



Creation of a Structural Database for Inhibition of Biofilm Formation

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BIOFILMS [1,2,3]

Biofilms are a community of individual bacteria glued together and enclosed in a self-produced EPS matrix attached to a surface.

- Bacteria in biofilms show differences in gene expression, resulting in a higher resistance to antibiotics and the host immune defenses.
 - They are responsibly for ca. 80% of bacterial infections in the body, including lung infections in cystic fibrosis patients.

Biofilm infections of medical apparatus are virtually impossible to eliminate, especially when they involve multi-drug resistant bacteria.



QUORUM-SENSING^[1,3]

Quorum-sensing (QS) is the cell-to-cell communication in bacteria. It involves a synthase that produces a diffusible molecule (autoinducer) and a receptor that detects the signal, resulting in altered gene expression and community behavior, such as biofilm formation or motility.



SYNTHASE

RECEPTOR

THE DATABASE



Code	Protein	Category	Classification	Autoinducer Type	Organism	Туре	Ligand	Mutation Pathway	Method	(Å)	Year	DOI	PDB Links	
2010	LasR	Receptor	Transcription	Acyl-Homoserine-Lactones	Pseudomonas aeruginosa	•	OC12-HSL	Νο	X-Ray Diffraction	1.8	2007	<u>10.1074/jbc.M700556200</u>	ChEMBL BindingDB ExPASy KeGG UniProt	
<u>31X3</u>	LasR	Receptor	Transcription	Acyl-Homoserine-Lactones	Pseudomonas aeruginosa	•	OC12-HSL	No	X-Ray Diffraction	1.4	2009	Not available	ChEMBL BindingDB ExPASy <u>KeGG</u> UniProt	 Ĵ
<u>4NG2</u>	LasR	Receptor	Transcription	Acyl-Homoserine-Lactones	Pseudomonas aeruginosa	•	OC12-HSL	No	X-Ray Diffraction	2.41	2013	<u>10.1073/pnas.1314415110</u>	ChEMBL BindingDB ExPASy <u>KeGG</u> UniProt	
<u>31X4</u>	LasR	Receptor	Transcription	Acyl-Homoserine-Lactones	Pseudomonas aeruginosa	•	<u>TX1</u>	No	X-Ray Diffraction	1.8	2009	<u>10.1016/j.chembiol.2009.09.0</u>	01 ChEMBL BindingDB ExPASy KeGG UniProt	
<u>31X8</u>	LasR	Receptor	Transcription	Acyl-Homoserine-Lactones	Pseudomonas aeruginosa	•	<u>TX3</u>	No	X-Ray Diffraction	1.8	2009	<u>10.1016/j.chembiol.2009.09.0</u>	ChEMBL BindingDB ExPASy ▲ KeGG UniProt	

	Year: 2007	DOI: <u>10.1074/jbc.M700556200</u>
5000 ·	PDB: 🗹 🛓	External links: <u>ChEMBL</u> - <u>BindingDB</u> - ExPASy - <u>KeGG</u> - <u>UniProt</u>
	OC12-HSL	
I I		
	ID: OHN	Name: N-3-oxo-dodecanoyl-L-homoserine Lactone
	Molecular Weight: 297.39	SMILES: CCCCCCCCC(=O)CC(=O)N[C@H]1CCOC1=O
	Formula: C16 H27 N O4	ldentifier: 3-oxo-N-[(3S)-2-oxooxolan-3-yl]dodecanamide
	Formal Charge: 0	InChI: InChI=1S/C16H27NO4/c1-2-3-4-5-6-7-8-9-13(18)12-15(19)17-14-10-11-21- 16(14)20/h14H,2-12H2,1H3,(H,17,19)/t14-/m0/s1
	Atom Count: 48	InChIKey: PHSRRHGYXQCRPU-AWEZNQCLSA-N
n n n n n n n n n n n n n n n n n n n	PDB codes: 2UV0, 3IX3, 4NG2	Type: Non-polymer
	Chiral Atom Count: 0	Chiral Atoms: n/a
	Bond Count: 48	Aromatic Bond Count: 0
	Leaving Atoms: n/a	

This database was built on MySQL (v74) and PHP (v7.0). The web interface was designed using HTML and CSS. LigPlot^[4] was used to obtain the map of interactions of the ligands and NGL viewer^[5,6] as an interactive web molecule visualizer.

References: [1] Worthington, R.J. et al., Org Biomol Chem, **2012**. 10(37): p. 7457-74 [2] Kamaruzzaman, N.F. et al., Materials, **2018**. 11(9): p.11-27 [3] Lazdunski, A.M. et al., Nat Rev Microb, **2004**. 2(7): p.581-592 [4] Wallace, A.C. *et al.*, Protein Eng, **1996**. 8(2): p.127-134 [5] Rose, A.S. *et al.*, Web3D'16, **2016**. p. 185-186. [6] Rose, A.S. *et al.*, Nucl Acids Res, **2015**. 43(W1): p.576-579

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