



## Supplemental Data

# ***Streptomyces lydicamycinicus* sp. nov. and its secondary metabolite biosynthetic gene clusters for polyketide and nonribosomal peptide compounds**

Hisayuki Komaki <sup>1,\*</sup>, Akira Hosoyama <sup>1</sup>, Yasuhiro Igarashi <sup>2</sup> and Tomohiko Tamura <sup>1</sup>

<sup>1</sup> Biological Resource Center, National Institute of Technology and Evaluation (NBRC); komaki-hisayuki@nite.go.jp, hosoyama-akira@nite.go.jp, tamura-tomohiko@nite.go.jp

<sup>2</sup> Biotechnology Research Center and Department of Biotechnology, Toyama Prefectural University; yas@pu-toyama.ac.jp

\* Correspondence: komaki-hisayuki@nite.go.jp; Tel.: +81-438-20-5764

**Table S1.** Closest homolog of PKSs and NRPSs in the gene clusters of *Streptomyces* sp. TP-A0598 . . . . . page 2

**Table S2.** Closest homolog of PKSs and NRPSs in the gene clusters of *Streptomyces angustmyceticus* NBRC 3934<sup>T</sup> . . . . . page 3

**Table S1.** Closest homolog of PKSs and NRPSs in the gene clusters of *Streptomyces* sp. TP-A0598.

Gene cluster	Locus tag (TPA0598)	I/S* (%)	Description and accession number of the closest homolog (homolog whose metabolite is experimentally identified)
<i>t1pks-1</i>	_10_00280	91/92	Phenolphthiocerol synthesis polyketide synthase type I Pks15/1, OSY45424
	_10_00270	86/87	Phthioceranic/hydroxyphthioceranic acid synthase, OSY45423
<i>t1pks-2</i>	_04_06320	99/99	3-oxoacyl-[acyl-carrier-protein] synthase 2, OSY38813
	_04_06310	98/98	Phthioceranic/hydroxyphthioceranic acid synthase, OSY38814
<i>t2pks-1</i>	_03_01500	99/100	$\beta$ -ketoacyl-[acyl-carrier-protein] synthase family protein, QEV50971
	_03_01510	99/99	ketosynthase chain-length factor, QEV50970
	_03_01520	100/100	acyl carrier protein, QEV50969
<i>t2pks-2 (oxy)</i>	_07_00590	93/95 (88/93)	Actinorhodin polyketide putative $\beta$ -ketoacyl synthase 1, OSY48324 (OxyA, AAZ78325)
	_07_00600	86/90 (77/84)	Actinorhodin polyketide putative $\beta$ -ketoacyl synthase 2, OSY48325 (OxyB, AAZ78326)
	_07_00610	83/90 (70/80)	Oxytetracycline polyketide synthase acyl carrier protein, OSY48326 (OxyC, AAZ78327)
	_03_03810	98/98	1,3,6,8-tetrahydroxynaphthalene synthase, GFE29002
<i>nrps-1</i>	_07_04820	97/98	non-ribosomal peptide synthetase, WP_085926581
	_07_04810	94/95	non-ribosomal peptide synthetase, WP_085926580
	_07_04800	96/96	non-ribosomal peptide synthetase, WP_085926605
	_07_04790	95/96	NAD-dependent epimerase/dehydratase family protein, WP_085926579
<i>nrps-2</i>	_02_01330	95/97	Tyrocidine synthase 3, OSY47214
	_02_01450	97/98	hypothetical protein Srufu_42150, GFE31835
	_02_01460	95/97	hypothetical protein Sgleb_38680, GFE15821
	_02_01470	96/97	non-ribosomal peptide synthetase, WP_085923271
<i>pks/nrps-1</i>	_03_00740	95/96	polyketide synthase, GFE28620
	_03_00750	93/95	hypothetical protein Srufu_10010, GFE28621
	_03_00760	94/96	type I polyketide synthase, WP_085923489
	_03_00770	92/95	polyketide synthase, AZS70416
	_03_00780	95/96	type I polyketide synthase, WP_085923487
	_03_00790	96/97	type I polyketide synthase, WP_085923486
	_03_00800	97/97	hypothetical protein Srufu_10060, GFE28626
	_03_00820	97/97	hypothetical protein Srufu_10080, GFE28628
_03_00840	95/96	hypothetical protein Srufu_10100, GFE28630	
<i>pks/nrps-2</i>	_08_01960	82/88	condensation protein, WP_107065154
	_08_01950	80/87	non-ribosomal peptide synthetase, WP_031138763
	_08_01940	80/85	type I polyketide synthase, WP_078904507
	_08_01890	76/82	amino acid adenylation domain-containing protein, WP_107066826

\*I/S, identity/similarity in amino acid sequence.

**Table S2.** Closest homolog of PKSs and NRPSs in the gene clusters of *Streptomyces angustmyceticus* NBRC 3934<sup>T</sup>

Gene cluster	Locus tag (San01_)	I/S* (%)	Description and accession number of the closest homolog (homolog whose metabolite is experimentally identified)
<i>t1pks-1*</i>	16600	83/85	type I polyketide synthase, WP_093491222
	16610	85/86	hypothetical protein Scani_28540, GFE06586
<i>t1pks-2*</i>	20810	95/97	ketoacyl synthase, WP_088797712
	20820	92/95	type I polyketide synthase, WP_093492590
<i>t1pks-3 (tsn)</i>	<i>s29-1<sup>t</sup></i>	97/98	type I polyketide synthetase (TsnB1), BAX57200
	RS35710 <sup>t</sup>	94/96	type I polyketide synthetase (TsnB1), BAX57200
	RS35715 <sup>t</sup>	95/97	type I polyketide synthetase (TsnB2), BAX57201
	RS31690 <sup>t</sup>	95/96	type I polyketide synthetase (TsnB2), BAX57201
	64470	95/97	type I polyketide synthetase (TsnB3), BAX57202
<i>t1pks-4</i>	<i>s04-1<sup>t</sup></i>	87/90	type I polyketide synthase (ScaP1), QBF51754
	RS35695 <sup>t</sup>	87/92	SDR family NAD(P)-dependent oxidoreductase, TXD00034 (86/90) (type I polyketide synthase (ScaP1), QBF51754)
	<i>s40-2<sup>t</sup></i>	94/96	Acyl transferase domain-containing protein, SOE09197 (94/97) (type I polyketide synthase (ScaP2), QBF51755)
	RS35360 <sup>t</sup>	89/92	SDR family NAD(P)-dependent oxidoreductase, TXD00033 (89/92) (type I polyketide synthase (ScaP2), QBF51755))
	71810	88/91	Type I polyketide synthase, CUW01173 (87/90) (type I polyketide synthase (ScaP3), QBF51756)
	RS35370 <sup>t</sup>	91/93	type I polyketide synthase, WP_093488014 (89/92) (type I polyketide synthase (ScaP4), QBF51757)
	RS35705 <sup>t</sup>	89/92	SDR family NAD(P)-dependent oxidoreductase, TXD00026 (85/90) (type I polyketide synthase (ScaP4), QBF51757)
	RS35690 <sup>t</sup>	86/89	type I polyketide synthase (ScaP4), QBF51757
	<i>s39-1<sup>t</sup></i>	94/97	type I polyketide synthase (ScaP5), QBF51758
	RS35595 <sup>t</sup>	89/92	type I polyketide synthase (ScaP5), QBF51758
	RS31970 <sup>t</sup>	90/93	hypothetical protein Stube_65570, GFE41884 (90/93) (type I polyketide synthase (ScaP5), QBF51758)
	65020	99/100	SDR family NAD(P)-dependent oxidoreductase, TXD00025 (89/92) (type I polyketide synthase (ScaP6), QBF51759)
	65010	92/94	hypothetical protein Stube_65590, GFE41886 (90/92) (type I polyketide synthase (ScaP7), QBF51760)
	64920	88/92	AMP-binding protein, TXD00261 (87/91) (type I polyketide synthase (ScaP8), QBF51769)
	<i>t2pks-1*</i>	26680	97/99
26670		99/99	ketosynthase chain-length factor, WP_088796350
26660		96/97	putative acyl carrier protein, GFE08130
<i>t2pks-3</i>		99/99	actinorhodin polyketide putative β-ketoacyl synthase 1, GFE06353
	00550		(TxnA1, AKT74262) (86/92)
		96/97	actinorhodin polyketide putative β-ketoacyl synthase 1, GFE06352
	00560		(78/87) (TxnA2, AKT74261)
	00570	98/98	actinorhodin polyketide synthase acyl carrier protein, GFE06351 (73/85) (TxnA3, AKT74260)
00580	87/88	hypothetical protein Scani_26180, GFE06350 (63/70) (TxnA4, AKT74259)	
<i>t3pks-1 (rpp)*</i>	24600	97/98	1,3,6,8-tetrahydroxynaphthalene synthase, GFE07918
<i>nrps-1*</i>	06160	92/95	non-ribosomal peptide synthetase, WP_088801550
	06150	87/90	non-ribosomal peptide synthetase, WP_129297982
	06140	90/92	amino acid adenylation domain-containing protein, SED80324
	06130	88/91	non-ribosomal peptide synthetase/polyketide synthase, KOG49533
<i>nrps-3</i>	24170	91/93	amino acid adenylation domain-containing protein, WP_129292551
	24160	91/93	non-ribosomal peptide synthetase, WP_093640679
<i>nrps-4</i>	36160	87/91	amino acid adenylation domain-containing protein, TXS70023

	<i>s07-1<sup>t</sup></i>	93/96	non-ribosomal peptide synthetase, partial, TXS70022
<i>nrps-5</i>	27520 <sup>t</sup>	90/93	amino acid adenylation domain-containing protein, TXS81310
	27580	85/88	amino acid adenylation domain-containing protein, TXS81304
	27590	89/92	amino acid adenylation domain-containing protein, TXS81303
<i>pks/nrps-3</i>	61570	82/89	SDR family NAD(P)-dependent oxidoreductase, WP_138902144
	61560	87/94	ACP S-malonyltransferase, MQS98670
	61550	81/88	hypothetical protein, MQS98671
	61530	82/88	amino acid adenylation domain-containing protein, WP_138902148 (54/64) (mixed NRPS PKS (GdnE), AFU82614)
	61520	74/82	thioesterase, WP_138902149
	61190	89/91	AMP-binding protein, WP_100605862
<i>pks/nrps-4</i>	12760	74/76	acyl carrier protein, WP_058042275
	12770	84/88	polyketide synthase, WP_058042274
	12780	88/93	amino acid adenylation domain-containing protein, WP_058042273
	12800	83/87	non-ribosomal peptide synthetase, WP_058042271
	12810	77/83	thioesterase, WP_058042270

\*I/S, identity/similarity in amino acid sequence.



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