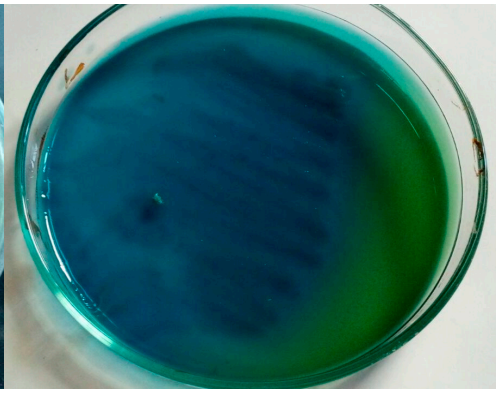
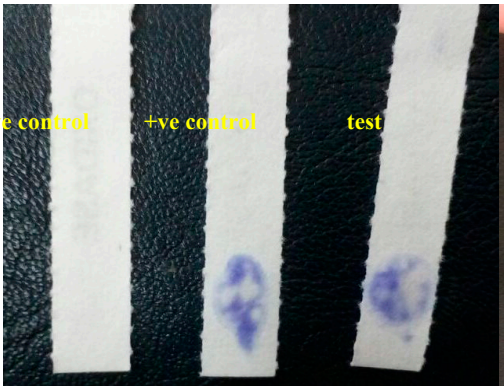
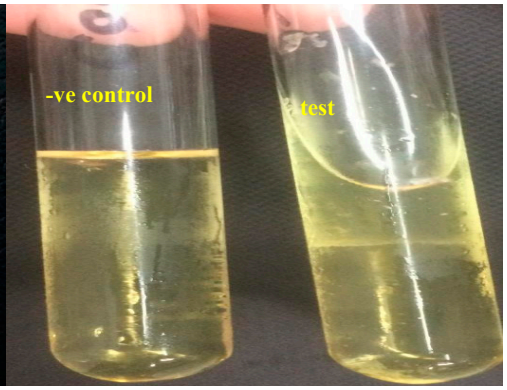
Pyocyanin pigment on cetrimide agar medium



Positive citrate test



Positive oxidase test



Positive gelatinase test

Triple sugar iron agar test tube (-ve)

Figure S1: Some morphological and biochemical characters of the isolated *P. aeruginosa*

Table S1. Physicochemical properties, water solubility and pharmacokinetic properties of *A. platensis* acetone extract by *Swiss ADME*.

Dominate compounds	**Linoleic acid ethyl ester**	**3,7,11,15-tetramethyl-2-hexadecen-1-ol**	***n*-hexadecanoic acid**	**11,14-eicosadienoic acid, methyl ester**	**Trans-13-octadecenoic acid**
Physicochemical Properties					
MW	312.44	256.42	338.61	366.53	296.49
#Heavy atoms	22	18	24	26	21
#H-bond acceptors	4	2	1	4	2
#H-bond donors	0	1	1	0	1
MlogP	3.55	4.19	5.91	4.36	4.8
MR	90.74	80.8	112.84	109.49	94.74
Solubility					
Esol log s	-3.69	-5.98	-5.02	-5.69	-5.41
Esol class	Soluble	Moderately soluble	Moderately soluble	Moderately soluble	Moderately soluble
Silicos-it logsw	-4.96	-5.51	-5.31	-6.17	-5.39
Silicos-it class	Moderately soluble	Moderately soluble	Moderately soluble	Poorly soluble	Moderately soluble
Pharmaco-kinetics					
Cyp1a2 inhibitor	No	No	Yes	Yes	Yes
Cyp2c19 inhibitor	No	No	No	No	No
Cyp2c9 inhibitor	No	Yes	Yes	Yes	Yes
Cyp2d6 inhibitor	No	No	No	No	No
Cyp3a4 inhibitor	Yes	No	No	No	No
Log kp (cm/s)	-4.85	-2.29	-2.77	-2.66	-2.6
Likeness drug					
Lipinski #violations	0	1	1	1	1
Bioavailability score	0.55	0.55	0.85	0.55	0.85
PAINS #alerts	0	0	0	0	0
Synthetic accessibility	3.11	4.3	2.31	3.41	3.07
Toxicity					
Hepatotoxicity	inactive	inactive	inactive	inactive	inactive
cytotoxicity	inactive	inactive	inactive	inactive	inactive

Table S2. Physicochemical properties, water solubility and pharmacokinetic properties of *P. scopulorum* methanol extract by *Swiss ADME*.

Dominate compounds	**Linolenic acid methyl ester**	**n-hexadecanoic acid methyl ester**	**3-bromo-4,5-dihydroxybenzaldehyde**	**Bis (3-bromo-4,5-dihydroxybenzyl) ether**	**3,4-dihydroxybenzaldehyde**
Physicochemical Properties					
MW	278.43	240.38	217.02	420.05	138.12
#Heavy atoms	20	17	11	21	10
#H-bond acceptors	0	0	3	5	3
#H-bond donors	1	0	2	4	2
MlogP	4.38	3.84	0.94	2.21	0.18
MR	88.99	75.03	43.58	85.28	35.88
Solubility					
Esol log s	-4.78	-3.86	-2.83	-4.51	-1.76
Esol class	Moderately soluble	Soluble	Soluble	Moderately soluble	Very soluble
Silicos-it logsw	-3.96	-4.49	-3.46	-4.77	-1.17
Silicos-it class	Soluble	Moderately soluble	Soluble	Moderately soluble	Soluble
Pharmaco-kinetics					
Cyp1a2 inhibitor	Yes	Yes	Yes	Yes	No
Cyp2c19 inhibitor	No	No	Yes	No	No
Cyp2c9 inhibitor	No	No	Yes	Yes	Yes
Cyp2d6 inhibitor	No	No	Yes	Yes	No
Cyp3a4 inhibitor	No	No	Yes	Yes	No
Log kp (cm/s)	-4.02	-6.3	-6.66	-6.71	-3.04
Likeness drug					
Lipinski #violations	1	0	0	0	0
Bioavailability score	0.85	0.55	0.55	0.55	0.55
PAINS #alerts	0	0	1	0	1
Synthetic accessibility	3.03	2.71	1.49	2.30	1
Toxicity					
Hepatotoxicity	inactive	inactive	Inactive	inactive	inactive
cytotoxicity	inactive	inactive	inactive	inactive	inactive

Table S3: Molecular docking data presents results from docking simulations of various phycocompounds from PME and AAE

Extract	phycocompounds	Est. Free Energy of Binding (kcal/mol)	Est. Inhibition Constant, Ki (mM)	vdW + Hbond + desolv Energy (kcal/mol)	Electrostatic Energy (kcal/mol)	Total Intermolec. Energy (kcal/mol)
PME	Linolenic acid methyl ester	-2.11	28.56	-5.02	+0.14	-4.88
	3-Bromo-4,5-dihydroxybenzaldehyde	-4.54	0.47	-3.65	-0.41	-4.06
	Bis (3-bromo-4,5-dihydroxybenzyl) ether	-4.59	0.43	-4.46	-0.35	-4.80
	3,4-dihydroxybenzaldehyde	-3.72	1.89	-3.91	-0.10	-4.01
	n-Hexadecanoic acid methyl ester	-1.31	110.00	-5.32	-0.03	-5.34
AAE	Linolenic acid ethyl ester	-1.59	68.60	-5.19	-0.07	-5.26
	11,14-Eicosadienoic acid, methyl ester	-2.50	14.71	-6.57	-0.05	-6.63
	trans-13-Octadecenoic acid	-2.59	12.55	-5.23	-0.93	-6.15
	3,7,11,15-Tetramethyl-2-hexadecen-1-ol	-2.75	9.66	-5.90	-0.04	-5.93
	n-Hexadecanoic acid	-1.96	36.36	-6.09	+0.38	-5.71

Table S4. Primer sequences used in this study.

Genes	Sequences
algD	F-CTACATCGAGACCGTCTGCC R-GCATCAACGAACCGAGCATC
pelF	F-GAGGTCAGCTACATCCGTCG R-TCATGCAATCTCCGTGGCTT
pslD	F- TGTACACCGTGCTCAACGAC R- CTTCCGGCCCGATCTTCATC
Reference gene *16S rRNA*	GCTGCCCTTTGTATTGTC AGATGTTGGGTTAAGTCCC