Supplementary material

to

A bacterial chemoreceptor that mediates chemotaxis to two different plant hormones

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Running Head: Chemotaxis to plant hormones

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Supplementary Table S1. Thermodynamic parameters derived from the microcalorimetric titrations of PcpI-LBD and E6B08_RS28125 with different ligands. Data were analyzed using the "One binding site model" of the MicroCal version of ORIGIN. The corresponding data are shown in Figures 5 and supplementary Figure S6.

Protein/Ligand	<i>Κ</i> ₀ (μΜ)	Δ <i>H</i> (kcal/mol)		
Pcpl-LBD ^a				
Salicylate	826 ± 34	-14.5 ± 5.7		
Benzoate	171 ± 14	-0.75 ± 0.03		
3-Methylbenzoate	91 ± 8	-0.37 ± 0.02		
E6B08_RS28125 ^b				
L-ornithine	0.93 ± 0.11	-10.13 ± 0.42		
L-histidine	3.28 ± 0.29	-8.43 ± 0.72		
L-arginine	29.5 ± 2.61	8.61 ± 0.3		

^aNo binding was detected for 2-aminobenzoate, 2-chlorobenzoate, 2-nitrobenzoate, 3-aminobenzoate, 3-nitrobenzoate, 4-hidroxybenzoate, acetyl salicylic acid, benzene, protocatechuate, vanillate, vanillin and quinate.

^bNo binding was detected for L-Lysine.

Strains and plasmids	Genotype or relevant characteristics ^a	Ref.
Strains		
Escherichia coli BL21(DE3)	F ⁻ ompT gal dcm lon $hsdS_B(r_B m_B^-) \lambda$ (DE3 [lacI lacUV5-	(Jeong e
Escherichia coli BE21(BE5)	T7p07 ind1 sam7 nin5]) [malB ⁺] _{K-12} (λ ^S)	al., 2009
	F ⁻ endA1 glnV44 thi-1 recA1 relA1 gyrA96	(Woodco
E. coli DH5α	$deoR \ nupG \ purB20 \ \varphi 80 dlacZ\Delta M15 \ \Delta(lacZYA-argF)U169,$	k et al.,
	hsdR17($r_{K}^{-}m_{K}^{+}$), λ^{-}	1989)
E. coli CC118λpir	araD Δ (ara, leu) Δ lacZ74 phoA20 galK thi-1 rspE rpoB argE	(Herrero
	recA1 λpir	al., 1990
		(Demarro <i>et al.</i> ,
<i>E. coli</i> β2163	F- RP4-2-Tc::Mu $\Delta dapA$::(<i>erm-pir</i>), Km ^R , Em ^R	
		2005)
D 1 1000	W 711.	(Laird an
Pseudomonas putida 1290	Wild type strain	Leveau,
D (1.1200 CL.)		2019)
P. putida 1290-CheA	$cheA::pCHESIQKmGm; Km^R, Gm^R$	This stud
<i>P. putida</i> 1290-IacA	<i>iacA</i> ::pCHESIΩKmGm; Km ^R , Gm ^R	This stud
<i>P. putida</i> 1290-RS07220	<i>E6B08_RS07220</i> ::pCHESIΩKmGm; Km ^R , Gm ^R	This stud
<i>P. putida</i> 1290-RS17840	<i>E6B08_RS17840</i> ::pCHESIΩKmGm; Km ^R , Gm ^R	This stud
<i>P. putida</i> 1290-RS22475	<i>E6B08_RS22475</i> ::pCHESIΩKmGm; Km ^R , Gm ^R	This stud
<i>P. putida</i> 1290-PcpI	$\Delta pcpI::Km; Km^R$	This stud
<i>P. putida</i> 1290-RS29420	<i>E6B08_RS29420</i> ::pCHESIΩKmGm; Km ^R , Gm ^R	This stud
P. putida 1290-RS30830	<i>E6B08_RS30830</i> ::pCHESIΩKmGm; Km ^R , Gm ^R	This stud
Pseudomonas aeruginosa PAO1	Wild type strain	(Stover e
-		<i>al.</i> , 2000
Pseudomonas putida KT2440	Wild-type, non-pathogenic soil bacterium	(Belda <i>et al.</i> , 2016)
Plasmids		<i>u</i> ., 2010
pET28b(+)	Km ^R ; Protein expression plasmid	Novager
pE1280(+)	Km ^R ; pET28b(+) derivative containing a DNA fragment	Novagen
pMAMV365	encoding PcpI-LBD cloned into the NdeI/BamHI	This stud
	Km ^R ; pET28b(+) derivative containing a DNA fragment	
pMAMV385	encoding <i>E6B08_RS28125</i> cloned into the NdeI/BamHI sites.	This stud
	The sequence predicted to be signal peptide was not included.	This stud
		(Obranic
pBBR1MCS-5_START	Gm ^R ; oriRK2 mobRK2	<i>al.</i> , 2013
		P. van
	Ap ^R , Km ^R , Gm ^R ; pUNφ18 bearing a HindIII fragment from	Dillewijn
pCHESIΩGmKm	pHP45 Ω Km (Ω -KmGm interposon) cloned at the HindIII site,	unpublish
	oriT RP4	d data
	Km ^R , Gm ^R ; PCR product containing a 0.8 kb region of <i>cheA</i>	
pMAMV352	was inserted into the EcoRI/SacI sites of pCHESIQKmGm	This stud
	Km ^R , Gm ^R ; PCR product containing a 0.8 kb region of <i>iacA</i>	T 1 · 1
	was inserted into the EcoRI/SacI sites of pCHESIQKmGm	This stud
pMAMV353		
pMAMV353		
-	Km ^R , Gm ^R ; PCR product containing a 0.9 kb region of	This stud
pMAMV353 pMAMV355	Km ^R , Gm ^R ; PCR product containing a 0.9 kb region of <i>E6B08_RS30830</i> was inserted into the EcoRI/SacI sites of	This stud
-	Km ^R , Gm ^R ; PCR product containing a 0.9 kb region of <i>E6B08_RS30830</i> was inserted into the EcoRI/SacI sites of pCHESIΩKmGm	This stud
pMAMV355	Km ^R , Gm ^R ; PCR product containing a 0.9 kb region ofE6B08_RS30830 was inserted into the EcoRI/SacI sites ofpCHESIΩKmGmKm ^R , Gm ^R ; PCR product containing a 0.7 kb region of	
pMAMV355	 Km^R, Gm^R; PCR product containing a 0.9 kb region of <i>E6B08_RS30830</i> was inserted into the EcoRI/SacI sites of pCHESIΩKmGm Km^R, Gm^R; PCR product containing a 0.7 kb region of <i>E6B08_RS17840</i> was inserted into the EcoRI/SacI sites of 	
pMAMV355	 Km^R, Gm^R; PCR product containing a 0.9 kb region of <i>E6B08_RS30830</i> was inserted into the EcoRI/SacI sites of pCHESIΩKmGm Km^R, Gm^R; PCR product containing a 0.7 kb region of <i>E6B08_RS17840</i> was inserted into the EcoRI/SacI sites of pCHESIΩKmGm 	
pMAMV355 pMAMV356	 Km^R, Gm^R; PCR product containing a 0.9 kb region of <i>E6B08_RS30830</i> was inserted into the EcoRI/SacI sites of pCHESIΩKmGm Km^R, Gm^R; PCR product containing a 0.7 kb region of <i>E6B08_RS17840</i> was inserted into the EcoRI/SacI sites of pCHESIΩKmGm Km^R, Gm^R; PCR product containing a 0.7 kb region of Km^R, Gm^R; PCR product containing a 0.7 kb region of Science (Science) 	This stud
pMAMV355 pMAMV356	 Km^R, Gm^R; PCR product containing a 0.9 kb region of <i>E6B08_RS30830</i> was inserted into the EcoRI/SacI sites of pCHESIΩKmGm Km^R, Gm^R; PCR product containing a 0.7 kb region of <i>E6B08_RS17840</i> was inserted into the EcoRI/SacI sites of pCHESIΩKmGm Km^R, Gm^R; PCR product containing a 0.7 kb region of <i>E6B08_RS22475</i> was inserted into the EcoRI/SacI sites of 	This stud
-	 Km^R, Gm^R; PCR product containing a 0.9 kb region of <i>E6B08_RS30830</i> was inserted into the EcoRI/SacI sites of pCHESIΩKmGm Km^R, Gm^R; PCR product containing a 0.7 kb region of <i>E6B08_RS17840</i> was inserted into the EcoRI/SacI sites of pCHESIΩKmGm Km^R, Gm^R; PCR product containing a 0.7 kb region of <i>E6B08_RS22475</i> was inserted into the EcoRI/SacI sites of pCHESIΩKmGm 	This stud
pMAMV355 pMAMV356	 Km^R, Gm^R; PCR product containing a 0.9 kb region of <i>E6B08_RS30830</i> was inserted into the EcoRI/SacI sites of pCHESIΩKmGm Km^R, Gm^R; PCR product containing a 0.7 kb region of <i>E6B08_RS17840</i> was inserted into the EcoRI/SacI sites of pCHESIΩKmGm Km^R, Gm^R; PCR product containing a 0.7 kb region of <i>E6B08_RS22475</i> was inserted into the EcoRI/SacI sites of 	This stud

Supplementary Table S2. Strains and plasmids used in this study.

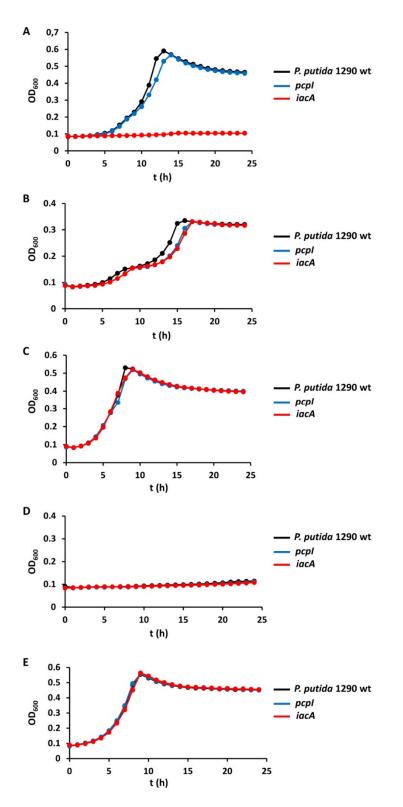
pMAMV361	Km ^R , Gm ^R ; PCR product containing a 0.7 kb region of <i>E6B08_RS07220</i> was inserted into the EcoRI/SacI sites of pCHESIΩKmGm	This study
pUC18Not	Ap ^R ; identical to pUC18 but with two NotI sites flanking pUC18 polylinker	(Herrero <i>et</i> <i>al.</i> , 1990)
p34S-Km3	Km ^R , Ap ^R ; <i>Km3</i> antibiotic cassette	(Dennis and Zylstra, 1998)
pMAMV366	Ap ^R ; 1.5-kb PCR product containing a 1086 bp deletion of <i>pcpI</i> inserted into the EcoRI/HindIII sites of pUC18Not	This study
pMAMV367	Ap ^R , Km ^R ; 0.95-kb BamHI fragment containing <i>km3</i> cassette of p34S-Km3 was inserted into BamHI site of <i>pcpI</i> in pMAMV366	This study
pKNG101	Sm ^R ; oriR6K mob sacBR	(Kaniga <i>et</i> <i>al.</i> , 1991)
pMAMV368	Sm ^R , Km ^R ; 2.5-kb NotI fragment of pMAMV367 was cloned at the same site in pKNG101	This study
pMAMV378	Gm ^R ; a 1.7-kb PCR fragment containing the <i>pcp1</i> gene cloned into the NdeI/BamHI sites of pBBR1-MCS-5_START	This study

^aAp, ampicillin; Km, kanamycin; Gm, gentamycin; Sm, streptomycin; Em, erythromycin.

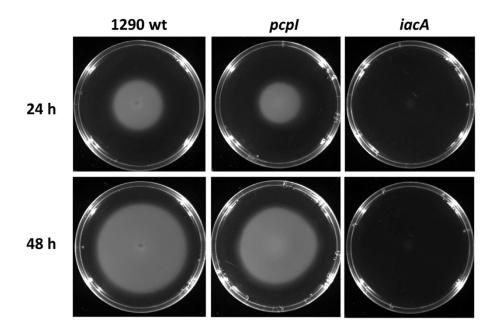
chcA-1290-EcoRI-FTATGAATTCCTTCAGCTCAACGAGCTGGTG omanaOnstruction of cheA matachcA-1290-SacI-RTAATGAACTCCGCTGCGTGATGCTGACCCOnstruction of cheA mataiacA-1290-SacI-RTAATGAATTCGAGTGGGACTGGGAACGA TATGAGCTCAAGTCGGGCAACGACGCOnstruction of cheA mataMCP30830-EcoRI-FTAATGAATTCGAGGGCAACTGGCAACGC TGGAGAAGCACTOnstruction of cheA mataMCP30830-SacI-RTAATGAACTCCGCGAACCTGGAAGCCGTGOnstruction of CBBB_RS30830 mutaMCP30830-SacI-RTAATGAACTCCGGCAACTGGACACGCGACGOnstruction of CBBB_RS20830 mutaMCP17840-SacI-RTAATGAACTCCGGCAACGTGGACACCTGACGOnstruction of CBBB_RS217540 mutaMCP22475-SacI-RTAATGAACTCCGGCAACGTGGCGGCTGCTCACCOnstruction of CBBB_RS22475 mutaMCP2240-EcoRI-FTAATGAACTCCGCGCACGTGACCCTOnstruction of CBBB_RS22475 mutaMCP2240-EcoRI-FTAATGAACTCCGGCGAGACCTGACCCTOnstruction of CBBB_RS22475 mutaMCP07220-EcoRI-FTAATGAACTCCGACGTGGTGGCTGGCTGGCACCOnstruction of CBBB_RS282475 mutaMCP0720-EcoRI-FTAATGAACTCCGACGCACTGACGCAGCACCOnstruction of CBBB_RS282475 mutaMCP0720-EcoRI-FTAATGAACTCCGACGCACGACGCACCOnstruction of CBBB_RS282275 mutaMCP0720-EcoRI-FTAATGAACTCCGACGCACGCACGCACCOnstruction of CBBB_RS282120-mutaRS28110-BamHI-RTAATGAACTCCGACGCACGCACGCACCOnstruction of CBBB_RS28125RS28110-BamHI-RTAATGAACTCCGACGCAGCACGCACACCOnstruction of CBBB_RS28125RS28110-BamHI-RTAATGAACTCCGACGCAGCGCACACCCOnstruction of CBBB_RS28125RS28110-BamHI-RTAATGAACTCCAGCAGC	Oligonucleotide	Sequence (5'-3')	Purpose	
cmeA-1290-BeoRI-FTAATGAATTCCGCTTCGGTGGACTGGACTGACCCConstruction of iacA mutantiaeA-1290-SacI-RTAATGACTCCAGGTGGTGGTGACGCACCGConstruction of iacA mutantMCP30830-EcoRI-FTAATGACTCCACATCTCGTGGACATGCCACCGConstruction of E6B08_RS30830 mutantMCP17840-EcoRI-FTAATGAATTCCGGCCAACCTGGACATGCTCAConstruction of E6B08_RS17840 mutantMCP22475-EcoRI-FTAATGAATTCCGGCCAACGTGGACATGCTCAConstruction of E6B08_RS17840 mutantMCP22475-SacI-RTAATGAATTCCGGCCAACGTGGACACCTATGConstruction of E6B08_RS22475 mutantMCP22475-SacI-RTAATGAGCTCCGCATTGCGGCGCCACTTCATCConstruction of E6B08_RS22475 mutantMCP29420-EcoRI-FGTCGACGAATTCCAGCAGATGACConstruction of E6B08_RS22475 mutantMCP07220-EcoRI-FTAATGACTCCGCGAGACCTGGTGGTGGTCACCConstruction of E6B08_RS29420 mutantMCP07220-SacI-RTAATGAATTCGAGAACCTGGTGGTGGTGGTGGCConstruction of E6B08_RS27220 mutantRS28110-EcoRI-FTAATGAATTCGAAAGCGTGGCGGAGAACCConstruction of E6B08_RS27220 mutantRS28110-BamHI-RTAATGGATCCCATGCGCGGGATCGACGCAAGGConstruction of E6B08_RS28110 (pcpl) mutantRS28110-MindII-RTAATGGATCCCAGGGCATGGACGGCATCConstruction of pET28- E6B08_RS28125-NdeI-FRS28110-Comple-BamHI-RTAATGGATCCTAAGGTCTGGCGGCAAGCCConstruction of pET28- E6B08_RS28125-NdeI-FRS28110-Comple-BamHI-RTAATGGATCCGATCAGGCAAGGCGATCCConstruction of pET28- E6B08_RS28125-NdeI-FF6B08_RS28125-NdeI-FTAATGGATCCTAATGCAGGCAAGCGGCATCConstruction of pET28- E6B08_RS28125-NdeI-FF6B08_RS28125-NdeI-FTAATGGATCCTA	cheA-1290-EcoRI-F	TAATGAATTCCTTCAGCTCAACGAGCTGGTGG		
iacA-1290-SacI-RTAATGAGCTCCAGGTTGGTGACGTCGACCGcmutantMCP30830-SacI-RTAATGAACTCCGAGCCACCTGGCAACGGConstruction of <i>E6008_RS30830</i> mutantMCP17840-EcoRI-FTAATGAATTCCGGCAACCTGGACATGCTCAConstruction of <i>E6008_RS17840</i> mutantMCP17840-SacI-RTAATGAACTCCGGCAACCTGGACATGCTGAConstruction of <i>E6008_RS17840</i> mutantMCP22475-SacI-RTAATGAACTCCGGCCAACGTGGACACCTATGConstruction of <i>E6008_RS22475</i> mutantMCP29420-EcoRI-FGTCGACGAATTCCAGCAGATGCACCCTATGConstruction of <i>E6008_RS22475</i> mutantMCP29420-SacI-RTAATGAGCTCCGCATGGGCGGGCACCTGACCConstruction of <i>E6008_RS22475</i> mutantMCP07220-SacI-RTAATGAACTCCGGCAGACCTGGTGGTGGCCConstruction of <i>E6008_RS22475</i> mutantMCP07220-SacI-RTAATGAATTCGAAAGCGTGGCGGAGAACCConstruction of <i>E6008_RS22475</i> mutantRS28110-EcoRI-FTAATGAATTCGAAAGCGTGGCGAGAACCConstruction of <i>E6008_RS22175</i> mutantRS28110-BamHI-RTAATGAATTCGACAGCATGAAGCGTGGCGAGAACCConstruction of <i>E6008_RS22110</i> (pcp1) mutantRS28110-BamHI-FTAATGAATTCGACAGTCAGGCATGACGCATCConstruction of <i>E6008_RS281210</i> (pcp1) mutantRS28110-BamHI-FTAATGAATCCCAGGGGATGGACGCATCConstruction of <i>E728</i> - Pep1-LBD (pMAMV355)RS28110-Comple-NdeI-FTAATGATCATATGCAGGGCATGGACGGCATCConstruction of pE728- Pep1-LBD (pMAMV355)RS28110-Comple-BamHI-RTAATGAATCCCAAGGCAAGCGGCATCGConstruction of pE728- Pep1-LBD (pMAMV355)RS28110-Comple-BamHI-RTAATGAATCCTAAGGCCGATGCAGGCAAGCConstruction of pE728- Pep1-LBD (pMAMV355)RS28110-Comple-BamHI-RTAATG	cheA-1290-SacI-R	TAATGAGCTCGTGCTCGCTGATGTCGTCACC		
IacA-1290-SacI-RIAATGAGCTCCACGTTGGGCACGTCGGCCACCGConstruction of E6008_R530830 mutantMCP30830-EcoRI-FTAATGAGCTCCACATCTCGGGCAAGGCCGTGConstruction of E6008_R530830 mutantMCP17840-EcoRI-FTAATGAGCTCGGTGCTCACCGCGTTGTTGGConstruction of E6008_R517840 mutantMCP22475-EcoRI-FTAATGAGCTCGGCAACGTCGACACCTATGConstruction of E6008_R522475 mutantMCP22475-SacI-RTAATGAGCTCCGCATTGCGCGCCACTTCATCConstruction of E6008_R522475 mutantMCP29420-EcoRI-FGTCGACGAATTCCAGCAGATGACConstruction of E6008_R522475 mutantMCP29420-EcoRI-FTAATGAGCTCCCTCGTCGTGGTGGTCACCConstruction of E6008_R529420 mutantMCP07220-EcoRI-FTAATGAGCTCCACGCGTGGTGGTCGCCConstruction of E6008_R529420 mutantRS28110-EcoRI-FTAATGAATTCGCAGACCTGGTGGTGGTCGCConstruction of E6008_R52210 mutantRS28110-BamHI-RTAATGACTCCCATGCGCGGAGCCGCGAGAACCConstruction of E6008_R528110 (pcpl) mutantRS28110-BamHI-FTAATGGATCCCATGCGGCATCAGCGCATCCConstruction of E608_R528110 (pcpl) mutantRS28110-MidII-RTAATGGATCCCAGGCATGAGCGCATCConstruction of PE728- PCPI-LBD (pMAMV365)RS28110-SamHI-RTAATGGATCCCAGGCATGGTGGCGCGCGCATCConstruction of pE728- PCPI-LBD (pMAMV365)RS28110-Comple-BamHI-RTAATGGATCCGATGCGGCAGGCGAGCGCGCATCConstruction of pE728- PCPI-LBD (pMAMV378) for complementation assaysE6B08_RS28125-NdeI-FAACATATGATCGACGATGCGGCAAGCCGCGCAACCConstruction of pE728- PCBI-LBD (pMAMV378) for complementation assaysE6B08_RS28125-NdeI-FAACATATGGACCGACAGGGCAAGCCAAGCConstruction of pE728- <td>iacA-1290-EcoRI-F</td> <td>TAATGAATTCCGCTTCGGTGGACTGGAGTG</td> <td colspan="2">Construction of <i>iacA</i></td>	iacA-1290-EcoRI-F	TAATGAATTCCGCTTCGGTGGACTGGAGTG	Construction of <i>iacA</i>	
MCP30830-SacI-RTAATGAGCTCACATCTCGTGCAAGGCCGTGCONStruction of EGB08_RS30830 mutantMCP17840-EcoRI-FTAATGAATTCCCGCAACCTGGACATGCTCAConstruction of EGB08_RS17840 mutantMCP217840-SacI-RTAATGAGCTCGGTGCTCACCGCGTTGTTGGConstruction of EGB08_RS17840 mutantMCP22475-EcoRI-FTAATGAGCTCGGCAACGTCGACACCTATGConstruction of 	iacA-1290-SacI-R	290-SacI-R TAATGAGCTCCAGGTTGGTGACGTCGACCG		
MCF300305-3aFrKTAATGAGCTCACATCTCGTGCAACGCCUTGConstruction of E6B08_RS17840 mutantMCP17840-EcoRI-FTAATGAGCTCGGTGCTCACCGCGTTGTTGGConstruction of E6B08_RS17840 mutantMCP22475-EcoRI-FTAATGAGCTCGCATTGCGCGCCACTTCATCConstruction of E6B08_RS22475 mutantMCP29420-EcoRI-FGTCGACGAATTCCAGCAGCAGTGGCCACCTConstruction of E6B08_RS22475 mutantMCP29420-EcoRI-FGTCGACGAATTCCAGCAGAGAGCConstruction of E6B08_RS22420 mutantMCP07220-EcoRI-FTAATGAGCTCCGGCGAGAACCTGGTCGTCConstruction of E6B08_RS22420 mutantMCP07220-EcoRI-FTAATGAATTCGAAAGCGTGCGGCGAGAACCConstruction of E6B08_RS2220 mutantRS28110-EcoRI-FTAATGAATTCGAAAGCGTGCGGGAGAACCConstruction of E6B08_RS2220 mutantRS28110-BamHI-RTAATGGATCCGCGATCCAGGCAGGAACCConstruction of E6B08_RS2210 (pcpl) mutantRS28110-Ndel-FTAATAGGATCCGCGATCCAGGCATGAACCGCConstruction of pE128- Pcpl-LBD (pMAMV365)RS28110-SamHI-RTAATGGATCCCGAGTCTGGCCGGCGCGCATCConstruction of pBB1- MCS5_START-pcpl (pMAMV38) for complementation assaysE6B08_RS28125-Ndel-FAAACATATGATCGACGATCACGGCTAAGCConstruction of pE128- E6B08_RS28125-BamHI-RF6B08_S5770-qPCR-RAACAGGTCCGACAGCGATCACAGConstruction of pE128- E6B08_23075-qPCR-RE6B08_23075-qPCR-RCGACACTTGCGCAAGGCAATGqPCR analyses	MCP30830-EcoRI-F	TAATGAATTCGAGGCGCTACTGGCCAACG	Construction of	
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E6B08_23075-qPCR-R CGAGCAGTGGCAAGGCAATG qPCR analyses	E6B08_05770-qPCR-R	AACAGGTCCGACAGCGACTT	qPCR analyses	
	E6B08_23075-qPCR-F	GACAGCCTTGGCGATAACGG	qPCR analyses	
E6B08_26760-qPCR-F CAGCCTGATCGACCGTAGCA qPCR analyses	E6B08_23075-qPCR-R	CGAGCAGTGGCAAGGCAATG	qPCR analyses	
	E6B08_26760-qPCR-F	CAGCCTGATCGACCGTAGCA	qPCR analyses	

Supplementary Table S3. Oligonucleotides used in this study.

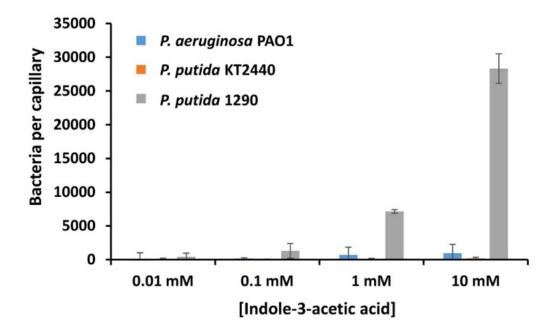
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E6B08_27055-qPCR-F	TTCGCAGCAGTTCCAGAACG	qPCR analyses
E6B08_27055-qPCR-R	ACTCGGTCAGCGAAGCCTTG	qPCR analyses
gyrB-1290-qPCR-F	CGTCAGCTGCCAGAGTTGGT	qPCR analyses
gyrB-1290-qPCR-R	GGCCTCGTCGTCCTTGATGT	qPCR analyses
E6B08_13285-qPCR-F2	CTCGATGGCCAGGACCTTTC	qPCR analyses
E6B08_13285-qPCR-R2	GCTTGGGCCAACGGTAGTTC	qPCR analyses
E6B08_28110-qPCR-F2	CGACAGCTCTTCGCCGACTA	qPCR analyses
E6B08_28110-qPCR-R2	GCGGACCTTGGTCTGGGAAAC	qPCR analyses



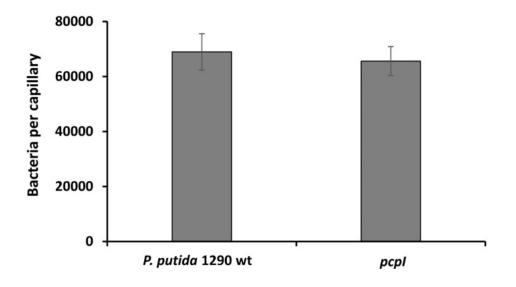
Supplementary Figure S1. Growth of *Pseudomonas putida* **1290 strains in minimal medium supplemented with different Pcpl ligands as sole carbon sources.** Five millimolar of indole-3-acetic acid (A), salicylic acid (B), benzoate (C), 3-methylbenzoate (D) and glucose (E, positive control) were used. Wild type *P. putida* 1290 was grown at 30 °C using Bioscreen Microbiological Growth Analyser (Oy Growth Curves Ab Ltd, Helsinki, Finland) under shaking. Data were registered each hour. Shown are mean and standard deviation of five biological replicates.



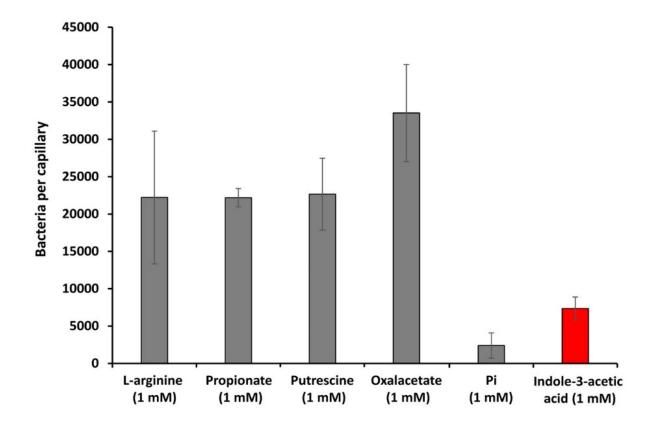
Supplementary Figure S2. Swimming plate motility assays of *Pseudomonas putida* 1290 strains grown in minimal medium supplemented with indole-3-acetic acid as sole carbon source. The bioassays were repeated at least three times, and representative results are shown.



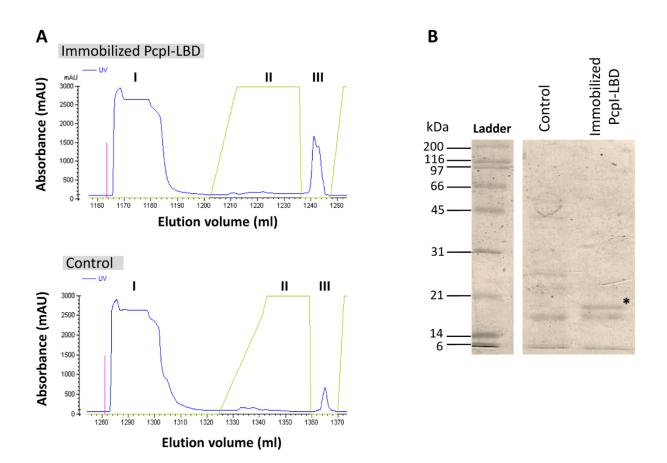
Supplementary Figure S3. Quantitative chemotaxis assays of different *Pseudomonas* strains towards different concentrations of indole-3-acetic acid. Data are means and standard deviations from three independent experiments conducted in triplicate.



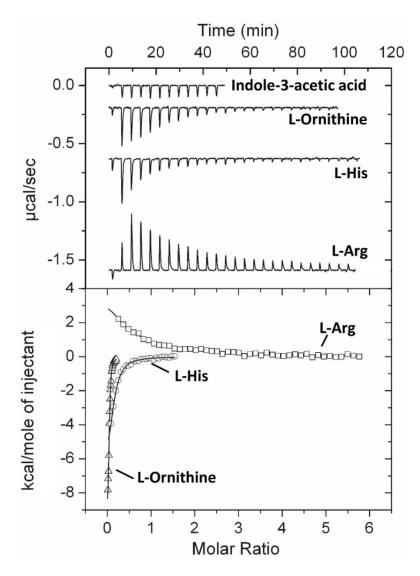
Supplementary Figure S4. The mutation of *E6B08_RS28110* (*pcpl*) has no impact on the general chemotactic responses of *P. putida* 1290. Quantitative capillary chemotaxis assays of the wild type and *pcpl* mutant strains to 0.1% (w/v) casamino acids are shown. Data are means and standard deviations from three independent experiments conducted in triplicate.



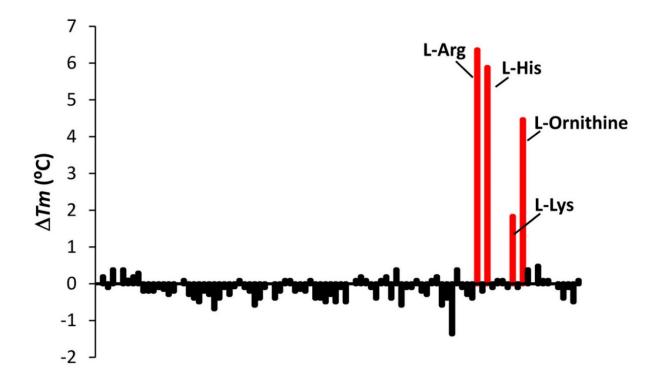
Supplementary Figure S5. Chemotactic responses of *Pseudomonas putida* 1290 to different chemoeffectors. Data are means and standard deviations from three independent experiments conducted in triplicate.



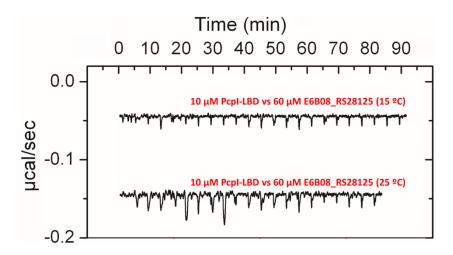
Supplementary Figure S6. Pull-down experiment on immobilized Pcpl-LBD. A, FPLC (fast protein liquid chromatography) chromatogram profiles showing: (I) the injection of *Pseudomonas putida* 1290 protein extracts onto a HisTrap column without (negative control) or with immobilized Pcpl-LBD; (II) protein elution using a guanidine hydrochloride gradient; and (III) Pcpl-LBD protein release using a gradient of imidazole. **B**, SDS-PAGE gel of the pull-down experiment on immobilized Pcpl-LBD. Shown are proteins eluted using a 0–6 M guanidine hydrochloride gradient in the control experiment (i.e. no Pcpl-LBD immobilized on the column) and when Pcpl-LBD was immobilized on the column. The asterisk indicates the protein band that was excised and subjected to analysis by MALDI-TOF mass spectrometry. This protein was identified as the peptidyl-prolyl *cis-trans* isomerase (PPlase) E6B08_RS26110 and regarded as an artefact of the experiment. PPlases assist protein folding by catalyzing the *cis-trans* isomerization of peptide bonds preceding prolyl residues (Göthel *et al.*, 1999).

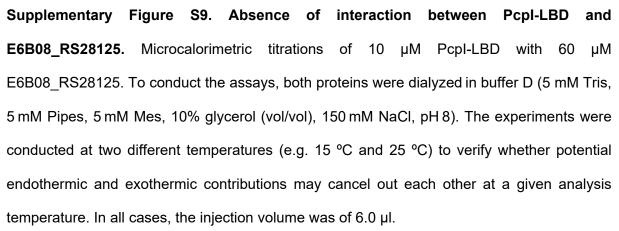


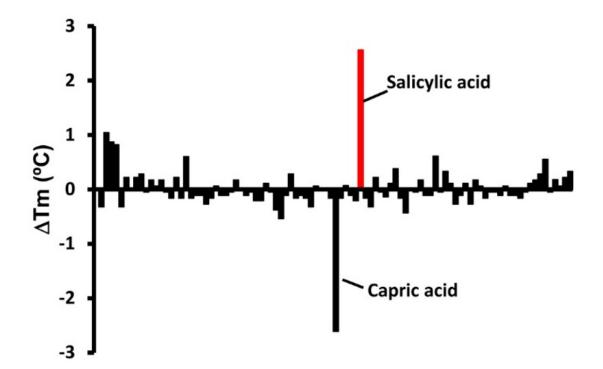
Supplementary Figure S7. The solute binding protein E6B08_RS28125 binds L-arginine, L-histidine and L-ornithine. Microcalorimetric titrations of E6B08_RS28125 with indole-3acetic acid, L-Arg, L-His and L-ornithine. Upper graphs show raw titration data, while lower graphs show integrated corrected peak areas of the titration data fit using the "one binding site model." The derived thermodynamic parameters are provided in Suppl. Table S1.



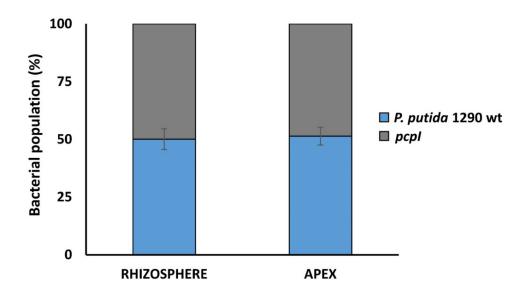
Supplementary Figure S8. Differential scanning fluorimetry-based thermal shift assays to identify E6B08_RS28125 ligands. Differential scanning fluorimetry thermal shift assays of *P. putida* 1290 E6B08_RS28125 using the 95 compounds present in the compound array PM2A (Biolog) that can serve as carbon sources. Shown are the changes in the midpoint of protein unfolding transitions (Tm) with respect to the ligand-free protein.



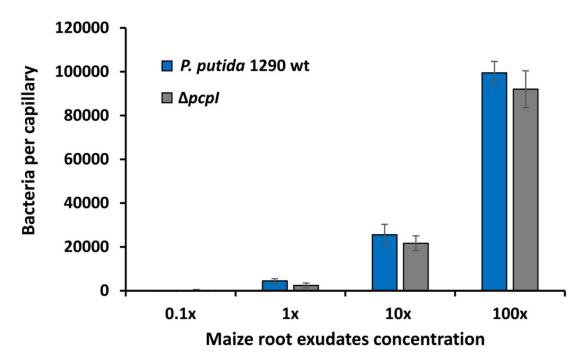




Supplementary Figure S10. Differential scanning fluorimetry based thermal shift assays to identify Pcpl ligands. Shown are midpoint of protein unfolding transitions (Tm) changes for each of the 95 compounds present in the Biolog PM2A compound array of carbon sources with respect to the Tm of the ligand-free protein (39.6 °C). Microcalorimetric titrations with capric acid revealed no binding.



Supplementary Figure S11. Competitive root colonization of *Pseudomonas putida* 1290 and a mutant defective in *pcpl*. The figure represents the percentage of bacteria recovered either from the rhizosphere or root tips of maize (*Zea mays*) plants. Percentage of the wild type and mutant strain in the initial inoculum was $50 \pm 1\%$. Data are the means and standard deviations of eight plants after 10 days of colonization.



Supplementary Figure S12. Quantitative capillary chemotaxis assays of *Pseudomonas putida* 1290 strains to different concentrations of maize root exudates. Data are means and standard deviations from three individual experiments conducted in triplicate.

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