Structural characterization of bacterial proteins involved in antibiotic resistance and peptidoglycan biosynthesis

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Appendix

1. Nucleotide sequences of *ylmE*

>Wild type *ylmE* (SCO2080) with 0 flanks (2232970 to 2233689)

ATGACGGACCGTAAGCACGAACTCGCCGCGAACCTGGCGAAAGTGGAACAGCGCATCACCGACG
CGTGCGCGGCCGCGGGCCGCCCGCGCCAGGACGTGACCCTCATCGTGGTCACCAAGACCTACC
CGGCGGACGATGTGCGCATTCTCTCGGAACTCGGGGTGCGCCACGTCGCGGAGAACCGCGACCA
GGACGCGGCGCCCAAGGCCGCCGCCTGCTCGGATCTGCCGCTTTCCTGGCATTTCGTCGGACAG
TTGCAGACGAACAAGGTGCGTTCCGTGGTCGGTTACGCGGATGTCGTGCAGTCCGTCGACCGGG
CCCGGCTGGTCACGGCGCTGTCGAAGGAGGCCGTACGGGCCGGACGTGAGGTGGGCTGTCTCC
TCCAGGTGGCCCTCGACGCGGAGGAGGGCGGGCGCGGGGAGCGCGGCGGTGTCCCGCCCGCC
GGAATCGAAGAGTTGGCCGACCTGGTCGCCGGATCGGAGGGGCTGCGCCTCGACGGACTGATGA
CCGTGGCCCCGCTCAGCGGCGAGTACGCCGGACGCCAACAGGCGGCGTTCGAGCACCTCATGG
ATTTGTCGACCCGCGTGCGCCGGACCCATCCGGCTGCGAACATGGTCTCCGCGGGGATGAGTGC
GGACCTCGAACAGGCCGTGGCCGCCGGAGCGACACATGTACGCGTCGGCACTGCGGTACTCGGA
GTCCGACCCAGGCTCGGGTAA

>Sequence optimized *ylmE* (SCO2080) for expression in *E. coli*

CCATGGTGATTGGTCAGCGTGATACCGTTAATGGTGCACATTTTGGTTTTACCGATCGTTGGGGTG
GTGTTAGCGCAGTTCCGTATGAAGAACTGAATCTGGGTGGTGCAGTTGGTGATGATCCGGGTGCA
GTTACCGCAAATCGTGAACTGGCAGCAAAAAGCCTGGGTGTTGATCCGGCACGTGTTGTTTGGAT
GAATCAGGTTCATGGTGCAGATGTTGCCGTTGTTGATGCACCGTGGGGTGATCGTCCGGTTCCGC
GTGTTGATGCGGTTGTTACCGCAGAACGTGGTCTGGCACTGGCAGTTCTGACCGCAGATTGTGTT
CCGGTTCTGCTGGCAGATCCGGTTAGCGGTGTTGCAGCAGCAGCACATGCAGGTCGTCCGGGTC
TGGTTGCCGGTGTGGTTCCGGCAGCAGTTCGTGCAATGGCAGAACTGGGTGCAGATCCTGCCCG
TATTGTTGCACGTACCGGTCCGGCAGTTTGTGGTCGTTGTTATGAAGTTCCGGAAGAAATGCGTGC
AGAAGTTGCAGCCGTTGAACCGGCAGCATATGCAGAAACCGGTTGGGGTACACCGGCACTGGAT
GTTTCAGCCGGTGTTCATGCACAGCTGGAACGTCTGGGTGTGCATGATCGTGCCCAGAGTCCGGT
TTGTACCCGTGAAAGCGCAGATCATTTTAGCTATCGTCGTGATCGTACCACCGGTCGTCTGGCAGG
TTATGTTTGGCTGGATTAACTCGAG

2. Nucleotide sequences of *ftsZ*

>Wild type *ftsZ* (SCO2082) with 0 flanks (2234421 to 2235620)

GTGGCAGCACCGCAGAACTACCTCGCAGTCATCAAAGTCATCGGTGTCGGCGGCGGTGGTGTCA
ATGCCATCAACCGGATGATCGAGGTCGGTCTCAAGGGCGTCGAGTTCATCGCCATCAACACCGAC
GCGCAGGCGCTGTTGATGAGCGACGCCGACGTCAAGCTCGACGTCGGCCGCGAACTCACCCGCG
GACTCGGCGCCGGAGCCAACCCGGCCGTAGGCCGCAAGGCCGCCGAGGACCACCGCGAGGAGA
TCGAGGAGGTCCTCAAGGGGGCCGACATGGTCTTCGTGACAGCCGGTGAAGGCGGCGGCACCG
GCACCGGCGGCGCGCCCGTCGTGGCCAACATCGCCCGCTCGCTGGGCGCCCTCACCATCGGCG
TGGTCACCCGCCCGTTCACCTTCGAGGGACGGCGCCGGGCCAACCAGGCCGAGGACGGCATCG
CGGAACTCCGCGAAGAGGTCGACACCCTCATCGTCATCCCCAACGACCGGCTGCTGTCCATCTCG
GACCGCCAGGTCAGCGTGCTCGACGCGTTCAAGTCCGCCGACCAGGTGCTGCTCTCCGGTGTGC
AGGGCATCACCGACCTCATCACCACCCCCGGCCTGATCAACCTGGACTTCGCCGACGTGAAGTCG
GTCATGTCCGAGGCGGGTTCGGCCCTCATGGGCATCGGCTCCGCCCGCGGCGACGACCGCGCG
GTGGCCGCCGCCGAGATGGCGATCTCCTCGCCGCTGCTCGAGGCGTCCATCGACGGCGCCCGC
GGCGTGCTGCTCTCCATCTCCGGCGGCTCCGACCTCGGCCTGTTCGAGATCAACGAGGCCGCCC
AGCTGGTCAGCGAGGCCGCGCACCCCGAGGCCAACATCATCTTCGGCGCGGTCATCGACGACGC
CCTCGGCGACGAGGTGCGGGTCACCGTGATCGCGGCCGGTTTCGACGGGGGCCAGCCGCCGTC
CAAGCGGGACAACGTCCTCGGGTCCTCCTCGGCCAAGCGCGAGGAGCCCACCCCGGCCCGGCC
GTCCGAGAGCCGTCCGTCCTTCGGCTCGCTCGGCAGCGTCAAGCCGAAGGAGGAGCCGGAGCC
GGCCCCCGTGCCGGAGCCGGTCGCCGACCTGCCGGTCTCCCCGCCGCCGGTCCCGCCGTCGCG
GACCTACTCGGACAGCGCGGCCGAGGAACTGGACGTGCCGGACTTCCTGAAGTGA

>Sequence optimized *ftsZ* (SCO2082) for expression in *E. coli*

CCATGGTTGCAGCACCGCAGAATTATCTGGCAGTTATTAAAGTTATTGGTGTGGGTGGTGGTGGC
GTTAATGCAATTAATCGTATGATTGAAGTGGGTCTGAAAGGCGTTGAATTTATTGCCATTAATACCG
ATGCACAGGCACTGCTGATGAGTGATGCAGATGTTAAACTGGATGTTGGTCGTGAACTGACCCGT
GGTCTGGGTGCCGGTGCAAATCCGGCAGTTGGTCGTAAAGCAGCCGAAGATCATCGTGAAGAAAT
TGAAGAAGTGCTGAAAGGGGCAGATATGGTTTTTGTTACCGCAGGCGAAGGTGGTGGTACAGGCA
CCGGTGGTGCACCGGTTGTTGCAAATATTGCACGTAGCCTGGGTGCACTGACCATTGGTGTTGTT
ACCCGTCCGTTTACCTTTGAAGGTCGTCGTCGTGCAAATCAGGCCGAAGATGGTATTGCAGAACTG
CGCGAAGAAGTTGATACCCTGATTGTTATTCCGAATGATCGTCTGCTGAGCATTAGCGATCGTCAG
GTTAGCGTTCTGGATGCATTTAAAAGCGCAGATCAGGTGCTGCTGAGCGGTGTTCAGGGTATTACC
GATCTGATTACCACACCGGGTCTGATTAATCTGGATTTTGCCGATGTTAAAAGCGTTATGAGCGAA
GCAGGTAGCGCACTGATGGGTATTGGTAGTGCACGTGGTGATGATCGTGCAGTTGCAGCAGCAGA
AATGGCAATTAGCAGTCCGCTGCTGGAAGCAAGCATTGATGGTGCCCGTGGTGTTCTGCTGTCAA
TTAGCGGTGGTAGCGATCTGGGTCTGTTTGAAATCAATGAAGCAGCACAGCTGGTTAGCGAAGCC
GCACATCCGGAAGCAAATATCATTTTTGGTGCCGTTATTGATGATGCCCTGGGTGATGAAGTTCGT
GTTACCGTTATTGCAGCAGGTTTTGATGGTGGTCAGCCTCCGAGCAAACGTGATAATGTTCTGGGT
AGCAGCAGCGCAAAACGTGAAGAACCGACACCGGCACGTCCGAGCGAAAGCCGTCCGAGCTTTG
GTTCACTGGGTAGCGTTAAACCGAAAGAAGAACCGGAACCAGCACCGGTTCCAGAACCTGTTGCC
GATCTGCCGGTTAGTCCGCCTCCGGTTCCGCCTAGCCGTACCTATAGCGATAGCGCAGCGGAAGA
ACTGGACGTTCCGGATTTTCTGAAATAACTCGAG

3. YlmE biochemical characterization

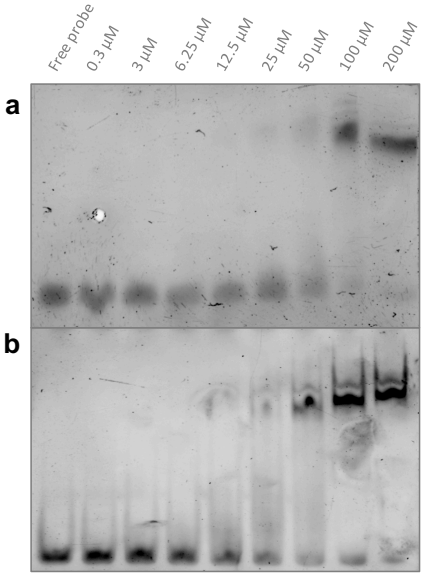

Figure A3.1. YlmE binding to DNA. *Electrophoretic Mobility Shift Assays (EMSA's) to test YlmE binding to (a) ss-[Cy5]drenagB, (b) ds-[Cy5]drenagB. Each DNA substrate was used at a concentration of 0.2 µM in a final volume of 12 µL. YlmE concentration varied between 0 and 200 µM. The electrophoresis was done using TAE gels and imaged by detecting the fluorescent signal of the Cy5 label.*

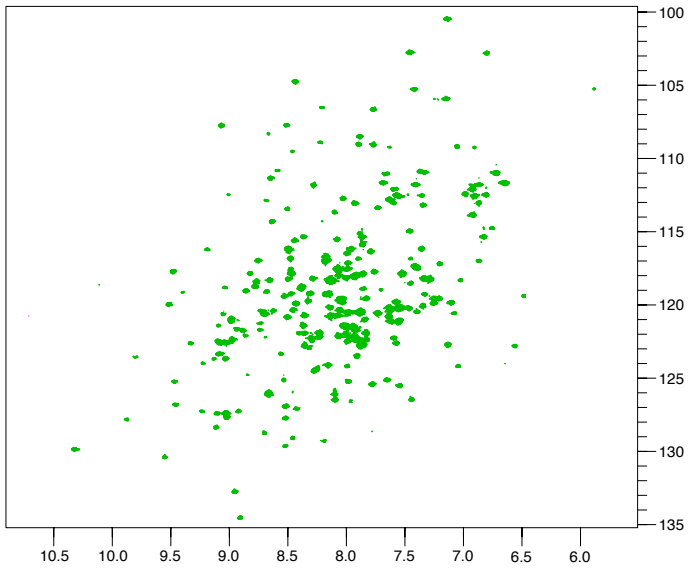

Figure A3.2. *^{1}H-^{15}N-HSQC-NMR spectrum of ^{15}N-labelled NHis-YlmE. The chemical shifts of ^{1}H and ^{15}N atoms are on the x- and y-axis, respectively.*

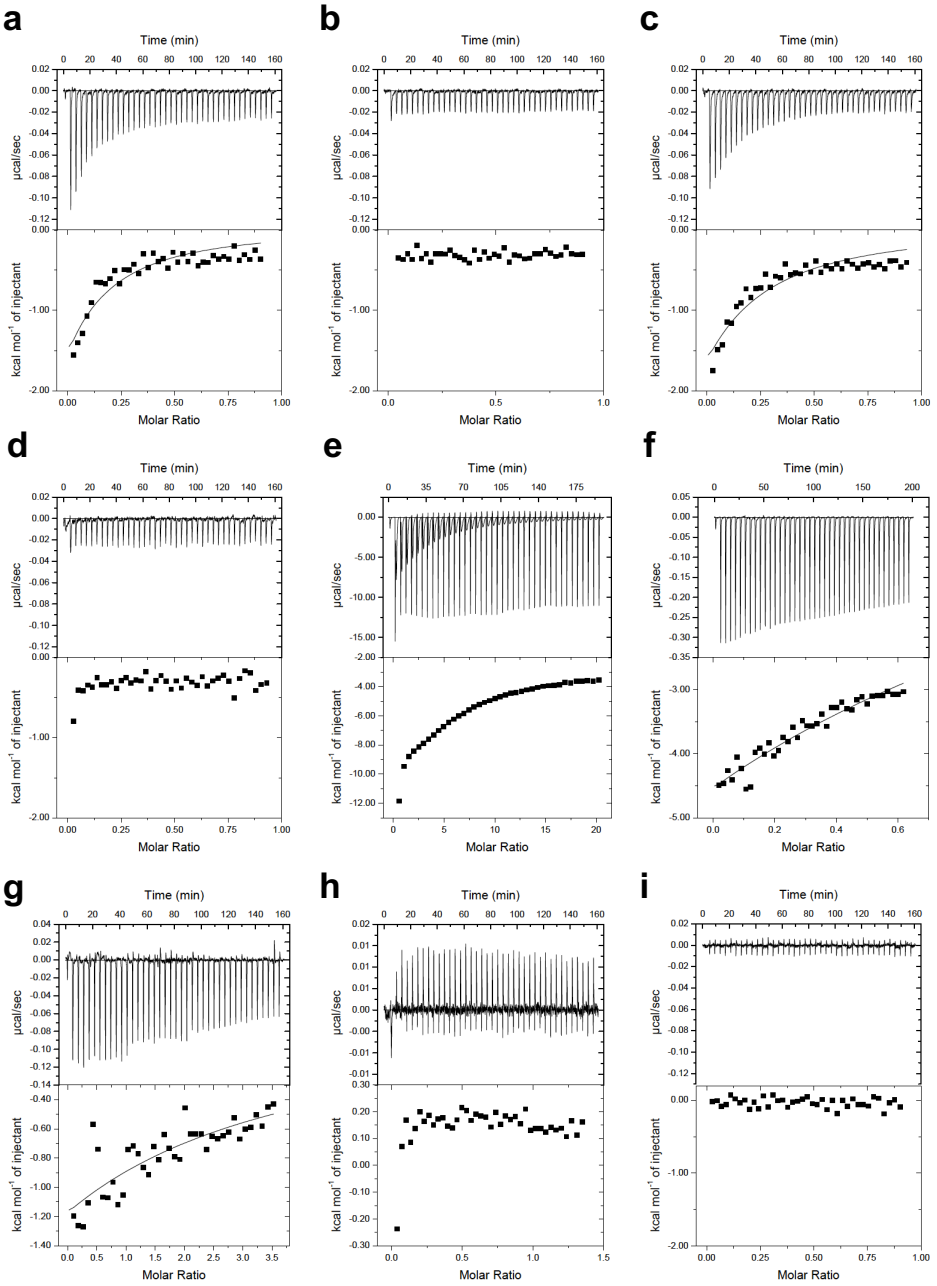

Figure A3.3. Calorimetric interaction study of YlmE with cell division proteins FtsZ and SsgB. *(a) YlmE titration into monomeric FtsZ, and control titration of YlmE into ITC buffer (b). (c) Titration of Alr into monomeric FtsZ, and control dilution experiment of Alr into ITC buffer (d). (e) FtsZ polymerization was induced by titrating GTP into FtsZ, and (f) binding of YlmE to FtsZ protofilaments was followed by titrating YlmE directly in the sample cell after GTP. (g) YlmE titration into SsgB. (h) SsgB was titrated into monomeric FtsZ, and the dilution of SsgB into ITC buffer was also checked (i).*

4. Full list of identified proteins from pull-down experiments

Table A4.1. Pull-down assay 1.

The reported numbers indicate the total spectrum counts for each protein.

Identified Proteins	SCOXXXX	Accession Number (Code_STRCO)	Alr	FtsZ	BlaC	YlmE
Dihydrolipoyl dehydrogenase	2180	Q9S2Q6	41	39	41	36
YlmE	2080	Q9S2X1	8	10	11	31
Alr	4745	ALR	28	3	0	0
Enolase 1	3096	ENO1	22	19	18	13
Putative oligopeptide-binding lipoprotein	5477	O86572	38	21	14	35
Putative inosine-5'-monophosphate dehydrogenase	4771	Q9L0I6	21	11	12	19
Polyribonucleotide nucleotidyltransferase Pnp	5737	PNP	12	26	14	9
Alanine dehydrogenase	1773	Q9S227	10	15	11	9
30S ribosomal protein S1	1998	Q9S2K5	15	14	16	14
Probable cytosol aminopeptidase PepA	2179	AMPA	14	10	11	14
Ribonuclease Z Rnz	2547	RNZ	0	0	0	25
Malate dehydrogenase Mdh	4827	MDH	14	13	5	8
Adenylosuccinate synthetase PurA	3629	PURA	11	6	6	8
Solute-binding protein	6009	O50503	10	9	3	9
Putative nitrite/sulphite reductase	6102	Q9ADG1	13	8	7	13
Citrate synthase	2736	Q9R339	13	14	5	6
Bifunctional purine biosynthesis protein PurH	4814	PUR9	9	12	8	4
Glutamine synthetase GlnA	2198	GLN1B	4	5	7	3
Aconitate hydratase	5999	Q7AKF3	4	14	8	5
30S ribosomal protein S15 RpsO	5736	RS15	1	0	1	13
Nucleoside diphosphate kinase Ndk	2612	NDK	6	9	5	3
Putative secreted protein	2116	Q9S2M7	7	2	5	5
Delta-1-pyrroline-5-carboxylate dehydrogenase	5520	Q8CJR1	2	16	4	0
Histidine ammonia-lyase HutH	4932	HUTH	4	8	5	3
Bifunctional protein FolD	4824	FOLD	11	2	1	2
Single-stranded DNA-binding protein 2	3907	SSB2	2	2	2	9
Putative secreted protein	4471	Q9F2R8	4	3	2	5
Cobalamin biosynthesis protein	1849	Q9RJ19	2	14	3	2
Uncharacterized protein	2368	Q9KY22	3	6	7	2
Adenosylhomocysteinase	3023	SAHH	1	14	3	0
Xaa-Pro aminopeptidase 1 PepPI	3970	AMPP1	1	11	2	0
Putative aminotransferase	5655	O86744	0	15	1	0
Tellurium resistance protein	0641	Q8CK50	4	4	4	1
Glyceraldehyde-3-phosphate dehydrogenase	7511	Q93J08	2	7	1	0
Uncharacterized protein	1424	Q9RKY3	6	5	2	4

Identified Proteins	SCOXXXX	Accession Number (Code_STRCO)	Alr	FtsZ	BlaC	YlmE
Glyceraldehyde-3-phosphate dehydrogenase Gap	1947	G3P	4	8	2	0
Pyridoxal 5'-phosphate synthase subunit PdxS	1523	PDXS	1	5	3	0
Superoxide dismutase	0999	Q7AKR0	1	3	2	0
Probable M18 family aminopeptidase 2 ApeB	3801	APEB	3	1	2	3
Aspartate-tRNA ligase AspS	3795	SYD	1	4	0	1
Putative oxidoreductase	4919	Q9EWF0	3	5	3	0
Fructose-bisphosphate aldolase Fba	3649	ALF	1	6	1	1
Elongation factor Tu-1	4662	EFTU1	2	1	3	1
Superoxide dismutase [Ni] SodN	5254	SODN	1	2	1	0
Putative cystathionine beta-synthase	3077	Q9KZ71	3	5	2	3
Probable cytochrome c oxidase subunit 2 CtaC	2156	COX2	5	0	0	3
Glycine dehydrogenase (decarboxylating) GcvP	1378	GCSP	1	10	1	0
Putative 4-aminobutyrate aminotransferase	5676	O86823	1	3	2	0
Uncharacterized protein	4253	Q9L0N8	0	0	0	7
Putative polyguluronate lyase	3497	Q9RKE1	2	1	2	3
Cytochrome c oxidase subunit 1-alpha CtaD1	2155	COX1A	4	0	0	3
Methionine aminopeptidase Map	4724	Q7AKJ0	3	0	0	1
Putative tellurium resistance protein	4277	Q9KXW4	3	3	2	0
Uncharacterized protein	5843	O50517	3	0	0	2
Glutamate binding protein	5776	O50494	6	0	0	1
Putative aminotransferase	3622	Q9XAI0	0	6	2	0
Agmatinase	2770	Q8CJY5	0	4	1	0
Putative lipoprotein	4885	Q9AK41	5	0	0	3
tRNA pseudouridine synthase A TruA	4731	TRUA	0	0	0	5
Uncharacterized protein TerB	3767	Q9F2L4	1	2	1	1
Probable cysteine desulfurase Csd	1921	CSD	0	3	4	0
Lipoprotein	1557	Q9L1C5	4	1	0	0
Putative prolyl aminopeptidase	0805	Q9RD72	0	5	0	0
FtsZ	2082	FTSZ	0	4	0	0
Ribonuclease PH Rph	2904	RNPH	4	1	0	0
Delta-aminolevulinic acid dehydratase HemB	3311	HEM2	0	7	0	0
Putative exonuclease	6341	O86610	0	0	0	3
Putative cystathionine gamma-synthase	1294	Q93IX6	2	1	1	1
50S ribosomal protein L2 RplB	4705	RL2	1	1	3	1
DNA-directed RNA polymerase subunit beta' RpoC	4655	RPOC	1	0	0	3
Uncharacterized protein	3353	Q9X8L7	2	1	0	3
Probable amino acid ABC transporter	2828	Q9RDC3	3	1	0	0
Uncharacterized protein	1623	Q9RJ78	3	0	0	0

Identified Proteins	SCOXXXX	Accession Number (Code_STRCO)	Alr	FtsZ	BlaC	YlmE
Uncharacterized protein	6042	O69830	1	0	0	2
HTH-type transcriptional repressor DasR	5231	DASR	0	0	4	0
UDP-N-GlcNAc 1-carboxyvinyltransferase MurA	2949	Q9L1U5	0	3	0	0
Catalase	0379	Q9RJK9	0	3	0	0
Uncharacterized protein	1777	Q9S223	0	3	0	0
Uncharacterized protein	2497	Q9RDC6	0	0	0	3
Urocanate hydratase HutU	3073	HUTU	0	2	0	0
Probable endonuclease 4 Nfo	2111	END4	0	0	0	2
Inosine-5'-monophosphate dehydrogenase GuaB	4770	Q9L0I7	0	0	0	2
Cholesterol esterase	5420	Q9L2A2	0	0	0	2
Large Ala/Glu-rich protein	5397	Q9L2C3	0	0	0	2
Probable oxidoreductase	0884	Q9RD26	0	2	0	0
Putative zinc-containing dehydrogenase	0179	Q9RIY6	0	2	0	0
50S ribosomal protein L29 RpmC	4710	RL29	0	0	0	2

Table A4.2. Pull-down assay 2.

W: lysate of S. coelicolor M145; Δ: lysate of the ylmE mutant of S. coelicolor; D: DNaseI treatment; R: RNaseA treatment. The reported numbers indicate the total spectrum counts for each protein.

Identified Proteins	SCO XXXX	Accession Number (Code_STRCO)	YlmE								FtsZ		BlaC			
			W	Δ	WD	WR	WDR	ΔD	ΔR	ΔDR	W	Δ	W	Δ	WD	WR	WDR
YlmE	2080	Q9S2X1	67	233	196	76	306	222	88	262	1	0	0	7	1	0	12
30S ribosomal protein S7 RspG	4660	RS7	18	4	21	64	60	4	5	4	0	0	0	0	0	2	4
50S ribosomal protein L1 RplA	4649	RL1	54	0	93	29	2	3	0	0	0	0	0	0	1	2	3
50S ribosomal protein L24 RplX	4713	RL24	7	0	6	31	19	0	0	0	2	0	1	0	7	28	26
50S ribosomal protein L2 RplB	4705	RL2	13	0	17	15	52	0	0	1	0	0	0	0	1	0	6
FtsZ	2082	FTSZ	0	0	1	0	0	0	0	0	28	80	0	0	0	0	0
50S ribosomal protein L9 RplI	3909	RL9	15	0	31	23	9	0	0	0	0	0	0	0	3	13	12
Translation initiation factor IF-3 InfC	1600	IF3	9	3	11	12	35	3	4	5	0	0	0	0	0	1	8
Probable cytosol aminopeptidase PepA	2179	AMPA	9	4	20	0	10	23	7	21	0	0	0	0	0	0	1
30S ribosomal protein S9 RpsI	4735	RS9	8	2	4	18	33	2	0	1	2	0	2	0	0	3	7
Translation initiation factor IF-1 InfA	4725	IF1	1	8	2	6	11	3	4	9	1	4	1	6	4	11	10
Type III pantothenate kinase CoaX	3380	COAX	2	26	7	0	0	13	5	23	0	0	0	0	0	0	0
60 kDa chaperonin 1 GroL1	4762	CH601	15	15	1	6	3	4	11	2	0	0	1	4	0	6	7
30S ribosomal protein S15 RpsO	5736	RS15	15	2	14	5	7	6	2	3	0	0	0	0	0	1	3
Dihydrolipoyl dehydrogenase	2180	Q9S2Q6	9	4	0	1	5	7	2	4	0	0	3	2	1	2	15
Sporulation transcription regulator WhiA	1950	WHIA	2	3	7	8	30	4	6	3	0	0	0	0	0	0	4
30S ribosomal protein S18 1 RpsR1	3908	RS181	6	0	1	33	20	0	0	0	0	0	0	0	0	1	0
30S ribosomal protein S10 RpsJ	4701	RS10	4	0	2	8	5	2	0	0	4	1	2	0	2	9	11
50S ribosomal protein L6 RplF	4717	RL6	9	0	7	19	11	0	0	0	0	0	0	0	0	0	5
50S ribosomal protein L13 RplM	4734	RL13	5	0	2	19	5	0	0	0	0	0	0	0	1	11	12
30S ribosomal protein S1	1998	Q9S2K5	8	11	1	0	3	13	0	1	0	0	0	0	0	0	6
30S ribosomal protein S3 RpsC	4708	RS3	16	5	6	2	5	8	2	2	0	0	0	0	0	0	1

Identified Proteins	SCO XXXX	Accession Number (Code_STRCO)	YlmE								FtsZ		BlaC				
			W	Δ	WD	WR	WDR	ΔD	ΔR	ΔDR	W	Δ	W	Δ	WD	WR	WDR
30S ribosomal protein S4 RpsD	1505	RS4	12	2	3	3	3	4	2	1	0	0	0	0	1	0	1
30S ribosomal protein RpsB	5624	RS2	2	10	1	0	6	8	3	3	0	0	0	0	0	0	0
50S ribosomal protein L17 RplQ	4730	RL17	8	0	4	14	4	0	0	0	0	0	0	0	1	5	2
Putative tetR-family transcription regulator	4421	Q9F367	0	0	3	3	6	5	4	19	0	0	0	0	0	0	0
50S ribosomal protein L23 RplW	4704	Q9L0D8	6	0	1	22	1	0	0	0	0	0	0	0	0	8	3
50S ribosomal protein RplT	1598	RL20	10	0	2	17	5	0	0	0	0	0	0	0	0	1	0
Gap	1947	G3P	8	2	0	4	3	0	0	0	3	1	1	1	0	4	9
50S ribosomal protein L15 RplO	4721	RL15	7	0	10	9	2	0	0	0	0	0	0	0	0	3	6
30S ribosomal protein S8 RpsH	4716	RS8	8	0	4	0	1	4	1	4	0	0	0	0	0	0	0
30S ribosomal protein S6 RpsF	3906	RS6	4	0	0	15	14	0	0	1	0	0	0	0	0	1	0
60 kDa chaperonin 2 GroL2	4296	CH602	4	4	0	0	3	3	1	0	0	2	1	3	2	4	7
50S ribosomal protein L19 RplS	5595	RL19	7	0	4	6	5	0	0	2	0	0	0	0	4	0	3
30S ribosomal protein S16 RpsP	5591	RS16	2	0	0	10	10	0	0	0	0	0	0	0	0	0	0
50S ribosomal protein L33 2 RpmG2	4635	RL332	0	0	2	10	8	0	0	0	2	0	0	0	3	5	3
50S ribosomal protein L27 RpmA	2596	RL27	2	0	0	10	1	0	0	0	1	0	2	0	1	14	2
Elongation factor Tu-1	4662	EFTU1	2	5	1	2	3	0	1	0	1	1	1	1	1	3	3
50S ribosomal protein L29 RpmC	4710	RL29	8	1	5	1	1	2	2	2	0	0	0	0	0	0	0
50S ribosomal protein L3 RplC	4702	RL3	5	0	0	7	1	0	0	0	0	0	0	0	2	8	8
30S ribosomal protein S17 RpsQ	4711	RS17	2	0	0	4	0	0	0	0	2	0	2	1	0	5	0
50S ribosomal protein L36 1 RpmJ1	4726	RL361	1	0	2	4	13	0	0	1	0	0	0	0	1	2	4
DNA-binding protein HU 1 Hup1	2950	DBH1	10	2	0	7	1	1	3	0	0	0	0	0	0	0	0
30S ribosomal protein S13	1480	Q9KXR9	3	0	4	5	12	0	0	0	0	0	0	0	0	0	1

Identified Proteins	SCO XXXX	Accession Number (Code_STRCO)	YlmE								FtsZ		BlaC				
			W	Δ	WD	WR	WDR	ΔD	ΔR	ΔDR	W	Δ	W	Δ	WD	WR	WDR
50S ribosomal protein L21 RplU	2597	RL21	1	0	0	6	3	0	0	0	0	0	0	0	0	4	5
Putative inosine-5'-monophosphate dehydrogenase	4771	Q9L0I6	0	4	0	0	7	3	4	3	0	0	0	0	0	0	0
CYTH-like hypothetical secreted protein	0544	Q9RK66	0	9	0	0	0	7	1	6	0	0	0	0	0	0	0
Ribonuclease PH Rph	2904	RNPH	2	17	0	0	0	4	0	0	0	0	0	0	0	0	0
Phenylacetic acid degradation protein PaaB	7472	Q93JC4	0	5	0	0	0	6	1	7	0	2	0	5	0	0	0
Putative secreted protease	2920	Q9S2G1	0	6	0	0	0	10	1	4	0	0	0	0	0	0	0
50S ribosomal protein L18 RplR	4718	RL18	4	0	1	10	0	0	0	0	0	0	0	0	0	6	3
50S ribosomal protein L11 RplK	4648	RL11	1	1	1	2	2	1	1	1	0	0	0	0	0	0	1
Putative D-alanyl-D-alanine	3811	Q9XA66	1	4	4	0	0	5	4	1	0	0	0	0	0	0	0
Uncharacterized protein	0838	Q9XA87	0	6	0	0	0	6	2	2	0	0	0	0	0	0	0
50S ribosomal protein L4 RplD	4703	RL4	8	0	0	10	0	0	0	0	0	0	0	0	1	0	0
Translation initiation factor IF-2	5706	IF2	3	0	1	1	7	0	0	0	0	0	0	0	0	0	5
50S ribosomal protein L14 RplN	4712	RL14	4	0	0	3	2	1	0	0	0	0	0	0	0	3	3
50S ribosomal protein L30 RpmD	4720	RL30	1	0	1	1	2	0	0	0	6	0	1	0	1	2	1
Uncharacterized protein	4246	Q9L0P5	0	2	0	0	0	4	4	6	0	0	0	0	0	0	0
30S ribosomal protein S13 RpsM	4727	RS13	6	0	0	5	0	0	0	0	0	0	0	0	0	1	0
30S ribosomal protein S14 type Z RpsZ	4715	RS14Z	1	0	1	4	4	0	0	0	0	0	0	0	1	1	2
SsrA-binding protein SmpB	2966	SSRP	0	0	4	2	5	0	0	0	0	0	0	0	0	0	5
Uncharacterized protein	1858	Q93RW8	0	0	1	0	6	1	0	4	0	0	0	0	0	0	0
50S ribosomal protein L32-1 RpmF1	5571	RL321	2	0	0	8	2	0	0	0	0	0	0	0	0	2	1
30S ribosomal protein S20 RpsT	2563	RS20	2	0	0	8	1	0	0	0	0	0	0	0	0	2	0
Glyceraldehyde-3-phosphate dehydrogenase	7511	Q93J08	0	3	0	0	1	4	1	1	0	0	0	1	0	0	0

Identified Proteins	SCO XXXX	Accession Number (Code_STRCO)	YlmE								FtsZ		BlaC				
			W	A	WD	WR	WDR	AD	AR	ADR	W	A	W	A	WD	WR	WDR
Malate dehydrogenase Mdh	4827	MDH	0	2	0	0	1	4	0	0	0	0	0	0	0	0	3
Putative 3-oxoacyl-[acyl-carrier protein] reductase	6282	Q93S07	0	4	0	0	0	2	1	1	0	1	0	1	0	0	0
Alanine dehydrogenase	1773	Q9S227	0	1	0	0	0	3	0	0	0	0	2	1	0	0	1
DNA-directed RNA polymerase subunit beta' RpoC	4655	RPOC	2	5	0	0	0	2	0	1	0	0	0	0	0	0	0
tRNA pseudouridine synthase A TruA	4731	TRUA	2	4	2	0	0	3	0	0	0	0	0	0	0	0	0
DNA-binding protein HU2	5556	DBH2	0	0	0	7	3	0	0	0	0	0	0	0	0	0	0
Putative ATP-binding protein	3261	Q9X8D4	0	1	1	0	0	2	1	3	0	0	0	0	0	0	0
Jag	3884	Q7BUY9	3	1	0	1	2	0	0	0	0	0	0	0	0	0	0
50S ribosomal protein L28-1 RpmB1	5564	RL28A	0	0	0	3	2	0	0	0	0	0	0	0	0	2	0
30S ribosomal protein S5 RpsE	4719	RS5	7	0	0	3	0	0	0	0	0	0	0	0	0	0	0
Uncharacterized, RNA binding protein	1991	Q9S2L2	0	0	0	2	7	0	0	0	0	0	0	0	0	0	0
Methionine aminopeptidase Map	4724	Q7AKJ0	0	0	0	0	6	0	0	0	0	0	0	0	0	0	0
Predicted RNA-binding protein YlqC	5592	Y5592	3	1	1	2	1	0	0	0	0	0	0	0	0	0	0
30S ribosomal protein S11 RpsK	4728	RS11	1	0	0	4	0	0	0	0	0	0	0	0	0	1	0
Putative TetR-family transcriptional regulator	3129	Q9K3T5	0	3	0	0	2	3	0	0	0	0	0	0	0	0	0
Dihydrolipoamide acetyltransferase of pyruvate dehydrogenase	3815	Q9XA62	0	1	0	0	0	3	0	2	0	0	0	0	0	0	0
50S ribosomal protein L35 RpmI	1599	RL35	0	0	0	4	0	0	0	0	0	0	0	0	1	3	0
ATP synthase subunit delta AtpH	5370	ATPD	0	0	0	0	3	0	0	0	0	0	0	0	0	0	4
Putative tetR-family transcriptional regulatory protein	7518	Q93J02	0	0	0	0	6	0	0	1	0	0	0	0	0	0	0
Chaperone protein DnaJ 1	3669	DNAJ1	1	1	2	0	2	1	0	0	0	0	0	0	0	0	0
50S ribosomal protein L5 RplE	4714	RL5	3	0	0	2	0	0	0	0	0	0	0	0	0	0	1
Putative transcriptional regulator	1839	Q9RJ29	0	0	0	3	3	0	0	0	0	0	0	0	0	0	0

Identified Proteins	SCO XXXX	Accession Number (Code_STRCO)	YlmE								FtsZ		BlaC				
			W	Δ	WD	WR	WDR	ΔD	ΔR	ΔDR	W	Δ	W	Δ	WD	WR	WDR
30S ribosomal protein S12 RpsL	4659	RS12	5	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Uncharacterized protein	5154	Q9FBK4	0	0	0	1	5	0	0	0	0	0	0	0	0	0	0
50S ribosomal protein L31 RpmE	5359	RL31	0	0	0	1	0	0	0	0	1	0	0	0	0	2	1
Tellurium resistance protein	0641	Q8CK50	0	2	0	0	0	2	0	0	0	0	0	1	0	0	0
Transcriptional regulator	6312	Q7AKE7	0	0	0	0	0	0	2	2	0	0	0	0	0	0	0
Uncharacterized protein	2368	Q9KY22	0	2	0	0	1	1	0	0	0	0	0	0	0	0	0
Single-stranded DNA-binding protein 2 Ssb2	3907	SSB2	0	2	0	0	0	0	3	0	0	0	0	0	0	0	0
Uncharacterized protein	4247	Q9L0P4	0	0	0	0	0	3	0	1	0	0	0	0	0	0	0
Uncharacterized protein	2370	Q9KY20	0	0	0	4	0	0	1	0	0	0	0	0	0	0	0
Uncharacterized protein	3793	Q9F325	0	0	0	0	0	0	0	5	0	0	0	0	0	0	0
50S ribosomal protein L25 RplY	3124	RL25	0	0	0	2	0	0	0	0	0	0	0	0	0	1	1
Uncharacterized protein	1511	Q8CK26	0	1	0	0	2	0	0	0	0	0	0	0	0	0	1
Trigger factor	2620	TIG	0	0	0	0	1	0	0	0	1	0	0	0	0	2	0
Uncharacterized protein	3843	Q9XA21	0	0	0	0	0	0	0	0	0	1	0	2	0	0	0
Putative transcriptional factor regulator	4232	Q9L0Q9	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0
Putative secreted protein	7657	Q9F3N0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0
Putative alcohol dehydrogenase	0199	Q9RI47	0	2	0	0	0	0	0	0	0	1	0	0	0	0	0
Uncharacterized protein	4048	Q9AK69	0	0	0	0	0	1	0	0	0	2	0	0	0	0	0
Putative LuxR family two-component response regulator	0204	Q9RI42	0	2	0	0	0	1	0	0	0	0	0	0	0	0	0
50S ribosomal protein L22 RplV	4707	RL22	1	0	0	2	0	0	0	0	0	0	0	0	0	0	0
Serine hydroxymethyltransferase GlyA	5470	GLYA	0	2	0	0	0	1	0	0	0	0	0	0	0	0	0
Uncharacterized protein	1790	Q9S210	1	0	0	0	2	0	0	0	0	0	0	0	0	0	0

			YlmE								FtsZ		BlaC				
Identified Proteins	**SCO XXXX**	**Accession Number (Code_STRCO)**	**W**	**Δ**	**WD**	**WR**	**WDR**	**ΔD**	**ΔR**	**ΔDR**	**W**	**Δ**	**W**	**Δ**	**WD**	**WR**	**WDR**
Putative transcriptional regulatory protein	2105	Q8CK07	0	0	0	0	0	0	1	2	0	0	0	0	0	0	0
Possible regulator protein	0168	Q9RIZ7	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0
Uncharacterized protein	2936	Q9S2E8	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
Flavin prenyltransferase UbiX	4492	UBIX	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
Putative TetR-family regulator	0857	Q9RCV4	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
Glucose-6-phosphate 1-dehydrogenase Zwf	6661	O88017 (+1)	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0

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Curriculum vitae

Raffaella Tassoni was born on July 27th, 1989, in Atri, a small city in Abruzzo, Italy, and grew up in Roseto degli Abruzzi, where she also attended school. She moved to Milano, in 2008 to gain a Bachelor degree in Biotechnology, and later a Master degree in Industrial Biotechnology at Milano Bicocca University. For her Master thesis, she spent ten months working on the biodegradation of water micropollutants in the laboratory of Prof. Dr. Dirk Springael at KU Leuven University, Belgium. In December 2013, she moved to Leiden, The Netherlands, to start her PhD at Leiden University under the supervision of Prof. Dr. Marcellus Ubbink, Prof. Dr. Gilles P. van Wezel, and Dr. Navraj S. Pannu. During this time, she attended several conferences and Summer Schools, where she presented and discussed her work.

- CHAINS, Veldhoven (The Netherlands), December 2013 and December 2017
- ESRF Users Meeting, Grenoble (France), February 8-10 2016
- 16th International Conference on the Crystallization of Biological Macromolecules, Prague (Czech Republic), July 2-7 2016
- CCP4 Study Weekend, Nottingham (UK), 2016, 2017
- 50th Course Erice, Integrative structural biology, Erice (Italy), June 2-5 2017
- AIC International School, Bridging the gap between cryo-EM and crystallography, Pavia (Italy), September 3-6 2017

Publications

1. **W., Elings; R., Tassoni; S., van der Schoot; W., Luu; J., Kynast; L., Dai; A., Blok; M., Timmer; B., Florea; N. S., Pannu; M., Ubbink.** Phosphate Promotes the Recovery of *Mycobacterium tuberculosis* β-Lactamase from Clavulanic Acid Inhibition. *Biochemistry* **2017** 56 (47), 6257-6267.
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2. **R., Tassoni; L., van der Aart; M., Ubbink; G. P., van Wezel; N. S. Pannu.** Structural and Functional Characterization of the Alanine Racemase from *Streptomyces coelicolor* A3(2). *Biochem. Biophys. Res. Commun.* **2017** 483 (1), 122-128.
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3. **J., T'Syen; R., Tassoni; L., Hansen; S. J., Sorensen; B., Leroy; A., Sekhar; R., Wattiez; R., De Mot; D., Springael.** Identification of the Amidase BbdA That Initiates Biodegradation of the Groundwater Micropollutant 2,6-dichlorobenzamide (BAM) in *Aminobacter* sp. MSH1. *Environmental Science and Technology* **2015** 49 (19), 11703-11713.
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4. **R., Tassoni; W., Elings; A. Blok; N. S., Pannu; M., Ubbink.** Crystallographic Studies of Acylation and Pre-Acylation States of BlaC from *Mycobacterium tuberculosis* with Clavulanic Acid, Sulbactam, Tazobactam and Avibactam. ***In preparation***.

5. **R., Tassoni; M. C., Janssen; P. Wolff; P. A., van Veelen; M., Ubbink; G. P., van Wezel; N. S., Pannu.** The Cell-division Related Protein YlmE from *Streptomyces coelicolor* A3(2) Binds to tRNA-like Molecules. ***In preparation***.