKKE.N	AAPAMPMGGGMGGM	544	540	3.376	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	E.AAPAMPMGGGM+16GGMAGNKKE.N	AAPAMPMGGGMGGM	544	540	2.977	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	E.AAPAMPMGGGM+16GGMAGNK.K	AAPAMPMGGGMGGM	544	540	2.7	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	E.AAPAM+16PMGGGM+16GGMAGNK.K	AAPAMPMGGGMGGM	544	540	2.213	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	*.EAAPAMPMGGGMGGMAGNK.K	EAAPAMPMGGGMGGM	544	540	4.316	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	*.EAAPAM+16PMGGGM+16GGMAGNK.K	EAAPAMPMGGGMGGM	544	540	2.749	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	E.AAPAMPMGGGMGGMPAGNKK.E	AAPAMPMGGGMGGMP	544	541	4.586	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	E.AAPAMPMGGGMGGMPAGNKKE.N	AAPAMPMGGGMGGMP	544	541	4.377	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	E.AAPAMPMGGGMGGMPAGNK.K	AAPAMPMGGGMGGMP	544	541	4.297	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	E.AAPAMPM+16GGGMGGMPAGNK.K	AAPAMPMGGGMGGMP	544	541	3.181	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	E.AAPAM+16PMGGGMGGMPAGNKK.E	AAPAMPMGGGMGGMP	544	541	2.678	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	*.EAAPAMPMGGGMGGMPAGNKK.E	EAAPAMPMGGGMGGMP	544	541	4.564	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	*.EAAPAMPMGGGMGGMPAGNK.K	EAAPAMPMGGGMGGMP	544	541	3.383	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	*.EAAPAMPMGGGM+16GGMPAGNKK.E	EAAPAMPMGGGMGGMP	544	541	3.163	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	*.EAAPAMPMGGGMGGM+16PAGNKK.E	EAAPAMPMGGGMGGMP	544	541	2.925	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	*.EAAPAMPMGGGM+16GGMPAGNK.K	EAAPAMPMGGGMGGMP	544	541	2.886	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	E.AAPAMPMGGGMGGMPGAGNKK.E	AAPAMPMGGGMGGMPG	544	542	4.131	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	*.EAAPAMPMGGGMGGMPGAGNK.K	EAAPAMPMGGGMGGMPG	544	542	4.525	0.000
sp|P94798|CH60_FRATH	60 kDa chaperonin groL	*.EAAPAMPMGGGM+16GGMPGAGNK.K	EAAPAMPMGGGMGGMPG	544	542	3.26	0.000
sp|Q2A1K3|ACON_FRATH	Aconitate hydratase acn	K.AFAEALVHEQGLHGFGLTDEQAGNK.K	AFAEALVHEQGLHGFGLTDEQ	937	412	3.539	0.002
sp|Q2A1K3|ACON_FRATH	Aconitate hydratase acn	E.IAAIQSHVAGNK.K	IAAIQSHV	937	605	4.165	0.000
sp|Q2A1K3|ACON_FRATH	Aconitate hydratase acn	E.IAAIQSHVIAGNK.K	IAAIQSHVI	937	606	4.222	0.000
sp|Q2A1K3|ACON_FRATH	Aconitate hydratase acn	E.IAAIQSHVIAGNKKE.N	IAAIQSHVI	937	606	3.407	0.000
sp|Q2A1K3|ACON_FRATH	Aconitate hydratase acn	E.IAAIQSHVINAGNK.K	IAAIQSHVIN	937	607	4.061	0.000
sp|Q2A1K3|ACON_FRATH	Aconitate hydratase acn	E.IAAIQSHVINSAGNK.K	IAAIQSHVINS	937	608	4.375	0.000
sp|Q2A1K3|ACON_FRATH	Aconitate hydratase acn	E.IAAIQSHVINSAGNKKE.N	IAAIQSHVINS	937	608	3.388	0.000
sp|Q2A1K3|ACON_FRATH	Aconitate hydratase acn	E.IAAIQSHVINSDAGNK.K	IAAIQSHVINSD	937	609	4.339	0.000
sp|Q2A1K3|ACON_FRATH	Aconitate hydratase acn	E.IAAIQSHVINSDAGNKKE.N	IAAIQSHVINSD	937	609	3.123	0.000
sp|Q2A1M0|EFTU_FRATH	Elongation factor Tu tuf	R.KFDEIDSAAGNKK.E	KFDEIDSA	394	53	3.636	0.008
sp|Q2A1M0|EFTU_FRATH	Elongation factor Tu tuf	R.KFDEIDSAPEEAGNK.K	KFDEIDSAPEE	394	56	2.885	0.002
sp|Q2A1M0|EFTU_FRATH	Elongation factor Tu tuf	E.IDSAPEEKARGITINTSAGNKKE.N	IDSAPEEKARGITINTS	394	66	2.499	0.000

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

splQ2A1M0lEFTU_FRATH	Elongation factor Tu tuf	R.GITINTSHAGNK.K	GITINTSH	394	67	3.017	0.000
splQ2A1M0lEFTU_FRATH	Elongation factor Tu tuf	R.GITINTSHVAGNK.K	GITINTSHV	394	68	4.062	0.000
splQ2A1M0lEFTU_FRATH	Elongation factor Tu tuf	R.GITINTSHVAGNKK.E	GITINTSHV	394	68	2.985	0.002
splQ2A1M0lEFTU_FRATH	Elongation factor Tu tuf	R.HYAHVDC+57PGHADAGNKK.E	HYAHVDCPGHAD	394	87	3.035	0.000
splQ2A1M0lEFTU_FRATH	Elongation factor Tu tuf	K.IVELVQAAGNKK.E	IVELVQA	394	195	4.019	0.001
splQ2A1M0lEFTU_FRATH	Elongation factor Tu tuf	K.IVELVQAMDDYIAGNKK.E	IVELVQAMDDYI	394	200	3.202	0.002
splQ2A1M0lEFTU_FRATH	Elongation factor Tu tuf	K.IVELVQAMDDYIPAGNKK.E	IVELVQAMDDYIP	394	201	4.26	0.000
splQ2A1M0lEFTU_FRATH	Elongation factor Tu tuf	E.LVQAMDDYIPAGNKKE.N	LVQAMDDYIP	394	201	4.164	0.000
splQ2A1M0lEFTU_FRATH	Elongation factor Tu tuf	K.IVELVQAMDDYIPAPAGNK.K	IVELVQAMDDYIPAP	394	203	4.352	0.000
splQ2A1M0lEFTU_FRATH	Elongation factor Tu tuf	E.LVQAMDDYIPAPAGNK.K	LVQAMDDYIPAP	394	203	4.076	0.000
splQ2A1M0lEFTU_FRATH	Elongation factor Tu tuf	E.LVQAMDDYIPAPAGNKKENR.V	LVQAMDDYIPAP	394	203	2.94	0.007
splQ2A1M0lEFTU_FRATH	Elongation factor Tu tuf	E.LVQAM+16DDYIPAPAGNK.K	LVQAMDDYIPAP	394	203	2.403	0.000
splQ2A1M0lEFTU_FRATH	Elongation factor Tu tuf	E.LVQAMDDYIPAPERDTEKAGNKKENR.V	LVQAMDDYIPAPERDTEK	394	209	3.577	0.000
splQ2A1M0lEFTU_FRATH	Elongation factor Tu tuf	E.LVQAMDDYIPAPERDTEKAGNKKE.N	LVQAMDDYIPAPERDTEK	394	209	2.667	0.001
splQ2A1M0lEFTU_FRATH	Elongation factor Tu tuf	E.LVQAMDDYIPAPERDTEKPAGNKKE.N	LVQAMDDYIPAPERDTEKP	394	210	2.429	0.000
splQ2A1M0lEFTU_FRATH	Elongation factor Tu tuf	E.LVQAMDDYIPAPERDTEKPFAGNKK.E	LVQAMDDYIPAPERDTEKPF	394	211	2.822	0.000
splQ2A1M0lEFTU_FRATH	Elongation factor Tu tuf	E.LVQAMDDYIPAPERDTEKPFAGNKKE.N	LVQAMDDYIPAPERDTEKPF	394	211	2.68	0.000
splQ2A1M0lEFTU_FRATH	Elongation factor Tu tuf	R.DTEKPFIAGNKK.E	DTEKPFI	394	212	3.946	0.000
splQ2A1M0lEFTU_FRATH	Elongation factor Tu tuf	E.LVQAMDDYIPAPERDTEKPFIAGNKK.E	LVQAMDDYIPAPERDTEKPFI	394	212	3.343	0.000
splQ2A1M0lEFTU_FRATH	Elongation factor Tu tuf	E.RDTEKPFIAGNKKE.N	RDTEKPFI	394	212	4.16	0.001
splQ2A1M0lEFTU_FRATH	Elongation factor Tu tuf	E.RDTEKPFIAGNK.K	RDTEKPFI	394	212	3.637	0.001
splQ2A1M0lEFTU_FRATH	Elongation factor Tu tuf	R.DTEKPFILAGNK.K	DTEKPFIL	394	213	4.103	0.000
splQ2A1M0lEFTU_FRATH	Elongation factor Tu tuf	R.DTEKPFILAGNKK.E	DTEKPFIL	394	213	4.094	0.000
splQ2A1M0lEFTU_FRATH	Elongation factor Tu tuf	K.IVELVQAMDDYIPAPERDTEKPFILAGNKK.E	IVELVQAMDDYIPAPERDTEKPFIL	394	213	2.934	0.000
splQ2A1M0lEFTU_FRATH	Elongation factor Tu tuf	E.LVQAMDDYIPAPERDTEKPFILAGNKK.E	LVQAMDDYIPAPERDTEKPFIL	394	213	2.886	0.000
splQ2A1M0lEFTU_FRATH	Elongation factor Tu tuf	E.RDTEKPFILAGNK.K	RDTEKPFIL	394	213	3.97	0.000
splQ2A1M0lEFTU_FRATH	Elongation factor Tu tuf	E.RDTEKPFILAGNKKE.N	RDTEKPFIL	394	213	3.949	0.000
splQ2A1M0lEFTU_FRATH	Elongation factor Tu tuf	R.DTEKPFILPAGNKK.E	DTEKPFILP	394	214	4.303	0.000
splQ2A1M0lEFTU_FRATH	Elongation factor Tu tuf	R.DTEKPFILPAGNK.K	DTEKPFILP	394	214	3.299	0.000
splQ2A1M0lEFTU_FRATH	Elongation factor Tu tuf	E.RDTEKPFILPAGNK.K	RDTEKPFILP	394	214	3.803	0.000
splQ2A1M0lEFTU_FRATH	Elongation factor Tu tuf	R.DTEKPFILPIAGNK.K	DTEKPFILPI	394	215	4.267	0.000
splQ2A1M0lEFTU_FRATH	Elongation factor Tu tuf	R.DTEKPFILPIEDAGNKK.E	DTEKPFILPIED	394	217	3.306	0.003
splQ2A1M0lEFTU_FRATH	Elongation factor Tu tuf	E.LVQAMDDYIPAPERDTEKPFILPIEDAGNKKE.N	LVQAMDDYIPAPERDTEKPFILPIED	394	217	2.37	0.000

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

sp|Q2A1M0|EFTU_FRATH	Elongation factor Tu tuf	R.DTEKPFILPIEDVAGNKK.E	DTEKPFILPIEDV	394	218	4.36	0.000
sp|Q2A1M0|EFTU_FRATH	Elongation factor Tu tuf	E.LVQAMDDYIPAPERDTEKPFILPIEDVAGNKKE.N	LVQAMDDYIPAPERDTEKPFILPIEDV	394	218	3.696	0.000
sp|Q2A1M0|EFTU_FRATH	Elongation factor Tu tuf	E.RDTEKPFILPIEDVAGNKKE.N	RDTEKPFILPIEDV	394	218	3.051	0.000
sp|Q2A1M0|EFTU_FRATH	Elongation factor Tu tuf	R.DTEKPFILPIEDVFAGNKK.E	DTEKPFILPIEDVF	394	219	4.295	0.000
sp|Q2A1M0|EFTU_FRATH	Elongation factor Tu tuf	R.DTEKPFILPIEDVFAGNK.K	DTEKPFILPIEDVF	394	219	4.196	0.000
sp|Q2A1M0|EFTU_FRATH	Elongation factor Tu tuf	E.LVQAMDDYIPAPERDTEKPFILPIEDVFAGNKKE.N	LVQAMDDYIPAPERDTEKPFILPIEDVF	394	219	3.454	0.000
sp|Q2A1M0|EFTU_FRATH	Elongation factor Tu tuf	E.RDTEKPFILPIEDVFAGNK.K	RDTEKPFILPIEDVF	394	219	3.421	0.000
sp|Q2A1M0|EFTU_FRATH	Elongation factor Tu tuf	R.DTEKPFILPIEDVFSAGNKK.E	DTEKPFILPIEDVFS	394	220	3.831	0.000
sp|Q2A1M0|EFTU_FRATH	Elongation factor Tu tuf	R.DTEKPFILPIEDVFSIAGNK.K	DTEKPFILPIEDVFSI	394	221	4.523	0.000
sp|Q2A1M0|EFTU_FRATH	Elongation factor Tu tuf	R.DTEKPFILPIEDVFSIAGNKK.E	DTEKPFILPIEDVFSI	394	221	4.403	0.000
sp|Q2A1M0|EFTU_FRATH	Elongation factor Tu tuf	R.DTEKPFILPIEDVFSISAGNKK.E	DTEKPFILPIEDVFSIS	394	222	3.081	0.000
sp|Q2A1M0|EFTU_FRATH	Elongation factor Tu tuf	R.DTEKPFILPIEDVFSISAGNK.K	DTEKPFILPIEDVFSIS	394	222	2.68	0.001
sp|Q2A1M0|EFTU_FRATH	Elongation factor Tu tuf	R.DTEKPFILPIEDVFSISGAGNKK.E	DTEKPFILPIEDVFSISG	394	223	3.523	0.000
sp|Q2A1M0|EFTU_FRATH	Elongation factor Tu tuf	R.DTEKPFILPIEDVFSISGAGNK.K	DTEKPFILPIEDVFSISG	394	223	3.272	0.000
sp|Q2A1M0|EFTU_FRATH	Elongation factor Tu tuf	E.RGVVNVGDEAGNKK.E	RGVVNVGDE	394	242	3.257	0.008
sp|Q2A1M0|EFTU_FRATH	Elongation factor Tu tuf	R.GVVNVGDEVAGNKK.E	GVVNVGDEV	394	243	4.127	0.003
sp|Q2A1M0|EFTU_FRATH	Elongation factor Tu tuf	*.RGVVNVGDEVAGNKKE.N	RGVVNVGDEV	394	243	4.11	0.000
sp|Q2A1M0|EFTU_FRATH	Elongation factor Tu tuf	R.GVVNVGDEVEVVGAGNKK.E	GVVNVGDEVEVVG	394	247	3.474	0.000
sp|Q2A1M0|EFTU_FRATH	Elongation factor Tu tuf	E.VVGIRPTAGNK.K	VVGIRPT	394	251	3.508	0.004
sp|Q2A1M0|EFTU_FRATH	Elongation factor Tu tuf	E.VVGIRPTQAGNK.K	VVGIRPTQ	394	252	3.946	0.008
sp|Q2A1M0|EFTU_FRATH	Elongation factor Tu tuf	R.KLLDRGEAGAGNKK.E	KLLDRGEAG	394	272	3.834	0.003
sp|Q2A1M0|EFTU_FRATH	Elongation factor Tu tuf	K.LLDRGEAGAGNKK.E	LLDRGEAG	394	272	3.347	0.003
sp|Q2A1M0|EFTU_FRATH	Elongation factor Tu tuf	R.KLLDRGEAGDAGNKK.E	KLLDRGEAGD	394	273	3.957	0.000
sp|Q2A1M0|EFTU_FRATH	Elongation factor Tu tuf	R.KLLDRGEAGDNVGIAGNKK.E	KLLDRGEAGDNVGI	394	277	3.159	0.000
sp|Q2A1M0|EFTU_FRATH	Elongation factor Tu tuf	R.GQVLC+57KPAGNKK.E	GQVLCKP	394	296	3.243	0.000
sp|Q2A1M0|EFTU_FRATH	Elongation factor Tu tuf	R.GQVLC+57KPGAGNK.K	GQVLCKPG	394	297	3.336	0.000
sp|Q2A1M0|EFTU_FRATH	Elongation factor Tu tuf	R.GQVLC+57KPGSAGNK.K	GQVLCKPGS	394	298	3.681	0.000
sp|Q2A1M0|EFTU_FRATH	Elongation factor Tu tuf	R.GQVLC+57KPGSAGNKK.E	GQVLCKPGS	394	298	3.243	0.001
sp|Q2A1M0|EFTU_FRATH	Elongation factor Tu tuf	R.GQVLC+57KPGSIAGNKK.E	GQVLCKPGSI	394	299	3.555	0.003
sp|Q2A1M0|EFTU_FRATH	Elongation factor Tu tuf	R.GQVLC+57KPGSIAGNK.K	GQVLCKPGSI	394	299	2.917	0.006
sp|Q2A1M3|RL11_FRATH	50S ribosomal protein L1	E.MKTPPASAGNKKE.N	MKTPPAS	144	78	2.081	0.001
sp|Q2A1M3|RL11_FRATH	50S ribosomal protein L1	E.MKTPPASYAGNKKE.N	MKTPPASY	144	79	3.919	0.000
sp|Q2A1M3|RL11_FRATH	50S ribosomal protein L1	E.M+16KTPPASYAGNKKE.N	MKTPPASY	144	79	3.35	0.001

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

sp|Q2A1M3|RL11_FRATH	50S ribosomal protein L1	K.TPPASYAGNKK.E	TPPASY	144	79	3.766	0.003
sp|Q2A1M3|RL11_FRATH	50S ribosomal protein L1	K.TPPASYLAGNK.K	TPPASYL	144	80	3.582	0.000
sp|Q2A1M3|RL11_FRATH	50S ribosomal protein L1	K.TPPASYLAGNKK.E	TPPASYL	144	80	2.012	0.001
sp|Q2A1M3|RL11_FRATH	50S ribosomal protein L1	E.IAKVKDPAGNKKE.N	IAKVKDP	144	116	2.149	0.000
sp|Q2A1M3|RL11_FRATH	50S ribosomal protein L1	E.IAKVKDPDLAGNKKE.N	IAKVKDPDL	144	118	3.565	0.000
sp|Q2A1M3|RL11_FRATH	50S ribosomal protein L1	E.IAKVKDPDLTAAAGNKKE.N	IAKVKDPDLTAA	144	121	3.485	0.000
sp|Q2A1M3|RL11_FRATH	50S ribosomal protein L1	E.IAKVKDPDLTAADAGNKKE.N	IAKVKDPDLTAAD	144	122	2.94	0.003
sp|Q2A1M4|RL1_FRATH	50S ribosomal protein L1	D.FDVVAGNKKE.N	FDVV	232	115	4.055	0.001
sp|Q2A1M5|RL10_FRATH	50S ribosomal protein L1	E.ALATLLNAGNKKE.N	ALATLLN	172	141	3.834	0.001
sp|Q2A1M5|RL10_FRATH	50S ribosomal protein L1	E.ALATLLNIMQAAGNKKE.N	ALATLLNIMQA	172	145	4.296	0.000
sp|Q2A1M5|RL10_FRATH	50S ribosomal protein L1	E.ALATLLNIMQAAGNK.K	ALATLLNIMQA	172	145	2.422	0.001
sp|Q2A1M5|RL10_FRATH	50S ribosomal protein L1	R.EEALATLLNIMQAPVTAGNKK.E	EEALATLLNIMQAPVT	172	148	2.596	0.001
sp|Q2A1M5|RL10_FRATH	50S ribosomal protein L1	R.TLNEIPSQAGNKK.E	TLNEIPSQ	172	160	4.016	0.000
sp|Q2A1M5|RL10_FRATH	50S ribosomal protein L1	R.TLNEIPSQAAGNKK.E	TLNEIPSQA	172	161	3.555	0.002
sp|Q2A1M5|RL10_FRATH	50S ribosomal protein L1	R.TLNEIPSQAAGNK.K	TLNEIPSQA	172	161	3.474	0.008
sp|Q2A1M5|RL10_FRATH	50S ribosomal protein L1	E.IPSQAVAGNKKE.N	IPSQAV	172	162	3.975	0.009
sp|Q2A1M5|RL10_FRATH	50S ribosomal protein L1	R.TLNEIPSQAVAGNKK.E	TLNEIPSQAV	172	162	4.302	0.000
sp|Q2A1M5|RL10_FRATH	50S ribosomal protein L1	R.TLNEIPSQAVAGNK.K	TLNEIPSQAV	172	162	4.165	0.000
sp|Q2A1M5|RL10_FRATH	50S ribosomal protein L1	R.VFAAVGDAGNKK.E	VFAAVGD	172	170	3.902	0.004
sp|Q2A1M5|RL10_FRATH	50S ribosomal protein L1	R.VFAAVGDSKAGNK.K	VFAAVGDSK	172	172	3.418	0.000
sp|Q2A1M6|RL7_FRATH	50S ribosomal protein L7	E.DKFGVSAAGNKKE.N	DKFGVSA	125	35	4.247	0.000
sp|Q2A1M6|RL7_FRATH	50S ribosomal protein L7	K.FGVSAAGNK.K	FGVSA	125	35	2.912	0.009
sp|Q2A1M6|RL7_FRATH	50S ribosomal protein L7	E.DKFGVSAAAAGNKKE.N	DKFGVSAAA	125	37	4.313	0.001
sp|Q2A1M6|RL7_FRATH	50S ribosomal protein L7	K.FGVSAAAAGNK.K	FGVSAAA	125	37	4.11	0.002
sp|Q2A1M6|RL7_FRATH	50S ribosomal protein L7	K.FGVSAAAAGNKK.E	FGVSAAA	125	37	3.416	0.000
sp|Q2A1M6|RL7_FRATH	50S ribosomal protein L7	E.DKFGVSAAAAAGNKKE.N	DKFGVSAAAA	125	38	4.398	0.000
sp|Q2A1M6|RL7_FRATH	50S ribosomal protein L7	K.FGVSAAAAAGNK.K	FGVSAAAA	125	38	3.938	0.005
sp|Q2A1M6|RL7_FRATH	50S ribosomal protein L7	K.FGVSAAAAAGNKK.E	FGVSAAAA	125	38	3.581	0.000
sp|Q2A1M6|RL7_FRATH	50S ribosomal protein L7	*.DKFGVSAAAAVAGNKKE.N	DKFGVSAAAAV	125	39	4.08	0.006
sp|Q2A1M6|RL7_FRATH	50S ribosomal protein L7	K.FGVSAAAAVAGNK.K	FGVSAAAAV	125	39	4.43	0.004
sp|Q2A1M6|RL7_FRATH	50S ribosomal protein L7	K.FGVSAAAAVAGNKK.E	FGVSAAAAV	125	39	4.386	0.001
sp|Q2A1M6|RL7_FRATH	50S ribosomal protein L7	D.KFGVSAAAAVAGNKK.E	KFGVSAAAAV	125	39	3.363	0.001
sp|Q2A1M6|RL7_FRATH	50S ribosomal protein L7	E.DKFGVSAAAAVAAGNKKE.N	DKFGVSAAAAVA	125	40	4.076	0.000

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

sp|Q2A1M6|RL7_FRATH	50S ribosomal protein L7	K.FGVSAAAAVAAGNKK.E	FGVSAAAAVA	125	40	4.458	0.000
sp|Q2A1M6|RL7_FRATH	50S ribosomal protein L7	K.FGVSAAAAVAAGNK.K	FGVSAAAAVA	125	40	4.397	0.000
sp|Q2A1M6|RL7_FRATH	50S ribosomal protein L7	E.DKFGVSAAAAVAVAGNKKE.N	DKFGVSAAAAVAV	125	41	4.262	0.000
sp|Q2A1M6|RL7_FRATH	50S ribosomal protein L7	K.FGVSAAAAVAVAGNK.K	FGVSAAAAVAV	125	41	4.465	0.000
sp|Q2A1M6|RL7_FRATH	50S ribosomal protein L7	K.FGVSAAAAVAVAGNKK.E	FGVSAAAAVAV	125	41	4.423	0.000
sp|Q2A1M6|RL7_FRATH	50S ribosomal protein L7	K.MMEDKFGVSAAAAVAVAGNKK.E	MMEDKFGVSAAAAVAV	125	41	3.226	0.000
sp|Q2A1M6|RL7_FRATH	50S ribosomal protein L7	E.DKFGVSAAAAVAVAAAGNKKE.N	DKFGVSAAAAVAVAA	125	43	4.196	0.000
sp|Q2A1M6|RL7_FRATH	50S ribosomal protein L7	K.FGVSAAAAVAVAAAGNK.K	FGVSAAAAVAVAA	125	43	2.708	0.000
sp|Q2A1M6|RL7_FRATH	50S ribosomal protein L7	E.FDVVLVDAAGNKKE.N	FDVVLVDA	125	66	3.981	0.000
sp|Q2A1M6|RL7_FRATH	50S ribosomal protein L7	E.FDVVLVDAGAGNKKE.N	FDVVLVDAG	125	67	2.513	0.001
sp|Q2A1M6|RL7_FRATH	50S ribosomal protein L7	E.FDVVLVDAGSNKAGNKKE.N	FDVVLVDAGSNK	125	70	4.338	0.000
sp|Q2A1M6|RL7_FRATH	50S ribosomal protein L7	E.FDVVLVDAGSNKIAGNKKE.N	FDVVLVDAGSNKI	125	71	4.27	0.000
sp|Q2A1M6|RL7_FRATH	50S ribosomal protein L7	E.FDVVLVDAGSNKIAAGNKKE.N	FDVVLVDAGSNKIA	125	72	4.373	0.000
sp|Q2A1M6|RL7_FRATH	50S ribosomal protein L7	E.FDVVLVDAGSNKIAAAGNKKE.N	FDVVLVDAGSNKIAA	125	73	4.417	0.000
sp|Q2A1M6|RL7_FRATH	50S ribosomal protein L7	D.VVLVDAGSNKIAAAGNKKE.N	VVLVDAGSNKIAA	125	73	3.422	0.000
sp|Q2A1M6|RL7_FRATH	50S ribosomal protein L7	E.FDVVLVDAGSNKIAAIAGNKKE.N	FDVVLVDAGSNKIAAI	125	74	4.353	0.009
sp|Q2A1M6|RL7_FRATH	50S ribosomal protein L7	D.VVLVDAGSNKIAAIAGNKKE.N	VVLVDAGSNKIAAI	125	74	3.202	0.000
sp|Q2A1M6|RL7_FRATH	50S ribosomal protein L7	E.FDVVLVDAGSNKIAAIKAGNKKE.N	FDVVLVDAGSNKIAAIK	125	75	3.567	0.002
sp|Q2A1M6|RL7_FRATH	50S ribosomal protein L7	E.FDVVLVDAGSNKIAAIKAAGNK.K	FDVVLVDAGSNKIAAIKA	125	76	3.519	0.000
sp|Q2A1M6|RL7_FRATH	50S ribosomal protein L7	E.FDVVLVDAGSNKIAAIKAAGNKKE.N	FDVVLVDAGSNKIAAIKA	125	76	2.705	0.001
sp|Q2A1M6|RL7_FRATH	50S ribosomal protein L7	E.FDVVLVDAGSNKIAAIKAVAGNKKE.N	FDVVLVDAGSNKIAAIKAV	125	77	3.568	0.000
sp|Q2A1M6|RL7_FRATH	50S ribosomal protein L7	R.GATGLGLAGNKK.E	GATGLGL	125	85	3.621	0.005
sp|Q2A1M6|RL7_FRATH	50S ribosomal protein L7	R.GATGLGLAGNKKE.N	GATGLGL	125	85	3.541	0.008
sp|Q2A1M6|RL7_FRATH	50S ribosomal protein L7	E.AKDAVEGTAGNKKE.N	AKDAVEGT	125	95	3.738	0.000
sp|Q2A1M6|RL7_FRATH	50S ribosomal protein L7	E.AKDAVEGTPAGNKKE.N	AKDAVEGTP	125	96	4.2	0.000
sp|Q2A1M6|RL7_FRATH	50S ribosomal protein L7	E.AKDAVEGTPAGNKK.E	AKDAVEGTP	125	96	2.774	0.000
sp|Q2A1M6|RL7_FRATH	50S ribosomal protein L7	K.DAVEGTPAGNKK.E	DAVEGTP	125	96	3.345	0.006
sp|Q2A1M6|RL7_FRATH	50S ribosomal protein L7	E.AKDAVEGTPFAGNKKE.N	AKDAVEGTPF	125	97	4.27	0.000
sp|Q2A1M6|RL7_FRATH	50S ribosomal protein L7	K.DAVEGTPFAGNKK.E	DAVEGTPF	125	97	3.944	0.000
sp|Q2A1M6|RL7_FRATH	50S ribosomal protein L7	K.DAVEGTPFTVKAGNK.K	DAVEGTPFTVK	125	100	4.156	0.000
sp|Q2A1M6|RL7_FRATH	50S ribosomal protein L7	E.GTPFTVKAGNKKE.N	GTPFTVK	125	100	3.714	0.002
sp|Q2A1M8|RPOC_FRATH	DNA-directed RNA polym	E.KAIKRLRAGNKK.E	KAIKRLR	1417	220	2.106	0.009
sp|Q2A1R5|LOLA_FRATH	Outer-membrane lipoprot	D.IAQFPYLIAGNKK.E	IAQFPYLI	205	111	3.26	0.000

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

sp|Q2A1R5|LOLA_FRATH	Outer-membrane lipoprot	K.VSNDIAQFPYLIAGNKK.E	VSNDIAQFPYLI	205	111	4.262	0.000
sp|Q2A1R5|LOLA_FRATH	Outer-membrane lipoprot	K.KVSNDIAQFPYLILAGNKK.E	KVSNDIAQFPYLIL	205	112	3.391	0.000
sp|Q2A1R5|LOLA_FRATH	Outer-membrane lipoprot	K.VSNDIAQFPYLILAGNKK.E	VSNDIAQFPYLIL	205	112	3.811	0.000
sp|Q2A1R5|LOLA_FRATH	Outer-membrane lipoprot	K.VSNDIAQFPYLILAGNK.K	VSNDIAQFPYLIL	205	112	3.619	0.000
sp|Q2A1R5|LOLA_FRATH	Outer-membrane lipoprot	D.IAQFPYLILLAGNK.K	IAQFPYLILL	205	113	3.719	0.000
sp|Q2A1R5|LOLA_FRATH	Outer-membrane lipoprot	K.VSNDIAQFPYLILLAGNK.K	VSNDIAQFPYLILL	205	113	4.573	0.000
sp|Q2A1R5|LOLA_FRATH	Outer-membrane lipoprot	K.VSNDIAQFPYLILLAGNKK.E	VSNDIAQFPYLILL	205	113	4.477	0.000
sp|Q2A1R5|LOLA_FRATH	Outer-membrane lipoprot	K.VSNDIAQFPYLILLSAGNK.K	VSNDIAQFPYLILLS	205	114	4.357	0.000
sp|Q2A1R5|LOLA_FRATH	Outer-membrane lipoprot	E.FNNVKTDVDISNTSFAGNKKE.N	FNNVKTDVDISNTSF	205	188	3.099	0.006
sp|Q2A1R5|LOLA_FRATH	Outer-membrane lipoprot	K.APQNTDIIAGNKK.E	APQNTDII	205	199	3.953	0.001
sp|Q2A205|FETP_FRATH	Probable Fe(2+)-traffickir	K.FLFEGKEEKPAGNKK.E	FLFEGKEEKP	87	81	2.925	0.004
sp|Q2A260|PDXS_FRATH	Pyridoxal biosynthesis lya	R.AIVSAVTAGNKK.E	AIVSAVT	287	253	4.299	0.000
sp|Q2A260|PDXS_FRATH	Pyridoxal biosynthesis lya	R.AIVSAVTAGNKKE.N	AIVSAVT	287	253	2.641	0.000
sp|Q2A260|PDXS_FRATH	Pyridoxal biosynthesis lya	R.AIVSAVTYAGNKK.E	AIVSAVTY	287	254	4.425	0.000
sp|Q2A260|PDXS_FRATH	Pyridoxal biosynthesis lya	R.AIVSAVTYYNDAKAGNK.K	AIVSAVTYYNDAK	287	259	4.39	0.000
sp|Q2A269|PNP_FRATH	Polyribonucleotide nucleo	K.TYAAGKIAGNK.K	TYAAGKI	693	72	2.834	0.008
sp|Q2A278|ENO_FRATH	Enolase eno	K.VQLVGDDLFVTNPSILAKAGNKK.E	VQLVGDDLFVTNPSILAK	456	326	2.929	0.003
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	R.NLNKLDSAGNKK.E	NLNKLDS	741	51	3.865	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	R.NLNKLDSPAGNKK.E	NLNKLDSP	741	52	3.762	0.006
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	R.NLNKLDSPMAGNKK.E	NLNKLDSPM	741	53	4.088	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	R.NLNKLDSPMDKAGNK.K	NLNKLDSPMDK	741	55	4.144	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	R.NLNKLDSPMDKDAGNKK.E	NLNKLDSPMDKD	741	56	4.183	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	R.NLNKLDSPMDKDAGNKKENR.V	NLNKLDSPMDKD	741	56	3.7	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	R.NLNKLDSPM+16DKDAGNKK.E	NLNKLDSPMDKD	741	56	2.837	0.001
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	R.NLNKLDSPMDKDYAGNKK.E	NLNKLDSPMDKDY	741	57	4.129	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	R.NLNKLDSPMDKDYNAGNKK.E	NLNKLDSPMDKDYN	741	58	3.475	0.007
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	R.NLNKLDSPMDKDYNAGNKKENR.V	NLNKLDSPMDKDYN	741	58	3.427	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	R.NLNKLDSPMDKDYNYAGNKK.E	NLNKLDSPMDKDYNY	741	59	3.383	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.LDSPMDKDYNYHQAGNKK.E	LDSPMDKDYNYHQ	741	61	2.729	0.001
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.DYNYHQAAGNKK.E	DYNYHQA	741	62	2.477	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	R.NLNKLDSPMDKDYNYHQAAGNKK.E	NLNKLDSPMDKDYNYHQA	741	62	3.092	0.001
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	R.NLNKLDSPMDKDYNYHQAAGNK.K	NLNKLDSPMDKDYNYHQA	741	62	2.964	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	R.NLNKLDSPM+16DKDYNYHQAAGNKK.E	NLNKLDSPMDKDYNYHQA	741	62	2.703	0.008

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

splQ2A298lKATG_FRATH	Catalase-peroxidase katG	K.KLDTEQLAGNKK.E	KLDTEQL	741	71	3.797	0.006
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	K.DMQDLAGNKK.E	DMQDL	741	78	3.701	0.002
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	D.TEQLKKDMQDLAGNKKE.N	TEQLKKDMQDL	741	78	4.004	0.001
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	K.DMQDLLTQAGNKK.E	DMQDLLTQ	741	81	4.039	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	K.DMQDLLTQAGNK.K	DMQDLLTQ	741	81	3.819	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	K.DMQDLLTQSQAGNKK.E	DMQDLLTQSQ	741	83	4.317	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	K.DMQDLLTQSQDWAGNKK.E	DMQDLLTQSQDW	741	85	4.28	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.QLKKDMQDLLTQSQDWAGNKKE.N	QLKKDMQDLLTQSQDW	741	85	2.301	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	K.DMQDLLTQSQDWWPADFAGNKK.E	DMQDLLTQSQDWWPADF	741	90	4.42	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	*.DMQDLLTQSQDWWPADFGAGNKK.E	DMQDLLTQSQDWWPADFG	741	91	4.445	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	D.MQDLLTQSQDWWPADFGAGNKKE.N	MQDLLTQSQDWWPADFG	741	91	3.728	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	*.DMQDLLTQSQDWWPADFGNYGPFFAGNKK.E	DMQDLLTQSQDWWPADFGNYGPFF	741	97	3.192	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	D.M+16QDLLTQSQDWWPADFGNYGPFFAGNKKE.	MQDLLTQSQDWWPADFGNYGPFF	741	97	2.803	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	K.DMQDLLTQSQDWWPADFGNYGPFFIAGNKK.E	DMQDLLTQSQDWWPADFGNYGPFFI	741	98	3.711	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	R.LSWHDAGAGNKK.E	LSWHDAG	741	106	3.998	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	R.LSWHDAGAGNK.K	LSWHDAG	741	106	3.723	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	R.LSWHDAGTAGNKK.E	LSWHDAGT	741	107	4.261	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	R.LSWHDAGTYAGNKK.E	LSWHDAGTY	741	108	4.241	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	R.LSWHDAGTYAGNK.K	LSWHDAGTY	741	108	4.202	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	R.FSPLNSWAGNK.K	FSPLNSW	741	130	4.242	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	R.FSPLNSWAGNKK.E	FSPLNSW	741	130	3.745	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	R.FSPLNSWPAGNK.K	FSPLNSWP	741	131	2.809	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	R.FSPLNSWPDAGNK.K	FSPLNSWPD	741	132	4.409	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	R.FSPLNSWPDAGNKK.E	FSPLNSWPD	741	132	4.325	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	R.FSPLNSWPDNAGNKK.E	FSPLNSWPDN	741	133	4.252	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	R.FSPLNSWPDNVAGNK.K	FSPLNSWPDNV	741	134	4.371	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	R.FSPLNSWPDNVAGNKK.E	FSPLNSWPDNV	741	134	4.198	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	R.FSPLNSWPDNVNAGNK.K	FSPLNSWPDNVN	741	135	4.49	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	R.FSPLNSWPDNVNAGNKK.E	FSPLNSWPDNVN	741	135	3.908	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	R.FSPLNSWPDNVNLAGNK.K	FSPLNSWPDNVNL	741	136	4.425	0.001
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	R.FSPLNSWPDNVNLAGNKK.E	FSPLNSWPDNVNL	741	136	4.403	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	K.YGDAVSWAGNKK.E	YGDAVSW	741	156	4.209	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	K.YGDAVSWSDLIAGNK.K	YGDAVSWSDLI	741	160	3.423	0.000

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.YGDAVSWSDLIVLAGTAGNKK.E	YGDAVSWSDLIVLAGT	741	165	2.082	0.002
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.YGDAVSWSDLIVLAGTVAGNKK.E	YGDAVSWSDLIVLAGTV	741	166	3.521	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.YGDAVSWSDLIVLAGTVSLAGNKK.E	YGDAVSWSDLIVLAGTVSL	741	168	3.142	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.SMGMKPIAGNKKE.N	SMGMKPI	741	176	4.136	0.001
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.SMGMKPIAGNK.K	SMGMKPI	741	176	4.059	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.SMGMKPIAGNKK.E	SMGMKPI	741	176	3.953	0.001
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.SM+16GMKPIAGNKK.E	SMGMKPI	741	176	2.875	0.008
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.SMGM+16KPIAGNK.K	SMGMKPI	741	176	2.158	0.009
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.SM+16GMKPIAGNK.K	SMGMKPI	741	176	2.066	0.001
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.SMGMKPIGAGNK.K	SMGMKPIG	741	177	4.05	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.SMGMKPIGAGNKK.E	SMGMKPIG	741	177	3.914	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.SMGMKPIGAGNKKE.N	SMGMKPIG	741	177	3.353	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.SMGMKPIGFAGNKK.E	SMGMKPIGF	741	178	3.56	0.010
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.SMGMKPIGFAAGNK.K	SMGMKPIGFA	741	179	4.181	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.PIGFAFAGNK.K	PIGFAF	741	180	4.208	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.SMGMKPIGFAFAGNK.K	SMGMKPIGFAF	741	180	4.257	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.SMGMKPIGFAFAGNKK.E	SMGMKPIGFAF	741	180	3.632	0.001
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.PIGFAFGAGNK.K	PIGFAFG	741	181	3.285	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.SMGMKPIGFAFGAGNK.K	SMGMKPIGFAFG	741	181	4.317	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.SMGMKPIGFAFGAGNKK.E	SMGMKPIGFAFG	741	181	3.374	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.SMGMKPIGFAFGREDDWQGDDTAGNKK.E	SMGMKPIGFAFGREDDWQGDDT	741	191	3.463	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	D.GKLAPAYAAAGNKKE.N	GKLAPAYAA	741	216	4.064	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.LAPAYAAAGNKK.E	LAPAYAA	741	216	4.343	0.005
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.LAPAYAAAGNK.K	LAPAYAA	741	216	3.59	0.003
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.LAPAYAAAGNKKE.N	LAPAYAA	741	216	3.574	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	D.GKLAPAYAATAGNKKE.N	GKLAPAYAAT	741	217	4.354	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	*.GKLAPAYAATQAGNKKE.N	GKLAPAYAATQ	741	218	2.477	0.002
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.LAPAYAATQAGNKK.E	LAPAYAATQ	741	218	4.535	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.LAPAYAATQAGNKKE.N	LAPAYAATQ	741	218	4.162	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.LAPAYAATQAGNK.K	LAPAYAATQ	741	218	4.129	0.004
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.LAPAYAATQMAGNKK.E	LAPAYAATQM	741	219	4.439	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.LAPAYAATQMAGNK.K	LAPAYAATQM	741	219	4.285	0.003
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.LAPAYAATQM+16AGNK.K	LAPAYAATQM	741	219	4.071	0.000

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.LAPAYAATQM+16AGNKK.E	LAPAYAATQM	741	219	3.861	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.LAPAYAATQMGAGNKK.E	LAPAYAATQMG	741	220	4.531	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.LAPAYAATQM+16GAGNK.K	LAPAYAATQMG	741	220	3.997	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.LAPAYAATQMGAGNK.K	LAPAYAATQMG	741	220	3.852	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.LAPAYAATQM+16GAGNKK.E	LAPAYAATQMG	741	220	3.751	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.LAPAYAATQM+16GAGNKKE.N	LAPAYAATQMG	741	220	2.991	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.LAPAYAATQMGLAGNK.K	LAPAYAATQMGL	741	221	4.48	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.LAPAYAATQMGLAGNKK.E	LAPAYAATQMGL	741	221	4.444	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.LAPAYAATQM+16GLAGNK.K	LAPAYAATQMGL	741	221	3.917	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.LAPAYAATQM+16GLAGNKK.E	LAPAYAATQMGL	741	221	3.772	0.001
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.LAPAYAATQMGLIAGNK.K	LAPAYAATQMGLI	741	222	4.401	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.LAPAYAATQMGLIAGNKK.E	LAPAYAATQMGLI	741	222	4.001	0.001
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.LAPAYAATQM+16GLIAGNK.K	LAPAYAATQMGLI	741	222	3.973	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.LAPAYAATQMGLIYAGNKK.E	LAPAYAATQMGLIY	741	223	4.457	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.LAPAYAATQM+16GLIYAGNK.K	LAPAYAATQMGLIY	741	223	3.989	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.LAPAYAATQMGLIYAGNK.K	LAPAYAATQMGLIY	741	223	3.968	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.LAPAYAATQMGLIYVAGNKK.E	LAPAYAATQMGLIYV	741	224	4.405	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.LAPAYAATQMGLIYVAGNK.K	LAPAYAATQMGLIYV	741	224	4.3	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.LAPAYAATQM+16GLIYVAGNK.K	LAPAYAATQMGLIYV	741	224	4.017	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.LAPAYAATQMGLIYVNAGNKK.E	LAPAYAATQMGLIYVN	741	225	4.31	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.LAPAYAATQMGLIYVNAGNK.K	LAPAYAATQMGLIYVN	741	225	3.691	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.LAPAYAATQMGLIYVNPAGNK.K	LAPAYAATQMGLIYVNP	741	226	4.483	0.001
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.LAPAYAATQM+16GLIYVNPAGNK.K	LAPAYAATQMGLIYVNP	741	226	4.053	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.LAPAYAATQMGLIYVNPEGAGNK.K	LAPAYAATQMGLIYVNPEG	741	228	3.742	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.LAPAYAATQMGLIYVNPEGAGNKK.E	LAPAYAATQMGLIYVNPEG	741	228	2.394	0.005
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.LAPAYAATQMGLIYVNPEGPAGNKK.E	LAPAYAATQMGLIYVNPEGP	741	229	4.408	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.LAPAYAATQMGLIYVNPEGPAGNK.K	LAPAYAATQMGLIYVNPEGP	741	229	3.411	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.LAPAYAATQMGLIYVNPEGPDAGNK.K	LAPAYAATQMGLIYVNPEGPD	741	230	3.63	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.LAPAYAATQMGLIYVNPEGPDGKPAGNK.K	LAPAYAATQMGLIYVNPEGPDGKP	741	233	3.538	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.LAPAYAATQMGLIYVNPEGPDGKPAGNKK.E	LAPAYAATQMGLIYVNPEGPDGKP	741	233	2.966	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.LAPAYAATQM+16GLIYVNPEGPDGKPAGNKK.E	LAPAYAATQMGLIYVNPEGPDGKP	741	233	2.544	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	R.AMGMTDKAGNK.K	AMGMTDK	741	254	3.318	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	R.AMGMTDKEAGNKK.E	AMGMTDKE	741	255	3.416	0.001

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

splQ2A298lKATG_FRATH	Catalase-peroxidase katG	R.AMGMTDKETAGNKK.E	AMGMTDKET	741	256	3.908	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	R.AMGMTDKETVAGNKK.E	AMGMTDKETV	741	257	4.097	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.IRQAFRAMGMTDKETVAGNKKE.N	IRQAFRAMGMTDKETV	741	257	2.392	0.008
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	R.AMGMTDKETVAAGNKK.E	AMGMTDKETVA	741	258	4.017	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	R.AMGMTDKETVALIAAGNKK.E	AMGMTDKETVALIA	741	261	3.446	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.TVALIAAGNKKE.N	TVALIA	741	261	3.766	0.009
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.TVALIAAGNKK.E	TVALIA	741	261	3.321	0.002
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.TVALIAGAGNKKE.N	TVALIAG	741	262	4.13	0.002
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	R.AMGMTDKETVALIAGGAGNKK.E	AMGMTDKETVALIAGG	741	263	3.784	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	*.ETVALIAGGAGNKK.E	ETVALIAGG	741	263	3.895	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.TVALIAGGAGNKKE.N	TVALIAGG	741	263	4.323	0.001
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.TVALIAGGAGNKK.E	TVALIAGG	741	263	4.264	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.TVALIAGGAGNK.K	TVALIAGG	741	263	2.87	0.001
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.TVALIAGGHAGNK.K	TVALIAGGH	741	264	4.266	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.TVALIAGGHAGNKK.E	TVALIAGGH	741	264	4.256	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.TVALIAGGHAGNKKE.N	TVALIAGGH	741	264	3.847	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	*.ETVALIAGGHTAGNKK.E	ETVALIAGGHT	741	265	4.084	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.TVALIAGGHTAGNKKE.N	TVALIAGGHT	741	265	4.279	0.002
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.TVALIAGGHTAGNK.K	TVALIAGGHT	741	265	4.243	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.TVALIAGGHTAGNKK.E	TVALIAGGHT	741	265	4.099	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	R.AMGMTDKETVALIAGGHTFAGNKK.E	AMGMTDKETVALIAGGHTF	741	266	3.476	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	*.ETVALIAGGHTFAGNK.K	ETVALIAGGHTF	741	266	4.047	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	*.ETVALIAGGHTFAGNKK.E	ETVALIAGGHTF	741	266	3.277	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.TVALIAGGHTFAGNK.K	TVALIAGGHTF	741	266	4.351	0.001
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.TVALIAGGHTFAGNKKE.N	TVALIAGGHTF	741	266	3.845	0.001
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.TVALIAGGHTFGAGNKKE.N	TVALIAGGHTFG	741	267	4.127	0.001
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.TVALIAGGHTFGAGNKK.E	TVALIAGGHTFG	741	267	2.952	0.004
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.TVALIAGGHTFGKTHGAGNKKE.N	TVALIAGGHTFGKTHG	741	271	2.855	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	K.THGAVAGNKK.E	THGAV	741	273	3.935	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	K.THGAVAGNK.K	THGAV	741	273	2.131	0.003
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.TVALIAGGHTFGKTHGAVAGNKKE.N	TVALIAGGHTFGKTHGAV	741	273	3.767	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	K.THGAVPEAGNKK.E	THGAVPE	741	275	3.949	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	K.THGAVPEAGNK.K	THGAVPE	741	275	3.194	0.000

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.THGAVPEAGNKKENR.V	THGAVPE	741	275	2.376	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.THGAVPEDKAGNK.K	THGAVPEDK	741	277	3.374	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.THGAVPEDKAGNKK.E	THGAVPEDK	741	277	2.988	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.THGAVPEDKVAGNK.K	THGAVPEDKV	741	278	3.913	0.005
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.THGAVPEDKVAGNKK.E	THGAVPEDKV	741	278	3.867	0.004
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.THGAVPEDKVAGNKKENR.V	THGAVPEDKV	741	278	3.423	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.DKVKQAIGAGNKKE.N	DKVKQAIG	741	283	3.915	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.QAIGPAAGNKK.E	QAIGPA	741	285	2.192	0.009
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.VKQAIGPAAGNKK.E	VKQAIGPA	741	285	3.14	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.DKVKQAIGPAPAGNKKE.N	DKVKQAIGPAP	741	286	4.293	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.QAIGPAPAGNKK.E	QAIGPAP	741	286	2.862	0.006
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.DKVKQAIGPAPDAGNKKE.N	DKVKQAIGPAPD	741	287	4.357	0.001
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.QAIGPAPDAGNKKENR.V	QAIGPAPD	741	287	2.506	0.003
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.DKVKQAIGPAPDKAGNKKE.N	DKVKQAIGPAPDK	741	288	4.206	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.DKVKQAIGPAPDKAAGNKKE.N	DKVKQAIGPAPDKA	741	289	3.303	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.DKVKQAIGPAPDKAPAGNKKE.N	DKVKQAIGPAPDKAP	741	290	3.333	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.QAIGPAPDKAPAGNKK.E	QAIGPAPDKAP	741	290	2.824	0.004
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.QAIGPAPDKAPIAGNK.K	QAIGPAPDKAPI	741	291	3.211	0.002
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.QAIGPAPDKAPIAGNKK.E	QAIGPAPDKAPI	741	291	2.616	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.DKVKQAIGPAPDKAPIEAGNKKE.N	DKVKQAIGPAPDKAPIE	741	292	3.3	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.QAIGPAPDKAPIEAGNKKENR.V	QAIGPAPDKAPIE	741	292	3.289	0.005
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.QAIGPAPDKAPIEAGNKK.E	QAIGPAPDKAPIE	741	292	2.925	0.005
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.QAIGPAPDKAPIEQAGNKK.E	QAIGPAPDKAPIEQ	741	293	3.521	0.009
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.QAIGPAPDKAPIEQQAGNKK.E	QAIGPAPDKAPIEQQ	741	294	2.515	0.001
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.QAIGPAPDKAPIEQQGAGNKK.E	QAIGPAPDKAPIEQQG	741	295	3.081	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.APIEQQGLAGNKK.E	APIEQQGL	741	296	4.234	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.QAIGPAPDKAPIEQQGLAGNKK.E	QAIGPAPDKAPIEQQGL	741	296	2.796	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.QAIGPAPDKAPIEQQGLAGNK.K	QAIGPAPDKAPIEQQGL	741	296	2.582	0.003
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.APIEQQGLGAGNKK.E	APIEQQGLG	741	297	4.049	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.QAIGPAPDKAPIEQQGLGAGNK.K	QAIGPAPDKAPIEQQGLG	741	297	3.537	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.QAIGPAPDKAPIEQQGLGAGNKK.E	QAIGPAPDKAPIEQQGLG	741	297	3.18	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.APIEQQGLGWAGNKK.E	APIEQQGLGW	741	298	4.069	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.APIEQQGLGWAGNK.K	APIEQQGLGW	741	298	2.371	0.005

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.QAIGPAPDKAPIEQQGLGWAGNK.K	QAIGPAPDKAPIEQQGLGW	741	298	3.382	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.QAIGPAPDKAPIEQQGLGWAGNKK.E	QAIGPAPDKAPIEQQGLGW	741	298	2.051	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.APIEQQGLGWHAGNK.K	APIEQQGLGWH	741	299	4.157	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.APIEQQGLGWHNAGNK.K	APIEQQGLGWHN	741	300	4.081	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.APIEQQGLGWHNAGNKK.E	APIEQQGLGWHN	741	300	2.758	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.QAIGPAPDKAPIEQQGLGWHNAGNK.K	QAIGPAPDKAPIEQQGLGWHN	741	300	2.938	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	*.APIEQQGLGWHNSAGNK.K	APIEQQGLGWHNS	741	301	4.21	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	*.APIEQQGLGWHNSAGNKK.E	APIEQQGLGWHNS	741	301	4.089	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.QAIGPAPDKAPIEQQGLGWHNSAGNK.K	QAIGPAPDKAPIEQQGLGWHNS	741	301	3.16	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	*.APIEQQGLGWHNSYAGNK.K	APIEQQGLGWHNSY	741	302	4.164	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	*.APIEQQGLGWHNSYAGNKK.E	APIEQQGLGWHNSY	741	302	3.041	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.QAIGPAPDKAPIEQQGLGWHNSYAGNKK.E	QAIGPAPDKAPIEQQGLGWHNSY	741	302	2.036	0.003
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.APIEQQGLGWHNSYGAGNK.K	APIEQQGLGWHNSYG	741	303	4.205	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.QAIGPAPDKAPIEQQGLGWHNSYGAGNK.K	QAIGPAPDKAPIEQQGLGWHNSYG	741	303	2.678	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.QAIGPAPDKAPIEQQGLGWHNSYGAGNKK.E	QAIGPAPDKAPIEQQGLGWHNSYG	741	303	2.387	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.APIEQQGLGWHNSYGTAGNK.K	APIEQQGLGWHNSYGT	741	304	3.042	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.QAIGPAPDKAPIEQQGLGWHNSYGTAGNK.K	QAIGPAPDKAPIEQQGLGWHNSYGT	741	304	2.734	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.QAIGPAPDKAPIEQQGLGWHNSYGTGAGNKK.E	QAIGPAPDKAPIEQQGLGWHNSYGTG	741	305	2.428	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.QAIGPAPDKAPIEQQGLGWHNSYGTGAGNK.K	QAIGPAPDKAPIEQQGLGWHNSYGTG	741	305	2.008	0.003
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.QAIGPAPDKAPIEQQGLGWHNSYGTGNAGNK.K	QAIGPAPDKAPIEQQGLGWHNSYGTGN	741	306	2.971	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.APIEQQGLGWHNSYGTGNGAGNKK.E	APIEQQGLGWHNSYGTGNG	741	307	2.102	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.QAIGPAPDKAPIEQQGLGWHNSYGTGNGAGNK.K	QAIGPAPDKAPIEQQGLGWHNSYGTGNG	741	307	2.057	0.001
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.APIEQQGLGWHNSYGTGNGDAGNKK.E	APIEQQGLGWHNSYGTGNGD	741	308	2.072	0.001
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.APIEQQGLGWHNSYGTGNGDDTAGNKK.E	APIEQQGLGWHNSYGTGNGDDT	741	310	2.318	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.GSWTSTPAGNKKE.N	GSWTSTP	741	323	3.679	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.GSWTSTPAGNKKENR.V	GSWTSTP	741	323	3.394	0.003
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.GSWTSTPTAGNKKE.N	GSWTSTPT	741	324	3.715	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.GSWTSTPTFAGNKKENR.V	GSWTSTPTF	741	325	4.272	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.GSWTSTPTFAGNKKE.N	GSWTSTPTF	741	325	3.935	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.GSWTSTPTFAGNKK.E	GSWTSTPTF	741	325	3.432	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.GSWTSTPTFAGNK.K	GSWTSTPTF	741	325	2.13	0.002
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.GSWTSTPTFWAGNKKE.N	GSWTSTPTFW	741	326	4.054	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.GSWTSTPTFWAGNKK.E	GSWTSTPTFW	741	326	3.546	0.000

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.GSWTSTPTFWNAGNKKE.N	GSWTSTPTFWN	741	327	4.213	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.GSWTSTPTFWNAGNKK.E	GSWTSTPTFWN	741	327	4.202	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.GSWTSTPTFWNHAGNK.K	GSWTSTPTFWNH	741	328	4.195	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.GSWTSTPTFWNHAGNKK.E	GSWTSTPTFWNH	741	328	3.959	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.GSWTSTPTFWNHDAGNKK.E	GSWTSTPTFWNHD	741	329	4.103	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.GSWTSTPTFWNHDFAGNK.K	GSWTSTPTFWNHDF	741	330	4.256	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.GSWTSTPTFWNHDFAGNKKE.N	GSWTSTPTFWNHDF	741	330	4.096	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.GSWTSTPTFWNHDFLAGNK.K	GSWTSTPTFWNHDFL	741	331	4.369	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.GSWTSTPTFWNHDFLAGNKK.E	GSWTSTPTFWNHDFL	741	331	3.719	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.GSWTSTPTFWNHDFLAGNKKE.N	GSWTSTPTFWNHDFL	741	331	2.282	0.003
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.GSWTSTPTFWNHDFLHAGNK.K	GSWTSTPTFWNHDFLH	741	332	4.074	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.GSWTSTPTFWNHDFLHAGNKK.E	GSWTSTPTFWNHDFLH	741	332	2.904	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.GSWTSTPTFWNHDFLHNAGNKK.E	GSWTSTPTFWNHDFLHN	741	333	3.632	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.GSWTSTPTFWNHDFLHNLAGNK.K	GSWTSTPTFWNHDFLHNL	741	334	3.732	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.GSWTSTPTFWNHDFLHNLAGNKKE.N	GSWTSTPTFWNHDFLHNL	741	334	3.331	0.004
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.GSWTSTPTFWNHDFLHNLAGNKK.E	GSWTSTPTFWNHDFLHNL	741	334	2.931	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.GSWTSTPTFWNHDFLHNLYAGNKK.E	GSWTSTPTFWNHDFLHNLY	741	335	3.513	0.005
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.GSWTSTPTFWNHDFLHNLYAGNKKE.N	GSWTSTPTFWNHDFLHNLY	741	335	3.212	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.GSWTSTPTFWNHDFLHNLYNAGNK.K	GSWTSTPTFWNHDFLHNLYN	741	336	3.589	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.GSWTSTPTFWNHDFLHNLYNAGNKK.E	GSWTSTPTFWNHDFLHNLYN	741	336	3.339	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.GSWTSTPTFWNHDFLHNLYNLAGNK.K	GSWTSTPTFWNHDFLHNLYNL	741	337	3.34	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.GSWTSTPTFWNHDFLHNLYNLDAGNKK.E	GSWTSTPTFWNHDFLHNLYNLD	741	338	3.712	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.GSWTSTPTFWNHDFLHNLYNLDAGNKKE.N	GSWTSTPTFWNHDFLHNLYNLD	741	338	2.447	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.GSWTSTPTFWNHDFLHNLYNLDWAGNKK.E	GSWTSTPTFWNHDFLHNLYNLDW	741	339	3.769	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	K.KTLSPAGAGNKK.E	KTLSPAG	741	347	2.005	0.005
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	K.TLSPAGAGNKK.E	TLSPAG	741	347	2.707	0.001
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	K.KTLSPAGAAGNKK.E	KTLSPAGA	741	348	3.569	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	K.TLSPAGAAGNKK.E	TLSPAGA	741	348	4.21	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	K.TLSPAGAAGNK.K	TLSPAGA	741	348	3.182	0.006
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	K.KTLSPAGAHAGNKK.E	KTLSPAGAH	741	349	2.201	0.001
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	K.TLSPAGAHAGNKKE.N	TLSPAGAH	741	349	4.153	0.001
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	K.TLSPAGAHAGNKK.E	TLSPAGAH	741	349	4.148	0.005
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	K.TLSPAGAHAGNK.K	TLSPAGAH	741	349	4.128	0.008

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.TLSPAGAHAGNKKENR.V	TLSPAGAH	741	349	2.567	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.KTLSPAGAHQAGNKK.E	KTLSPAGAHQ	741	350	3.064	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.TLSPAGAHQAGNKK.E	TLSPAGAHQ	741	350	4.368	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.TLSPAGAHQAGNK.K	TLSPAGAHQ	741	350	4.257	0.008
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.TLSPAGAHQAGNKKE.N	TLSPAGAHQ	741	350	4.215	0.001
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.TLSPAGAHQAGNKKENR.V	TLSPAGAHQ	741	350	3.528	0.001
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.TLSPAGAHQWAGNKKE.N	TLSPAGAHQW	741	351	4.383	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.TLSPAGAHQWAGNKK.E	TLSPAGAHQW	741	351	4.379	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.TLSPAGAHQWAGNK.K	TLSPAGAHQW	741	351	4.352	0.003
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.TLSPAGAHQWTAGNK.K	TLSPAGAHQWT	741	352	4.384	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.TLSPAGAHQWTAGNKK.E	TLSPAGAHQWT	741	352	4.31	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.TLSPAGAHQWTPAGNK.K	TLSPAGAHQWTP	741	353	4.462	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.TLSPAGAHQWTPAGNKK.E	TLSPAGAHQWTP	741	353	4.411	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.TLSPAGAHQWTPTAGNKK.E	TLSPAGAHQWTPT	741	354	4.363	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.TLSPAGAHQWTPTAGNK.K	TLSPAGAHQWTPT	741	354	4.323	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.TLSPAGAHQWTPTNAGNK.K	TLSPAGAHQWTPTN	741	355	4.28	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.TLSPAGAHQWTPTNAGNKK.E	TLSPAGAHQWTPTN	741	355	4.235	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.TLSPAGAHQWTPTNAKPENMVAGNKK.E	TLSPAGAHQWTPTNAKPENMV	741	362	2.933	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.NMVPAGNKKE.N	NMVP	741	363	3.089	0.009
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.TLSPAGAHQWTPTNAKPENMVPAGNK.K	TLSPAGAHQWTPTNAKPENMVP	741	363	3.17	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.TLSPAGAHQWTPTNAKPENMVPAGNKK.E	TLSPAGAHQWTPTNAKPENMVP	741	363	3.107	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.TLSPAGAHQWTPTNAKPENMVPDAGNK.K	TLSPAGAHQWTPTNAKPENMVPD	741	364	3.376	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.NMVPDAAGNKKE.N	NMVPDA	741	365	3.447	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.NM+16VPDAAGNKKE.N	NMVPDA	741	365	2.968	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.TLSPAGAHQWTPTNAKPENMVPDAAGNK.K	TLSPAGAHQWTPTNAKPENMVPDA	741	365	3.554	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.TLSPAGAHQWTPTNAKPENMVPDAAGNKK.E	TLSPAGAHQWTPTNAKPENMVPDA	741	365	3.512	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.NMVPDAHAGNKK.E	NMVPDAH	741	366	4.156	0.009
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.NMVPDAHAGNKKE.N	NMVPDAH	741	366	3.777	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.NM+16VPDAHAGNKKE.N	NMVPDAH	741	366	3.609	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.NMVPDAHAGNK.K	NMVPDAH	741	366	3.579	0.004
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.NM+16VPDAHAGNK.K	NMVPDAH	741	366	3.06	0.004
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.NMVPDAHKAGNKKE.N	NMVPDAHK	741	367	3.827	0.002
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.NMVPDAHKAGNK.K	NMVPDAHK	741	367	2.865	0.003

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

splQ2A298lKATG_FRATH	Catalase-peroxidase katG	K.HKPIMFTAGNK.K	HKPIMFT	741	378	3.893	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	K.HKPIMFTAGNKK.E	HKPIMFT	741	378	3.838	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	K.HKPIM+16FTAGNKK.E	HKPIMFT	741	378	3.049	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	K.HKPIM+16FTAGNK.K	HKPIMFT	741	378	2.092	0.008
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	K.HKPIMFTTAGNKK.E	HKPIMFTT	741	379	4.081	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	K.HKPIM+16FTTAGNKK.E	HKPIMFTT	741	379	2.194	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	K.HKPIMFTTDAGNK.K	HKPIMFTTD	741	380	4.35	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	K.HKPIMFTTDAGNKK.E	HKPIMFTTD	741	380	4.297	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	K.HKPIM+16FTTDAGNKK.E	HKPIMFTTD	741	380	3.24	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	K.HKPIMFTTDLAGNK.K	HKPIMFTTDL	741	381	4.3	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	K.HKPIMFTTDLAGNKK.E	HKPIMFTTDL	741	381	3	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	K.HKPIMFTTDLAAGNK.K	HKPIMFTTDLA	741	382	4.073	0.002
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	K.HKPIMFTTDLALKEDAGNKK.E	HKPIMFTTDLALKED	741	386	3.268	0.001
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	K.HKPIMFTTDLALKEDDAGNKK.E	HKPIMFTTDLALKEDD	741	387	3.153	0.002
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	D.LALKEDDAGNKKE.N	LALKEDD	741	387	3.736	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	K.HKPIMFTTDLALKEDDGAGNKK.E	HKPIMFTTDLALKEDDG	741	388	3.691	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	K.HKPIMFTTDLALKEDDGAGNK.K	HKPIMFTTDLALKEDDG	741	388	3.518	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	D.LALKEDDGAGNKKE.N	LALKEDDG	741	388	3.895	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	K.HKPIMFTTDLALKEDDGFAGNKK.E	HKPIMFTTDLALKEDDGF	741	389	3.477	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	K.HKPIM+16FTTDLALKEDDGFAGNKK.E	HKPIMFTTDLALKEDDGF	741	389	3.152	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	D.LALKEDDGFAGNKKE.N	LALKEDDGF	741	389	4.356	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.DDGFNKAGNKKE.N	DDGFNK	741	391	2.781	0.008
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	D.LALKEDDGFNKAGNKKE.N	LALKEDDGFNK	741	391	4.132	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	K.HKPIMFTTDLALKEDDGFNKYTQAGNKK.E	HKPIMFTTDLALKEDDGFNKYTQ	741	394	2.823	0.001
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	K.HKPIM+16FTTDLALKEDDGFNKYTQAGNKK.E	HKPIMFTTDLALKEDDGFNKYTQ	741	394	2.295	0.005
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	K.HKPIMFTTDLALKEDDGFNKYTQEFAGNK.K	HKPIMFTTDLALKEDDGFNKYTQEF	741	396	2.347	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	K.YTQEFYNNAGNKK.E	YTQEFYNN	741	399	3.893	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.FYNNPAGNKKENR.V	FYNNP	741	400	4.004	0.009
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.FYNNPAGNKK.E	FYNNP	741	400	3.777	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.FYNNPAGNKKE.N	FYNNP	741	400	3.711	0.002
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	K.YTQEFYNNPAGNKK.E	YTQEFYNNP	741	400	3.953	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.FYNNPEEFAGNKKE.N	FYNNPEEF	741	403	4.169	0.005
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.FYNNPEEFAGNKKENR.V	FYNNPEEF	741	403	2.891	0.003

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.FYNNPEEFKAGNKKE.N	FYNNPEEFK	741	404	4.189	0.009
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.FYNNPEEFKAGNKK.E	FYNNPEEFK	741	404	3.891	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.FYNNPEEFKAGNKKENR.V	FYNNPEEFK	741	404	3.279	0.008
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.YTQEFYNNPEEFKAGNK.K	YTQEFYNNPEEFK	741	404	4.2	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	R.YIGPWIPAGNKK.E	YIGPWIP	741	431	4.227	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	R.YIGPWIPAGNK.K	YIGPWIP	741	431	4.014	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	R.YIGPWIPAGNKKE.N	YIGPWIP	741	431	2.397	0.008
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	R.YIGPWIPEQAGNKK.E	YIGPWIPEQ	741	433	4.498	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	R.YIGPWIPEQAGNK.K	YIGPWIPEQ	741	433	3.519	0.002
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	R.YIGPWIPEQNAGNKK.E	YIGPWIPEQN	741	434	4.545	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	R.YIGPWIPEQNFAGNK.K	YIGPWIPEQNF	741	435	3.903	0.008
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	R.YIGPWIPEQNFIAGNK.K	YIGPWIPEQNFI	741	436	4.63	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	R.YIGPWIPEQNFIAGNKK.E	YIGPWIPEQNFI	741	436	4.499	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	R.YIGPWIPEQNFIWAGNK.K	YIGPWIPEQNFIW	741	437	4.505	0.006
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.QNFIWQAGNKKE.N	QNFIWQ	741	438	2.926	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.QNFIWQAGNKK.E	QNFIWQ	741	438	2.833	0.005
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	R.YIGPWIPEQNFIWQAGNK.K	YIGPWIPEQNFIWQ	741	438	3.333	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	R.YIGPWIPEQNFIWQDAGNK.K	YIGPWIPEQNFIWQD	741	439	4.507	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	R.YIGPWIPEQNFIWQDAGNKKENR.V	YIGPWIPEQNFIWQD	741	439	3.001	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	R.YIGPWIPEQNFIWQDPAGNKK.E	YIGPWIPEQNFIWQDP	741	440	2.567	0.003
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.QNFIWQDPVAGNKKE.N	QNFIWQDPV	741	441	3.622	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	R.YIGPWIPEQNFIWQDPVAGNK.K	YIGPWIPEQNFIWQDPV	741	441	4.475	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	R.YIGPWIPEQNFIWQDPVPAGNK.K	YIGPWIPEQNFIWQDPVP	741	442	4.384	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	R.YIGPWIPEQNFIWQDPVPAGNKK.E	YIGPWIPEQNFIWQDPVP	741	442	3.588	0.003
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	D.PVPAAGNKKE.N	PVPA	741	443	3.847	0.001
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	R.YIGPWIPEQNFIWQDPVPAAGNK.K	YIGPWIPEQNFIWQDPVPA	741	443	3.808	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	D.PVPAAAGNKKE.N	PVPAA	741	444	4.198	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.QNFIWQDPVPAAAGNKKE.N	QNFIWQDPVPAA	741	444	3.945	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	R.YIGPWIPEQNFIWQDPVPAAAGNK.K	YIGPWIPEQNFIWQDPVPAA	741	444	4.34	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	D.PVPAADAGNKK.E	PVPAAD	741	445	4.159	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	D.PVPAADAGNKKE.N	PVPAAD	741	445	4.022	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	D.PVPAADAGNK.K	PVPAAD	741	445	2.415	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	R.YIGPWIPEQNFIWQDPVPAADAGNK.K	YIGPWIPEQNFIWQDPVPAAD	741	445	3.924	0.005

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

splQ2A298lKATG_FRATH	Catalase-peroxidase katG	R.YIGPWIPEQNFIWQDPVPAADAGNKK.E	YIGPWIPEQNFIWQDPVPAAD	741	445	3.233	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	D.PVPAADYAGNKK.E	PVPAADY	741	446	3.946	0.008
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.QNFIWQDPVPAADYKQVSAGNKKE.N	QNFIWQDPVPAADYKQVS	741	450	2.861	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	K.QVSTQDIAQLAGNKK.E	QVSTQDIAQL	741	457	2.88	0.001
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	K.QVSTQDIAQLEQDIIAGNKK.E	QVSTQDIAQLEQDII	741	462	2.363	0.001
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	K.QVSTQDIAQLEQDIINSGAGNKK.E	QVSTQDIAQLEQDIINSG	741	465	2.681	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.QDIINSGLTAGNKKE.N	QDIINSGLT	741	467	3.384	0.009
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.QDIINSGLTNAGNKKE.N	QDIINSGLTN	741	468	3.058	0.001
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.QDIINSGLTNQQLAGNKKE.N	QDIINSGLTNQQL	741	471	3.641	0.002
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.QDIINSGLTNQQLIAGNKKE.N	QDIINSGLTNQQLI	741	472	3.963	0.002
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.QDIINSGLTNQQLIKAGNKKE.N	QDIINSGLTNQQLIK	741	473	2.534	0.005
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.QDIINSGLTNQQLIKTAGNKKE.N	QDIINSGLTNQQLIKT	741	474	2.811	0.001
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.QDIINSGLTNQQLIKTAAGNKKE.N	QDIINSGLTNQQLIKTA	741	475	2.642	0.001
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.QDIINSGLTNQQLIKTAWDSAGNKKE.N	QDIINSGLTNQQLIKTAWDS	741	478	2.801	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.QDIINSGLTNQQLIKTAWDSASAGNKKE.N	QDIINSGLTNQQLIKTAWDSAS	741	480	2.666	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	K.TAWDSASAGNK.K	TAWDSAS	741	480	2.467	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.QDIINSGLTNQQLIKTAWDSASTAGNKKE.N	QDIINSGLTNQQLIKTAWDSAST	741	481	2.305	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	K.TAWDSASTAGNKK.E	TAWDSAST	741	481	4.115	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.QDIINSGLTNQQLIKTAWDSASTYAGNKKE.N	QDIINSGLTNQQLIKTAWDSASTY	741	482	2.471	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	R.IALAPEKAGNK.K	IALAPEK	741	502	3.542	0.009
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	R.IALAPEKDAGNKK.E	IALAPEKD	741	503	4.087	0.001
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	R.IALAPEKDWAGNKK.E	IALAPEKDW	741	504	4.378	0.009
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	R.IALAPEKDWAGNKKENR.V	IALAPEKDW	741	504	3.71	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	R.IALAPEKDWQAGNKK.E	IALAPEKDWQ	741	505	3.652	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	R.IALAPEKDWQMNEAGNK.K	IALAPEKDWQMNE	741	508	3.162	0.001
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	R.IALAPEKDWQMNEPAGNKK.E	IALAPEKDWQMNEP	741	509	4.158	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	R.IALAPEKDWQMNEPAKLEAGNKK.E	IALAPEKDWQMNEPAKLE	741	513	3.374	0.003
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	R.IALAPEKDWQMNEPAKLEVAGNKK.E	IALAPEKDWQMNEPAKLEV	741	514	3.161	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	R.IALAPEKDWQM+16NEPAKLEVAGNKK.E	IALAPEKDWQMNEPAKLEV	741	514	2.562	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	R.IALAPEKDWQMNEPAKLEVVAGNKK.E	IALAPEKDWQMNEPAKLEVV	741	515	3.552	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	R.IALAPEKDWQMNEPAKLEVVLAGNKK.E	IALAPEKDWQMNEPAKLEVVL	741	516	3.447	0.000
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	K.LEVVLAGNKK.E	LEVVL	741	516	3.07	0.002
splQ2A298lKATG_FRATH	Catalase-peroxidase katG	E.IQTNFAGNKKE.N	IQTNF	741	526	3.625	0.004

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.LKEIQTNFAGNKK.E	LKEIQTNF	741	526	3.93	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.LKEIQTNFAGNK.K	LKEIQTNF	741	526	3.902	0.001
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.IQTNFNAGNKKE.N	IQTNFN	741	527	3.821	0.005
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.IQTNFNAGNKKENR.V	IQTNFN	741	527	3.264	0.003
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.LKEIQTNFNAGNKK.E	LKEIQTNFN	741	527	3.986	0.008
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.IQTNFNNAGNKKE.N	IQTNFNN	741	528	3.859	0.003
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.LKEIQTNFNNAGNKK.E	LKEIQTNFNN	741	528	4.004	0.001
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	*.EIQTNFNNSAGNKK.E	EIQTNFNNS	741	529	3.325	0.008
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.IQTNFNNSAGNKKE.N	IQTNFNNS	741	529	3.849	0.004
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.IQTNFNNSKAGNKKE.N	IQTNFNNSK	741	530	3.861	0.002
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.IQTNFNNSKTDAGNKKE.N	IQTNFNNSKTD	741	532	3.746	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.IQTNFNNSKTDGAGNKKE.N	IQTNFNNSKTDG	741	533	4.177	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.IQTNFNNSKTDGAGNKKENR.V	IQTNFNNSKTDG	741	533	3.331	0.001
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.IQTNFNNSKTDGTAGNKKE.N	IQTNFNNSKTDGT	741	534	4.108	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.IQTNFNNSKTDGTAGNKKENR.V	IQTNFNNSKTDGT	741	534	3.13	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.IQTNFNNSKTDGTKAGNKKE.N	IQTNFNNSKTDGTK	741	535	2.778	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.IQTNFNNSKTDGTKVAGNKKE.N	IQTNFNNSKTDGTKV	741	536	4.088	0.003
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.IQTNFNNSKTDGTKVSAGNKKE.N	IQTNFNNSKTDGTKVS	741	537	3.209	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.IQTNFNNSKTDGTKVSLAGNKKE.N	IQTNFNNSKTDGTKVSL	741	538	2.814	0.003
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.IQTNFNNSKTDGTKVSLAAGNKKE.N	IQTNFNNSKTDGTKVSLA	741	539	3.277	0.002
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.VSLAAGNKK.E	VSLA	741	539	2.851	0.006
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.IQTNFNNSKTDGTKVSLADLAGNKKE.N	IQTNFNNSKTDGTKVSLADL	741	541	3.268	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.VSLADLAGNKK.E	VSLADL	741	541	3.733	0.003
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.VSLADLIVAGNKK.E	VSLADLIV	741	543	4.24	0.001
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.VSLADLIVLAGNKK.E	VSLADLIVL	741	544	4.341	0.009
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.VSLADLIVLAGNK.K	VSLADLIVL	741	544	3.055	0.006
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.VSLADLIVLGAGNKK.E	VSLADLIVLG	741	545	4.356	0.001
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	D.LIVLGGAGNKKE.N	LIVLGG	741	546	4.069	0.002
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.VSLADLIVLGGAGNKK.E	VSLADLIVLGG	741	546	4.205	0.001
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	D.LIVLGGNAGNKKE.N	LIVLGGN	741	547	4.123	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.VSLADLIVLGGNAGNKK.E	VSLADLIVLGGN	741	547	4.409	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	D.LIVLGGNVAGNKKE.N	LIVLGGNV	741	548	3.206	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.VSLADLIVLGGNVAGNKK.E	VSLADLIVLGGNV	741	548	4.488	0.000

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.VSLADLIVLGGNVAGNK.K	VSLADLIVLGGNV	741	548	4.163	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.VSLADLIVLGGNVGAGNK.K	VSLADLIVLGGNVG	741	549	3.422	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.VSLADLIVLGGNVGVAGNKK.E	VSLADLIVLGGNVGV	741	550	4.472	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.VSLADLIVLGGNVGVAGNK.K	VSLADLIVLGGNVGV	741	550	4.039	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.VSLADLIVLGGNVGVEQAGNKK.E	VSLADLIVLGGNVGVEQ	741	552	4.386	0.002
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.VSLADLIVLGGNVGVEQAAAGNK.K	VSLADLIVLGGNVGVEQAA	741	554	3.942	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.QAAKQAGYNIAGNKKE.N	QAAKQAGYNI	741	561	2.533	0.001
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.QAAKQAGYNIQAGNKKE.N	QAAKQAGYNIQ	741	562	2.706	0.008
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.QAGYNIQMPFAGNK.K	QAGYNIQMPF	741	565	2.708	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.QAGYNIQMPFVAGNKK.E	QAGYNIQMPFV	741	566	3.187	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.QAGYNIQMPFVPGAGNK.K	QAGYNIQMPFVPG	741	568	3.349	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	R.TDATQAQTAGNKK.E	TDATQAQT	741	577	3.55	0.008
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	R.TDATQAQTDAGNKK.E	TDATQAQTD	741	578	3.883	0.002
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	R.TDATQAQTDAGNKKENR.V	TDATQAQTD	741	578	3.568	0.003
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.SFNYLKTAGNKKE.N	SFNYLKT	741	587	3.959	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.SFNYLKTKSDAGNKKE.N	SFNYLKTKSD	741	590	4.178	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.SFNYLKTKSDGAGNKKE.N	SFNYLKTKSDG	741	591	4.094	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.SDGFAGNKK.E	SDGF	741	592	3.428	0.001
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.SFNYLKTKSDGFAGNKKE.N	SFNYLKTKSDGF	741	592	3.047	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.TKSDGFAGNKK.E	TKSDGF	741	592	3.272	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.SDGFINAGNKK.E	SDGFIN	741	594	4.033	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.TKSDGFINAGNKK.E	TKSDGFIN	741	594	3.915	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.TKSDGFINYAGNKK.E	TKSDGFINY	741	595	3.711	0.004
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.SFNYLKTKSDGFINYTDGAGNKKE.N	SFNYLKTKSDGFINYTDG	741	598	3.52	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.SFNYLKTKSDGFINYTDGSIAGNKKE.N	SFNYLKTKSDGFINYTDGSI	741	600	3.513	0.006
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.SFNYLKTKSDGFINYTDGSIAGNK.K	SFNYLKTKSDGFINYTDGSI	741	600	3.104	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.SFNYLKTKSDGFINYTDGSISAAGNKKE.N	SFNYLKTKSDGFINYTDGSISA	741	602	3.518	0.003
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.SFNYLKTKSDGFINYTDGSISADAGNKKE.N	SFNYLKTKSDGFINYTDGSISAD	741	603	3.633	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.SFNYLKTKSDGFINYTDGSISADKLAGNKKE.N	SFNYLKTKSDGFINYTDGSISADKL	741	605	3.197	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.SDGFINYTDGSISADKLPQTLAGNKK.E	SDGFINYTDGSISADKLPQTL	741	609	3.548	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.LPQTLVAGNK.K	LPQTLV	741	610	4.094	0.009
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.TKSDGFINYTDGSISADKLPQTLVAGNKK.E	TKSDGFINYTDGSISADKLPQTLV	741	610	3.745	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.ASMLDLNIPAGNKK.E	ASMLDLNIP	741	621	4.051	0.000

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.MTVLVGGAGNKKE.N	MTVLVGG	741	629	3.982	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.M+16TVLVGGAGNKKE.N	MTVLVGG	741	629	3.027	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.GVLTTTPAGNKKE.N	GVLTTTP	741	649	3.921	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.GVLTTTPAGNKK.E	GVLTTTP	741	649	2.121	0.008
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.GVLTTTPGAGNKKE.N	GVLTTTPG	741	650	3.429	0.001
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.GVLTTTPGQAGNKKE.N	GVLTTTPGQ	741	651	4.01	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.GVLTTTPGQAGNKK.E	GVLTTTPGQ	741	651	2.323	0.001
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.GVLTTTPGQLAGNKKE.N	GVLTTTPGQL	741	652	4.237	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.GVLTTTPGQLAGNKK.E	GVLTTTPGQL	741	652	3.196	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.GVLTTTPGQLAGNK.K	GVLTTTPGQL	741	652	2.859	0.002
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.GVLTTTPGQLNAGNKK.E	GVLTTTPGQLN	741	653	4.199	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.GVLTTTPGQLNAGNKKE.N	GVLTTTPGQLN	741	653	3.521	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.GVLTTTPGQLNNAGNKKE.N	GVLTTTPGQLNN	741	654	4.152	0.002
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.GVLTTTPGQLNNSAGNKKE.N	GVLTTTPGQLNNS	741	655	4.165	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.GVLTTTPGQLNNSFAGNKKE.N	GVLTTTPGQLNNSF	741	656	4.26	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.GVLTTTPGQLNNSFFAGNK.K	GVLTTTPGQLNNSFF	741	657	4.38	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.GVLTTTPGQLNNSFFAGNKKE.N	GVLTTTPGQLNNSFF	741	657	2.29	0.003
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.GVLTTTPGQLNNSFFVAGNK.K	GVLTTTPGQLNNSFFV	741	658	4.36	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.GVLTTTPGQLNNSFFVNLLAGNK.K	GVLTTTPGQLNNSFFVNLL	741	661	2.79	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	E.GVLTTTPGQLNNSFFVNLLDMSTAGNKKE.N	GVLTTTPGQLNNSFFVNLLDMST	741	665	2.767	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.WTASPVDLAGNKK.E	WTASPVDL	741	696	3.834	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.WTASPVDLIAGNKK.E	WTASPVDLI	741	697	4.181	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.WTASPVDLIAGNK.K	WTASPVDLI	741	697	3.183	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.QKWTASPVDLIFAGNKK.E	QKWTASPVDLIF	741	698	2.523	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.WTASPVDLIFAGNKK.E	WTASPVDLIF	741	698	4.366	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.WTASPVDLIFAGNK.K	WTASPVDLIF	741	698	4.147	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.WTASPVDLIFGSAGNK.K	WTASPVDLIFGS	741	700	3.453	0.000
sp|Q2A298|KATG_FRATH	Catalase-peroxidase katG	K.FVNDFAGNKK.E	FVNDF	741	724	3.76	0.004
sp|Q2A2B1|GPMI_FRATH	2,3-bisphosphoglycerate-	K.TIFNFEKAGNK.K	TIFNFEK	512	512	3.277	0.009
sp|Q2A2E4|RL21_FRATH	50S ribosomal protein L2	K.VSSISLAGNKK.E	VSSISL	104	104	3.943	0.000
sp|Q2A2J0|SYT_FRATH	Threonyl-tRNA synthetas	R.TPLIADFSLAGNKK.E	TPLIADFSL	634	301	3.137	0.001
sp|Q2A2J2|RL35_FRATH	50S ribosomal protein L3	K.VDTTSLVQQMPAGNKK.E	VDTTSLVQQMP	65	63	4.247	0.000
sp|Q2A311|DCD_FRATH	Deoxycytidine triphospha	E.FKIFTNINSSAGNKKE.N	FKIFTNINSS	188	62	2.988	0.002

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

splQ2A311lDCD_FRATH	Deoxycytidine triphospha	E.GVAQMLFFAGNKKE.N	GVAQMLFF	188	160	4.095	0.001
splQ2A311lDCD_FRATH	Deoxycytidine triphospha	K.IYANEGVAQMLFFAGNK.K	IYANEGVAQMLFF	188	160	4.237	0.000
splQ2A311lDCD_FRATH	Deoxycytidine triphospha	E.GVAQMLFFQSAGNKKE.N	GVAQMLFFQS	188	162	4.051	0.000
splQ2A311lDCD_FRATH	Deoxycytidine triphospha	E.TSYADKGGKYQGQVGAGNKKE.N	TSYADKGGKYQGQVG	188	182	3.125	0.000
splQ2A311lDCD_FRATH	Deoxycytidine triphospha	E.TSYADKGGKYQGQVGVAGNKKE.N	TSYADKGGKYQGQVGV	188	183	3.333	0.000
splQ2A311lDCD_FRATH	Deoxycytidine triphospha	K.YQGQVGVAGNKK.E	YQGQVGV	188	183	3.714	0.000
splQ2A311lDCD_FRATH	Deoxycytidine triphospha	E.TSYADKGGKYQGQVGVTAGNKKE.N	TSYADKGGKYQGQVGVT	188	184	3.324	0.000
splQ2A311lDCD_FRATH	Deoxycytidine triphospha	K.YQGQVGVTAGNKK.E	YQGQVGVT	188	184	4.222	0.008
splQ2A311lDCD_FRATH	Deoxycytidine triphospha	E.TSYADKGGKYQGQVGVTLAGNKKE.N	TSYADKGGKYQGQVGVTL	188	185	3.511	0.007
splQ2A311lDCD_FRATH	Deoxycytidine triphospha	K.YQGQVGVTLAGNKK.E	YQGQVGVTL	188	185	4.148	0.000
splQ2A311lDCD_FRATH	Deoxycytidine triphospha	E.TSYADKGGKYQGQVGVTLPAGNKKE.N	TSYADKGGKYQGQVGVTLP	188	186	3.367	0.000
splQ2A311lDCD_FRATH	Deoxycytidine triphospha	K.YQGQVGVTLPAGNKK.E	YQGQVGVTLP	188	186	4.278	0.009
splQ2A327lDNAJ_FRATH	Chaperone protein dnaJ d	R.YDQFGHAGVAGNKK.E	YDQFGHAGV	371	74	3.905	0.008
splQ2A327lDNAJ_FRATH	Chaperone protein dnaJ d	R.YDQFGHAGVAGNK.K	YDQFGHAGV	371	74	2.235	0.006
splQ2A327lDNAJ_FRATH	Chaperone protein dnaJ d	R.YDQFGHAGVNQQSGAGNK.K	YDQFGHAGVNQQSG	371	79	3.591	0.000
splQ2A328lDNAK_FRATH	Chaperone protein dnaK c	K.IIGIDLGTTNSC+57LAAGNKK.E	IIGIDLGTTNSCLA	642	17	2.507	0.005
splQ2A328lDNAK_FRATH	Chaperone protein dnaK c	R.IINEPTAAALAYGAGNKKE.N	IINEPTAAALAYG	642	182	3.198	0.002
splQ2A328lDNAK_FRATH	Chaperone protein dnaK c	R.IINEPTAAALAYGVDAGNK.K	IINEPTAAALAYGVD	642	184	4.184	0.000
splQ2A328lDNAK_FRATH	Chaperone protein dnaK c	R.IINEPTAAALAYGVDAGNKKE.N	IINEPTAAALAYGVD	642	184	2.535	0.006
splQ2A328lDNAK_FRATH	Chaperone protein dnaK c	E.SLVSDLVMRSLEPCAGNKKE.N	SLVSDLVMRSLEPC	642	322	3.34	0.008
splQ2A328lDNAK_FRATH	Chaperone protein dnaK c	E.AVAVGAAAGNKKE.N	AVAVGAA	642	378	4.03	0.003
splQ2A328lDNAK_FRATH	Chaperone protein dnaK c	E.AVAVGAAIAGNKKE.N	AVAVGAAI	642	379	4.102	0.003
splQ2A328lDNAK_FRATH	Chaperone protein dnaK c	E.AVAVGAAIQAGNKKE.N	AVAVGAAIQ	642	380	4.046	0.000
splQ2A328lDNAK_FRATH	Chaperone protein dnaK c	E.AVAVGAAIQAGNKK.E	AVAVGAAIQ	642	380	3.518	0.000
splQ2A328lDNAK_FRATH	Chaperone protein dnaK c	E.AVAVGAAIQGAGNKKE.N	AVAVGAAIQG	642	381	4.215	0.000
splQ2A328lDNAK_FRATH	Chaperone protein dnaK c	E.AVAVGAAIQGGAGNKKE.N	AVAVGAAIQGG	642	382	3.841	0.000
splQ2A328lDNAK_FRATH	Chaperone protein dnaK c	R.KDVNPDEAVAVGAAIQGGVLAGAGNK.K	KDVNPDEAVAVGAAIQGGVLAG	642	386	3.753	0.000
splQ2A328lDNAK_FRATH	Chaperone protein dnaK c	R.KDVNPDEAVAVGAAIQGGVLAGDVKAGNK.K	KDVNPDEAVAVGAAIQGGVLAGDVK	642	389	3.618	0.000
splQ2A328lDNAK_FRATH	Chaperone protein dnaK c	E.AVAVGAAIQGGVLAGDVKDVLAGNKKE.N	AVAVGAAIQGGVLAGDVKDVL	642	392	3.198	0.000
splQ2A328lDNAK_FRATH	Chaperone protein dnaK c	D.VLLLDVAGNKK.E	VLLLDV	642	396	3.586	0.001
splQ2A328lDNAK_FRATH	Chaperone protein dnaK c	D.VLLLDVTAGNKKE.N	VLLLDVT	642	397	3.36	0.000
splQ2A328lDNAK_FRATH	Chaperone protein dnaK c	K.DVLLLDVTPAGNKK.E	DVLLLDVTP	642	398	3.357	0.001
splQ2A328lDNAK_FRATH	Chaperone protein dnaK c	K.DVLLLDVTPLSAGNKK.E	DVLLLDVTPLS	642	400	2.813	0.003

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

splQ2A328lDNAK_FRATH	Chaperone protein dnaK c	D.VTPLSAGNKKE.N	VTPLS	642	400	2.8	0.008
splQ2A328lDNAK_FRATH	Chaperone protein dnaK c	K.DVLLLDVTPLSLAGNKK.E	DVLLLDVTPLSL	642	401	4.353	0.000
splQ2A328lDNAK_FRATH	Chaperone protein dnaK c	D.VTPLSLAGNKKE.N	VTPLSL	642	401	4.04	0.000
splQ2A328lDNAK_FRATH	Chaperone protein dnaK c	D.VTPLSLAGNKK.E	VTPLSL	642	401	3.987	0.000
splQ2A328lDNAK_FRATH	Chaperone protein dnaK c	D.VTPLSLGAGNKKE.N	VTPLSLG	642	402	3.422	0.001
splQ2A328lDNAK_FRATH	Chaperone protein dnaK c	K.DVLLLDVTPLSLGIAGNKK.E	DVLLLDVTPLSLGI	642	403	4.429	0.000
splQ2A328lDNAK_FRATH	Chaperone protein dnaK c	K.DVLLLDVTPLSLGIAGNK.K	DVLLLDVTPLSLGI	642	403	4.414	0.000
splQ2A328lDNAK_FRATH	Chaperone protein dnaK c	D.VTPLSLGIAGNKKE.N	VTPLSLGI	642	403	4.278	0.006
splQ2A328lDNAK_FRATH	Chaperone protein dnaK c	D.VTPLSLGIAGNK.K	VTPLSLGI	642	403	2.898	0.006
splQ2A328lDNAK_FRATH	Chaperone protein dnaK c	K.DVLLLDVTPLSLGIETMGGVAGNKK.E	DVLLLDVTPLSLGIETMGGV	642	409	2.546	0.002
splQ2A328lDNAK_FRATH	Chaperone protein dnaK c	E.TMGGVMTAGNKKE.N	TMGGVMT	642	411	3.633	0.000
splQ2A328lDNAK_FRATH	Chaperone protein dnaK c	E.ADKKFHDLVAGNKKE.N	ADKKFHDLV	642	535	4.229	0.000
splQ2A328lDNAK_FRATH	Chaperone protein dnaK c	K.FHDLVAGNKK.E	FHDLV	642	535	4.034	0.004
splQ2A328lDNAK_FRATH	Chaperone protein dnaK c	K.FHDLVAGNK.K	FHDLV	642	535	3.648	0.000
splQ2A328lDNAK_FRATH	Chaperone protein dnaK c	E.ADKKFHDLVTAGNKKE.N	ADKKFHDLVT	642	536	2.891	0.001
splQ2A328lDNAK_FRATH	Chaperone protein dnaK c	K.FHDLVTAGNK.K	FHDLVT	642	536	3.683	0.001
splQ2A328lDNAK_FRATH	Chaperone protein dnaK c	K.FHDLVTAGNKK.E	FHDLVT	642	536	3.426	0.000
splQ2A328lDNAK_FRATH	Chaperone protein dnaK c	E.ADKKFHDLVTAAGNKKE.N	ADKKFHDLVTA	642	537	2.786	0.000
splQ2A328lDNAK_FRATH	Chaperone protein dnaK c	K.FHDLVTAAGNKK.E	FHDLVTA	642	537	4.141	0.000
splQ2A328lDNAK_FRATH	Chaperone protein dnaK c	K.FHDLVTAAGNK.K	FHDLVTA	642	537	4.098	0.000
splQ2A328lDNAK_FRATH	Chaperone protein dnaK c	R.NTADNLIHAGNKK.E	NTADNLIH	642	546	3.358	0.000
splQ2A328lDNAK_FRATH	Chaperone protein dnaK c	R.NTADNLIHSAGNK.K	NTADNLIHS	642	547	3.748	0.000
splQ2A328lDNAK_FRATH	Chaperone protein dnaK c	R.NTADNLIHSAGNKK.E	NTADNLIHS	642	547	3.735	0.000
splQ2A328lDNAK_FRATH	Chaperone protein dnaK c	R.NTADNLIHSAGNKKE.N	NTADNLIHS	642	547	3.412	0.000
splQ2A328lDNAK_FRATH	Chaperone protein dnaK c	R.NTADNLIHSSAGNKK.E	NTADNLIHSS	642	548	3.959	0.000
splQ2A328lDNAK_FRATH	Chaperone protein dnaK c	R.KAIQELGAGNKK.E	KAIQELG	642	556	3.899	0.001
splQ2A328lDNAK_FRATH	Chaperone protein dnaK c	E.LGDKVTAAGNKKE.N	LGDKVTA	642	561	3.906	0.008
splQ2A328lDNAK_FRATH	Chaperone protein dnaK c	E.LGDKVTAAGNKK.E	LGDKVTA	642	561	2.143	0.000
splQ2A328lDNAK_FRATH	Chaperone protein dnaK c	E.AATKGDDKQAIEAAGNKK.E	AATKGDDKQAIEA	642	588	2.147	0.003
splQ2A328lDNAK_FRATH	Chaperone protein dnaK c	E.AFAPAGNKKE.N	AFAP	642	599	3.994	0.001
splQ2A328lDNAK_FRATH	Chaperone protein dnaK c	K.ALEEAFAPAGNKK.E	ALEEAFAP	642	599	2	0.005
splQ2A328lDNAK_FRATH	Chaperone protein dnaK c	E.AFAPIAQAGNKKE.N	AFAPIAQ	642	602	3.873	0.000
splQ2A328lDNAK_FRATH	Chaperone protein dnaK c	E.AFAPIAQAGNK.K	AFAPIAQ	642	602	3.142	0.005

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

sp|Q2A328|DNAK_FRATH	Chaperone protein dnaK c	K.ALEEAFAPIAQAGNK.K	ALEEAFAPIAQ	642	602	4.218	0.000
sp|Q2A328|DNAK_FRATH	Chaperone protein dnaK c	E.AFAPIAQKAAGNKKE.N	AFAPIAQKA	642	604	3.066	0.000
sp|Q2A328|DNAK_FRATH	Chaperone protein dnaK c	K.AYAEQAQAAGAQAGNK.K	AYAEQAQAAGAQ	642	615	4.189	0.000
sp|Q2A328|DNAK_FRATH	Chaperone protein dnaK c	K.AYAEQAQAAGAQGGAGNKK.E	AYAEQAQAAGAQGG	642	617	4.206	0.001
sp|Q2A328|DNAK_FRATH	Chaperone protein dnaK c	E.QAQAAGAQGGAKAEEPAGNKKE.N	QAQAAGAQGGAKAEEP	642	623	2.923	0.001
sp|Q2A328|DNAK_FRATH	Chaperone protein dnaK c	K.AEEPKKEEDVAGNKK.E	AEEPKKEEDV	642	629	4.098	0.000
sp|Q2A328|DNAK_FRATH	Chaperone protein dnaK c	K.AEEPKKEEDVVAGNKK.E	AEEPKKEEDVV	642	630	3.633	0.000
sp|Q2A332|RL13_FRATH	50S ribosomal protein L1	K.VYAGEAHPAGNKK.E	VYAGEAHP	142	131	3.607	0.000
sp|Q2A332|RL13_FRATH	50S ribosomal protein L1	K.VYAGEAHPHAGNKK.E	VYAGEAHPH	142	132	3.833	0.000
sp|Q2A332|RL13_FRATH	50S ribosomal protein L1	K.VYAGEAHPHAGNK.K	VYAGEAHPH	142	132	3.073	0.000
sp|Q2A332|RL13_FRATH	50S ribosomal protein L1	K.VYAGEAHPHTAAGNKK.E	VYAGEAHPHTA	142	134	3.5	0.004
sp|Q2A332|RL13_FRATH	50S ribosomal protein L1	K.VYAGEAHPHTAQAGNKK.E	VYAGEAHPHTAQ	142	135	2.531	0.009
sp|Q2A332|RL13_FRATH	50S ribosomal protein L1	K.VYAGEAHPHTAQQPAGNKK.E	VYAGEAHPHTAQQP	142	137	3.198	0.000
sp|Q2A369|PGK_FRATH	Phosphoglycerate kinase	K.YIPVAC+57AGILLTNEIQAGNKK.E	YIPVACAGILLTNEIQ	392	172	3.831	0.000
sp|Q2A369|PGK_FRATH	Phosphoglycerate kinase	K.LSVLNNLLAGNK.K	LSVLNNLL	392	205	3.972	0.000
sp|Q2A3H5|RL9_FRATH	50S ribosomal protein L9	E.AAVAVADAIKAGNKKE.N	AAVAVADAIK	151	73	3.8	0.000
sp|Q2A3H5|RL9_FRATH	50S ribosomal protein L9	E.AAVAVADAIKDAGNKKE.N	AAVAVADAIKD	151	74	4.144	0.000
sp|Q2A3H5|RL9_FRATH	50S ribosomal protein L9	E.AAVAVADAIKDKVAGNKKE.N	AAVAVADAIKDKV	151	76	3.262	0.000
sp|Q2A3H5|RL9_FRATH	50S ribosomal protein L9	E.AAVAVADAIKDKVYAGNKKE.N	AAVAVADAIKDKVY	151	77	3.587	0.000
sp|Q2A3H5|RL9_FRATH	50S ribosomal protein L9	E.AAVAVADAIKDKVYTAGNKKE.N	AAVAVADAIKDKVYT	151	78	3.316	0.000
sp|Q2A3H5|RL9_FRATH	50S ribosomal protein L9	K.VNVVAAEAAGNKK.E	VNVVAAEA	151	151	4.132	0.003
sp|Q2A3H7|RS6_FRATH	30S ribosomal protein S6	E.AITEPSVAGNKKE.N	AITEPSV	111	101	4.139	0.000
sp|Q2A3H7|RS6_FRATH	30S ribosomal protein S6	E.AITEPSVMAGNKKE.N	AITEPSVM	111	102	4.407	0.000
sp|Q2A3H7|RS6_FRATH	30S ribosomal protein S6	E.AITEPSVM+16AGNKKE.N	AITEPSVM	111	102	2.957	0.002
sp|Q2A3H7|RS6_FRATH	30S ribosomal protein S6	*.EAITEPSVMAGNKK.E	EAITEPSVM	111	102	2.777	0.006
sp|Q2A3H7|RS6_FRATH	30S ribosomal protein S6	E.AITEPSVMMEAGNKK.E	AITEPSVMME	111	104	3.809	0.000
sp|Q2A3H7|RS6_FRATH	30S ribosomal protein S6	E.AITEPSVM+16MEAGNKK.E	AITEPSVMME	111	104	2.612	0.002
sp|Q2A3H7|RS6_FRATH	30S ribosomal protein S6	E.AITEPSVMM+16EAGNKK.E	AITEPSVMME	111	104	2.571	0.000
sp|Q2A3M7|HSLU_FRATH	ATP-dependent hsl prote	K.KMRIKDAIAGNKKE.N	KMRIKDAI	455	234	3.448	0.000
sp|Q2A3R0|Y929_FRATH	UPF0082 protein FTL_09	K.VMALIDKLEDLDYVQSVYSNANFAGNKK.E	VMALIDKLEDLDYVQSVYSNANF	248	239	3.513	0.000
sp|Q2A3R0|Y929_FRATH	UPF0082 protein FTL_09	K.VMALIDKLEDLDYVQSVYSNANFTQAGNK.K	VMALIDKLEDLDYVQSVYSNANFTQ	248	241	3.672	0.000
sp|Q2A3R0|Y929_FRATH	UPF0082 protein FTL_09	E.LIEQIGAGNKKE.N	LIEQIG	248	248	3.748	0.006
sp|Q2A3T5|HFQ_FRATH	Protein hfq hfq	K.HAISTIVAGNK.K	HAISTIV	109	63	4.112	0.001

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

splQ2A3T5lHFQ_FRATH	Protein hfq hfq	K.HAISTIVPAGNK.K	**HAISTIVP**	109	64	4.17	0.000
splQ2A3T5lHFQ_FRATH	Protein hfq hfq	K.HAISTIVPAGNKKE.N	**HAISTIVP**	109	64	3.618	0.000
splQ2A3T5lHFQ_FRATH	Protein hfq hfq	K.HAISTIVPAAGNK.K	**HAISTIVPA**	109	65	4.23	0.005
splQ2A3T5lHFQ_FRATH	Protein hfq hfq	R.M+16VYSSFNAGNKK.E	MVYSSFN	109	76	3.396	0.000
splQ2A3T5lHFQ_FRATH	Protein hfq hfq	R.MVYSSFNAGNK.K	MVYSSFN	109	76	3.296	0.000
splQ2A3T5lHFQ_FRATH	Protein hfq hfq	R.MVYSSFNPAGNKK.E	MVYSSFNP	109	77	4.247	0.000
splQ2A3T5lHFQ_FRATH	Protein hfq hfq	R.M+16VYSSFNPAGNKK.E	MVYSSFNP	109	77	3.205	0.000
splQ2A3T5lHFQ_FRATH	Protein hfq hfq	R.MVYSSFNPYHAGNK.K	MVYSSFNPYH	109	79	4.095	0.000
splQ2A3T5lHFQ_FRATH	Protein hfq hfq	R.MVYSSFNPYHQNSAGNK.K	MVYSSFNPYHQNS	109	82	4.369	0.000
splQ2A3T5lHFQ_FRATH	Protein hfq hfq	R.M+16VYSSFNPYHQNSAGNK.K	MVYSSFNPYHQNS	109	82	3.576	0.000
splQ2A3T5lHFQ_FRATH	Protein hfq hfq	R.MVYSSFNPYHQNSNDEQDENVDDIAGNKK.E	MVYSSFNPYHQNSNDEQDENVDDI	109	93	3.429	0.000
splQ2A3U2lTIG_FRATH	Trigger factor tig	E.NMQAQQAGFAGNKKE.N	NMQAQQAGF	438	438	3.851	0.000
splQ2A419lAROK_FRATH	Shikimate kinase aroK	K.NIFLIGPVAGNK.K	NIFLIGPV	176	13	3.372	0.001
splQ2A419lAROK_FRATH	Shikimate kinase aroK	K.ISTFLVEAGNKK.E	ISTFLVE	176	172	3.304	0.000
splQ2A4C6lPANB_FRATH	3-methyl-2-oxobutanoate	E.TKANTFPAGNKKE.N	TKANTFP	265	256	4.084	0.000
splQ2A4C6lPANB_FRATH	3-methyl-2-oxobutanoate	E.TKANTFPTAGNKKE.N	TKANTFPT	265	257	4.133	0.000
splQ2A4C6lPANB_FRATH	3-methyl-2-oxobutanoate	K.ANTFPTKEHC+57AGNKK.E	ANTFPTKEHC	265	261	2.353	0.000
splQ2A4C6lPANB_FRATH	3-methyl-2-oxobutanoate	K.ANTFPTKEHC+57YAGNKK.E	ANTFPTKEHCY	265	262	3.034	0.000
splQ2A4C6lPANB_FRATH	3-methyl-2-oxobutanoate	K.ANTFPTKEHC+57YDAGNKK.E	ANTFPTKEHCYD	265	263	2.824	0.000
splQ2A4C6lPANB_FRATH	3-methyl-2-oxobutanoate	K.ANTFPTKEHC+57YDYAGNKK.E	ANTFPTKEHCYDY	265	264	2.878	0.000
splQ2A4C6lPANB_FRATH	3-methyl-2-oxobutanoate	E.HC+57YDYAGNKKE.N	HCYDY	265	264	3.517	0.000
splQ2A4C6lPANB_FRATH	3-methyl-2-oxobutanoate	K.ANTFPTKEHC+57YDYC+57AGNKK.E	ANTFPTKEHCYDYC	265	265	2.646	0.000
splQ2A4C6lPANB_FRATH	3-methyl-2-oxobutanoate	E.HC+57YDYC+57AGNKKE.N	HCYDYC	265	265	3.607	0.000
splQ2A4C7lPANC_FRATH	Pantothenate synthetase	E.LTNKINSAGNKKE.N	LTNKINS	261	223	3.113	0.000
splQ2A4C7lPANC_FRATH	Pantothenate synthetase	E.LTNKINSTAGNKKE.N	LTNKINST	261	224	3.659	0.000
splQ2A4C7lPANC_FRATH	Pantothenate synthetase	E.LTNKINSTGAGNKKE.N	LTNKINSTG	261	225	3.815	0.000
splQ2A4C7lPANC_FRATH	Pantothenate synthetase	E.LTNKINSTGAAGNKKE.N	LTNKINSTGA	261	226	4.049	0.000
splQ2A4R2lRL33_FRATH	50S ribosomal protein L3	K.M+16EIKKYDAGNK.K	MEIKKYD	51	36	3.023	0.004
splQ2A4R5lMINE_FRATH	Cell division topological s	E.VNIPFNAGNKKE.N	VNIPFN	90	90	4	0.000
splQ2A4U1lSYGA_FRATH	Glycyl-tRNA synthetase a	R.HAISAGNKKE.N	HAIS	296	258	3.05	0.005
splQ2A4V1lGCSPA_FRATH	Probable glycine dehydro	K.VLIAEALAGNKK.E	VLIAEAL	455	161	3.334	0.001
splQ2A4V1lGCSPA_FRATH	Probable glycine dehydro	R.VASISHENTQTLATAGNKK.E	VASISHENTQTLAT	455	369	4.254	0.000
splQ2A4Y0lPSD_FRATH	Phosphatidylserine decar	E.ENKNNIAGNKK.E	ENKNNI	283	270	2.716	0.004

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

sp|Q2A4Y0|PSD_FRATH	Phosphatidylserine decarb	K.IQVNQDLALIAGNKK.E	IQVNQDLALI	283	281	4.149	0.002
sp|Q2A4Y0|PSD_FRATH	Phosphatidylserine decarb	K.IQVNQDLALITAGNKK.E	IQVNQDLALIT	283	282	4.207	0.000
sp|Q2A5B4|ACCA_FRATH	Acetyl-coenzyme A carbo	K.DLLPLIFTDFQELHGAGNK.K	DLLPLIFTDFQELHG	315	84	2.703	0.000
sp|Q2A5B6|SECB2_FRATH	Protein-export protein sec	K.GGFLPLNLAPIAGNK.K	GGFLPLNLAPI	147	130	4.351	0.000
sp|Q2A5B6|SECB2_FRATH	Protein-export protein sec	K.GGFLPLNLAPINFDAGNK.K	GGFLPLNLAPINFD	147	133	3.242	0.000
sp|Q2A5B6|SECB2_FRATH	Protein-export protein sec	K.GGFLPLNLAPINFDAAGNK.K	GGFLPLNLAPINFDA	147	134	3.605	0.000
sp|Q2A5B6|SECB2_FRATH	Protein-export protein sec	K.GGFLPLNLAPINFDAIAGNK.K	GGFLPLNLAPINFDAI	147	135	4.406	0.000
sp|Q2A5B6|SECB2_FRATH	Protein-export protein sec	K.GGFLPLNLAPINFDAIYAGNK.K	GGFLPLNLAPINFDAIY	147	136	3.674	0.005
sp|Q2A5B6|SECB2_FRATH	Protein-export protein sec	K.GGFLPLNLAPINFDAIYLAGNK.K	GGFLPLNLAPINFDAIYL	147	137	2.708	0.000
sp|Q2A5E0|HTPG_FRATH	Chaperone protein htpG h	E.TVNNTKAIAGNKKE.N	TVNNTKAI	628	235	3.678	0.000
sp|Q2A5E5|RPOA1_FRATH	DNA-directed RNA polyme	R.VLLSSLSGAAGNKK.E	VLLSSLSGA	323	55	3.223	0.000
sp|Q2A5F4|RL18_FRATH	50S ribosomal protein L1	R.EHGLQFAGNKK.E	EHGLQF	117	117	3.165	0.009
sp|Q2A5F4|RL18_FRATH	50S ribosomal protein L1	R.EHGLQFAGNK.K	EHGLQF	117	117	2.244	0.003
sp|Q2A5G4|RS3_FRATH	30S ribosomal protein S3	K.IQIERPAAGNKK.E	IQIERPA	223	61	3.648	0.000
sp|Q2A5G8|RL23_FRATH	50S ribosomal protein L2	K.LAEGHDIAGNKK.E	LAEGHDI	99	93	3.952	0.009
sp|Q2A5G8|RL23_FRATH	50S ribosomal protein L2	K.LAEGHDINAGNKK.E	LAEGHDIN	99	94	3.813	0.000
sp|Q2A5G8|RL23_FRATH	50S ribosomal protein L2	E.GHDINFAGNKKE.N	GHDINF	99	95	3.812	0.008
sp|Q2A5G8|RL23_FRATH	50S ribosomal protein L2	E.GHDINFAGNKK.E	GHDINF	99	95	3.456	0.000
sp|Q2A5G8|RL23_FRATH	50S ribosomal protein L2	K.LAEGHDINFAGNK.K	LAEGHDINF	99	95	4.258	0.000
sp|Q2A5G8|RL23_FRATH	50S ribosomal protein L2	K.LAEGHDINFAGNKK.E	LAEGHDINF	99	95	4.242	0.000
sp|Q2A5G8|RL23_FRATH	50S ribosomal protein L2	E.GHDINFVAGNKKE.N	GHDINFV	99	96	3.948	0.003
sp|Q2A5G8|RL23_FRATH	50S ribosomal protein L2	K.LAEGHDINFVAGNK.K	LAEGHDINFV	99	96	4.216	0.004
sp|Q2A5G8|RL23_FRATH	50S ribosomal protein L2	E.GHDINFVGAGNKKE.N	GHDINFVG	99	97	4.063	0.001
sp|Q2A5G8|RL23_FRATH	50S ribosomal protein L2	K.LAEGHDINFVGAGNKK.E	LAEGHDINFVG	99	97	4.199	0.000
sp|Q2A5H2|EFG_FRATH	Elongation factor G fusA	E.ANVGNPQVAAGNKKE.N	ANVGNPQVA	704	487	4.278	0.000
sp|Q2A5H6|DUT_FRATH	Deoxyuridine 5'-triphosph	R.FAQLVIVPVVQAAGNK.K	FAQLVIVPVVQA	148	124	2.34	0.001
sp|Q2A5I1|EFTS_FRATH	Elongation factor Ts tsf	*.KALVAAAGDAGNKKE.N	KALVAAAGD	289	33	3.238	0.009
sp|Q2A5I1|EFTS_FRATH	Elongation factor Ts tsf	K.TVEAETLGAAGNKK.E	TVEAETLGA	289	152	4.189	0.001
sp|Q2A5I1|EFTS_FRATH	Elongation factor Ts tsf	E.AETLGAYIHAGNK.K	AETLGAYIH	289	155	3.207	0.000
sp|Q2A5I1|EFTS_FRATH	Elongation factor Ts tsf	K.TVEAETLGAYIHAGNK.K	TVEAETLGAYIH	289	155	3.771	0.000
sp|Q2A5I1|EFTS_FRATH	Elongation factor Ts tsf	E.TLGAYIHGAGNK.K	TLGAYIHG	289	156	4.162	0.000
sp|Q2A5I1|EFTS_FRATH	Elongation factor Ts tsf	E.TLGAYIHGSAGNKKE.N	TLGAYIHGS	289	157	3.734	0.000
sp|Q2A5I1|EFTS_FRATH	Elongation factor Ts tsf	E.TLGAYIHGSAGNK.K	TLGAYIHGS	289	157	2.478	0.002

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

sp|Q2A5I1|EFTS_FRATH	Elongation factor Ts tsf	K.TVEAETLGAYIHGSAGNK.K	TVEAETLGAYIHGS	289	157	2.841	0.000
sp|Q2A5I1|EFTS_FRATH	Elongation factor Ts tsf	K.IGVVAALAGNK.K	IGVVAAL	289	165	3.804	0.000
sp|Q2A5I1|EFTS_FRATH	Elongation factor Ts tsf	K.IGVVAALEGGAGNKK.E	IGVVAALEGG	289	168	3.163	0.000
sp|Q2A5I1|EFTS_FRATH	Elongation factor Ts tsf	K.DVAMHVAAAGNK.K	DVAMHVAA	289	182	3.127	0.000
sp|Q2A5I1|EFTS_FRATH	Elongation factor Ts tsf	K.DVAMHVAAAAGNK.K	DVAMHVAAA	289	183	4.032	0.000
sp|Q2A5I1|EFTS_FRATH	Elongation factor Ts tsf	*.DVAMHVAAANAGNK.K	DVAMHVAAAN	289	184	4.198	0.000
sp|Q2A5I1|EFTS_FRATH	Elongation factor Ts tsf	D.VAM+16HVAAANAGNK.K	VAMHVAAAN	289	184	3.2	0.004
sp|Q2A5I1|EFTS_FRATH	Elongation factor Ts tsf	*.DVAM+16HVAAANPAGNK.K	DVAMHVAAANP	289	185	3.727	0.000
sp|Q2A5I1|EFTS_FRATH	Elongation factor Ts tsf	*.DVAMHVAAANPAGNKK.E	DVAMHVAAANP	289	185	3.538	0.000
sp|Q2A5I1|EFTS_FRATH	Elongation factor Ts tsf	*.DVAMHVAAANPAGNK.K	DVAMHVAAANP	289	185	3.475	0.000
sp|Q2A5I1|EFTS_FRATH	Elongation factor Ts tsf	D.VAMHVAAANPAGNK.K	VAMHVAAANP	289	185	3.259	0.000
sp|Q2A5I1|EFTS_FRATH	Elongation factor Ts tsf	E.IFTAQAKEAGNKK.E	IFTAQAKE	289	211	3.128	0.002
sp|Q2A5I1|EFTS_FRATH	Elongation factor Ts tsf	E.SGKPAEIIAGNKKE.N	SGKPAEII	289	219	4.185	0.002
sp|Q2A5I1|EFTS_FRATH	Elongation factor Ts tsf	E.SGKPAEIIAGNK.K	SGKPAEII	289	219	3.295	0.000
sp|Q2A5I1|EFTS_FRATH	Elongation factor Ts tsf	R.LDVGEGIAGNKK.E	LDVGEGI	289	272	4.243	0.000
sp|Q2A5I2|RS2_FRATH	30S ribosomal protein S2	K.TVPLFQDAVNFVGKTVAAGNKK.E	TVPLFQDAVNFVGKTVA	239	60	2.276	0.005
sp|Q2A5I8|SYE_FRATH	Glutamyl-tRNA synthetas	D.QEIFSIEEMIAGNKK.E	QEIFSIEEMI	468	282	3.645	0.002
sp|Q2A5L0|LPXD1_FRATH	UDP-3-O-[3-hydroxymyris	K.ILELFSVPYPAGNK.K	ILELFSVPYP	347	100	3.698	0.000
sp|Q2A5L0|LPXD1_FRATH	UDP-3-O-[3-hydroxymyris	E.KAVIDPTAAGNKKE.N	KAVIDPTA	347	115	2.794	0.003
sp|Q2A5V4|TRPA_FRATH	Tryptophan synthase alph	E.M+16KAATLNAGNKKE.N	MKAATLN	269	269	2.644	0.003
sp|Q2A5X7|RS20_FRATH	30S ribosomal protein S2	K.ENFTKVVAGNK.K	ENFTKVV	90	55	2.351	0.009
sp|Q9ZAW3|FTSZ_FRATH	Cell division protein ftsZ f	K.VVGVGGGGGNAVQHMAGNK.K	VVGVGGGGGNAVQHM	381	30	2.752	0.000
sp|Q9ZAW3|FTSZ_FRATH	Cell division protein ftsZ f	K.HVDSIITVPNEKLLAGNKKE.N	HVDSIITVPNEKLL	381	169	2.462	0.000
sp|Q9ZAW3|FTSZ_FRATH	Cell division protein ftsZ f	K.VTVVVTGAGNKK.E	VTVVVTG	381	314	3.939	0.002
sp|Q9ZAW3|FTSZ_FRATH	Cell division protein ftsZ f	K.VTVVVTGIAGNKK.E	VTVVVTGI	381	315	3.536	0.000
sp|Q9ZAW3|FTSZ_FRATH	Cell division protein ftsZ f	K.TSSLQQSASSAGNKK.E	TSSLQQSASS	381	338	3.442	0.000
sp|Q9ZAW3|FTSZ_FRATH	Cell division protein ftsZ f	E.KTSSLQQSASSFAGNKKE.N	KTSSLQQSASSF	381	339	4.376	0.000
sp|Q9ZAW3|FTSZ_FRATH	Cell division protein ftsZ f	E.KTSSLQQSASSFAGNK.K	KTSSLQQSASSF	381	339	4.107	0.000
sp|Q9ZAW3|FTSZ_FRATH	Cell division protein ftsZ f	K.TSSLQQSASSFAGNK.K	TSSLQQSASSF	381	339	4.277	0.000
sp|Q9ZAW3|FTSZ_FRATH	Cell division protein ftsZ f	K.TSSLQQSASSFAGNKK.E	TSSLQQSASSF	381	339	4.021	0.003
sp|Q9ZAW3|FTSZ_FRATH	Cell division protein ftsZ f	E.KTSSLQQSASSFSAGNKKE.N	KTSSLQQSASSFS	381	340	4.208	0.000
sp|Q9ZAW3|FTSZ_FRATH	Cell division protein ftsZ f	K.TSSLQQSASSFSAGNKK.E	TSSLQQSASSFS	381	340	4.01	0.000
sp|Q9ZAW3|FTSZ_FRATH	Cell division protein ftsZ f	E.KTSSLQQSASSFSNKAGNKKE.N	KTSSLQQSASSFSNK	381	342	2.823	0.000

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

sp|Q9ZAW3|FTSZ_FRATH	Cell division protein ftsZ f	E.KTSSLQQSASSFSNKTAGNKKE.N	KTSSLQQSASSFSNKT	381	343	3.317	0.000
sp|Q9ZAW3|FTSZ_FRATH	Cell division protein ftsZ f	E.KTSSLQQSASSFSNKTSAGNKKE.N	KTSSLQQSASSFSNKTS	381	344	2.991	0.000
sp|Q9ZAW3|FTSZ_FRATH	Cell division protein ftsZ f	E.KTSSLQQSASSFSNKTSAAGNKKE.N	KTSSLQQSASSFSNKTSA	381	345	2.728	0.000
sp|Q9ZAW3|FTSZ_FRATH	Cell division protein ftsZ f	E.KTSSLQQSASSFSNKTSAPAGNKKE.N	KTSSLQQSASSFSNKTSAP	381	346	3.001	0.000
sp|Q9ZAW3|FTSZ_FRATH	Cell division protein ftsZ f	K.TSAPFAGNKK.E	TSAPF	381	347	2.982	0.006
sp|Q9ZAW3|FTSZ_FRATH	Cell division protein ftsZ f	E.TEVVTGAAGNKKE.N	TEVVTGA	381	358	2.904	0.005
sp|Q9ZAW3|FTSZ_FRATH	Cell division protein ftsZ f	E.TEVVTGASNAGNKKE.N	TEVVTGASN	381	360	3.277	0.001
sp|Q9ZAW3|FTSZ_FRATH	Cell division protein ftsZ f	E.TEVVTGASNAAGNKKE.N	TEVVTGASNA	381	361	4.301	0.001
sp|Q9ZAW3|FTSZ_FRATH	Cell division protein ftsZ f	E.TEVVTGASNAPAGNKKE.N	TEVVTGASNAP	381	362	4.31	0.000
sp|Q9ZAW3|FTSZ_FRATH	Cell division protein ftsZ f	E.TEVVTGASNAPKAGNKKE.N	TEVVTGASNAPK	381	363	4.36	0.000
sp|Q9ZAW3|FTSZ_FRATH	Cell division protein ftsZ f	E.TEVVTGASNAPKTAGNKKE.N	TEVVTGASNAPKT	381	364	4.232	0.000
sp|Q9ZAW3|FTSZ_FRATH	Cell division protein ftsZ f	E.TEVVTGASNAPKTAGNKKENR.V	TEVVTGASNAPKT	381	364	3.467	0.000
sp|Q9ZAW3|FTSZ_FRATH	Cell division protein ftsZ f	E.TEVVTGASNAPKTDSAGNKKE.N	TEVVTGASNAPKTDS	381	366	4.234	0.000
sp|Q9ZAW3|FTSZ_FRATH	Cell division protein ftsZ f	E.VVTGASNAPKTDSAGNKKE.N	VVTGASNAPKTDS	381	366	2.752	0.000
sp|Q9ZAW3|FTSZ_FRATH	Cell division protein ftsZ f	E.VVTGASNAPKTDSDDVNKAGNKKE.N	VVTGASNAPKTDSDDVNK	381	371	2.168	0.001
sp|Q9ZAW3|FTSZ_FRATH	Cell division protein ftsZ f	E.TEVVTGASNAPKTDSDDVNKSDIPSFLRAGNKKE.	TEVVTGASNAPKTDSDDVNKSDIPSFLR	381	379	3.109	0.000
tr|Q2A144|Q2A144_FRATH	Peptide methionine sulfo	K.HNQSVYTQILPSTHFAGNKK.E	HNQSVYTQILPSTHF	229	169	3.6	0.000
tr|Q2A144|Q2A144_FRATH	Peptide methionine sulfo	K.AESYHQDYHHKAGNK.K	AESYHQDYHHK	229	182	3.895	0.000
tr|Q2A193|Q2A193_FRATH	Glutamine synthetase FTL	E.VYNPDGQTPHAAGNKK.E	VYNPDGQTPHA	345	91	2.063	0.005
tr|Q2A193|Q2A193_FRATH	Glutamine synthetase FTL	K.DILNYGHNLAGNKK.E	DILNYGHNL	345	280	4.018	0.001
tr|Q2A193|Q2A193_FRATH	Glutamine synthetase FTL	K.DILNYGHNLAGNK.K	DILNYGHNL	345	280	2.061	0.009
tr|Q2A1C0|Q2A1C0_FRATH	Outer membrane protein	E.TVPTALGAGNKKE.N	TVPTALG	509	117	3.218	0.000
tr|Q2A1C4|Q2A1C4_FRATH	Amidophosphoribosyltran	E.KAYMVAAGNKKE.N	KAYMVA	496	206	2.736	0.003
tr|Q2A1C8|Q2A1C8_FRATH	Putative uncharacterized	E.VGSTYNYQRVNADDQDKFTIEAGNKK.E	VGSTYNYQRVNADDQDKFTIE	132	53	2.954	0.000
tr|Q2A1C8|Q2A1C8_FRATH	Putative uncharacterized	K.TSANSSYQYSYVAGNKK.E	TSANSSYQYSYV	132	90	2.877	0.000
tr|Q2A1C8|Q2A1C8_FRATH	Putative uncharacterized	K.IRNDNVINAAGNKK.E	IRNDNVINA	132	128	3.69	0.000
tr|Q2A1E1|Q2A1E1_FRATH	Lipase/acyltransferase FT	K.PKVLAGNK.K	PKVL	183	113	3.865	0.008
tr|Q2A1E1|Q2A1E1_FRATH	Lipase/acyltransferase FT	K.PKVLAGNKK.E	PKVL	183	113	3.283	0.009
tr|Q2A1F6|Q2A1F6_FRATH	NADH-quinone oxidoredu	K.LLAAVGSVNIAGNKK.E	LLAAVGSVNI	788	348	3.067	0.000
tr|Q2A1F6|Q2A1F6_FRATH	NADH-quinone oxidoredu	R.LAADNIQYIALAGNKK.E	LAADNIQYIAL	788	438	4.072	0.000
tr|Q2A1I4|Q2A1I4_FRATH	Putative uncharacterized	K.SLANNIVSFAGNKK.E	SLANNIVSF	947	152	3.184	0.000
tr|Q2A1I4|Q2A1I4_FRATH	Putative uncharacterized	K.SLANNIVSFLAGNK.K	SLANNIVSFL	947	153	4.078	0.000
tr|Q2A1I8|Q2A1I8_FRATH	Citrate synthase FTL_17	E.IINKMPVAGNKK.E	IINKMPV	419	114	2.948	0.004

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

tr|Q2A1I8|Q2A1I8_FRATH	Citrate synthase FTL_178	K.LGHSDNPLAGNKK.E	LGHSDNPL	419	333	3.941	0.000
tr|Q2A1I8|Q2A1I8_FRATH	Citrate synthase FTL_178	K.LGHSDNPLLTVAGNK.K	LGHSDNPLLTV	419	336	3.328	0.000
tr|Q2A1I8|Q2A1I8_FRATH	Citrate synthase FTL_178	K.LFSNVDFYSGIIAGNK.K	LFSNVDFYSGII	419	366	3.849	0.008
tr|Q2A1J2|Q2A1J2_FRATH	Succinate dehydrogenase	K.FIGPSGLLQAAGNK.K	FIGPSGLLQA	233	173	3.304	0.001
tr|Q2A1J4|Q2A1J4_FRATH	Dihydrolipoamide succinyl	E.DVKKAVASVAGNKKE.N	DVKKAVASV	489	243	3.562	0.000
tr|Q2A1J4|Q2A1J4_FRATH	Dihydrolipoamide succinyl	K.AVASVNKPAGNKK.E	AVASVNKP	489	246	2.733	0.002
tr|Q2A1J4|Q2A1J4_FRATH	Dihydrolipoamide succinyl	K.AVASVNKPQAGNK.K	AVASVNKPQ	489	247	3.777	0.009
tr|Q2A1J4|Q2A1J4_FRATH	Dihydrolipoamide succinyl	K.AVASVNKPQQAGNK.K	AVASVNKPQQ	489	248	4.096	0.008
tr|Q2A1J4|Q2A1J4_FRATH	Dihydrolipoamide succinyl	K.AVASVNKPQQQAGNK.K	AVASVNKPQQQ	489	249	3.459	0.009
tr|Q2A1J4|Q2A1J4_FRATH	Dihydrolipoamide succinyl	K.AVASVNKPQQQAGNKK.E	AVASVNKPQQQ	489	249	2.764	0.000
tr|Q2A1J4|Q2A1J4_FRATH	Dihydrolipoamide succinyl	K.AVASVNKPQQQTAGNK.K	AVASVNKPQQQT	489	250	4.098	0.000
tr|Q2A1J4|Q2A1J4_FRATH	Dihydrolipoamide succinyl	K.AVASVNKPQQQTAGNKK.E	AVASVNKPQQQT	489	250	3.057	0.000
tr|Q2A1J4|Q2A1J4_FRATH	Dihydrolipoamide succinyl	K.AVASVNKPQQQTVAGNK.K	AVASVNKPQQQTV	489	251	4.332	0.000
tr|Q2A1J4|Q2A1J4_FRATH	Dihydrolipoamide succinyl	K.AVASVNKPQQQTVAGNKK.E	AVASVNKPQQQTV	489	251	3.481	0.000
tr|Q2A1J4|Q2A1J4_FRATH	Dihydrolipoamide succinyl	K.AVASVNKPQQQTVVAGNK.K	AVASVNKPQQQTVV	489	252	4.401	0.000
tr|Q2A1J4|Q2A1J4_FRATH	Dihydrolipoamide succinyl	K.AVASVNKPQQQTVVAGNKK.E	AVASVNKPQQQTVV	489	252	3.026	0.000
tr|Q2A1J4|Q2A1J4_FRATH	Dihydrolipoamide succinyl	K.AVASVNKPQQQTVVINQGAAGNK.K	AVASVNKPQQQTVVINQGA	489	257	3.189	0.000
tr|Q2A1J4|Q2A1J4_FRATH	Dihydrolipoamide succinyl	K.AVASVNKPQQQTVVINQGAAGNKK.E	AVASVNKPQQQTVVINQGA	489	257	3.146	0.000
tr|Q2A1J4|Q2A1J4_FRATH	Dihydrolipoamide succinyl	E.LIEDPNRILLQAGNKKE.N	LIEDPNRILLQ	489	488	3.071	0.000
tr|Q2A1S0|Q2A1S0_FRATH	GlpX protein FTL_1701	R.HITAEHSFAGNKK.E	HITAEHSF	328	317	3.719	0.000
tr|Q2A1S0|Q2A1S0_FRATH	GlpX protein FTL_1701	R.HITAEHSFAGNK.K	HITAEHSF	328	317	3.575	0.000
tr|Q2A1U2|Q2A1U2_FRATH	Putative uncharacterized	K.ALKDTGYNTTAGNKK.E	ALKDTGYNTT	337	63	4.164	0.000
tr|Q2A1U2|Q2A1U2_FRATH	Putative uncharacterized	E.KALKDTGYNTTAGNKKE.N	KALKDTGYNTT	337	63	4.025	0.002
tr|Q2A1U2|Q2A1U2_FRATH	Putative uncharacterized	K.ILLDALLDKNIDIIAGNKK.E	ILLDALLDKNIDII	337	99	4.115	0.000
tr|Q2A1U2|Q2A1U2_FRATH	Putative uncharacterized	K.ILLDALLDKNIDIIWAGNKK.E	ILLDALLDKNIDIIW	337	100	3.226	0.001
tr|Q2A1U2|Q2A1U2_FRATH	Putative uncharacterized	K.ILLDALLDKNIDIIWFAGNKK.E	ILLDALLDKNIDIIWF	337	101	3.612	0.000
tr|Q2A1U2|Q2A1U2_FRATH	Putative uncharacterized	K.ILLDALLDKNIDIIWFLKAGNK.K	ILLDALLDKNIDIIWFLK	337	103	3.079	0.000
tr|Q2A1U2|Q2A1U2_FRATH	Putative uncharacterized	K.GGGGAFNAGNKK.E	GGGGAFN	337	110	3.058	0.008
tr|Q2A1U2|Q2A1U2_FRATH	Putative uncharacterized	K.GGGGAFNLLPYLYDAGNKK.E	GGGGAFNLLPYLYD	337	117	4.249	0.000
tr|Q2A1U2|Q2A1U2_FRATH	Putative uncharacterized	K.GGGGAFNLLPYLYDHAGNKK.E	GGGGAFNLLPYLYDH	337	118	2.875	0.003
tr|Q2A1U2|Q2A1U2_FRATH	Putative uncharacterized	K.GGGGAFNLLPYLYDHINEAGNK.K	GGGGAFNLLPYLYDHINE	337	121	2.976	0.008
tr|Q2A1U2|Q2A1U2_FRATH	Putative uncharacterized	K.ILVGFSDVTAAGNKK.E	ILVGFSDVTA	337	138	4.34	0.000
tr|Q2A1U2|Q2A1U2_FRATH	Putative uncharacterized	K.ILVGFSDVTAIAGNKK.E	ILVGFSDVTAI	337	139	4.368	0.000

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

tr|Q2A1U2|Q2A1U2_FRATH Putative uncharacterized	K.ILVGFSDVTAIAGNK.K	ILVGFSDVTAI	337	139	4.284	0.000
tr|Q2A1U2|Q2A1U2_FRATH Putative uncharacterized	K.SLHGVVAAAGNK.K	SLHGVVAA	337	158	3.915	0.000
tr|Q2A1U2|Q2A1U2_FRATH Putative uncharacterized	R.IPNITEIAGNKK.E	IPNITEI	337	186	4.078	0.009
tr|Q2A1U2|Q2A1U2_FRATH Putative uncharacterized	E.IINNGISAGNKKE.N	IINNGIS	337	192	3.542	0.002
tr|Q2A1U2|Q2A1U2_FRATH Putative uncharacterized	E.IINNGISYDKAGNKKE.N	IINNGISYDK	337	195	3.859	0.000
tr|Q2A1U2|Q2A1U2_FRATH Putative uncharacterized	E.IINNGISYDKLAGNKKE.N	IINNGISYDKL	337	196	4.144	0.000
tr|Q2A1U2|Q2A1U2_FRATH Putative uncharacterized	K.TFNRPVYAGNK.K	TFNRPVY	337	301	3.947	0.000
tr|Q2A1U2|Q2A1U2_FRATH Putative uncharacterized	K.TFNRPVYAGNKK.E	TFNRPVY	337	301	3.382	0.006
tr|Q2A1V9|Q2A1V9_FRATH Hypothetical membrane p	R.NQIIQSSYQKPSSDTTSQQPSTPAAAGNK.K	NQIIQSSYQKPSSDTTSQQPSTPAA	438	120	3.595	0.000
tr|Q2A1V9|Q2A1V9_FRATH Hypothetical membrane p	K.IPVLIPTAGNK.K	IPVLIPT	438	152	4.291	0.001
tr|Q2A1V9|Q2A1V9_FRATH Hypothetical membrane p	K.IPVLIPTDAGNKK.E	IPVLIPTD	438	153	4.164	0.000
tr|Q2A1V9|Q2A1V9_FRATH Hypothetical membrane p	E.TYKSNLDTAGNKKE.N	TYKSNLDT	438	167	4.065	0.001
tr|Q2A1V9|Q2A1V9_FRATH Hypothetical membrane p	E.TYKSNLDTQIAGNKKE.N	TYKSNLDTQI	438	169	4.278	0.000
tr|Q2A1V9|Q2A1V9_FRATH Hypothetical membrane p	E.TYKSNLDTQINAGNKKE.N	TYKSNLDTQIN	438	170	4.234	0.003
tr|Q2A1V9|Q2A1V9_FRATH Hypothetical membrane p	E.TYKSNLDTQINSAGNKKE.N	TYKSNLDTQINS	438	171	4.081	0.000
tr|Q2A1V9|Q2A1V9_FRATH Hypothetical membrane p	E.TYKSNLDTQINSDNIQEAGNKK.E	TYKSNLDTQINSDNIQE	438	176	2.84	0.001
tr|Q2A207|Q2A207_FRATH Stringent starvation prote	K.KRLFARDSVKKAGNKKE.N	KRLFARDSVKK	209	190	2.354	0.005
tr|Q2A221|Q2A221_FRATH Acetyl-CoA carboxylase,	K.NNTAAITSVVSAAPVASNVAGNKK.E	NNTAAITSVVSAAPVASNV	157	54	2.733	0.001
tr|Q2A221|Q2A221_FRATH Acetyl-CoA carboxylase,	K.NNTAAITSVVSAAPVASNVASAAPAGNKK.E	NNTAAITSVVSAAPVASNVASAAP	157	59	2.264	0.000
tr|Q2A221|Q2A221_FRATH Acetyl-CoA carboxylase,	K.NNTAAITSVVSAAPVASNVASAAPAVATAGNKK	NNTAAITSVVSAAPVASNVASAAPAVA	157	63	2.328	0.001
tr|Q2A221|Q2A221_FRATH Acetyl-CoA carboxylase,	K.NNTAAITSVVSAAPVASNVASAAPAVATAAGNK	NNTAAITSVVSAAPVASNVASAAPAVA	157	64	3.155	0.000
tr|Q2A221|Q2A221_FRATH Acetyl-CoA carboxylase,	K.NNTAAITSVVSAAPVASNVASAAPAVATAATSA	NNTAAITSVVSAAPVASNVASAAPAVA	157	67	2.728	0.001
tr|Q2A221|Q2A221_FRATH Acetyl-CoA carboxylase,	K.NNTAAITSVVSAAPVASNVASAAPAVATAATSA	NNTAAITSVVSAAPVASNVASAAPAVA	157	68	2.645	0.000
tr|Q2A221|Q2A221_FRATH Acetyl-CoA carboxylase,	K.NNTAAITSVVSAAPVASNVASAAPAVATAATSA	NNTAAITSVVSAAPVASNVASAAPAVA	157	70	2.471	0.000
tr|Q2A221|Q2A221_FRATH Acetyl-CoA carboxylase,	E.ISGEEIKSPAGNKKE.N	ISGEEIKSP	157	87	3.902	0.000
tr|Q2A221|Q2A221_FRATH Acetyl-CoA carboxylase,	K.SPMVGTFAGNKK.E	SPMVGTF	157	92	4.106	0.000
tr|Q2A221|Q2A221_FRATH Acetyl-CoA carboxylase,	K.SPMVGTFAGNK.K	SPMVGTF	157	92	3.142	0.000
tr|Q2A221|Q2A221_FRATH Acetyl-CoA carboxylase,	K.SPM+16VGTFAGNK.K	SPMVGTF	157	92	3.066	0.000
tr|Q2A221|Q2A221_FRATH Acetyl-CoA carboxylase,	K.SPMVGTFYGASSAGNKK.E	SPMVGTFYGASS	157	97	4.189	0.000
tr|Q2A221|Q2A221_FRATH Acetyl-CoA carboxylase,	K.SPMVGTFYGASSAGNKKENR.V	SPMVGTFYGASS	157	97	3.551	0.000
tr|Q2A221|Q2A221_FRATH Acetyl-CoA carboxylase,	K.VNLAEEISGEEIKSPMVGTFYGASSAGNKK.E	VNLAEEISGEEIKSPMVGTFYGASS	157	97	3.103	0.000
tr|Q2A221|Q2A221_FRATH Acetyl-CoA carboxylase,	K.SPMVGTFYGASSPAGNKK.E	SPMVGTFYGASSP	157	98	2.828	0.000
tr|Q2A221|Q2A221_FRATH Acetyl-CoA carboxylase,	K.VNLAEEISGEEIKSPMVGTFYGASSPAGNKK.E	VNLAEEISGEEIKSPMVGTFYGASSP	157	98	3.382	0.000

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

tr|Q2A221|Q2A221_FRATH Acetyl-CoA carboxylase,	K.SPMVGTFYGASSPDAAPAGNKK.E	SPMVGTFYGASSPDAAP	157	102	4.195	0.000
tr|Q2A221|Q2A221_FRATH Acetyl-CoA carboxylase,	K.DGVPVQFDQPLFIIAGNK.K	DGVPVQFDQPLFII	157	156	4.493	0.002
tr|Q2A221|Q2A221_FRATH Acetyl-CoA carboxylase,	K.DGVPVQFDQPLFIIAGNKK.E	DGVPVQFDQPLFII	157	156	4.377	0.005
tr|Q2A234|Q2A234_FRATH Putative uncharacterized	R.GMPNGIIAGNKK.E	GMPNGII	239	59	2.28	0.003
tr|Q2A234|Q2A234_FRATH Putative uncharacterized	R.GMPNGIIHAGNKK.E	GMPNGIIH	239	60	3.217	0.000
tr|Q2A234|Q2A234_FRATH Putative uncharacterized	R.GMPNGIIHTAGNKK.E	GMPNGIIHT	239	61	2.988	0.000
tr|Q2A234|Q2A234_FRATH Putative uncharacterized	E.IVVPLMYVDSAGNKKE.N	IVVPLMYVDS	239	88	4.551	0.000
tr|Q2A234|Q2A234_FRATH Putative uncharacterized	E.IVVPLMYVDSSGAGNKKE.N	IVVPLMYVDSSG	239	90	4.109	0.002
tr|Q2A234|Q2A234_FRATH Putative uncharacterized	E.IVVPLMYVDSSGKAGNKKE.N	IVVPLMYVDSSGK	239	91	3.072	0.001
tr|Q2A234|Q2A234_FRATH Putative uncharacterized	E.IVVPLMYVDSSGKPTAGNKK.E	IVVPLMYVDSSGKPT	239	93	2.45	0.000
tr|Q2A234|Q2A234_FRATH Putative uncharacterized	E.SFVFAGNAGNKKE.N	SFVFAGN	239	127	4.06	0.001
tr|Q2A234|Q2A234_FRATH Putative uncharacterized	E.AGTAVANAGNKK.E	AGTAVAN	239	138	3.302	0.008
tr|Q2A234|Q2A234_FRATH Putative uncharacterized	E.AGTAVANAGNKKE.N	AGTAVAN	239	138	3.067	0.001
tr|Q2A234|Q2A234_FRATH Putative uncharacterized	E.AGTAVANQAGNKK.E	AGTAVANQ	239	139	3.679	0.002
tr|Q2A234|Q2A234_FRATH Putative uncharacterized	E.AGTAVANQAGNKKE.N	AGTAVANQ	239	139	2.544	0.006
tr|Q2A234|Q2A234_FRATH Putative uncharacterized	E.AGTAVANQKAGNKKE.N	AGTAVANQK	239	140	3.306	0.000
tr|Q2A234|Q2A234_FRATH Putative uncharacterized	E.AGTAVANQKSDIAGNKKE.N	AGTAVANQKSDI	239	143	4.033	0.000
tr|Q2A234|Q2A234_FRATH Putative uncharacterized	E.AGTAVANQKSDIYAGNKKE.N	AGTAVANQKSDIY	239	144	2.973	0.000
tr|Q2A234|Q2A234_FRATH Putative uncharacterized	E.AGTAVANQKSDIYKNAGNKKE.N	AGTAVANQKSDIYKN	239	146	2.86	0.000
tr|Q2A234|Q2A234_FRATH Putative uncharacterized	E.AGTAVANQKSDIYKNGAGNKKE.N	AGTAVANQKSDIYKNG	239	147	2.532	0.000
tr|Q2A234|Q2A234_FRATH Putative uncharacterized	E.AGTAVANQKSDIYKNGGAGNKKE.N	AGTAVANQKSDIYKNGG	239	148	2.766	0.005
tr|Q2A234|Q2A234_FRATH Putative uncharacterized	E.AGTAVANQKSDIYKNGGVAGNKKE.N	AGTAVANQKSDIYKNGGV	239	149	3.297	0.000
tr|Q2A234|Q2A234_FRATH Putative uncharacterized	E.AGTAVANQKSDIYKNGGVIAGNKKE.N	AGTAVANQKSDIYKNGGVI	239	150	3.05	0.000
tr|Q2A234|Q2A234_FRATH Putative uncharacterized	E.AGTAVANQKSDIYKNGGVINPNDGAGNKKE.N	AGTAVANQKSDIYKNGGVINPNDG	239	155	3.489	0.000
tr|Q2A234|Q2A234_FRATH Putative uncharacterized	E.AQVQDGGTTMFAKAAAGNKKE.N	AQVQDGGTTMFAKAA	239	176	2.266	0.001
tr|Q2A234|Q2A234_FRATH Putative uncharacterized	K.VTATC+57TNYPAGNKK.E	VTATCTNYP	239	229	3.675	0.000
tr|Q2A234|Q2A234_FRATH Putative uncharacterized	K.VTATC+57TNYPVAQAGNK.K	VTATCTNYPVAQ	239	232	3.909	0.000
tr|Q2A234|Q2A234_FRATH Putative uncharacterized	K.VTATC+57TNYPVAQFAGNK.K	VTATCTNYPVAQF	239	233	3.576	0.000
tr|Q2A237|Q2A237_FRATH DNA mismatch repair prot	K.LALAPAGNKK.E	LALAP	600	82	4.209	0.005
tr|Q2A237|Q2A237_FRATH DNA mismatch repair prot	K.LALAPAGNKKE.N	LALAP	600	82	3.105	0.001
tr|Q2A254|Q2A254_FRATH Hypothetical membrane p	K.FYKKAGNKKE.N	FYKK	637	139	2.451	0.004
tr|Q2A259|Q2A259_FRATH DNA gyrase subunit B FTL	R.SAAEVILTVLHAGNK.K	SAAEVILTVLH	803	101	4.336	0.000
tr|Q2A274|Q2A274_FRATH Putative uncharacterized	E.LLSSSLAAGNKKE.N	LLSSSLA	190	140	2.973	0.001

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

tr|Q2A274|Q2A274_FRATH Putative uncharacterized	K.IPGLATNGNIDMIFAGNK.K	IPGLATNGNIDMIF	190	164	2.371	0.000
tr|Q2A274|Q2A274_FRATH Putative uncharacterized	K.AGVYQFAPGHVAAGNK.K	AGVYQFAPGHVA	190	180	4.152	0.000
tr|Q2A274|Q2A274_FRATH Putative uncharacterized	K.AGVYQFAPGHVAAAGNK.K	AGVYQFAPGHVAA	190	181	4.417	0.000
tr|Q2A274|Q2A274_FRATH Putative uncharacterized	K.AGVYQFAPGHVAAYAGNK.K	AGVYQFAPGHVAAY	190	182	4.062	0.000
tr|Q2A284|Q2A284_FRATH Chitinase family 18 protei	K.DLEIERPAGNKK.E	DLEIERP	764	149	3.562	0.000
tr|Q2A284|Q2A284_FRATH Chitinase family 18 protei	K.VDGKDLEIERPAGNKK.E	VDGKDLEIERP	764	149	2.989	0.000
tr|Q2A284|Q2A284_FRATH Chitinase family 18 protei	R.KYNPYDFAGNKK.E	KYNPYDF	764	183	4.096	0.003
tr|Q2A284|Q2A284_FRATH Chitinase family 18 protei	*.KYNPYDFKYDKLNTIIAGNKK.E	KYNPYDFKYDKLNTII	764	192	3.343	0.000
tr|Q2A284|Q2A284_FRATH Chitinase family 18 protei	K.YNPYDFKYDKLNTIIAGNKK.E	YNPYDFKYDKLNTII	764	192	3.259	0.000
tr|Q2A284|Q2A284_FRATH Chitinase family 18 protei	K.LNTIIYAFAGNK.K	LNTIIYAF	764	195	3.157	0.000
tr|Q2A284|Q2A284_FRATH Chitinase family 18 protei	K.VAMQPWAAGNKK.E	VAMQPWA	764	513	2.873	0.000
tr|Q2A284|Q2A284_FRATH Chitinase family 18 protei	K.VAMQPWAYSPSAGNK.K	VAMQPWAYSPS	764	517	2.725	0.002
tr|Q2A284|Q2A284_FRATH Chitinase family 18 protei	E.NSASISWAGNKKE.N	NSASISW	764	590	3.17	0.000
tr|Q2A284|Q2A284_FRATH Chitinase family 18 protei	E.NSASISWNKAGNKKE.N	NSASISWNK	764	592	3.938	0.000
tr|Q2A292|Q2A292_FRATH Glycerophosphoryl dieste	K.TPIKDLTAGNKK.E	TPIKDLT	344	99	3.45	0.000
tr|Q2A292|Q2A292_FRATH Glycerophosphoryl dieste	K.KYTVGYIKPAGNKK.E	KYTVGYIKP	344	113	4.062	0.000
tr|Q2A292|Q2A292_FRATH Glycerophosphoryl dieste	K.YTVGYIKPAGNKK.E	YTVGYIKP	344	113	3.353	0.000
tr|Q2A292|Q2A292_FRATH Glycerophosphoryl dieste	K.KYTVGYIKPDSAGNKK.E	KYTVGYIKPDS	344	115	3.996	0.000
tr|Q2A292|Q2A292_FRATH Glycerophosphoryl dieste	K.YTVGYIKPDSAGNKK.E	YTVGYIKPDS	344	115	3.314	0.000
tr|Q2A292|Q2A292_FRATH Glycerophosphoryl dieste	K.MYPNHIGAGNKK.E	MYPNHIG	344	126	3.685	0.000
tr|Q2A292|Q2A292_FRATH Glycerophosphoryl dieste	K.M+16YPNHIGAGNKK.E	MYPNHIG	344	126	2.305	0.002
tr|Q2A292|Q2A292_FRATH Glycerophosphoryl dieste	K.MYPNHIGMDNVAGNKK.E	MYPNHIGMDNV	344	130	3.574	0.000
tr|Q2A292|Q2A292_FRATH Glycerophosphoryl dieste	E.VINYVKSNAGNKKE.N	VINYVKSN	344	145	3.926	0.000
tr|Q2A292|Q2A292_FRATH Glycerophosphoryl dieste	E.VINYVKSNVAGNKKE.N	VINYVKSNV	344	146	4.243	0.001
tr|Q2A292|Q2A292_FRATH Glycerophosphoryl dieste	E.VINYVKSNVGAGNKKE.N	VINYVKSNVG	344	147	4.178	0.000
tr|Q2A292|Q2A292_FRATH Glycerophosphoryl dieste	E.VINYVKSNVGSAGNKKE.N	VINYVKSNVGS	344	148	4.241	0.000
tr|Q2A292|Q2A292_FRATH Glycerophosphoryl dieste	E.IKTNAGNKKENR.V	IKTN	344	159	3.379	0.009
tr|Q2A292|Q2A292_FRATH Glycerophosphoryl dieste	E.IKTNPYDLEAGNKK.E	IKTNPYDLE	344	164	3.566	0.000
tr|Q2A292|Q2A292_FRATH Glycerophosphoryl dieste	K.WTAPLDPKDYNYNYPLMVKAGNK.K	WTAPLDPKDYNYNYPLMVK	344	254	3.088	0.010
tr|Q2A292|Q2A292_FRATH Glycerophosphoryl dieste	K.KLGGIFWEPAGNKK.E	KLGGIFWEP	344	263	3.983	0.000
tr|Q2A292|Q2A292_FRATH Glycerophosphoryl dieste	K.LGGIFWEPFAGNK.K	LGGIFWEPF	344	264	4.387	0.000
tr|Q2A292|Q2A292_FRATH Glycerophosphoryl dieste	K.KLGGIFWEPFEKDLTKAGNK.K	KLGGIFWEPFEKDLTK	344	270	3.036	0.000
tr|Q2A292|Q2A292_FRATH Glycerophosphoryl dieste	E.AAKGLDLAGNKKE.N	AAKGLDL	344	331	3.845	0.000

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

tr|Q2A292|Q2A292_FRATH Glycerophosphoryl diester	E.AAKGLDLPAGNKKE.N	AAKGLDLP	344	332	3.346	0.000
tr|Q2A292|Q2A292_FRATH Glycerophosphoryl diester	K.GLDLPPAYPNIPAGNK.K	GLDLPPAYPNIP	344	339	3.883	0.000
tr|Q2A292|Q2A292_FRATH Glycerophosphoryl diester	K.GLDLPPAYPNIPFAGNK.K	GLDLPPAYPNIPF	344	340	2.705	0.000
tr|Q2A294|Q2A294_FRATH D-alanyl-D-alanine carbox	K.LLTGIAGLAGNKK.E	LLTGIAGL	176	85	3.878	0.000
tr|Q2A294|Q2A294_FRATH D-alanyl-D-alanine carbox	K.LLTGIAGLLAGNK.K	LLTGIAGLL	176	86	4.098	0.001
tr|Q2A294|Q2A294_FRATH D-alanyl-D-alanine carbox	K.LLTGIAGLLFAGNK.K	LLTGIAGLLF	176	87	4.125	0.000
tr|Q2A2A3|Q2A2A3_FRATH Translation initiation inhib	E.AVAITNAGNKKE.N	AVAITN	126	126	3.847	0.000
tr|Q2A2A7|Q2A2A7_FRATH Putative uncharacterized	K.TTAAEVSAGNKK.E	TTAAEVS	169	60	4.029	0.009
tr|Q2A2A7|Q2A2A7_FRATH Putative uncharacterized	E.VSKKLDKTAGNKKE.N	VSKKLDKT	169	66	4.114	0.000
tr|Q2A2A7|Q2A2A7_FRATH Putative uncharacterized	E.VSKKLDKTAGNKKENR.V	VSKKLDKT	169	66	3.43	0.006
tr|Q2A2A7|Q2A2A7_FRATH Putative uncharacterized	E.VSKKLDKTSKDVEAGNKKE.N	VSKKLDKTSKDVE	169	71	3.013	0.003
tr|Q2A2A7|Q2A2A7_FRATH Putative uncharacterized	E.VSKKLDKTSKDVEAGNKKENR.V	VSKKLDKTSKDVE	169	71	2.337	0.004
tr|Q2A2A7|Q2A2A7_FRATH Putative uncharacterized	E.VSKKLDKTSKDVEKAGNKKENR.V	VSKKLDKTSKDVEK	169	72	3.624	0.000
tr|Q2A2A7|Q2A2A7_FRATH Putative uncharacterized	E.VSKKLDKTSKDVEKAGNKKE.N	VSKKLDKTSKDVEK	169	72	3.033	0.001
tr|Q2A2A7|Q2A2A7_FRATH Putative uncharacterized	E.VSKKLDKTSKDVEKDAGNKKE.N	VSKKLDKTSKDVEKD	169	73	3.237	0.000
tr|Q2A2A7|Q2A2A7_FRATH Putative uncharacterized	E.VSKKLDKTSKDVEKDAGNKKENR.V	VSKKLDKTSKDVEKD	169	73	2.277	0.000
tr|Q2A2A7|Q2A2A7_FRATH Putative uncharacterized	K.TSKDVEKDAAGNKK.E	TSKDVEKDA	169	74	3.921	0.000
tr|Q2A2A7|Q2A2A7_FRATH Putative uncharacterized	E.VSKKLDKTSKDVEKDAAGNKKENR.V	VSKKLDKTSKDVEKDA	169	74	3.394	0.000
tr|Q2A2A7|Q2A2A7_FRATH Putative uncharacterized	E.VSKKLDKTSKDVEKDAAGNKKE.N	VSKKLDKTSKDVEKDA	169	74	3.026	0.000
tr|Q2A2A7|Q2A2A7_FRATH Putative uncharacterized	K.DVEKDASAGNKK.E	DVEKDAS	169	75	3.425	0.003
tr|Q2A2A7|Q2A2A7_FRATH Putative uncharacterized	E.VSKKLDKTSKDVEKDASAGNKKENR.V	VSKKLDKTSKDVEKDAS	169	75	3.577	0.010
tr|Q2A2A7|Q2A2A7_FRATH Putative uncharacterized	K.TSKDVEKDASQAGNKK.E	TSKDVEKDASQ	169	76	3.302	0.001
tr|Q2A2A7|Q2A2A7_FRATH Putative uncharacterized	K.TSKDVEKDASQAAGNKK.E	TSKDVEKDASQA	169	77	3.382	0.000
tr|Q2A2A7|Q2A2A7_FRATH Putative uncharacterized	E.VSKKLDKTSKDVEKDASQAAGNKKE.N	VSKKLDKTSKDVEKDASQA	169	77	3.374	0.001
tr|Q2A2A7|Q2A2A7_FRATH Putative uncharacterized	K.DASQAADAGNKK.E	DASQAAD	169	79	2.877	0.001
tr|Q2A2A7|Q2A2A7_FRATH Putative uncharacterized	E.VSKKLDKTSKDVEKDASQAADAGNKKE.N	VSKKLDKTSKDVEKDASQAAD	169	79	3.635	0.001
tr|Q2A2A7|Q2A2A7_FRATH Putative uncharacterized	E.VSKKLDKTSKDVEKDASQAADAGNK.K	VSKKLDKTSKDVEKDASQAAD	169	79	3.256	0.000
tr|Q2A2A7|Q2A2A7_FRATH Putative uncharacterized	K.DASQAADIAGNKK.E	DASQAADI	169	80	4.002	0.000
tr|Q2A2A7|Q2A2A7_FRATH Putative uncharacterized	K.TSKDVEKDASQAADIAGNKK.E	TSKDVEKDASQAADI	169	80	3.18	0.001
tr|Q2A2A7|Q2A2A7_FRATH Putative uncharacterized	E.VSKKLDKTSKDVEKDASQAADIAGNKKE.N	VSKKLDKTSKDVEKDASQAADI	169	80	3.219	0.010
tr|Q2A2A7|Q2A2A7_FRATH Putative uncharacterized	K.DASQAADILVAGNKK.E	DASQAADILV	169	82	4.115	0.000
tr|Q2A2A7|Q2A2A7_FRATH Putative uncharacterized	K.DVEKDASQAADILVAGNKK.E	DVEKDASQAADILV	169	82	3.02	0.000
tr|Q2A2A7|Q2A2A7_FRATH Putative uncharacterized	E.VSKKLDKTSKDVEKDASQAADILVAGNKKE.N	VSKKLDKTSKDVEKDASQAADILV	169	82	3.68	0.003

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

tr|Q2A2A7|Q2A2A7_FRATH Putative uncharacterized	K.KILNTAGNKK.E	KILNT	169	94	2.634	0.005
tr|Q2A2A7|Q2A2A7_FRATH Putative uncharacterized	E.NAKKILNTAGNKKE.N	NAKKILNT	169	94	4.239	0.001
tr|Q2A2A7|Q2A2A7_FRATH Putative uncharacterized	K.ANQASQSLAGNKK.E	ANQASQSL	169	103	3.665	0.000
tr|Q2A2A7|Q2A2A7_FRATH Putative uncharacterized	K.ANQASQSLGAGNKK.E	ANQASQSLG	169	104	3.373	0.004
tr|Q2A2A7|Q2A2A7_FRATH Putative uncharacterized	E.NAKKILNTKANQASQSLGAGNK.K	NAKKILNTKANQASQSLG	169	104	2.768	0.000
tr|Q2A2A7|Q2A2A7_FRATH Putative uncharacterized	K.ANQASQSLGQAGNKK.E	ANQASQSLGQ	169	105	3.958	0.000
tr|Q2A2A7|Q2A2A7_FRATH Putative uncharacterized	K.ANQASQSLGQMAGNKK.E	ANQASQSLGQM	169	106	3.9	0.000
tr|Q2A2A7|Q2A2A7_FRATH Putative uncharacterized	K.ANQASQSLGQMAAGNKK.E	ANQASQSLGQMA	169	107	3.831	0.000
tr|Q2A2A7|Q2A2A7_FRATH Putative uncharacterized	K.ANQASQSLGQMAAGNK.K	ANQASQSLGQMA	169	107	2.838	0.000
tr|Q2A2A7|Q2A2A7_FRATH Putative uncharacterized	K.ANQASQSLGQMADAGNKK.E	ANQASQSLGQMAD	169	108	4.054	0.000
tr|Q2A2A7|Q2A2A7_FRATH Putative uncharacterized	K.ANQASQSLGQMADDAEKDTSQAAAGNKK.E	ANQASQSLGQMADDAEKDTSQAA	169	118	3.695	0.000
tr|Q2A2A7|Q2A2A7_FRATH Putative uncharacterized	K.ANQASQSLGQMADDAEKDTSQAATAGNKK.E	ANQASQSLGQMADDAEKDTSQAAT	169	119	3.318	0.000
tr|Q2A2A7|Q2A2A7_FRATH Putative uncharacterized	D.TSQAATTIAAGNKK.E	TSQAATTIA	169	122	3.365	0.000
tr|Q2A2A7|Q2A2A7_FRATH Putative uncharacterized	D.TSQAATTIANKAGNKKE.N	TSQAATTIANK	169	124	2.218	0.000
tr|Q2A2A7|Q2A2A7_FRATH Putative uncharacterized	K.AAQSKLVQQTDKAGNKKE.N	AAQSKLVQQTDK	169	138	2.734	0.000
tr|Q2A2A7|Q2A2A7_FRATH Putative uncharacterized	K.LVQQTDKAGNK.K	LVQQTDK	169	138	3.053	0.003
tr|Q2A2A7|Q2A2A7_FRATH Putative uncharacterized	K.LVQQTDKAGNKK.E	LVQQTDK	169	138	2.755	0.000
tr|Q2A2A7|Q2A2A7_FRATH Putative uncharacterized	E.KTVTNSQDKVQAGNK.K	KTVTNSQDKVQ	169	155	2.774	0.000
tr|Q2A2A7|Q2A2A7_FRATH Putative uncharacterized	K.TVTNSQDKVQAGNKK.E	TVTNSQDKVQ	169	155	4.081	0.001
tr|Q2A2A7|Q2A2A7_FRATH Putative uncharacterized	E.KTVTNSQDKVQNAGNKKE.N	KTVTNSQDKVQN	169	156	2.598	0.005
tr|Q2A2A7|Q2A2A7_FRATH Putative uncharacterized	E.KTVTNSQDKVQNAGNKK.E	KTVTNSQDKVQN	169	156	2.549	0.000
tr|Q2A2A7|Q2A2A7_FRATH Putative uncharacterized	K.TVTNSQDKVQNAGNKK.E	TVTNSQDKVQN	169	156	3.605	0.000
tr|Q2A2A7|Q2A2A7_FRATH Putative uncharacterized	E.KTVTNSQDKVQNFAGNKKE.N	KTVTNSQDKVQNF	169	157	3.133	0.007
tr|Q2A2A7|Q2A2A7_FRATH Putative uncharacterized	E.KTVTNSQDKVQNFKQAGNKKE.N	KTVTNSQDKVQNFKQ	169	159	2.73	0.000
tr|Q2A2A7|Q2A2A7_FRATH Putative uncharacterized	E.KTVTNSQDKVQNFKQGAGNKKE.N	KTVTNSQDKVQNFKQG	169	160	2.514	0.001
tr|Q2A2A7|Q2A2A7_FRATH Putative uncharacterized	E.KTVTNSQDKVQNFKQGFAGNKKE.N	KTVTNSQDKVQNFKQGF	169	161	2.939	0.000
tr|Q2A2A7|Q2A2A7_FRATH Putative uncharacterized	E.KTVTNSQDKVQNFKQGFDAGNKKE.N	KTVTNSQDKVQNFKQGFD	169	162	2.933	0.000
tr|Q2A2A7|Q2A2A7_FRATH Putative uncharacterized	E.KTVTNSQDKVQNFKQGFDDGSAGNKKE.N	KTVTNSQDKVQNFKQGFDDGS	169	165	2.994	0.000
tr|Q2A2A7|Q2A2A7_FRATH Putative uncharacterized	E.KTVTNSQDKVQNFKQGFDDGSDNTFAGNKKE.N	KTVTNSQDKVQNFKQGFDDGSDNTF	169	169	3.363	0.000
tr|Q2A2B3|Q2A2B3_FRATH Cytidine deaminase FTL_	K.ELLPYIFSAGNKK.E	ELLPYIFS	133	132	4.008	0.000
tr|Q2A2B3|Q2A2B3_FRATH Cytidine deaminase FTL_	K.ELLPYIFSAGNK.K	ELLPYIFS	133	132	4.002	0.000
tr|Q2A2B3|Q2A2B3_FRATH Cytidine deaminase FTL_	E.LLPYIFSAGNKKE.N	LLPYIFS	133	132	4.265	0.001
tr|Q2A2B3|Q2A2B3_FRATH Cytidine deaminase FTL_	K.ELLPYIFSLAGNKK.E	ELLPYIFSL	133	133	4.359	0.000

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

tr|Q2A2B3|Q2A2B3_FRATH	Cytidine deaminase FTL_	K.ELLPYIFSLAGNK.K	ELLPYIFSL	133	133	3.298	0.000
tr|Q2A2C3|Q2A2C3_FRATH	Inosine-5-monophosphate	E.SHVHNVAGNK.K	SHVHNV	486	475	2.835	0.000
tr|Q2A2C3|Q2A2C3_FRATH	Inosine-5-monophosphate	R.TEPTFVQITGAGFNESHVHNVAGNK.K	TEPTFVQITGAGFNESHVHNV	486	475	2.519	0.002
tr|Q2A2C3|Q2A2C3_FRATH	Inosine-5-monophosphate	E.SHVHNVTITKAGNK.K	SHVHNVTITK	486	479	3.686	0.000
tr|Q2A2C4|Q2A2C4_FRATH	Thiamine pyrophosphokin	E.FIDIYSRYFFAGNK.K	FIDIYSRYFF	217	134	2.386	0.009
tr|Q2A2C8|Q2A2C8_FRATH	DNA excision repair enzy	R.FKPKKENEQRAGNK.K	FKPKKENEQR	940	217	4.203	0.003
tr|Q2A2E7|Q2A2E7_FRATH	Major facilitator superfam	*.IKNMIAAAAGNK.K	IKNMIAAA	404	356	2.88	0.001
tr|Q2A2F5|Q2A2F5_FRATH	Enoyl-[acyl-carrier-protei	K.VWDGLDAIVHSIAFAGNK.K	VWDGLDAIVHSIAF	260	93	4.168	0.000
tr|Q2A2F5|Q2A2F5_FRATH	Enoyl-[acyl-carrier-protei	E.VVHVDAGAGNKKE.N	VVHVDAG	260	250	4.185	0.000
tr|Q2A2F5|Q2A2F5_FRATH	Enoyl-[acyl-carrier-protei	E.VVHVDAGYAGNKKE.N	VVHVDAGY	260	251	4.24	0.000
tr|Q2A2G0|Q2A2G0_FRATH	Putative uncharacterized	D.LVNELNSITAGNKK.E	LVNELNSIT	269	262	3.201	0.008
tr|Q2A2G7|Q2A2G7_FRATH	UDP-glucose 4-epimerase	R.DYIHVVDLAIGHILAGNKK.E	DYIHVVDLAIGHIL	339	246	3.287	0.000
tr|Q2A2K4|Q2A2K4_FRATH	Peptidyl-prolyl cis-trans is	K.VHGPVQTQAGNKK.E	VHGPVQTQ	92	80	4.142	0.000
tr|Q2A2K5|Q2A2K5_FRATH	Cold-shock DEAD-box pro	K.DFSQLGLNQDIVDTVIAGNKK.E	DFSQLGLNQDIVDTVI	569	23	2.117	0.006
tr|Q2A2L3|Q2A2L3_FRATH	Glutathione peroxidase FT	K.TIPEDLIPDIDNFLAGNK.K	TIPEDLIPDIDNFL	156	154	3.421	0.001
tr|Q2A2M0|Q2A2M0_FRATH	Putative uncharacterized	D.FKYEKDFTTFGAGNK.K	FKYEKDFTTFG	287	276	2.301	0.002
tr|Q2A2M0|Q2A2M0_FRATH	Putative uncharacterized	K.YEKDFTTFGAGNKKE.N	YEKDFTTFG	287	276	3.419	0.003
tr|Q2A2Q0|Q2A2Q0_FRATH	Prephenate dehydratase	*.IFEKNKRNHAGNKK.E	IFEKNKRNH	280	147	2.05	0.005
tr|Q2A2Q8|Q2A2Q8_FRATH	Outer membrane associat	K.YFAVQYNQAGNKK.E	YFAVQYNQ	392	115	4.173	0.000
tr|Q2A2Q8|Q2A2Q8_FRATH	Outer membrane associat	K.YFAVQYNQAGNK.K	YFAVQYNQ	392	115	4.04	0.000
tr|Q2A2Q8|Q2A2Q8_FRATH	Outer membrane associat	K.YFAVQYNQLAGNK.K	YFAVQYNQL	392	116	4.112	0.000
tr|Q2A2Q8|Q2A2Q8_FRATH	Outer membrane associat	K.YFAVQYNQLAGNKK.E	YFAVQYNQL	392	116	4.046	0.003
tr|Q2A2Q8|Q2A2Q8_FRATH	Outer membrane associat	K.YFAVQYNQLVAGNKK.E	YFAVQYNQLV	392	117	4.296	0.000
tr|Q2A2Q8|Q2A2Q8_FRATH	Outer membrane associat	K.YFAVQYNQLVAGNK.K	YFAVQYNQLV	392	117	4.248	0.000
tr|Q2A2Q8|Q2A2Q8_FRATH	Outer membrane associat	K.YFAVQYNQLVGAGNK.K	YFAVQYNQLVG	392	118	4.297	0.000
tr|Q2A2Q8|Q2A2Q8_FRATH	Outer membrane associat	K.YFAVQYNQLVGAGNKK.E	YFAVQYNQLVG	392	118	4.256	0.000
tr|Q2A2Q8|Q2A2Q8_FRATH	Outer membrane associat	R.VFAGLGEGAGNKK.E	VFAGLGEG	392	127	4.366	0.000
tr|Q2A2Q8|Q2A2Q8_FRATH	Outer membrane associat	R.VFAGLGEGVAGNKK.E	VFAGLGEGV	392	128	4.022	0.000
tr|Q2A2Q8|Q2A2Q8_FRATH	Outer membrane associat	R.VFAGLGEGVVAGNKK.E	VFAGLGEGVV	392	129	4.24	0.000
tr|Q2A2Q8|Q2A2Q8_FRATH	Outer membrane associat	E.GVVNAGNKKE.N	GVVN	392	130	3.568	0.009
tr|Q2A2Q8|Q2A2Q8_FRATH	Outer membrane associat	R.VFAGLGEGVVNAGNKK.E	VFAGLGEGVVN	392	130	4.388	0.000
tr|Q2A2Q8|Q2A2Q8_FRATH	Outer membrane associat	R.VFAGLGEGVVNAGNK.K	VFAGLGEGVVN	392	130	3.617	0.000
tr|Q2A2Q8|Q2A2Q8_FRATH	Outer membrane associat	E.GVVNFAGNKKE.N	GVVNF	392	131	3.356	0.002

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

tr|Q2A2Q8|Q2A2Q8_FRATH	Outer membrane associat	R.VFAGLGEGVVNFAGNK.K	VFAGLGEGVVNF	392	131	4.484	0.000
tr|Q2A2Q8|Q2A2Q8_FRATH	Outer membrane associat	R.VFAGLGEGVVNFAGNKK.E	VFAGLGEGVVNF	392	131	3.953	0.000
tr|Q2A2Q8|Q2A2Q8_FRATH	Outer membrane associat	E.GVVNFSAGNKKE.N	GVVNFS	392	132	3.774	0.000
tr|Q2A2Q8|Q2A2Q8_FRATH	Outer membrane associat	R.VFAGLGEGVVNFSAGNKK.E	VFAGLGEGVVNFS	392	132	4.334	0.000
tr|Q2A2Q8|Q2A2Q8_FRATH	Outer membrane associat	R.VFAGLGEGVVNFSAGNK.K	VFAGLGEGVVNFS	392	132	4.121	0.000
tr|Q2A2Q8|Q2A2Q8_FRATH	Outer membrane associat	E.GVVNFSNAGNKKE.N	GVVNFSN	392	133	3.907	0.000
tr|Q2A2Q8|Q2A2Q8_FRATH	Outer membrane associat	R.VFAGLGEGVVNFSNAGNK.K	VFAGLGEGVVNFSN	392	133	4.414	0.000
tr|Q2A2Q8|Q2A2Q8_FRATH	Outer membrane associat	E.GVVNFSNNAGNKKE.N	GVVNFSNN	392	134	3.897	0.000
tr|Q2A2Q8|Q2A2Q8_FRATH	Outer membrane associat	E.GVVNFSNNTAGNKKE.N	GVVNFSNNT	392	135	4.061	0.000
tr|Q2A2Q8|Q2A2Q8_FRATH	Outer membrane associat	R.VFAGLGEGVVNFSNNTAGNKK.E	VFAGLGEGVVNFSNNT	392	135	4.446	0.000
tr|Q2A2Q8|Q2A2Q8_FRATH	Outer membrane associat	R.VFAGLGEGVVNFSNNTMAGNK.K	VFAGLGEGVVNFSNNTM	392	136	4.287	0.000
tr|Q2A2Q8|Q2A2Q8_FRATH	Outer membrane associat	R.VFAGLGEGVVNFSNNTMFAGNKK.E	VFAGLGEGVVNFSNNTMF	392	137	3.578	0.000
tr|Q2A2Q8|Q2A2Q8_FRATH	Outer membrane associat	R.VFAGLGEGVVNFSNNTMFAGNK.K	VFAGLGEGVVNFSNNTMF	392	137	2.748	0.000
tr|Q2A2Q8|Q2A2Q8_FRATH	Outer membrane associat	E.GVVNFSNNTMFTAGNKKE.N	GVVNFSNNTMFT	392	138	3.793	0.000
tr|Q2A2Q8|Q2A2Q8_FRATH	Outer membrane associat	R.VFAGLGEGVVNFSNNTMFTAGNKK.E	VFAGLGEGVVNFSNNTMFT	392	138	3.392	0.000
tr|Q2A2Q8|Q2A2Q8_FRATH	Outer membrane associat	R.NVQASVAGNKK.E	NVQASV	392	176	3.554	0.000
tr|Q2A2Q8|Q2A2Q8_FRATH	Outer membrane associat	R.NVQASVDAGNKK.E	NVQASVD	392	177	3.985	0.000
tr|Q2A2Q8|Q2A2Q8_FRATH	Outer membrane associat	R.YIQTMAPAGNKK.E	YIQTMAP	392	186	2.871	0.001
tr|Q2A2Q8|Q2A2Q8_FRATH	Outer membrane associat	R.YIQTM+16APSAGNK.K	YIQTMAPS	392	187	3.125	0.000
tr|Q2A2Q8|Q2A2Q8_FRATH	Outer membrane associat	R.YIQTMAPSAGNK.K	YIQTMAPS	392	187	2.606	0.001
tr|Q2A2Q8|Q2A2Q8_FRATH	Outer membrane associat	R.YIQTMAPSNAGNK.K	YIQTMAPSN	392	188	3.89	0.000
tr|Q2A2Q8|Q2A2Q8_FRATH	Outer membrane associat	R.YIQTMAPSNAGNKK.E	YIQTMAPSN	392	188	3.654	0.000
tr|Q2A2Q8|Q2A2Q8_FRATH	Outer membrane associat	R.YIQTMAPSNIAGNKK.E	YIQTMAPSNI	392	189	4.151	0.000
tr|Q2A2Q8|Q2A2Q8_FRATH	Outer membrane associat	R.YIQTMAPSNIAGNK.K	YIQTMAPSNI	392	189	3.53	0.000
tr|Q2A2Q8|Q2A2Q8_FRATH	Outer membrane associat	R.YIQTM+16APSNIAGNKK.E	YIQTMAPSNI	392	189	3.288	0.000
tr|Q2A2Q8|Q2A2Q8_FRATH	Outer membrane associat	R.YIQTMAPSNISAGNKK.E	YIQTMAPSNIS	392	190	4.12	0.008
tr|Q2A2Q8|Q2A2Q8_FRATH	Outer membrane associat	R.YIQTMAPSNISGAGNKK.E	YIQTMAPSNISG	392	191	4.035	0.000
tr|Q2A2Q8|Q2A2Q8_FRATH	Outer membrane associat	R.YIQTMAPSNISGAAGNK.K	YIQTMAPSNISGA	392	192	3.747	0.009
tr|Q2A2Q8|Q2A2Q8_FRATH	Outer membrane associat	R.AGTNMIGAGLAGNKK.E	AGTNMIGAGL	392	205	4.255	0.000
tr|Q2A2Q8|Q2A2Q8_FRATH	Outer membrane associat	R.AGTNMIGAGLTAGNKK.E	AGTNMIGAGLT	392	206	4.185	0.000
tr|Q2A2S5|Q2A2S5_FRATH	Putative uncharacterized	D.ALWAVAGNKKE.N	ALWAV	353	77	2.465	0.009
tr|Q2A2S5|Q2A2S5_FRATH	Putative uncharacterized	E.DALWAVAGNKKE.N	DALWAV	353	77	2.955	0.005
tr|Q2A2S5|Q2A2S5_FRATH	Putative uncharacterized	K.LALEDALWAVAGNK.K	LALEDALWAV	353	77	3.19	0.000

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

tr|Q2A2S5|Q2A2S5_FRATH	Putative uncharacterized	E.DALWAVNFAGNKKE.N	DALWAVNF	353	79	4.184	0.001
tr|Q2A2S5|Q2A2S5_FRATH	Putative uncharacterized	K.LALEDALWAVNFAGNKK.E	LALEDALWAVNF	353	79	4.217	0.000
tr|Q2A2S5|Q2A2S5_FRATH	Putative uncharacterized	E.DALWAVNFYQKAGNKKE.N	DALWAVNFYQK	353	82	2.563	0.010
tr|Q2A2S5|Q2A2S5_FRATH	Putative uncharacterized	E.DALWAVNFYQKNGAAGNKKE.N	DALWAVNFYQKNGA	353	85	3.095	0.000
tr|Q2A2S5|Q2A2S5_FRATH	Putative uncharacterized	R.LYSYLVYLIGELAGNKK.E	LYSYLVYLIGEL	353	105	4.454	0.000
tr|Q2A2S5|Q2A2S5_FRATH	Putative uncharacterized	E.LDHISPVETGAGNKKE.N	LDHISPVETG	353	236	3.837	0.001
tr|Q2A2S5|Q2A2S5_FRATH	Putative uncharacterized	R.EAIQQPYAPAFVVIADAGNKKE.N	EAIQQPYAPAFVVIAD	353	271	2.878	0.000
tr|Q2A2T7|Q2A2T7_FRATH	Short-chain dehydrogenas	R.ILPTNILDNFLAGNK.K	ILPTNILDNFL	274	271	3.727	0.000
tr|Q2A2W1|Q2A2W1_FRAT	Putative uncharacterized	E.IVFVSDDFLEVHLAGNK.K	IVFVSDDFLEVHL	166	47	2.932	0.001
tr|Q2A2W3|Q2A2W3_FRAT	2-amino-4-hydroxy-6-hyd	*.MQYIIGIGTNSAGNKK.E	MQYIIGIGTNS	421	11	2.147	0.002
tr|Q2A2X0|Q2A2X0_FRATH	ATP-dependent RNA helic	D.QPKAQANRIKAGNK.K	QPKAQANRIK	441	75	2.676	0.002
tr|Q2A2X4|Q2A2X4_FRATH	Pyruvate/2-oxoglutarate	E.LVTLVAGNKK.E	LVTLV	453	453	2.935	0.009
tr|Q2A2Y3|Q2A2Y3_FRATH	Signal recognition particle	K.KSLTPDQAGNKK.E	KSLTPDQ	458	72	3.582	0.000
tr|Q2A2Y3|Q2A2Y3_FRATH	Signal recognition particle	K.KSLTPDQAGNK.K	KSLTPDQ	458	72	3.233	0.008
tr|Q2A2Y3|Q2A2Y3_FRATH	Signal recognition particle	K.KSLTPDQAGNKKENR.V	KSLTPDQ	458	72	2.154	0.003
tr|Q2A2Z0|Q2A2Z0_FRATH	Putative uncharacterized	K.VLNSQLLSAGNKK.E	VLNSQLLS	136	119	3.322	0.006
tr|Q2A2Z4|Q2A2Z4_FRATH	Putative uncharacterized	E.TTVKSDSILAGNKKE.N	TTVKSDSIL	229	49	4.041	0.000
tr|Q2A2Z4|Q2A2Z4_FRATH	Putative uncharacterized	E.TTVKSDSILVAGNKKE.N	TTVKSDSILV	229	50	4.393	0.000
tr|Q2A2Z4|Q2A2Z4_FRATH	Putative uncharacterized	E.TTVKSDSILVQVAGNKKE.N	TTVKSDSILVQV	229	52	4.275	0.000
tr|Q2A2Z4|Q2A2Z4_FRATH	Putative uncharacterized	D.SILVQVTAGNKKE.N	SILVQVT	229	53	3.927	0.000
tr|Q2A2Z4|Q2A2Z4_FRATH	Putative uncharacterized	E.TTVKSDSILVQVTAGNKKE.N	TTVKSDSILVQVT	229	53	2.955	0.001
tr|Q2A2Z4|Q2A2Z4_FRATH	Putative uncharacterized	K.SDSILVQVTGAGNKK.E	SDSILVQVTG	229	54	3.964	0.000
tr|Q2A2Z4|Q2A2Z4_FRATH	Putative uncharacterized	D.SILVQVTGAGNKKE.N	SILVQVTG	229	54	3.832	0.000
tr|Q2A2Z4|Q2A2Z4_FRATH	Putative uncharacterized	E.TTVKSDSILVQVTGAGNKKE.N	TTVKSDSILVQVTG	229	54	4.145	0.000
tr|Q2A2Z4|Q2A2Z4_FRATH	Putative uncharacterized	E.TTVKSDSILVQVTGYATAGNKKE.N	TTVKSDSILVQVTGYAT	229	57	3.445	0.000
tr|Q2A2Z4|Q2A2Z4_FRATH	Putative uncharacterized	E.TTVKSDSILVQVTGYATTTAGNKKE.N	TTVKSDSILVQVTGYATTT	229	59	3.325	0.000
tr|Q2A2Z4|Q2A2Z4_FRATH	Putative uncharacterized	E.TTVKSDSILVQVTGYATTTLEAGNKK.E	TTVKSDSILVQVTGYATTTLE	229	61	3.316	0.000
tr|Q2A2Z4|Q2A2Z4_FRATH	Putative uncharacterized	E.KQNDVEKQIAGNKKE.N	KQNDVEKQI	229	70	3.535	0.000
tr|Q2A2Z4|Q2A2Z4_FRATH	Putative uncharacterized	E.KQNDVEKQISAGNKKE.N	KQNDVEKQIS	229	71	3.889	0.000
tr|Q2A2Z4|Q2A2Z4_FRATH	Putative uncharacterized	E.KQNDVEKQISDAGNKKE.N	KQNDVEKQISD	229	72	3.971	0.000
tr|Q2A2Z4|Q2A2Z4_FRATH	Putative uncharacterized	E.KQISDNVAGNKKE.N	KQISDNV	229	74	3.807	0.006
tr|Q2A2Z4|Q2A2Z4_FRATH	Putative uncharacterized	E.KQISDNVNAGNKKE.N	KQISDNVN	229	75	3.474	0.005
tr|Q2A2Z4|Q2A2Z4_FRATH	Putative uncharacterized	E.KQNDVEKQISDNVNAGNKKE.N	KQNDVEKQISDNVN	229	75	3.89	0.000

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

tr|Q2A2Z4|Q2A2Z4_FRATH	Putative uncharacterized	E.KQISDNVNNAGNKKE.N	KQISDNVNN	229	76	3.851	0.000
tr|Q2A2Z4|Q2A2Z4_FRATH	Putative uncharacterized	E.KQISDNVNNIAGNKKE.N	KQISDNVNNI	229	77	3.924	0.000
tr|Q2A2Z4|Q2A2Z4_FRATH	Putative uncharacterized	E.KQNDVEKQISDNVNNIAGNKKE.N	KQNDVEKQISDNVNNI	229	77	3.03	0.002
tr|Q2A2Z4|Q2A2Z4_FRATH	Putative uncharacterized	K.QISDNVNNIAGNKK.E	QISDNVNNI	229	77	2.276	0.003
tr|Q2A2Z4|Q2A2Z4_FRATH	Putative uncharacterized	E.KQISDNVNNIVAGNKKE.N	KQISDNVNNIV	229	78	4.064	0.001
tr|Q2A2Z4|Q2A2Z4_FRATH	Putative uncharacterized	E.KQNDVEKQISDNVNNIVAGNKKE.N	KQNDVEKQISDNVNNIV	229	78	3.109	0.003
tr|Q2A2Z4|Q2A2Z4_FRATH	Putative uncharacterized	E.KQISDNVNNIVKAGNKKE.N	KQISDNVNNIVK	229	79	2.8	0.001
tr|Q2A2Z4|Q2A2Z4_FRATH	Putative uncharacterized	E.KQNDVEKQISDNVNNIVKAGNKKE.N	KQNDVEKQISDNVNNIVK	229	79	3.112	0.000
tr|Q2A2Z4|Q2A2Z4_FRATH	Putative uncharacterized	E.KQNDVEKQISDNVNNIVKSEAGNKK.E	KQNDVEKQISDNVNNIVKSE	229	81	2.816	0.000
tr|Q2A2Z4|Q2A2Z4_FRATH	Putative uncharacterized	K.VKNIEQTAGNKK.E	VKNIEQT	229	90	3.637	0.001
tr|Q2A2Z4|Q2A2Z4_FRATH	Putative uncharacterized	K.NIEQTTAGNKK.E	NIEQTT	229	91	3.709	0.000
tr|Q2A2Z4|Q2A2Z4_FRATH	Putative uncharacterized	K.VKNIEQTTAGNKK.E	VKNIEQTT	229	91	3.856	0.000
tr|Q2A2Z4|Q2A2Z4_FRATH	Putative uncharacterized	K.NIEQTTSAGNKK.E	NIEQTTS	229	92	2.948	0.002
tr|Q2A2Z4|Q2A2Z4_FRATH	Putative uncharacterized	K.NIEQTTSNAGNKK.E	NIEQTTSN	229	93	3.657	0.000
tr|Q2A2Z4|Q2A2Z4_FRATH	Putative uncharacterized	K.VKNIEQTTSNAGNKK.E	VKNIEQTTSN	229	93	3.929	0.000
tr|Q2A2Z4|Q2A2Z4_FRATH	Putative uncharacterized	K.NIEQTTSNSGAAGNKK.E	NIEQTTSNSGA	229	96	3.529	0.000
tr|Q2A2Z4|Q2A2Z4_FRATH	Putative uncharacterized	K.NIEQTTSNSGAIAGNKK.E	NIEQTTSNSGAI	229	97	4.036	0.000
tr|Q2A2Z4|Q2A2Z4_FRATH	Putative uncharacterized	K.VKNIEQTTSNSGAIAGNKK.E	VKNIEQTTSNSGAI	229	97	3.768	0.000
tr|Q2A2Z4|Q2A2Z4_FRATH	Putative uncharacterized	K.NIEQTTSNSGAINAGNKK.E	NIEQTTSNSGAIN	229	98	4.061	0.000
tr|Q2A2Z4|Q2A2Z4_FRATH	Putative uncharacterized	R.ISQSDLNAGNKK.E	ISQSDLN	229	113	4.038	0.000
tr|Q2A2Z4|Q2A2Z4_FRATH	Putative uncharacterized	R.ISQSDLNNAGNKK.E	ISQSDLNN	229	114	3.969	0.001
tr|Q2A2Z4|Q2A2Z4_FRATH	Putative uncharacterized	R.ISQSDLNNLQAGNKK.E	ISQSDLNNLQ	229	116	4.105	0.000
tr|Q2A2Z4|Q2A2Z4_FRATH	Putative uncharacterized	R.LVVDVLDAGNKK.E	LVVDVLD	229	136	4.236	0.006
tr|Q2A2Z4|Q2A2Z4_FRATH	Putative uncharacterized	R.LVVDVLDYAGNKK.E	LVVDVLDY	229	137	4.225	0.000
tr|Q2A2Z4|Q2A2Z4_FRATH	Putative uncharacterized	R.LVVDVLDYAGNK.K	LVVDVLDY	229	137	3.168	0.000
tr|Q2A2Z4|Q2A2Z4_FRATH	Putative uncharacterized	R.LVVDVLDYNAGNKK.E	LVVDVLDYN	229	138	4.411	0.000
tr|Q2A2Z4|Q2A2Z4_FRATH	Putative uncharacterized	R.LVVDVLDYNPAGNKK.E	LVVDVLDYNP	229	139	4.448	0.000
tr|Q2A2Z4|Q2A2Z4_FRATH	Putative uncharacterized	R.LVVDVLDYNPPAGNKK.E	LVVDVLDYNPP	229	140	4.4	0.000
tr|Q2A2Z4|Q2A2Z4_FRATH	Putative uncharacterized	R.LVVDVLDYNPPAAGNKK.E	LVVDVLDYNPPA	229	141	4.444	0.000
tr|Q2A2Z4|Q2A2Z4_FRATH	Putative uncharacterized	R.LVVDVLDYNPPAAGNK.K	LVVDVLDYNPPA	229	141	4.364	0.000
tr|Q2A2Z4|Q2A2Z4_FRATH	Putative uncharacterized	K.LFNDTKDYLAAGNKK.E	LFNDTKDYLA	229	164	3.031	0.000
tr|Q2A2Z4|Q2A2Z4_FRATH	Putative uncharacterized	K.LFNDTKDYLANAGNKK.E	LFNDTKDYLAN	229	165	3.818	0.000
tr|Q2A2Z4|Q2A2Z4_FRATH	Putative uncharacterized	K.LFNDTKDYLANFAGNKK.E	LFNDTKDYLANF	229	166	4.262	0.000

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

tr|Q2A2Z4|Q2A2Z4_FRATH Putative uncharacterized	K.DYLANFNKAGNK.K	DYLANFNK	229	168	3.871	0.000
tr|Q2A2Z4|Q2A2Z4_FRATH Putative uncharacterized	K.LFNDTKDYLANFNKAGNK.K	LFNDTKDYLANFNK	229	168	3.208	0.001
tr|Q2A2Z4|Q2A2Z4_FRATH Putative uncharacterized	K.QTNSNYTIQSAGNKK.E	QTNSNYTIQS	229	178	3.49	0.000
tr|Q2A2Z4|Q2A2Z4_FRATH Putative uncharacterized	K.QTNSNYTIQSIQAGNKK.E	QTNSNYTIQSIQ	229	180	3.416	0.000
tr|Q2A2Z4|Q2A2Z4_FRATH Putative uncharacterized	K.QTNSNYTIQSIQAGNK.K	QTNSNYTIQSIQ	229	180	2.691	0.000
tr|Q2A2Z4|Q2A2Z4_FRATH Putative uncharacterized	K.TAYSGDAAGNKK.E	TAYSGDA	229	204	3.742	0.002
tr|Q2A2Z4|Q2A2Z4_FRATH Putative uncharacterized	K.TAYSGDANSNSSNPAGNKK.E	TAYSGDANSNSSNP	229	211	4.079	0.006
tr|Q2A2Z4|Q2A2Z4_FRATH Putative uncharacterized	K.TAYSGDANSNSSNPVAVTQAGNK.K	TAYSGDANSNSSNPVAVTQ	229	216	4.072	0.000
tr|Q2A2Z4|Q2A2Z4_FRATH Putative uncharacterized	D.INIKANVAGNKKE.N	INIKANV	229	224	3.917	0.009
tr|Q2A306|Q2A306_FRATH Putative uncharacterized	D.WKKIDAGAGNKKE.N	WKKIDAG	631	304	2.982	0.003
tr|Q2A319|Q2A319_FRATH Cobalamin (Vitamin B12)	K.LPVTVLSGFLAGNK.K	LPVTVLSGFL	405	13	4.284	0.000
tr|Q2A319|Q2A319_FRATH Cobalamin (Vitamin B12)	R.SFVYHSINPAGNK.K	SFVYHSINP	405	268	3.593	0.000
tr|Q2A347|Q2A347_FRATH Putative uncharacterized	D.NNELPLIAAGNK.K	NNELPLIA	1093	100	2.848	0.002
tr|Q2A355|Q2A355_FRATH Putative uncharacterized	K.NISLNNFVAGNKK.E	NISLNNFV	257	36	2.243	0.009
tr|Q2A357|Q2A357_FRATH Putative uncharacterized	K.KNATIFLNLNEFC+57AGNKK.E	KNATIFLNLNEFC	191	51	3.209	0.000
tr|Q2A357|Q2A357_FRATH Putative uncharacterized	E.FC+57PTNIAAAGNKKE.N	FCPTNIAA	191	57	3.665	0.000
tr|Q2A357|Q2A357_FRATH Putative uncharacterized	K.KNATIFLNLNEFCPTNIAACKDENDAGNKK.E	KNATIFLNLNEFCPTNIAACKDEND	191	63	2.172	0.000
tr|Q2A357|Q2A357_FRATH Putative uncharacterized	K.NATIFLNLNEFC+57PTNIAACKDENDNNCIYITEL	NATIFLNLNEFCPTNIAACKDENDNNCIYI	191	72	2.001	0.000
tr|Q2A357|Q2A357_FRATH Putative uncharacterized	R.IYYYLAVAGNK.K	IYYYLAV	191	86	4.043	0.001
tr|Q2A357|Q2A357_FRATH Putative uncharacterized	R.IYYYLAVAGNKK.E	IYYYLAV	191	86	4.043	0.000
tr|Q2A357|Q2A357_FRATH Putative uncharacterized	R.IYYYLAVPAGNKK.E	IYYYLAVP	191	87	4.437	0.000
tr|Q2A357|Q2A357_FRATH Putative uncharacterized	R.IYYYLAVPIAGNKK.E	IYYYLAVPI	191	88	4.383	0.000
tr|Q2A357|Q2A357_FRATH Putative uncharacterized	R.IYYYLAVPIAGNK.K	IYYYLAVPI	191	88	3.915	0.000
tr|Q2A357|Q2A357_FRATH Putative uncharacterized	R.IYYYLAVPITAGNK.K	IYYYLAVPIT	191	89	4.125	0.000
tr|Q2A357|Q2A357_FRATH Putative uncharacterized	R.IYYYLAVPITAGNKK.E	IYYYLAVPIT	191	89	3.368	0.000
tr|Q2A357|Q2A357_FRATH Putative uncharacterized	K.DLTILYKHDKEESAGNKK.E	DLTILYKHDKEES	191	107	3.052	0.000
tr|Q2A357|Q2A357_FRATH Putative uncharacterized	K.DLTILYKHDKEESPAGNKK.E	DLTILYKHDKEESP	191	108	3.216	0.000
tr|Q2A357|Q2A357_FRATH Putative uncharacterized	K.HDKEESPPAGNKK.E	HDKEESPP	191	109	2.222	0.003
tr|Q2A357|Q2A357_FRATH Putative uncharacterized	K.HDKEESPPEAGNKK.E	HDKEESPPE	191	110	3.775	0.000
tr|Q2A357|Q2A357_FRATH Putative uncharacterized	*.DLTILYKHDKEESPPEAAGNKK.E	DLTILYKHDKEESPPEA	191	111	3.581	0.000
tr|Q2A357|Q2A357_FRATH Putative uncharacterized	K.HDKEESPPEAAGNKK.E	HDKEESPPEA	191	111	4.023	0.000
tr|Q2A357|Q2A357_FRATH Putative uncharacterized	K.DLTILYKHDKEESPPEAIAGNK.K	DLTILYKHDKEESPPEAI	191	112	3.634	0.000
tr|Q2A357|Q2A357_FRATH Putative uncharacterized	K.HDKEESPPEAIAGNKK.E	HDKEESPPEAI	191	112	4.152	0.000

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

trlQ2A357lQ2A357_FRATH Putative uncharacterized	K.HDKEESPPEAIAGNK.K	HDKEESPPEAI	191	112	3.312	0.000
trlQ2A357lQ2A357_FRATH Putative uncharacterized	K.SVKDLTILYKHDKEESPPEAIAGNKK.E	SVKDLTILYKHDKEESPPEAI	191	112	3.456	0.000
trlQ2A357lQ2A357_FRATH Putative uncharacterized	*.DLTILYKHDKEESPPEAINAGNKK.E	DLTILYKHDKEESPPEAIN	191	113	3.702	0.000
trlQ2A357lQ2A357_FRATH Putative uncharacterized	K.HDKEESPPEAINAGNKK.E	HDKEESPPEAIN	191	113	4.131	0.000
trlQ2A357lQ2A357_FRATH Putative uncharacterized	K.HDKEESPPEAINAGNK.K	HDKEESPPEAIN	191	113	3.87	0.000
trlQ2A357lQ2A357_FRATH Putative uncharacterized	K.SVKDLTILYKHDKEESPPEAINAGNKK.E	SVKDLTILYKHDKEESPPEAIN	191	113	3.405	0.000
trlQ2A357lQ2A357_FRATH Putative uncharacterized	K.DLTILYKHDKEESPPEAINIAGNKK.E	DLTILYKHDKEESPPEAINI	191	114	3.791	0.000
trlQ2A357lQ2A357_FRATH Putative uncharacterized	K.HDKEESPPEAINIAGNK.K	HDKEESPPEAINI	191	114	4.28	0.000
trlQ2A357lQ2A357_FRATH Putative uncharacterized	K.HDKEESPPEAINIAGNKK.E	HDKEESPPEAINI	191	114	4.036	0.000
trlQ2A357lQ2A357_FRATH Putative uncharacterized	K.DLTILYKHDKEESPPEAINIC+57LAGNKKE.N	DLTILYKHDKEESPPEAINICL	191	116	3.243	0.000
trlQ2A357lQ2A357_FRATH Putative uncharacterized	K.DLTILYKHDKEESPPEAINIC+57LSLAGNKK.E	DLTILYKHDKEESPPEAINICLSL	191	118	3.177	0.000
trlQ2A357lQ2A357_FRATH Putative uncharacterized	K.HDKEESPPEAINIC+57LSLAGNKK.E	HDKEESPPEAINICLSL	191	118	3.252	0.000
trlQ2A357lQ2A357_FRATH Putative uncharacterized	K.NNKYETYAGNKK.E	NNKYETY	191	127	3.813	0.000
trlQ2A357lQ2A357_FRATH Putative uncharacterized	K.NNKYETYYSQVAGNKK.E	NNKYETYYSQV	191	131	4.02	0.000
trlQ2A357lQ2A357_FRATH Putative uncharacterized	E.TYYSQVAGNKKE.N	TYYSQV	191	131	3.768	0.000
trlQ2A357lQ2A357_FRATH Putative uncharacterized	E.TYYSQVAGNKK.E	TYYSQV	191	131	2.276	0.001
trlQ2A357lQ2A357_FRATH Putative uncharacterized	K.NNKYETYYSQVIAGNKK.E	NNKYETYYSQVI	191	132	3.927	0.000
trlQ2A357lQ2A357_FRATH Putative uncharacterized	K.NNKYETYYSQVIAGNK.K	NNKYETYYSQVI	191	132	3.857	0.000
trlQ2A357lQ2A357_FRATH Putative uncharacterized	E.TYYSQVIAGNKKE.N	TYYSQVI	191	132	3.818	0.001
trlQ2A357lQ2A357_FRATH Putative uncharacterized	K.NNKYETYYSQVIYNAGNKK.E	NNKYETYYSQVIYN	191	134	3.187	0.001
trlQ2A357lQ2A357_FRATH Putative uncharacterized	E.TYYSQVIYNWFAGNKKE.N	TYYSQVIYNWF	191	136	4.179	0.000
trlQ2A357lQ2A357_FRATH Putative uncharacterized	K.NNKYETYYSQVIYNWFVSAGNK.K	NNKYETYYSQVIYNWFVS	191	138	2.17	0.002
trlQ2A357lQ2A357_FRATH Putative uncharacterized	E.TYYSQVIYNWFVSAGNKKE.N	TYYSQVIYNWFVS	191	138	3.151	0.000
trlQ2A357lQ2A357_FRATH Putative uncharacterized	E.TYYSQVIYNWFVSSAGNKKE.N	TYYSQVIYNWFVSS	191	139	2.923	0.000
trlQ2A357lQ2A357_FRATH Putative uncharacterized	E.GSIFINKDINNSNNYDKGNFAGNKKE.N	GSIFINKDINNSNNYDKGNF	191	167	2.301	0.000
trlQ2A357lQ2A357_FRATH Putative uncharacterized	R.IADGWAPAGNKK.E	IADGWAP	191	181	3.163	0.000
trlQ2A357lQ2A357_FRATH Putative uncharacterized	R.IADGWAPPAGNK.K	IADGWAPP	191	182	4.232	0.001
trlQ2A357lQ2A357_FRATH Putative uncharacterized	R.IADGWAPPAGNKK.E	IADGWAPP	191	182	3.898	0.001
trlQ2A357lQ2A357_FRATH Putative uncharacterized	R.IADGWAPPHAGNK.K	IADGWAPPH	191	183	4.356	0.000
trlQ2A357lQ2A357_FRATH Putative uncharacterized	R.IADGWAPPHAGNKK.E	IADGWAPPH	191	183	4.243	0.000
trlQ2A357lQ2A357_FRATH Putative uncharacterized	R.IADGWAPPHYAGNK.K	IADGWAPPHY	191	184	4.091	0.000
trlQ2A357lQ2A357_FRATH Putative uncharacterized	R.IADGWAPPHYEKAGNK.K	IADGWAPPHYEK	191	186	3.894	0.003
trlQ2A358lQ2A358_FRATH Intracellular growth locus,	E.IYDFPLLTLAGNK.K	IYDFPLLTL	398	156	2.724	0.000

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

tr|Q2A358|Q2A358_FRATH Intracellular growth locus,	R.LVPEIYDFPLLTLAGNK.K	LVPEIYDFPLLTL	398	156	4.499	0.000
tr|Q2A358|Q2A358_FRATH Intracellular growth locus,	R.LVPEIYDFPLLTLNAGNK.K	LVPEIYDFPLLTLN	398	157	4.434	0.000
tr|Q2A359|Q2A359_FRATH Intracellular growth locus,	R.TDPTAC+57IGSHPAGNK.K	TDPTACIGSHP	209	30	2.444	0.004
tr|Q2A359|Q2A359_FRATH Intracellular growth locus,	R.LSITPGSAGNKK.E	LSITPGS	209	80	2.411	0.002
tr|Q2A359|Q2A359_FRATH Intracellular growth locus,	R.LSITPGSINPTAGNK.K	LSITPGSINPT	209	84	3.926	0.000
tr|Q2A359|Q2A359_FRATH Intracellular growth locus,	E.KVSSILQAGNKKE.N	KVSSILQ	209	110	4.015	0.001
tr|Q2A359|Q2A359_FRATH Intracellular growth locus,	K.VSSILQAGNKK.E	VSSILQ	209	110	3.234	0.002
tr|Q2A359|Q2A359_FRATH Intracellular growth locus,	E.KVSSILQASAGNKK.E	KVSSILQAS	209	112	3.09	0.002
tr|Q2A359|Q2A359_FRATH Intracellular growth locus,	K.VSSILQASAGNKK.E	VSSILQAS	209	112	3.676	0.000
tr|Q2A359|Q2A359_FRATH Intracellular growth locus,	K.VSSILQASAAGNKK.E	VSSILQASA	209	113	4.328	0.000
tr|Q2A359|Q2A359_FRATH Intracellular growth locus,	K.VSSILQASATDAGNKK.E	VSSILQASATD	209	115	3.956	0.000
tr|Q2A359|Q2A359_FRATH Intracellular growth locus,	K.AFSISIEPAGNKK.E	AFSISIEP	209	160	3.928	0.000
tr|Q2A359|Q2A359_FRATH Intracellular growth locus,	K.AFSISIEPTELAGNKK.E	AFSISIEPTEL	209	163	4.31	0.000
tr|Q2A359|Q2A359_FRATH Intracellular growth locus,	K.AFSISIEPTELMAGNK.K	AFSISIEPTELM	209	164	3.509	0.000
tr|Q2A359|Q2A359_FRATH Intracellular growth locus,	K.AFSISIEPTELMGVAGNKK.E	AFSISIEPTELMGV	209	166	4.545	0.000
tr|Q2A359|Q2A359_FRATH Intracellular growth locus,	E.LMGVAGNKKE.N	LMGV	209	166	3.234	0.008
tr|Q2A359|Q2A359_FRATH Intracellular growth locus,	K.DGMSYHIAGNKK.E	DGMSYHI	209	175	4.1	0.006
tr|Q2A359|Q2A359_FRATH Intracellular growth locus,	K.DGMSYHIISAGNKK.E	DGMSYHIIS	209	177	3.945	0.000
tr|Q2A359|Q2A359_FRATH Intracellular growth locus,	K.DGM+16SYHIISAGNKK.E	DGMSYHIIS	209	177	3.544	0.005
tr|Q2A359|Q2A359_FRATH Intracellular growth locus,	K.DGMSYHIISAGNK.K	DGMSYHIIS	209	177	2.959	0.001
tr|Q2A359|Q2A359_FRATH Intracellular growth locus,	K.DGMSYHIISIDGLTTSQGSLAGNKK.E	DGMSYHIISIDGLTTSQGSL	209	188	3.39	0.000
tr|Q2A359|Q2A359_FRATH Intracellular growth locus,	K.DGMSYHIISIDGLTTSQGSLPAGNKK.E	DGMSYHIISIDGLTTSQGSLP	209	189	3.494	0.000
tr|Q2A359|Q2A359_FRATH Intracellular growth locus,	K.DGMSYHIISIDGLTTSQGSLPVAGNK.K	DGMSYHIISIDGLTTSQGSLPV	209	190	4.329	0.000
tr|Q2A359|Q2A359_FRATH Intracellular growth locus,	K.DGMSYHIISIDGLTTSQGSLPVC+57AGNKK.E	DGMSYHIISIDGLTTSQGSLPVC	209	191	3.487	0.000
tr|Q2A359|Q2A359_FRATH Intracellular growth locus,	K.IGYIAAAAGNK.K	IGYIAAA	209	209	4.211	0.002
tr|Q2A359|Q2A359_FRATH Intracellular growth locus,	K.IGYIAAAAGNKKE.N	IGYIAAA	209	209	3.82	0.002
tr|Q2A359|Q2A359_FRATH Intracellular growth locus,	K.IGYIAAAAGNKK.E	IGYIAAA	209	209	3.721	0.002
tr|Q2A368|Q2A368_FRATH Pyruvate kinase FTL_114	K.VIIAGQVAGNKK.E	VIIAGQV	478	477	3.976	0.000
tr|Q2A370|Q2A370_FRATH Glyceraldehyde-3-phosph	K.ALHDLANIESGFAGNK.K	ALHDLANIESGF	333	173	3.074	0.000
tr|Q2A370|Q2A370_FRATH Glyceraldehyde-3-phosph	K.AIGLVIPAGNKKE.N	AIGLVIP	333	222	2.578	0.004
tr|Q2A370|Q2A370_FRATH Glyceraldehyde-3-phosph	R.VPVATGSLTELVAVAGNK.K	VPVATGSLTELVAV	333	248	2.902	0.000
tr|Q2A370|Q2A370_FRATH Glyceraldehyde-3-phosph	R.VVEYFGALAGNKK.E	VVEYFGAL	333	333	4.298	0.000
tr|Q2A372|Q2A372_FRATH Putative uncharacterized	D.LKDIIKEEILLDLPLIPKKDTSTAGNK.K	LKDIIKEEILLDLPLIPKKDTST	167	136	2.133	0.000

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

tr|Q2A377|Q2A377_FRATH 3-oxoacyl-(Acyl-carrier-pr	K.YITGQTLHVAGNK.K	YITGQTLHV	247	240	3.245	0.000
tr|Q2A378|Q2A378_FRATH Acyl carrier protein FTL_	R.VNHIIVEQLGVKEEDLKPEASAGNK.K	VNHIIVEQLGVKEEDLKPEAS	94	43	3.384	0.000
tr|Q2A378|Q2A378_FRATH Acyl carrier protein FTL_	R.VNHIIVEQLGVKEEDLKPEASFAGNKK.E	VNHIIVEQLGVKEEDLKPEASF	94	44	3.452	0.000
tr|Q2A378|Q2A378_FRATH Acyl carrier protein FTL_	K.DVYDYIAGNKK.E	DVYDYI	94	88	3.904	0.000
tr|Q2A378|Q2A378_FRATH Acyl carrier protein FTL_	R.TVKDVYDYIAGNKK.E	TVKDVYDYI	94	88	4.164	0.000
tr|Q2A378|Q2A378_FRATH Acyl carrier protein FTL_	K.DVYDYIESKAGNK.K	DVYDYIESK	94	91	4.156	0.000
tr|Q2A378|Q2A378_FRATH Acyl carrier protein FTL_	R.TVKDVYDYIESKAGNK.K	TVKDVYDYIESK	94	91	3.345	0.000
tr|Q2A378|Q2A378_FRATH Acyl carrier protein FTL_	E.SKDVGAGNKKE.N	SKDVG	94	94	2.824	0.003
tr|Q2A383|Q2A383_FRATH Inositol-1-monophosphat	K.EAGAVVTNIHGTSDLDSGLIVAGNKK.E	EAGAVVTNIHGTSDLDSGLIV	262	243	3.148	0.000
tr|Q2A3A5|Q2A3A5_FRATH Putative uncharacterized	R.NIDKDKDDEAGNKK.E	NIDKDKDDE	152	134	3.208	0.001
tr|Q2A3A5|Q2A3A5_FRATH Putative uncharacterized	R.NIDKDKDDENAGNKK.E	NIDKDKDDEN	152	135	3.98	0.000
tr|Q2A3A5|Q2A3A5_FRATH Putative uncharacterized	R.NIDKDKDDENPNAGNKK.E	NIDKDKDDENPN	152	137	3.446	0.000
tr|Q2A3A5|Q2A3A5_FRATH Putative uncharacterized	R.NIDKDKDDENPNAGNK.K	NIDKDKDDENPN	152	137	3.375	0.000
tr|Q2A3A5|Q2A3A5_FRATH Putative uncharacterized	R.NIDKDKDDENPNLAGNKK.E	NIDKDKDDENPNL	152	138	3.802	0.001
tr|Q2A3A5|Q2A3A5_FRATH Putative uncharacterized	R.NIDKDKDDENPNLAAGNKK.E	NIDKDKDDENPNLA	152	139	3.346	0.000
tr|Q2A3A5|Q2A3A5_FRATH Putative uncharacterized	R.NIDKDKDDENPNLANAGNKK.E	NIDKDKDDENPNLAN	152	140	3.393	0.000
tr|Q2A3A5|Q2A3A5_FRATH Putative uncharacterized	R.NIDKDKDDENPNLANLAGNKK.E	NIDKDKDDENPNLANL	152	141	3.456	0.000
tr|Q2A3A5|Q2A3A5_FRATH Putative uncharacterized	R.NIDKDKDDENPNLANLAAGNKK.E	NIDKDKDDENPNLANLA	152	142	3.287	0.000
tr|Q2A3A5|Q2A3A5_FRATH Putative uncharacterized	R.NIDKDKDDENPNLANLAAGNK.K	NIDKDKDDENPNLANLA	152	142	3.175	0.000
tr|Q2A3A5|Q2A3A5_FRATH Putative uncharacterized	R.NIDKDKDDENPNLANLATPAPAGNK.K	NIDKDKDDENPNLANLATPAP	152	146	3.429	0.000
tr|Q2A3A5|Q2A3A5_FRATH Putative uncharacterized	R.NIDKDKDDENPNLANLATPAPAGNKK.E	NIDKDKDDENPNLANLATPAP	152	146	3.107	0.000
tr|Q2A3A5|Q2A3A5_FRATH Putative uncharacterized	R.NIDKDKDDENPNLANLATPAPTAGNK.K	NIDKDKDDENPNLANLATPAPT	152	147	3.757	0.000
tr|Q2A3B3|Q2A3B3_FRATH Macrophage infectivity pc	K.SKLTPDQMAGNKK.E	SKLTPDQM	96	79	3.875	0.006
tr|Q2A3B3|Q2A3B3_FRATH Macrophage infectivity pc	K.LTPDQMQAGNKK.E	LTPDQMQ	96	80	3.93	0.000
tr|Q2A3B3|Q2A3B3_FRATH Macrophage infectivity pc	K.SKLTPDQMQAGNKK.E	SKLTPDQMQ	96	80	4.105	0.000
tr|Q2A3B3|Q2A3B3_FRATH Macrophage infectivity pc	K.SKLTPDQM+16QAGNKK.E	SKLTPDQMQ	96	80	2.035	0.000
tr|Q2A3B3|Q2A3B3_FRATH Macrophage infectivity pc	K.LTPDQMQNAGNKK.E	LTPDQMQN	96	81	3.931	0.001
tr|Q2A3B3|Q2A3B3_FRATH Macrophage infectivity pc	K.SKLTPDQMQNAGNKK.E	SKLTPDQMQN	96	81	4.181	0.000
tr|Q2A3B3|Q2A3B3_FRATH Macrophage infectivity pc	K.LTPDQMQNAAGNKK.E	LTPDQMQNA	96	82	4.21	0.000
tr|Q2A3B3|Q2A3B3_FRATH Macrophage infectivity pc	K.LTPDQM+16QNAAGNK.K	LTPDQMQNA	96	82	3.212	0.002
tr|Q2A3B3|Q2A3B3_FRATH Macrophage infectivity pc	K.SKLTPDQMQNAAGNKK.E	SKLTPDQMQNA	96	82	4.238	0.000
tr|Q2A3B3|Q2A3B3_FRATH Macrophage infectivity pc	K.SKLTPDQM+16QNAAGNKK.E	SKLTPDQMQNA	96	82	2.87	0.000
tr|Q2A3B3|Q2A3B3_FRATH Macrophage infectivity pc	K.SKLTPDQMQNAMAGNKK.E	SKLTPDQMQNAM	96	83	4.077	0.000

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

tr|Q2A3B3|Q2A3B3_FRATH	Macrophage infectivity pc	K.SKLTPDQMQNAM+16AGNKK.E	SKLTPDQMQNAM	96	83	3.204	0.000
tr|Q2A3B3|Q2A3B3_FRATH	Macrophage infectivity pc	K.SKLTPDQMQNAMIAGNKK.E	SKLTPDQMQNAMI	96	84	4.246	0.002
tr|Q2A3B3|Q2A3B3_FRATH	Macrophage infectivity pc	K.SKLTPDQMQNAMIEFQAGNK.K	SKLTPDQMQNAMIEFQ	96	87	3.391	0.000
tr|Q2A3B5|Q2A3B5_FRATH	Peptide methionine sulfox	D.QPYPDYKKVAGNK.K	QPYPDYKKV	284	169	2.391	0.003
tr|Q2A3B8|Q2A3B8_FRATH	Putative uncharacterized	K.THQNHEHKHQDDAGNKKE.N	THQNHEHKHQDD	117	17	2.489	0.000
tr|Q2A3B8|Q2A3B8_FRATH	Putative uncharacterized	K.HQDDC+57GHAGNKK.E	HQDDCGH	117	20	2.196	0.003
tr|Q2A3B8|Q2A3B8_FRATH	Putative uncharacterized	K.HGDHYDYLHDGHAGNKK.E	HGDHYDYLHDGH	117	36	4.047	0.000
tr|Q2A3B8|Q2A3B8_FRATH	Putative uncharacterized	K.HGDHYDYLHDGHLHHAGNK.K	HGDHYDYLHDGHLHH	117	39	3.129	0.000
tr|Q2A3B8|Q2A3B8_FRATH	Putative uncharacterized	E.VTEKNPDGC+57AGNKKE.N	VTEKNPDGC	117	60	3.311	0.003
tr|Q2A3B8|Q2A3B8_FRATH	Putative uncharacterized	K.NPDGC+57HPIAGNK.K	NPDGCHPI	117	63	3.071	0.008
tr|Q2A3B8|Q2A3B8_FRATH	Putative uncharacterized	E.VTEKNPDGC+57HPIKEDAGNKK.E	VTEKNPDGCHPIKED	117	66	2.651	0.008
tr|Q2A3B8|Q2A3B8_FRATH	Putative uncharacterized	E.DC+57SSHVHGPNCAGNK.K	DCSSHVHGPNC	117	76	2.659	0.001
tr|Q2A3B8|Q2A3B8_FRATH	Putative uncharacterized	R.LHHPHGDAGNKK.E	LHHPHGD	117	101	3.366	0.000
tr|Q2A3B8|Q2A3B8_FRATH	Putative uncharacterized	R.LHHPHGDAGNK.K	LHHPHGD	117	101	2.419	0.002
tr|Q2A3B8|Q2A3B8_FRATH	Putative uncharacterized	R.LHHPHGDHCDDHGPVEAGNK.K	LHHPHGDHCDDHGPVE	117	110	2.945	0.000
tr|Q2A3B8|Q2A3B8_FRATH	Putative uncharacterized	R.LHHPHGDHC+57DDHGPVEAGNK.K	LHHPHGDHCDDHGPVE	117	110	2.87	0.000
tr|Q2A3B8|Q2A3B8_FRATH	Putative uncharacterized	R.LHHPHGDHC+57DDHGPVEVAGNK.K	LHHPHGDHCDDHGPVEV	117	111	2.871	0.000
tr|Q2A3B8|Q2A3B8_FRATH	Putative uncharacterized	R.LHHPHGDHC+57DDHGPVEVIAGNK.K	LHHPHGDHCDDHGPVEVI	117	112	3.121	0.000
tr|Q2A3D0|Q2A3D0_FRATH	Putative uncharacterized	R.SSGTKPADLIANDIMLPAGNK.K	SSGTKPADLIANDIMLP	196	118	2.459	0.006
tr|Q2A3D0|Q2A3D0_FRATH	Putative uncharacterized	*.KLSLDVYHVAGNK.K	KLSLDVYHV	196	183	4.103	0.000
tr|Q2A3D0|Q2A3D0_FRATH	Putative uncharacterized	K.LSLDVYHVAGNK.K	LSLDVYHV	196	183	4.209	0.000
tr|Q2A3D0|Q2A3D0_FRATH	Putative uncharacterized	K.LSLDVYHVAGNKK.E	LSLDVYHV	196	183	4.15	0.000
tr|Q2A3D0|Q2A3D0_FRATH	Putative uncharacterized	D.VYHVAGNKKE.N	VYHV	196	183	2.659	0.005
tr|Q2A3D0|Q2A3D0_FRATH	Putative uncharacterized	D.VYHVYQAGNK.K	VYHVYQ	196	185	3.845	0.002
tr|Q2A3D0|Q2A3D0_FRATH	Putative uncharacterized	D.VYHVYQAGNKKE.N	VYHVYQ	196	185	3.346	0.001
tr|Q2A3E4|Q2A3E4_FRATH	Inorganic pyrophosphatas	E.IEKSVKNAGNKKE.N	IEKSVKN	173	171	3.646	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carbox	D.PYFNGANAGNKK.E	PYFNGAN	444	36	3.964	0.008
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carbox	E.LDAPAWVTM+16AGNK.K	LDAPAWVTM	444	60	3.371	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carbox	R.PANIELDAPAWVTM+16AGNK.K	PANIELDAPAWVTM	444	60	2.738	0.001
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carbox	R.NLVTGMDVVSGAGNKK.E	NLVTGMDVVSG	444	142	2.64	0.001
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carbox	E.YIGGTTQAFAGNKKE.N	YIGGTTQAF	444	160	3.799	0.005
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carbox	E.YIGGTTQAFTAGNKKE.N	YIGGTTQAFT	444	161	4.299	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carbox	E.YIGGTTQAFTDLAGNKKE.N	YIGGTTQAFTDL	444	163	4.368	0.000

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carbox	K.AIGMNNTHAGNKK.E	AIGMNNTH	444	177	4.061	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carbox	K.AIGMNNTHAGNK.K	AIGMNNTH	444	177	3.748	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carbox	K.AIGMNNTHFAGNKK.E	AIGMNNTHF	444	178	4.064	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carbox	K.AIGM+16NNTHFAGNKK.E	AIGMNNTHF	444	178	3.034	0.003
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carbox	K.AIGMNNTHFAAGNKK.E	AIGMNNTHFA	444	179	3.98	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carbox	K.AIGMNNTHFANPAGNKK.E	AIGMNNTHFANP	444	181	2.676	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carbox	K.AIGMNNTHFANPDAGNKK.E	AIGMNNTHFANPD	444	182	3.456	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carbox	K.AIGMNNTHFANPDGAGNKK.E	AIGMNNTHFANPDG	444	183	3.387	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carbox	K.AIGMNNTHFANPDGLAGNKK.E	AIGMNNTHFANPDGL	444	184	4.117	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carbox	K.AIGMNNTHFANPDGLPGAGNK.K	AIGMNNTHFANPDGLPG	444	186	2.366	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carbox	K.AIGMNNTHFANPDGLPGGAGNK.K	AIGMNNTHFANPDGLPGG	444	187	2.133	0.004
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carbox	K.AIGMNNTHFANPDGLPGGEQAGNKK.E	AIGMNNTHFANPDGLPGGEQ	444	189	3.503	0.006
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carbox	K.AIGMNNTHFANPDGLPGGEQYAGNKK.E	AIGMNNTHFANPDGLPGGEQY	444	190	3.871	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carbox	K.AIGMNNTHFANPDGLPGGEQYTTAGNKK.E	AIGMNNTHFANPDGLPGGEQYTT	444	192	3.498	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carbox	K.AIGMNNTHFANPDGLPGGEQYTTAAGNKK.E	AIGMNNTHFANPDGLPGGEQYTTA	444	193	3.924	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carbox	K.AIGMNNTHFANPDGLPGGEQYTTAHAGNK.K	AIGMNNTHFANPDGLPGGEQYTTAH	444	194	3.982	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carbox	K.AIGMNNTHFANPDGLPGGEQYTTAHDMAAGNKK.	AIGMNNTHFANPDGLPGGEQYTTAHDM	444	197	3.104	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carbox	K.AIGMNNTHFANPDGLPGGEQYTTAHDMALLAGN	AIGMNNTHFANPDGLPGGEQYTTAHDM	444	199	3.824	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carbox	R.SYIYNFPAGNKK.E	SYIYNFP	444	208	4.2	0.001
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carbox	R.SYIYNFPEAGNKK.E	SYIYNFPE	444	209	4.184	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carbox	R.SYIYNFPEAAGNKK.E	SYIYNFPEA	444	210	4.154	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carbox	E.AYKVYDDKGLVAGNKKE.N	AYKVYDDKGLV	444	220	4.285	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carbox	E.AYKVYDDKGLVWAGNKKE.N	AYKVYDDKGLVW	444	221	3.345	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carbox	E.AYKVYDDKGLVWNATKQDSVSIAAGNKKE.N	AYKVYDDKGLVWNATKQDSVSIA	444	232	3.592	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carbox	D.SVSIADRAGNKKE.N	SVSIADR	444	234	2.753	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carbox	R.ATGNVIESAGNKK.E	ATGNVIES	444	251	4.072	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carbox	R.ATGNVIESYTVKAGNK.K	ATGNVIESYTVK	444	255	3.95	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carbox	E.SYTVKDLDAGNKKE.N	SYTVKDLD	444	258	4.169	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carbox	E.SYTVKDLDDQAKDKAGNKKE.N	SYTVKDLDDQAKDK	444	264	3.279	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carbox	E.SYTVKDLDDQAKDKC+57AGNKKE.N	SYTVKDLDDQAKDKC	444	265	2.601	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carbox	E.SYTVKDLDDQAKDKC+57NAGNKKENR.V	SYTVKDLDDQAKDKCN	444	266	2.659	0.003
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carbox	E.SYTVKDLDDQAKDKC+57NKLAGNKKE.N	SYTVKDLDDQAKDKCNKL	444	268	2.745	0.010
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carbox	E.SYTVKDLDDQAKDKC+57NKLFAGNKKE.N	SYTVKDLDDQAKDKCNKLF	444	269	2.997	0.000

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carboxy	E.SYTVKDLDDQAKDKC+57NKLFPAGNKKE.N	SYTVKDLDDQAKDKCNKLFP	444	270	3.118	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carboxy	K.GDNFVLQAGNK.K	GDNFVLQ	444	278	2.772	0.002
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carboxy	R.LLFTFDGAGNKK.E	LLFTFDG	444	290	4.359	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carboxy	R.LLFTFDGAGNK.K	LLFTFDG	444	290	3.246	0.002
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carboxy	K.TGHTDAAGYC+57LVAGNK.K	TGHTDAAGYCLV	444	307	3.62	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carboxy	K.TGHTDAAGYC+57LVSAGNKK.E	TGHTDAAGYCLVS	444	308	3.688	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carboxy	K.TGHTDAAGYC+57LVSSAGNK.K	TGHTDAAGYCLVSS	444	309	2.265	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carboxy	R.FISVVLGTAGNKK.E	FISVVLGT	444	324	2.687	0.001
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carboxy	R.FISVVLGTTAGNKK.E	FISVVLGTT	444	325	3.711	0.003
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carboxy	R.FISVVLGTTSAGNKK.E	FISVVLGTTS	444	326	3.689	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carboxy	E.NVLLYKANSAGNKKE.N	NVLLYKANS	444	355	4.208	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carboxy	K.ANSPVTIAGNKK.E	ANSPVTI	444	359	3.744	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carboxy	K.ANSPVTISAGNKK.E	ANSPVTIS	444	360	2.993	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carboxy	K.ANSPVTISAAGNKK.E	ANSPVTISA	444	361	3.937	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carboxy	E.NVLLYKANSPVTISADAGNKKE.N	NVLLYKANSPVTISAD	444	362	3.603	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carboxy	K.ANSPVTISADNIPAGNKK.E	ANSPVTISADNIP	444	365	4.377	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carboxy	E.NVLLYKANSPVTISADNIPAGNKKE.N	NVLLYKANSPVTISADNIP	444	365	3.378	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carboxy	E.NVLLYKANSPVTISADNIPNAAGNKKE.N	NVLLYKANSPVTISADNIPNA	444	367	3.126	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carboxy	*.KLTVASNQNIAGNK.K	KLTVASNQNI	444	381	3.393	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carboxy	K.LTVASNQNIAGNKK.E	LTVASNQNI	444	381	4.14	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carboxy	K.LTVASNQNIAGNK.K	LTVASNQNI	444	381	3.975	0.001
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carboxy	K.LTVASNQNIYKTVPAGNKKE.N	LTVASNQNIYKTVP	444	386	2.493	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carboxy	E.FNPNLNAAGNKKE.N	FNPNLNA	444	405	3.235	0.002
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carboxy	E.FNPNLNAPAGNKKE.N	FNPNLNAP	444	406	4.022	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carboxy	E.FNPNLNAPAGNKK.E	FNPNLNAP	444	406	3.139	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carboxy	E.FNPNLNAPIAGNKKE.N	FNPNLNAPI	444	407	4.269	0.001
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carboxy	E.FNPNLNAPIAGNK.K	FNPNLNAPI	444	407	4.181	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carboxy	K.QGIEFNPNLNAPIAGNK.K	QGIEFNPNLNAPI	444	407	4.051	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carboxy	K.TGQNVGNAGNKK.E	TGQNVGN	444	415	3.23	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carboxy	K.TGQNVGNLAGNK.K	TGQNVGNL	444	416	3.826	0.002
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carboxy	K.TGQNVGNLVAGNKK.E	TGQNVGNLV	444	417	3.782	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carboxy	K.TGQNVGNLVIAGNKK.E	TGQNVGNLVI	444	418	4.132	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carboxy	K.TGQNVGNLVIAGNK.K	TGQNVGNLVI	444	418	2.302	0.002

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carbox	K.TGQNVGNLVITAGNKK.E	TGQNVGNLVIT	444	419	4.109	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carbox	K.TGQNVGNLVITLAGNK.K	TGQNVGNLVITL	444	420	4.31	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carbox	K.TGQNVGNLVITLGAGNK.K	TGQNVGNLVITLG	444	421	3.885	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carbox	K.TGQNVGNLVITLGDTAGNKK.E	TGQNVGNLVITLGDT	444	423	2.881	0.001
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carbox	E.IASIPVVAGNKKE.N	IASIPVV	444	433	3.897	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carbox	E.IASIPVVAAGNKKE.N	IASIPVVA	444	434	4.006	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carbox	E.IASIPVVAMAGNK.K	IASIPVVAM	444	435	4.179	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carbox	E.IASIPVVAMAGNKKE.N	IASIPVVAM	444	435	4.031	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carbox	E.IASIPVVAM+16AGNK.K	IASIPVVAM	444	435	3.415	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carbox	E.IASIPVVAMNAGNKKE.N	IASIPVVAMN	444	436	3.747	0.001
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carbox	E.IASIPVVAMNAGNK.K	IASIPVVAMN	444	436	3.633	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carbox	E.IASIPVVAMNNVSAGNK.K	IASIPVVAMNNVS	444	439	2.988	0.000
tr|Q2A3E5|Q2A3E5_FRATH	D-alanyl-D-alanine carbox	E.IASIPVVAMNNVSQAGNK.K	IASIPVVAMNNVSQ	444	440	3.729	0.006
tr|Q2A3E6|Q2A3E6_FRATH	Putative uncharacterized	K.EISAHPEVHMVAGNK.K	EISAHPEVHMV	94	93	4.156	0.000
tr|Q2A3E6|Q2A3E6_FRATH	Putative uncharacterized	E.VHMVAGNKK.E	VHMV	94	93	4.098	0.000
tr|Q2A3E6|Q2A3E6_FRATH	Putative uncharacterized	E.VHMVAGNKKE.N	VHMV	94	93	3.955	0.000
tr|Q2A3E6|Q2A3E6_FRATH	Putative uncharacterized	E.VHM+16VAGNKKE.N	VHMV	94	93	2.252	0.002
tr|Q2A3E6|Q2A3E6_FRATH	Putative uncharacterized	E.VHMVLAGNKK.E	VHMVL	94	94	3.392	0.003
tr|Q2A3E6|Q2A3E6_FRATH	Putative uncharacterized	E.VHMVLAGNKKE.N	VHMVL	94	94	2.521	0.006
tr|Q2A3F2|Q2A3F2_FRATH	RNA polymerase sigma fa	R.VPVHMIETINAGNKK.E	VPVHMIETIN	577	425	2.113	0.004
tr|Q2A3F6|Q2A3F6_FRATH	D-alanyl-D-alanine carbox	R.IVELSNASNIAGNKK.E	IVELSNASNI	467	206	2.429	0.000
tr|Q2A3G5|Q2A3G5_FRATH	Putative uncharacterized	K.KDEYIEINLAGNKK.E	KDEYIEINL	188	12	2.552	0.006
tr|Q2A3J9|Q2A3J9_FRATH	Putative uncharacterized	K.ITHAAGNKK.E	ITHA	167	79	2.572	0.002
tr|Q2A3K0|Q2A3K0_FRATH	AhpC/Tsa family protein	D.FAKAAGNKKE.N	FAKA	199	31	3.571	0.005
tr|Q2A3K2|Q2A3K2_FRATH	Putative uncharacterized	R.AAAGLSGAYDIAGNKK.E	AAAGLSGAYDI	496	257	2.854	0.000
tr|Q2A3L0|Q2A3L0_FRATH	Biofunctional protein, glu	E.AYSAAGNKK.E	AYSA	410	410	2.284	0.006
tr|Q2A3L6|Q2A3L6_FRATH	Putative uncharacterized	K.FLNLDFNRQKVIGAGNK.K	FLNLDFNRQKVIG	128	50	2.465	0.008
tr|Q2A3M3|Q2A3M3_FRAT	Tyrosyl-tRNA synthetase	R.FHSKEDAESAHQDFAGNKK.E	FHSKEDAESAHQDF	396	312	3.203	0.000
tr|Q2A3M3|Q2A3M3_FRAT	Tyrosyl-tRNA synthetase	E.SAHQDFIAGNKKE.N	SAHQDFI	396	313	4.138	0.005
tr|Q2A3N1|Q2A3N1_FRATH	Soluble pyridine nucleotid	R.FANNEIDVFAGNKK.E	FANNEIDVF	466	99	3.051	0.002
tr|Q2A3P2|Q2A3P2_FRATH	Ribose-phosphate pyroph	R.FKDGEIHVVLNAGNKK.E	FKDGEIHVVLN	322	46	4.542	0.009
tr|Q2A3P2|Q2A3P2_FRATH	Ribose-phosphate pyroph	K.VITLAPLLAQIAGNK.K	VITLAPLLAQI	322	301	3.938	0.000
tr|Q2A3P2|Q2A3P2_FRATH	Ribose-phosphate pyroph	K.VITLAPLLAQIVAGNK.K	VITLAPLLAQIV	322	302	3.766	0.000

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

tr|Q2A3P4|Q2A3P4_FRATH	Major facilitator superfam	K.VAADVLPAGNKK.E	VAADVLP	332	113	2.883	0.003
tr|Q2A3P4|Q2A3P4_FRATH	Major facilitator superfam	K.YLSFAAGNKKE.N	YLSFA	332	191	2.957	0.001
tr|Q2A3P8|Q2A3P8_FRATH	Putative uncharacterized	K.VYLSGLFSDVC+57AGNK.K	VYLSGLFSDVC	167	113	2.987	0.000
tr|Q2A3Q1|Q2A3Q1_FRATH	Histidine decarboxylase F	D.NFYIHLDGAGNKKE.N	NFYIHLDG	378	195	3.225	0.002
tr|Q2A3R1|Q2A3R1_FRATH	DJ-1/PfpI family protein F	E.SVKIVSTPAAGNKKE.N	SVKIVSTPA	219	194	3.753	0.000
tr|Q2A3R1|Q2A3R1_FRATH	DJ-1/PfpI family protein F	E.KVVSYIAGNKKE.N	KVVSYI	219	219	2.626	0.002
tr|Q2A3R3|Q2A3R3_FRATH	Ferritin-like protein FTL_(	R.NFNAPSLAGNK.K	NFNAPSL	166	166	3.773	0.000
tr|Q2A3R3|Q2A3R3_FRATH	Ferritin-like protein FTL_(	R.NFNAPSLAGNKK.E	NFNAPSL	166	166	3.513	0.000
tr|Q2A3T8|Q2A3T8_FRATH	Histone-like protein HU fo	K.GLKDAVKAGNK.K	GLKDAVK	90	90	3.237	0.008
tr|Q2A3T9|Q2A3T9_FRATH	ATP-dependent protease	K.ALLLLSYLAGNK.K	ALLLLSYL	774	203	3.082	0.000
tr|Q2A3T9|Q2A3T9_FRATH	ATP-dependent protease	E.QVKAIYKELGEAAGNKKE.N	QVKAIYKELGEA	774	247	2.71	0.000
tr|Q2A3V2|Q2A3V2_FRATH	Putative uncharacterized	D.CDEIKLLDILNWFAGNKK.E	CDEIKLLDILNWF	316	97	2.442	0.009
tr|Q2A3V3|Q2A3V3_FRATH	Beta-lactamase FTL_087	E.NKYDGKIGIYTLNTDDKTNIAGNKKE.N	NKYDGKIGIYTLNTDDKTNI	287	49	3.242	0.000
tr|Q2A3V3|Q2A3V3_FRATH	Beta-lactamase FTL_087	E.SYHFAGNKK.E	SYHF	287	57	3.678	0.001
tr|Q2A3V3|Q2A3V3_FRATH	Beta-lactamase FTL_087	K.YNESYHFAGNKK.E	YNESYHF	287	57	4.085	0.001
tr|Q2A3V3|Q2A3V3_FRATH	Beta-lactamase FTL_087	K.YNESYHFAGNK.K	YNESYHF	287	57	3.992	0.002
tr|Q2A3V3|Q2A3V3_FRATH	Beta-lactamase FTL_087	E.SYHFPAGNKK.E	SYHFP	287	58	3.355	0.001
tr|Q2A3V3|Q2A3V3_FRATH	Beta-lactamase FTL_087	K.YNESYHFPAGNKK.E	YNESYHFP	287	58	4.113	0.000
tr|Q2A3V3|Q2A3V3_FRATH	Beta-lactamase FTL_087	E.SYHFPIAGNKK.E	SYHFPI	287	59	3.483	0.000
tr|Q2A3V3|Q2A3V3_FRATH	Beta-lactamase FTL_087	E.SYHFPIAGNKKE.N	SYHFPI	287	59	2.717	0.002
tr|Q2A3V3|Q2A3V3_FRATH	Beta-lactamase FTL_087	K.YNESYHFPIAGNKK.E	YNESYHFPI	287	59	4.058	0.001
tr|Q2A3V3|Q2A3V3_FRATH	Beta-lactamase FTL_087	K.YNESYHFPIAGNK.K	YNESYHFPI	287	59	4.003	0.000
tr|Q2A3V3|Q2A3V3_FRATH	Beta-lactamase FTL_087	E.SYHFPIC+57AGNK.K	SYHFPIC	287	60	2.233	0.009
tr|Q2A3V3|Q2A3V3_FRATH	Beta-lactamase FTL_087	K.YNESYHFPIC+57AGNK.K	YNESYHFPIC	287	60	3.946	0.004
tr|Q2A3V3|Q2A3V3_FRATH	Beta-lactamase FTL_087	K.YNESYHFPIC+57AGNKK.E	YNESYHFPIC	287	60	3.944	0.001
tr|Q2A3V3|Q2A3V3_FRATH	Beta-lactamase FTL_087	E.SYHFPIC+57SVAGNKK.E	SYHFPICSV	287	62	3.85	0.000
tr|Q2A3V3|Q2A3V3_FRATH	Beta-lactamase FTL_087	E.SYHFPIC+57SVAGNKKE.N	SYHFPICSV	287	62	2.255	0.001
tr|Q2A3V3|Q2A3V3_FRATH	Beta-lactamase FTL_087	K.YNESYHFPIC+57SVAGNK.K	YNESYHFPICSV	287	62	3.885	0.000
tr|Q2A3V3|Q2A3V3_FRATH	Beta-lactamase FTL_087	E.SYHFPIC+57SVFAGNKK.E	SYHFPICSVF	287	63	4.091	0.005
tr|Q2A3V3|Q2A3V3_FRATH	Beta-lactamase FTL_087	E.SYHFPIC+57SVFAGNKKE.N	SYHFPICSVF	287	63	4.034	0.002
tr|Q2A3V3|Q2A3V3_FRATH	Beta-lactamase FTL_087	K.FLLVGAIAGNK.K	FLLVGAI	287	71	4.111	0.001
tr|Q2A3V3|Q2A3V3_FRATH	Beta-lactamase FTL_087	K.KIPINQDDIAGNKK.E	KIPINQDDI	287	93	3.792	0.000
tr|Q2A3V3|Q2A3V3_FRATH	Beta-lactamase FTL_087	K.TLTISQLNAGNKK.E	TLTISQLN	287	116	4.007	0.000

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

tr|Q2A3V3|Q2A3V3_FRATH	Beta-lactamase FTL_087	K.TLTISQLNYAAILSDSPASNIAGNKK.E	TLTISQLNYAAILSDSPASNI	287	129	2.391	0.003
tr|Q2A3V3|Q2A3V3_FRATH	Beta-lactamase FTL_087	E.INYTQPHSNAGNKKE.N	INYTQPHSN	287	169	4.063	0.000
tr|Q2A3V3|Q2A3V3_FRATH	Beta-lactamase FTL_087	E.INYTQPHSNIAGNK.K	INYTQPHSNI	287	170	3.842	0.000
tr|Q2A3V3|Q2A3V3_FRATH	Beta-lactamase FTL_087	K.LGDNDTIITADEPEINYTQPHSNIAGNK.K	LGDNDTIITADEPEINYTQPHSNI	287	170	3.36	0.000
tr|Q2A3V3|Q2A3V3_FRATH	Beta-lactamase FTL_087	K.HKDIFIKAGNK.K	HKDIFIK	287	201	3.567	0.001
tr|Q2A3V3|Q2A3V3_FRATH	Beta-lactamase FTL_087	D.VAIIWAGNKKE.N	VAIIW	287	243	4.004	0.001
tr|Q2A3V3|Q2A3V3_FRATH	Beta-lactamase FTL_087	D.VAIIWPAGNKKE.N	VAIIWP	287	244	3.541	0.001
tr|Q2A3V3|Q2A3V3_FRATH	Beta-lactamase FTL_087	K.NQQPIALGAGNK.K	NQQPIALG	287	253	3.565	0.000
tr|Q2A3V3|Q2A3V3_FRATH	Beta-lactamase FTL_087	K.NQQPIALGAGNKK.E	NQQPIALG	287	253	3.296	0.000
tr|Q2A3V3|Q2A3V3_FRATH	Beta-lactamase FTL_087	K.NQQPIALGIAGNK.K	NQQPIALGI	287	254	4.064	0.000
tr|Q2A3V3|Q2A3V3_FRATH	Beta-lactamase FTL_087	K.NQQPIALGIAGNKK.E	NQQPIALGI	287	254	3.045	0.001
tr|Q2A3V3|Q2A3V3_FRATH	Beta-lactamase FTL_087	K.NQQPIALGILAGNK.K	NQQPIALGIL	287	255	4.433	0.000
tr|Q2A3V3|Q2A3V3_FRATH	Beta-lactamase FTL_087	K.NQQPIALGILAGNKK.E	NQQPIALGIL	287	255	4.197	0.000
tr|Q2A3V3|Q2A3V3_FRATH	Beta-lactamase FTL_087	K.NQQPIALGILYAGNK.K	NQQPIALGILY	287	256	4.309	0.000
tr|Q2A3V3|Q2A3V3_FRATH	Beta-lactamase FTL_087	K.NQQPIALGILYTAGNK.K	NQQPIALGILYT	287	257	3.185	0.003
tr|Q2A3V3|Q2A3V3_FRATH	Beta-lactamase FTL_087	K.NQQPIALGILYTNAGNK.K	NQQPIALGILYTN	287	258	4.051	0.000
tr|Q2A3V3|Q2A3V3_FRATH	Beta-lactamase FTL_087	K.NQQPIALGILYTNPAGNKK.E	NQQPIALGILYTNP	287	259	4.425	0.000
tr|Q2A3V3|Q2A3V3_FRATH	Beta-lactamase FTL_087	K.NQQPIALGILYTNPAGNK.K	NQQPIALGILYTNP	287	259	4.406	0.000
tr|Q2A3V3|Q2A3V3_FRATH	Beta-lactamase FTL_087	K.NQQPIALGILYTNPNAGNK.K	NQQPIALGILYTNPN	287	260	4.366	0.003
tr|Q2A3V3|Q2A3V3_FRATH	Beta-lactamase FTL_087	K.NQQPIALGILYTNPNDKNAAGNKK.E	NQQPIALGILYTNPNDKNA	287	264	2.871	0.010
tr|Q2A3V3|Q2A3V3_FRATH	Beta-lactamase FTL_087	K.NQQPIALGILYTNPNDKNAPSNAGNKK.E	NQQPIALGILYTNPNDKNAPSN	287	267	3.151	0.000
tr|Q2A3V3|Q2A3V3_FRATH	Beta-lactamase FTL_087	K.NAPSNEEIIQAGNK.K	NAPSNEEIIQ	287	272	3.784	0.008
tr|Q2A3V3|Q2A3V3_FRATH	Beta-lactamase FTL_087	E.IIQQAAKLIANDAGNKKE.N	IIQQAAKLIAND	287	281	4.205	0.000
tr|Q2A3V3|Q2A3V3_FRATH	Beta-lactamase FTL_087	E.IIQQAAKLIANDLAGNKKE.N	IIQQAAKLIANDL	287	282	3.196	0.000
tr|Q2A3V3|Q2A3V3_FRATH	Beta-lactamase FTL_087	K.LIANDLAGNKK.E	LIANDL	287	282	3.708	0.005
tr|Q2A3V3|Q2A3V3_FRATH	Beta-lactamase FTL_087	E.IIQQAAKLIANDLTNAGNKKE.N	IIQQAAKLIANDLTN	287	284	3.389	0.000
tr|Q2A3V3|Q2A3V3_FRATH	Beta-lactamase FTL_087	K.LIANDLTNAGNKK.E	LIANDLTN	287	284	3.437	0.000
tr|Q2A3V3|Q2A3V3_FRATH	Beta-lactamase FTL_087	E.IIQQAAKLIANDLTNTAGNKKE.N	IIQQAAKLIANDLTNT	287	285	3.393	0.000
tr|Q2A3V3|Q2A3V3_FRATH	Beta-lactamase FTL_087	K.LIANDLTNTAGNK.K	LIANDLTNT	287	285	4.176	0.000
tr|Q2A3V3|Q2A3V3_FRATH	Beta-lactamase FTL_087	K.LIANDLTNTAGNKK.E	LIANDLTNT	287	285	4.116	0.000
tr|Q2A3V3|Q2A3V3_FRATH	Beta-lactamase FTL_087	E.IIQQAAKLIANDLTNTYAGNKKE.N	IIQQAAKLIANDLTNTY	287	286	4.145	0.002
tr|Q2A3V3|Q2A3V3_FRATH	Beta-lactamase FTL_087	K.LIANDLTNTYAGNKK.E	LIANDLTNTY	287	286	3.943	0.005
tr|Q2A3W0|Q2A3W0_FRATI	Putative uncharacterized	K.FLGYIDRAGNKK.E	FLGYIDR	59	48	2.904	0.005

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

tr|Q2A3W0|Q2A3W0_FRAT	Putative uncharacterized	K.FLGYIDRIIAGNKK.E	FLGYIDRII	59	50	2.114	0.005
tr|Q2A3W3|Q2A3W3_FRAT	Putative uncharacterized	D.FNLIGENVLAGAGNK.K	FNLIGENVLAG	485	404	2.319	0.005
tr|Q2A3Y0|Q2A3Y0_FRATH	Putative uncharacterized	E.VVDKNNGNTGWINLDKLAGNKKE.N	VVDKNNGNTGWINLDKL	176	110	2.853	0.000
tr|Q2A3Y0|Q2A3Y0_FRATH	Putative uncharacterized	E.YTKVQDQKISAGNKKE.N	YTKVQDQKIS	176	142	3.933	0.002
tr|Q2A3Y0|Q2A3Y0_FRATH	Putative uncharacterized	E.YTKVQDQKISQAGNKKE.N	YTKVQDQKISQ	176	143	3.1	0.000
tr|Q2A3Y0|Q2A3Y0_FRATH	Putative uncharacterized	E.YTKVQDQKISQLAGNKKE.N	YTKVQDQKISQL	176	144	4.199	0.000
tr|Q2A3Y0|Q2A3Y0_FRATH	Putative uncharacterized	K.ISQLHAMAGNK.K	ISQLHAM	176	147	3.731	0.001
tr|Q2A3Y0|Q2A3Y0_FRATH	Putative uncharacterized	K.ISQLHAMAGNKK.E	ISQLHAM	176	147	3.535	0.000
tr|Q2A3Y0|Q2A3Y0_FRATH	Putative uncharacterized	K.ISQLHAM+16AGNK.K	ISQLHAM	176	147	3.303	0.000
tr|Q2A3Y2|Q2A3Y2_FRATH	Preprotein translocase, s	K.LINVATIQSALGSAGNK.K	LINVATIQSALGS	645	432	2.755	0.000
tr|Q2A3Y2|Q2A3Y2_FRATH	Preprotein translocase, s	K.LINVATIQSALGSQFAGNK.K	LINVATIQSALGSQF	645	434	3.9	0.000
tr|Q2A3Y4|Q2A3Y4_FRATH	Isochorismatase hydrolas	E.ASLTNLSRIADIVDIDDFIAGNKKE.N	ASLTNLSRIADIVDIDDFI	190	190	3.675	0.000
tr|Q2A404|Q2A404_FRATH	Hypothetical lipoprotein F	K.SYQYENVAGNKK.E	SYQYENV	130	102	3.973	0.003
tr|Q2A404|Q2A404_FRATH	Hypothetical lipoprotein F	K.SYQYENVETALVSLVAGNKK.E	SYQYENVETALVSLV	130	110	2.568	0.001
tr|Q2A404|Q2A404_FRATH	Hypothetical lipoprotein F	K.SYQYENVETALVSLVAGNKKE.N	SYQYENVETALVSLV	130	110	2.043	0.001
tr|Q2A404|Q2A404_FRATH	Hypothetical lipoprotein F	E.TALVSLVAGNKKE.N	TALVSLV	130	110	4.081	0.006
tr|Q2A404|Q2A404_FRATH	Hypothetical lipoprotein F	K.SYQYENVETALVSLVESAGNKK.E	SYQYENVETALVSLVES	130	112	2.583	0.001
tr|Q2A404|Q2A404_FRATH	Hypothetical lipoprotein F	K.SYQYENVETALVSLVESSSTAGNKK.E	SYQYENVETALVSLVESSST	130	115	2.471	0.007
tr|Q2A405|Q2A405_FRATH	Putative uncharacterized	E.RAQGAAYVPPAGNKK.E	RAQGAAYVPP	83	47	4.224	0.000
tr|Q2A405|Q2A405_FRATH	Putative uncharacterized	E.RAQGAAYVPPDAGNKKE.N	RAQGAAYVPPD	83	48	2.387	0.002
tr|Q2A405|Q2A405_FRATH	Putative uncharacterized	R.AQGAAYVPPDREFAGNKK.E	AQGAAYVPPDREF	83	51	3.176	0.001
tr|Q2A405|Q2A405_FRATH	Putative uncharacterized	R.AQGAAYVPPDREFIAGNKK.E	AQGAAYVPPDREFI	83	52	2.941	0.001
tr|Q2A405|Q2A405_FRATH	Putative uncharacterized	R.LFWSYSRPAGNKK.E	LFWSYSRP	83	83	3.611	0.000
tr|Q2A420|Q2A420_FRATH	Type IV pilin multimeric o	E.FAGLNLVVAGNK.K	FAGLNLVV	590	207	2.822	0.001
tr|Q2A422|Q2A422_FRATH	Type IV pili glycosylation	E.RHSIPIFLAGNKK.E	RHSIPIFL	198	107	2.241	0.001
tr|Q2A441|Q2A441_FRATH	Gamma-glutamyltranspep	K.LAEDGIPVSYDLHQSLVTAKPWAGNK.K	LAEDGIPVSYDLHQSLVTAKPW	601	218	3.665	0.000
tr|Q2A441|Q2A441_FRATH	Gamma-glutamyltranspep	K.ITTDKHIPSKDIAGNKK.E	ITTDKHIPSKDI	601	399	2.806	0.000
tr|Q2A441|Q2A441_FRATH	Gamma-glutamyltranspep	K.LQTTHFSAGNK.K	LQTTHFS	601	416	3.058	0.000
tr|Q2A460|Q2A460_FRATH	Oxidoreductase, short-ch	E.VVIAATKAGNKKE.N	VVIAATK	240	237	4.269	0.000
tr|Q2A460|Q2A460_FRATH	Oxidoreductase, short-ch	E.VVIAATKAGNKK.E	VVIAATK	240	237	2.291	0.009
tr|Q2A460|Q2A460_FRATH	Oxidoreductase, short-ch	E.VVIAATKQAGNKKE.N	VVIAATKQ	240	238	4.081	0.000
tr|Q2A460|Q2A460_FRATH	Oxidoreductase, short-ch	E.VVIAATKQPAGNKKE.N	VVIAATKQP	240	239	4.078	0.000
tr|Q2A460|Q2A460_FRATH	Oxidoreductase, short-ch	E.VVIAATKQPAAGNKKE.N	VVIAATKQPA	240	240	3.819	0.000

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

tr|Q2A484|Q2A484_FRATH	Ribonuclease E FTL_0717	K.TTQATALTIAGNKK.E	TTQATALTI	843	420	4.105	0.000
tr|Q2A490|Q2A490_FRATH	Proton-dependent oligope	K.QLQNLVVAGNKKE.N	QLQNLVV	197	130	2.375	0.004
tr|Q2A4A7|Q2A4A7_FRATH	Putative uncharacterized	E.YILDHNIVNAGNKKE.N	YILDHNIVN	232	112	3.186	0.000
tr|Q2A4A7|Q2A4A7_FRATH	Putative uncharacterized	K.NTQNFFKPLAGNK.K	NTQNFFKPL	232	228	3.938	0.000
tr|Q2A4D9|Q2A4D9_FRATH	Putative uncharacterized	K.GLHANQAAGNKK.E	GLHANQA	544	105	2.262	0.000
tr|Q2A4D9|Q2A4D9_FRATH	Putative uncharacterized	E.GLSIANLAAAVAAGNKKE.N	GLSIANLAAAVA	544	127	3.562	0.000
tr|Q2A4D9|Q2A4D9_FRATH	Putative uncharacterized	K.VEGLSIANLAAAVANSNLVSSEVAGNKK.E	VEGLSIANLAAAVANSNLVSSEV	544	136	2.832	0.000
tr|Q2A4D9|Q2A4D9_FRATH	Putative uncharacterized	K.VEGLSIANLAAAVANSNLVSSEVDPAGNKK.E	VEGLSIANLAAAVANSNLVSSEVDP	544	138	2.367	0.005
tr|Q2A4D9|Q2A4D9_FRATH	Putative uncharacterized	K.QLADNQGLFSIAMNSLGQTIYNLEIAGNKK.E	QLADNQGLFSIAMNSLGQTIYNLEI	544	164	2.699	0.000
tr|Q2A4D9|Q2A4D9_FRATH	Putative uncharacterized	E.INYNYNNSAGNKKE.N	INYNYNNS	544	171	2.722	0.002
tr|Q2A4D9|Q2A4D9_FRATH	Putative uncharacterized	E.INYNYNNSTIAGNKKE.N	INYNYNNSTI	544	173	4.108	0.001
tr|Q2A4D9|Q2A4D9_FRATH	Putative uncharacterized	K.GSPIIQVFSALAGNK.K	GSPIIQVFSAL	544	341	3.409	0.000
tr|Q2A4D9|Q2A4D9_FRATH	Putative uncharacterized	K.LNLLPYLGAGNK.K	LNLLPYLG	544	394	2.921	0.003
tr|Q2A4D9|Q2A4D9_FRATH	Putative uncharacterized	K.LNLLPYLGIAGNK.K	LNLLPYLGI	544	395	3.824	0.000
tr|Q2A4D9|Q2A4D9_FRATH	Putative uncharacterized	K.FLQQTLSAFAAGNK.K	FLQQTLSAFA	544	471	2.192	0.008
tr|Q2A4D9|Q2A4D9_FRATH	Putative uncharacterized	K.ANKPVNENALLNMLVAAGNK.K	ANKPVNENALLNMLVA	544	501	3.021	0.000
tr|Q2A4D9|Q2A4D9_FRATH	Putative uncharacterized	E.NALLNMLVAAGNK.K	NALLNMLVA	544	501	2.392	0.000
tr|Q2A4E4|Q2A4E4_FRATH	Hypothetical membrane p	E.IQDIPKNQTLAGNKKE.N	IQDIPKNQTL	361	252	4.219	0.002
tr|Q2A4H6|Q2A4H6_FRATH	Putative uncharacterized	K.IADLNETYQHNINDILIESLEHAGNK.K	IADLNETYQHNINDILIESLEH	146	98	2.98	0.001
tr|Q2A4H6|Q2A4H6_FRATH	Putative uncharacterized	K.IADLNETYQHNINDILIESLEHAGNKK.E	IADLNETYQHNINDILIESLEH	146	98	2.384	0.001
tr|Q2A4H6|Q2A4H6_FRATH	Putative uncharacterized	K.KAVSAYYAGNKK.E	KAVSAYY	146	107	3.903	0.002
tr|Q2A4I2|Q2A4I2_FRATH	Transcription termination	K.YFAVKAGNKK.E	YFAVK	420	113	4.06	0.000
tr|Q2A4I2|Q2A4I2_FRATH	Transcription termination	K.YFAVKAGNK.K	YFAVK	420	113	3.721	0.000
tr|Q2A4K2|Q2A4K2_FRATH	ATp-dependent helicase	E.LFTAAGNKKE.N	LFTA	1444	1310	3.439	0.002
tr|Q2A4K4|Q2A4K4_FRATH	Isocitrate dehydrogenase	K.TFNTILAQIAGNK.K	TFNTILAQI	738	738	2.706	0.000
tr|Q2A4K6|Q2A4K6_FRATH	Long chain fatty acid CoA	K.KVPLNIDIPAGNKKE.N	KVPLNIDIP	562	21	2.215	0.008
tr|Q2A4K8|Q2A4K8_FRATH	Fusion product of 3-hydr	K.IAVLGAGTAGNKK.E	IAVLGAGT	898	127	4.125	0.002
tr|Q2A4K8|Q2A4K8_FRATH	Fusion product of 3-hydr	K.IAVLGAGTMGAQAGNK.K	IAVLGAGTMGAQ	898	131	3.628	0.000
tr|Q2A4L9|Q2A4L9_FRATH	Putative uncharacterized	K.TISDQVIGAIYPLAGNKK.E	TISDQVIGAIYPL	327	242	2.563	0.009
tr|Q2A4L9|Q2A4L9_FRATH	Putative uncharacterized	K.TISDQVIGAIYPLQVAGNK.K	TISDQVIGAIYPLQV	327	244	3.693	0.000
tr|Q2A4L9|Q2A4L9_FRATH	Putative uncharacterized	K.TISDQVIGAIYPLQVLAGNK.K	TISDQVIGAIYPLQVL	327	245	4.221	0.000
tr|Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized	K.SSAEEILNDVMENYIDQAGNKK.E	SSAEEILNDVMENYIDQ	476	84	2.341	0.008
tr|Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized	E.NYIDQNNLRDRAGNKKE.N	NYIDQNNLRDR	476	90	2.066	0.006

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

tr|Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized	E.NYIDQNNLRDRYDYVGSAIGTASVAGNKKE.N	NYIDQNNLRDRYDYVGSAIGTASV	476	103	2.55	0.000
tr|Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized	R.DRYDYVGSAIGTASVNQTNSAGNKK.E	DRYDYVGSAIGTASVNQTNS	476	108	2.916	0.000
tr|Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized	R.DRYDYVGSAIGTASVNQTNSNYVAGNKK.E	DRYDYVGSAIGTASVNQTNSNYV	476	111	3.423	0.000
tr|Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized	K.AQAEYISFAGNKK.E	AQAEYISF	476	132	4.004	0.000
tr|Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized	K.AQAEYISFIAGNKK.E	AQAEYISFI	476	133	4.191	0.000
tr|Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized	E.YISFISAAGNKKE.N	YISFISA	476	135	3.564	0.006
tr|Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized	E.YISFISANAGNKKE.N	YISFISAN	476	136	4.181	0.002
tr|Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized	K.SLNIDSTQGSAGNKK.E	SLNIDSTQGS	476	151	4.261	0.000
tr|Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized	K.SLNIDSTQGSTAGNKK.E	SLNIDSTQGST	476	152	4.227	0.000
tr|Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized	E.YISFISANTKVNKSLNIDSTQGSTAGNK.K	YISFISANTKVNKSLNIDSTQGST	476	152	3.207	0.000
tr|Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized	K.SLNIDSTQGSTAAGNKK.E	SLNIDSTQGSTA	476	153	2.612	0.000
tr|Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized	E.IDTYADKAGNKKE.N	IDTYADK	476	162	3.898	0.009
tr|Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized	E.IDTYADKPAGNKKE.N	IDTYADKP	476	163	3.465	0.006
tr|Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized	E.IDTYADKPKQGTAGNKKE.N	IDTYADKPKQGT	476	167	3.427	0.001
tr|Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized	E.IDTYADKPKQGTQAAIAGNKKE.N	IDTYADKPKQGTQAAI	476	171	3.034	0.000
tr|Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized	E.IDTYADKPKQGTQAAIDAGNKKE.N	IDTYADKPKQGTQAAID	476	172	2.356	0.000
tr|Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized	E.IDTYADKPKQGTQAAIDAKAGNKKE.N	IDTYADKPKQGTQAAIDAK	476	174	2.241	0.000
tr|Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized	E.IDTYADKPKQGTQAAIDAKQKALDEAGNKK.E	IDTYADKPKQGTQAAIDAKQKALDE	476	180	2.1	0.001
tr|Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized	K.SLTTGFGNLAGNKK.E	SLTTGFGNL	476	224	4.249	0.001
tr|Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized	K.SLTTGFGNLSAGNKK.E	SLTTGFGNLS	476	225	3.938	0.000
tr|Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized	K.SLTTGFGNLSGAGNKK.E	SLTTGFGNLSG	476	226	4.014	0.000
tr|Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized	K.SLTTGFGNLSGLAGNKK.E	SLTTGFGNLSGL	476	227	4.323	0.000
tr|Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized	K.SLTTGFGNLSGLAGNK.K	SLTTGFGNLSGL	476	227	4.069	0.000
tr|Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized	K.SLTTGFGNLSGLLAGNK.K	SLTTGFGNLSGLL	476	228	4.342	0.000
tr|Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized	K.SLTTGFGNLSGLLAGNKK.E	SLTTGFGNLSGLL	476	228	4.111	0.000
tr|Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized	K.SLTTGFGNLSGLLPAGNK.K	SLTTGFGNLSGLLP	476	229	4.074	0.000
tr|Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized	K.SLTTGFGNLSGLLPIKTFAGNKK.E	SLTTGFGNLSGLLPIKTF	476	233	3.234	0.000
tr|Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized	K.DGNAAIGVVAGNKK.E	DGNAAIGVV	476	246	2.567	0.009
tr|Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized	E.KDGNAAIGVVAGNKKE.N	KDGNAAIGVV	476	246	3.908	0.000
tr|Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized	K.GMFEDIKHGAGNKK.E	GMFEDIKHG	476	263	3.805	0.000
tr|Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized	K.GMFEDIKHGNEAGNKK.E	GMFEDIKHGNE	476	265	3.949	0.000
tr|Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized	K.GMFEDIKHGNEPVAGNKK.E	GMFEDIKHGNEPV	476	267	3.144	0.000
tr|Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized	K.GMFEDIKHGNEPVIAGNKK.E	GMFEDIKHGNEPVI	476	268	3.38	0.000

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

tr|Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized	K.GMFEDIKHGNEPVIVAGNKK.E	GMFEDIKHGNEPVIV	476	269	3.013	0.000
tr|Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized	K.GMFEDIKHGNEPVIVAGNKKE.N	GMFEDIKHGNEPVIV	476	269	2.751	0.000
tr|Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized	K.HGNEPVIVAGNK.K	HGNEPVIV	476	269	3.813	0.000
tr|Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized	K.HGNEPVIVAGNKK.E	HGNEPVIV	476	269	3.694	0.000
tr|Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized	R.VGFGEDNKPAGNKK.E	VGFGEDNKP	476	304	4.111	0.000
tr|Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized	R.VGFGEDNKPAGNK.K	VGFGEDNKP	476	304	3.545	0.000
tr|Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized	R.VGFGEDNKPYILAAGNK.K	VGFGEDNKPYILA	476	308	4.422	0.000
tr|Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized	R.VGFGEDNKPYILAAGNKK.E	VGFGEDNKPYILA	476	308	4.293	0.000
tr|Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized	R.VGFGEDNKPYILAYAGNKK.E	VGFGEDNKPYILAY	476	309	3.098	0.000
tr|Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized	R.VGFGEDNKPYILAYGQAGNK.K	VGFGEDNKPYILAYGQ	476	311	2.731	0.001
tr|Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized	R.VGFGEDNKPYILAYGQGSAGNKK.E	VGFGEDNKPYILAYGQGS	476	313	3.394	0.000
tr|Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized	R.VGFGEDNKPYILAYGQGSYNGPAGNKK.E	VGFGEDNKPYILAYGQGSYNGP	476	317	2.389	0.000
tr|Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized	R.ANLVTLIAGQMAGNK.K	ANLVTLIAGQM	476	348	4.006	0.000
tr|Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized	R.ANLVTLIAGQM+16AGNK.K	ANLVTLIAGQM	476	348	2.6	0.000
tr|Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized	R.ANLVTLIAGQMSAGNK.K	ANLVTLIAGQMS	476	349	2.625	0.000
tr|Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized	E.DISSTLAKNTKTQAGNKKE.N	DISSTLAKNTKTQ	476	371	2.288	0.000
tr|Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized	R.RIDATAGNKK.E	RIDAT	476	379	2.712	0.006
tr|Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized	R.RIDATDIAGNKK.E	RIDATDI	476	381	4.025	0.003
tr|Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized	E.KTLSTYYAGNKKE.N	KTLSTYY	476	389	4.058	0.000
tr|Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized	E.KTLSTYYKAGNKKE.N	KTLSTYYK	476	390	4.004	0.001
tr|Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized	R.YKLPGTENAGNKK.E	YKLPGTEN	476	415	4.087	0.002
tr|Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized	R.YKLPGTENIIAGNKK.E	YKLPGTENII	476	417	3.942	0.001
tr|Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized	R.YKLPGTENIIAGNK.K	YKLPGTENII	476	417	3.85	0.001
tr|Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized	R.YKLPGTENIIYGAGNK.K	YKLPGTENIIYG	476	419	4.055	0.000
tr|Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized	R.YKLPGTENIIYGAGNKK.E	YKLPGTENIIYG	476	419	3.888	0.000
tr|Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized	E.NIIYGVVLAGNKKE.N	NIIYGVVL	476	422	4.127	0.000
tr|Q2A4M0|Q2A4M0_FRATH	Putative uncharacterized	K.YLNQYAGNKK.E	YLNQY	476	476	3.615	0.003
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	K.LATIDDQDPNAGNKK.E	LATIDDQDPN	178	44	3.839	0.000
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	K.LATIDDQDPNYKAIAGNKK.E	LATIDDQDPNYKAI	178	48	2.881	0.000
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	K.GEWIEVVDAGNKK.E	GEWIEVVD	178	59	4.232	0.002
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	K.GEWIEVVDNAGNKK.E	GEWIEVVDN	178	60	4.03	0.009
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	E.WIEVVDNKAGNKKE.N	WIEVVDNK	178	61	4.172	0.000
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	E.VVDNKDGAGNKKE.N	VVDNKDG	178	63	3.847	0.000

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	E.WIEVVDNKDGAGNKKE.N	WIEVVDNKDG	178	63	3.967	0.000
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	K.GEWIEVVDNKDGSVAGNKK.E	GEWIEVVDNKDGSV	178	65	4.089	0.000
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	E.VVDNKDGSVAGNKKE.N	VVDNKDGSV	178	65	4.174	0.001
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	E.VVDNKDGSVAGNKK.E	VVDNKDGSV	178	65	2.248	0.001
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	K.GEWIEVVDNKDGSVGAGNKK.E	GEWIEVVDNKDGSVG	178	66	3.322	0.001
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	E.VVDNKDGSVGAGNKKE.N	VVDNKDGSVG	178	66	3.938	0.000
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	E.VVDNKDGSVGAGNKK.E	VVDNKDGSVG	178	66	2.561	0.000
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	E.WIEVVDNKDGSVGAGNKKE.N	WIEVVDNKDGSVG	178	66	3.228	0.000
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	K.DGSVGWAGNKK.E	DGSVGW	178	67	3.095	0.002
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	E.VVDNKDGSVGWAGNKKE.N	VVDNKDGSVGW	178	67	4.265	0.000
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	E.WIEVVDNKDGSVGWAGNKKE.N	WIEVVDNKDGSVGW	178	67	2.292	0.000
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	K.DGSVGWVAGNKK.E	DGSVGWV	178	68	4.212	0.002
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	E.VVDNKDGSVGWVAGNKKE.N	VVDNKDGSVGWV	178	68	4.249	0.002
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	E.VVDNKDGSVGWVKAGNKKE.N	VVDNKDGSVGWVK	178	69	4.232	0.001
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	E.WIEVVDNKDGSVGWVKAGNKKE.N	WIEVVDNKDGSVGWVK	178	69	2.481	0.001
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	E.VVDNKDGSVGWVKQAGNKKE.N	VVDNKDGSVGWVKQ	178	70	4.105	0.001
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	E.WIEVVDNKDGSVGWVKQAGNKKE.N	WIEVVDNKDGSVGWVKQ	178	70	2.917	0.000
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	K.TSQAISKAGNK.K	TSQAISK	178	82	3.003	0.009
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	K.TSQAISKDPAGNKK.E	TSQAISKDP	178	84	3.474	0.003
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	K.TSQAISKDPIAGNKK.E	TSQAISKDPI	178	85	4.29	0.000
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	K.TSQAISKDPIAGNKKENR.V	TSQAISKDPI	178	85	3.42	0.001
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	K.TSQAISKDPIEAGNKKENR.V	TSQAISKDPIE	178	86	4.385	0.000
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	K.TSQAISKDPIEAGNKK.E	TSQAISKDPIE	178	86	3.682	0.009
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	K.TSQAISKDPIEQAGNKK.E	TSQAISKDPIEQ	178	87	4.3	0.000
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	K.TSQAISKDPIEQAGNKKENR.V	TSQAISKDPIEQ	178	87	3.358	0.000
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	K.DPIEQMAGNKK.E	DPIEQM	178	88	4.151	0.000
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	D.PIEQMAGNKK.E	PIEQM	178	88	3.689	0.006
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	K.TSQAISKDPIEQMAGNKK.E	TSQAISKDPIEQM	178	88	4.265	0.000
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	K.TSQAISKDPIEQMAGNK.K	TSQAISKDPIEQM	178	88	4.151	0.000
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	K.TSQAISKDPIEQM+16AGNKK.E	TSQAISKDPIEQM	178	88	3.287	0.000
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	K.TSQAISKDPIEQMAGNKKENR.V	TSQAISKDPIEQM	178	88	3.247	0.003
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	K.TSQAISKDPIEQM+16AGNKKENR.V	TSQAISKDPIEQM	178	88	2.5	0.000
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	K.TSQAISKDPIEQMMAGNKK.E	TSQAISKDPIEQMM	178	89	4.16	0.000

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	K.TSQAISKDPIEQMMAAGNKK.E	TSQAISKDPIEQMMA	178	90	4.371	0.000
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	K.TSQAISKDPIEQMMAAGNK.K	TSQAISKDPIEQMMA	178	90	4.232	0.000
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	K.TSQAISKDPIEQM+16MAAGNKK.E	TSQAISKDPIEQMMA	178	90	3.628	0.000
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	K.TSQAISKDPIEQMM+16AAGNKK.E	TSQAISKDPIEQMMA	178	90	2.691	0.001
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	K.TSQAISKDPIEQMMANAGNKK.E	TSQAISKDPIEQMMAN	178	91	3.77	0.000
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	K.TSQAISKDPIEQM+16MANAGNKK.E	TSQAISKDPIEQMMAN	178	91	2.717	0.000
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	K.TSQAISKDPIEQMMANAGNK.K	TSQAISKDPIEQMMAN	178	91	2.068	0.001
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	K.DPIEQMMANFAGNK.K	DPIEQMMANF	178	92	3.56	0.009
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	K.QQQLLDQHAGNKKENR.V	QQQLLDQH	178	102	3.325	0.005
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	K.QQQLLDQHAGNKK.E	QQQLLDQH	178	102	3.231	0.000
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	K.QQQLLDQHAGNK.K	QQQLLDQH	178	102	2.652	0.009
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	*.KQQQLLDQHFAGNK.K	KQQQLLDQHF	178	103	3.612	0.009
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	K.QQQLLDQHFAGNKKE.N	QQQLLDQHF	178	103	3.427	0.000
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	K.QQQLLDQHFAGNKK.E	QQQLLDQHF	178	103	3.376	0.000
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	K.QQQLLDQHFAGNK.K	QQQLLDQHF	178	103	2.962	0.002
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	K.QQQLLDQHFAGNKKENR.V	QQQLLDQHF	178	103	2.126	0.004
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	K.QQQLLDQHFNAGNKKE.N	QQQLLDQHFN	178	104	3.432	0.003
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	K.MLANIDQAGNK.K	MLANIDQ	178	112	3.724	0.009
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	K.M+16LANIDQAGNKK.E	MLANIDQ	178	112	3.39	0.006
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	K.M+16LANIDQAGNK.K	MLANIDQ	178	112	3.286	0.002
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	K.MLANIDQNAGNK.K	MLANIDQN	178	113	4.154	0.000
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	K.MLANIDQNAGNKK.E	MLANIDQN	178	113	4.088	0.000
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	K.M+16LANIDQNAGNKK.E	MLANIDQN	178	113	3.496	0.002
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	K.MLANIDQNAGNKKENR.V	MLANIDQN	178	113	3.145	0.002
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	K.M+16LANIDQNAGNKKENR.V	MLANIDQN	178	113	2.3	0.003
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	K.MLANIDQNIAGNKK.E	MLANIDQNI	178	114	4.231	0.000
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	K.MLANIDQNIAGNK.K	MLANIDQNI	178	114	3.985	0.002
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	K.M+16LANIDQNIAGNK.K	MLANIDQNI	178	114	3.939	0.003
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	K.M+16LANIDQNIAGNKK.E	MLANIDQNI	178	114	3.649	0.002
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	K.MLANIDQNIAAGNKK.E	MLANIDQNIA	178	115	4.061	0.009
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	K.MLANIDQNIAQAGNKK.E	MLANIDQNIAQ	178	116	4.181	0.000
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	K.M+16LANIDQNIAQAGNKK.E	MLANIDQNIAQ	178	116	3.704	0.001
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	K.MLANIDQNIAQMQAGNKK.E	MLANIDQNIAQMQ	178	118	4.277	0.001

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	K.M+16LANIDQNIAQMQAGNKK.E	MLANIDQNIAQMQ	178	118	3.589	0.008
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	K.MLANIDQNIAQMQAGNKKENR.V	MLANIDQNIAQMQ	178	118	3.406	0.000
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	K.MLANIDQNIAQM+16QAGNKK.E	MLANIDQNIAQMQ	178	118	3.382	0.001
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	K.M+16LANIDQNIAQM+16QAGNKK.E	MLANIDQNIAQMQ	178	118	2.28	0.001
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	K.MLANIDQNIAQMQAQAGNKK.E	MLANIDQNIAQMQAQ	178	120	4.219	0.001
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	K.MLANIDQNIAQM+16QAQAGNKK.E	MLANIDQNIAQMQAQ	178	120	2.989	0.010
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	K.MLANIDQNIAQMQAQPAGNK.K	MLANIDQNIAQMQAQP	178	121	4.287	0.000
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	K.MLANIDQNIAQMQAQPAGNKK.E	MLANIDQNIAQMQAQP	178	121	4.227	0.000
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	K.MLANIDQNIAQM+16QAQPAGNK.K	MLANIDQNIAQMQAQP	178	121	3.997	0.000
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	K.MLANIDQNIAQM+16QAQPAGNKK.E	MLANIDQNIAQMQAQP	178	121	3.561	0.000
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	K.M+16LANIDQNIAQMQAQPAGNKK.E	MLANIDQNIAQMQAQP	178	121	3.535	0.000
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	K.M+16LANIDQNIAQM+16QAQPAGNKK.E	MLANIDQNIAQMQAQP	178	121	3.109	0.003
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	K.M+16LANIDQNIAQM+16QAQPAGNK.K	MLANIDQNIAQMQAQP	178	121	2.921	0.000
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	K.MLANIDQNIAQMQAQPNAGNK.K	MLANIDQNIAQMQAQPN	178	122	4.352	0.000
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	K.MLANIDQNIAQM+16QAQPNAGNK.K	MLANIDQNIAQMQAQPN	178	122	4.123	0.000
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	K.MLANIDQNIAQMQAQPNAGNKK.E	MLANIDQNIAQMQAQPN	178	122	4.113	0.000
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	K.M+16LANIDQNIAQMQAQPNAGNK.K	MLANIDQNIAQMQAQPN	178	122	3.86	0.000
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	K.MLANIDQNIAQMQAQPNAGNKKENR.V	MLANIDQNIAQMQAQPN	178	122	3.367	0.000
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	K.MLANIDQNIAQM+16QAQPNAGNKK.E	MLANIDQNIAQMQAQPN	178	122	3.263	0.007
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	K.M+16LANIDQNIAQMQAQPNAGNKK.E	MLANIDQNIAQMQAQPN	178	122	3.154	0.003
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	K.MLANIDQNIAQMQAQPNSAGNK.K	MLANIDQNIAQMQAQPNS	178	123	4.346	0.001
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	K.MLANIDQNIAQM+16QAQPNSAGNK.K	MLANIDQNIAQMQAQPNS	178	123	3.913	0.000
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	K.MLANIDQNIAQMQAQPNSAGNKK.E	MLANIDQNIAQMQAQPNS	178	123	3.79	0.008
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	K.MLANIDQNIAQM+16QAQPNSAGNKK.E	MLANIDQNIAQMQAQPNS	178	123	3.504	0.004
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	K.M+16LANIDQNIAQMQAQPNSAGNKK.E	MLANIDQNIAQMQAQPNS	178	123	3.161	0.001
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	K.MLANIDQNIAQMQAQPNSTAGNKKENR.V	MLANIDQNIAQMQAQPNST	178	124	3.548	0.000
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	K.AKNNPQVAGNK.K	AKNNPQV	178	132	4.044	0.006
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	K.AKNNPQVAGNKK.E	AKNNPQV	178	132	3.852	0.009
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	K.AKNNPQVAGNKKE.N	AKNNPQV	178	132	3.227	0.000
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	K.NNPQVAGNKK.E	NNPQV	178	132	3.824	0.008
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	K.AKNNPQVLAGNKKE.N	AKNNPQVL	178	133	3.718	0.000
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	K.AKNNPQVLAGNKKENR.V	AKNNPQVL	178	133	2.49	0.001
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	K.AKNNPQVLAGNKK.E	AKNNPQVL	178	133	2.435	0.009

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	K.NNPQVLKAGNKKE.N	NNPQVLK	178	134	3.854	0.001
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	K.FSSITIAGNKK.E	FSSITI	178	141	4.108	0.003
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	K.FSSITIAGNK.K	FSSITI	178	141	2.708	0.003
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	K.KFSSITIAGNKK.E	KFSSITI	178	141	4.167	0.000
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	K.KFSSITIAGNK.K	KFSSITI	178	141	3.981	0.000
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	*.KFSSITINAGNKK.E	KFSSITIN	178	142	4.17	0.000
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	*.KFSSITINAGNK.K	KFSSITIN	178	142	4.06	0.000
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	K.FSSITINSAGNKK.E	FSSITINS	178	143	4.036	0.000
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	K.FSSITINSAGNK.K	FSSITINS	178	143	4.01	0.001
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	*.KFSSITINSAGNK.K	KFSSITINS	178	143	4.229	0.000
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	*.KFSSITINSAGNKK.E	KFSSITINS	178	143	4.224	0.000
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	K.FSSITINSDAGNKK.E	FSSITINSD	178	144	4.112	0.000
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	K.FSSITINSDAGNKKE.N	FSSITINSD	178	144	2.805	0.000
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	*.KFSSITINSDAGNKK.E	KFSSITINSD	178	144	4.303	0.000
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	*.KFSSITINSDAGNK.K	KFSSITINSD	178	144	4.115	0.000
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	*.KFSSITINSDAGNKKENR.V	KFSSITINSD	178	144	3.543	0.000
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	K.FSSITINSDGAGNKK.E	FSSITINSDG	178	145	3.981	0.002
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	K.FSSITINSDGAGNKKENR.V	FSSITINSDG	178	145	2.048	0.002
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	*.KFSSITINSDGAGNKKENR.V	KFSSITINSDG	178	145	4.272	0.001
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	*.KFSSITINSDGAGNKK.E	KFSSITINSDG	178	145	3.998	0.006
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	*.KFSSITINSDGAGNKKE.N	KFSSITINSDG	178	145	3.978	0.000
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	K.IVKKTEDGNGAGNKKENR.V	IVKKTEDGNG	178	159	2.479	0.004
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	K.KTEDGNGNIAGNKK.E	KTEDGNGNI	178	161	3.673	0.005
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	K.KTEDGNGNIAGNK.K	KTEDGNGNI	178	161	3.081	0.008
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	K.KTEDGNGNIQAGNKK.E	KTEDGNGNIQ	178	162	4.068	0.006
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	K.KTEDGNGNIQTAGNKK.E	KTEDGNGNIQT	178	163	3.648	0.000
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	K.KTEDGNGNIQTVAGNKK.E	KTEDGNGNIQTV	178	164	4.106	0.002
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	K.KTEDGNGNIQTVAGNK.K	KTEDGNGNIQTV	178	164	3.177	0.003
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	K.EIPADQAGNKK.E	EIPADQ	178	172	3.335	0.000
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	K.EIPADQLAGNKK.E	EIPADQL	178	173	3.963	0.000
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	E.IPADQLAGNKKE.N	IPADQL	178	173	4.078	0.000
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	E.IPADQLAGNKK.E	IPADQL	178	173	3.146	0.000
trlQ2A4M3lQ2A4M3_FRATH	Outer membrane protein	E.KEIPADQLAGNKKE.N	KEIPADQL	178	173	4.23	0.000

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	E.KEIPADQLAGNKK.E	KEIPADQL	178	173	3.768	0.004
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	*.EIPADQLGAGNKK.E	EIPADQLG	178	174	3.658	0.000
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	E.IPADQLGAGNKKE.N	IPADQLG	178	174	4.04	0.001
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	E.KEIPADQLGAGNKKE.N	KEIPADQLG	178	174	4.269	0.000
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	E.KEIPADQLGAGNK.K	KEIPADQLG	178	174	3.933	0.000
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	*.EIPADQLGTAGNKK.E	EIPADQLGT	178	175	2.548	0.001
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	E.IPADQLGTAGNKKE.N	IPADQLGT	178	175	4.252	0.000
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	E.IPADQLGTAGNKK.E	IPADQLGT	178	175	3.852	0.000
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	E.KEIPADQLGTAGNKKE.N	KEIPADQLGT	178	175	4.057	0.000
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	*.EIPADQLGTIAGNKK.E	EIPADQLGTI	178	176	4.072	0.004
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	E.IPADQLGTIAGNKKE.N	IPADQLGTI	178	176	4.314	0.002
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	E.IPADQLGTIAGNKK.E	IPADQLGTI	178	176	4.216	0.009
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	E.KEIPADQLGTIAGNKKE.N	KEIPADQLGTI	178	176	4.302	0.000
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	E.IPADQLGTIKAGNKKE.N	IPADQLGTIK	178	177	4.149	0.005
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	E.KEIPADQLGTIKAGNKKE.N	KEIPADQLGTIK	178	177	4.044	0.000
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	E.IPADQLGTIKLAGNKKE.N	IPADQLGTIKL	178	178	4.338	0.001
tr|Q2A4M3|Q2A4M3_FRATH	Outer membrane protein	E.KEIPADQLGTIKLAGNKKE.N	KEIPADQLGTIKL	178	178	3.263	0.001
tr|Q2A4M9|Q2A4M9_FRATH	Delta 9 acyl-lipid fatty aci	E.TSGLAFVFWGGILSTAGNK.K	TSGLAFVFWGGILST	212	123	2.387	0.008
tr|Q2A4N4|Q2A4N4_FRATH	Two-component response	E.LALLAILVQNAGAGNK.K	LALLAILVQNAG	228	170	3.158	0.000
tr|Q2A4N4|Q2A4N4_FRATH	Two-component response	K.INIPNFIQTIAGNK.K	INIPNFIQTI	228	214	3.553	0.000
tr|Q2A4N4|Q2A4N4_FRATH	Two-component response	R.GVGYFVQAGNKK.E	GVGYFVQ	228	222	4.086	0.003
tr|Q2A4P7|Q2A4P7_FRATH	Outer membrane protein	K.IAVVNPVEIFNDSDLGSVAGNK.K	IAVVNPVEIFNDSDLGSV	167	41	4.309	0.000
tr|Q2A4P7|Q2A4P7_FRATH	Outer membrane protein	K.KLENDLKAGNKK.E	KLENDLK	167	51	3.791	0.001
tr|Q2A4P7|Q2A4P7_FRATH	Outer membrane protein	K.KLENDLKPAGNKK.E	KLENDLKP	167	52	4.023	0.000
tr|Q2A4P7|Q2A4P7_FRATH	Outer membrane protein	E.NDLKPAGNKKENR.V	NDLKP	167	52	2.965	0.000
tr|Q2A4P7|Q2A4P7_FRATH	Outer membrane protein	E.NDLKPAGNKKE.N	NDLKP	167	52	2.143	0.008
tr|Q2A4P7|Q2A4P7_FRATH	Outer membrane protein	K.KLENDLKPDAGNKK.E	KLENDLKPD	167	53	4.204	0.000
tr|Q2A4P7|Q2A4P7_FRATH	Outer membrane protein	K.KLENDLKPDAGNKKENR.V	KLENDLKPD	167	53	3.148	0.003
tr|Q2A4P7|Q2A4P7_FRATH	Outer membrane protein	K.KLENDLKPDAAGNKK.E	KLENDLKPDA	167	54	4.199	0.000
tr|Q2A4P7|Q2A4P7_FRATH	Outer membrane protein	E.NDLKPDAAGNKK.E	NDLKPDA	167	54	3.58	0.000
tr|Q2A4P7|Q2A4P7_FRATH	Outer membrane protein	K.KLENDLKPDATAGNKK.E	KLENDLKPDAT	167	55	4.141	0.003
tr|Q2A4P7|Q2A4P7_FRATH	Outer membrane protein	E.NDLKPDATAGNKKE.N	NDLKPDAT	167	55	3.828	0.005
tr|Q2A4P7|Q2A4P7_FRATH	Outer membrane protein	E.NDLKPDATAGNKK.E	NDLKPDAT	167	55	3.619	0.003

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

tr|Q2A4P7|Q2A4P7_FRATH Outer membrane protein	E.NDLKPDATAGNKKENR.V	NDLKPDAT	167	55	3.552	0.001
tr|Q2A4P7|Q2A4P7_FRATH Outer membrane protein	E.NDLKPDATKAGNKKE.N	NDLKPDATK	167	56	4.281	0.000
tr|Q2A4P7|Q2A4P7_FRATH Outer membrane protein	E.NDLKPDATKAGNKKENR.V	NDLKPDATK	167	56	2.924	0.008
tr|Q2A4P7|Q2A4P7_FRATH Outer membrane protein	E.NDLKPDATKLAGNKKE.N	NDLKPDATKL	167	57	4.102	0.000
tr|Q2A4P7|Q2A4P7_FRATH Outer membrane protein	E.NDLKPDATKLKAGNKKE.N	NDLKPDATKLK	167	58	3.992	0.001
tr|Q2A4P7|Q2A4P7_FRATH Outer membrane protein	K.LKQEQDAGNKKENR.V	LKQEQD	167	62	3.663	0.001
tr|Q2A4P7|Q2A4P7_FRATH Outer membrane protein	K.LKQEQDAGNK.K	LKQEQD	167	62	2.942	0.005
tr|Q2A4P7|Q2A4P7_FRATH Outer membrane protein	E.NDLKPDATKLKQEQDAGNKKE.N	NDLKPDATKLKQEQD	167	62	3.411	0.003
tr|Q2A4P7|Q2A4P7_FRATH Outer membrane protein	E.NDLKPDATKLKQEQDAGNKKENR.V	NDLKPDATKLKQEQD	167	62	3.062	0.000
tr|Q2A4P7|Q2A4P7_FRATH Outer membrane protein	K.LKQEQDNIAGNKK.E	LKQEQDNI	167	64	3.706	0.005
tr|Q2A4P7|Q2A4P7_FRATH Outer membrane protein	K.LKQEQDNIAGNKKENR.V	LKQEQDNI	167	64	3.669	0.001
tr|Q2A4P7|Q2A4P7_FRATH Outer membrane protein	K.LKQEQDNIMAGNKK.E	LKQEQDNIM	167	65	3.903	0.006
tr|Q2A4P7|Q2A4P7_FRATH Outer membrane protein	K.LKQEQDNIMAGNK.K	LKQEQDNIM	167	65	2.875	0.003
tr|Q2A4P7|Q2A4P7_FRATH Outer membrane protein	K.LKQEQDNIMQAGNKK.E	LKQEQDNIMQ	167	66	4.104	0.008
tr|Q2A4P7|Q2A4P7_FRATH Outer membrane protein	K.LKQEQDNIMQQAGNKK.E	LKQEQDNIMQQ	167	67	4.101	0.000
tr|Q2A4P7|Q2A4P7_FRATH Outer membrane protein	K.LKQEQDNIM+16QQAGNKK.E	LKQEQDNIMQQ	167	67	3.178	0.005
tr|Q2A4P7|Q2A4P7_FRATH Outer membrane protein	K.TLQNNSAAGNKK.E	TLQNNSA	167	76	3.632	0.000
tr|Q2A4P7|Q2A4P7_FRATH Outer membrane protein	K.TLQNNSATAGNKK.E	TLQNNSAT	167	77	3.352	0.000
tr|Q2A4P7|Q2A4P7_FRATH Outer membrane protein	K.TLQNNSATAGNK.K	TLQNNSAT	167	77	2.574	0.002
tr|Q2A4P7|Q2A4P7_FRATH Outer membrane protein	K.TLQNNSATMTKAGNK.K	TLQNNSATMTK	167	80	3.386	0.000
tr|Q2A4P7|Q2A4P7_FRATH Outer membrane protein	E.LDKKQQQIQAGNKKE.N	LDKKQQQIQ	167	91	3.816	0.000
tr|Q2A4P7|Q2A4P7_FRATH Outer membrane protein	E.LDKKQQQIQQAGNKKE.N	LDKKQQQIQQ	167	92	3.684	0.000
tr|Q2A4P7|Q2A4P7_FRATH Outer membrane protein	K.KQQQIQQEQQAGNKK.E	KQQQIQQEQQ	167	95	3.006	0.002
tr|Q2A4P7|Q2A4P7_FRATH Outer membrane protein	K.SELDKKQQQIQQEQQAGNK.K	SELDKKQQQIQQEQQ	167	95	2.495	0.004
tr|Q2A4P7|Q2A4P7_FRATH Outer membrane protein	K.SELDKKQQQIQQEQQNFAAGNKK.E	SELDKKQQQIQQEQQNFA	167	98	2.941	0.000
tr|Q2A4P7|Q2A4P7_FRATH Outer membrane protein	E.YTAKDKLAGNKKE.N	YTAKDKL	167	115	4.015	0.002
tr|Q2A4P7|Q2A4P7_FRATH Outer membrane protein	E.YTAKDKLSKAGNKKE.N	YTAKDKLSK	167	117	4.205	0.005
tr|Q2A4P7|Q2A4P7_FRATH Outer membrane protein	E.YTAKDKLSKAGNKKENR.V	YTAKDKLSK	167	117	2.884	0.000
tr|Q2A4P7|Q2A4P7_FRATH Outer membrane protein	*.KFQASFDKAGNK.K	KFQASFDK	167	125	3.847	0.001
tr|Q2A4P7|Q2A4P7_FRATH Outer membrane protein	K.NYNVVLTAGNKK.E	NYNVVLT	167	141	3.924	0.000
tr|Q2A4P7|Q2A4P7_FRATH Outer membrane protein	K.NYNVVLTTQAGNK.K	NYNVVLTTQ	167	143	3.944	0.000
tr|Q2A4P7|Q2A4P7_FRATH Outer membrane protein	K.NYNVVLTTQAAGNKK.E	NYNVVLTTQA	167	144	4.107	0.000
tr|Q2A4P7|Q2A4P7_FRATH Outer membrane protein	E.LMNKDSEAGNKK.E	LMNKDSE	167	167	3.814	0.000

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

tr|Q2A4P7|Q2A4P7_FRATH	Outer membrane protein	E.LMNKDSEAGNKKE.N	LMNKDSE	167	167	3.342	0.000
tr|Q2A4P8|Q2A4P8_FRATH	Outer membrane protein	K.ERPIIAGAGNKKE.N	ERPIIAG	792	100	2.972	0.006
tr|Q2A4Q7|Q2A4Q7_FRATH	Transposase isftu1	D.FRDIVINKAGNKKE.N	FRDIVINK	239	15	2.723	0.009
tr|Q2A4Q9|Q2A4Q9_FRATH	ATP-dependent DNA helic	E.FADM+16LDKHAGNKK.E	FADMLDKH	679	657	3.58	0.002
tr|Q2A4Q9|Q2A4Q9_FRATH	ATP-dependent DNA helic	E.FADM+16LDKHAGNK.K	FADMLDKH	679	657	2.98	0.005
tr|Q2A4Q9|Q2A4Q9_FRATH	ATP-dependent DNA helic	E.FADM+16LDKHYPEAGNK.K	FADMLDKHYPE	679	660	2.42	0.002
tr|Q2A4T3|Q2A4T3_FRATH	Spermidine synthase FTL_	*.MIANINNKKIAGNK.K	MIANINNKKI	289	10	2.811	0.004
tr|Q2A4U2|Q2A4U2_FRATH	4-alpha-glucanotransfera	D.LPIYAGNKK.E	LPIY	487	214	3.538	0.002
tr|Q2A4U9|Q2A4U9_FRATH	Shikimate 5-dehydrogena	E.EDIIEAWGLAGNKK.E	EDIIEAWGL	281	281	3.153	0.008
tr|Q2A4V2|Q2A4V2_FRATH	Glycine cleavage system	D.AYAKTLAGNKKE.N	AYAKTL	127	125	3.839	0.000
tr|Q2A4W8|Q2A4W8_FRAT	DNA topoisomerase IV su	K.FIPYDKDLKMLAAGNK.K	FIPYDKDLKMLA	741	645	2.733	0.006
tr|Q2A4X1|Q2A4X1_FRATH	Methionine aminopeptida	K.GIEVVKPGNHFGDIGAAGNKK.E	GIEVVKPGNHFGDIGA	256	151	2.612	0.000
tr|Q2A4X3|Q2A4X3_FRATH	Cold shock protein FTL_0	R.KGPEAINIEVAGNK.K	KGPEAINIEV	67	66	4.122	0.000
tr|Q2A4X3|Q2A4X3_FRATH	Cold shock protein FTL_0	R.KGPEAINIEVLAGNKK.E	KGPEAINIEVL	67	67	3.018	0.003
tr|Q2A4Z1|Q2A4Z1_FRATH	Putative uncharacterized	E.LLLKLQQQVQQLQGAGNK.K	LLLKLQQQVQQLQG	551	86	3.999	0.004
tr|Q2A4Z1|Q2A4Z1_FRATH	Putative uncharacterized	E.ADAQAWFGSAVTKAQSAGQLAGNKKE.N	ADAQAWFGSAVTKAQSAGQL	551	255	3.307	0.000
tr|Q2A4Z1|Q2A4Z1_FRATH	Putative uncharacterized	K.AQSAGQLAGNKK.E	AQSAGQL	551	255	2.933	0.002
tr|Q2A4Z1|Q2A4Z1_FRATH	Putative uncharacterized	K.YRPSVGSFGGGGAGNKK.E	YRPSVGSFGGGG	551	328	2.619	0.001
tr|Q2A504|Q2A504_FRATH	DNA topoisomerase I FTL	E.PLKKPKDAGNKKENR.V	PLKKPKD	764	682	2.409	0.000
tr|Q2A510|Q2A510_FRATH	Oligopeptidase A FTL_04	D.KLFSAGNKK.E	KLFS	668	30	2.841	0.002
tr|Q2A516|Q2A516_FRATH	UDP-N-acetylglucosamine	*.QAMTYAAMAAGNKK.E	QAMTYAAMA	434	249	2.248	0.003
tr|Q2A518|Q2A518_FRATH	Putative uncharacterized	K.KPTQC+57SDYAGNKK.E	KPTQCSDY	291	278	2.669	0.000
tr|Q2A543|Q2A543_FRATH	Mannose-6-phosphate iso	K.IITVKPQGQLSAGNK.K	IITVKPQGQLS	120	41	3.546	0.002
tr|Q2A544|Q2A544_FRATH	Amino acid permease FTL	D.KFAAVFAFVAGNKKE.N	KFAAVFAFV	464	286	2.545	0.001
tr|Q2A563|Q2A563_FRATH	Putative uncharacterized	E.YFLVLPEQYAGNK.K	YFLVLPEQY	168	168	2.512	0.005
tr|Q2A565|Q2A565_FRATH	Putative uncharacterized	D.HCKIKAGNKK.E	HCKIK	119	119	3.304	0.004
tr|Q2A598|Q2A598_FRATH	Dihydrolipoyl dehydrogen	E.VISGLNHSFDPLVIPSVAAGNKKE.N	VISGLNHSFDPLVIPSVA	470	349	2.094	0.006
tr|Q2A599|Q2A599_FRATH	Pyruvate dehydrogenase,	K.VKTQGSAPVAGNKK.E	VKTQGSAPV	531	188	2.431	0.000
tr|Q2A599|Q2A599_FRATH	Pyruvate dehydrogenase,	K.QQAATPAAPTAGNK.K	QQAATPAAPT	531	214	2.151	0.001
tr|Q2A599|Q2A599_FRATH	Pyruvate dehydrogenase,	K.QQAATPAAPTPAAGNK.K	QQAATPAAPTPA	531	216	3.068	0.000
tr|Q2A599|Q2A599_FRATH	Pyruvate dehydrogenase,	K.QQAATPAAPTPASAGNK.K	QQAATPAAPTPAS	531	217	3.633	0.000
tr|Q2A599|Q2A599_FRATH	Pyruvate dehydrogenase,	K.QQAATPAAPTPASSAGNK.K	QQAATPAAPTPASS	531	218	4.013	0.000
tr|Q2A599|Q2A599_FRATH	Pyruvate dehydrogenase,	K.QQAATPAAPTPASSAGNKK.E	QQAATPAAPTPASS	531	218	3.504	0.002

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

tr|Q2A599|Q2A599_FRATH	Pyruvate dehydrogenase,	K.QQAATPAAPTPASSSAGNK.K	QQAATPAAPTPASSS	531	219	3.683	0.000
tr|Q2A599|Q2A599_FRATH	Pyruvate dehydrogenase,	K.QQAATPAAPTPASSSVNAGNK.K	QQAATPAAPTPASSSVN	531	221	3.835	0.000
tr|Q2A599|Q2A599_FRATH	Pyruvate dehydrogenase,	E.YAVDNSNAHASPAGNKKE.N	YAVDNSNAHASP	531	234	4.387	0.000
tr|Q2A599|Q2A599_FRATH	Pyruvate dehydrogenase,	E.YAVDNSNAHASPAAGNKK.E	YAVDNSNAHASPA	531	235	4.369	0.000
tr|Q2A599|Q2A599_FRATH	Pyruvate dehydrogenase,	E.YAVDNSNAHASPAAGNK.K	YAVDNSNAHASPA	531	235	4.312	0.000
tr|Q2A599|Q2A599_FRATH	Pyruvate dehydrogenase,	E.YAVDNSNAHASPAAGNKKE.N	YAVDNSNAHASPA	531	235	3.066	0.000
tr|Q2A599|Q2A599_FRATH	Pyruvate dehydrogenase,	E.YAVDNSNAHASPAVAGNKKE.N	YAVDNSNAHASPAV	531	236	3.099	0.000
tr|Q2A599|Q2A599_FRATH	Pyruvate dehydrogenase,	E.YAVDNSNAHASPAVRAGNKKE.N	YAVDNSNAHASPAVR	531	237	2.818	0.000
tr|Q2A599|Q2A599_FRATH	Pyruvate dehydrogenase,	K.HAVTQVQAGNKK.E	HAVTQVQ	531	276	3.935	0.001
tr|Q2A599|Q2A599_FRATH	Pyruvate dehydrogenase,	K.HAVTQVQAGNK.K	HAVTQVQ	531	276	3.903	0.001
tr|Q2A599|Q2A599_FRATH	Pyruvate dehydrogenase,	K.VAASGSGLDLAGNKK.E	VAASGSGLDL	531	289	4.355	0.000
tr|Q2A599|Q2A599_FRATH	Pyruvate dehydrogenase,	R.YC+57QILSDAGNKK.E	YCQILSD	531	525	3.825	0.000
tr|Q2A5A0|Q2A5A0_FRATH	Pyruvate dehydrogenase,	R.WNSTVIVAAAGNKK.E	WNSTVIVAA	893	96	3.97	0.000
tr|Q2A5D8|Q2A5D8_FRATH	NAD(P)-specific glutamat	R.VPWVDKDGNIAGNKK.E	VPWVDKDGNI	449	74	3.903	0.005
tr|Q2A5D8|Q2A5D8_FRATH	NAD(P)-specific glutamat	R.HIGPDIDVPAGDIGVGAGNK.K	HIGPDIDVPAGDIGVG	449	172	3.287	0.000
tr|Q2A5D8|Q2A5D8_FRATH	NAD(P)-specific glutamat	E.TLQGKTVVTSGYGNAGNK.K	TLQGKTVVTSGYGN	449	243	2.551	0.000
tr|Q2A5D8|Q2A5D8_FRATH	NAD(P)-specific glutamat	K.TVVTSGYGNVAWGVCAGNK.K	TVVTSGYGNVAWGVC	449	249	4.09	0.000
tr|Q2A5H7|Q2A5H7_FRATH	Phosphatidate cytidylyltra	R.QKIDAIAAGNKKE.N	QKIDAIA	264	101	3.96	0.002
tr|Q2A5J9|Q2A5J9_FRATH	Pyrrolidone-carboxylate p	E.KYNPDVIIAGNKKE.N	KYNPDVII	222	84	4.263	0.001
tr|Q2A5J9|Q2A5J9_FRATH	Pyrrolidone-carboxylate p	E.RVAINVDDAAGNKKE.N	RVAINVDDA	222	107	4.294	0.001
tr|Q2A5J9|Q2A5J9_FRATH	Pyrrolidone-carboxylate p	K.ISANGENAAGNKK.E	ISANGENA	222	129	3.504	0.000
tr|Q2A5J9|Q2A5J9_FRATH	Pyrrolidone-carboxylate p	K.ISANGENAYFAGNKK.E	ISANGENAYF	222	131	3.177	0.000
tr|Q2A5J9|Q2A5J9_FRATH	Pyrrolidone-carboxylate p	E.NAYFSKLAGNKKE.N	NAYFSKL	222	134	4.155	0.000
tr|Q2A5J9|Q2A5J9_FRATH	Pyrrolidone-carboxylate p	K.IQAAIQAQGIAGNKK.E	IQAAIQAQGI	222	148	4.212	0.000
tr|Q2A5J9|Q2A5J9_FRATH	Pyrrolidone-carboxylate p	K.IQAAIQAQGIPAAGNK.K	IQAAIQAQGIPA	222	150	4.349	0.000
tr|Q2A5J9|Q2A5J9_FRATH	Pyrrolidone-carboxylate p	K.IQAAIQAQGIPAYAGNK.K	IQAAIQAQGIPAY	222	151	4.439	0.000
tr|Q2A5J9|Q2A5J9_FRATH	Pyrrolidone-carboxylate p	K.IQAAIQAQGIPAYIAGNK.K	IQAAIQAQGIPAYI	222	152	4.289	0.000
tr|Q2A5J9|Q2A5J9_FRATH	Pyrrolidone-carboxylate p	K.IQAAIQAQGIPAYIAGNKK.E	IQAAIQAQGIPAYI	222	152	2.304	0.005
tr|Q2A5J9|Q2A5J9_FRATH	Pyrrolidone-carboxylate p	K.IQAAIQAQGIPAYISAGNK.K	IQAAIQAQGIPAYIS	222	153	4.382	0.000
tr|Q2A5J9|Q2A5J9_FRATH	Pyrrolidone-carboxylate p	K.IQAAIQAQGIPAYISAGNKK.E	IQAAIQAQGIPAYIS	222	153	3.045	0.001
tr|Q2A5J9|Q2A5J9_FRATH	Pyrrolidone-carboxylate p	K.IQAAIQAQGIPAYISDAGNKK.E	IQAAIQAQGIPAYISD	222	154	3.047	0.000
tr|Q2A5J9|Q2A5J9_FRATH	Pyrrolidone-carboxylate p	K.IQAAIQAQGIPAYISDSAGNKK.E	IQAAIQAQGIPAYISDS	222	155	3.458	0.000
tr|Q2A5J9|Q2A5J9_FRATH	Pyrrolidone-carboxylate p	K.IQAAIQAQGIPAYISDSAGTAGNKK.E	IQAAIQAQGIPAYISDSAGT	222	158	3.367	0.000

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

tr|Q2A5J9|Q2A5J9_FRATH	Pyrrolidone-carboxylate p	K.IQAAIQAQGIPAYISDSAGTYVAGNKK.E	IQAAIQAQGIPAYISDSAGTYV	222	160	2.364	0.000
tr|Q2A5L5|Q2A5L5_FRATH	Cytochrome O ubiquinol c	R.PTWSHSNKLEIICWAGNKK.E	PTWSHSNKLEIICW	300	89	2.412	0.005
tr|Q2A5L7|Q2A5L7_FRATH	Cytochrome d terminal ox	R.QPWTVYDQLPTSIAGNKKE.N	QPWTVYDQLPTSI	584	527	2.024	0.001
tr|Q2A5M6|Q2A5M6_FRATH	Acyltransferase FTL_018	K.FSPKNWGIWIVVAGNKK.E	FSPKNWGIWIVV	307	17	3.123	0.008
tr|Q2A5N2|Q2A5N2_FRATH	Putative uncharacterized	K.QHQQLVGSDPAGNKK.E	QHQQLVGSDP	152	93	2.695	0.001
tr|Q2A5N2|Q2A5N2_FRATH	Putative uncharacterized	K.QHQQLVGSDPSAGNKK.E	QHQQLVGSDPS	152	94	2.553	0.000
tr|Q2A5N2|Q2A5N2_FRATH	Putative uncharacterized	K.QHQQLVGSDPSTWTPAGNKK.E	QHQQLVGSDPSTWTP	152	98	2.41	0.002
tr|Q2A5N2|Q2A5N2_FRATH	Putative uncharacterized	E.NYRGWQGYC+57FPAEQAGNKKE.N	NYRGWQGYCFPAEQ	152	127	3.09	0.000
tr|Q2A5V5|Q2A5V5_FRATH	Putative uncharacterized	K.NKVPVHLAGNKK.E	NKVPVHL	117	19	2.644	0.008
tr|Q2A5V6|Q2A5V6_FRATH	ClpB protein FTL_0094	R.YELHHGVAGNKK.E	YELHHGV	859	363	3.802	0.000
tr|Q2A5V6|Q2A5V6_FRATH	ClpB protein FTL_0094	E.YKGLEELWKAAGNKKE.N	YKGLEELWKA	859	464	2.224	0.008
tr|Q2A5V6|Q2A5V6_FRATH	ClpB protein FTL_0094	E.LQYGKIPAGNKKE.N	LQYGKIP	859	507	3.292	0.006
tr|Q2A5V6|Q2A5V6_FRATH	ClpB protein FTL_0094	E.IADVVSKATAGNKKE.N	IADVVSKAT	859	546	3.639	0.000
tr|Q2A5V6|Q2A5V6_FRATH	ClpB protein FTL_0094	E.IADVVSKATGAGNKKE.N	IADVVSKATG	859	547	4.079	0.000
tr|Q2A5V6|Q2A5V6_FRATH	ClpB protein FTL_0094	R.SGLSDPNRPAGNK.K	SGLSDPNRP	859	599	3.677	0.000
tr|Q2A5V6|Q2A5V6_FRATH	ClpB protein FTL_0094	R.SGLSDPNRPIAGNK.K	SGLSDPNRPI	859	600	4.209	0.000
tr|Q2A5V6|Q2A5V6_FRATH	ClpB protein FTL_0094	R.SGLSDPNRPIGAGNK.K	SGLSDPNRPIG	859	601	4.478	0.000
tr|Q2A5V6|Q2A5V6_FRATH	ClpB protein FTL_0094	R.SGLSDPNRPIGAGNKK.E	SGLSDPNRPIG	859	601	2.011	0.001
tr|Q2A5V6|Q2A5V6_FRATH	ClpB protein FTL_0094	R.SGLSDPNRPIGSAGNK.K	SGLSDPNRPIGS	859	602	4.236	0.000
tr|Q2A5V6|Q2A5V6_FRATH	ClpB protein FTL_0094	K.AHADIFNILLQVLDDAGNK.K	AHADIFNILLQVLDD	859	698	2.287	0.005
tr|Q2A5V6|Q2A5V6_FRATH	ClpB protein FTL_0094	E.FVNRVDDAIVFEAGNKK.E	FVNRVDDAIVFE	859	765	3.114	0.003
tr|Q2A5V7|Q2A5V7_FRATH	Chitinase FTL_0093	K.AKPAPVPAGNKK.E	AKPAPVP	730	173	3.41	0.001
tr|Q2A5V7|Q2A5V7_FRATH	Chitinase FTL_0093	K.TTGLPQTIAGNKK.E	TTGLPQTI	730	251	3.625	0.000
tr|Q2A5V7|Q2A5V7_FRATH	Chitinase FTL_0093	E.LYTINPNNPEPAGNKK.E	LYTINPNNPEP	730	272	3.28	0.000
tr|Q2A5V7|Q2A5V7_FRATH	Chitinase FTL_0093	E.LYTINPNNPEPITLGAGNK.K	LYTINPNNPEPITLG	730	276	4.296	0.000
tr|Q2A5V7|Q2A5V7_FRATH	Chitinase FTL_0093	K.KVLSSDASAGNKK.E	KVLSSDAS	730	293	3.657	0.002
tr|Q2A5V7|Q2A5V7_FRATH	Chitinase FTL_0093	E.IYVAKNIAGNKKE.N	IYVAKNI	730	301	4.015	0.003
tr|Q2A5V7|Q2A5V7_FRATH	Chitinase FTL_0093	K.NIMPNPIAGNK.K	NIMPNPI	730	306	3.229	0.000
tr|Q2A5V7|Q2A5V7_FRATH	Chitinase FTL_0093	K.NIMPNPIIAGNKK.E	NIMPNPII	730	307	3.976	0.000
tr|Q2A612|Q2A612_FRATH	Acid phosphatase FTL_0	*.APFANIENAAGNKK.E	APFANIENA	351	44	2.677	0.005
tr|Q2A627|Q2A627_FRATH	Single-stranded DNA-bind	E.INSSNFDAGNKKE.N	INSSNFD	158	153	3.955	0.000
tr|Q2A632|Q2A632_FRATH	Outer membrane protein	E.TSPLGKAKVTAGNK.K	TSPLGKAKVT	179	46	2.445	0.002
tr|Q2A632|Q2A632_FRATH	Outer membrane protein	K.LKPQMDAGNKK.E	LKPQMD	179	57	4.253	0.004

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

tr|Q2A632|Q2A632_FRATH Outer membrane protein	K.LKPQMDAGNK.K	LKPQMD	179	57	3.502	0.009
tr|Q2A632|Q2A632_FRATH Outer membrane protein	K.LKPQM+16DQAGNKK.E	LKPQMDQ	179	58	2.494	0.004
tr|Q2A632|Q2A632_FRATH Outer membrane protein	K.LKPQMDQLKAGNK.K	LKPQMDQLK	179	60	3.992	0.000
tr|Q2A632|Q2A632_FRATH Outer membrane protein	K.LKPQMDQLKQNITAAGNKKE.N	LKPQMDQLKQNITA	179	65	3.046	0.003
tr|Q2A632|Q2A632_FRATH Outer membrane protein	E.KDDVQAGNKKE.N	KDDVQ	179	81	3.483	0.001
tr|Q2A632|Q2A632_FRATH Outer membrane protein	K.VNVYTQEKDDVQAGNKK.E	VNVYTQEKDDVQ	179	81	2.622	0.008
tr|Q2A632|Q2A632_FRATH Outer membrane protein	E.KVNVYTQEKDDVQTAGNKK.E	KVNVYTQEKDDVQT	179	82	3.377	0.000
tr|Q2A632|Q2A632_FRATH Outer membrane protein	K.VNVYTQEKDDVQTAGNKK.E	VNVYTQEKDDVQT	179	82	4.145	0.000
tr|Q2A632|Q2A632_FRATH Outer membrane protein	K.DAQSADKVAGNKK.E	DAQSADKV	179	98	3.726	0.001
tr|Q2A632|Q2A632_FRATH Outer membrane protein	K.DAQSADKVEAGNKK.E	DAQSADKVE	179	99	3.92	0.001
tr|Q2A632|Q2A632_FRATH Outer membrane protein	E.KDDVQTDDSKGDTKDAQSADKVEAGNKK.E	KDDVQTDDSKGDTKDAQSADKVE	179	99	2.645	0.000
tr|Q2A632|Q2A632_FRATH Outer membrane protein	K.DAQSADKVENQAGNKK.E	DAQSADKVENQ	179	101	3.631	0.003
tr|Q2A632|Q2A632_FRATH Outer membrane protein	K.DAQSADKVENQDKQQAQAAGNKK.E	DAQSADKVENQDKQQAQA	179	108	2.889	0.001
tr|Q2A632|Q2A632_FRATH Outer membrane protein	E.NQDKQQAQADLEKAGNK.K	NQDKQQAQADLEK	179	112	3.353	0.001
tr|Q2A632|Q2A632_FRATH Outer membrane protein	K.AM+16KDYQAGNKK.E	AMKDYQ	179	118	2.669	0.000
tr|Q2A632|Q2A632_FRATH Outer membrane protein	E.KAMKDYQAGNKKE.N	KAMKDYQ	179	118	3.592	0.001
tr|Q2A632|Q2A632_FRATH Outer membrane protein	E.KAMKDYQAGNKK.E	KAMKDYQ	179	118	3.458	0.004
tr|Q2A632|Q2A632_FRATH Outer membrane protein	K.AMKDYQNAGNKK.E	AMKDYQN	179	119	4.112	0.002
tr|Q2A632|Q2A632_FRATH Outer membrane protein	K.AM+16KDYQNAGNKK.E	AMKDYQN	179	119	2.264	0.008
tr|Q2A632|Q2A632_FRATH Outer membrane protein	E.KAMKDYQNAGNKKE.N	KAMKDYQN	179	119	3.594	0.003
tr|Q2A632|Q2A632_FRATH Outer membrane protein	K.AMKDYQNLAGNKK.E	AMKDYQNL	179	120	4.126	0.003
tr|Q2A632|Q2A632_FRATH Outer membrane protein	K.AM+16KDYQNLAGNKK.E	AMKDYQNL	179	120	3.035	0.003
tr|Q2A632|Q2A632_FRATH Outer membrane protein	E.KAMKDYQNLAGNKKE.N	KAMKDYQNL	179	120	4.177	0.001
tr|Q2A632|Q2A632_FRATH Outer membrane protein	E.KAMKDYQNLAGNKK.E	KAMKDYQNL	179	120	4.022	0.000
tr|Q2A632|Q2A632_FRATH Outer membrane protein	E.KAMKDYQNLAGNK.K	KAMKDYQNL	179	120	3.9	0.000
tr|Q2A632|Q2A632_FRATH Outer membrane protein	E.KAM+16KDYQNLAGNKKE.N	KAMKDYQNL	179	120	2.805	0.000
tr|Q2A632|Q2A632_FRATH Outer membrane protein	K.AMKDYQNLMAGNKK.E	AMKDYQNLM	179	121	4.305	0.000
tr|Q2A632|Q2A632_FRATH Outer membrane protein	K.AMKDYQNLM+16AGNKK.E	AMKDYQNLM	179	121	3.433	0.000
tr|Q2A632|Q2A632_FRATH Outer membrane protein	K.AM+16KDYQNLMAGNKK.E	AMKDYQNLM	179	121	3.209	0.002
tr|Q2A632|Q2A632_FRATH Outer membrane protein	E.KAMKDYQNLMAGNKKE.N	KAMKDYQNLM	179	121	4.086	0.000
tr|Q2A632|Q2A632_FRATH Outer membrane protein	E.KAMKDYQNLMAGNKK.E	KAMKDYQNLM	179	121	3.985	0.000
tr|Q2A632|Q2A632_FRATH Outer membrane protein	E.KAMKDYQNLM+16AGNKKE.N	KAMKDYQNLM	179	121	3.185	0.000
tr|Q2A632|Q2A632_FRATH Outer membrane protein	E.KAMKDYQNLMNAGNKKE.N	KAMKDYQNLMN	179	122	4.019	0.002

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

trlQ2A632lQ2A632_FRATH Outer membrane protein	K.AMKDYQNLMNQAGNKK.E	AMKDYQNLMNQ	179	123	4.151	0.002
trlQ2A632lQ2A632_FRATH Outer membrane protein	K.MASDDADAGNKKENR.V	MASDDAD	179	133	4.393	0.003
trlQ2A632lQ2A632_FRATH Outer membrane protein	K.MASDDADAGNKK.E	MASDDAD	179	133	3.899	0.000
trlQ2A632lQ2A632_FRATH Outer membrane protein	K.MASDDADAAGNKK.E	MASDDADA	179	134	4.124	0.000
trlQ2A632lQ2A632_FRATH Outer membrane protein	K.MASDDADAFKAGNK.K	MASDDADAFK	179	136	4.313	0.000
trlQ2A632lQ2A632_FRATH Outer membrane protein	K.MASDDADAFKDAAGNKK.E	MASDDADAFKDA	179	138	4.179	0.000
trlQ2A632lQ2A632_FRATH Outer membrane protein	K.MASDDADAFKDAAGNKKENR.V	MASDDADAFKDA	179	138	3.357	0.000
trlQ2A632lQ2A632_FRATH Outer membrane protein	D.ALIKASAAGNKKE.N	ALIKASA	179	144	3.769	0.001
trlQ2A632lQ2A632_FRATH Outer membrane protein	D.ALIKASAQAGNKKE.N	ALIKASAQ	179	145	3.95	0.000
trlQ2A632lQ2A632_FRATH Outer membrane protein	K.ASAQVAKAGNK.K	ASAQVAK	179	148	3.406	0.000
trlQ2A632lQ2A632_FRATH Outer membrane protein	K.EKQLDAIAGNKK.E	EKQLDAI	179	155	3.565	0.004
trlQ2A632lQ2A632_FRATH Outer membrane protein	E.KQLDAIAGNKKE.N	KQLDAI	179	155	3.944	0.005
trlQ2A632lQ2A632_FRATH Outer membrane protein	E.KQLDAIAGNKK.E	KQLDAI	179	155	3.799	0.000
trlQ2A632lQ2A632_FRATH Outer membrane protein	*.EKQLDAILPAGNKK.E	EKQLDAILP	179	157	3.701	0.000
trlQ2A632lQ2A632_FRATH Outer membrane protein	E.KQLDAILPAGNKK.E	KQLDAILP	179	157	4.093	0.000
trlQ2A632lQ2A632_FRATH Outer membrane protein	E.KQLDAILPAGNKKE.N	KQLDAILP	179	157	4.015	0.000
trlQ2A632lQ2A632_FRATH Outer membrane protein	K.QLDAILPAGNKK.E	QLDAILP	179	157	2.011	0.006
trlQ2A632lQ2A632_FRATH Outer membrane protein	D.AILPAAGNKKE.N	AILPA	179	158	3.644	0.005
trlQ2A632lQ2A632_FRATH Outer membrane protein	E.KQLDAILPAAGNK.K	KQLDAILPA	179	158	4.047	0.000
trlQ2A632lQ2A632_FRATH Outer membrane protein	E.KQLDAILPAEAGNKKE.N	KQLDAILPAE	179	159	4.203	0.000
trlQ2A632lQ2A632_FRATH Outer membrane protein	*.EKQLDAILPAEMAGNKK.E	EKQLDAILPAEM	179	160	4.069	0.000
trlQ2A632lQ2A632_FRATH Outer membrane protein	E.KQLDAILPAEMAGNKKE.N	KQLDAILPAEM	179	160	4.295	0.000
trlQ2A632lQ2A632_FRATH Outer membrane protein	*.EKQLDAILPAEMSAGNKK.E	EKQLDAILPAEMS	179	161	3.25	0.000
trlQ2A632lQ2A632_FRATH Outer membrane protein	E.KQLDAILPAEMSAGNKKE.N	KQLDAILPAEMS	179	161	4.239	0.009
trlQ2A632lQ2A632_FRATH Outer membrane protein	*.EKQLDAILPAEMSLAGNKK.E	EKQLDAILPAEMSL	179	162	4.185	0.000
trlQ2A632lQ2A632_FRATH Outer membrane protein	E.KQLDAILPAEMSLAGNKKE.N	KQLDAILPAEMSL	179	162	4.243	0.001
trlQ2A632lQ2A632_FRATH Outer membrane protein	E.KQLDAILPAEM+16SLAGNKKE.N	KQLDAILPAEMSL	179	162	3.807	0.000
trlQ2A632lQ2A632_FRATH Outer membrane protein	K.QLDAILPAEMSLAGNKK.E	QLDAILPAEMSL	179	162	4.071	0.000
trlQ2A632lQ2A632_FRATH Outer membrane protein	K.QLDAILPAEMSLAGNK.K	QLDAILPAEMSL	179	162	3.506	0.000
trlQ2A632lQ2A632_FRATH Outer membrane protein	E.KQLDAILPAEMSLYNVAGNKKE.N	KQLDAILPAEMSLYNV	179	165	3.353	0.000
trlQ2A632lQ2A632_FRATH Outer membrane protein	E.MSLYNVAGNKKE.N	MSLYNV	179	165	4.04	0.001
trlQ2A632lQ2A632_FRATH Outer membrane protein	E.M+16SLYNVAGNKKE.N	MSLYNV	179	165	3.314	0.003
trlQ2A632lQ2A632_FRATH Outer membrane protein	E.MSLYNVAGNK.K	MSLYNV	179	165	3.152	0.004

Table S2. Junction peptides identified by MudPIT-LC-MS-MS analysis of *F. tularensis* tmRNA- tagged proteins.

tr|Q2A632|Q2A632_FRATH Outer membrane protein	K.QLDAILPAEMSLYNVAGNKK.E	QLDAILPAEMSLYNV	179	165	3.256	0.004
tr|Q2A632|Q2A632_FRATH Outer membrane protein	E.MSLYNVDAGNKKE.N	MSLYNVD	179	166	4.096	0.000
tr|Q2A632|Q2A632_FRATH Outer membrane protein	E.KQLDAILPAEMSLYNVDSIAGNKKE.N	KQLDAILPAEMSLYNVDSI	179	168	3.637	0.000
tr|Q2A632|Q2A632_FRATH Outer membrane protein	E.MSLYNVDSIAGNKKE.N	MSLYNVDSI	179	168	4.228	0.000
tr|Q2A632|Q2A632_FRATH Outer membrane protein	E.MSLYNVDSIAGNKK.E	MSLYNVDSI	179	168	3.482	0.000
tr|Q2A632|Q2A632_FRATH Outer membrane protein	K.QLDAILPAEMSLYNVDSIAGNKK.E	QLDAILPAEMSLYNVDSI	179	168	4.271	0.000
tr|Q2A632|Q2A632_FRATH Outer membrane protein	E.KQLDAILPAEMSLYNVDSIDVTKDVIAAGNKKE.N	KQLDAILPAEMSLYNVDSIDVTKDVIA	179	176	3.179	0.001
tr|Q2A632|Q2A632_FRATH Outer membrane protein	E.MSLYNVDSIDVTKDVIAKAGNKKE.N	MSLYNVDSIDVTKDVIAK	179	177	3.271	0.000
tr|Q2A632|Q2A632_FRATH Outer membrane protein	E.MSLYNVDSIDVTKDVIAKMQAGNKKE.N	MSLYNVDSIDVTKDVIAKMQ	179	179	3.077	0.000
tr|Q2A639|Q2A639_FRATH DNA polymerase III, beta	R.LNISQNQLLLSANNPDAGNK.K	LNISQNQLLLSANNPD	367	300	4.385	0.009

Table S3. List of oligonucleotide primers used in this study.

Primer Name	Primer Sequence
ssrA-UPfw-MluI	5'-CCACGCGTCGGTATTATTGCACTATCATCGGC-3'
ssrA-DNrev-MluI	5'-CCACGCGTGATTATTATTCAAAGTTTTTTGGTGGAGGCGG-3'
smpB-UPfw-MluI	5'-GGA CGC GTC AAG CTC GTA CAT CTG TGC GG-3'
smpB-DNfw-MluI	5'-CCACGCGTGGTCTTTGTCATTTATTTATAAGCC-3'
smpB-UP200-EcoRI	5'-GGAATTCCAATGTCATAACACATCGGTAG-3'
smpB-DN200-BamHI	5'-GGGATCCGAGACTGATCTAGTGTATATACATG-3'
EBS-Universal	5’-CGAAATTAGAAACTTGCGTTCAGTAAAC-3’
ssrA147-IBS	5’AAAACTCGAGATAATTATCCTTAAGCAACTTTGCTGTGCGCCCAGATAGGG TG-3’
ssrA147s-EBS1d	5'- CAG ATT GTA CAA ATG TGG TGA TAA CAG ATA AGT CTT TGC TGC TAA CTT ACC TTT CTT TGT -3'
ssrA147s-EBS2	5'- TGA ACG CAA GTT TCT AAT TTC GAT TTT GCT TCG ATA GAG GAA AGT GTC T -3'
ssrA174-IBS	5’-AAAACTCGAGATAATTATCCTTAGCCTACTCTAGCGTGCGCCCAGATAGGGTG-3’
ssrA174s-EBS1d	5'- CAG ATT GTA CAA ATG TGG TGA TAA CAG ATA AGT CTC TAG CTT TAA CTT ACC TTT CTT TGT -3'
ssrA174s-EBS2	5'- TGA ACG CAA GTT TCT AAT TTC GAT TTA GGC TCG ATA GAG GAA AGT GTC T -3'
smpB255-IBS	5’-AAAACTCGAGATAATTATCCTTAGCAGCCACACGCGTGCGCCCAGATAGGGTG-3’
SmpB255-EBS1	5'- CAG ATT GTA CAA ATG TGG TGA TAA CAG ATA AGT CAC ACG CAA TAA CTT ACC TTT CTT TGT -3'
smpB255-EBS2	5'- TGA ACG CAA GTT TCT AAT TTC GAT TGC TGC TCG ATA GAG GAA AGT GTC T -3'
ssrA-DDmut-S	5’- TTGCTGCTGTTGCTAAAGATGACTAGTCTAGCTTAATAAC-3’
ssrA-DDmut-AS	5’- GTTATTAAGCTAGACTAGTCATCTTTAGCAACAGCAGCAA-3’
ssrA-His6-MutF	5’- CGACAGCAACTTTGCTCATCATCATCACCATCACTAGTCTAGCTTAATAAC-3’
ssrA-His6-MutR	5’-GTTATTAAGCTAGACTAGTGATGGTGATGATGATGAGCAAAGTTGCTGTCG-3’
ssrA-His6stem-MutF	5’-CATCATCACCATCACTAGTCGATGGTAATATGCTATATGCGCACGGATATGATAG-3’
ssrA-His6stem-MutR	5’- CTATCATATCCGTGCGCATATAGCATATTACCATCGACTAGTGATGGTGATGATG-3’
ssrA-Ala5Glu-mutF	5’-CTGGCAACAAAAAAGAAAACCGCGTAGCGGC-3’
ssrA-Ala5Glu-mutR	5’- GCCGCTACGCGGTTTTCTTTTTTGTTGCCAG-3’