## Direct modulation of T-box riboswitch-controlled transcription by protein synthesis inhibitors

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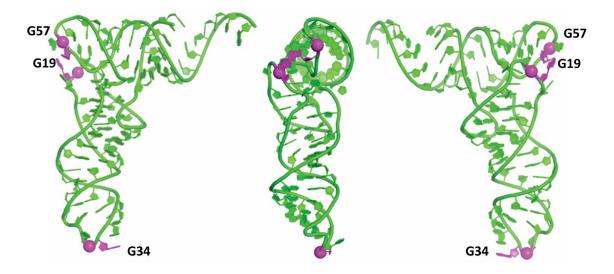
## Supplementary Table S1 Sequences of tRNAs and the T-boxes used for the phylogenetic analyses

			D-stem		D-	46	Ac-stem	Ac-loop	Ac-stem		T-stem	T-loop	T-stem	Acc-stem		CC
	1	8	10	14	stem 22	26	27	32	39	44	49	54	61	66	73	74
aur	GCGGGAA	TA	GCTC	AGT <mark>T</mark> -GGTA	GAGC	G	TCTCC	TTGCCAA	GGAGA	AGGTC	GCGAG	TTCGAGT	CTCGT	TTCCCGC	Т	CCI
	GCGGGAG	TA	GCGC	AATGGTA	GCGC	A	TCTGC	CT <mark>T</mark> CCAA	GCAGA	TGGTT	GCGAG	TTCGAGT	CTCGT	CTCCCGC	Т	CCI
aur	GCGGGAA	TG	GCGC	AATT-GGCA	GCGC	Α	TCTGT	TTCCCAA	ACAGA	AGGTT	GCGGG	TTCGAAC	CCCGT	TTCCCGC	Т	
The state of the s	GCGGGAG	TA	GCTC	AGCT-GGTA	GAGC	A	CTACC	TTGCCAA	GGTAG	ATGTC	GCGAG	TTCGAAT	CTCGT	CTCCCGC		CCZ
The second second	GCGGGAA	TA	GCTC	AGTT-GGTA	GAGC	G	TCAGC	TTCCCAA	GCTGA	ATGTC	GCGAG	TTCGAGT	CTCGT	TTCCCGC	Т	
	GCGGAAG	TG	GTGT	AGTGGTA AGTGGTA	GCAC GAAC	A A	GCAGC CCACC	CT <mark>T</mark> CCAA TTGCCAA	GCTTC GGTGG	TGG-C GGGTC	CTCGG GCGGG	TTCGAAT TTCGAAT	CCCCT	ATCCCGC CTTCCGC		CCI
	GCGGGTG	TA	GTTT	AGTGGTA	AAAC	C	TCAGC	CTTCCAA	GCTGA	TGT-C	GTGAG	TTCGATT	CTCAT	CACCCGC		CC
	GCGGGTG	TA	GTTT	AGTGGTA	AAAC	C	TCAGC	CTTCCAA	GCTGA	TGT-C	GTGGG	TTCGATT	CCCAT	CACCCGC		CC
	CGGAAG	TA	GTTC	AGTGGTA	GAAT	A	CAACC	TTGCCAA	GGTTG	GGGTC	GCGGG	TTCGAAT	CCCGT	CTTCCGC		CC
	CGGGTG	TA	GTTT	AGTGGTA	AAAC	А	AGAGC	CTTCCAA	GCTCT	GGT-C	GAGAG	TTCGATT	CTCTT	CACCCGC		CC
tet G	GCGGGAG	TG	GCTC	AGTGGTA	GAGC	G	TCACC	TTGCCAA	GGTGA	ACGTC	GTGGG	TTCGAAT	CCCAT	CTTCCGC	Т	CC.
tet G	GCGGGTG	TA	GCTC	AATGGTA	GAGT	Т	CCAGC	CTTCCAA	GCTGG	CTG-T	GAGAG	TTCGATT	CTCTT	CACCCGC	Т	CC.
bot G	GCGGGTG	TA	ACTC	AATGGTA	GAGT	G	CTAGC	CT <mark>TCC</mark> AA	GCTAG	TTA-C	GAGGG	TTCGATT	CCCTT	CACCCGC	Т	CC
bot G	GCGAGAG	TA	GTTC	AGTGGTA	GAAC	A	CTAGC	TTCCCAA	GCTAG	TTGCC	GCGGG	TTCGATC	CCCGT	TTCTCGC	Т	CC
bot G	GCGGGAG	TG	GCTC	AGTGGTA	GAGC	G	TCACC	TTGCCAA	GGTGA	ACGTC	GCGAG	TTCGAAT	CTCGT	CTTCCGC	Т	CC
ace G	GCGGGAA	TA	GCTC	AGTGGTA	GAGC	A	CTAGC	TTCCCAA	GCTGG	GTGCC	GCGGG	TTCGATA	CCCGT	TTCCCGC	Т	CC
		TG	GCTC	AGTGGTA	GAGC	G	TCACC	TTGCCAA	GGTGA	ACGTC	GCGAG	TTCGAAT	CTCGT	CTTCCGC	Т	
	GCGGGTG	TA	ACTC	AATGGTA	GAGT	G	CTAGC	CTTCCAA	GCTAG	TTA-C	GAGGG	TTCGATT	CCCTC	TACCCGC	Т	
	GCGGGAA	TA	GTTC	AGTGGTA	GAGC	G	CAACC	TTGCCAA	GGTTG	AAGTC	GCGAG	TTCGAAT	CTCGT	TTCCCGC	200	CC
	GCGGGTG	TA	GCTC	AATGGTA	GAGT	T	CTGGC	CTTCCAA	GCCAG	CTG-T	GAGGG	TTCGATC	CCCTT	CACCCGC	T	
	CGGAAA	TA TA	GCTC	AGTGGTA AGTGGTA	GAGC	A C	CCACC	TTGCCAA CTTCCAA	GGTGG GCTGT	GGGTC	GCGGG	TTCGAAC TTCGATT	CCCGT	TTTCCGC	T	
	GCGGGTG GCAGAAG	TA	GTTC	AGCGGTA	AAAC GAAT	A	ACAGC CAACC	TTGCCAA	GGTTG	TGT-C GGGTC	GCGAG GCGGG	TTCGATT	CCCGT	CTTCTGC	Т	
	GCGGGTG	TA	GTTT	AATGGCA	AAAC	C	TCAGC	CTTCCAA	GCTGA	TGT-T	GTGGG	TTCGATT	CCCAT	CACCCGC	Т	
	GCGGGAG	TA	GTTC	AACT-TTT-A	GAAC	A	CGTTC	CTTCCCG	GAACG	AGG-T	ATAGG	TGCAAAT	CCTAT	CTTCCGC	T	
	GCGGGAG	TA	GTTC	AACT-TTTA	GAAC	A	CGTTC	CTTCCCG	GAACG	AGG-T	ATAGG	TGTAAAT	CCTAT	CTTCCGC		CC
	CGGGAG	TA	TTTC	AACT-CTTA	GAAT	A	CATTC	CTTCCTG	GAATG	AGG-T	ATAGG	TGTAAAT	CCTAT	CTTCCGC	Т	
	GCGGAAG	TA	GTTC	AGTGGTA	GAAC	А	CCACC	TTGCCAA	GGTGG	GGGTC	GCGGG	TTCGAAT	CCCGT	CTTCCGC		CC
HATTER STATE OF THE STATE OF TH	GCGGGTG	TA	GTTT	AATGGCA	AAAC	С	TCAGC	CTTCCAA	GCTGA	TGT-T	GTGGG	TTCGATT	CCCAT	CACCCGC	Т	CC
epi G	GCGGGAG	TA	GTTC	AACT-CTCA	GAAC	A	CATTC	CT <mark>TCC</mark> CG	GAATG	AGA-T	ATAGG	TGTAAAT	CCTAT	CTTCCGC	Т	CC
epi G	GCGGGAG	TA	GTTC	AACT-CTCA	GAAC	A	CATTC	CT <b>TCC</b> CG	GAATG	AGA-T	ATAGG	TGCAAAT	CCTAT	CTTCCGC	Т	CC
epi G	GCGGGAG	TA	GTTC	AAC <mark>T-CT</mark> TA	GAAC	Α	CATTC	CT <mark>TCC</mark> CG	GAATG	AGA-T	ATAGG	TGTAAAT	CCTAT	CTTCCGC	Т	CC
sap G	GCAGAAG	TA	GTTC	AGCGGTA	GAAT	A	CGACC	TTGCCAA	GGTCG	GGGTC	GCGGG	TTCGAAT	CCCGT	CTTCTGC	Т	CC
sap G	GCGGGTG	TA	GTTT	AATGGCA	AAAC	C	TCAGC	CT <mark>TCC</mark> AA	GCTGA	TGT-T	GTGGG	TTCGATT	CCCAT	CACCCGC	Т	CC
san G	GCGAACG	TA	GTTC	AGTGGTA	GAAC	A	TCACC	TTGCCAA	GGTGG	GGGTC	GCGGG	TTCGAAT	CCCGT	CGTTCGC		CC
	GCGGGTG	TA	GTTT	AGTGGTA	AAAC	T	ACAGC	CTTCCAA	GCTGT	TGT-C	GCGAG	TTCGATT	CTCGT	CACCCGC		CC
	GCGAACG	TA	GTTC	AGTGGTA	GAAC	A	TCACC	TTGCCAA	GGTGG	GGGTC	GCGGG	TTCGAAT	CCCGT	CGTTCGC		CC
	GCGAACG	TA	GTTC	AGTGGTA	GAAC	A	TCACC	TTGCCAA	GGTGG	GGGTC	GCGGG	TTCGAAC	CTATA	CGTAGGT		CC
	GCGGGTG	TA	GTTT	AGTGGTA	AAAC	C	ACAGC	CTTCCAA	GCTGT	TGT-C	GCGAG	TTCGATT	CTCGT	CACCCGC		CC
	GCGGGTG	TA	GTTT	AGTGGTA	AAAC	T	ACAGC	CT <mark>TCC</mark> AA TTGCCAA	GCTGT	TGT-C GGGTC	GCGAG	TTCGATT	CTCGT	CACCCGC		CC
	GCGAACG GCGGGTG	TA	GTTC	AGTGGTA AGTGGTA	GAAC	A	CCACC ACAGC	CTTCCAA	GGTGG GCTGT	TGT-C	GCGAG GCGAG	TTCGATT	CCCGT	CACCCGC	- 22	CC
-2220-000	GCGAACG	TA	GTTC	AGTGGTA	GAAC	A	TCACC	TTGCCAA	GGTGA	GGGTC	GCGGG	TTCGAAC	CCCGT	CGTTCGC		CC
	CGGGTG	TA	GTTT	AGTGGTA	AAAC	T	ACAGC	CTTCCAA	GCTGT	TGT-C	GCGAG	TTCGATT	CTCGT	CACCCGC	Т	
	GCGGAAG	TA	GTTC	AGTGGTA	GAAC	A	TCACC	TTGCCAA	GGTGG	GGGTC	GCGGG	TTCGAAC	CCCGT	CTTCCGC	Т	
		TA		AGCGGTA	GAAC	A	TCACC	TTGCCAA		GGGTC	GCGGG	TTCGAAC		CTTCCGC		CC
		TA		AGTGGTA	AAAC		ACAGC	CTTCCAA	The second secon	TGT-C	GTGGG	TTCGATT		CACCCGC		CC
		TA		AGTGGTA	GAAC	А		TTGCCAA	No. of the Control of	GGGTC	GCGGG	TTCGAAC		CTTCCGC	Т	CC
mon G		TA	GTTC	AGCGGTA	GAAC	А	TCACC	TTGCCAA	GGTGG	GGGTC	GCGGG	TTCGAAC		CTTCCGC	Т	
	GCGGAAG				AAAC	Т	ACAGC		GCTGT							CC

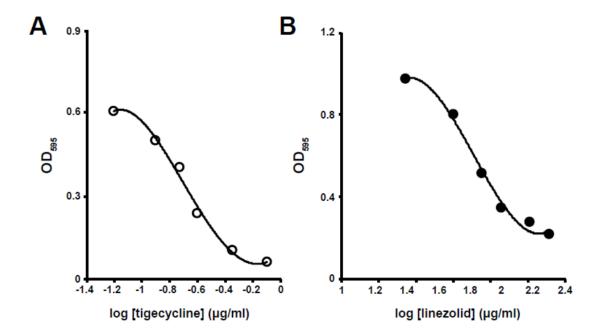
The annotation numbers used are: Haur\_4697: *H. aurantiacus* ATCC 23779; Dgeo\_1716: *D. geothermalis* DSM 11300; BSU25270: *B. subtilis* str. 168; BCE\_5053: *B. cereus* ATCC 14579; CTC00212: *C. tetani* E88; CBO3517: *C. botulinum* str. ATCC 3502; CAC3195: *C. acetobutylicum* ATCC 824; EF2408: *E. faecalis* V583; SA1394: *S. aureus* N315; SE1252: *S. epidermidis* ATCC 12228; SSP1191: *S. saprophyticus* ATCC 15305; SSA\_1881: *S. sanguinis* SK36; SMU\_444: *S. mutans* UA159; SP\_1477: *S. pneumoniae* TIGR4; SAG0268: *S. agalactiae* 2603V/R; lin1496: *L. innocua* Clip11262; Imo1459: *L. monocytogenes* EGD-e.

## SUPPLEMENTARY FIGURES LEGENDS

**Supplementary Figure S1** 3D representation of tRNA<sup>Gly</sup><sub>GCC</sub>. The main positions that were found protected by tigecycline and neomycin B are indicated.



**Supplementary Figure S2** IC<sub>50</sub> values calculation for tigecycline and linezolid (0.103  $\mu$ g/ml and 85.43  $\mu$ g/ml, respectively).



## **Supplementary Methods**

In vitro transcription and purification of S. aureus GT-box and P1 tRNAGINGCC

The S. aureus GT-box and P1 tRNAGIYGCC are cloned into pUC57 vector by GenScript and pUC18 vector, respectively (33). Both plasmid constructs were designed with a T7 promoter leader sequence and the terminal BstNI restriction enzyme recognition site. After BstNI digestion and linearization, the plasmids were treated with phenol:chloroform:isoamyl alcohol (25:24:1), precipitated with ethanol and used as template for subsequent in vitro transcription using T7 RNA polymerase. The linearization efficiency was confirmed on a 1% agarose gel. Run-off in vitro transcription reactions were carried out at 30°C for the GT-box and 37°C, for the P1 tRNA<sup>Gly</sup><sub>GCC</sub> for 16 h. The reactions mixtures contained 10 µg of purified linear plasmids as template, 500U T7 RNA polymerase (Takara), 2 mM of each ribonucleotide (rUTP, rGTP, rCTP, rATP), 160 U RNasin (Takara), 8U inorganic pyrophosphatase (New England Biolabs) and DTT (5mM final concentration) up to a final volume 500µL. The reactions were stopped by placing the mixture on ice followed by DNase I digestion of the template, phenol:chloroform:isoamyl alcohol (25:24:1) extraction, and ethanol precipitation. Subsequently the transcripts were purified on an 8 or 10% PAGE/8M urea. The band corresponding to the correct transcript length was excised after visualization under a UV lamp and the transcript was eluted in the presence of buffer containing 10mM Tris-HCl pH7.5, 300mM KCI, 1mM EDTA at 4°C for 16 h in continuous shaking. The eluted transcripts were ethanol precipitated, denatured by heating at 65 °C for 5 min and refolded with slow cooling in the presence of the same buffer with the addition of 1 mM MgCl<sub>2</sub>. After refolding the transcripts were loaded on a gel filtration column (Superdex 200 10/ 300 GL-ÄKTA FPLC system) using the same buffer to be further purified from nucleotides and unwanted bulky conformations (i.e. dimers), unless indicated otherwise. After elution, the properly folded and structured transcripts were analysed for size and quality on an 8 or 10% PAGE/8M Urea. Representative chromatographs and gels stained with methylene blue (0.025%) are presented in Supplementary Figure S3.

**Supplementary Figure S3** Chromatographs corresponding to purification of T-box (upper panel) and P1 tRNA (lower panel) on a gel filtration column column (Superdex 200 10/ 300 GL-ÄKTA FPLC system). The inserts correspond to eluted transcripts analysed for purity and correct size on 8 or 10% PAGE/8M urea.

