Interaction of ArmZ with the DNA-binding domain of MexZ induces expression of *mexXY* multidrug efflux pump genes and antimicrobial resistance in *Pseudomonas aeruginosa*

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Supplementary figures, tables and data sets.



Figure S1. Impact of CyaA complementation on the cellular level of CyaT18- fused proteins. Western blot analysis of CyaT18, CyaT18-MexZ and CyaT18-ArmZ levels in *E. coli* BTH101 double transformants (as on Fig. 1A). Cells from cultures used for β -galactosidase assays were diluted in fresh medium, grown to OD₆₀₀ = 0.6, harvested and boiled in the loading buffer. Cell extracts corresponding to 300 µl (A) or 1.2 ml of cultures (B) were separated on 10% polyacrylamide gels and analyzed by Western blot using anti CyaT18 antibodies. PonceauS staining of membranes after transfer was shown as a loading control (bottom panels).



Figure S2. ArmZ interactions with MexZ WT and R3S, K6E, R13H, K53E mutants. Purified MexZ-His₆ (WT or mutant, 150 μ g) was mixed with 1 mg of extract from *E. coli* BL21 (DE3) pKAB28.6 cells overproducing FLAG-ArmZ and transferred to a Ni-NTA column. After washing the bound proteins were eluted using imidazole gradient. Eluates were separated by SDS-PAGE, followed by Coomassie staining (**A**) or Western blot analysis using anti-FLAG antibodies (**B**).

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Consensus	<u>10</u> 20	- EA - ETRQ - ILDAA 30 4	F-E-GVS-TSL-DI 0 50	60	H F K N K - D L F 70 80	90	<u>к-РР</u> 100	110	120	130
B. ubonensis MSMB22 AJX13909	MRYSI	EHKHET <mark>R</mark> ARILDAASRL	FREEGYGGSGIGPL	TKAAGVTNGAFYG	HF <mark>K</mark> SKGEAFRSVVLAG	LDQLRQGVAAF	(AEHG)	ARWRRPFVSF	YL GPRRTC -	
A. xylosoxidans CKH02195		EESQRTRDRILDAAEHV	FLSKGGASTTMSDI	ADFAGVSRGAVYG	HY <mark>K</mark> NKIDVCIAMCDRA	L	GEAV	SLTRVSTDGE	ALESLYASMRQYVQ)IY
B. cepacia ATCC 25416 ALK18596	MARKTR	EESLAIKHRILDAAELV	LLEKGVGTTAMADL	AEAAGMSRGAVYG	HYRNKIEVCLAMCDRA HYRNKMEVCLAMCDRA	FARTSEGFDAGI	GQ-1 GLPP	LATLRRAASH	YLQECGEPGPM	
B. ubonensis MSMB22 AJX16992	MARKTR	EESLAI <mark>K</mark> HRILDAAELV	LLEKGVAQTAMADL	AEAAGMSRGAVYG	HY <mark>K</mark> NKMEVCLAMCDRA	FARTSEGFEAG	G QPA	LDTLRRAASH	YLEQCGEPGSM	
P. protegens CHAU AGL83159 C. serinivorans ABU03706		EEAQETRSQILEAAEKA EEAOETRTKLLDAAEHL	FYERGVARTTLADI	AALAGVTRGAIYW	HFSNKADLVQAMLDSL HFKDKGDLFNAMMDRI	REPLDEMAAASE TLPF-EAAVES	1MCSP DA	LGCMRKLLIHI IOAMRDHALL ⁻	LFHQVALDPKT TMDOLSHDPOL	
D. acidovorans SPH-1 ABX33148	MAGLNDGRKYILARRTK	EDAFATRNSLLDAAEQV	FYEQGVARASLNEI	AQRAGATRGAVYW	HFKDKLDLFYAMLDRV	TLPLEQA - VYSI	CEDDSECDA	LEYVRRLMAV	VFGRIADDDST	
C. testosteroni TK102 AIJ44552	MARRTK	AEADETRTKLLDAAEEV	FFEKGVSRTSLGDI	AQRAGATRGAVYW	HF <mark>K</mark> DKMDVFVSMLGRI	CLPFEEICDD-	- RYGDL - LP		VFESLDEDERR	
R. solanacearum GM1000 AIJ44552 B ubonensis MSMB22 AIX15925		EEALETRNRILDAAEEV	FFEKGVSHTSLSD1	AUAAGVIRGAIYW	HFANKADVFAAMCERV	LLPIDELKKLP	ADAPG-S-NP	LGELRNVANF	CLLGVORDSOL	
B. cepacia ATCC 25416 ALK16488	MV <mark>R</mark> RTK	EEALET <mark>R</mark> NRILDAAEHV	FFEKGVSHTSLADI	AQHAGVTRGAIYW	HF <mark>A</mark> NKSELFDAMFDRV	FLPIDELKRMPI	DAPG-G-NP	LDKIRQILIW	CLLGVQRDAQL	
N. elongata sp. glycolytica ATCC 29315 AJE17632		AEAQKTREQLLQSALDT	FYRQGVAKNPLQAI	ARNAGVTRGALYW	HFKNKEELFEELFRQT	FENFRTTFSDSI	KKAD-K-QG	LKQLLNS	IFAHIKHDELH	
<i>P. stuertii</i> MRSN 2154 AFH92876	MARKTK	QQAEETRQEILDAAIKT	FSERGVSATSLADI	AKSAGVTRGAIYW	HFKNKVDLFHQACESS	DSQIQQAENYY	RLKYS-N-DP	LAILKEILVY	ILTDFIESPKN	
X. bovienii SS-2004 CBJ80742	MYV-NHPQVKNKVYGTKMA <mark>R</mark> KT <mark>K</mark>	QKAKET <mark>R</mark> QQIIEAAIKV	FSERGVSATSLSDI	AIAASVTRGAIYW	HF <mark>KNKIDLISAVCKM</mark> H	ENKIDELEKEY	QAKYP - N - NP	LLALRSLLIFI	LLKMMIDDSRN	
X. hominickii AOM41130 P. mirabilia HI4320, CAP40437	MNVCKSPSVKNKVYGTKMARKTK	QQAKKTRQQIIEAAIKT	FSERGVSATSLADI	AIAAGVTRGAIYW	HFKNKTDLLSVVCKMP HEKNKVDLETEACELT	EYKIDELEKEY() T K Y P - N - N P) S K Y P - D - D P	LIALRSLLIF	ILGMMINDVQH TLTSTVEDPKH	
M. morganii KT AGG32267	MARKTK	QQAGETRRQIIDAALTA	FSEQGVSATSLVDI	AKQAGVTRGAIYW	HFKNKVDLFTEVCSIT	DTKIGFIEQEY	RAKYP - D - NP	LLVFKKILIY	ILTSVASDPKM	
P. fontium AKJ41702	MGRKTK	QASLET <mark>R</mark> QQILDAAMQE	FARRGVSSTSLNDI	ALAAGVTRGAIYW	HF <mark>KNKVDIFNAMWTQV</mark>	ESSIDDVELRY	RNQFP-S-EP	LSALRQTMIY	VLQTTVTDPRR	
S. tonticola DSM 45/6 AKG/020/ P. carotovorum PC1 ACT12120		QQAQETRQQILDAAVRE KOAOETROOILDTALRV	FSERGVSATSLIDI FSEHGVSATSLSDI	ATAAGVIRGAIYW	HFKNKVDLFNEVWELS	ESKIGDLELEY) T K F P - D - N P	LRILREILIY. LRVMRELLIY	MLRLTVSDTHW	
K. cowanii JCM 10956 DSM 18146 APZ05603	MARKTK	QQALETRQHILDVAMRL	FSRQGVSSTSLAEI	AQAAGVTRGAIYW	HF <mark>K</mark> NKSDLFSEIWELS	ESSIGDLETEY	RAKFP - G - DP	LSVLREILVY	ILEATVVEERR	
E. coli UMN026 CAR11718		QEAQETRQHILDVALRL	FSQQGVSSTSLGEI	AKAAGVTRGAIYW	HF <mark>K</mark> DKSDLFSEIWELS	ESNIGELELEY(AKFP-G-DP	LSVLREILIH	VLESTVTEERR	
<i>E. coli</i> O157:H7 S. Sakal BAB33940 <i>E. coli</i> O104:H4 s. 2011C-3493 AFS75705	MARKTK	QEAQETRQHILDVALRL	FSQQGVSSTSLGEI	AKAAGVIRGAIYW	HFKDKSDLFSEIWELS	ESNIGELELEY	AKFP-S-DP	LSVLREILIH	VLESTVTEERR	
E. coli O83:H1 s. NRG 857C ADR25868	MARKTK	QEAQETRQHILDVALRL	FSQQGVSSTSLGEI	AKAAGVTRGAIYW	HF <mark>K</mark> DKSDLFSEIWELS	ESNIGELELEY	AKFP - G - DP	LSVLREILIH	LESTVTEERR	
S. flexneri 2a / 301 AAN42064		QEAQETRQHILDVALRL OFAOFTROHILDVALRL	FSQQGVSSTSLGEI	AKAAGVTRGAIYW	HFKDKSDLFSEIWELS HEKDKSDLESETWELS	ESNIGELELEY(2 A K F P - G - D P	LSVLREILIH	VLESTVTEERR VLESTVTEERR	
S. dysenteriae Sd197 ABB60663	MARKTK	QEAQETRQHILDVALRL	FSQQGVSSTSLGEI	AKAAGVTRGAIYW	HFKDKSDLFSEIWELS	ESNIGELELEY	AKFP-G-DP	LSVLREILIH	LESTVTEERR	
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Conservation Consensus	R EI_FHKCEFVGEN	1 R - L Y - F		LPA-LD-RRAAI-L	R GL - ENWLF - P	- SFDL A	- V D L	- SP - LR		
Conservation Consensus	<u>RЕТ_FHKCEFVGEN</u> 140 150	160 17	RIELC	LPA-LD-RRAAI-L 190	RGL-ENWLF-P	SFDL A 220	230	- SP - L R 240	250	
Conservation Consensus B. ubonensis MSMB22 AJX13909	<u>Rеі_fнксеfvgen</u> 140 150 AlgesCalpsls	160 17	RIELC 0 180 ALRQIVDEVSSGLG	190 BDAPDDARAIAFLA	RGL-ENWLF-P 200 210 LLSGGVTLARAVRDPA	-SFDLA 220 LAERIADAVGQ	230 (AVVIAECAE	- SP-LR 240 VQPEKRRE	250	199
Conservation Consensus B. ubonensis MSMB22 AJX13909 A. xylosoxidans CKH02195 P. aeruginosa PAO1 AAG05408	REI_FHKCEFVGEN 140 150 ALGESCALPSLS AEEGSVQRVLEILYLKCERSDEN CEPGSVQRVLEILYLKCERSDEN	1R-LY-F 160 17 PEVMRADDDT-RDAYEQ APLLRRRDLWERHALRT FPLLRRRFLLEKOGORE	ALRQIVDEVSSGLG	190 DAPDDARAIAFLA PRALDVRLSNVYL PARLDVFLASTYL	RGL-ENWLF-P 200 210 LLSGGVTLARAVRDPA HSLIEGVFGTICWSDR	-SFDLA 220 LAERIADAVGQ LKGDIWPRVERI LRDDPWNRAERI	230 (AVVIAECAE (LRAAIDTLR	- SP - LR 240 VQPEKRRE	250 TPQAA	199 212 210
Conservation Consensus B. ubonensis MSMB22 AJX13909 A. xylosoxidans CKH02195 P. aeruginosa PAO1 AAG05408 B. cepacia ATCC 25416 ALK18596	A EI_FHKCEFVGEN 140 150 A EGSVQRVLEILYLKCERSDEN CEPGSVQRVLEILYLKCERSDEN CEPGSVQRVLEILYLKCERSDEN QRVLVILYTKCEQSEEN	160 17 PEVMRADDDT-RDAYEQ APLLRRRDLWERHALRT EPLLRRRELLEKQGQRF GALQRRRMLLELQMLRI	ALRQIVDEVSSGLG GLRQIRAVSREDL TKALLRAIAAGEL	190 DAPDDARAIAFLA PRALDVRLSNVYL AADLDVHLAAVYL	RGL-ENWLF-P 200 210 LLSGGVTLARAVRDPA HSLIEGVFGTICWSDR QSLWDGICGTLAWTER VSLLEGVFASMIWTNR	SFDLA 220 LAERIADAVGQ LKGDIWPRVERI LRDDPWNRAERI LRDDPWNRAERI LRGNLWNDAEAI	230 (AVVIAECAE 1LRAAIDTLR 1FRAGLDSLR 1LDAGFDTVR	-SP-LR 240 VQPEKRRE	250 TPQAA LADA KLPD	199 212 210 215
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Conservation Consensus B. ubonensis MSMB22 AJX13909 A. xylosoxidans CKH02195 P. aeruginosa PAO1 AAG05408 B. cepacia ATCC 25416 ALK18596 B. ubonensis MSMB22 AJX16992 P. protegens CHA0 AGL83159 C. serinivorans ARU03706 D. acidovorans SPH-1 ABX33148 C. testosteroni TK102 AIJ44552 P. solanacearum GM1000 AIJ44552	R EI_FHKCEFVGEN 140 150 AEEGSVQRVLEILYLKCERSDEN CEPGSVQRVLEILYLKCERSDEN QRVLVILYTKCEQSEEN QRVLVILYTKCEQCDEN QRVLVILYTKCEQCDEN QRVLVILYTKCEQCDEN QRVLVILYTKCEQCDEN QRVLVILYTKCEQCDEN QRVLVILYTKCEQCDEN	160 17 PEVMRADDDT - RDAYEQ APLLRRRDLWERHALRT EPLLRRRELLEKQGQRF GALQRRRMLLELQMLRI GALLRRRLLLELQMLRI CDLRRQRRAASLDCNVH LQIRERHEWASQRHIQR MPVQERNRAALDSFSAQ ADVRLQHIESSGFAREK	ALRQIVDEVSSGLG SEKLLRAAVSREDL GLRQIRRAVERGEL TKALLRRAIAAGGEV IELALRNAVNRGQL IAHAVREWAQCGAH LELALRAAAESQSL FARDLAAAAEGQSL	190 DAPDDARAIAFLA PRALDVRLSNVYL PARLDVELASIYL AADLDVHLAAVYL AADLDVHLAAVYL PENLDAARAAITL PLNATPEQIANGF TMSMPAPQASIAL RLSVSPEEAALGL PPDI DVPLAVAHE	RGL-ENWLF-P 200 210 LLSGGVTLARAVRDPA HSLIEGVFGTICWSDR QSLWDGICGTLAWTER VSLLEGVFASMIWTNR VSLLEGVFASMIWTNR HAFIDGILYQWLLAPD HSLFVGLMYQWLLTP- CAMFDGLLQSWLLG-R HSLFVGLIHGWVLTEG HASEGGTMGDYLEYP	220 LAERIADAVGQ LKGDIWPRVERI LRGDDPWNRAERI LRGNLWNDAEAI LRGNLWNDAEAI SFALHTEAERI - TFDLQETSRCQ - AFDLKQVGAQ - SFSLVKVGSMS - ASSLAVKRERI	230 AVVIAECAE ILRAAIDTLR IFRAGLDSLR ILDAGFDTVR ILDAGFDAVR VIDIGLDMLR CLDAFLRGAG AVDVCLRGLG SVDVYLSGLG	- SP-LR 240 VQPEKRRE SSPQLR SSPYLL TSAALRGRAH TSAALRHAQH SAALRHAQH LSPNLRH LGAVLNQR FTVPQAQ FRVNL YSPALRLAQP	250 - TPQAA	199 212 210 215 215 210 208 221 206 219
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Figure S3. Sequence alignment of the MexZ orthologs identified in genomes encoding ArmZ/PA5470 orthologs. Gene groups encoding clustered orthologs of *P. aeruginosa* MexZ/MexX/MexY or ArmZ/PA5470 were

identified in bacterial genomes (Refseq 91, reference and representative genomes) using MultiGeneBlast. All accessions are included in Data set S3.

Conservation Consersus	HAR IN ANT							
A4G05408 1145004628 . 6 nobable transminional regulator (Desurformnas aerupinosa DAO11	10 20 50	40 50 60 70	80 90 100 11	0 120 13	130 140	150 160 170	180 190 200 210 220 230	240 250 260 270 280 290 300 310 320 330 340 350
AAK90186.2] transcriptional regulator, TetR family [Agrobacterium fabrum str. CS8]	M RRTKAEAEET	RQAI LAAAERVFFKKGVANSSLDEVAAAAGVTRGAI YWHSSK	ADLFIGLYESVALPE-	SDLLDFG-DPDLK	KGTA LL- A	KI EEATCKWLALLAEDEQRQRI MTI SL- RTNY	- SDEFAPVLHAQEELDRHHKDVLEAAFQRVQSEGVFNDNWTAESALGALYWLLKG	VYDWLTG_KR_FDUXKEGAEAMHA_LLKK_GFQRPVP 10
AALS2612.1] transcriptional regulator, tetr family [Brucella melitensis by. 1 str. 10m] AAN67010.1[AE016329_5 Probable HTH-type transcriptional regulator TtgR [Pseudomonas putida KT2440]	MVRRTKEEAQET	RAQI I EAAERAFYKRGVARTTLADI AELAGVTRGAI YMHENK	AELVQALLDSLHETH-	DHLAR ASE SE	EDEL - D PL- GO	CMRKLLLQVF NELVLDARTRRI NEI LHHKCEF-	- TDDMCEI RQQRQSAVLDCHKGI TLALANAVRRGQLPGELDVERAAVAMFAYVDG-	I LI GRWLING - KU FUL I MUSRU SI E VI C. SLAV. FANI FU. 200 LI GRWLINF. DS. VULLGVERWORGEDM.R. SPAL RK. 201
AAOS//S3.1] transcriptional regulator, letik Taminy [Pseudomonas syringae pv. tomato str. DC.3000] AAQ58114.1] acrab operon repressor [Chromobacterium violaceum ATCC 12472]	MARKTREEAQT	ROOLLEAAEQAFYERGVARTILADIAILAGVIRGAIYWHFNNK RQQLLDAAEQLFSEQGVSRTTLAEIATAAGLTRGAVYWHFONK	LDLYRAMLDRVSPSF-	···· DDMREQLLLVA····	NTD PA- QA	ALWQHSHRLLALI EHDPQVRRILLI LFMRSEY	OGELAPI HEECI AHMHEARGLLSQVVGAAKARGQTYDCVDPDEVAVALQSLHDG	- ITYQWLUV DS-FSLPAEAEQUVDVCLDMLKFSPTLKV KNSP
AAU49084.1 transcriptional regulator, TetR family [Burkholderia mallei ATCC 23344] AAY39036.1 transcriptional regulator, TetR family [Pseudomonas syringae pv. syringae B728a]	MARRTKEEALAT MVRRTKEEAQIT	RDRI LDAAEHVFFEKGVSHTSLADI AQHAGVTRGAI YWHFASK RSQI LEAAEQAFYERGVARTTLADI ATLAGVTRGAI YWHFNNK	SELFDAMFDRVLLPI- ADLVQAMLDSLQEPL-	DELKA GTG EP DEMAQ ASQ SE	EPH- A- D PL - GF SEEEE- D PL - GC	RIREILIWCLLGAARDPQLRRVFSILFMKCEY CMRNLLIHLFHELALDPKTRRINEILFHKCEF	 VADMGPLLQRNREGMRDALRNI EADLAQGVANGQLPADLDTWRATLMLHTLVSG- TDEMCDFRRQRQDNAI QCHDRI TLGLNNAVRQGQLPKRLDTARAAVALFAYVNG- 	- FVRDMLMLP - GE - I DAERHAEK V VDGCF DMLRMSPAMRK - DD
AAZ46899.1 transcriptional regulator, TetR family [Dechloromonas aromatica RCB] ABB74000.1 transcriptional regulator, TetR family [Nitrosospira multiformis ATCC 25196]	MVRKTKEEAEQT MARKTKENAELT	RKHLI DAARTVFHECGVSRSTLEKI AKAAGVTRGAVYWHFKOK RORI VDAAROVFLERGVARSTMEHI AREAGVTRGAI YWHFNNK	AELFFAMREDVFAPM TELIQAMREQVFLPLI	/ERTDALLLS DRMDDTLLV	- DQFAN PL - DA - EGVDD PL - AG	AI EASI KEFFRVLDDCSVVREVFEI MI SRCEY	 VDEFAAVQEEVGRPAQTFLAKI ERVYLQAAERGTLRQGLDPHATAKDTWAFTTG VDEFAMVLQQI LFNCAHI SEKLKLVYERARMQQLLHSSHDLVQLAI DTHLFFI G 	LUH MUKDT EG NORTHÄLELTEN EL
ABD69792.1 transcriptional regulator, TetR family [Rhodoferax ferrireducens T118] ABE32227.11 transcriptional regulator, TetR family [Paraburkholderia xenovorans LB400]	MARCTKEEALAT	RNRLLDAAEHVFAEKGVSRTSLHDI AEAAGVSRGAI YWHFKNK	ADLFNAMMERTTLPL-	EDAL HQ I GD	DDPELDPL-HE	ELORAILDTMRKITLDERTRRVFEVATLKVEY	 VDELLAVKARHLQCYVEGVGQMERSLREAALRRGAPLRVSLSMAAQGLHALVVG- VEEMGPVMVRYQTNMREGLAKIEGGLRNAISKGOMPADLDTKLAAAMVHAEVSG- 	- LI HSWL LAP - QA. FEL VGVÄEMALGYYLAG GL VPAPEO- QAAPAP- 21 BUM LEP - DA. TE GAHAVQMWC GME DAL KI SPAPEO- QAAPAP- 21 BUM LEP - DA. TEF GAHAVQMWC GME DAL KI SPAPENG GAAPAP- 21 BUM LEP - DA. TEF GAHAVQMWC GME DAL KI SPAPENG - 2010
ABF10459.1 DNA-binding transcriptional repressor [Cupriavidus metallidurans CH34]	MVRRTKEEALET	RNRI LDAAEAVFHARGVARPSLADI AEAAGVTRGAI YWHFKNK	SDVFAAMCDRVNLPV-	EALCS PERI A	ASQE- D PL - GS	SI RDI CAFVF RQTVNNPQWRRVFEI I FHKCEM	- VEDNGAL FVRQRQSHQEGTVKMREHLRLAMERGQLPADLDLPLAVNAFHAALGG-	- VLAHWLF5P - ED DFELAREAERLADAFIDTERLSPALRV-GVYRPMAPLDÄEMAALCEROPOOPOALAPT-
ABM38187.1] transcriptional regulatory protein [Aeronionias inforophila subsp. hydrophila ACC 7505] ABM38187.1] transcriptional regulator, TetR family [Polaronionas naphthalenivorans CJ2]	MKSFSGDTEVARRTKEEALVT	RNKLLDAAECLFQSQGVSRTTLQDIALRAGATRGAVYWHFKDK	ADLFNAMMERVTLPL-	EAYFNHE- AAP AET	TSSDAY PL - EF	RMRNAILKALNQI VNDPQTRRVLEVATQKVEY	- I EELKTI RLRHLAVRNGFLCRVQQGLDAASRHENLKLPLSSALAAQGLHALI DG	LI ONWLIDP - DA FDLLEAGOSTNULYFTGLGFGSEPOS LAPAAGKK- 23
ABP86442.1] transcriptional regulator, letk family [i/seudomonas mendocina ymp] ABR62218.1] transcriptional regulator, TetR family [Sinorhizobium medicae WSM419]	MVRRIKEEAQAT M RRTKADAEAT	ROKILCAAERMEEKKOVPNTTLEEVAKAASVIRGAIYWHEENK	TDLFLALYEAVPLPH-	EDM A- R- EI E TE	EAFDTL-AI	I VESATSDWLTTLAADEQRQRI LAI ML- RCDY-	TGELLGLKERMOAL SAECDORI AKALSNAVGROUPAELDCKKAAVCLHATMEG DNDMSAVLVRQREI EERHDALLELAFARALARGOMQEHWTPPSATRALRWMMMG	LETWILL'UP- S-FDLANDARAU UD UDMENSPALERWY FIG LETWILLEG RR. FDLVI GREALINE - LFA - SFRO- EAAAPONLATI GDESAPHRR. 222
ACB35969.1 transcriptional regulator, TetR family [Leptothrix cholodnii SP-6] ACC69669.1 transcriptional regulator, TetR family [Paraburkholderia phymatum STM815]	MVRRTKEEAAAT MVRRTKEEAQET	REHLLDTAEQVFLARGVSRASLLDI AAAAGLTRGAI YWHFKDK RTRI LDAAEQVFSEKGVSRTSLADI AQTAGVTRGAI YWHFANK	AELFLAMLDRIMLPC- GELFTEMFDRVLLPL-	EAASCDL-TLQAG	AGGDFEQML DPNEA-DPL-GF	RQAVLQPLQRLCADERTRRVFTVIIHRTEY RLIEICTVCLRDTANDPHRRRVFDILFHKCEF	 GDDMLSVRTRHLQAIADWFAGMATLLRSARQQRLIHADVDPDLAARGLFALVDG- VEEMGPVMARYQNTMREGLTNIQTCMRNAISKGQLPADMNVPVAASMVHAFISG- 	- LLSQATLAS- DP-ATMLAAGEQAVSI FLAGLRADRTA 200 SLKDMLYVP-EV-LDFGRHÄRQMVESMD DALR. SPALRM-GA 201
ACD28862.1 transcriptional regulator, TetR family [Ralstonia pickettii 123] ACO75905.1 transcriptional regulator, TetR family [Laribacter hongkongensis HLHK9]	MVRRTKEEALET MRRTKEEAAQT	RNRI LDAAEDVFYARGVARTSLSDI AQAAGVTRGAI YWHFRNK RAALLDAAEQLFAERGVSRTSLADI AAAAGVTRGAVYWHFRNK	ADVFAAMCERVKLPM- SDLYTALHERVRLPL-	ETMCT PLG VE SARF D AL	/E-AD-DPL-GE ALMQESGPLLDF	ELRTVGNFLLRQLVEDAHWRKVFEIMFNKCEF RLEVILTDILTDLVTNPQRQRVMDILLHKSEY	 VEDTSPILKRQQESFEEGMAHLTSIIEQATRRGQLPADLDIPLAVAHFHATFNG- IEELRPAIERLVESHEGNQTRLRDVFSAAQASGEMRADVDPLTAAEMVMFFMHG- 	- IMGDYLFYP- DV: SSLATKRERLLDØCI DTLKYAPSLRL-EPAAAATVRTGAPA. 22 - TLSGWLMFPRCH-YPLAGRAPALVALLVRGLRSGA. 200
ACP27244.1 transcriptional regulator, TetR family [Sinorhizobium fredii NGR234] ACT46915.1 transcriptional regulator, TetR family [Methylotenera mobilis JLW8]	MIL	RRKILSAAERVFYKKGVSGTTLDEVASEAGVTRGAIYWHFANK	TDLFLALYDAVPLPQ-	EDM A- R- EI E TE KRAL DO- VK PF ON	EAFDTL-AI	I VEAATGDWL DMLAADEQRORI LAI ML - RCDY	 DNEMSTVLDRQKEMEERHTAMLELAFARALERGQLRENWTPAAAVRALHWMMMG- TPDLLHLRYAWEKORI VOLEKLLKDSI ALGELKLNDDFELI SLYCOSI LEG- 	- LGTDWL FG - RR - FDL AAEGROAL RR - LFE SFRO TI PAVSVA 210 VFSI VY FGUN, PD TORWARED LCFF GIORITYK 2000
ACT47793.1 transcriptional regulator, TetR family [Methylotenera mobilis JLW8] ACT50943.11 transcriptional regulator, TetR family [Methyloxogus glucosetrophys SIP3-4]		ROKI VDAARTVFLARGVSRSTLEHI ASQAEVTRGAVYWHFKNK	TEI FHAI R EQVFLPLI	DRMDDTLAISA	ADNSQN PL - DO	QI EASMCSTI QALNDNI EMREI YEI MMI KCEY	VDEFALVLHQI MNNCSSLVEKI EATYARAQSONLLASSI TPGALALDTHLFFGG VDEFAEVI ODI ANNCSNI SRNI FRAVORAOFI DI L DTSCTPEFYAMDTYLFFSG	LLH MWKDA-DC-SKFRYQAIDLIKSHIKLRRK
ACT51956.1 [transcriptional regulator, TetR family [Methylovorus glucosetrophus SIP3-4]	MARKTKEDSQRT	RDLI LDAAEHVI YERGMSLTTMANI ADAANVSRGAVYGHYKGK	VELAI AMA	ERAI HT- AP SLER	- GPEEP AL- VI	YLKRYCLHEVHSYI DASSLQRVLFI LYVRI DD	- TPE LVSI RERWEQKRAAVI AQCLQAAI QEGSLAADSDVALYTLYVQAQI EG-	- I FS I FF NHD- TT - I DKNDI AERILGS MGLERIT LPARP
AD049571.1] transcriptional regulator, tett family [Dickeya Zeae Ecitisa6] AD049571.1] transcriptional regulator, TetR family [[Enterobacter] lignolyticus SCF1]	MARKTKQQALET	RQHI L DVAL RL FSQQQVSSTSLADI AKAAGVTRGAI YWHFKNK	SDLFSEI WQLSEFSI-	ADLET EYR AK	AKFPD- D PL- SA	VLREI LVYI LEATVI DERRRLLMEI I FHKCEF-	- VGEMAEVQLVQRGLCLESYDRI EFTLNECMRARLLPVNLLTRRAAI LMRGYI SG-	LIEWWELE LP ES FOLKNEAT L'UGEL DEN OCCUT LRA - V. S - PAV.
ADU39638.1] regulatory protein TetR [Variovorax paradoxus EPS] ADX44384.1] transcriptional regulator, TetR family [Acidovorax avenae subsp. avenae ATCC 19860]	MARRIKEEAMAT MARRTKEDAVAT	RNRLLDAAELLFQAQQVSQTSLQQIAQQAGATRGATYWHFKDK RNSLLDAAEHVFYQKGVSNASLNDIAQAAGATRGATYWHFKDK	ADLFNAMMERVILPL- VDLFNAMMERVTLPL-	ECASG G CAD	AAGSDDPL-VE ADHGRMPPL-QF	EI EEGMVHALTEMITDPOVRRVFDVATHKVEY	- THOMAS VOORHEDARNAC VVDFEXALREAARRAHVKEP VPGHVAAQGMHALT SG- - VGELSAVRDRHVEASLEFRRQFAAELALAASDQGVELPSSAEVAALGEQALFDG-	- LI QWWLLDP 1 A - FDLYPTORRTFRYTLAGLOFERPAIG-TAVAHEAETAVA LMQVWLLDG AA- FGLAETGRAAVDÄYLRGLGFDVSASF-DPLSAGI PWKI CQASRNAVP
AEB82825.1 Tetracycline transcriptional repressor MAATS-type domain-containing protein [Alicycliphilus denitrificans K601] AEF20872.1 Tetracycline transcriptional repressor MAATS-type domain-containing protein [Pseudomonas fulva 12-X]	MARRTKEDADAT MARRTKEEAEET	RNALLDAAELVFYEKGVARASLSEI AQAAGATRGAI YWHFKDK RAHI LDAAERVFYANGVSGTSLADI ASAAGVTRGAI YWHFONK	VDLFNAMMDRATLPL- VDVFQAMLDRRMLPQ-	EGVCN A GEA	AAYAKE PL - VO GEDEP- D PL - GN	QLRGMVELLLRSVVSDAHMRRVFEIALYRVEY NMRQLLVQLLARMQADSECRRVGEILQYKCEY	 VSELSGVRERHLAAHARFQALLERNLSLAAAQASLALPMSAAMAAAGLHALFNG- NAELGDLRKRMQAFQQECDQRIARTLRNAVKRGQLPADLDCQRAAICLHAYMDG- 	- LL Q5WL LGE - AS - FDL PAT GRAAVDAY LRGL GF HV
AEG95873.1 DNA-binding transcriptional regulator EnvR [Klebsiella aerogenes KCTC 2190] AEG97506.1 DNA-binding transcriptional repressor AcrR [Klebsiella aerogenes KCTC 2190]	MLNWL-VYQSILYSPLGSEWEKVMARKTKEDALRT	ROLLI ESAI QOFAQRGVTNTTLTDI ADAAGVTRGAVYWHFSSK ROLI LDVALRLFSQQGVSSTSLAAI AKAAGVTRGAI YWHFKNK	AELFNEMW	ELLPH QQW EL SDLEV EYR AK	LDNQ- N PL - TO AKFPN- D PL - SV	GLRKKFITGLQYIAENPRQQALLQILYHKCEF	 TSDMLPESEI RKRI GF- NYAI I RDVLQCCVRNRLLPAETNI EI TLI I LHGAFTG- VGEMAVVQQAQRSLWLESYDRI EQTLKDCI TAQQLPANLLTRRAAI LMRSYLSG- 	- II KNWLMDP - EQ - FNLYQQAPULVDNI MSALSLQPDHS - VVKI - AAV
AEI78972.1 transcriptional regulator TetR/AcrR family [Cupriavidus necator N-1] AEV26249.1 transcriptional regulator [Azospira orvzae PS]		RHRI LDAAEAVFHARGVARPSLADI AEAAGVTRGAI YWHFKNK RREI I DAARCVFHECGVSRTSLEKI ARVAGVTRGAVYWHFENK	SDVFAAMCDRVNLPV- AELFFAMREDSLA-VL	EALCD PER LA	ARQE - D PL - GO	GIRDICAYVMRQTVINPRWRRVFEIIFHKCEM	 VQDNGAI FERQRQSHQDGLI KMREHLRLALERGQLPADLDLDLAVNAFHAAI GG- VDEFA0VLOEVNKPCMDFLAKLI RSYORAADKGYLRPGLDPEGAAYDTLSFTAG- 	- VLAHWLFSP - OD - FDLDANAERMSDAFI DT LKFSPALRH- GYVPRPMAALDRELSTLCQQACPNAOPGGLETGDLVP - 225 2550 PG DLIRLKVPDM ROHLLRRP - 2000
AEV61378.1 EmhR [Pseudomonas fluorescens F113] AEW63533 11 DNA-hinding transmittional regulator Env9 [Kleheialla pnaumoniae suben, pnaumoniae HS11286]	MVRRTKEEAQET	RSQLLEAAEQAFFERGVARTTLADIATLAGVTRGALYWHFSNK	ADLLQAML DTLHEPL	· · · · DELAR- · · ASE- · · RE	EEEL - D PL - GO	CIRKLLVRLFQDVALDPKTRRINEILFHKCEF	TDEMCDLRQQRREVSLDCNVRI ALSLRNAMKRGQLPDDLDPERAAVAI HAYI DG SDMI SEVEL ROPLGE, NYSLLGGL OCCVRNNLL PAETNI EMILLVL HSAESG	I LYOWL LAP - DS - FALAAEAEBWEI GLDMI HLSPSLRK - 220 LI KYNK LAP - DS - FALAAEAEBWEI GLDMI HLSPSLRK - 221 LI KYNK LAP - OR - FRI VORGAN VON MAVVLAABI SG - PALB - I VN. 110
AFE3555.1 DNA-blinding transcriptional regulator Eriv (recolumn predmining adaption predmining transcriptional regulator Eriv (recolumn predmining adaption predmining transcriptional regulator Eriv (recolumn predmining adaption pre	MARKTKSQALET	RQQI LDAAVREFSARGVSSTSLTDI ANAAGVTRGAI YWHFRNK	VELFNAI W EAYESRI -	KVLEV EYQ TK	KFPN- N PL - RI	LREI LI YI LVATVTDSQRKALMEI I FHKCEF	- VGENTSVHEARKALYMEGYGKI ERI LVRCI EEKQLPANLDTRQAAVI LRAYLSG-	LMENVLFIP - ES - FDLEGNAGREVDTYI DMLRHSSFLTM - I K
AFJ47530.1 aCAB operon repressor [Shimwellia blattae DSM 4461 = NBKC 105725] AFK54506.1 transcription regulator protein [Tistrella mobilis KA081020-065]	MARRTKEDAEKT	RQQI LDAAAAAFDAEGVAACALEHVARLAGVTRGAT WHEKKK	SDLLDAMLERVRLPQ-	···· EQVMEDLAAGRI ····	TDR- RPL- DL	LFHETSRDALSMI VNDERRRLVFRI I FTRI DQ-	- VGEMAAAREAQKKLCMEGTDRIEHALQKCITAGLLPADLINIKAAVLMISTICG - AHEQSPLHERQQADRVHFMTLIRQIMARAAEAGDLAPGWTPETAMRVAHAMFHG-	- LINEIWALT IP - UL F DE LINESAVI VID EL ENFERCIES VII - A PEN - PESAG- GE- AVSDML VLD - E - ARL ADELALT LIDAE DIT MITLOSKY DPRI. ND GOGCLLER AL PVGEG- 233
AFT69929.1 MAATS-type transcriptional repressor [Alcanivorax dieselolei 85] AGQ29802.1 transcriptional regulator [Serratia liquefaciens ATCC 27592]	MRRTKAEAQET MARKTKQQAQET	REQILDAAERVFHEKGVSRTSLNDIAGAAGFTRGAIYWHFKNK RQHILDAAVREFSERGVSATSLTDIATAAGVTRGAIYWHFKNK	HDVFAAMLERKRLPL- VDLFNEVWELSESKI-	EALAQ RAE HP GDLEL EYQ AK	1PEEK- D PL - GF AKYPE- N PL - RI	RLREFLIYVLCETVRDPSRRRVLEIIFOKCEF	 TVETDPLMARQKESFLEASKSMRIILGRAIERGQLPESLNIERAVTLLHVQVCG- VGEMLPLQDARKVLYLEGYDRIESVLRNSMRHGQLPADLHTRRASIILRAYITG- 	- LLYVWLLVP - ET - FDL EOGRAAHHVDCYLNTLASCPSI SGRPDSPS - 211 - LMENWLPM - ES - FDL KARAVLL DSFI EMAQFSPT IRI - KPEEGELAAQPLSAEHHHL - 222
AHF77985.1 DNA-binding transcriptional repressor [Sodalis praecaptivus] AHJ74949.1 DNA-binding transcriptional repressor AcrR [Kosakonia sacchari SP1]	MARKTKRQAQET MARKTKQQALET	ROHILDAAI KAFSERGVSATSLNDI AALAGVTRGAI YWHFKNK ROHILDVAMRLFSQNGVSATSLAEI AQAAGVTRGAI YWHFKNK	AELFNEILHTADSKV- SDLFSEIWELSESSI-	RDFET EYQ TK SDLET EYR AK	"KYPD- N PL - Y\ AKFPD- D PL - S\	VLTETMIYILDATVSNRQWRELMEIVFHKCEF VLREILVYILEATVVEERRRLMMEIIFHKCEF	 VGEMALYQEVRSQLFDECYGRLEATLGRCIAQRQLPATLHCRRAAIMLRASMSG- VGEMAIVQEAQRNLCLESYDRIELTLRECMQAKLLPDNLLTRRVAVLIRAYVSG- 	L MENNULF IP GS. F DL QADSRTL VF ÅLI DML RMSPNLRC - E OHD - ÅP - QTV - 211 - MENNULF AP- QS. F DL KERÄRDY SVLLEMCQL CPT LEMC - L NA - 111
AHY12302.1 transcriptional regulator [Citrobacter freundii CFNIH1] AJJ09385.1 Transcription repressor of multidrug efflux pump acrAB operon, TetR (AcrR) family [Edwardsiella anguillarum ET080	813] MARKTKQQAQET 813] MARKTKQQAQET	ROHI LDVALRLFSQQGVSSTSLAEI AKAAGVTRGAI YWHFKNK ROOI LDAAI REFSVRGVAATSLNDI ANAAGVTRGAI YWHFKNK	SDLFSEIWELAKPNI- TDIFHAVWAFMESRI-	DELET EYQ AK	KFPD-DPL-SV KFPD-DPL-RI	VLREILIYVLEATVTEERRRLLLEIIFHKCEF	 VGE MASVQLAQRSLCI ENYDRI EQTLRQCMNANMLPENLNTRRVAVLLRSYVTG VGE MRALGERRKVMYLESYTRI ERVLOHCI FLEOLPANLDTLRSAI ALRSYMTG 	LIENWLFAP-ES-FDLKKDÄREYVAVLEMCLLCPSLRV-N-VAK-SC 115. MESVLFP-DR-FDLOOGAI PLVDRVJ.MAR.HEPPLRA. DAVCAPNDTSVVESAFPATRNSVDKDE-221
AIR02571.1 transcriptional regulator [Pluralibacter gergoviae] AIR05455.1 transcriptional regulator [Cederea neteri]	MARKTKQQAMET	ROHI L DVAL RL FSQQGVSSTSLÄET AKAAGVTRGAT VWFKNK	SDLFCEI WQLSESCI - SEI ESEI WEI TESSI -	TDKET EYR AG	QLPG- D PL - SV	VLTNI LI YI LEATVMEERRRLLMEI I FHKCEF	 VGE MAAVRHOORNE CI ESYDRI EQI LNECI AAGOLPEDLETROAAI EMRSYI SG. VGELEVI ODABRTI YMEGNERI FAALORCI DAGKI PSSI RI SLAVTI MRSYI TG. 	. IVENUE FAP- DS- FELKKEARNYVNI LEMY OF CPT LRA- APQA- ESS- 21 ENNI VAP- ET- EDI HAR ANDFI AVI LEMY OF CPT IN- PA- 11 ENNI VAP- ET- EDI HAR ANDFI AVI LEMY OF CPT IN- PA-
AIR67014.1 transcriptional regulator [Pantoea rwandensis]	MARKTKAQALET	RNQI LDAALAHESEHGVAATSLADI ATAAGVTRGAI YWHEKNK	ADVLHEI W LRCDAGL-	DDVEL EYQ TK	KYPG- D PL - SV	VI RSMLI YI L DATAKDPORRALMEI I FHKCEF	VGEMSTLQDMRQSLLLECYDRIELVLRECIEVGQLPARLNTLQSARLMCGYING TOP CONTROL OF CONTROL O	- MRENNE FRP - QA - FDL AAR APQLUDAF I DM RLS PTING - AR
AI10696.1] retik ramity transcriptional regulator ("Seducinonas mizosphaerae) AIU26411.1] TetR family transcriptional regulator [Pandoraea pnomenusa]	MARRTKEEALET	RNLLLDTAETVFAQKGVSRTSLADI AEAAGLTRGAI YWHFKNK	I DLFNAMTDRI RLPM-	ERM D EEC AE	AEPEDGD PM- VF	RMHEI CKLVLKETARNERRRRVLDI LFHKCEY-	TDEMEDMARQROSUSEDENVALERSERNAVIREQUIPPEDIOLVRAATAETATT DG TNEMLSVLERQREACADGKQRI MRDMERALARGQLPAQLDTRRAAT MLHALVVG	MISOWELVP-DS-FDLTVCARATWIDVSEULSELITALIAN 410 MISOWELPP-D-YDLGVCDAVVDGFDM-RTSP-AMRRPGTPAVONATV-222
AJD47870.1 transcriptional regulator TtgR [Alcanivorax pacificus W11-5] AJG21555.1 Transcription repressor of multidrug efflux pump acrAB operon, TetR (AcrR) family [Cupriavidus basilensis]	MARRTKAEAMET MVRRTKEEALET	REQILDAAELVFHRKGVSCTSLNDIAAEAGVTRGAIYWHFKNK RHRILDAAEAVFHARGVARPSLADIAEAAGVTRGAIYWHFKNK	HDVFIAMAERRRVPF- SDVFAAMSDRVHLPL-	DTLLR QAM LP EALCE PGR I A	ASQE - D PL - GA	AIRAVMVTMLNELASDPQKRRLFEIYFLRCEY	 TAETLPLLNHRQDGFRQVSGYLAEGFRNAVRREQLPAGLDI NKAVVQFHAQLTG- VADNGAI FERQRQSHQEGTVKMREHLRMAVDRGQLPADLDLDLAVNVFHASI GG- 	- LIFTWL QP - ES - FCL ROOGTE L VDGF HTL RHCPYL QQSDPVANA - M. SHWL RAP - ED - FDL ETNAERVANAER TDT KF SPALRO, G'VARRVYKLEEEVASMCQEAKKKAET GQAAQALATKALPG- 255
AJQ93422.1 transcriptional regulator [Gynuella sunshinyii YC6258] AJW43866.1 TetR family transcriptional regulator [Ralstonia mannitoliiytica]	MARKTKEAAQET MVRRTKEEALET	YQALLDAAENEFSRHGVSATTLNDI ALAAGVTRGALYHYFGOK RNRI LDAAEDVFYARGVARTSLSDI AQAAGVTRGAI YWHFRNK	QALI AALI DRCFYPM- TDVF SAMC ERVKLPM-	EQLTL SQC ETMCS PPG VE	AETSM L- KK /E- AD- D PL- GE	KLHVCCLAYLTLIAKDRSAQNVQTITMHKCEM ELRNVGNFLLRQLVEDAHWRKVFEIMFNKCEF	 VDAHDTI HEHYRNLRNEI YREMKQDLEQAI NCGDLPDHI DPHQVAVALFSI TQG- VEDTSPI LKRQQESYEEGMARLSSI I EQATRRGQLPADLDI PLAVAHFHAAFNG- 	- I VYAWLADP - MY CDLI ROGMANI DTYLAGI TSPLIS
AJW96568.1 bacterial regulatory s, tetR family protein [Burkholderia gladioli] AJW97309.1 HTH-type transcriptional regulator ttgR [Burkholderia gladioli]	MRRTKEEALAT	RARI LOSAVQAFLRQGLSHTSLADI AGVAGVTRGAVYGHFRNK RNGI LDAAEHVFFEKGVSHTTLADI AQHAGVTRGAI YWHFANK	SALFEAMLEHAGLPV- GELFDAMFDRVFLPI-	DPFLI AWH	- APEPD PL - EC	QLRAALVRHLARVLSNGVARRVYSIVHSRCEV	 SEETREFWEKVHMGRRAAEQRI VDALADAHAQGQLADNADI AQLAAFTHASLMG VADLEPLLORNRAGMSEALHNI EGDMKOAVADGELPADLDTWRATLMLHTLVSG 	- FFI RSLAEQ- AS-1 APROSAEHVVDLAFLLERPFEAAD- 190 - VRDMU, MLP - DE I DAEOHAEPL VDAVFUDMERLSPALERA - KPAA- 212 MARTINE - DE I DAEOHAEPL VDAVFUDMERLSPALERA - KPAA-
AKE93595.1 transcription repressor of multidrug efflux pump [Cronobacter sakazakii] AKE97035.1 DNA-binding transcriptional repressor AcrR [Cronobacter sakazakii]		ROOLI DAAI FTFAERGVAHTTLTDI AQAAQVTRGAVYWHFASK	ADLFNEI WQQQLPVR- SDLFSEI W	EI I RP NI P EE	EAWR-DPL-RL	LERETFIAVLQYIASSPRORALLQILYRKCEF	DEEMMPESEI RERI GF- SRHYI GELLRRGI ADKQI AGSLDVDI MLTI LHGCLSG- VGEMAVVODAHRSI CFOSYDRI EHTLROCI OSGMI PENI OTRRAAI LMRSYI SG-	
AKJ31763.1 TetR/AcrR family transcriptional regulator, acrAB operon repressor [[Polyangium] brachysporum] AKI 34143.1 transcriptional regulator [Klebelella ovytoca]		RRQI LAAARETFHSRGVGNTSLEHI AQAAGLTRGAI YWHFANK	EQLEKAMCQEVTIPLV	DQMDYTLLQ	- DPHAD PL - QF	RVANFLMQFVAALSQNSSLLSTMEILNFKCEF	VGELARDLTDYI ERNEECLAKLQQAYLAASRAQQLRPGLTPKLAALETLVFLTG SSDMMPEAFI RKRI GE, SYPLI RSI OLCI RNGL PVETNVELSI VLHSAFTG	- LLR- LRLLGV- PA- FOKCPELKALI AAHVDSRRLCLKSAG-
AKL2714.1 transcriptional regulator [Klebsiella oxytoca]	MARKTKQQALET	ROHI L DVALRLFSQQGVSSTSLAAI AKEAGVTRGAI YWHFKNK	SDLFNEI W	NDLEV EYR AK	KFPN- D PL- SV	VVREILVYI LEATVTEKRRRLMMEI I FHKCEF	VGENVTLQEAQRSLCLESYDRI EQTLNECI AAKMLPANLLTRRAAI UNRSYLSG AGAUNTAL AAKMLPANLLTRRAAI UNRSYLSG AGAUNTAL AAKMLPANLLTRRAAI UNRSYLSG	- LMENULLAP - NA FDLQHEARAYVETLLEMYQLCPSLRS- SEG- AEA-
AKN04185.1] tetk tamily transcriptional regulator [Herbaspinilum seropedicae] AKZ61497.1] TetR family transcriptional regulator [Herbaspirillum hiltneri N3]	MARSIKEEALET	RSRILDAAEQVFHERGVSQISLADVAKAAEVIRGAITWHFKNK RSRILDAAEQVFYERGVSHTSLADVAKAADVTRGAIYWHFKNK	SDLFDAMCERVRLPM- SDLFDAMCERVRLPM-	EAI ME ANA DE	DERVT- D PL- GE	EFI KGGVYVLKQAAT DPRCRKVFDI I FNKCEF	ADAHDPI LI RORECHVDIGMERE EQI LGNAVARGQEPATEDI REACEMI HATESG VDHNDPI LMRORECHMOGMERMEQI LTNSI ARGQEPPENI NI RRACEMAHAMESG	- LLTUWFFSF- DS- FDLVSEUEWULAASMHALKTAPSLUK-K-21
ALD92077.1 Transcriptional regulator [Cupriavidus gilardii CR3] ALJ27113.1 Tetk family regulatory protein [Stenotrophomonas acidaminiphila]	MARRTKEEALET MSAVSNGSAMARKSKEDAQAT	RHRI LDAAEAVEHARGVARPSLADI AEAAGVTRGAI YWHEKNK REGI LDAAI ACEHEHGVVGTTLAMI ATRAGYTRGAVYWHEKNK	SDLFAAMCDRVHLPV- TEVLEAMIERDRMPF-	VQRLQRT- YAP	ASQE- D PL- GO QRQT PI - LD	GIRDIVALVFRETVVNPQWRRVFEIVFHKCEM	 VDDNGAI LERQRQSHEQGLLKMREHLRLAVDRGQLSADLDLDLAVNAFHAAI GG- SSESLSVQAMQRQNSQEELDMVTRTLERARELGQLRPGVDPAAASRMLHI SLTG- 	- VLAHWLFAP-GD-FDLNADAEHLADVFVDTLRFAPSLKK GYVPRFMARLDEEMAALRLKVQQCCAGG- ALYNAMQP-FC VDLERGLMMDVVLLAVYRGVPCPG GVFPAQADSSAGV0- 333
ALT00232.1 TetR family transcriptional regulator [Lacimicrobium alkaliphilum] ALV08763.1 TetR family transcriptional regulator [Roseateles depolymerans]	MVRRTKAEAEAT MYVYPSTMPDMARRTKQEAQET	RATILDAAERQFFEQGVSRTTLDKIARAAGVTRGAVYWHFDNK RTRLLDAAEQLFHERGVSRTSLQDIAQTAGVTRGAVYWHFEDK	SDLFSAMLERIRLPF- VQLFDAMMERATMPL-	RMMLS EMD EV EEGI EA AT	EVAGA- D SL - QS ATSPSPDR PL - ED	SVRDI MIRSLQI VGESEQHRRVLSI VFHRCEY DLRLGLLNVFHCTVNNTRTRAFEIANLRVEF	- I DELNPAVHEQEKLDMEVQQTLERAFERARQSGQLNPDVSPGLAASALHAYI SG- - VGEMARI LERKVAAHRDWTLHNRSAFERAI ALGQLPADLDTQRAAI GLMALVGG-	- LI GKFLLTP - NQ- CDLSQSAPALI DCFLDGVKKCQST- 200 - LLHHWMLDP - ES- FDLVELGQAQLEHYLSSLAVPVANRFPSLTEAERRTLGRQAVCDANRSRDATPADSPAPPPAADPT- 260
AMA45143.1 TetR family transcriptional regulator [Pseudomonas montellii] AML59731.1 Transcription repressor of multidrug efflux pump acrAB operon, TetR (AcrR) family [Serratia rubidaea]	MVRRTKEEAQET MARKTKOQAQET	RNQI LEAAEKAFYNRGVARTTLAEI AELAGVTRGAI YWHFNNK RQQI LDAAVREFSERGVSATSLADI ATAAGVTRGAI YWHFKNK	AELI EALL ESLRETL- VDLFNEVW ELSESKI-	DPLAR ASE SE GDLEI EYQ AK	EDEL - D PL - GO AKF PD- N PL - RI	CTRQLLVRLFREVVQDSRTRRIHEILHYKCEF	 TDDMCEI RQQRQSSI VECHESI SLAVTNAVRRGQLPDALDTDRAALALFAYI DG VGEMMQLHDI HKVLYLESYEHI ESVLRNSMRCGQLPADLHTRRAAVI LRAYVTG 	- LVKRWLLP- DS-FDLLGDADKWADTGLDMERWSPALRK- 210 - LMENNUEMP-ETF-FDLKGEÄAALVDGFLEHWOYCPETTRV- SPSE-RAALTP- 220
AMP03358.1 bacterial regulatory s, tetR family protein [Collimonas pratensis] AMR66063.1 TetR family transcriptional regulator [Pseudomonas alcaligenes]	MARSTKEEALET M. BRTKEOAEOT	RGRI LDAAAEVFHQHGVARTTLADVASAADVTRGAI YWHFKNK	SDLFDAMCERVRLPM- AHLFHELL	EAM E KTA DE	DENAH- D PL - NO PAAGD PL - LS	QFRNRCLFTLQEATLNLQSRKIFEIVLHKCEL	VDPQDPI YI RQHECFLQGRTDI ERLLRFAVAKGQLPRDLDPI LAAVMVQGLLFG TDELREAERRHNAFI DOFI ALVEALFALPDSOARLRPGLTPRLAARALHAOI LG	I NWWFSP-HS-FD.TENVSKVVDNCI HMFKTSPFMK-NAPA 210 LFDWFRP-OL FDPLSDTALI DA LMO CEL DOWNPAR 210 DOWNPAR 2
AMR68377.1 TetR family transcriptional regulator [Pseudomonas alcaligenes]	MARRIKEEAEET	ROSI L DAAERLEHDOGVSRTSLADI ASAAGVTRGAI YWHENK	VDLFQAMLERLHLPL-	EELAQ ASE SE	EDEP-NPL-GO	QTRELLVRLLRNVELDAQTRRI QEI LQHKCEY	- TDDL GDL RQK MQAL HLECDERI EKSL RNAVSKAQL PADL DCRRATL CL HGV VHG-	L DANVEL AP - GC DSL AE CARSF VOAL DMER CSHAL RR - R VL ONVEL AP - GL COLAU C GREVYOAL DMER CSHAL RR - RMOL VL ONVEL AP - GL COLAU C GREVYOAL DMER AS RR - RMOL
ANI7200.1] Tett family transcriptional regulator [Pseudonnas citronellois]	M-RRTKEDSERT	RQTI L DSAEAL FLENGVSSTSLEEI ARNAGVTRGAVYWHFENK	AHLFNELLAQVRLPP-	EQLAL - R- LSG CD	DGI DPL-QS	SLFDLCVEVVHSLAQNAQKRRVLTILMQRCEF	- TEELREAI LRHNAFI ROFI DL CEQLFARDKCRVRLLPGVTPKTASRAVHGLI HG	LINDWLRDP - QL F DPLQDAEALLEP - LFR - GL RDWSQAGAQASAS
ANK /418.1] letk family transcriptional regulator [Ensirer adhaerens] ANO52636.1 hypothetical protein BA177_16880 [Woeseia oceani]	MARKTKOEALET	RONI LSAAEKVETEKGVSNITLEELAKAAGVIRGATTWEFANK	TDLFLACH	···· DVSWGCGNCT····	PGKD PL- ES	SIRRQAVDCLQRAVADPNTKQVWDILLHKCEN-	DGDLGEVLARQEELDEHHNVVEELAFSKALARGOMHETWIPASATRTEHWMMLG VDDAAVMKSRLRKARTECAHNVTELFEAAI QAGQLPRSTDVLTAI SGLFCYI EG	LU WULFG-RI - FULFACGREULS M- LFA-SFAR-SFAR-SFAR-1 AVVA
ANY60870.1 TetR family transcriptional regulator [Comamonas aquatica] AOA73649.1 TetR family transcriptional regulator [Stenotrophomonas rhizophila]	MARRTKEDAEAT MARKTKEAAQAT	RNKLLDAAAEVFFAKGVAGASLSEVAQAAGLTRGAIYWHFKDK REGILDAAQSCFHEFGVANTSLAMIGERAGYTRGAVYWHFKNK	VDLFDALMQRTTLPF- TEVLTAMIDRERVPF-	EQAWEAG- QAKF MQHG I ERLRRT- TSS	IGAVLPEIL-GV RRNTPV-LE	VLRMVFRSVSTDTATRRVFDIALYKVEC DLRSALLVSFRELATDERLRNMMEIML-RNDL	 VGELLDVRQRRI EGALRFALQI EQALLLAAQQEGVCLPVSGQNAARGLQAI FDG- SVESQAMQQLQLEASREELAI FSAAFERARELGQLREGVDVDTVARI I STSLTG- 	- VL HF WLL QDG- QS - FDL EA EGML AVAL Y LK GLE FD L QKE - IA - 21 - VL YSAML EP - FL - FEL QNGT QT L QVF QAF VK PG GAP PEAL PT DD A - 222
AOE40459.1 DNA-binding transcriptional repressor AcrR [Pantoea agglomerans] AOP77053.1 DNA-binding transcriptional repressor AcrR [Enterobacter hormaechei subsp. steigerwaltii]	MARKTKAQALET MARKTKQQALET	RHQILDAAI VLESQQGVSATSLADI ATAASVTRGAI YWHEKNK RQHILDVAMRLESQQGVSATSLAQI AQAAGVTRGAI YWHEKDK	ADVL HEI W L RCDAGL- SDLF GEI W ELSESSI -	DDVEL EYQ TK SDLES EYR AK	"KYPG- D PL - S\ \KFPH- D PL - S\	VLRAMLVYIFDATAKDPQRRALMEIIFHKCEF VLREILVYILEATVVEERRRLMMEIIFHKCEF	 VGEMSALKNMQQSLLLECYDKI EDVLRQCI EAGQLPGSLSTRQAALI LRGYVNG- VGEMAVVQQAQRDLCLESYDRI EQVLTECMQAKMLPATLLTRRAAI LMRSYI SG- 	- MMES WL FAP - DS - FDL AGDAPTL VNAFI DMLR LSPTLTA - TAHH 21 - LMENNL FAP - ES - FDL REARSYVEI FLENCOL CPTLOS - KLSP - RSA - 21
AOP79864.1 acrEF/envCD operon transcriptional regulator [Enterobacter hormaechei subsp. steigerwaltii] APA86732.1 TetR family transcriptional regulator [Paraburkholderia sprentiae WSM5005]	MARKKKEEAQKT MVRRTKEEALET	ROQLIEAAI GLFATRGVSSTTLTDI ADAAQLTRGAVYWHSSK RNRILDAAEQVFFEKGVSRTSLADI AQAAGVTRGAIYWHFAHK	AEI F NAI W DQQL P MR- SEL F T AMF DRVL L P L	EMI RD RLI LS DELKA ASL DP	.SEND- D PL- LM DPNEA- D PL- GF	MLREQFIVALQYIASEPRQYALLQILYHKCEF	 HDDVI SECEI RKRI GL- NDDYLRKTLKRCI SRNVI SSQTNI ELALI VFHAFFSG- VEDMGPVMERYQTNMREGLAKI AGGLRNAI SKGQMPADLDTKLAAAMVHAFVGG- 	VI KNWLMDS NN- FNLYKQAPALVDNI LATLINI TRVAPV VYDT AS- 211 SLRDMLFLP DA- TDFGAHAQRMVEAMFDALRLSPALRT- SAAA- 214
APR93689.1 TetR family transcriptional regulator [Pandoraea thiooxydans] APW43538.1 TetR family transcriptional regulator [Rhodoferax saidenbachensis]		RHQI L DAAEQVFFEQGVSRTSLADI ATAAGVTRGAI YWHFKNK	ADLFTAMFDRIRLPM- GEIFHAMM	ET MVE RCRI S	SDPDPDPA-QT	TLRRVFTQVLCETARNPHRRRVLDILFHKCEY	- TEEMGPVMERHQEACADGRNRMERCLCDAVSLGQLPADLDTRRAAVLMHAMLTG- VDFLOSMRERHLAGRNECLDDMHRLMOLARDKGOLREMDLRHATLGLFALLGG-	- LI SNWLFLP- · RS- FDLEAEASAMADGFFDMLRYSPALR- · · VATAN
APW45976.1 TetR family transcriptional regulator [Rhodoferax antarcticus]	M	ROQLLQAAVRVFAEKGVSRTSLQDI AEAAGTTRGAI YWHFKNK	ADLENAMM	···· EQAMQH-····· I GH	HDPAQD PL - AE	ELEYALLQTMRDIVSNASTRAVFEIAIMKVEY	VDELLGI KERHI QAFADGTREI TRSLREAAGRRGI HLPVNPEVAAHGLHALM/G- VDESOM LBI REAHDSMI DI ETEMI XVAOGRNMI SDDWPEDAARVI VCVVGG-	- LI HSWMLSP - EA - FDLVVVSQSAVRAQLAGLGLHLSV
ARJAO38.1] DNA-binding transcriptional representant [Pantoea alhagi]	MARKTKQQALET	RHQI LDAAI ARFSEFGVSATSLADI ATAAGVTRGAI YWHFKNK	TDLLNEI W AQSESGL-	EDVEQ EYQ AK	KYPD- D PL - SV	VMRAMLRYVFEAPARDQRRSLLEI I FHKCEF	- VGEMLPLQI MQQNLYLECYEKI EQSLSHCI KAGQLPAELNMRRAAI VI RGYVTG-	VENWLEMP - DS - FD EQDAPILVETLIDM KTSPSLSQ - PAFS QI 20
ARN18553.1] TetR family transcriptional regulator [Rhizobacter gummiphilus] ARO87289.1] TetR family transcriptional regulator [Nitrosospira lacus]	MarktkeeaQel	RNRIT DAAERVELERGVSRISENEI AAAAGVIRGAI YWHEODK RORLI QAAREVELARGVSRITMEHI AVQAGVTRGAI YWHENNK	I ALFQAMREQVFLPLI	DRMDDTLLV-	- ERSED PL- AG	CI EKFLOGTI QI LTDSI ETRQI YEI MMI KCEY	- VEETKAVRDRHI SHRGERLEQMERAMATAATRGEVRGDVPASVAACGEHALTSG - VDEFATVLRQI LSNCSGI EEKLKLVYERAKTREQLHI SHDPSQLATDTHLFFTG-	LFOWALLOF-EA-FDLNAVGLOADDFVAGGFKPD 200
ARQ46881.1 HTH-type transcriptional regulator TtgR [Oxalobacter formigenes] ARU96054.1 DNA-binding transcriptional repressor AcrR [Tatumella citrea]	MEGAVRKKPLET MARKTKEQALET	RERI LDAAEDVFNARGVSRTTLNEI AEAAGVTRGAI YWHFKNK RNQI I EAAI HCFSTNGVSSTSLSDI ATRAGVTRGAI YWHFKNK	VELFEAMCDRVRGPM- IDILNEIWLQCDAHL-	KALVE KTA DK DELEQ EYQ I Q	QYPD- D PL - EC QYPD- D PL - AC	QLSAGHENLMQGIIDNPHYRKVLNILFHKCEY QMKALLVTLLQSTVTDRSRRALMEIIFHKCEF	 TDESDAI VI QQKEWQTYCNSMI QNTLSNAQLRKQLPEDLDI GLASRLMGFTFSG- VGEMETFQKI QQSLLLECYPKI EASLHNCI CQGQLPPNLNTRQAAI LMRSYI SG- 	- LLRSWLFMP-DS-FDLIEDTKRVNNALFAMLRHNPHLKK. 210 - LNENWLFP-AS-FNLEKAPDLVEAFIDMLRSPALCK. 210 - 110
ASI69424.1 [TetR family transcriptional regulator [Diaphorobacter polyhydroxybutyrativorans] ASM76281.1 [TetR family transcriptional regulator [Vitreoscilla filiformis]	MARRTKEDADAT MARKTKAEAEET	RNSLLDAAERVFYEKGVSRASLSDI AQAAGATRGAI YWHFKDK RQQI LDAAEQVFLRQGVSRTSLQEVASAAGVTRGAI YWHFADK	VDLFNAMMDRVTHPL- AALFHAMMDRVILPC-	EQVGS K SAS EAALADV- MAG PP	SMATLPPL-EF	RLRSMVDFVQRTIVQDERTRRVFEIALYRVEY	 VNDL AAVRDNHI EGCADF CALI EGELRSAAE DONL QL PMEPHT AAMGVQAL F DG TGDMASEQERHRQSVSHYL DQL EALLARAQRAGALASMPPARVSAL GL FAI VDG 	- LL QSWL [TH - GR. F DL VTVSRGAI DÄYLRG[GFRL - 200 LMYHWTLSP. FS. FDL VAVGGOTI GHFLGQ RAATPGAP- APTPPONPSAPÄP- SI - 220
BAL96565.1 transcriptional regulator, TetR family [Rubrivivax gelatinosus IL144] BANS0089.1 TetR family transcriptional regulator TbR [Pseudomonas resinovorans NBRC 106553]	MARRTKEEAEAT	RARI L DAAEREFHNNGVSGTSLEDI ARAAGVTRGAI YWHFRDK	AALFEAMMERVVLPL-	ETEMLR AGD	SDPEVAD PL - TL SEDEP- D PL - GE	LVRQATLGALRAAVEDEQARRVLEIALHKVEY	VNEMQGVRERRI ACLVERI GHLAAMFERAQAAGQI RLAMPAMTAAGGLHALI DG- TEELGDI RRKMODI SADCDI RLAKAL RNAVSRGOL PGDI DCRRAAL SVHAVMEG-	LLHNWMLDP-GA-FDLVACGEALLDBYFRG[N-AFA- 2007W1U-FG-FSIAFERFWINDFRGFN-AFA- 2017W1U-FG-FSIAFERFWINDFRGFN-GAG- 2017W1U-FG-FSIAFERFWINDFRGFN-GAG-
BAN50773.1 hypothetical protein PCA10_50410 [Pseudomonas resinovorans NBRC 106553] BAN99511 11 tet8 (amily transcriptional regulator [Plautia stali symbion?]	M RTKEEAEKT	RI AL LOAAEHL FLESGVARTSLEQI ARAAGVTRGAVYWHFONK	AHLENEML	EQM E- R- LYG CN	NGQDPM-LS	SLRDLCLDAVVNLAKDAQRQRIFTILLHRCEF	TEELREAEERHYAFVDQFI QLSHDLFDRPTCRERLRPGI TPLLASRAVHGLLVG VGENSTI MAMOOGMI QACYDRI FEVI RSCI FAGOL PASI NTROAAL I MRGYLSG	LF5DWTRDP-KL-FDPLTDSEPMLDA-MFR-GLVKDWD- 2005WFRDP-KL-FDPLTDSEPMLDA-MFR-GLVKDWD- 2015WFRW-FN-DS-FDLVSEADIVERENTING FSBTIAG
CAC41578.1 Putative transcriptional regulator [Sinorhizobium mellioti 1021]	M RRTKADAEAT	ROKI LCAAERMFYKKGVPNTTLEEVAKEAGVTRGAI YWHFANK	TDLFLALYEAVPLPH-	EDMI A- R- EI E TE	EAFDTL-AI	VESATSDWLTTLAADEQRQRILAIML-RCDY	- DNDMSAVLVRQREI EERHDALLELAFARALERGOLQEHWAPPTAARALRWMMMG-	LCTEWLFG - RF FDLVAQGSEALQS - LFA - GFR - VPARGDTSSRL
CAUG5025.1] Bacterial regulatory proteins, lettr family (Nitrosomonas europaea ALC: 19/16) CAH34804.1] TetR family regulatory protein [Burkholderia pseudomallei K96243]	MARRIKEEALAT	RDRI L DAAEUVI ECKGMGKTTMGDI AHAANVSKGAVTGHTKNK	SELFDAMFDRVLLPI-	DELKA GTG EP	PH- A- D PL- GF	RI REI LI WCLLGAARDPQLRRVFSI LFMKCEY-	- VADMGPLLQRNREGMRDALRNI EADLAQGVANGQLPADLDTWRATLMLHTLVSG-	FYRONUM, WP. GE I DAEHAEK LYOGO MURSTANKA DD. 21
CAH35804.1 TetR family regulatory protein [Burkholderia pseudomallei K96243] CAL13135.1 putative tetR-family transcriptional regulatory protein [Yersinia enterocolitica subsp. enterocolitica 8081]	MARKTREESLNT MARKTKQQAEET	KNRI LDAAELVLLEKGVGQTAMADI AEAAGMSRGAVYGHFNGK RQQI LDAAVREFSAHGVSGTSLTDI AVAAGVTRGAI YWHFKNK	VDLFNEVW ······ELSESKV·	DRAF SRAVE GF DL	- SDERP AL- AT KYPD- N PL - RI	ILREILIYVLVSTREDCRRALMEIVFHKCEF	 SEENAPLMRRRALYELQTERI AKALERRAVAAGELDASEDVHLAGVYLESLEG- VGEMTSFHDARKVEDLASYERI ESVEQGEI DANQEPVNEDTRRAAT I MRAYTTG- 	- IFGSM WTH-LR-GDRWRDAEAMIDAGVDTLRASPALRV- AEACAARGLPRANVH
CAL16414.1 transcriptional regulator TtgR [Alcanivorax borkumensis SK2] CAL21726.1 putative tetR-family transcriptional regulatory protein [Yersinia pestis CO92]	MVRRTKAEAMET MARKTKOKAEET	RTHI LDAAEQVFHRKGVLSASLHDI ACEAGVTRGAI YWHFKNK RQQI LDAAVREFSAHGVSRTSLTDI AI AAGVTRGAI YWHFKNK	HDVFVAMADRRLPF- VDLFNEVWELSESKI-	EALAQ RAE AD	ADDEA - D PM- GF AKYPD- N PL - RI	RLREFMVYLLQQVAQDPSQRRVFEIIFQKCEF ILRELLIYILVSTREDRRRRALMEIVFHKCEF	 SDENRDLLLRQRDACRDASDGLETTFRNAI AKGQLPAGLNI GRAVTLLHSLLNG- VGEMTSVHDARKVLDLASYERI ESVLQGCI DANQLPVNLNTHRAAI I MRAYI TG- 	- VI MYWL DP - 5V - FDL ADAAPDYVDTFLFSL ORSPSLVVGEGSV - LMENUL MP - ES - FDL KOEAPVL I ORV LEMIC GOFS ELRM - EMNS - RVSD - 201
CAL62832.1 putative transcriptional regulator acrR (Potential acrAB operon repressor) [Herminiimonas arsenicoxydans] CAQ47464.1 putative TetR family regulatory protein [Stenotrophomonas maltophilia K279a]	MARCTKEEALET MARKTKEDTOAT	RSRI I DAAEEVFHARGLAQSTLSDVALAADVTRGAI YWHF <mark>KN</mark> K REGI LDAAEACFHEHGVARTTLEMI GARAGYTRGAVYWHFKNK	GDLFDAMCERVRLPL- SEVLAAIVERVHLPF-	ESLAA TPF EC	QYAH- N PL - GH QRDT PV- HD	HLRNTWAFMKNVVSDTRSRKVLDIIFLRSEL DLRAVMIHSFIELSEDERLRKTMEIML-RSDA	 VDRDDPI WRQQHCYEKGLDNMERI LKEAVALDQLPKDLDTRLAAI SLHSHVI G SADTRVLTEMQQAGFRDALDRMERALRRARDLGQLREGADPKI AARMLHATVLG 	LL MNWLFSP GS- FALAEVAPAVI DGCLESLACATSMRL KT
CAX58569.1 Putative repressor for the acrAB genes [Erwinia billingiae Eb661] CBW75923.1 AcrAB generon repressor [Paraburkholderia rhizoxinica HKI 454]	MARKTKQQALET MCNSSGPLVPALOFAQORLRNNETMBRTKFAALET	RNHI I DAAI GRESEHGVSKTSLADI ATAAGVTRGAI YWEKNK	ADLLNEIWAQSESGL- ADLFTAMVDRVTLPM-	EDLEL EYQ LK	.KYPS- D PL - SV SREO- D PL - GE	VMRAMI TYVLEATARDQRRRSLEI I FHKCEF	 VGEMTTLQMMQQTLYLECYEKIEEVLRQCIEAGQLPVELDTRRTAVVMRAYITG TEDMGPVLERHRNATRDGRARLEVGLRNAMAKGOLSAELDPRRGAOLLHAFFGG 	- MENWLFMP-ES-FDLADDAPOLVEVLIDMLHSPALRT- RAH- 1. RDWLIDH-TS-IALOPERFLADSFAMIHSPATITA - PRLRR. 21
CCE98188.1 HTH-type transcriptional regulator [Sinorhizobium fredii HH103] CDG10962 11 DNA-biding transcriptional genessor [Seratia messenses subra massesses Dh11]	M RRTKADAEET	RRKI LSAAERVFYKKGVSGTTLDEI ASEAGVTRGAI YWHFANK	TDLFLALYEAVPLPH-	EDM A- R- EI E TE	EAFDTL-AI	I VEEATVDWLDLLARDEQRQRILAIMELENRCET	DDDMSTVLI KQKVVDERHNAI LEHAFARALERGQLQETWTPASAVRTLNWMMG VGEMMPLI DSRKVI YLAGVERI FAVI VNCI HUGO BADI UTDALI V DOVIT	- LCTDWLIFG- RR-FDLAGEGRDALGR LFE - SFRR VVEKNEQVSA 21
CDG16602.1 HTH-type transcriptional regulator AcrR [Xenorhabdus doucetiae]	MARK IN QAQE I MNVCKSASVKNKVYGTKMARKTKQQANQT	ROQI I DAAI KTFSERGVSATSLEDI ATAAGVTRGAI TWEFKNK	TDLLSVI C RMPEHKI	DELEK EYQ SK	KYPD- N PL- RV	TLRYLLI STLQMMI DDSQI RQLI EI FFHKCEF	VGEI SPLI AEI REKCI SDDQKI EKMLKACI QSGELPCNLDFKRSAI MLRALMTG	- TLEWISFSP- DS-FNI QEQAVHLVDSFI DTLKYSHILKN- SEKN- 23
CERCI940.1[transcriptional regulator, letk tamily [Neornizobium galegae bv. orientalis str. HAMBI 540] CERCI940.1[transcriptional repressor for multidrug efflux pump (TetR/AcrR family) [Xenorhabdus nematophila AN6/1]	MNVCKSASVKNKVYGI KMARKTKQQAKQT	RQQI I DAAI KTFSERGVSATSLSDI AI AAGVTRGAI YWHFKNK	TDLLSTVCKMPEDKI-	GALER EYQ AK	KYPN- N PE- LA	ALRSLLIFMLRMMMHDTEYRLLIEIFFHKCEF	- VGEI SSLEDELRETCI SDYEKI EKWLACCI QSGELPHNLELRRAAI MLKALMTG-	
SAY51600.1 mtrCDE transcriptional repressor [Neisseria weaveri] SDR69473.1 transcriptional regulator, TetR family [Pseudomonas litoralis]		REYLMLAALDTFYTKGVARASLNEI AQAAGVTRGALYWHFKNK RNQII DAAELCFFNKGVSHTSLAEI AKTAGVTRGAI YWHFENK	EDLFDALFQHIFNDFSGRMWADI- GEVLDALLVRAKTPI-	QHLEE ASR NS	ENASPNMWEN SDEP-DPL-GP	NLRQTLLNLYERLETNETHRKFI SI LHLKCEH RLQAMI AEVFRQAEQDPATRRI NEI VFHKCEY	 I EQNKAI VELMSKYNMMMEQMTKAI VLCI SQEKLPQNLDVNLASI YLKSVCTG- T DQMCDLREYMRQLRLQSDSKLESALRNAI SKDQLPAQLDVSMAAHSLHAFVI G- 	- LTQI WLINP AR- FDLQSAAPAI I DTALTALQHCPSLQKDYAV- 21: - MLDI WLLRP ED- FSLAERADQLAQTVI DMLRGSPAMRS- A- 21:
SDS60140.1 transcriptional regulator, TetR family [Pseudomonas xinjiangensis] SDS92323.1 TetR/AcrR family transcriptional regulator, acrAB operon repressor [Pseudomonas sabulinigri]	MVRTKEEALAT MVRTKEEAFET	RSQI I DAAEKCFHNKGLSRTSLADI ASAAGVTRGAI YWH ODK RORI I DAAQQCFHEKGVSRASLTDI AQAAGVTRGAI YWH ODK	SELLEALLERATMPL- ADLLDALFQRI HMPL-	QPLEE ASL NR EALSE ATR NP	IRNEV-DPL-AF	RMRDLI I EI FRGVATDSDI RRI NEI LLHKCEY LFRELLTEVFRRVESDPTNRQVHEI I FLKCEF	 TDEMCDLRKRMVLFRRSCDDNI AAGLTNAI SRQQLPADLDVPLAARCVHSFI VG TDEPCGPKKHLQAMRQEHDNQVLTTLRLAVARGELPADLDMELALLCLHSFI VG 	TI DQWLMCP GH- VDLAAQAGSLADAVLDMVRLSTALRR - SQ
SDT24907.1 transcriptional regulator, TetR family [Pseudomonas oryzae] SDT97650.1 transcriptional regulator, TetR family [Pseudomonas guangdongensis]	MARTKEEAAAT MARTKEEAOET	ROQI L DSAERVFAAKGVAHTTMADI AADAGVSRGAVYWHFTSK RNOI L DSAERVFASKGVTHSTMADI AADAGVSRGALYWHFTSK	ADVFNAMLTRQHDAN- TDIFHAMFVROHDAN-	KVVCA AAR DP KVVCA AAR DP	OPEEC- D PL- GO OPDEP- D PL- GO	QI RNI LVHFLCKTVHDPQQRRVNEI FHHKCEL QMRSI LSHFLRKVVEDPQQRRVCEI LHHKCEL	 AGDQESLREQLQATGDEI DRDI ALSLRNAI SRGQLPADLDLTRAAI GMHAYI HG AGEQAALRQHLQATGEEI DQDI ALSLRHAI ORGOLPANLDLORAAVAVHAYI HG 	LINNWLLRP DS-FALDREAGALVDALLDMLRYSPALRL PAA
SEH77664.1 tetr bacterial regulatory protein hth signature [Akkermansia glycaniphila] SEI13197.1 transcriptional regulator, TetR family [Pseudomonas fuscovacinae]		RDAI LDAAEVVFLKKGVTHASMADI AEQAGVSRGAVYGHYKNK RKOI LEAAEKAFYERGVARTTLADI ATLAGVTRGAI YWHENK	MELGLAMC	QRAFEADDYWKE	EGKAVN- VSPL - EF	RLRRQHLFHMKQYCESDTQRRVLEILYTRCERTPI CMRRLLIHLFQQIALDPKVRRINEILFHKCFF	ENDEMLRLKEQFEKECEDDHMLL LNEAVSSGELPRDLDVGLAFAFLNTMVCGQ - TDEMCDLRRORRAVSLDCNAHI ELALRNAVNRGOLPEDLDTARAALTI HAWVDG-	CSLLMCKEMTPEE-FMLALEPFLDASLDAMRHSPALRKR
B5M06_RS04695[transcriptional regulator, [Comamonas kerstersii strain 8943]	MURTKADAEAT	RDQLLDAAQTVFYEKGVAGASLAEVAKEAGLTRGAI YWHFEDK	VDLFNMPCCAEPRCLLSRHCRRRRLQTAI ALL	WRWFWTLFAWCCTASV-RMP	RIPGEFLILPSI	KPSVWASFWRCVSVVCRKRRSLSCTWSMY		14

Figure S4. Sequence alignment of the MexZ orthologs identified in genomes not encoding ArmZ/PA5470 orthologs. Gene groups encoding clustered orthologs of *P. aeruginosa* MexZ/MexX/MexY or ArmZ/PA5470 were identified in bacterial genomes (Refseq 91, reference and representative genomes) using MultiGeneBlast. MexZ orthologs from Data set S1 excluding those listed in Data set S3were used.

Table S1 Plasmids used in this study.

Name	Relevant features	Origin
pABB28.2	pET28a based expression vector with T7p-flag-mcs ¹ , Kan ^R	(1)
pAKE600	suicide vector, $oriV_{MB1}$, $sacB$ cassette, Amp^{R}	(2)
pET28mod	<i>oriV</i> _{MB1} , <i>T7</i> p, <i>lacO</i> , <i>his</i> ₆ - <i>tag</i> , pET28a modified to remove the T7 tag, Kan ^R	(3)
pGBT30	<i>oriV</i> _{MB1} , <i>lacI</i> ^{<i>q</i>} , <i>tac</i> p, expression vector, Amp ^R	(4)
pKAB240	pBAD24 derivative; <i>araC-araBADp-mcs-rrnBt</i> cassette flanked by NsiI restriction sites, Amp ^R	(1)
pKAB600	pAKE600 with <i>PA5412/PA5413</i> intergenic region of PAO1161 with internal PstI site, Amp^{R}	(1)
pKAB601	pKAB600 with araC-araBADp-mcs-rrnBt cassette inserted into PstI site, Amp ^R	(1)
pKGB8	broad host range expression vector, <i>ori</i> _{IncA/C} , <i>araC-araBAD</i> p, Chl ^R ,	(1)
pLKB2	pKT25 with modified mcs, lacp-cyaT25-mcs, Kan ^R	(5, 6)
pLKB4	pUT18C with modified mcs, lacp-cyaT18-mcs, Amp ^R	(5, 6)
pPT01	$oriV_{SC101}$, promoter-less xylE cassette, Kan ^R	(7)
pUC19	$oriV_{MB1}$, $lacZ\alpha$ with mcs, Amp^{R}	(8)

¹*mcs*- multiple cloning site

Table S2 Plasmids constructed in this study.

Name	Relevant features and construction					
pLKB4 deriv	atives (BACTH vectors)					
pKAB18.1	<i>cyaT18-mexZ</i> translational fusion; PCR amplified <i>mexZ</i> (<i>PA2020</i>) using primers #3 and #4, digested with EcoRI and BgIII and inserted between EcoRI and BamHI sites of pLKB4					
pKAB18.2	<i>cyaT18-armZ</i> translational fusion; <i>armZ</i> (<i>PA5471</i>) amplified using primers #5 and # 6, digested with EcoRI and MfeI and inserted into EcoRI site of pLKB4					
pKAB18.3	$cyaT18$ -mexZ ($\Delta N8$) translational fusion; 5' truncated mexZ allele amplified using primers #8 and #10, digested with EcoRI and MfeI and inserted into the EcoRI site of pLKB4					
pKAB18.4	<i>cyaT18-mexZ</i> (Δ N26) translational fusion; 5' truncated <i>mexZ</i> allele amplified using primers #9 and #10, digested with EcoRI and MfeI and inserted into EcoRI site of pLKB4					
pKAB18.5	<i>cyaT18-mexZ</i> (Δ C9) translational fusion; 3' truncated <i>mexZ</i> allele amplified using primers #11 and #12, digested with EcoRI and MfeI and inserted into EcoRI site of pLKB4					
pKAB18.6	<i>cyaT18-mexZ</i> (Δ C31) translational fusion; 3' truncated <i>mexZ</i> allele amplified using primers #11 and #13, digested with EcoRI and MfeI and inserted into EcoRI site of pLKB4					
pKAB18.7	<i>cyaT18-mexZ</i> (Δ C61) translational fusion; 3' truncated <i>mexZ</i> allele amplified using primers #11 and #14, digested with EcoRI and MfeI and inserted into EcoRI site of pLKB4					
pKAB18.8	<i>cyaT18-mexZ</i> _{R3S} translational fusion; library clone, 9G>C change in <i>mexZ</i>					
pKAB18.9	<i>cyaT18-mexZ</i> _{K6E} translational fusion; library clone, 16A>G change in $mexZ$					
pKAB18.10	cyaT18-mexZ _{R13H} translational fusion; library clone, 38G>A change in mexZ					
pKAB18.11	cyaT18-mexZ _{K53E} translational fusion; library clone, 157A>G change in mexZ					
pKAB18.12	cyaT18-mexZ _{K53M} translational fusion; library clone, 158A>T change in mexZ					
pKAB18.13	<i>cyaT18-mexZ</i> _{K53N} translational fusion; library clone, 159G>T change in <i>mexZ</i>					
pKAB18.14	<i>cyaT18-mexZ</i> _{K53Q} translational fusion; library clone, 157A>C change in <i>mexZ</i>					
pKAB18.15	cyaT18-mexZ _{K53E} translational fusion; library clone, 158A>C change in mexZ					
pLKB2 deriv	atives (BACTH vectors)					
pKAB25.1	<i>cyaT25-mexZ</i> translational fusion; <i>mexZ</i> excised as EcoRI-SmaI fragment from pKAB18.1 and inserted into pLKB2					
pKAB25.2	<i>cyaT25-armZ</i> translational fusion; <i>armZ</i> excised as EcoRI-BamHI fragment from pKAB18.3 and inserted into pLKB2					
pKAB25C	pLKB2 with Kan ^R marker replaced by Chl ^R ; PCR amplified <i>cat</i> from pKGB8 using primers #26 and #27 was digested with BgIII and NsbI and inserted into BgIII and NsbI digested pLKB2					
pKAB25C.2	<i>cyaT25-armZ</i> translational fusion, Chl ^R ; <i>armZ</i> excised as EcoRI-KpnI fragment from pKAB18.3 and inserted into pKAB25C					
pAKE600 ba	sed suicide vectors used in allele replacement					
pKAB610	<i>araC-araBAD</i> p- <i>armZ</i> -T _{rnB} flanked by sequences allowing insertion in <i>PA5412/PA5413</i> intergenic region; NsiI fragment from pKAB244 was inserted into PstI site of pKAB600					
pKAB611	<i>mexZ</i> deletion cassette; Gibson assembly of HindIII digested pAKE600 and two PCR fragments corresponding to PAO1 coordinates 2212177-2212676 and 2213164–2213664, amplified using pairs of primers #28/ #29 and #30/ #31, respectively					

pKAB612	<i>armZ</i> deletion cassette; Gibson assembly of SmaI digested pAKE600 and two PCR fragments corresponding to PAO1 coordinates 6161187–6160688 and 6159714– 6159214 amplified using pairs of primers #32/ #33 and #34/ #35, respectively
pKAB613	$mexZ_{R3S}$ mutagenesis cassette; PCR fragments amplified with primers #28/ #36 and #37/ #14 were used as a template in overlap PCR (primers #28 and #14). MunI and XbaI digested product was inserted between EcoRI and XbaI sites in pAKE600. Introduction of a NheI site facilitated the identification of mutagenic allele in the genome.
pKAB614	<i>mexZ</i> _{K6E} mutagenesis cassette; PCR fragments amplified with primers $#28/#38$ and $#39/#14$ were used as a template in overlap PCR (primers $#28$ and $#14$). MunI and XbaI digested product was inserted between EcoRI and XbaI sites in pAKE600. Introduction of a PauI site facilitated the identification of mutagenic allele in the genome.
pKAB615	$mexZ_{R13H}$ mutagenesis cassette; PCR fragments amplified with primers #28 / #40 and #41 / #14 were used as a template in overlap PCR (primers #28 and #14). MunI and XbaI digested product was inserted between EcoRI and XbaI sites in pAKE600. Introduction of a PagI site facilitated the identification of mutagenic allele in the genome.
pKAB616	<i>mexZ</i> _{K53E} mutagenesis cassette; PCR fragments amplified with primers $#1 / #42$ and $#43 / #14$ were used as a template in overlap PCR (primers $#1$ and $#14$). MunI and BamHI digested product was inserted between EcoRI and BamHI sites in pAKE600. Elimination of the XmiI site facilitated the identification of mutagenic allele in the genome.

pET28 based expression vectors

pKAB28	pET28mod with deletion of his_{δ} -tag and EcoRI site adjacent to RBS; PCR product obtained using primers #21/ #22 and pET28mod as a template, digested with BgIII and EcoRI, replaced the corresponding fragment in pET28mod
pKAB28.1	mexZ-his ₆ translational fusion; EcoRI-BlpI mexZ-his ₆ fragment from pKAB20.4 was ligated with pKAB28
pKAB28.2	$mexZ_{R3S}$ -his ₆ translational fusion; 218 bp EcoRI-KpnI $mexZ$ fragment of pKAB18.9 replaced the corresponding fragment in pKAB28.1
pKAB28.3	$mexZ_{K6E}$ -his ₆ translational fusion; 218 bp EcoRI-KpnI $mexZ$ fragment of pKAB18.10 replaced the corresponding fragment in pKAB28.1
pKAB28.4	$mexZ_{R13H}$ -his ₆ translational fusion; 218 bp EcoRI-KpnI $mexZ$ fragment of pKAB18.11 replaced the corresponding fragment in pKAB28.1
pKAB28.5	$mexZ_{K53E}$ -his ₆ translational fusion; 218 bp EcoRI-KpnI $mexZ$ fragment of pKAB18.12 replaced the corresponding fragment in pKAB28.1
pKAB28.6	<i>flag-armZ</i> translational fusion; <i>armZ</i> excised as EcoRI-KpnI fragment from pKAB18.3 was inserted between EcoRI and KpnI sites in pABB28.2
pKAB28.7	pET28mod with BamHI and ScaI sites in <i>mcs</i> ; synthetic DNA fragment obtained by annealing of oligonucleotides #24 and #25 inserted between EcoRI and SaII sites in pET28mod
pKAB28.8	<i>his</i> ₆ - <i>armZ</i> translational fusion; <i>armZ</i> excised as EcoRI-BamHI fragment from pKAB18.3 was inserted between EcoRI and BamHI sites of pKAB28.7
pKAB28.9	<i>flag-mexZ</i> translational fusion; <i>mexZ</i> (EcoRI-SalI fragment from pKAB18.1) inserted between EcoRI and SalI sites of pABB28.2.
Other plasmi	ids
pKAB8	expression vector with <i>araC-araBAD</i> p;. pKGB8 digested with XhoI, treated with Klenow fragment (filling-in 3' recessed ends) and self-ligated
pKAB10.1	<i>mexXYp-xylE</i> transcriptional fusion, <i>mexX-mexZ</i> intergenic region amplified using primers #1 and #2 and PAO1161 genomic DNA digested with BamHI and BgIII and inserted into BamHI site,

	upstream of promoterless xylE in pPT0I
pKAB19.1	cloning intermediate; pUC19 digested with BamHI and HindIII, blunted by filling-in 3' recessed ends using Klenow fragment, and self-ligated
pKAB19.2	cloning intermediate; Three fragments amplified with primer pairs #15/ #16, #17/ #18 and #19/ #20 and pKAB28.9 as template were used in overlap PCR using primers #15 and #20 to yield a 992 bp product containing <i>flag-mexZ-his</i> ₆ . PCR product was inserted as EcoRI, SmaI fragment into pKAB19.1.
pKAB20	pUC19 derivative with <i>flag-mcs</i> (MunI, HindIII, NotI, XhoI, BamHI)- <i>his</i> ₆ ; allows in frame attachment of <i>flag</i> to 5' and/or <i>his</i> ₆ to the 3' of a gene. The <i>mexZ</i> stuffer removed from pKAB19.2 by HindIII digestion and vector self-ligation.
pKAB20.4	mexZ-his ₆ translational fusion; $mexZ$ gene without stop codon amplified using primers #3/ #23, digested with EcoRI and BamHI and inserted between EcoRI and BamHI sites of pKAB20.
pKAB244	<i>araC-araBADp-armZ-T_{rmB}</i> cassette; <i>armZ</i> excised as EcoRI-KpnI fragment from pKAB18.3 inserted between EcoRI-KpnI sites in pKAB240
pKAB301	<i>tac</i> p- <i>armZ</i> transcriptional fusion; <i>armZ</i> excised as EcoRI-KpnI fragment from pKAB18.3 inserted between EcoRI-KpnI sites in pGBT30
pKAB302	<i>tacp-armZ/PA5470</i> transcriptional fusion; <i>armZ-PA5470</i> operon amplified using primers #5 and #47, digested with EcoRI and KpnI and inserted between EcoRI-KpnI sites in pGBT30
pKAB801	<i>araC-araBAD</i> p- <i>mexZ</i> transcriptional fusion; <i>mexZ</i> excised as EcoRI-SacI fragment from pKAB18.1 cloned into pKAB8

PCR was performed using PAO1161Rif^R genomic DNA as a template, unless stated otherwise.

Number	Sequence (5'-3')
#1	GTCA <u>GGATCC</u> GGGTGTCCCTCGATTCG
#2	TATA <u>AGATCT</u> TGAACGTCCTCACAAGGGAA
#3	TATA <u>GAATTC</u> ATGGCCAGGAAAACCAAAG
#4	CG <u>AGATCTGTCGAC</u> TGCACATCAGCGAGGAAGA
#5	TATA <u>GAATTC</u> ATGGGCAACTACATCAAGCC
#6	TATA <u>CAATTG</u> TCATCGGCAGCACTCCC
#7	TGTGCTGCAAGGCGATTAAG
#8	ATA <u>AAGCTTGAATTC</u> ATGTCCCAGAAAACCCGCGA
#9	TATA <u>GAATTC</u> ATGAAGGGCGTGGGCACC
#10	ATAT <u>CAATTG</u> TCAGGCGTCCGCCAGC
#11	TATA <u>GAATTC</u> ATGGCCAGGAAAACCAAAG
#12	ATAT <u>CAATTG</u> TCAACTGCGCAGGCTGTCG
#13	ATAT <u>CAATTG</u> TCAGCGCTCGGTCCAGG
#14	ATAT <u>CAATTG</u> TCATTCGCCGCGTTCCAC
#15	GTCA <u>GAATTC</u> ATGGACTACAAGGACGACGA
#16	GCCATAAGCTTCAATTGCGATCCGCGACCCATTT
#17	TCG <u>CAATTGAAGCTT</u> ATGGCCAGGAAAACCAA
#18	ACC <u>GGATCCCTCGAG</u> TGCGGCCG
#19	ACTCGAG <u>GGATCCGGTTCC</u> GGTCACCACCACCACCACCACT
#20	TATA <u>CCCGGG</u> TCGACCCGTTTAGAGGCCCCAAG
#21	GTCCGGCGTAGAGGATCG
#22	GCAT <u>GAATTC</u> CTCCTTCTTAAAGTTAAACAAAATTATTTC
#23	GTAT <u>GGATCC</u> GGCGTCCGCCAGCAA
#24	AATTC <u>GGATCCGAGCTCAGTACT</u> G
#25	TCGAC <u>AGTACTGAGCTCGGATCC</u> G
#26	CGATC <u>AGATCT</u> TTTGGCGAAAATGAGACGTT
#27	GTAC <u>TGCGCA</u> TTAATTGCGTTGCGCTCAC
#28	CGGT <u>GAATTCTCTAGA</u> ACAGGGCGCCGCGGCTGAT
#29	GCGATTGC <u>AAGCTT</u> TGAACGTCCTCACAAGGGAAAGGCG
#30	GACGTTCA <u>AAGCTT</u> GCAATCGCTCTGGGACGG
#31	GA <u>CCATGG</u> CTGCAGATCTCTGCGGACGATTGCAG
#32	AG <u>CCATGGTCGAC</u> CCCCTGCGCGAGGTCTACG

Table S3 Oligonucleotides used in this study

#33	GGTCGCCA	<u>CCCGGG</u> GTAGTTGCCCATAATCCAATCC
#34	GCAACTAC	<u>CCCGGG</u> TGGCGACCGCCAGCTGA
#35	TAATCCC <u>GC</u>	ATCCCCGAAGAGCGCAGGGTCTCGAAAC
#36	TTGGTTTT <u>G</u>	CTAGCCACTGAACGTCC
#37	TCAGTG <u>GC</u>	TAGCAAAACCAAAGAGG
#38	CTTCGGTTT	T <u>GCGCGC</u> CACTGAACGTCCTCAC
#39	AGTG <u>GCGC</u>	<u>GC</u> AAAACCGAAGAGGAATCCCA
#40	ATGCCG <u>TCA</u>	<u>ATGA</u> GTTTTCTGGGATTCCTC
#41	CAGAAAAC	TCATGA CGGCATACTCGATG
#42	TTCTCGTAG	TGGCCATAGACCGCACCGCGAGAAAC
#43	GTCTATGGC	CACTACGAGAACAAGATCGAGGTCTG
#44	CGGATGTAC	CTGGAAACGGTG
#45	CGGGGGCTG	GCTTAACTATG
#46	TCGTATGTT	GTGTGGAATTGTG
#47	ATA <u>GGTACC</u>	GAAGCTGCGCAAGGAAGTG
qPCR prin	ners	
Number	Name	Sequence (5'-3')
#48	NADB_F	CTACCTGGACATCAGCCACA
#49	NADB_R	GGTAATGTCGATGCCGAAGT
#50	qPA5471_F	CGGCGGACAAACTGGAAAAG
#51	qPA5471_R	TAGATCCAGGGCTTCGATGC
#52	qMexY1_F	TGCCCAACGACATCTACTTC
#53	qMexY1_R	ATGCCTTCCTGGTAATGGTC

Restriction sites are underlined.

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