Table 2. **Candidate nZUR-binding sites in proteobacteria and pZUR-binding sites in the *Bacillus* group**

Genome	Genes and operons	Site or consensus	Score	Position
γ-Proteobacteria		**GAAATGTTATANTATAACATTTC**		
EC	*znuA <> znuC-znuB* *	GAAATGTTATAATATcACAcTTC	7.04	+3
	zinT (b1973)	tAtATGTTAcAATATAACATTaC	5.89	–57
	L31p (ykgM)	GttATGTTATAAcATAACAggTa	4.91	–28
ST	*znuA <> znuC-znuB*	agAATGTTATAATATcACATTTC	7.00	–36
	zinT (STY1858)	GcAATGTTATAATATAACAaTca	6.11	–50
	L31p (rpmE2)	ttAtTGTTATgTTATAACATaat	5.00	–36
KP	*znuA <> znuC-znuB*	tgAATGTTATAATATcACATcaC	6.57	–35
	zinT	GAtATGTTATATcgTAACAaTTt	5.05	–53
	znuC2-znuB2	ttAtTGTTATgTTATAACATTaa	5.49	–106
YP	*znuA <> znuC-znuB*	tgAATGTTATAATATtACgcTTt	5.59	–52
	L31p-L36p (YP03134-5)	atgATGTTAcATTATAACATact	5.33	–37
VC	*znuA <> znuC-znuB*	GttATGTTATAAagTAACATTca	5.30	–49
	L31p-L36p (VC0878-9)	aAAATGTTATAAcATAACAaTTt	5.83	–41
α-Proteobacteria (*Rhodobacter* group)		**GATATGTTATAACATATC**		
RC	*znuA <> zur-znuB-znuC*	GtTATcTcATAACATAga	5.18	–58
RS	*znuA <> zur-znuB-znuC*	cATgcGTTATAcCATATC	5.35	+1
		GtTATGaTATAACgTAat	4.58	–48
	yrpE	GATATGTaATAACATATC	6.31	–45
α-Proteobacteria (*Agrobacterium* group)		**GTAATGTNATNACATTAC**		
AT	*yrpE (AGR_C_1935)*	GTAATGTtATtACgTTAC	5.80	–52
	znuA <> znuC-znuB-zur (AGR_C_2805<>4-2-1)	taAATGTaATaACATaAC	5.69	–37
BM	*znuA <> znuC-znuB-zur (BMEII0178<>7-5)*	GTAATaaaATaACATatC	5.21	–80
SM	*znuA <> znuC-znuB-zur (SMc04245<>4-2)*	tTgATGTaATaACATaAC	5.65	–87
	zinL (SMc03799)	GaAATGTaATaACgTatC	5.35	–73
ML	*znuC-znuB-zinA (Mll8315-3)*	cTAATGTaATaACATcAC	5.36	–68

Table 2, *continued*

Genome	_Genes and operons	Site	Score	Pos.
Gram-positive bacteria (*Bacillus* group)		**TAAATCGTAATNATTACGATTTA**		
BS	*adcA-adcC-adcB (ycdHIyceA)**	aAAATCGTtATCATTttGATTTt	6.05	–53
	*yciC **	TAAATCGTAATCATTctatTTTA	6.31	–38
	*yciA-yciB **	TAAATaGTAATTATTACGATTTg	6.75	–45
	zinT (yrpE)	TAAATCGTAATGtTTtCGATTTA	6.56	–41
	S14p (yhzA)	TAAATCGTAAcAATTtCGATTTA	6.52	–41
	L31p (ytiA)	TAAAaCGTAATTATTACGATTTA	7.00	–38
	L33p1	TAAAaCGTAATCATTACGtTTTA	6.86	–16
BH	*adcA (BH2760)*	cAAATCGTAAcTATTcCGATaTA	6.27	–66
	yciC (BH1790)	cAAAgCGTAATTATTACGATTTA	6.69	–196
	yciA (BH0998)	TAAATCGTAATTATTcttATTTA	6.53	–40
	yciC2 (BH0366)	TAAATaGgAATTATTACGATTTA	6.80	–41
	adcC-adcB-zur (BH1396-4)	TAAATCGgAATGATTcttAaTat	5.11	–73
BE	*adcA*	cAAATCGTAATGATTACGATaTA	6.78	–62
	adcC-adcB	cAAATCGgAATGATTctGAaTTA	5.98	–40
BA	*adcC-adcB-zur*	TAAATCGgAATCATTctGAaTTA	6.15	–40
	yciC	TAAATCGTAATTATTACGcTTTg	6.69	–45
LM	*adcA-adcC-adcB (lmo0153-5)*	cAAATaagAATTATTACGtTTTg	6.01	–98
	adcC2-adcB2-zur (zurAMR)	tAAtTCGaAgTaATTACGATTTA	5.75	–88
	S14p (lmo1882)	TAAATCGgAATGATTAttATTTA	6.57	–38
LI	*adcA-adcC-adcB (lin0193-1)*	cAAATaagAATGATTACGtTTTA	6.22	–98
	adcC2-adcB2-zur (zurAMR)	TAAtTCGaAgTaATTACGATTTA	5.75	–88
	S14p (lin195)	TAAATCGgAATGATTAttATTTA	6.57	–37
SA	*adcA (SAV2390)*	TAAAaCGTAAaGATTACtATTTA	6.43	–33
	yciC (SAV0438)	TAAAaCGgAATTATTcCtATTTA	6.50	–51
	S14p (SAV1320)	TAAATCGTAATAATTACGATTTg	7.01	–46
	adcC-adcB-zur (SAV1545-3)	TgAgTCGTAAaCATTACtgTTTA	4.99	–68
EF	*adcA-adcC-adcB*	cAAATCGTAAaTATTACGgTTTA	6.16	–50
	zur	TAAATCagAATCATTACGAaaTA	6.00	–79
	S14p-L33p4-yciC	cAAATCGTAAcCATTACGATTTA	6.70	–52

Positions (column 4) are given with respect to the translation start sites of the first gene in an operon. The training set is underlined. Known sites are marked by asterisks (*). Genes forming candidate operons are separated by dashes (–). Operons transcribed in opposite directions (divergons) are separated by less than/greater than signs (</>). pZUR and nZUR**,** ZUR proteins from Gram-positive and -negative bacteria, respectively.