Design, Synthesis and Evaluation of New 1*H*benzo[*d*]imidazole based PqsR Inhibitors as Adjuvant Therapy for *Pseudomonas aeruginosa* Infections

Fadi Soukarieh^{*a,1,3}, Alaa Mashabi^{a,2, r}, William Richardson², Eduard Vico Oton^{1[†]}, Manuel
Romero^{1,3|}, Jean-Frédéric Dubern¹, Shaun N. Robertson^{1,3}, Simone Lucanto^{1,3}, Zoe MarkhamLee², Tomás Sou^{4|}, Irena Kukavica-Ibrulj⁵, Roger C. Levesque⁵, Christel A.S. Bergstrom⁴, Nigel
Halliday¹, Barrie Kellam², Jonas Emsley^{2,3}, Stephan Heeb¹, Paul Williams^{1,3}, Michael J.
Stocks^{*2,3}, and Miguel Cámara^{*1,3}.

^a These authors contributed equally to this study.

² School of Pharmacy, University of Nottingham Biodiscovery Institute, University of Nottingham, Nottingham, NG7 2RD, UK.

³ The National Biofilms Innovation Centre, University of Nottingham Biodiscovery Institute, University of Nottingham, Nottingham, NG7 2RD, UK.

⁴ Department of Pharmacy, Uppsala University, Uppsala, SE-751 23, Sweden

⁵ Institut de Biologie Intégrative et des Systèmes, Université Laval, Quebec G1V 0A6, Canada.

¹ School of Life Sciences, University of Nottingham Biodiscovery Institute, University of Nottingham, NG7 2RD, UK.

Corresponding Authors

Dr Fadi Soukarieh

fadi.soukarieh@nottingham.ac.uk

Professor Michael Stocks

michael.stocks@nottingham.ac.uk

Professor Miguel Cámara,

miguel.camara@nottingham.ac.uk

Table of Contents

Table S1	S4
Figures S1-S41	85
References	S37

Table S1. Bacterial strains and plasmids used in this study

Strain or plasmid	Relevant characteristics	Reference or	
		origin	
PAO1-L	Wound isolate, wild type PAO1, Lausanne subline.	B. Holloway,	
		<i>via</i> D. Haas	
PAO1-L mCTX::PpqsA-lux	PAO1-L with chromosomal mini-CTX::P _{pqsA} -lux insertion; Tc^R	1	
PAO1-N	Wound isolate, wild type PAO1, Nottingham subline	2	
PA14	Burn isolate, wild type UCBPP-PA14	3, 4	
PALESB58	CF isolate	5	
IPCD1451	CF isolate, >95% related to PAO1, IPCD ID 1451	6, 7	
IPCD1350	CF isolate, >95% related to PA14, IPCD ID 1350	6, 7	
IPCD1331	CF isolate, >95% related to PAK, IPCD ID 1331	6, 7	
IPCD48	CF isolate, >95% related to PA7, IPCD ID 48	6-8	
PA14 mCTX::P _{pqsA} -lux	PA14 with chromosomal mini-CTX::P _{pqsA} -lux insertion; Tc^{R}	1	
Plasmids			
mini-CTX::P _{pqsA} -lux	R6K-based mini-CTX suicide plasmid for the chromosomal	9	
	insertion of a P_{pqsA} -Iux transcriptional reporter fusion; Tc^R		
pMMG	pME6032 Δ <i>lacl</i> constitutively expressing GFP from the P _{tac}	10	
	promoter		



Figure S1: Schematic representation of the measurement between the *ortho*- position of the phenoxy ring of **6f** and the oxygen atom of the Tyrosine 258 (PqsR ligand binding domain).



Note: Sigma fits < 0.05 indicates high probability of correct MF

Figure S2. HRMS spectrum of 6b.



Note: Sigma fits < 0.05 indicates high probability of correct MF

Figure S3. HRMS spectrum of 6r.



Expected Formula C24 H27 CIT N4 O2				Adduct(s): H, Na, NH4, C3H5h			SHONZ, TAUICAI	
#	meas. m/z	theo. m/z	Err [ppm]	Sigma	Formula	Adduct	Adduct Mass	
1	439.1905	439.1895	2.10	0.0043	C24H28CIN4O2	M+H	1.0078	
1	461.1712	461.1715	0.60	0.0121	C24H27CIN4NaO2	M+Na	22.9898	

Note: Sigma fits < 0.05 indicates high probability of correct MF

Figure S4. HRMS spectrum of 6l.



Figure S5. HRMS spectrum of 6k.



Note: Sigma fits < 0.05 indicates high probability of correct MF

Figure S6. HRMS spectrum of 6c.

+MS, 0.7-0.9min #28-34



Generate Molecular Formula Parameters

No of Most Intense MS Peaks Analysed 5

Char	ge Tolerand	ce sigma_lii	mit Ca	alibration				
	+1 6 pp	m 0	.08	TRUE				
Form	ula Min C	1 H 0 N 0 O	0	Fo	rmula Max	C50 H100 N10 O10	H Na NH4 C3H5N2	
#	meas. m/z	theo. m/z	Err [ppm]	Sigma		Formula		
2	417.1518	417.1520	0.50	0.0038	C 19 H 20 N	7 Na 1 O 3		
		417.1533	3.70	0.0040	C 21 H 22 N	4 Na 1 O 4		
		417.1531	3.10	0.0040	C 20 H	23 N 3 O 7		
		417.1530	3.10	0.0042	C 19 H 1	7 N 10 O 2		
		417.1517	0.20	0.0061	C 17 H 1	5 N 13 O 1		
	Note: Sigma fits < 0.05 indicates high probability of correct MF							

Figure S7. HRMS spectrum of 6t.

Sample-ID	pazfs2_005	Lab	C13
Submitter	Fadi Soukarieh (pazfs2)	Supervisor	Mike Stocks (pazmjs)
Analysis Name	pazfs2_005_653078_7_01_133763.d	Acquisition Date	8/9/2023 10:43:23 AM
Ionisation Mode	ESI Positive	Instrument	Bruker MicroTOF

+MS, 0.7-0.9min #27-33



Figure S8. HRMS spectrum of 6h.

Sample-ID	pazfs2_006	Lab	C13
Submitter	Fadi Soukarieh (pazfs2)	Supervisor	Mike Stocks (pazmjs)
Analysis Name	pazfs2_006_653079_8_01_133764.d	Acquisition Date	8/9/2023 10:45:53 AM
Ionisation Mode	ESI Positive	Instrument	Bruker MicroTOF

+MS, 0.7-0.9min #28-34



Figure S9. HRMS spectrum of 6j.

Sample-ID	pazfs2_	007	Lab	C13
Submitter	Fadi So	ukarieh (pazfs2)	Supervisor	Mike Stocks (pazmjs)
Analysis Name	pazfs2_	007_653080_9_01_133765.d	Acquisition Date	8/9/2023 10:48:23 AM
Ionisation Mode	ESI	Positive	Instrument	Bruker MicroTOF

+MS, 0.7-0.9min #28-34



Figure S10. HRMS spectrum of 6g.

1

Sample-ID	pazfs2_	008	Lab	C13
Submitter	Fadi So	ukarieh (pazfs2)	Supervisor	Mike Stocks (pazmjs)
Analysis Name	pazfs2_	008_653081_10_01_133766.d	Acquisition Date	8/9/2023 10:50:52 AM
Ionisation Mode	ESI	Positive	Instrument	Bruker MicroTOF

+MS, 0.7-0.9min #28-34



Figure S11. HRMS spectrum of 6q.



Note: Sigma fits < 0.05 indicates high probability of correct MF

Figure S12. HRMS spectrum of 6v.



Note: Sigma fits < 0.05 indicates high probability of correct MF

Figure S13. HRMS spectrum of 60.



onu	+1	6 ppm	0.08	3-0	Licearo	both	langen i	false	Unit	false	TRUE
Expe	ected	Formula	C21 H2	3 CI1 F1 N4	02				Addu	ict(s): H, N	a, NH4, C3H5N2, radical
#	meas	s.m/z t	heo.m/z	Err [ppm]	Sigma	F	ormula	Add	uct	Adduct Mass	
1	417	7.1500	417.1488	2.90	0.0042	C21H23C	CIFN4O2		M+	-0.0005	

Note: Sigma fits < 0.05 indicates high probability of correct MF

Figure S14. HRMS spectrum of **6n**.



Note: Sigma fits < 0.05 indicates high probability of correct MF

Figure S15. HRMS spectrum of 6e.

Sample-ID	pazfs2_SEN086_Me	Lab	C13
Submitter	Fadi Soukarieh (pazfs2)	Supervisor	Mike Stocks (pazmjs)
Analysis Name	pazfs2_SEN086_Me_653090_16_01_1337	Acquisition Date	8/9/2023 12:31:19 PM
Ionisation Mode	ESI Positive	Instrument	Bruker MicroTOF

+MS, 0.7-0.9min #28-34



Note: Sigma fits < 0.05 indicates high probability of correct MF

Figure S16. HRMS spectrum of 6a.



Note: Sigma fits < 0.05 indicates high probability of correct MF

Figure S17. HRMS spectrum of 6f.

Sample-ID	pazfs2_	SEN089	Lab	C13
Submitter	Fadi So	ukarieh (pazfs2)	Supervisor	Mike Stocks (pazmjs)
Analysis Name	pazfs2_	SEN089_653091_17_01_133774.d	Acquisition Date	8/9/2023 12:33:49 PM
Ionisation Mode	ESI	Positive	Instrument	Bruker MicroTOF



Note: Sigma fits < 0.05 indicates high probability of correct MF

Figure S18. HRMS spectrum of 6w.







Figure S20. ¹³C-NMR spectrum of **6f**.







Figure S22. ¹³C-NMR spectrum of **6n**.







Figure S24. ¹³C-NMR spectrum of **6k.**







Figure S26. ¹³C-NMR spectrum of **6c**







Figure S28. ¹H-NMR spectrum of 6j



Figure S30. ¹H-NMR spectrum of **6v**.







Figure S32. ¹³C-NMR spectrum of **60**.









Figure S34. ¹³C-NMR spectrum of **6i**.

Figure S35. LCMS spectrum of 6q.





Figure S36. LCMS spectrum of 6k.



Figure S37. LCMS spectrum of 6c.



Figure S38. LCMS spectrum of 60.



Figure S39. LCMS spectrum of 6f.



Figure S40. LCMS spectrum of 6e.

Printing Time: 13:21:15 Printing Date: 24 August 2023



Figure S41. LCMS spectrum of 6a.

References

(1) Soukarieh, F.; Vico Oton, E.; Dubern, J. F.; Gomes, J.; Halliday, N.; de Pilar Crespo, M.; Ramirez-Prada, J.; Insuasty, B.; Abonia, R.; Quiroga, J.; et al. In Silico and in Vitro-Guided Identification of Inhibitors of Alkylquinolone-Dependent Quorum Sensing in *Pseudomonas aeruginosa*. *Molecules* **2018**, *23* (2). DOI: 10.3390/molecules23020257.

(2) Dubern, J.-F.; Romero, M.; Mai-Prochnow, A.; Messina, M.; Trampari, E.; Gijzel, H. N.-V.; Chan, K.-G.; Carabelli, A. M.; Barraud, N.; Lazenby, J.; et al. ToxR is a c-di-GMP binding protein that modulates surface-associated behaviour in *Pseudomonas aeruginosa. npj Biofilms and Microbiomes* **2022**, 8 (1). DOI: 10.1038/s41522-022-00325-9.

(3) Rahme, L. G.; Stevens, E. J.; Wolfort, S. F.; Shao, J.; Tompkins, R. G.; Ausubel, F. M. Common virulence factors for bacterial pathogenicity in plants and animals. *Science* **1995**, *268* (5219), 1899-1902. DOI: 10.1126/science.7604262.

(4) Lee, D. G.; Urbach, J. M.; Wu, G.; Liberati, N. T.; Feinbaum, R. L.; Miyata, S.; Diggins, L. T.; He, J.; Saucier, M.; Déziel, E.; et al. Genomic analysis reveals that *Pseudomonas aeruginosa* virulence is combinatorial. *Genome Biol* 2006, *7* (10), R90. DOI: 10.1186/gb-2006-7-10-r90.
(5) Winstanley, C.; Langille, M. G. I.; Fothergill, J. L.; Kukavica-Ibrulj, I.; Paradis-Bleau, C.; Sanschagrin, F.; Thomson, N. R.; Winsor, G. L.; Quail, M. A.; Lennard, N.; et al. Newly introduced genomic prophage islands are critical determinants of in vivo competitiveness in the Liverpool Epidemic Strain of *Pseudomonas aeruginosa. Genome Res* 2009, *19* (1), 12-23. DOI: 10.1101/gr.086082.108.

(6) Freschi, L.; Jeukens, J.; Kukavica-Ibrulj, I.; Boyle, B.; Dupont, M. J.; Laroche, J.; Larose, S.; Maaroufi, H.; Fothergill, J. L.; Moore, M.; et al. Clinical utilization of genomics data produced by the international *Pseudomonas aeruginosa* consortium. *Front Microbiol* **2015**, *6*, 1036. DOI: 10.3389/fmicb.2015.01036.

(7) Freschi, L.; Vincent, A. T.; Jeukens, J.; Emond-Rheault, J. G.; Kukavica-Ibrulj, I.; Dupont, M. J.; Charette, S. J.; Boyle, B.; Levesque, R. C. The *Pseudomonas aeruginosa* Pan-Genome Provides New Insights on Its Population Structure, Horizontal Gene Transfer, and Pathogenicity. *Genome Biol Evol* **2019**, *11* (1), 109-120. DOI: 10.1093/gbe/evy259.

(8) Roy, P. H.; Tetu, S. G.; Larouche, A.; Elbourne, L.; Tremblay, S.; Ren, Q.; Dodson, R.; Harkins, D.; Shay, R.; Watkins, K.; et al. Complete genome sequence of the multiresistant taxonomic outlier *Pseudomonas aeruginosa* PA7. *PLoS One* 2010, *5* (1), e8842. DOI: 10.1371/journal.pone.0008842.
(9) Diggle, S. P.; Matthijs, S.; Wright, V. J.; Fletcher, M. P.; Chhabra, S. R.; Lamont, I. L.; Kong, X.; Hider, R. C.; Cornelis, P.; Cámara, M.; et al. The *Pseudomonas aeruginosa* 4-quinolone signal molecules HHQ and PQS play multifunctional roles in quorum sensing and iron entrapment. *Chem Biol* 2007, *14* (1), 87-96. DOI: 10.1016/j.chembiol.2006.11.014.

(10) Popat, R.; Crusz, S. A.; Messina, M.; Williams, P.; West, S. A.; Diggle, S. P. Quorum-sensing and cheating in bacterial biofilms. *Proc Biol Sci* **2012**, *279* (1748), 4765-4771. DOI: 10.1098/rspb.2012.1976.