

Figure S1. Purification of *FtRNAP* σ^{70} -(MglA-SspA) complex and analyses of distinct α subunit contacts, related to Figure 1

A SDS silver stain gel showing *FtRNAP* σ^{70} -(MglA-SspA) complex purifications. Lane 1 is the molecular weight standard. Lane 2 is purification of complex in which β' -TAP was used to pulldown the *FtRNAP* σ^{70} -(MglA-SspA) complex. Lane 3 shows a similar purification in which an MglA-CBP tagged protein was used to pulldown the *FtRNAP* σ^{70} -(MglA-SspA) complex. **B** Ribbon diagram showing specific $\alpha 1$ - $\alpha 2$ contacts with β and β' . **C** Close up showing contacts that are specific for $\alpha 1$ interactions with β and $\alpha 2$ interactions with β' . $\alpha 1$, $\alpha 2$, β and β' are colored as in Figure 1A.

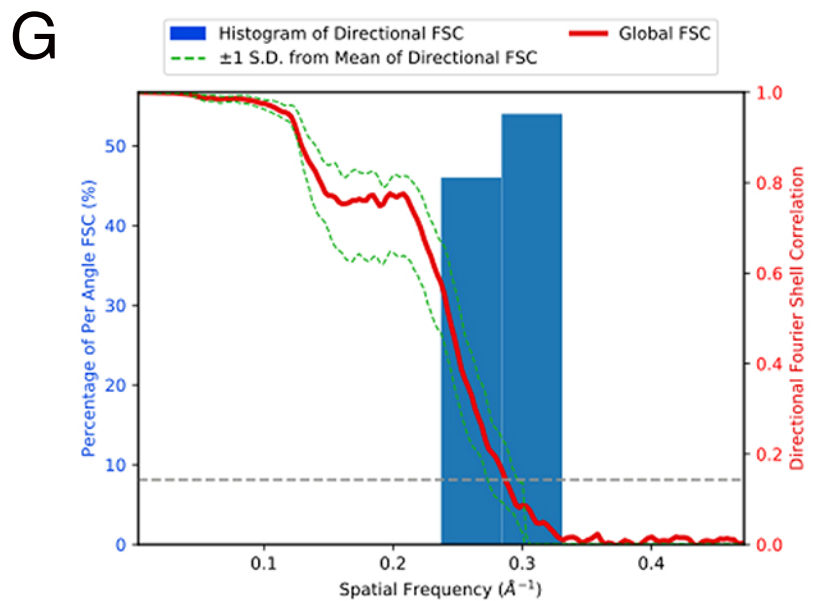
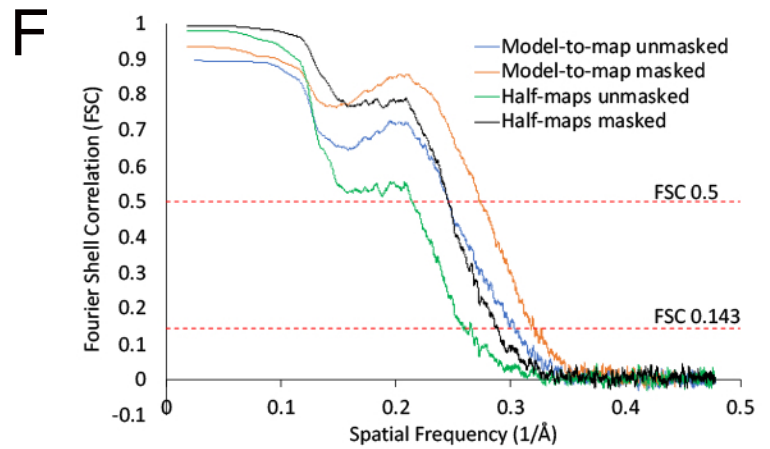
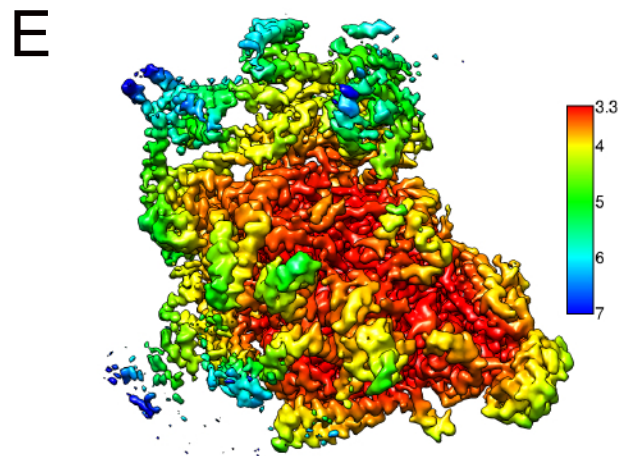
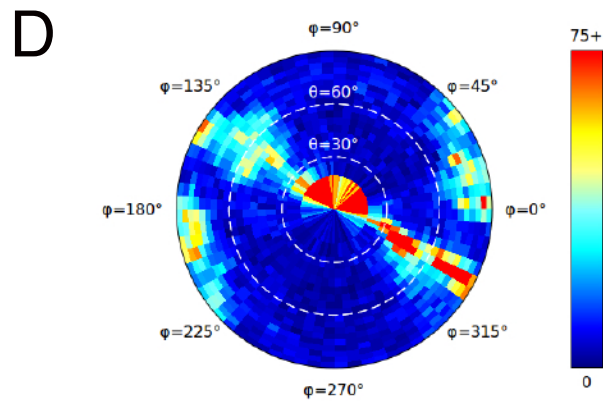
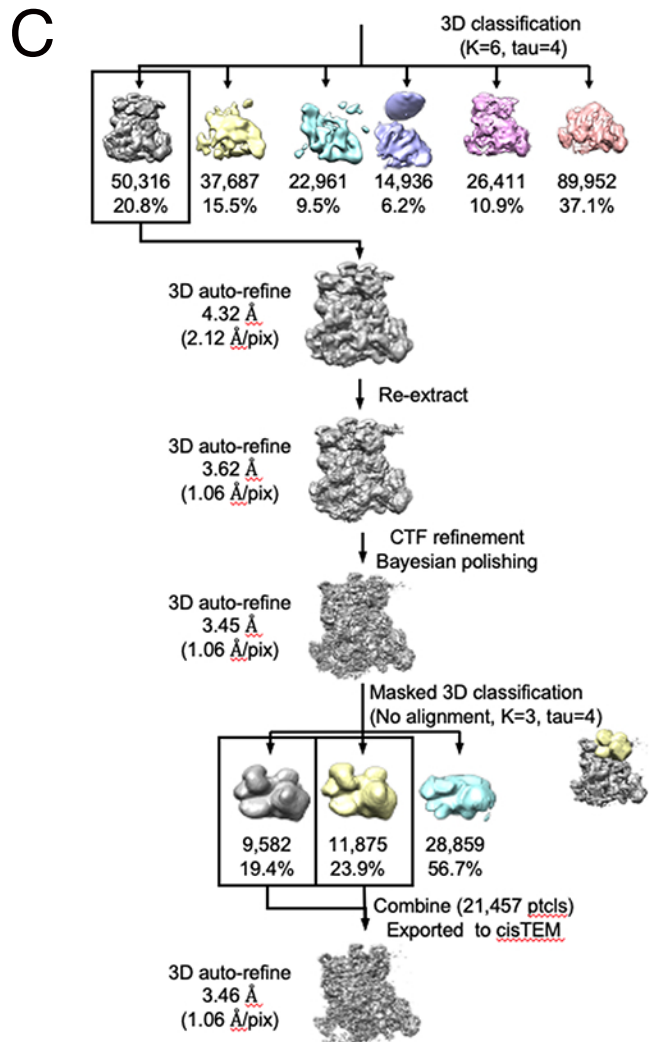
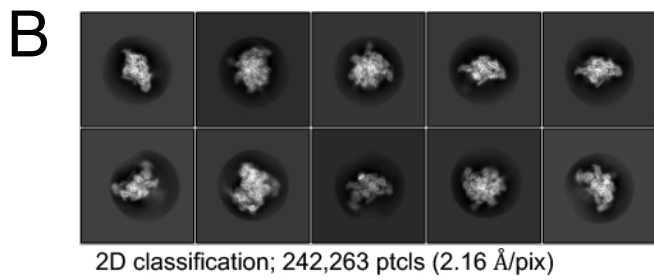
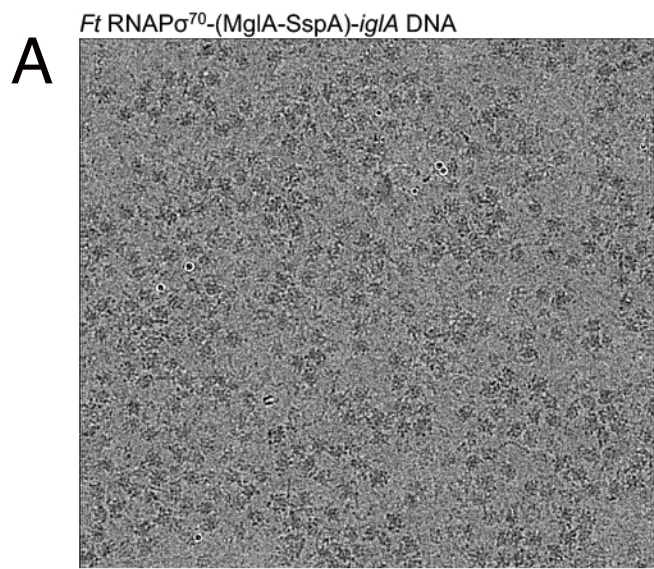
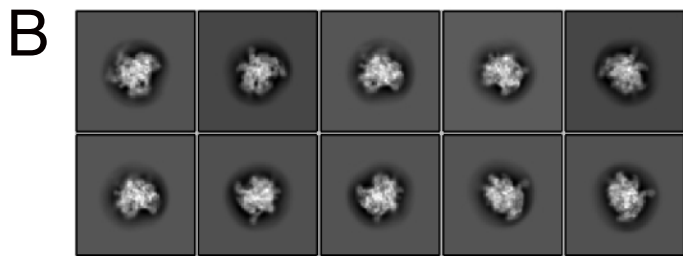
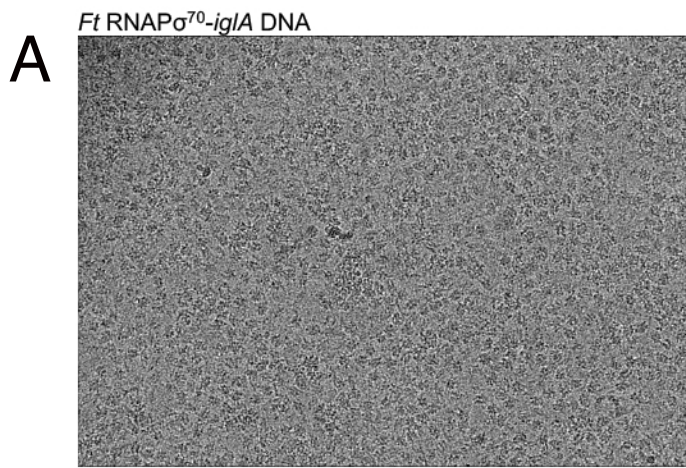
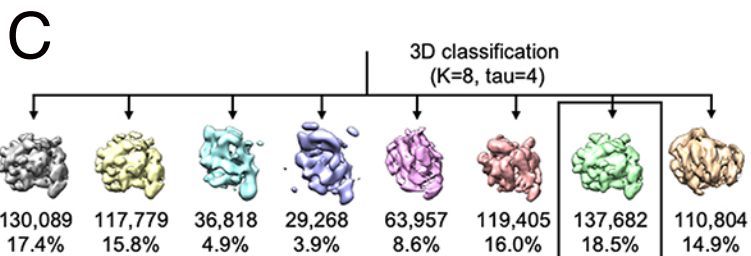


Figure S2. Cryo-EM data processing workflow of the *FtRNAP* σ^{70} -(MglA-SspA)-DNA dataset, related to Figure 1

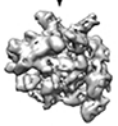
A A representative micrograph from a *FtRNAP* σ^{70} -(MglA-SspA)-DNA complex grid. **B** A subset of the 2D classes showing clear structural features. **C** Flow chart of the data processing strategy. **D** Angular distribution plot of the final particle set. **E** Final map colored by local resolution. **F** Masked and unmasked half-map FSC curves were used to determine global resolution of 3.46 Å. **G** Directional 3D FSC plot calculated using 3DFSC.



2D classification; 745,802 ptcls (4.32 Å/pix)

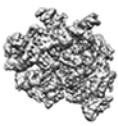


3D auto-refine
8.56 Å
(4.28 Å/pix)



Re-extract

3D auto-refine
3.25 Å
(1.07 Å/pix)



CTF refinement (2 rds)
Bayesian polishing (2 rds)

3D auto-refine
2.98 Å
(1.07 Å/pix)

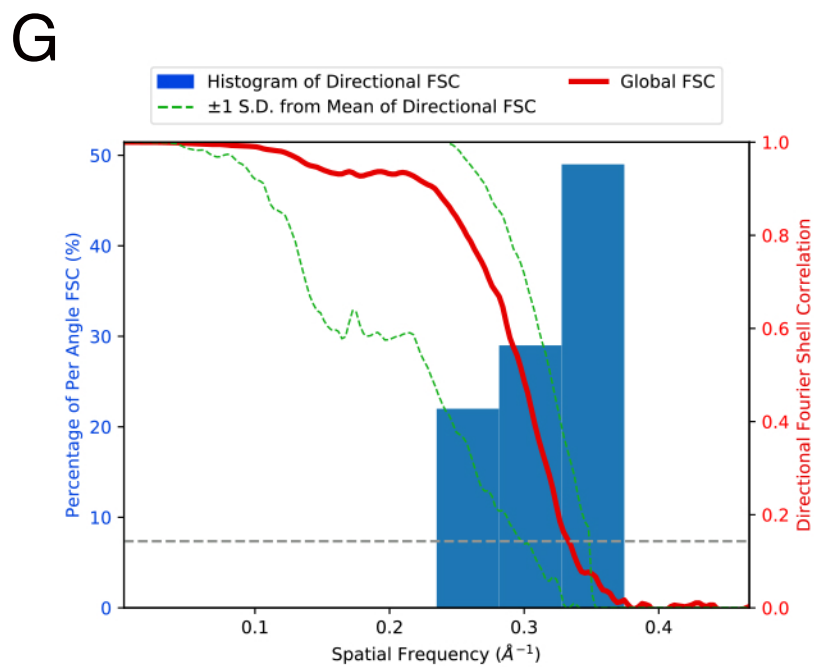
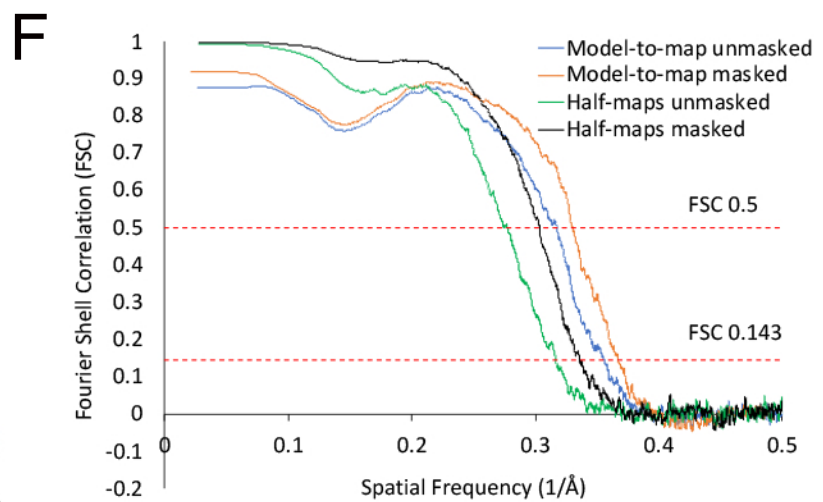
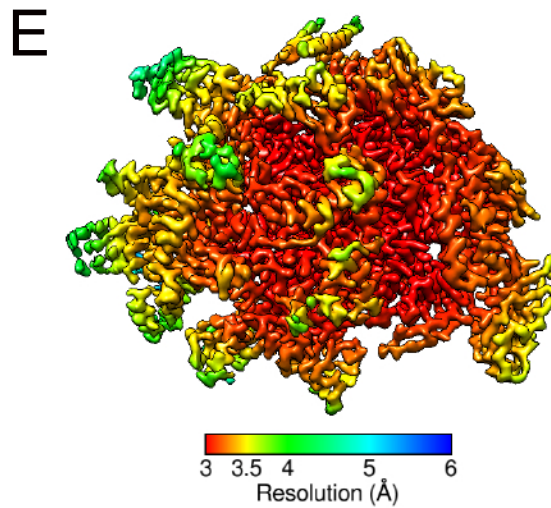
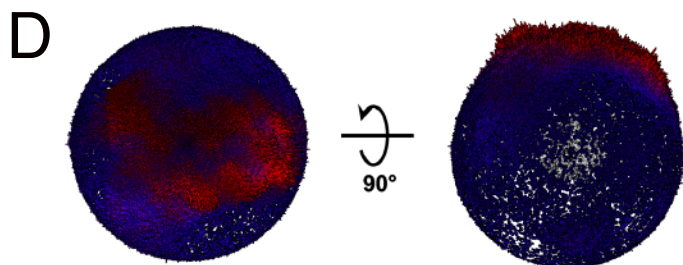
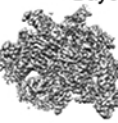
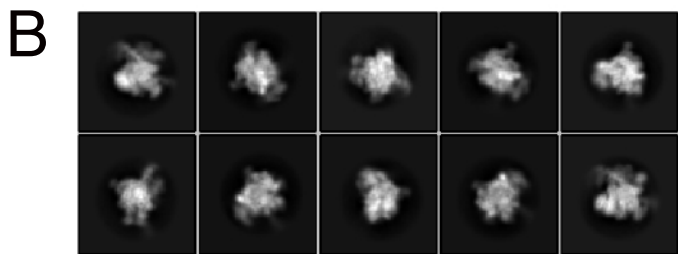
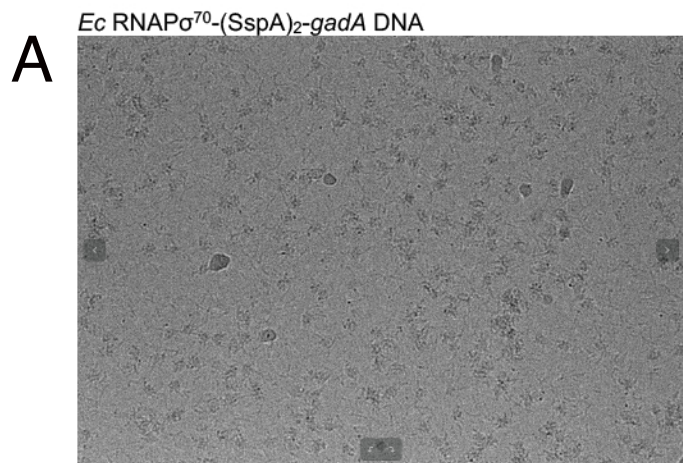


Figure S3. Cryo-EM data processing workflow of the *FtRNAP* σ^{70} -DNA dataset, related to Figure 1

A A representative micrograph from the *FtRNAP* σ^{70} -DNA dataset. **B** A subset of the 2D classes showing clear structural features. **C** Flow chart of the data processing strategy. **D** Angular distribution map of the final particle set used in the reconstruction. Each orientation is represented by a colored cylinder, ranging from blue to red, with a height proportional to the number of particles in that orientation. **E** Final map colored by local resolution. **F** Masked and unmasked half-map and model FSC curves used to determine global resolution. **G** Directional 3D FSC plot calculated using 3DFSC.



2D classification; 393,711 ptcls (4.4 Å/pix)

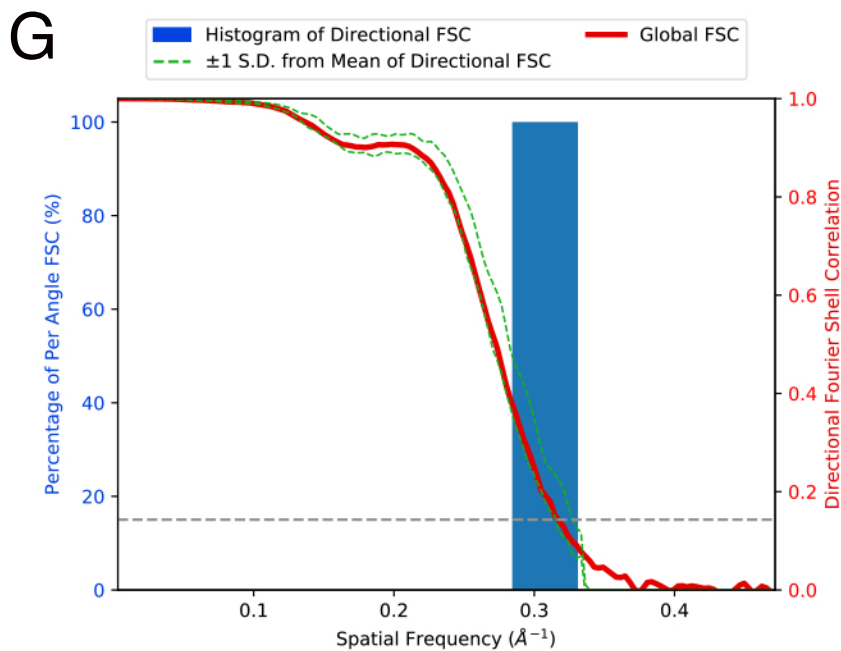
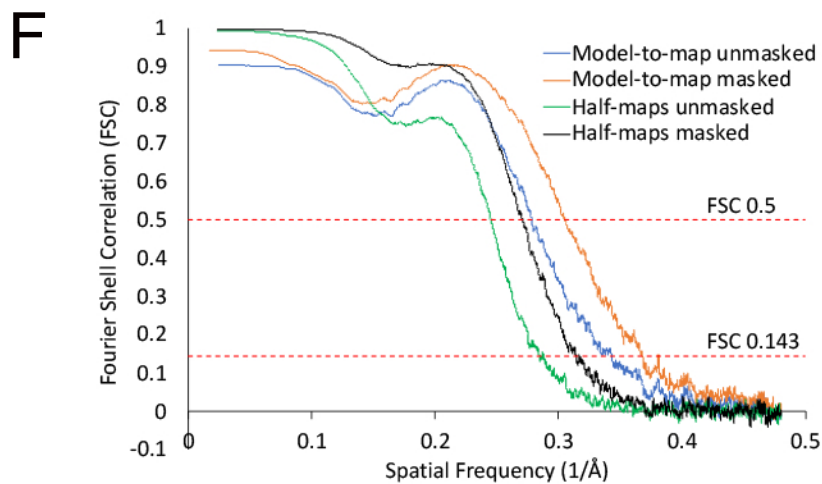
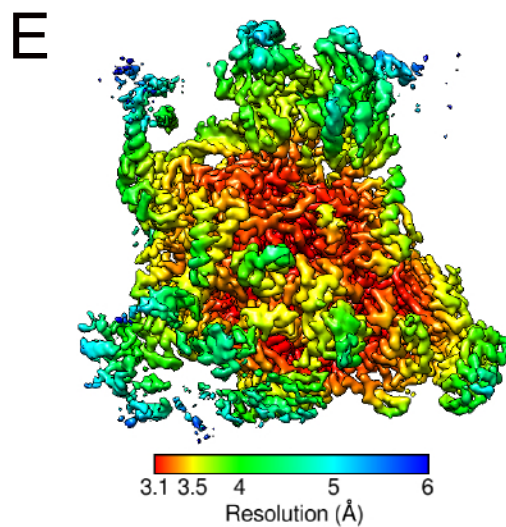
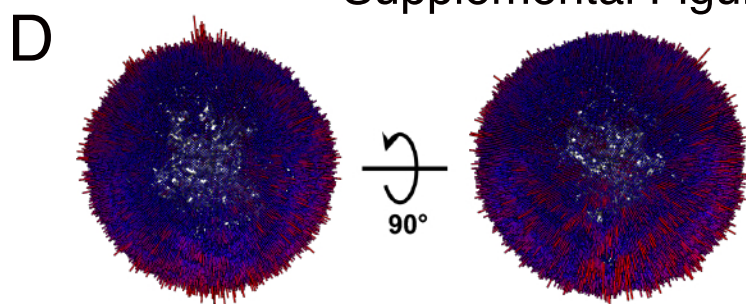
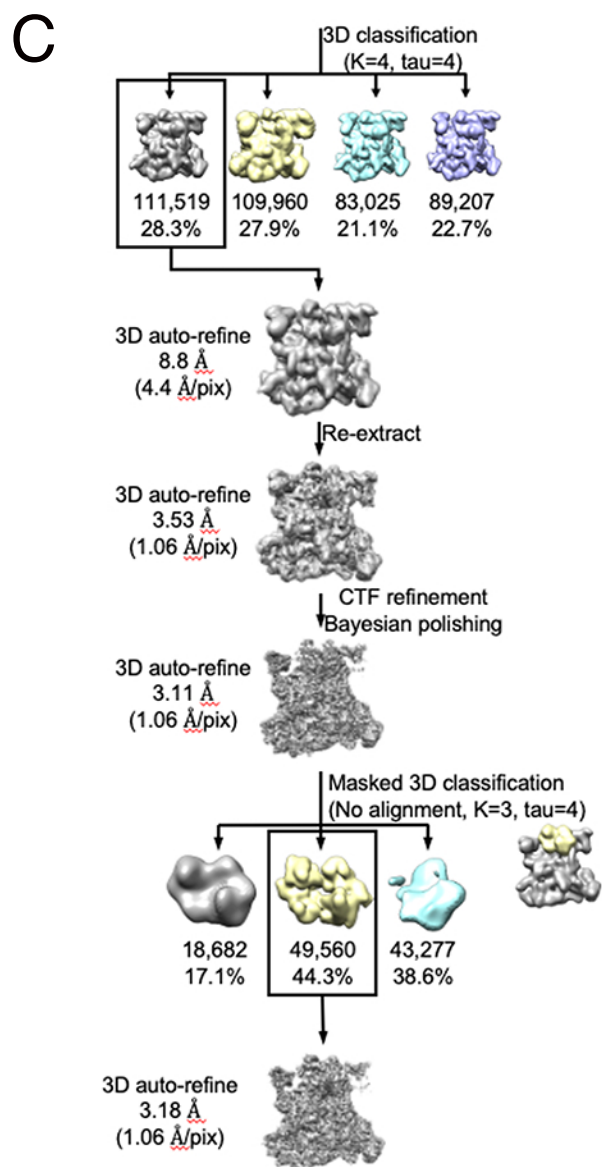


Figure S4. Cryo-EM data processing workflow of the *Ec*RNAP σ^{70} -(SspA)₂-DNA dataset, related to Figure 2

A A representative micrograph of the *Ec*RNAP σ^{70} -(SspA)₂-DNA complex. **B** A subset of the 2D classes showing clear structural features. **C** Flow chart of the data processing strategy. **D** Angular distribution map of the final particle set used in the reconstruction. **E** Final map colored by local resolution. **F** Masked and unmasked half-map FSC curves were used to determine the global resolution of 3.20 Å. **G** Directional 3D FSC plot calculated using 3DFSC.

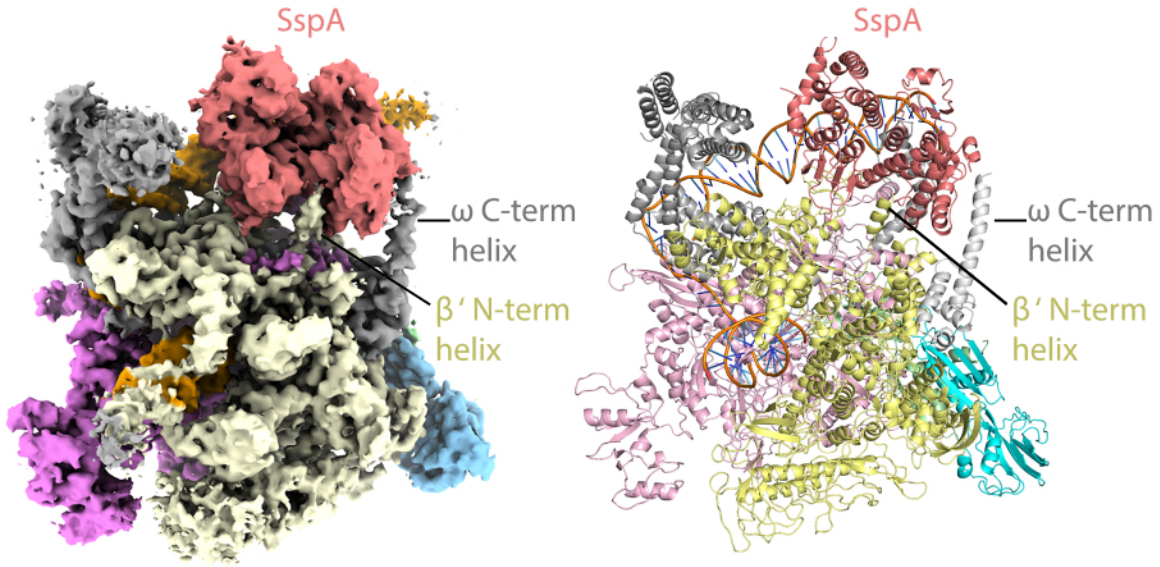
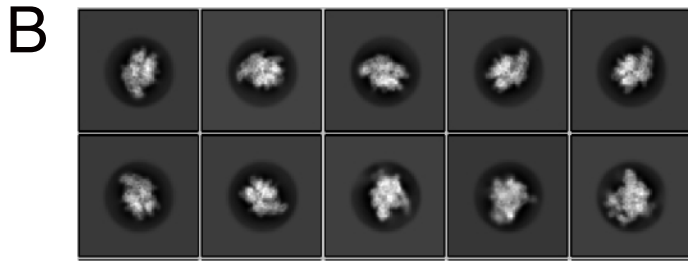
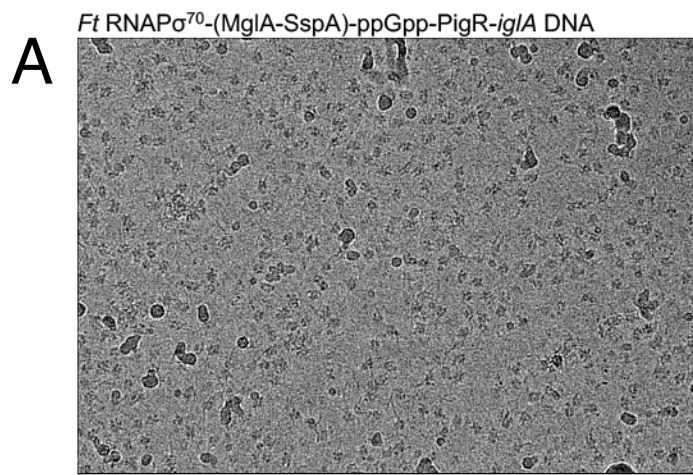


Figure S5. Additional interactions between *Ec*SspA and the *Ec*RNAP β' and ω subunits, related to Figure 2

Final *Ec*RNAP σ^{70} -(SspA)₂-DNA map (left) and model (right) colored by subunit. The N-terminal helix of β' contacts both SspA monomers and the C-terminal helix of ω contacts one SspA monomer.



2D classification; 1,901,718 ptcls (4.28 Å/pix)

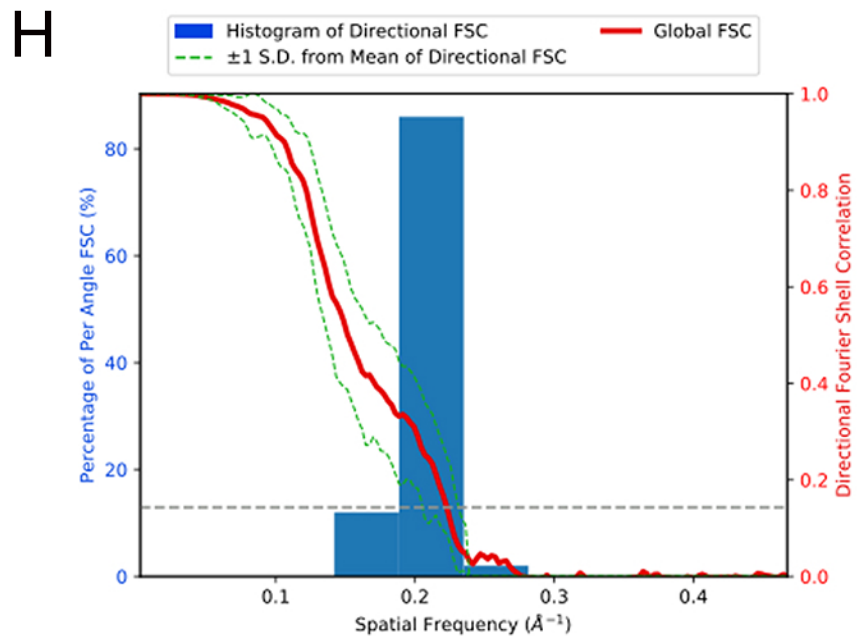
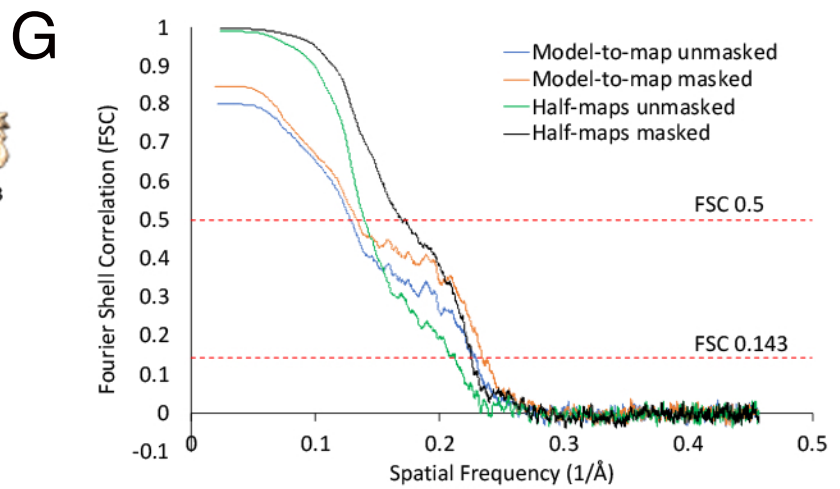
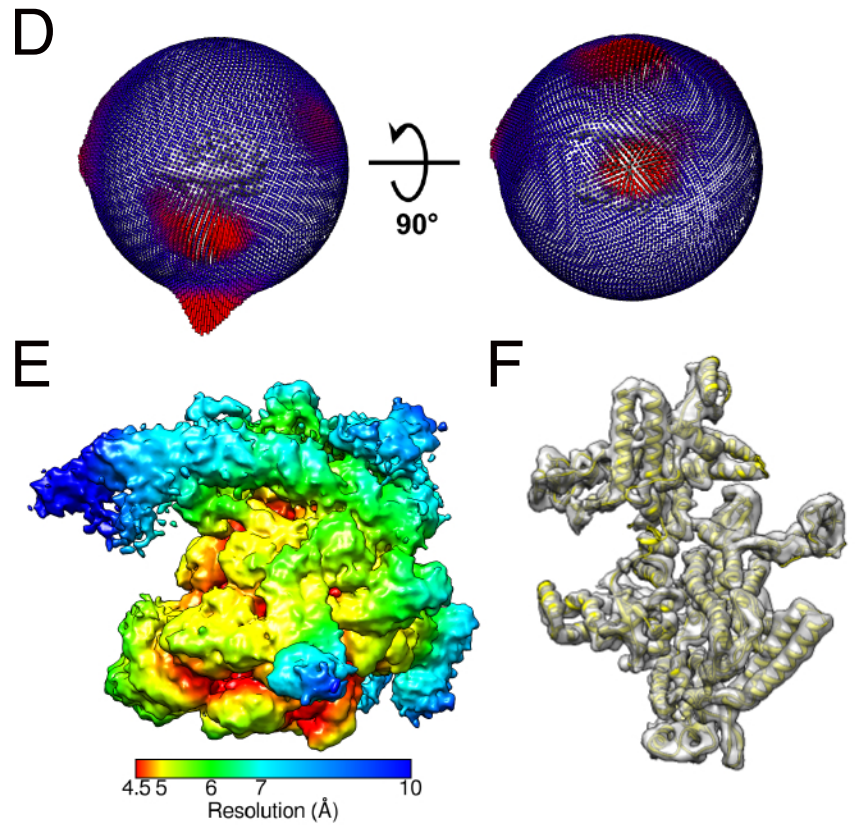
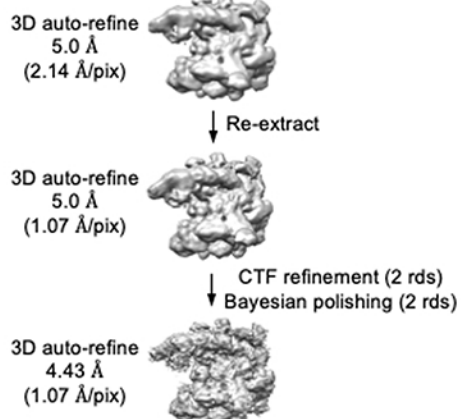
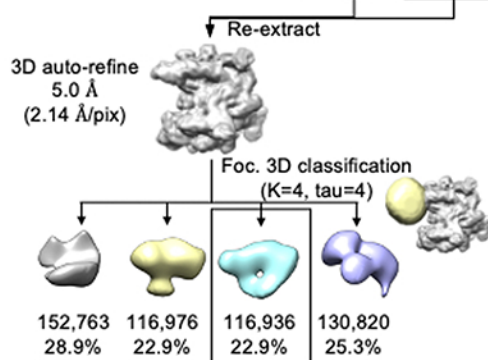
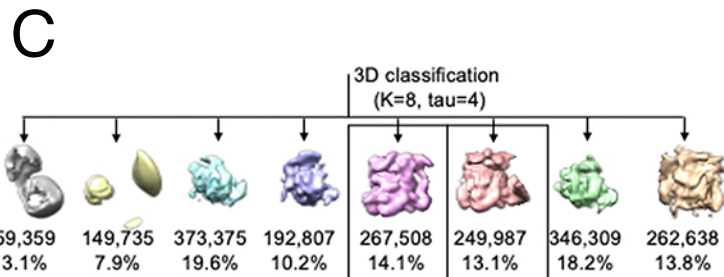


Figure S6. Cryo-EM data processing workflow of the *Ft*RNAP σ^{70} -(MglA-SspA)-ppGpp-PigR-DNA dataset, related to Figure 4

A A representative micrograph of the *Ft*RNAP σ^{70} -(MglA-SspA)-ppGpp-PigR-DNA complex. **B** A subset of the 2D classes showing clear structural features. **C** Flow chart of the data processing strategy. **D** Angular distribution maps of the final particle set used in the reconstruction. **E** Final map colored by local resolution. **F** Map-model overlay for the β' core subunit included to show map quality. **G** Masked and unmasked half-map FSC curves were used to determine the global resolution. **H** Directional 3D FSC plot calculated using 3DFSC.

A PigR-independent promoters activated by MglA-SspA

Promoter		-35		-10	TSS
<i>FTL_1174*</i>	AGTTAAATAAGT	TTCTTA	TAGCATACATTTTGTTA	AAATATTCT	A
<i>FTL_0488*</i>	TTTATTTTGAAC	TTCATA	TTCAGTGACACAATCTC	TATAATTCAAT	A
<i>FTL_1345*</i>	AAGCTTTTAATA	AATACA	AAACGGCAATAATTTG	TATTATACTCTTTCCTA	A
<i>FTL_1511*</i>	TAATATAAAACT	TTGCTA	TTTGATACCAAAAGAG	TAATTAATATTTGT	G
<i>FTL_1012*</i>	CAAAGCTATTTT	TTTTTA	TAAACTTCTTTGTTAC	TATATACCT.	A
<i>FTL_0361*</i>	TAAGGCTTGAAA	ATTTTA	GTATTTAACGTCATC	TTTATACAC.	A
<i>FTL_1046*</i>	TATAACTTACTG	TATTTA	TAAGAGATAAAAATGC	TATTAT CTCGGTT	A
Consensus		TTGACA		TATAAT	

*TSS estimated using RNA-Seq data

B PigR-dependent promoters

Promoter		UP	PRE	UP		-35		-10	TSS
<i>iglA</i>	AATGATCTGGGTTTAAAT	TT AGCTGT AATAAA	CA	TTGTGT	TATTGGCGTTATTAAGG	TA ACTT	GCTTAT	A	
<i>FTL_0026</i>	AATACTATAAAAATAGTA	TT TGCAGT AAAAA	AG	TGTTAA	TCAGTTTTGTGAGGTAC	TAAAA T	TAAATAT	A	
<i>pigR*</i>	ATCTACTAAACTGAAATA	AT TGCTGT AGAAA	AGG	TTGTTG	CAAATGATAAAAAAATG	TAAGAT	GAATAGT	T	
<i>FTL_1219</i>	TAAATAAAATAAAAATAT	TT TGCTATA AAAT	TTAT	TTCAAA	ATGAAATTGATTAATGCA	TACTTA	CTGATA	A	
<i>FTL_0170*</i>	CCTTTAAGGTATATAATC	CAC GCTGT AACAT	AGAG	TATTCT	TTTTAAAAATTTGTGTT	TATAGT	ATAGC	A	
<i>FTL_0221*</i>	ATTTTTATCATTTTTAA	TT TGCTGT AGTAA	ATTA	TCGAGC	AGAGTATTTTTTGT	TAGACT	GTAAAA	A	
<i>pdpA</i>	ACTTTATCGTCAGACCAA	TT AGCTGT AACA	TA	TAGTCA	ATAGATAAGTGCTTATG	TAAAA T	GACTTT	A	
<i>FTL_0207*</i>	GAGCTAAATGCTGCAATA	TAT GCTGT A AAAAG	ATT	TTAATA	ATTATCATGAGCTGC	TAAAT T	TAATT	A	
<i>FTL_0816*</i>	AATATGCAATAATTA AAA	TAT TGCCGT AGAAA	AG	TTTATA	GGGTTGTTTGTA ACTGT	TACGAT	GAAAAC	A	
<i>FTL_0067*</i>	CTAAGGCTCTAATAAAGA	CT TGCTATA AAGA	TGA	TTTAGT	TTAGAGACCTGGTATG	TAAAA T	TGAGAT	A	
<i>FTL_1832*</i>	TCTCTAGACCCTTATTTT	TT TGCAATA AAAA	A	TTGTAT	TTTATACTTAAATAAAC	GATAAT	GATATTC	G	
<i>FTL_1218</i>	ATATTTGTAATTAAGAT	GAT TGCCATA AAAT	CTA	TAAACA	GCTAAAAATCAAAAAGG	TATAAT	TGTTGT	A	

*TSS estimated using RNA-Seq data

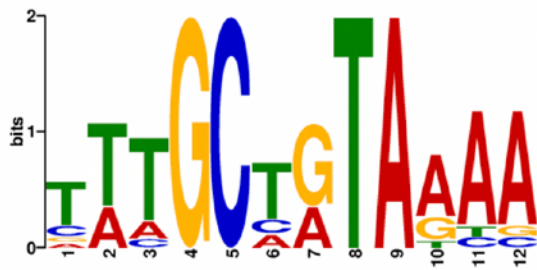
C MEME motif derived from PRE containing/PigR-dependent promoters

Figure S7. PigR-independent and PigR-dependent MglA-SspA regulated promoters, related to Figure 7

A Promoters identified from RNA-Seq experiments that are activated by >2.2 fold MglA-SspA in a PigR-independent manner ($\Delta pigR$). The predicted -35 and -10 promoter elements are labeled and underlined. Also labeled and highlighted in yellow are the predicted transcription start site (TSS) of each promoter. Base pairs shown to be involved in direct contacts with residues of the $\sigma 4$ (-35 element) or $\sigma 2$ (-10) element (Campbell et al., 2002) are highlighted in yellow. “Consensus” refers to the optimal element motifs from well-studied σ^{70} proteins, *E. coli* and *Taq*. **B** Promoters that MglA-SspA activate in a PigR-dependent manner. The -35, -10 and TSS are labeled and highlighted as in A. Also bolded and underlined are the predicted PRE sites. **C** MEME identified from PigR-dependent promoters sequences. The MEME pattern shows that in addition to the PRE, the bps that surround the PRE are also highly conserved, AT-rich regions. Transcription start sites were either previously identified (Ramsey et al., 2015) or estimated from published RNA-Seq data (Ramsey and Dove, 2016). For MEME analyses, DNA sequences corresponding to the transcription start site and 66 - 71 bp upstream were submitted to MEME (version 5.1.1) for twelve promoters tightly controlled by PigR (with transcripts reduced 26 - 4.4-fold in abundance in the absence of PigR).

Table S1 : Cryo-EM data collection, refinement, and validation statistics

	<i>Ft RNAPσ^{70}-(MglA-SspA)-iglA</i> PDB: 6WMR EMD-21851	<i>Ft RNAPσ^{70}-iglA</i> PDB: 6WMP EMD-21850	<i>Ec RNAPσ^{70}-(SspA)-gadA</i> PDB: 6WMU EMD-21853	<i>Ft RNAPσ^{70}-(MglA-SspA)-ppGpp-PigR-iglA</i> PDB: 6WMT EMD-21852
Data collection and Processing				
Electron microscope	Titan Krios (Duke)	Titan Krios (Duke)	Titan Krios (PNCC)	Titan Krios (Duke)
Detector	Falcon III	K3	K3	K3
Magnification	75,000x	22,500x	81,000x	22,500x
Voltage (keV)	300	300	300	300
Electron exposure (e-/Å ²)	42	60	50	60
Defocus range (μm)	-1.0 to -2.5	-1.0 to -2.0	-1.0 to -3.0	-1.25 to -2.75
Pixel size (Å)	1.06	1.07	0.53	1.07
Total extracted particles (no.)	618,526	1,503,586	672,043	3,485,423
Refined particles (no.)	242,263	745,802	393,711	1,901,718
Reconstruction				
Final particles (no.)	21,457	137,682	49,560	116,936
Symmetry imposed	C1	C1	C1	C1
FSC 0.143 (unmasked/masked) (Å)	3.86/3.46	3.16/2.98	3.52/3.18	4.78/4.43
Map sharpening B-factor (Å ²)	-90	-37	-47	0
Refinement				
Model composition				
Non-hydrogen atoms	30,441	22,296	34,094	31,926
Protein residues	3,743	2,879	4,121	3,890
Nucleotides	81	47	86	116
Ions/Ligands	3	3	3	5
MolProbity score	3.12	2.96	3.17	3.04
Clash score	16.43	9.38	20.86	57.80
Bonds (RMSD)				
Bond lengths (Å)	0.008	0.011	0.016	0.013
Bond angles (°)	0.776	0.922	0.999	1.483
Ramachandran plot (%)				
Favored (%)	85.20	86.17	88.02	96.11
Allowed (%)	14.67	13.62	11.69	3.32
Disallowed (%)	0.13	0.21	0.29	0.57

Table S2: New MglA regulon revealed by RNA-seq studies, related to Figure 2

Locus Number	Gene name	Gene product	Δ mglA pF compared to LVS pF			Δ pigR pF compared to LVS pF			Previous MglA Regulon*
			Mean of normalized read counts	log-2 Fold Change	adjusted p-value	Mean of normalized read counts	log-2 Fold Change	adjusted p-value	
FTL_0111	<i>iglA</i>	intracellular growth locus, subunit A	3414.2	-4.93	5.9E-116	3414.2	-4.75	1.3E-108	yes
FTL_0026	-	3-hydroxyisobutyrate dehydrogenase	576.7	-4.46	2.8E-63	576.7	-4.34	4.2E-58	yes
FTL_0449	<i>pigR</i>	pathogenicity island gene regulator	6782.1	-4.10	3.7E-48	6782.1	-7.26	2.0E-110	yes
FTL_0112	<i>iglB</i>	intracellular growth locus, subunit B	10167.4	-3.96	2.3E-59	10167.4	-3.75	3.2E-53	yes
FTL_1219	-	hypothetical protein	5828.6	-3.84	3.3E-118	5828.6	-2.77	2.6E-62	yes
FTL_0170	-	hypothetical protein	131.1	-3.72	4.0E-45	131.1	-4.40	4.2E-44	no
FTL_0348	-	-	475.3	-3.71	5.7E-64	475.3	-4.45	1.0E-73	yes
FTL_0221	-	amino acid permease	1158.6	-3.68	1.4E-45	1158.6	-4.40	7.7E-61	yes
FTL_0349	-	-	115.3	-3.51	1.5E-36	115.3	-3.98	9.0E-37	yes
FTL_0126	<i>pdpA</i>	PdpA protein	711.9	-3.51	8.1E-32	711.9	-3.92	3.8E-38	yes
FTL_1213	-	hypothetical protein	926.2	-3.46	6.3E-33	926.2	-3.48	6.5E-33	yes
FTL_0121	<i>iglG</i>	hypothetical protein	871.7	-3.39	1.9E-49	871.7	-3.37	6.9E-48	yes
FTL_0113	<i>iglC</i>	intracellular growth locus, subunit C	14862.4	-3.20	4.8E-35	14862.4	-3.18	1.2E-34	yes
FTL_0207	-	pyrrolidone-carboxylate peptidase	2022.5	-3.15	4.4E-63	2022.5	-2.84	3.3E-51	yes
FTL_0816	-	hypothetical protein	132.6	-3.13	3.0E-34	132.6	-3.49	2.6E-35	no
FTL_0025	-	hypothetical protein	29.5	-3.11	7.9E-17	29.5	-3.66	6.5E-19	no
FTL_0120	<i>iglH</i>	hypothetical protein	413.5	-3.03	7.2E-24	413.5	-3.28	8.4E-27	yes
FTL_0208	-	putative cytochrome c-type biogenesis protein	326.1	-2.92	5.2E-43	326.1	-3.16	5.1E-46	yes
FTL_0114	<i>iglD</i>	intracellular growth locus, subunit D	4658.5	-2.83	1.0E-24	4658.5	-3.26	4.2E-32	yes
FTL_0027	-	3-hydroxyisobutyrate dehydrogenase	195.8	-2.79	1.5E-24	195.8	-3.33	4.5E-30	yes
FTL_0118	<i>iglI</i>	hypothetical protein	487.0	-2.74	2.5E-18	487.0	-3.01	3.1E-21	yes
FTL_0125	<i>pdpB</i>	PdpB protein	466.2	-2.70	3.1E-18	466.2	-3.46	8.8E-28	yes
FTL_0815	-	PRC-barrel protein	73.4	-2.59	4.6E-20	73.4	-3.26	7.5E-24	no
FTL_0067	-	-	37.5	-2.57	9.3E-14	37.5	-3.21	1.1E-16	yes
FTL_0879	-	beta-lactamase	1198.1	-2.55	9.9E-46	1198.1	-2.38	1.5E-39	yes
FTL_0117	<i>iglJ</i>	hypothetical protein	105.9	-2.41	3.3E-12	105.9	-2.61	3.3E-13	yes
FTL_0124	<i>iglE</i>	hypothetical protein	41.5	-2.41	4.9E-13	41.5	-3.38	1.0E-18	yes
FTL_1217	-	hypothetical protein	70.0	-2.33	1.6E-11	70.0	-2.11	3.4E-09	no
FTL_1832	<i>fsIA</i>	hypothetical protein	2659.1	-2.29	1.3E-104	2659.1	-1.59	8.0E-52	yes
FTL_0123	<i>vgrG</i>	hypothetical protein	93.7	-2.25	2.3E-11	93.7	-2.87	8.3E-16	yes
FTL_1218	-	hypothetical protein	597.6	-2.22	4.8E-07	597.6	-2.16	2.6E-06	yes
FTL_1202	-	hypothetical protein	777.0	-2.18	7.9E-07	777.0	-2.62	5.1E-09	yes
FTL_0941	-	hypothetical protein	1316.2	-2.17	6.2E-28	1316.2	-1.17	1.4E-08	no
FTL_0119	<i>dotU</i>	hypothetical protein	298.2	-2.14	9.1E-07	298.2	-2.56	1.0E-08	yes
FTL_0673	<i>panC</i>	pantoate-beta-alanine ligase	15958.0	-2.13	4.7E-29	15958.0	-1.44	2.0E-13	yes
FTL_0116	<i>pdpC</i>	PdpC protein	1605.0	-2.12	1.4E-08	1605.0	-2.43	1.6E-10	yes
FTL_0097	-	hypothetical protein	810.4	-2.12	2.2E-25	810.4	-3.02	6.1E-47	yes
FTL_1833	<i>fsiB</i>	hypothetical protein	485.0	-2.12	8.4E-44	485.0	-1.82	1.8E-32	no
FTL_0209	-	DNA polymerase III subunit chi	351.8	-2.11	3.5E-25	351.8	-2.18	1.3E-25	yes
FTL_0674	<i>panB</i>	3-methyl-2-oxobutanoate hydroxymethyltransferase	21424.2	-2.10	3.0E-28	21424.2	-1.37	3.7E-12	yes
FTL_0627	<i>mtB</i>	threonine efflux protein	268.4	-2.10	1.1E-16	268.4	-1.02	1.4E-04	no
FTL_0675	<i>panG</i>	hypothetical protein, putative ketopantoate reductase	4509.7	-2.09	3.5E-32	4509.7	-1.33	3.0E-13	yes
FTL_0282	-	hypothetical protein	157.0	-2.09	3.1E-23	157.0	-1.94	3.3E-19	no
FTL_0672	<i>panD</i>	aspartate alpha-decarboxylase	4620.1	-2.07	1.4E-26	4620.1	-1.38	4.4E-12	yes
FTL_1834	<i>fsiC</i>	diaminopimelate decarboxylase	722.8	-2.06	3.4E-45	722.8	-1.58	3.6E-27	yes
FTL_0543	-	-	768.0	-2.05	5.2E-28	768.0	-3.13	6.0E-58	yes
FTL_0491	-	outer membrane lipoprotein	1064.0	-2.01	1.1E-17	1064.0	-2.11	5.9E-19	yes
FTL_0499	-	S-adenosylmethionine decarboxylase	1641.0	-2.00	3.7E-28	1641.0	-1.16	6.2E-10	yes
FTL_0500	-	spermidine synthase	1282.1	-2.00	2.6E-20	1282.1	-1.06	4.1E-06	yes
FTL_0066	-	-	33.5	-1.97	2.9E-08	33.5	-2.90	7.6E-13	yes
FTL_1546	-	pyridoxal biosynthesis lyase Pdx5	2923.9	-1.94	8.5E-36	2923.9	-2.74	3.8E-68	yes
FTL_1091	-	-	47.9	-1.89	1.9E-12	47.9	-1.61	8.5E-09	no
FTL_0280	-	amino acid permease	366.8	-1.89	5.5E-27	366.8	-1.79	1.5E-23	no
FTL_0859	-	rubredoxin	246.7	-1.88	5.1E-30	246.7	0.06	8.2E-01	yes
FTL_1057	-	-	184.5	-1.87	1.2E-16	184.5	-1.68	3.7E-13	yes
FTL_1251	<i>dptA</i>	proton-dependent oligopeptide transport (POT) family protein	3093.6	-1.85	9.0E-69	3093.6	-1.02	1.6E-21	yes
FTL_0569	-	hypothetical protein	6072.5	-1.82	6.8E-26	6072.5	-2.65	3.2E-53	yes
FTL_0550	-	-	102.7	-1.78	7.5E-14	102.7	-2.54	1.2E-21	yes
FTL_0942	-	nicotinamide mononucleotide transport (NMT) family protein	1144.3	-1.78	5.8E-13	1144.3	-1.19	4.7E-06	yes
FTL_1876	-	outer membrane associated protein, fragment	613.5	-1.76	2.0E-23	613.5	-1.57	2.7E-18	yes
FTL_1225	-	hypothetical protein	1834.3	-1.76	1.3E-29	1834.3	-1.62	4.8E-25	yes
FTL_0924	-	proton-dependent oligopeptide transporter	37.2	-1.76	1.6E-05	37.2	-1.96	6.5E-06	yes
FTL_0767	-	hypothetical protein	566.9	-1.75	6.0E-20	566.9	-1.83	6.8E-21	yes
FTL_1790	<i>ampG</i>	major facilitator superfamily transporter	5492.3	-1.72	7.1E-44	5492.3	-1.29	6.0E-25	yes
FTL_1097	<i>fipA</i>	Macrophage infectivity potentiator, fragment, FipA	3157.7	-1.71	1.4E-38	3157.7	-0.07	7.3E-01	no
FTL_0671	-	pantothenate kinase	12136.8	-1.70	5.1E-21	12136.8	-1.25	1.9E-11	yes
FTL_1545	-	glutamine amidotransferase subunit PdxT	1428.2	-1.68	8.0E-28	1428.2	-2.77	1.2E-68	yes
FTL_1509	-	D-alanyl-D-alanine carboxypeptidase/D-alanyl-D-alanine-endopeptidase	285.3	-1.67	8.9E-26	285.3	-1.78	2.7E-27	yes
FTL_1096	<i>dsbA</i>	Disulfide bond formation protein A / FipB	9535.1	-1.66	1.8E-23	9535.1	-0.13	5.9E-01	no
FTL_0473	-	peptide deformylase	706.3	-1.66	4.4E-14	706.3	-2.12	1.7E-21	yes
FTL_0807	-	major facilitator transporter	604.4	-1.65	4.9E-27	604.4	-1.33	1.1E-17	no
FTL_0753	-	aminoacylase	174.1	-1.64	5.2E-13	174.1	-1.59	1.4E-11	yes
FTL_1317	-	hypothetical protein	1813.3	-1.60	6.1E-25	1813.3	-1.11	3.9E-12	no
FTL_1214	-	hypothetical protein	23.1	-1.60	1.8E-05	23.1	-2.67	4.0E-10	yes
FTL_1354	-	EamA family transporter	905.6	-1.59	8.1E-19	905.6	-0.99	1.6E-07	no
FTL_0122	<i>iglF</i>	hypothetical protein	81.8	-1.59	4.9E-06	81.8	-2.21	1.4E-09	yes
FTL_1892	-	hypothetical protein	1841.5	-1.58	1.5E-23	1841.5	-1.16	8.7E-13	no
FTL_1835	<i>fsiD</i>	hypothetical protein	461.0	-1.55	6.3E-30	461.0	-1.96	6.5E-43	yes
FTL_0265	-	hypothetical protein	1790.3	-1.54	8.4E-22	1790.3	-1.12	1.6E-11	no
FTL_0881	-	hypothetical protein	5.0	-1.54	2.5E-03	5.0	-1.50	6.7E-03	yes
FTL_0808	-	bifunctional 4'-phosphopantothencysteine decarboxylase, phosphopantothencysteine synthetase	1334.3	-1.53	1.7E-16	1334.3	-0.89	6.5E-06	yes
FTL_0457	-	cold shock protein	1412.7	-1.52	2.8E-24	1412.7	-0.20	3.1E-01	no
FTL_0814	-	hypothetical protein	127.0	-1.49	7.6E-14	127.0	-1.95	4.4E-19	no
FTL_0570	-	hypothetical protein	198.6	-1.48	1.1E-09	198.6	-2.16	2.2E-17	yes
FTL_0963	-	proton-dependent oligopeptide transport (POT) family protein	591.9	-1.48	2.4E-28	591.9	-1.09	1.3E-15	no
FTL_0130	-	isopropylmalate/homocitrate/citramalate synthase family protein	646.1	-1.44	4.7E-34	646.1	-1.30	3.8E-27	yes
FTL_0425	-	Type IV pilI glycosylation protein	1391.5	-1.43	1.0E-23	1391.5	-1.20	1.6E-16	yes
FTL_0953	-	hypothetical protein	512.9	-1.43	1.3E-03	512.9	-2.05	7.8E-06	no
FTL_0131	-	branched-chain amino acid aminotransferase	2131.1	-1.41	6.5E-38	2131.1	-1.38	7.6E-36	yes
FTL_1174	-	cystathionine beta-synthase (cystein synthase)	1399.7	-1.41	8.5E-14	1399.7	-0.80	7.6E-05	yes
FTL_1135	-	-	207.5	-1.37	2.2E-05	207.5	-1.09	1.9E-03	yes
FTL_0456	<i>rpsU</i>	30S ribosomal protein S21	4080.0	-1.37	2.2E-13	4080.0	0.18	4.8E-01	no
FTL_0448	-	hypothetical protein	412.7	-1.37	9.6E-16	412.7	-0.35	7.3E-02	yes
FTL_1146	<i>gapA</i>	glyceraldehyde-3-phosphate dehydrogenase	8411.6	-1.37	9.2E-15	8411.6	-0.75	7.4E-05	yes
FTL_1454	-	-	44.1	-1.35	3.3E-06	44.1	-0.19	6.3E-01	no
FTL_1345	-	-	927.0	-1.35	6.3E-21	927.0	-0.77	3.3E-07	no
FTL_0477	<i>gcvT</i>	glycine cleavage system aminomethyltransferase T	5119.7	-1.35	5.1E-20	5119.7	-0.23	2.3E-01	yes
FTL_R0002	-	-	1001.5	-1.34	4.0E-09	1001.5	0.20	5.4E-01	no
FTL_1556	-	hypothetical protein	229.4	-1.34	2.0E-09	229.4	-0.30	2.9E-01	yes
FTL_1485	-	hypothetical protein	507.9	-1.34	4.9E-14	507.9	-0.11	6.7E-01	yes
FTL_1224	-	thioredoxin	1287.7	-1.32	1.4E-15	1287.7	-0.99	8.2E-09	yes
FTL_0765	-	VacJ lipoprotein	573.1	-1.30	6.2E-11	573.1	-0.62	1.5E-15	no
FTL_0307	<i>coaE</i>	dephospho-CoA kinase	3558.5	-1.28	2.5E-65	3558.5	0.36	5.0E-06	yes
FTL_1511	-	glycerophosphoryl diester phosphodiesterase family protein	5147.3	-1.28	1.1E-26	5147.3	-0.31	2.3E-02	yes
FTL_0759	-	hypothetical protein	43.0	-1.28	5.0E-05	43.0	-1.27	2.0E-04	no
FTL_0190	-	major facilitator transporter	426.8	-1.28	4.3E-26	426.8	-0.04	8.1E-01	no
FTL_0748	-	major facilitator transporter	639.1	-1.25	1.0E-30	639.1	-0.05	7.6E-01	no

FTL 0572	-	hypothetical protein	10162.3	-1.25	6.9E-16	10162.3	-0.27	1.6E-01	yes
FTL 0809	-	-	1340.6	-1.24	4.7E-13	1340.6	-0.91	3.5E-07	yes
FTL 1012	-	hypothetical protein	611.5	-1.23	1.3E-23	611.5	-0.47	3.8E-04	no
FTL 0361	-	LemA-like protein	2923.7	-1.22	1.8E-15	2923.7	-0.59	4.0E-04	no
FTL 1046	<i>dacB</i>	D-alanyl-D-alanine carboxypeptidase	2518.0	-1.19	2.7E-31	2518.0	-0.17	1.8E-01	no
FTL 0385	-	-	781.7	-1.19	1.2E-11	781.7	-1.10	1.3E-09	yes
FTL 1739	-	S-adenosylmethionine synthetase	1558.4	-1.19	2.4E-09	1558.4	-0.76	4.3E-04	no
FTL 0858	-	hypothetical protein	480.5	-1.18	5.3E-11	480.5	-0.25	2.7E-01	no
FTL 0147	-	hypothetical protein	327.0	-1.18	1.5E-06	327.0	-1.85	2.1E-13	yes
FTL 0129	-	2-isopropylmalate synthase	1233.4	-1.18	2.5E-13	1233.4	-1.15	3.0E-12	yes
FTL 0786	-	N-acetylglucosamine-6-phosphate deacetylase	1565.2	-1.17	4.0E-14	1565.2	-0.05	8.5E-01	yes
FTL 0384	-	-	1146.2	-1.17	1.9E-11	1146.2	-0.71	1.4E-04	yes
FTL 1727	<i>ampD</i>	N-acetyl-anhydromuramyl-L-alanine amidase	589.1	-1.16	1.2E-27	589.1	-0.55	5.8E-07	no
FTL 1936	-	periplasmic solute binding family protein	5552.8	-1.15	5.8E-17	5552.8	-0.09	6.7E-01	no
FTL 0691	-	proton-dependent oligopeptide transport (POT) family protein	6993.0	-1.15	6.7E-72	6993.0	-0.79	2.2E-34	no
FTL 1147	<i>pgk</i>	phosphoglycerate kinase	6974.7	-1.15	7.0E-11	6974.7	-0.67	5.0E-04	yes
FTL 0663	-	hypothetical protein	29.2	-1.15	1.8E-02	29.2	-1.03	6.0E-02	yes
FTL 1458	<i>secA</i>	preprotein translocase subunit SecA	7842.9	-1.15	2.4E-19	7842.9	0.13	4.7E-01	no
FTL 0094	<i>cipB</i>	CipB protein	8887.1	-1.15	2.0E-09	8887.1	-0.97	1.0E-06	no
FTL 0937	-	hypothetical protein	428.5	-1.14	2.8E-14	428.5	-0.70	1.0E-05	no
FTL 0901	-	monooxygenase family protein	345.7	-1.13	2.7E-13	345.7	-0.19	3.4E-01	no
FTL 1212	<i>leuS</i>	leucyl-tRNA synthetase	6620.4	-1.12	1.2E-22	6620.4	0.12	4.3E-01	no
FTL 0099	-	tryptophan synthase subunit beta	2085.6	-1.11	2.0E-09	2085.6	-0.63	1.8E-03	yes
FTL 1075	-	hypothetical protein	2017.7	-1.11	5.8E-27	2017.7	0.30	8.2E-03	no
FTL 1148	<i>pyk</i>	pyruvate kinase	7457.6	-1.11	2.6E-08	7457.6	-0.49	3.2E-02	no
FTL 1013	-	hypothetical protein	770.7	-1.10	5.4E-04	770.7	-0.62	9.3E-02	no
FTL 0847	<i>yajC</i>	preprotein translocase family protein	2706.4	-1.10	2.6E-27	2706.4	-0.43	7.7E-05	no
FTL 0073	-	hypothetical protein	4022.1	-1.10	8.1E-18	4022.1	-0.44	2.0E-03	no
FTL 0478	-	glycine cleavage system H protein	3192.5	-1.10	6.9E-14	3192.5	-0.33	5.1E-02	no
FTL 0573	-	hypothetical protein	3994.4	-1.09	2.7E-30	3994.4	-0.43	3.1E-05	no
FTL 0222	-	hypothetical protein	1670.0	-1.08	2.5E-14	1670.0	-0.09	6.7E-01	yes
FTL 1360	<i>rpsU</i>	30S ribosomal protein S21	632.0	-1.08	2.0E-11	632.0	-0.04	8.9E-01	no
FTL 0098	<i>trpA</i>	tryptophan synthase subunit alpha	1172.9	-1.07	4.7E-08	1172.9	-0.66	2.2E-03	no
FTL 1344	-	hypothetical protein	94.9	-1.06	3.2E-06	94.9	0.38	1.4E-01	no
FTL 1094	-	-	217.1	-1.06	2.2E-04	217.1	-1.45	1.3E-06	no
FTL 0902	-	oxidoreductase	143.0	-1.06	1.4E-07	143.0	-0.31	2.0E-01	no
FTL 1223	-	hypothetical protein	584.5	-1.05	4.5E-07	584.5	-0.87	8.2E-05	no
FTL 0681	<i>potG</i>	ATP-binding cassette putrescine uptake system, ATP-binding protein	6004.2	-1.05	1.3E-17	6004.2	0.15	3.7E-01	no
FTL 1678	-	hypothetical protein	2661.2	-1.05	1.3E-04	2661.2	-1.66	2.0E-09	yes
FTL 1312	-	S-transferase	447.5	-1.04	1.2E-09	447.5	-0.92	3.0E-07	no
FTL 1494	-	hypothetical protein	2056.9	-1.04	8.9E-23	2056.9	0.04	8.0E-01	no
FTL 1045	-	lipoprotein	914.6	-1.04	1.5E-12	914.6	-0.34	4.3E-02	no
FTL 1269	-	-	14.7	-1.04	1.3E-02	14.7	-2.44	1.5E-07	no
FTL 0360	-	heat shock protein HtpX	2944.2	-1.03	1.6E-13	2944.2	-0.63	2.1E-05	no
FTL 1081	-	hypothetical protein	7.4	-1.03	4.2E-02	7.4	-1.44	8.3E-03	no
FTL 1015	-	AhpC/TSA family protein	6835.9	-1.02	7.0E-22	6835.9	-0.65	5.7E-09	no
FTL 1095	-	-	95.4	-1.02	5.8E-04	95.4	-1.34	2.6E-05	no
FTL 0834	-	rhodanese-like family protein	1931.1	-1.02	3.5E-35	1931.1	-0.30	9.1E-04	yes
FTL 1227	-	-	1334.1	-1.02	1.6E-14	1334.1	-1.00	9.6E-14	yes
FTL 0571	-	hypothetical protein	2277.5	-1.01	5.0E-42	2277.5	-0.21	1.6E-02	no
FTL 1901	-	hypothetical protein	138.7	-1.01	4.6E-06	138.7	-1.45	6.5E-10	yes
FTL R0044	<i>ffs</i>	4.5 S RNA	2885.6	-1.01	9.2E-05	2885.6	-0.33	3.2E-01	no
FTL 0466	-	soluble lytic murein transglycosylase	1555.4	-1.01	1.5E-21	1555.4	0.04	7.9E-01	no
FTL 0295	-	acetyl-CoA carboxylase carboxyltransferase subunit alpha	9506.9	-1.01	3.0E-17	9506.9	0.25	8.3E-02	yes
FTL 1568	-	LysR family transcriptional regulator	97.4	-1.01	8.7E-05	97.4	-0.95	6.0E-04	no
FTL 1145	-	transketolase	6600.6	-1.00	2.9E-14	6600.6	-0.03	8.8E-01	no
FTL 1056	-	-	33.7	-0.95	9.6E-04	33.7	-1.49	8.0E-06	yes
FTL 1092	-	-	33.4	-0.95	1.3E-03	33.4	-1.31	7.6E-05	yes
FTL 0379	-	methionine sulfoxide reductase B	360.0	-0.90	1.4E-11	360.0	-1.42	3.6E-24	yes
FTL 1508	-	-	13.2	-0.89	4.1E-02	13.2	-1.43	3.1E-03	yes
FTL 0115	<i>pdpE</i>	hypothetical protein	109.1	-0.87	8.8E-03	109.1	-2.19	2.3E-10	yes
FTL 0925	-	proton-dependent oligopeptide transport (POT) family protein	33.1	-0.86	4.0E-02	33.1	-1.09	1.7E-02	yes
FTL 0880	-	hypothetical protein	135.1	-0.85	2.6E-04	135.1	-1.42	1.1E-08	yes
FTL 1640	-	amino acid transporter protein, fragment	1004.5	-0.78	2.3E-15	1004.5	-1.25	1.6E-35	yes
FTL 1503	<i>dgt</i>	deoxyguanosinetriphosphate triphosphohydrolase	1223.7	-0.76	7.6E-07	1223.7	-0.05	1.6E-11	yes
FTL 1242	-	ThiI/PfpI family protein	487.2	-0.74	2.9E-08	487.2	-1.11	5.3E-16	yes
FTL 0155	-	-	172.7	-0.73	6.0E-03	172.7	-1.40	5.5E-07	yes
FTL 1196	-	hypothetical protein	36.2	-0.73	2.9E-02	36.2	-1.45	9.4E-05	yes
FTL 0952	-	hypothetical protein	14.9	-0.69	1.0E-01	14.9	-1.13	1.6E-02	no
FTL 0061	-	hypothetical protein	50.6	-0.67	7.4E-02	50.6	-1.46	2.2E-04	no
FTL 0161	-	-	449.0	-0.58	1.3E-02	449.0	-1.05	1.6E-05	yes
FTL 1226	-	-	291.8	-0.54	4.4E-03	291.8	-1.15	6.1E-09	yes
FTL 0160	-	LamB/YcsF family protein	437.6	-0.22	4.5E-01	437.6	-1.02	2.7E-04	no
FTL 1921	-	ABC transporter ATP-binding protein	182.6	0.00	9.9E-01	182.6	-1.34	4.6E-11	no
FTL 0812	-	-	35.8	0.12	7.2E-01	35.8	-1.11	7.7E-04	no
FTL 1068	<i>truA</i>	tRNA pseudouridine synthase A	297.4	0.12	4.0E-01	297.4	-1.13	8.8E-16	no
FTL 0159	-	hydrolase subunit	322.2	0.36	1.9E-01	322.2	-1.45	8.1E-08	no
FTL 0158	<i>acpA</i>	acid phosphatase, phospholipase C	2420.9	1.00	6.8E-14	2420.9	-0.33	3.6E-02	no
FTL 1322	-	-	20.3	1.00	3.6E-03	20.3	-0.30	5.8E-01	no
FTL 1465	-	hypothetical protein	109.6	1.00	9.6E-08	109.6	0.13	6.7E-01	no
FTL 0018	<i>isfU1</i>	transposase	590.1	1.01	4.9E-06	590.1	0.24	4.2E-01	yes
FTL 1600	-	periplasmic L-asparaginase II	170.3	1.01	4.6E-06	170.3	-0.53	5.2E-02	yes
FTL 1032	-	ribosomal-protein-alanine acetyltransferase	4.7	1.01	5.0E-02	4.7	0.30	6.9E-01	no
FTL 0563	-	-	8.7	1.02	3.1E-02	8.7	-0.82	1.7E-01	no
FTL 0006	-	indolepyruvate decarboxylase	152.9	1.03	1.0E-06	152.9	-0.06	8.6E-01	no
FTL 0272	-	diaminopimelate decarboxylase	73.9	1.03	1.2E-04	73.9	0.00	1.0E+00	no
FTL 1008	-	-	53.3	1.03	3.1E-06	53.3	0.36	2.3E-01	yes
FTL 0184	-	hypothetical protein	117.0	1.03	6.3E-07	117.0	-0.05	8.8E-01	no
FTL 0781	-	-	80.8	1.03	9.2E-07	80.8	-0.32	2.8E-01	no
FTL 1698	-	hypothetical protein	17.9	1.03	4.7E-03	17.9	0.00	1.0E+00	no
FTL 1651	-	-	15.1	1.04	4.2E-03	15.1	-0.21	7.3E-01	yes
FTL 1953	-	-	7.0	1.04	2.7E-02	7.0	-0.50	4.4E-01	no
FTL 1559	-	-	102.7	1.05	6.5E-09	102.7	-0.17	5.5E-01	no
FTL 1730	-	hypothetical protein	6.1	1.05	3.1E-02	6.1	0.19	8.1E-01	no
FTL 0003	-	hypothetical protein	6.2	1.05	3.3E-02	6.2	-0.43	5.4E-01	no
FTL 1504	<i>kotG</i>	peroxidase/catalase	56629.7	1.06	8.3E-06	56629.7	0.48	8.5E-02	yes
FTL 0103	-	hypothetical protein	1456.1	1.06	3.2E-09	1456.1	0.20	3.9E-01	no
FTL 1495	-	cysteine/glutathione ABC transporter membrane/ATP-binding protein	1022.8	1.06	9.1E-13	1022.8	0.22	2.6E-01	no
FTL 1281	-	hypothetical protein	86.3	1.06	2.1E-05	86.3	0.08	8.6E-01	no
FTL 1922	-	YggT family protein	481.7	1.07	9.3E-11	481.7	-0.31	1.4E-01	no
FTL 1870	-	-	23.4	1.07	1.7E-03	23.4	-0.04	9.5E-01	no
FTL 0134	-	hypothetical protein	14.7	1.07	5.1E-03	14.7	-0.34	5.6E-01	no
FTL 1715	<i>groES</i>	co-chaperonin GroES	5073.4	1.07	1.2E-05	5073.4	-0.18	6.0E-01	no
FTL 1555	-	hypothetical protein	164.5	1.08	1.3E-10	164.5	0.21	3.8E-01	no
FTL 1011	-	-	2.7	1.09	4.5E-02	2.7	-0.09	9.1E-01	yes
FTL 0621	-	-	552.5	1.09	1.8E-15	552.5	0.55	3.1E-04	no
FTL 0719	-	hypothetical protein	169.6	1.09	1.2E-05	169.6	-0.03	9.4E-01	no
FTL 0976	-	hypothetical protein	278.3	1.11	1.9E-09	278.3	0.03	9.3E-01	no
FTL 1776	-	hypothetical protein	281.7	1.12	4.6E-05	281.7	-0.70	2.9E-02	yes
FTL 0544	<i>ppk</i>	polyphosphate kinase 2	1045.7	1.12	2.4E-09	1045.7	0.63	2.2E-03	yes
FTL 0172	<i>murC</i>	UDP-N-acetylmuramate-L-alanine ligase	965.8	1.12	1.3E-21	965.8	-0.05	7.9E-01	no

FTL 1260	-	-	7.1	1.13	1.3E-02	7.1	0.46	4.6E-01	no
FTL 0484	<i>pgm</i>	phosphoglucosylase	2590.5	1.14	1.6E-17	2590.5	0.62	1.6E-05	no
FTL 0773	-	-	2.6	1.14	3.3E-02	2.6	0.21	7.9E-01	no
FTL 1010	-	-	20.7	1.14	2.7E-03	20.7	-0.09	9.0E-01	yes
FTL 1502	-	major facilitator transporter	32.3	1.15	1.7E-03	32.3	-0.50	3.2E-01	no
FTL 1156	-	hypothetical protein	9.0	1.16	2.3E-02	9.0	-0.70	2.8E-01	no
FTL 0162	-	hypothetical protein	51.8	1.16	9.4E-05	51.8	-0.44	2.8E-01	no
FTL 1770	-	Type IV pili nucleotide-binding protein	95.9	1.16	1.6E-05	95.9	0.10	8.3E-01	no
FTL 0957	<i>blaA</i>	Beta-lactamase class A	213.1	1.17	5.0E-10	213.1	0.30	2.2E-01	no
FTL 0038	<i>emrA2</i>	HlyD family secretion protein	1629.7	1.17	2.2E-05	1629.7	-0.14	7.5E-01	no
FTL 0485	<i>glgC</i>	glucose-1-phosphate adenyltransferase	3934.1	1.17	3.2E-11	3934.1	0.75	7.4E-05	yes
FTL 1289	-	hypothetical protein	3.1	1.19	2.8E-02	3.1	-0.17	8.3E-01	no
FTL 1367	-	hypothetical protein	91.9	1.19	7.0E-05	91.9	-0.41	3.1E-01	no
FTL 0056	-	NADH dehydrogenase	590.3	1.19	1.8E-11	590.3	-0.43	4.5E-02	yes
FTL 0710	-	chologlycine hydrolase family protein	17.4	1.19	6.7E-04	17.4	-0.17	7.8E-01	no
FTL 1632	-	hypothetical protein	25.9	1.20	2.8E-04	25.9	-0.06	9.1E-01	no
FTL 0163	-	MFS transporter	11.7	1.21	6.6E-03	11.7	-0.56	3.7E-01	no
FTL 1877	-	-	56.3	1.21	1.6E-06	56.3	-0.48	1.8E-01	no
FTL 1292	-	hypothetical protein	9.0	1.21	9.9E-03	9.0	0.34	6.2E-01	no
FTL 1758	-	hypothetical protein	53.3	1.22	5.7E-07	53.3	-0.07	8.8E-01	no
FTL 0347	-	hypothetical protein	148.7	1.22	5.5E-16	148.7	0.10	6.9E-01	no
FTL 1948	-	major facilitator transporter	247.0	1.22	4.2E-10	247.0	-0.16	5.8E-01	yes
FTL 0970	-	L-lactate dehydrogenase	89.6	1.22	6.0E-09	89.6	-0.03	9.4E-01	no
FTL 0751	-	lipoprotein	375.7	1.22	1.9E-26	375.7	-0.06	7.6E-01	no
FTL 0486	<i>glgA</i>	glycogen synthase	3201.6	1.22	5.5E-17	3201.6	0.64	4.7E-05	yes
FTL 1691	-	hypothetical protein	55.2	1.22	1.2E-07	55.2	0.10	8.0E-01	yes
FTL 1778	-	-	160.5	1.23	4.2E-07	160.5	-0.18	6.2E-01	no
FTL 0860	-	hypothetical protein	114.7	1.23	4.5E-10	114.7	-0.33	2.3E-01	yes
FTL 0450	<i>psd</i>	phosphatidylserine decarboxylase	1364.7	1.23	2.6E-10	1364.7	-0.04	8.9E-01	yes
FTL 1950	-	hypothetical protein	216.2	1.24	3.4E-14	216.2	0.40	4.3E-02	no
FTL 1347	-	hypothetical protein	58.4	1.26	4.9E-06	58.4	-0.33	4.2E-01	no
FTL 0971	-	FAD linked oxidase	169.7	1.26	1.4E-11	169.7	-0.12	6.8E-01	no
FTL 1927	-	-	45.9	1.27	1.5E-06	45.9	-0.52	1.7E-01	no
FTL 0791	-	hypothetical protein	12.6	1.28	9.7E-04	12.6	0.03	9.7E-01	no
FTL 0365	-	-	120.1	1.28	1.5E-10	120.1	0.17	5.8E-01	yes
FTL 1916	-	competence-like protein	109.1	1.29	1.2E-12	109.1	0.13	6.6E-01	no
FTL 0051	-	hypothetical protein	69.2	1.29	4.9E-07	69.2	0.13	7.5E-01	no
FTL 0044	-	transglutaminase	284.2	1.29	1.9E-17	284.2	0.46	9.0E-03	no
FTL 1054	-	putative alpha-xylosidase	146.1	1.30	5.6E-09	146.1	0.00	1.0E+00	yes
FTL 1945	-	hypothetical protein	115.9	1.30	5.4E-12	115.9	-0.55	2.6E-02	no
FTL 1777	-	-	95.1	1.31	1.6E-07	95.1	-0.44	1.9E-01	no
FTL 1368	-	hypothetical protein	32.9	1.31	5.1E-04	32.9	-0.90	6.1E-02	no
FTL 1175	-	-	18.2	1.32	6.2E-04	18.2	0.05	9.4E-01	no
FTL 0944	-	-	14.9	1.33	8.9E-04	14.9	-0.46	4.3E-01	no
FTL 1326	-	hypothetical protein	54.1	1.33	7.1E-07	54.1	0.46	1.9E-01	no
FTL 0344	-	hypothetical protein	23.1	1.33	1.3E-04	23.1	0.24	6.6E-01	no
FTL 0869	-	hypothetical protein	2.0	1.33	1.3E-02	2.0	0.32	6.7E-01	no
FTL 0735	-	-	10.7	1.33	1.9E-03	10.7	0.02	9.8E-01	yes
FTL 0842	-	transposase	10.9	1.34	1.2E-03	10.9	0.52	3.6E-01	no
FTL 1262	-	chorismate binding family protein	858.7	1.35	3.6E-10	858.7	0.21	4.8E-01	no
FTL 1565	-	-	53.1	1.35	1.2E-07	53.1	-0.25	5.3E-01	no
FTL 0366	-	-	28.5	1.35	2.7E-05	28.5	-0.04	9.5E-01	no
FTL 1373	-	hypothetical protein	69.5	1.36	6.7E-08	69.5	-0.52	1.4E-01	no
FTL 1261	-	anthranilate synthase component II	271.9	1.36	1.7E-26	271.9	0.17	3.6E-01	no
FTL 1690	-	hypothetical protein	64.3	1.36	1.2E-07	64.3	-0.45	2.2E-01	yes
FTL 1677	-	-	4.7	1.36	8.9E-03	4.7	-0.07	9.3E-01	no
FTL 0934	-	hypothetical protein	13.6	1.37	1.1E-03	13.6	0.06	9.3E-01	no
FTL 1320	-	hypothetical protein	13.2	1.38	2.6E-04	13.2	-0.35	5.7E-01	no
FTL 0171	-	tetrapyrrole methyltransferase family protein	370.1	1.40	1.3E-17	370.1	0.15	5.4E-01	no
FTL 0037	-	hypothetical protein	649.4	1.40	4.3E-11	649.4	-0.05	9.0E-01	no
FTL 0641	-	hypothetical protein	11.5	1.41	8.4E-04	11.5	0.55	3.4E-01	no
FTL 0973	-	-	147.2	1.42	4.0E-14	147.2	-0.11	7.3E-01	no
FTL 0432	-	hypothetical protein	92.2	1.42	3.5E-11	92.2	0.19	5.6E-01	no
FTL 0972	-	-	133.2	1.43	1.0E-12	133.2	0.22	4.6E-01	no
FTL 1752	-	helicase	114.3	1.44	1.9E-19	114.3	-0.24	3.3E-01	no
FTL 0826	-	-	46.8	1.46	1.2E-08	46.8	-0.06	8.9E-01	no
FTL 1682	-	hypothetical protein	7.0	1.48	1.8E-03	7.0	0.50	4.4E-01	no
FTL 1466	-	major facilitator transporter	55.4	1.48	9.2E-09	55.4	-0.15	7.3E-01	no
FTL 1857	-	-	28.3	1.49	3.4E-04	28.3	-0.17	8.0E-01	no
FTL 0997	-	hypothetical protein	16.5	1.50	1.4E-04	16.5	-0.20	7.6E-01	no
FTL 0819	-	-	12.4	1.50	5.3E-04	12.4	-0.32	6.4E-01	no
FTL 0528	-	Type III restriction enzyme	601.1	1.50	9.9E-31	601.1	0.17	3.4E-01	yes
FTL 1844	-	secretion protein	49.2	1.51	2.9E-10	49.2	0.40	2.3E-01	no
FTL 1378	-	-	71.5	1.52	2.0E-08	71.5	-0.07	8.9E-01	yes
FTL 1321	-	hypothetical protein	12.0	1.54	3.3E-04	12.0	-0.09	9.1E-01	no
FTL 1629	-	hypothetical protein	63.4	1.54	6.9E-09	63.4	-0.62	8.3E-02	no
FTL 1564	-	-	20.9	1.55	2.4E-05	20.9	-0.36	5.3E-01	no
FTL 1053	-	putative alpha-xylosidase	40.1	1.56	9.8E-07	40.1	0.00	9.9E-01	yes
FTL 0065	-	-	40.6	1.59	2.7E-08	40.6	-0.20	6.7E-01	yes
FTL 0559	-	hypothetical protein	23.9	1.59	2.7E-07	23.9	-0.36	4.6E-01	no
FTL 0558	-	oxidoreductase	39.4	1.63	8.4E-10	39.4	-0.02	9.7E-01	no
FTL 0409	-	purine/pyrimidine phosphoribosyl transferase family protein	124.9	1.64	6.9E-13	124.9	0.39	2.0E-01	no
FTL 1470	-	major facilitator transporter	56.5	1.66	4.5E-13	56.5	-0.10	8.2E-01	no
FTL 0636	-	NADH oxidase	82.2	1.66	3.5E-12	82.2	0.46	1.3E-01	no
FTL 0415	-	hypothetical protein	43.0	1.68	4.5E-11	43.0	-0.21	6.3E-01	no
FTL 0576	-	hypothetical protein	23.3	1.68	2.5E-07	23.3	0.11	8.6E-01	yes
FTL 0055	-	hypothetical protein	45.1	1.69	7.1E-09	45.1	0.04	9.4E-01	no
FTL 1562	-	-	220.8	1.72	5.3E-18	220.8	0.41	1.0E-01	no
FTL 1769	-	-	11.2	1.74	1.5E-05	11.2	0.49	3.9E-01	no
FTL 0050	-	hypothetical protein	13.8	1.75	1.0E-05	13.8	0.54	3.2E-01	no
FTL 0889	-	hypothetical protein	26.7	1.76	5.6E-08	26.7	0.31	5.2E-01	no
FTL 1314	-	hypothetical protein	37.6	1.76	4.3E-08	37.6	0.44	3.2E-01	no
FTL 1379	-	-	159.4	1.78	3.4E-24	159.4	-0.62	7.8E-03	yes
FTL 1563	-	-	99.3	1.80	2.4E-13	99.3	0.56	6.7E-02	no
FTL 1814	-	-	69.6	1.80	1.7E-09	69.6	0.08	8.8E-01	no
FTL 0577	-	hypothetical protein	12.1	1.81	3.8E-05	12.1	0.31	6.6E-01	yes
FTL 0998	-	hypothetical protein	8.9	1.82	4.3E-05	8.9	0.53	4.0E-01	no
FTL 0734	-	-	60.4	1.90	3.0E-16	60.4	-0.19	6.4E-01	yes
FTL 0527	-	endonuclease	34.9	1.91	2.7E-11	34.9	0.15	7.7E-01	no
FTL 1377	-	hypothetical protein	45.3	1.93	3.2E-12	45.3	0.13	8.0E-01	no
FTL 1052	-	putative glycosidase	5.5	1.94	6.9E-05	5.5	0.24	7.6E-01	yes
FTL 1675	-	-	15.5	1.94	2.1E-07	15.5	-0.11	8.8E-01	no
FTL 1380	-	-	25.0	1.97	1.8E-10	25.0	-0.05	9.3E-01	no
FTL 1853	-	lipoprotein	30.4	2.05	3.2E-13	30.4	0.12	8.1E-01	no
FTL 1628	-	hypothetical protein	55.9	2.06	4.5E-11	55.9	-0.10	8.6E-01	no
FTL 0352	-	hypothetical protein	11.6	2.06	9.2E-07	11.6	0.19	8.0E-01	no
FTL 0529	-	uracil-DNA glycosylase	168.9	2.17	3.0E-34	168.9	0.20	4.6E-01	yes
FTL 1103	-	-	34.3	2.22	7.5E-14	34.3	0.39	3.8E-01	yes
FTL 0340	-	hypothetical protein	11.0	2.29	1.6E-07	11.0	0.14	8.6E-01	no

*Previous MglA regulon based on Brotcck et al., 2006 and Charity et al., 2007

Table S3: Data collection and refinement statistics

	<i>Ft</i> (MgIA-SspA)- ppGpp-PigR complex
Data collection	
PDB code	6WEG
Space group	P2 ₁ 2 ₁ 2 ₁
Cell dimensions	
<i>a</i> , <i>b</i> , <i>c</i> (Å)	65.75, 113.56, 141.07
α , β , γ (°)	90.0, 90.0, 90.0
Resolution (Å)	88.46 (2.95)*
<i>R</i> _{sym}	0.091 (1.380)
<i>R</i> _{pim}	0.063 (0.950)
<i>I</i> / σ <i>I</i>	7.3 (1.2)
Completeness (%)	98.1 (99.2)
Redundancy	2.9 (2.9)
CC(1/2)	0.997 (0.338)
Refinement	
Resolution (Å)	88.46-2.95
No. reflections	22055
<i>R</i> _{work} / <i>R</i> _{free}	22.5/28.6
No. atoms	
Protein	6535
ppGpp/Mg ²⁺	74
Water	0
Ramachandran analyses	
Favored (%)	89.1
Disallowed (%)	0.0
R.m.s. deviations	
Bond lengths (Å)	0.004
Bond angles (°)	0.805

*Values in parentheses are for highest-resolution shell.