Strain(s) or plasmid	Relevant characteristics	Source or reference*	
<i>E. coli</i> strains			
DH5a	F <sup>-</sup> , ø80dlacZDM15, D( <i>lacZYA-argF</i> )U169, <i>deoR, recA1, endA1, hsdR17</i> ( <i>rK</i> <sup>-</sup> , <i>mK</i> <sup>+</sup> ),	Laboratory collection	
	phoA,supE44, l–, thi-1, gyrA96, relA1		
BL21	F <sup>-</sup> ,ompT, hsdS (rBB <sup>-</sup> mB <sup>-</sup> ), gal,dcm (DE3)	CWBIO	
BL21/pET28a	Kan <sup>r</sup> ; BL21 containing the pET28a vector	This study	
BL21/pET28a-osaR	Kan <sup>r</sup> ; BL21 containing the pET28a- <i>osaR</i> vector	This study	
BL21/pETMAL-osaR	Kan <sup>r</sup> ; BL21 containing the pETMAL- <i>osaR</i> vector	This study	
Transetta	<i>F</i> <sup>-</sup> <i>ompT hsdSB (rB</i> <sup>-</sup> <i>mB</i> <sup>-</sup> ) gal dcm lacY1 ahpC (DE3) gor522::Tn10 trxB pRARE	TransGen	
Transetta/pET28a-PA0055	Kan <sup>r</sup> ; Transetta containing the pETMAL- <i>PA0055</i> vector	This study	
P. aeruginosa strains			
PAK(WT)	wild-type strain	David Bradley <sup>a</sup>	
$\triangle osaR$	PAK $\triangle osaR(PA0056)$	(1)	
$\triangle osaR / osaR$	$\triangle osaR / pDN18- osaR, Tc^r; \triangle osaR$ containing the pDN18-osaR vector	This study	
PAK/pDN18	PAK/ pDN18, Tc <sup>r</sup> ; $\triangle osaR$ containing the pDN18 vector	This study	
∆osaR/pDN18	$\triangle osaR / pDN18$ , Tc <sup>r</sup> ; $\triangle osaR$ containing the pDN18 vector	This study	
$\triangle dsbM$	PAK $\triangle dsbM$ (PA0058)	(2)	
$\triangle dsbM/dsbM$	$\triangle dsbM$ /pDN18- $dsbM$ ,Tc <sup>r</sup> ; $\triangle dsbM$ containing the pDN18- $dsbM$ vector	This study	
$\triangle dsbM/pDN18$	$\triangle osaR$ / pDN18, Tc <sup>r</sup> ; $\triangle osaR$ containing the pDN18 vector	This study	
$\triangle osaR \triangle dsbM$	PAK $\triangle osaR \triangle dsbM$	This study	
$\triangle oxyR$	PAK $\triangle oxyR$	This study	
$\triangle oxyR \triangle osaR$	PAK $\triangle oxyR \triangle osaR$	This study	
$\triangle oxyR \triangle dsbM$	PAK $\triangle oxyR \triangle dsbM$	This study	
550E	PAK/pUCP19- <i>PA0055</i> , Cb <sup>r</sup> ; PAK containing the pUCP19- <i>PA0055</i> vector;	This study	
	Overexpression of PA0055 in WT		
56OE	PAK/pUCP19- <i>osaR</i> , Cb <sup>r</sup> ; PAK containing the TI pUCP19- <i>osaR</i> vector; Overexpression of		
580E	PAK/pUCP19- <i>dsbM</i> , Cb <sup>r</sup> ; PAK containing the	This study	

Table S1 Bacterial strains and plasmids used in this study

	pUCP19-dsbM vector; Overexpression of	
	<i>dsbM</i> in WT	
	$\triangle dsbM/dsbM; \triangle dsbM / pUCP19- dsbM$ ,	This study
$\triangle dsbM/58OE$	$Cb^{r}$ ; $\triangle dsbM$ containing the pUCP19- $dsbM$	
	vector; Overexpression of $dsbM$ in $\triangle dsbM$	
	$\triangle osaR/dsbM; \triangle osaR/pUCP19$ - $dsbM$ , Cb <sup>r</sup> ;	This study
$\triangle osaR/58OE$	$\triangle osaR$ containing the pUCP19-dsbM	
	vector; Overexpression of $dsbM$ in $\triangle osaR$	
PAK/pUCP19	Cb <sup>r</sup> ; PAK containing the pUCP19 vector	This study
$\triangle osaR/pUCP19$	$Cb^{r}$ ; $\triangle osaR$ containing the pUCP19 vector	This study
$\triangle dsbM/pUCP19$	$Cb^{r}$ ; $\triangle dsbM$ containing the pUCP19 vector	This study
PAK/Tn7:: P <sub>PA0057</sub> -gfp	PAK with $P_{PA0057}$ -gfp inserted on chromosome	This study
	with mini-Tn7T insertion; Gm <sup>r</sup>	
$\triangle osaR$ /Tn7:: P <sub>PA0057</sub> -gfp	$\triangle osaR$ with P <sub>PA0057</sub> -gfp inserted on	This study
	chromosome with mini-Tn7T insertion; Gm <sup>r</sup>	
Plasmids		
pET28a	Kan <sup>r</sup> ; vectors carry an N-terminal His-	Novagen
	Tag/thrombin/T7-Tag configuration plus an	
	optional C-terminal His-Tag sequence	
pETMALc-H	Kan <sup>r</sup> ; maltose-binding protein (MBP) fusion	(3)
	expression vector	
pDN18	Tc <sup>r</sup> ; Broad-host-range plasmid, IncP	(4)
pDN19lacΩ	Sp <sup>r</sup> Sm <sup>r</sup> Tc <sup>r</sup> ; Promoterless <i>lacZ</i> fusion vector	(4)
pUCP19	Ap <sup>r</sup> ; Broad-host-range shuttle vector	(5)
pMH305	Gm <sup>r</sup> ; pUCP22NotI-based expression vector	(6)
•	carrying a promoterless gfpmut3b* gene	
pUC18T-mini-Tn7T-Gm	mini-Tn7 base vector from insertion into	(7)
L	chromosome attTn7 site; Gm <sup>r</sup>	
pET28a-osaR	Kan <sup>r</sup> ; osaR cloned into pET28a at Nco I/Xho I	This study
	site	
pET28a-PA0055	Kan <sup>r</sup> ; PA0055 cloned into pET28a at Nde I/Eco	This study
	RI site	
pETMAL-osaR	Kan <sup>r</sup> ; pETMALc-H vector carrying the malE-	This study
	osaR fusion at Bam HI/Hind III.	-
pDN18- osaR	Tcr; osaR gene cloned into pDN18 for	This study
•	complement of <i>osaR</i> at <i>Eco</i> RI/ <i>Hind</i> III.	•
pDN18-dsbM	Tc <sup>r</sup> ; <i>dsbM</i> gene cloned into pDN18 for	This study
1	complement of <i>dsbM</i> at <i>Eco</i> RI/ <i>Hind</i> III.	2
pUCP19-PA0055	Ap <sup>r</sup> : <i>PA0055</i> gene cloned into pUCP19 for	This study
1	overexpression of PA0055 at <i>Hind</i> III/ <i>Eco</i> RI	·····j
pUCP19- osaR	Ap <sup>r</sup> : <i>osaR</i> gene cloned into nUCP19 for	This study
1	overexpression of <i>osaR</i> at <i>Hind</i> III/ <i>Eco</i> RI.	·····j
pUCP19- osaR-his	Ap <sup>r</sup> : <i>osaR-his</i> tag fusion cloned into pUCP19	This study
•		2

	for overexpression of <i>osaR</i> at <i>Hind</i> III/ <i>Eco</i> RI.	
pUCP19-dsbM	Apr; dsbM gene cloned into pUCP19 for	This study
	overexpression of <i>dsbM</i> at <i>Hind</i> III/ <i>Eco</i> RI.	
$P_{katA}$ -gfp	Gmr; pMH305 vector carrying the PkatA-gfp	This study
	fusion at <i>Eco</i> RI/ <i>Kpn</i> I.	
$P_{katB}$ -gfp	Gmr; pMH305 vector carrying the PkatB-gfp	This study
	fusion at <i>Eco</i> RI/Kpn I.	
PoxyR-gfp	Gmr; pMH305 vector carrying the PoxyR-gfp	This study
	fusion at <i>Eco</i> RI/ <i>Kpn</i> I.	
$P_{osaR}$ -lacZ	Spr Smr Tcr; PosaR-lacZ fusion reporter in	This study
	pDN19lac $\Omega$ at <i>Eco</i> RI/ <i>Bam</i> HI.	
$P_{PA0057}$ -lacZ	Spr Smr Tcr; PPA0057-lacZ fusion reporter in	This study
	pDN19lac $\Omega$ at <i>Eco</i> RI/ <i>Bam</i> HI.	
pTn7-P <sub>PA0057</sub> -gfp	Gmr; pUC18T-mini-Tn7T-Gm vector carrying	This study
	the P <sub>PA0057</sub> -gfp fusion at Eco RI/Sac I.	

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Gene (purpose)	size	Primer name	Primer sequence
	(bp)		
osaR(knock	1000	P0056YF	5'- ACCAGCAGTTCCGAGGACACG-3'
sequencing)		P0056YR	5'-ACTCCAGCGCAGCACCATCA -3'
dsbM(knock	1000	P0058YF	5'-CCGACCCACTCCTCCAACTC-3'
sequencing)		P0058YR	5'-TCCAGATAACTGCCGTCACTCC-3'
PA0055(overexpress	580	PA0055OEF	5'-CCCAAGCTTGATGTCCCTGTCGATCTACCA-3'
ion)		PA0055OER	5'-CCGGAATTCGGGTTTTCCGATCCATTC-3'
osaR	996	PA0056OEF	5'-CCCAAGCTTGATGGACCGCCTGACCG-3'
(overexpression)		PA0056OER	5'-CCGGAATTCCCAGACAGGGGATAAAGGTG-3'
dsbM(overexpressio	858	PA0058OEF	5'-CCCAAGCTTGATGAACGACCTCACCCTG-3'
n)		PA0058OER	5'-CCGGAATTCCGCCGATGCCGTCTTCT-3'
osaR (complement)	989	PA0056CF	5'-CCGGAATTCCATGGACCGCCTGACCGCC-3'
		PA0056CR	5'-CCCAAGCTTGGGGATAAAGGTGCGTCG-3'
dsbM (complement)	858	PA0058CF	5'-CCGGAATTCCATGAACGACCTCACCCTGC-3'
		PA0058CR	5'-CCCAAGCTTCGCCGATGCCGTCTTCTTC-3'
osaR (expression)	938	PA56EF	5'-
		PA56ER	CATGCCATGGGCATGGACCGCCTGACCGCCACT
			CGCG-3'
			5'-CCGCTCGAGCGCCAGCGCCAGGGGGCCCGC-
			3'
malE-osaR(fusion	949	3RH-PA56F	5'-CGCGGATCCATGGACCGCCTGACCGC-3'
expression)		3RH-PA56R	5'-CCCAAGCTTTCCAGCAGTCTACCCGGCTT-3'

Table S2. PO	CR prime	rs used in	this study

<i>malE-osaR(</i> fusion		CX-RHPA56F	5'-GGTCGTCAGACTGTCGATGAAGCC-3'
expression			
sequencing)			
PA0055(qPCR)	181	PA0055RTF	5'-GAGCTACGCGGATACGGAAAC-3'
		PA0055RTR	5'-GGCGAAGCCGAAGAGGAA-3'
PA0057(qPCR)	176	PA0057RTF	5'-GGGCCGATCCTCAAGGACAAC-3'
		PA0057RTR	5'-ACCAGCACGCCACCAACCAC-3'
<i>dsbM</i> (qPCR)	113	PA0058RTF	5'- GCCTGCGAGGTGACGGGTCTGG -3'
		PA0058RTR	5'- AGGTCATGGGGCATCACGTAGTGGC -3'
<i>rpsL</i> (qPCR)	150	rspLRTF	5'-ACGTGCCTGCGCTGCAAAC-3'
		rspLRTR	5'-CCCGAGGTGTCCAGCGAACC-3'
osaR F1(EMSA)	297	PA56J1F	5'-CGAGACCATCGCCCGGGACA-3'
		PA56J1R	5'-GTTCGGCGCTGGCGGCGAAG-3'
osaR F2IR(EMSA)	238	PA56F2JF	5'-CCTCCAACTCGGCGAGGTAGCG-3'
		PA56F2JR	5'-GCGACATGAGCGGTTCTCCAGG-3'
osaR IR(EMSA)	108	5657JGF	5'-TTCGCTCGATCCATGCAACAAAG-3'
		5657JGR	5'-CATGAGCGGTTCTCCAGGCAGT-3'
osaR F2IRC(EMSA)	90	F2JGMF	5'-CGATGACTTCGACGAAGACG-3'
		F2JGMR	5'- AAAAGCCCCGCAATAATCAC-3'
osaR F3(EMSA)	110	PA56J4F	5'-GCGCCATGGATTGCTTCGTT-3'
		PA56J4R	5'-CGGGGTTGTAGACCTCCAGCC-3'
EMSAc	185	EMSAcF	5'-GCTGTCCCATGAACTACGCC-3'
		EMSAcR	5'-GCCAGGATGTCCCAACTGAA-3'
flpJG(EMSA)	459	flpF	5'-GCCGAGGTATCCGAGCAACA -3'
		flpR	5'- GCAATCACCGAGACAGAGCC-3'
P <sub>PA0057</sub> (promoter-	421	P0057F	5'-CCGGAATTCCCGACCCACTCCTCCA-3'
lacZ)		P0057R	5'-CGCGGATCCTTAGCCCACCAGCAGTTCC-3'
P <sub>osaR</sub> (promoter-lacZ)	420	P0056F	5'-CCGGAATTCGCCCACCAGCAGTTCC-3'
····· ()		P0056R	5'-CGCGGATCCTTAGACCCACTCCTCCAACT-3"
<i>oxyR</i> (gPCR)	192	oxyR-F	5'-TCTTCGAGCGCAGCAAGAGCG-3'
, , ,		oxyR-R	5'-GAATCAGGTGCGGGAACAGGTAGG-3'
katA(gPCR)	124	katA-F	5'-GGCTTCTTCGAGCTGAACCGTAAC-3'
(-1 )		katA-R	5'-GACGGCCCTGGAGCATCTTGTC-3'
<i>katB</i> (gPCR)	103	katB-RTF	5'-CCGGTATTCGTGCGCTTCTCCG-3'
(-1 )		katB-RTR	5'-TGCCGTCTGCGGTATAGAACTTGGTG-3'
ahpB(gPCR)	188	ahoB-F	5'-GCCTTGCGTGCTTCGTTCCTG-3'
	100	ahpB-R	5'-GCGCTCGCCTTCATGCCTTTCTG-3'
ahnC(gPCR)	96	ahnC-RTF	5'-GCAAGTGGTCGGTCCTGATCTTCA-3'
	00	ahpC-RTR	5'-TCTGGAACTCGCCGTAGTTGTTGG-3'
ahnF(gPCR)	115	ahoF-RTF	5'-GGCATCGAGGGCACCTTCGAGTTC-3'
		ahnF-RTR	
$kat \Delta IG1(EMS\Delta)$	208	katΔIG1F	
	200	katΔIG1R	
		Rainjoin	J-100A0011010011A100A00-J

katAJG2(EMSA)	231	katA JG2F	5'-GTCGGCGGTGAAGTCGTAGAAGC -3'
		katA JG2R	5'-ACAACCTGTCGGCTGAACCAAGC-3'
katBJG1(EMSA)	235	katB JG1F	5'- ACTTCGCAGGCAAATAAGAAGGT-3'
		katB JG1R	5'- TGGAAGAGCTCCTAATGGCTTGT -3'
katBJG2(EMSA)	334	katBJG2F	5'- AATTCACTCAGAAGACCCATGG -3'
		katBJG2R	5'- TTATTTGCCTGCGAAGTTAGG -3'
oxyRJG(EMSA)	137	oxyRJGF	5'-GAAGCCGTCTCCTTCCTACAAC-3'
		oxyRJGR	5'-GGCTGCTCATCCGTTAAGATCG-3'
ahpBJG(EMSA)	237	ahpBJGF	5'-GGAATAGCCAGAGCAGGCGTGT-3'
		ahpBJGR	5'-TGTTGACCAGTACGCTCATCGC -3'
ahpFJG(EMSA)	175	ahpFJGF	5'- ACCTGGTCGGCAAGATCTAAGACCG-3'
		ahpFJGR	5'-GCGTCCAACATGGTTCAGCTCCTC-3'
ahpCJG1(EMSA)	203	ahpCJG1F	5'-GCACTGACGAGGGCAGGTTCTT-3'
		ahpCJG1R	5'-AACGGTTGGACTTGAGTGTTGATC-3'
ahpCJG2(EMSA)	217	ahpCJG2F	5'-GCTGCTCGGTGCCTGGTTGT-3'
		ahpCJG2R	5'- AACCTGCCCTCGTCAGTGCC -3'
katA(promoter-gfp)	398	katAPF	5'-CCGGAATTCGTCGGCGGTGAAGTCGTAGAA-3'
		katAP2R	5'-CGGGGTACC
			TTACTGCACGTTCTGGTTATCGACC-3'
katB(promoter-gfp)	564	katBPF	5'- CCGGAATTCAATTCACTCAGAAGACCCATG-3'
		katBP2R	5'-CGGGGTACC GGAAGAGCTCCTAATGGCT-3'
oxyR(promoter-gfp)	155	oxyRPF	5'-CCGGAATTC GAAGCCGTCTCCTTCCTACAAC-3'
		oxyRP2R	5'-CGGGGTACC GGCTGCTCATCCGTTAAGATCG-
			3'
oxyR(knock out)	424	oxyR-upF	5'-GGGGACAAGTTTGTACAAAAAAGCAGGCTC
			ATGCAACCAGCCCAGCACATG-3'
		oxyR-upR	5'-TCACATGGCTGCTCATCCGTTAAGATC-3'
oxyR(knock out)	474	oxyR-doF	5'-TGACCGAGCTGTCCAGGGTCCC-3'
		oxyR-doR	5'-GGGGACCACTTTGTACAAGAAAGCTGG
			GTAGCTGCTGGGTGAGTCCTTCG-3'
<i>oxyR</i> (knock	1990/13	oxyRseq-F	5'-TAGACCCCGGTGCTGGAGACG-3'
sequencing)	30	oxyRseq-R	5'-CGAGCGGGCCAAGTTGGTAAT-3'

Table S3. MIC of *P. aeruginosa* PAK,  $\triangle osaR$ ,  $\triangle dsbM$  and  $\triangle osaR \triangle dsbM$  against nonaminoglycosides antibiotics investigated.

	63		U		
Bacterial	Relevant	MIC of compound ( $\mu g m l^{-1}$ )			
strain	genotype	Chloramphenicol	Tetracycline	Ciprofloxacin	
PAK	WT	50	16	0.5	
$\Delta osaR$	$\Delta osaR$	50	16	0.5	
$\Delta dsbM$	$\Delta dsbM$	50	16	0.5	
$\Delta osaR\Delta dsbM$	$\Delta osaR\Delta dsbM$	50	16	0.5	



Fig. S1. The knocking out of *osaR* have no effect on growth rate. Overnight culture were diluted into fresh LB medium with 1/100,  $100\mu$ l of culture was transferred into each of the well of a 96-wells microplate,  $OD_{600}$  was measured every 30 minutes for 24 hours at 37°C 200 rpm in microplate reader.



**Fig. S2. The regulation of** *oxyR* **and the genes belonging to the OxyR regulon by OsaR is indirect**. (A)EMSA assays of OsaR-RE binding with promoter region of *oxyR*, *katA*, *katB*, *ahpB* and *ahpCF*; DNA fragments information are shown in (B). OsaR was used in the following concentration (nM): 0, 50, 100, 200. Black arrows indicate free DNA.

A MDRLTATRVFVEVIDSGSQTAAAERLDMSRAMVSRYLAELEEWVGARLLHRSTRRLSLTDAGAELLPQCREMLAVADAMQ ATGQTRRDSPRGTLRITSSLSFAQAWLTRAAAAFVERYPGTAIDLQVNSQVVNLVEERIDLALRIANQLDPNLIARRLGECRS VICAAPDYLRRHGTPRRPEDLALHNCLTYSYFGRSLWQEERDGEPTSVPVGGSLSANESTVLLEAAAAGAGISQQPLYSAAP LIRSGRLVALLPEWSPQVLGIHAVYASRRQMPPALRALLDFLVERMAADPHWDEAGPLALALEHHHHHHH-

1 C 69	2 C 161	3 C 166	4 (	C 189
C69 is 1	not SS-bou	nded	Scot	e = -36.8
C161 is	not SS-bo	unded	Scot	e = -33.9
C166 is	probably	SS-boun	ded	Score = -22.7
C189 is	probably	SS-boun	ded	Score = -13.3

## Gene seqence



## Fig. S3. Expression and purification of OsaR protein (C-D) and PA0055

**protein(E)**. (A) the amino sequence of OsaR, which have four cysteines in red color. C166 and C189 are located at regulate domain(RD) and form disulfide bond probably. (B) OsaR tertiary structure prediction. OsaR was expressed in BL21(DE3) host strain via pET28a insolubility (C) MBP- OsaR fusion expression (Lane 2), purification (Lane 3), cleavage(Lane 4) and Lane 1 is MBP expression control as followed by SDS-PAGE. (D) nonreducing SDS-PAGE of OsaR protein (purified with inclusion body; M:Protein marker. (E)PA0055 protein expression in the BL21(DE3) strain with pET28a vector. Lane 1, negative control; Lane 2 cell lysate supernatant; Lane 3, acquired pure PA0055 protein in 200 mM imidazole solution; Lane 4, pure PA0055 after ultra-filtration desalination). The same molecular weight marker was used for all SDS–PAGE analyses.



**Fig. S4. The EMSA of PA0055 protein with F2IR.** PA0055 used in the following concentration (nM) 0, 50, 100, 200, 400. All the data were obtained from at least three independent experiments.



Fig. S5. Promoter  $P_{PA0057}$  can be induced by carbenicillin. Bacteria were treated with given concentration of carbenicillin at the OD<sub>600</sub> of 0.4 in LB at 37°C. (B) OD<sub>600</sub> and (A) GFP fluorescence readings (relative fluorescence units/RFU) were measured every 30 minutes for 24 hours. All the data were obtained from at least three independent experiments with at least three replicates.

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