

Taxonomic description and complete genome of *Pseudomonas silvicola* sp. nov., a candidate biocontrol agent isolated from *Cunninghamia lanceolata*

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Supplementary materials

Table S1 Closest related species of *Pseudomonas* strain T1-3-2^T based on 16S rRNA from EzBioCloud database*

Name	Strain	Accession	Pairwise Similarity(%)	Completeness(%)
<i>P. silvicola</i>	T1-3-2^T	OM920535	-	-
<i>P. Vancouverensis</i>	ATCC 700688	AJ011507	99.21	100
<i>P. eucalypticola</i>	NP-1	MN238862	99.21	97.46922025
<i>P. moorei</i>	RW10	AM293566	99.20	100
<i>P. izuensis</i>	IzPS43_3003	MN865785	99.14	100
<i>P. koreensis</i>	Ps 9-14	AF468452	99.07	99.72583962
<i>P. kribbensis</i>	46-2	CP029608	98.85	100
<i>P. atacamensis</i>	M7D1	SSBS01000008	98.85	100
<i>P. glyciniae</i>	MS586	MG692779	98.85	100
<i>P. reinekei</i>	Mt-1	AM293565	98.78	100
<i>P. jessenii</i>	DSM 17150	NIWT01000013	98.64	100
<i>P. moraviensis</i>	CCM 7280	AY970952	98.64	100
<i>P. umsongensis</i>	DSM 16611	NIWU01000003	98.57	100
<i>P. mohnii</i>	DSM 18327	FNRV01000001	98.57	100
<i>P. granadensis</i>	LMG 27940	LT629778	98.57	100
<i>P. baetica</i>	a390	FM201274	98.42	99.10897875
<i>P. parafulva</i>	NBRC 16636	BBIU01000051	98.35	100
<i>P. neuropathica</i>	P155	LR797591	98.30	84.44139822
<i>P. laurylsulfativorans</i>	AP3_22	MF554631	98.28	100
<i>P. fulva</i>	NBRC 16637	BBIQ01000036	98.21	100
<i>P. batumici</i>	UCM B-321	JXDG01000105	98.21	100
<i>P. atagonensis</i>	PS14	MN396717	98.14	100
<i>P. mucoides</i>	P154a	LR797589	97.97	84.44139822
<i>P. graminis</i>	DSM 11363	Y11150	97.92	100
<i>P. rhizosphaerae</i>	DSM 16299	CP009533	97.92	100
<i>P. lutea</i>	DSM 17257	JRMB01000004	97.92	100
<i>P. baltica</i>	MBT-2	MW377590	97.92	100
<i>P. helmanticensis</i>	OHA11	HG940537	97.85	100
<i>P. massiliensis</i>	CB1	CCYK01000003	97.85	100
<i>P. coleopterorum</i>	Esc2Am	KM888184	97.85	99.04043866
<i>P. laurylsulfatiphila</i>	AP3_16	KY462012	97.78	100
<i>P. juntendi</i>	BML3	MK680061	97.78	100
<i>P. akapageensis</i>	PS24	MN382268	97.78	100
<i>P. defluvii</i>	WCHP16	KY979145	97.78	100
<i>P. kuykendallii</i>	NRRL B-59562	FNNU01000014	97.71	100

*Here are the species with valid names only in EzBioCloud database.

Table S2 Accession numbers of the sequences of the type strains of different *Pseudomonas* species used in the MLSA phylogenetic analysis.

Species	Type strain	16S	Gene and Accession number		
			<i>gyrB</i>	<i>rpoB</i>	<i>rpoD</i>
<i>P. silvicola</i>	T1-3-2 ^T	OM920535	ON243870	ON364553	ON364554
<i>P. eucalypticola</i>	NP-1 ^T	MN238862	MN233594	MN233595	MN233596
<i>P. coleopterorum</i>	Esc2Am ^T	KM888184	FNTZ010000 011:4674081- 4676604	KM888186	KM888187
<i>P. graminis</i>	DSM 11363 ^T	Y11150	FN554187	AJ717429	FN554469
<i>P. kuykendallii</i>	NRRL B-59562 ^T	JF749828	LT615253	FNNU01000 011:5421-955 5	LMG 26364
<i>P. lutea</i>	LMG 21974 ^T	AY364537	FN554198	FN554738	FN554480
<i>P. mohnii</i>	DSM 18327 ^T	AM293567	AM293561	FN554741	FN554487
<i>P. moorei</i>	DSM 12647 ^T	AM293566	TAM293560	FN554742	FN554489
<i>P. rhizosphaerae</i>	DSM 16299 ^T	CP009533	FN554224	FN554755	FN554510
<i>P. umsongensis</i>	LMG 21317 ^T	NR025227	FN554231	FN554763	FN554516
<i>P. vancouverensis</i>	ATCC 00688 ^T	AJ011507	FN554232	NZ_LT62980 3:6114764-61 15679	FN554517
<i>Cellvibrio japonicus</i>	Ueda107 ^T	NC010995:80 7088-808555	NC010995:3 980-6400	NC010995:8 21813-82589 8	NC010995:8 95987-89672 6
<i>P. fluorescens</i>	ATCC 13525 ^T	D84013	D86016	AJ717451	AB039545
<i>P. gessardii</i>	LMG 21604 ^T	AF074384	FN554186	AJ717438	FN554468
<i>P. meridiana</i>	CIP 108465 ^T	AJ537602	FN554203	FN554740	FN554485
<i>P. fragi</i>	CECT 446 ^T	AF094733	FN554184	AJ717444	FN554466
<i>P. mandelii</i>	LMG 21607 ^T	AF058286	FN554200	AJ717435	FN554482
<i>P. deceptionensis</i>	CECT 7677 ^T	GU936597	HE800476	HE800510	GU936596
<i>P. arsenicoxydans</i>	CECT 7543 ^T	FN645213	FN645139	HE800503	FN645160/H E800488
<i>P. koreensis</i>	LMG 21318 ^T	AF468452	FN554194	FN554737	FN554476
<i>P. corrugata</i>	ATCC 29736 ^T	D84012	AB039460	AJ717487	AB039566
<i>P. mediterranea</i>	CFBP 5447 ^T	AF386080	AM084678	AJ717449	AM084337
<i>P. chlororaphis</i>	DSM 6698 ^T	AY509898	FN554172	AJ717426	FN554453
subsp. <i>aureofaciens</i>					
<i>P. asplenii</i>	LMG 2137 ^T	AB021397	AB039455	AJ717432	AB039593
<i>P. fuscovaginae</i>	LMG 2158 ^T	FJ483519	FN554185	AJ717433	FN554467
<i>P. syringae</i>	NCPPB 281 ^T	DQ318866	AB039428	FN554759	AB039516
<i>P. abietaniphila</i>	ATCC 700689 ^T	AJ011504	FN554166	AJ717416	FN554447
<i>P. monteilii</i>	ATCC 700476 ^T	AF064458	FN554205	AJ717455	FN554488
<i>P. putida</i>	ATCC 12633 ^T	D84020	AB039451	AJ717474	AB039581
<i>P. soli</i>	LMG 27941 ^T	HF930598	LN851840	HF930596	HF930597
<i>P. taiwanensis</i>	DSM 21245 ^T	EU103629	FJ418634/HE 800487	HE577797	HE577796
<i>P. straminea</i>	LMG 21615 ^T	D84023	AB039410	FN554758	AB039600
<i>P. flavescens</i>	LMG 18387 ^T	U01916	FN554183	AJ717468	FN554465
<i>P. benzenivorans</i>	DSM 8628 ^T	FM208263	HE800472	HE800506	HE800490
<i>P. anguilliseptica</i>	LMG 21629 ^T	X99540	FN554168	AJ717417	FN554449
<i>P. peli</i>	LMG 23201 ^T	AM114534	FN554217	FN554750	FN554501

P. guineae M8^T AM491810 FN554189 FN554734 FN554471

Table S3 Type strains and their genome sources in the phylogenomic tree

Species	Deposit	GenBank assembly accession	Percent G+C	No. proteins
<i>Pseudomonas silvicola</i>	T1-3-2 ^T	CP093280	61.65	8117
<i>Pseudomonas reidholzensis</i>	CCOS 865	GCA_900536025	64.09	5441
<i>Pseudomonas ovata</i>	F51 ^I	GCA_003131185	61.94	5749
<i>Pseudomonas chlororaphis</i> <i>subsp. aurantiaca</i>	DSM 19603	GCF_003851835	62.86	6297
<i>Pseudomonas nabeulensis</i>	E10BT	GCA_004682045	60.29	6049
<i>Pseudomonas reinekei</i>	MT1	GCA_001945365	59.17	5603
<i>Pseudomonas eucalypticola</i>	NP-1 T	GCA_013374995	63.12	5596
<i>Pseudomonas kribbensis</i>	KCTC 32541T	GCF_003352185	60.55	5661
<i>Pseudomonas moorei</i>	DSM 12647	GCF_900102045	59.66	5989
<i>Pseudomonas tractae</i>	SNU WT1	GCA_004214895	61.83	5033
<i>Pseudomonas monteilii</i>	DSM 14164	GCA_000621245	61.49	5953
<i>Pseudomonas moraviensis</i>	LMG 24280	GCF_900105805	60.17	5351
<i>Pseudomonas koreensis</i>	LMG 21318	GCF_900101415	60.53	5467
<i>Pseudomonas koreensis</i>	JCM 14769	GCA_014646955	60.58	5520
<i>Pseudomonas rhizosphaerae</i>	DSM 16299	GCA_000761155	61.99	3893
<i>Pseudomonas glycinae</i>	MS586	GCA_001594225	60.48	5674
<i>Pseudomonas coleopterorum</i>	LMG 28558	GCA_900105555	62.03	4341
<i>Pseudomonas orientalis</i>	DSM 17489	GCF_001439815	60.51	5471
<i>Pseudomonas</i> <i>vancouverensis</i>	LMG 20222	GCF_900105825	60.11	5822
<i>Pseudomonas izuensis</i>	IzPS43_3003	GCA_009861505	59.62	6149

Table S4 Functional categories bases on eggNOG of the protein-coding genes of the *Pseudomonas silvicola* sp. nov.

Code	Description	CDS(%)
A	Translation, ribosomal structure and biogenesis	197 (2.80)
B	Transcription	604 (8.58)
C	Replication, recombination and repair	242(3.44)
D	Cell cycle control, cell division, chromosome partitioning	41(0.58)
E	Posttranslational modification, protein turnover, chaperones	192(2.73)
F	Cell wall/membrane/envelope biogenesis	378(5.37)
G	Cell motility	139(1.97)
H	Inorganic ion transport and metabolism	507(7.20)
I	Signal transduction mechanisms	343(4.87)
J	Energy production and conversion	440(6.25)
K	Carbohydrate transport and metabolism	474 (6.73)
L	Amino acid transport and metabolism	660 (9.37)
M	Nucleotide transport and metabolism	109 (1.55)
N	Coenzyme transport and metabolism	171 (2.43)
O	Lipid transport and metabolism	290 (4.12)
P	Secondary metabolites biosynthesis, transport and catabolism	175 (2.49)
Q	General function prediction only	631 (8.96)
S	Intracellular trafficking,secretion,and vesicular transport	128 (1.82)
T	RNA processing and modification	1 (0.01)
U	Chromatin structure and dynamics	1 (0.01)
V	Defense mechanisms	81 (1.15)
Z	Function unknown	1237 (17.57)

Table S5Genes related to carbohydrate-active enzymes (CAZymes) in *Pseudomonas silvicola* sp. nov.

Family of enzymes	AA	CBM	CE	GH	GT	PL
Number of genes	36	12	46	69	68	4
Percentage (%)	15.32%	5.11%	19.57%	29.36%	28.94%	1.70%

CBM. Carbohydrate-Binding Module; GH. Glycoside Hydrolase; GT. Glycosyl Transferase; PL. Polysaccharide lyases; AA. Auxiliary Activity; CE. Carbohydrate Esterase.

Table S6CAZymes involved in plant and fungal cell wall degradation identified in *Pseudomonas silvicola* sp. nov. genome

Substrate	Family enzymes	Annotation	Copy number
Endo- β -1,4-glucanase	GH5	endo- β -1,4-glucanase / cellulase (EC 3.2.1.4)	1
6-phospho- β -glucosidase	GH1/GH4	(6-phospho- β -glucosidase EC 3.2.1.86)	3
α -glucosidase	GH13/GH31/GH4	α -glucosidase (EC 3.2.1.20)	11
Endoglucanases	GH74	endoglucanase (EC 3.2.1.4)	1
Beta-1-3-glucan	GH1	endo-1.3- β -glucosidase (EC 3.2.1.39)	1
oligoxylolucan	GH74	oligoxylolucan reducing end-specific cellobiohydrolase (EC 3.2.1.150)	3
Cellulose	GH5	endo- β -1,4-glucanase / cellulase (EC 3.2.1.4)	1
Pectin	GH28	polygalacturonase (EC 3.2.1.15)	1
Polysaccharides	GH13	α -amylase (EC 3.2.1.1)	9
Polysaccharides	GH15	glucoamylase (EC 3.2.1.3)	2

Table S7Secondary metabolite gene clusters identified in the *Pseudomonas silvicola* sp. nov. using antiSMASH v. 5.0.0.

Cluster	Type	From	To	Size	Most similar known cluster	Similarity
r1c1	arylpoliene	432895	476490	43596	APE Vf	40%
r1c2	NRPS-like	1115614	1156761	41148	Mangotoxin	71%
r1c3	NRPS-like	1749641	1794415	44775		
r1c4	NAGGN	2661155	2675928	14774		
r1c5	NRPS	3771272	3813511	42240		
r1c6	hserlactone, NRPS	4587333	4646179	58847		
r1c7	LAP	4668739	4690735	21997		
r1c8	NRPS	5338387	5403272	64886	Orfamide	35%
r1c9	NRPS	5780918	5857722	76805	Pyoverdine	16%
r1c10	CDPS	6185239	6205976	20738		
r1c11	amglyccycl	6447315	6470458	23144	Acarbose	7%
r1c12	NRPS	6518068	6581825	63758	Enterobactin	16%
r1c13	lassopeptide	7152758	7177090	24333		
r2c1	NRPS	9846	57082	47237	Vanchrobactin	20%
r2c2	acyl_amino_acids	646308	706661	60354	Kanamycin	1%

Table S8 Genes attributed to biocontrol, plant growth promotion and colonization traits identified in *Pseudomonas* sp. T1-3-2^T strain genome.

Gene	#gene_ID	VFDB_gene_function/TrEMBL_annotation	Activity
<i>hcnC</i>	GE000002	hydrogen cyanide synthase HcnC	Production volatile organic compounds
<i>hcnB</i>	GE000004	hydrogen cyanide synthase HcnB	
<i>hcnC</i>	GE001730	FAD dependent oxidoreductase	
<i>hcnA</i>	GE003656	Ferredoxin	
<i>hcnB</i>	GE003657	hydrogene cyanide synthase HcnB	
<i>hcnC</i>	GE003658	hydrogen cyanide synthase HcnC	
<i>hcnC</i>	GE003705	FAD dependent oxidoreductase	
<i>hcnC</i>	GE003895	FAD dependent oxidoreductase	
<i>hcnC</i>	GE005055	hydrogen cyanide synthase HcnC	
<i>hcnC</i>	GE007597	hydrogen cyanide synthase HcnC	
<i>hcnC</i>	GE007739	hydrogen cyanide synthase HcnC	
<i>pdhB</i>	GE004635	AcoB	
<i>ilvC</i>	GE004386	hypothetical protein	
-	GE000032	Acetolactate synthase isozyme 3 small subunit	
-	GE000950	Acetolactate synthase isozyme 2 large subunit	
-	GE003312	Acetolactate synthase large subunit	
-	GE004667	Acetolactate synthase	
<i>bdh</i>	GE003968	meso-butanediol dehydrogenase / (S,S)-butanediol dehydrogenase / diacetyl reductase	Plant growth promotion
-	GE007338	meso-butanediol dehydrogenase / (S,S)-butanediol dehydrogenase / diacetyl reductase	
<i>trpE1</i>	GE001442	Anthranilate synthase component I	
<i>trpE2</i>	GE001443	Anthranilate synthase component I	
<i>trpG</i>	GE001444	Anthranilate synthase component II	
<i>trpD</i>	GE001445	anthranilate phosphoribosyltransferase	
<i>trpC</i>	GE001446	indole-3-glycerol phosphate synthase [EC:4.1.1.48]	
<i>trpA</i>	GE000792	tryptophan synthase alpha chain [EC:4.2.1.20]	
<i>trpB</i>	GE000791	tryptophan synthase beta chain [EC:4.2.1.20]	
<i>phzS</i>	GE003873	flavin dependent hydroxylase PhzS	
<i>phzS</i>	GE004361	flavin dependent hydroxylase PhzS	
<i>phzS</i>	GE004399	flavin dependent hydroxylase PhzS	
<i>phzS</i>	GE004789	flavin dependent hydroxylase PhzS	
<i>phzS</i>	GE005146	flavin dependent hydroxylase PhzS	
<i>phzH</i>	GE002430	phenazine-modifying enzyme	Antibiotics and secondary metbolites
<i>phzH</i>	GE006388	phenazine-modifying enzyme	
<i>phzH</i>	GE006395	phenazine-modifying enzyme	
<i>phzH</i>	GE006800	phenazine-modifying enzyme	
<i>phzG1</i>	GE006337	phenazine biosynthesis protein PhzG, pyridoxamine 5'-phosphate oxidase	
<i>phzF1</i>	GE005721	phenazine biosynthesis protein PhzF, isomerase	
<i>phzE1</i>	GE001444	phenazine biosynthesis protein PhzE	
<i>phzD1</i>	GE003827	phenazine biosynthesis protein PhzD,	

<i>phzD1</i>	GE004775	isochorismatase phenazine biosynthesis protein PhzD, isochorismatase	
<i>phzC1</i>	GE002549	phenazine biosynthesis protein PhzC	
<i>phzR</i>	GE001609	Transcriptional activator protein PhzR	
<i>ubiA</i>	GE000985	4-hydroxybenzoate polyprenyltransferase [EC:2.5.1.39]	
<i>pys2</i>	GE006724	pyocin	
-	GE002318	pyocin R2	
<i>prtN</i>	GE003123	Pyocin activator protein	
<i>entD</i>	GE002181	Enterobactin synthetase, component D:Phosphopantethiene-protein transferase domain	
<i>iucB</i>	GE005177	N-acetyltransferase IucB	
<i>bfrD</i>	GE001765	Probable TonB-dependent receptor BfrD	Siderophore biosynthesis
	GE002255	Probable TonB-dependent receptor BfrD	
	GE006409	Probable TonB-dependent receptor BfrD	
<i>bfd</i>	GE002210	Bacterioferritin-associated ferredoxin	
<i>bfd-like</i>	GE003894	Sarcosine oxidase subunit alpha	
<i>fiu</i>	#N/A	#N/A	
<i>exbB</i>	GE000648	biopolymer transport protein	Siderophore uptake
<i>exbD</i>	GE000647	biopolymer transport protein	
<i>tonB</i>	GE003685	TonB protein	
<i>pvdA</i>	GE005179	L-ornithine N5-oxygenase PvdA	
<i>pvdE</i>	GE005180	cyclic peptide transporter	
<i>pvdH</i>	GE003662	diaminobutyrate--2-oxoglutarate aminotransferase	
<i>pvdL</i>	GE005189	peptide synthase	
<i>pvdG</i>	GE005186	putative thioesterase	
<i>pvdS</i>	GE005167	ferric regulator PfrI	Pyoverdin biosynthesis
<i>pvdJ</i>	GE003031	thermophilic carboxylesterase Est2	
<i>pvdO</i>	GE004492	protein of unknown function DUF323	
<i>pvdN</i>	GE002272	aminotransferase, class V	
<i>pvdM</i>	GE001313	renal dipeptidase family protein	
<i>pvdP</i>	GE005173	twin-arginine translocation pathway signal	
<i>pvdI</i>	GE000363	peptide synthase	
<i>pvdQ</i>	GE001107	peptidase S45, penicillin amidase	
<i>menF</i>	GE004959	Isochorismate synthase EntC	Salicylic acid production
<i>pchB</i>	GE007843	isochorismate pyruvate lyase	
<i>afuA</i>	GE000558	iron(III) transport system substrate-binding protein	Iron transport, receptors and related protein
-	GE001183	iron(III) transport system substrate-binding protein	
-	GE007513	iron(III) transport system substrate-binding protein	

-	GE007990	iron(III) transport system substrate-binding protein
<i>FbpB</i>	GE007987	iron(III) transport system permease protein
-	GE007988	iron(III) transport system permease protein
<i>CysA 2</i>	GE001181	Sulfate/thiosulfate import ATP-binding protein
<i>FbpC</i>	GE006219	Fe(3+) ions import ATP-binding protein FbpC
<i>FbpC1</i>	GE007507	Fe(3+) ions import ATP-binding protein FbpC
<i>FbpC2</i>	GE007986	Fe(3+) ions import ATP-binding protein FbpC
<i>pqqF</i>	GE001377	PqqA binding protein
<i>pqqE</i>	GE001373	PqqA peptide cyclase
<i>pqqD1</i>	GE001374	pyrroloquinoline quinone biosynthesis protein D
<i>pqqD2</i>	GE006401	pyrroloquinoline quinone biosynthesis protein D
<i>pqqC</i>	GE001375	pyrroloquinoline-quinone synthase
<i>pqqB</i>	GE001376	pyrroloquinoline quinone biosynthesis protein B
<i>pqqA</i>	#N/A	pyrroloquinoline quinone biosynthesis protein A
<i>phnA</i>	GE001704	protein PhnA
-	GE002436	Polyphosphate:AMP phosphotransferase
-	GE006535	Polyphosphate:ADP phosphotransferase
-	GE007292	Polyphosphate:ADP phosphotransferase
<i>phoU</i>	GE000976	phosphate transport system protein
<i>PstB1</i>	GE000975	phosphate transport system ATP-binding protein
<i>PstB2</i>	GE005595	phosphate transport system ATP-binding protein
<i>pstA1</i>	GE000974	phosphate transport system permease protein
<i>pstA2</i>	GE005596	phosphate transport system permease protein
<i>pstC1</i>	GE000973	phosphate transport system permease protein
<i>pstC2</i>	GE005597	phosphate transport system permease protein
<i>pstS1</i>	GE000972	phosphate transport system substrate-binding protein
<i>pstS2</i>	GE005598	phosphate transport system substrate-binding protein
<i>pstS3</i>	GE005615	phosphate transport system substrate-binding protein
<i>phoQ1</i>	GE002184	two-component system.OmpR family. sensor kinase protein
<i>phoQ2</i>	GE004994	Virulence sensor histidine kinase PhoQ
<i>phoP</i>	GE002183	transcriptional regulatory protein PhoP, regulator of virulence determinants
-	GE005723	low-affinity inorganic phosphate transporter 1
-	GE007293	low-affinity inorganic phosphate transporter 1
-	GE007294	low-affinity inorganic phosphate transporter 1
<i>pqqL</i>	GE000540	Probable alpha-L-glutamate ligase
-	GE000781	--
-	GE001207	Uncharacterized zinc protease-like protein y4wB

Phosphate solubilization

-	GE005820	Probable alpha-L-glutamate ligase	
<i>gcd</i>	GE007549	Quinoprotein glucose dehydrogenase	
-	GE002074	Quinoprotein glucose dehydrogenase A	
-	GE003161	Quinoprotein glucose dehydrogenase A	
-	GE004272	Quinoprotein glucose dehydrogenase A	
-	GE007550	Glycerol dehydrogenase large subunit	
-	GE003340	Glycerol dehydrogenase large subunit	
<i>acdS</i>	GE001066	D-cysteine desulphydrase	ACC deaminase activity
	GE006028	1-aminocyclopropane-1-carboxylate deaminase	
<i>oxdD</i>	GE007831	aldoxime dehydratase	
<i>oxdD</i>	GE007832	aldoxime dehydratase	IAA production
-		oxidoreductase	
<i>fixI</i>	GE002644	Nitrogen fixation protein	Nitrogen fixation
<i>iscU</i>	GE006507	Iron-sulfur cluster assembly scaffold protein	
-	GE000456	glutamine synthetase	
<i>bglX</i>	GE001991	beta-glucosidase	Lytic enzymes production
-	GE005081	Beta-N-acetylglucosaminidase/beta-glucosidase	
<i>BglB1</i>	GE007372	6-phospho-beta-glucosidase BglB	
<i>BglB2</i>	GE007373	6-phospho-beta-glucosidase	
<i>AscB1</i>	GE007755	6-phospho-beta-glucosidase AscB	
<i>AscB2</i>	GE007756	6-phospho-beta-glucosidase AscB	
<i>AscB3</i>	GE007757	6-phospho-beta-glucosidase AscB	
-	GE000998	endoglucanase	
-	GE005135	endoglucanase	
<i>nagAl</i>	#N/A	#N/A	
<i>pvdQ</i>	GE001107	peptidase S45, penicillin amidase	Quorum quenching
<i>manD</i>	GE004872	mannitol 2-dehydrogenase	Mannitol dehydrogenase
<i>rhIB</i>	GE006625	ATP-dependent RNA helicase RhIB	Rhamnolipid production
<i>rhIE</i>	GE001258	ATP-dependent RNA helicase RhIE	
<i>rhIE</i>	GE001624	ATP-dependent RNA helicase RhIE	
<i>rhIA</i>	GE002026	rhamnosyltransferase chain A	
<i>algA</i>	GE006643	mannose-1-phosphate guanylyltransferase/mannose-6-phosphate isomerase	Exopolisacharydes biosynthesis <i>Alginate</i>
<i>algF</i>	GE006642	alginate biosynthesis protein AlgF	
<i>algJ</i>	GE005140	alginate o-acetyltransferase AlgJ	
<i>algI</i>	GE005139	membrane bound O-acyl transferase, MBOAT family protein	
<i>algL</i>	GE006639	poly(beta-D-mannuronate) lyase	
<i>algX</i>	GE006638	alginate biosynthesis protein AlgX	

<i>algG</i>	GE006637	Carbohydrate binding and sugar hydrolysis	
<i>algE</i>	GE006636	alginate biosynthesis protein AlgE	
<i>alg44</i>	GE006634	alginate biosynthesis protein Alg44	
<i>alg8</i>	GE006633	glycosyl transferase Alg8	
<i>algD</i>	GE006632	GDP-mannose 6-dehydrogenase AlgD	
<i>algI</i>	GE005139	membrane bound O-acyl transferase, MBOAT family protein	
<i>lpxL</i>	GE000811	lipid A biosynthesis lauroyl acyltransferase	
<i>lpxO</i>	GE004250	beta-hydroxylase	
<i>lpxC</i>	GE001884	UDP-3-O-acyl N-acetylglucosamine deacetylase	
<i>lpxB</i>	GE002296	lipid-A-disaccharide synthase	Lypopolysaccharides
<i>lpxA</i>	GE002295	lpxA	
<i>lpxD</i>	GE002293	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase	
<i>lpxH</i>	GE002671	UDP-2,3 diacylglucosamine hydrolase	
<i>flhG</i>	GE006257	ATPase, ParA family	Cell Motility
<i>flhF</i>	GE001169	flagellar biosynthesis protein	Flagellar assembly
<i>flhA</i>	GE001168	flagellar biosynthesis protein	
<i>flhB</i>	GE001167	flagellar biosynthetic protein FlhB	
<i>fliR</i>	GE001146	flagellar biosynthetic protein FliR	
<i>fliQ</i>	GE001147	flagellar biosynthetic protein FliQ	
<i>fliP</i>	GE001148	flagellar biosynthesis protein	
<i>MopB</i>	GE001149	flagellar protein FliO/FliZ	
<i>FliO</i>	GE006080	flagellar protein FliO/FliZ	
<i>fliNY</i>	GE001150	lagellar motor switch protein FliN/FliY	
<i>fliNY</i>	GE006081	lagellar motor switch protein FliN/FliY	
<i>fliM</i>	GE001151	flagellar motor switch protein FliM	
<i>fliL</i>	GE000568	flagellar basal body protein FliL	
<i>fliK</i>	GE001153	flagellar hook-length control protein	
<i>fliJ</i>	GE001154	flagellar protein FliJ	
<i>fliI</i>	GE001155	flagellum-specific ATP synthase	
<i>fliH</i>	GE001156	flagellar assembly protein	
<i>fliG</i>	GE001157	flagellar motor switch protein G	
<i>fliF</i>	GE001158	flagellar MS-ring protein	
<i>fliE</i>	GE001159	flagellar hook-basal body complex protein FliE	
<i>fliS</i>	GE001161	flagellar protein FliS	
<i>fliD</i>	GE001160	flagellar capping protein	
<i>fliC</i>	GE006101	flagellin FliC	

<i>flrC</i>	GE001350	FlaM
<i>fleQ</i>	GE006096	Sigma-54 Specific Transcriptional Regulator, Fis family
<i>fleL</i>	GE001145	flagellar hook-associated protein 3 FlgL
-	GE006122	flagellar hook-associated protein 3 FlgL
<i>flgK</i>	GE001144	flagellar hook-associated protein FlgK
<i>flgJ</i>	GE001143	flagellar rod assembly protein/muramidase FlgJ
<i>flgI</i>	GE001142	flagellar basal body P-ring protein
<i>flgH</i>	GE001141	flagellar basal body L-ring protein
<i>flgG</i>	GE001140	flagellar basal-body rod protein FlgG
<i>flgF</i>	GE001139	flagellar basal body rod protein FlgF
<i>motB</i>	GE000286	OmpA/MotB domain protein
<i>motA</i>	GE000287	chemotaxis MotA protein

<i>pilA/Flp</i>	GE000177	<i>pilus assembly protein Flp/PilA</i>
<i>pilJ</i>	GE000380	pilus biogenesis protein
<i>pilQ</i>	GE000390	type II and III secretion system protein:NolW-like:NolW-like
<i>pilP</i>	GE000391	type IV pilus assembly protein PilP
<i>pilO</i>	GE000392	type IV pilus biogenesis protein PilO
<i>pilN</i>	GE000393	type IV pilus inner membrane platform protein PilN
<i>pilM</i>	GE000394	type IV pilus biogenesis protein PilM
<i>pilT</i>	GE001227	twitching motility protein
<i>pilG</i>	GE001238	type IV pilus response regulator PilG
<i>pilH</i>	GE001239	type IV pilus response regulator PilH
<i>pilI</i>	GE001240	type IV pilus biogenesis protein PilI
<i>pilV</i>	GE001725	hypothetical protein
<i>pilW</i>	GE001726	type IV pilus assembly protein PilW
<i>pilX</i>	GE001727	type IV pilus assembly protein PilX
<i>PilY1</i>	GE001728	type IV pilus assembly protein PilY1
<i>pilE</i>	GE001729	type IV pilus biogenesis protein
<i>pilD</i>	GE001747	type IV pilus prepilin peptidase PilD
<i>pilC</i>	GE001748	type IV pilus biogenesis protein PilC
<i>pilB</i>	GE001749	ype IV pilus biogenesis protein PilB
<i>PilZ</i>	GE002594	type IV pilus assembly protein PilZ
<i>pilL</i>	GE003179	pilus biogenesis protein
<i>pilF</i>	GE006499	type IV pilus biogenesis protein PilF
<i>fimA</i>	GE004881	major type I subunit fimbrin (pilin)

Pilus assembly

<i>cheY</i>	GE000672	chemotaxis protein CheY
<i>cheV</i>	GE003084	chemotaxis protein

Chemotaxis

<i>cheB</i>	GE004858	chemotaxis-specific methylesterase	
<i>cheR</i>	GE004859	chemotaxis protein methyltransferase CheR	
<i>cheW</i>	GE006062	purine-binding chemotaxis protein	
<i>cheA</i>	GE006068	two-component sensor	
<i>cheZ</i>	GE006069	chemotaxis protein CheZ	
<i>cheR</i>	GE006133	chemotaxis protein methyltransferase CheR	
<i>wspF</i>	GE006371	two-component system, chemotaxis family, response regulator	
<i>wspE</i>	GE006372	two-component system, chemotaxis family, sensor histidine kinase and response regulator	
<i>wspD</i>	GE006373	chemotaxis-related protein	
<i>wspC</i>	GE006374	chemotaxis protein methyltransferase	
<i>wspB</i>	GE006375	chemotaxis-related protein	
<i>wspA</i>	GE006376	methyl-accepting chemotaxis protein	
<i>aer</i>	GE002652	aerotaxis receptor	
<i>aer</i>	GE006272	aerotaxis receptor	
<i>oxyR</i>	GE002526	LysR_substrate	
<i>sod2</i>	GE001820	superoxide dismutase. Fe-Mn family	
<i>grxC</i>	GE000465	glutaredoxin 3	
<i>ggt</i>	GE003902	gamma-glutamyltranspeptidase	
<i>ggt</i>	GE001198	gamma-glutamyltranspeptidase	
<i>ggt</i>	GE000009	gamma-glutamyltranspeptidase	
<i>mlrA</i>	GE000149	MerR family transcriptional regulator	
<i>pfpI</i>	GE000753	Catalase;Catalase-rel;Catalase_C	
-	GE001504	Catalase;Catalase-rel	
-	GE002404	Catalase	Oxidative/Stress response
-	GE004237	peroxidase	
-	GE004243	Catalase;Catalase-rel	
-	GE005438	Catalase	
<i>cotJC</i>	GE005550	Mn_catalase	
<i>gpx</i>	GE002234	Glutathione peroxidase	
<i>bsaA</i>	GE002557	Glutathione peroxidase homolog	
<i>btuE</i>	GE005624	Thioredoxin/glutathione peroxidase	
<i>btuE</i>	GE006695	Thioredoxin/glutathione peroxidase	
-	GE006953	Glutathione peroxidase	
<i>gsr</i>	GE004882	glutathione reductase (NADPH)	
<i>gshB</i>	GE001237	Glutathione synthetase	

