

NC_002755.2 *Mycobacterium tuberculosis* CDC1551, complete genome

1	NRPS	105314-123821						
		Distance						
	Score	From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
	75	430	106294	+	TTGGCAGCGCTTCGGCT	-	MT0106	dioxygenase, putative
	75	157	106567	+	CTGGCAGTCAAGGTGCC	-	MT0106	dioxygenase, putative
	81	323	109450	+	GTGGCGTGAACATTGCG	-	MT0109	hypothetical protein cation transporter E1-E2 family
	81	325	122488	-	GTGGAATAGCACTTGCC	-	MT0112	ATPase
	81	60	122247	+	ATGGCCCGCTGGATGCA	-	MT0113	hypothetical protein
2	PKS	485426-491388						
3	PKS	1313164-1328792						
		Distance						
	Score	From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
	78	341	1327340	-	CTGGCTCAGACCCTGCG	-	MT1222	acyl-CoA synthetase
4	PKS	1865066-1886258						
		Distance						
	Score	From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
	78	121	1866089	+	CTGGCACTGATGCTGGA	-	MT1701	polyketide synthase
	76	370	1878562	+	TTGCCACCGACCTTGAT	-	MT1704	polyketide synthase
5	PKS	2294295-2309319						
6	NRPS/PKS	2647576-2673168						
		Distance						
	Score	From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
	75	344	2649233	-	CCGGCCCCCGCGTTGCC	-	MT2439	hypothetical protein
	83	331	2651649	-	GAGGAACGCCTTTTGCT	dnaJ-2	MT2442	chaperone protein DnaJ
	78	334	2673502	-	CTGGCAGCCGTTTGCA	pchE	MT2451	dihydroaeruginic acid synthetase
7	PKS	3236513-3319822						
		Distance						
	Score	From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
	76	385	3236128	+	TCGGCACGCCTCGGGCT	-	MT2998	thioesterase
	75	1	3237290	+	TTCGCTGGACATTTGCT	-	MT2998.1	hypothetical protein
	77	349	3256220	+	CTGGGACTCGACTCGCT	-	MT3004	polyketide synthase
	78	23	3292184	-	GTGGCCGACCGTTTGCG	-	MT3021.1	polyketide synthase
	77	323	3296988	-	ATGGCACGGCGCTGGCG	-	MT3023	acyl-CoA synthetase
	79	490	3298272	+	TTGGCATCGATCTTGGG	-	MT3026	methyltransferase, putative
	78	477	3298285	+	TGGGCACGAATTCGCC	-	MT3026	methyltransferase, putative
	77	104	3298658	+	CTGCCATACTCCTTGCC	-	MT3026	methyltransferase, putative
	82	353	3303494	+	GTGGCATGCTCATTCT	-	MT3031	glycosyl transferase
	76	44	3303803	+	GTGGCTGCGGTATTGCC	-	MT3031	glycosyl transferase
	79	276	3306596	-	CTGGCAAGATCTTCGCC	-	MT3034	UDP-glucuronosyl and UDP-
	75	379	3308002	-	TTGGCCAGCTAGTTACT	-	MT3036	glucosyltransferase family protein
	76	106	3308155	-	GTGGCAGGGCCGTGAT	-	MT3037	hypothetical protein
	89	439	3311348	+	CTGGCACGCTACATGCA	-	MT3041.1	hypothetical protein

NC_008611.1 *Mycobacterium ulcerans* Agy99, complete genome

1	PKS	1803923-1835953						
		Distance						
	Score	From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
	77	280	1820828	+	CTGGACAAGTTATTGCT	pkS11	MUL_1656	chalcone synthase, Pks11

75	91	1821017	+	ATGTCACATGTGTTGAA	pks11	MUL_1656	chalcone synthase, Pks11
80	234	1834666	-	ATGGTGCCGCGAGTTGCT	-	MUL_1664	hypothetical protein
75	443	1834875	-	ACGGCACAGCATTTCG	-	MUL_1664	hypothetical protein
75	322	1835436	-	CTGGATCCCGTTTTCG	-	MUL_1665	antibiotic resistance ABC transporter, efflux protein

2 PKS 2211634-2271101

Score	Distance		Strand	Sequence	Gene	Synonym	Protein Name
	From ORF	N					
75	133	2213368	+	CGGGCACACCGAGTGCG	-	MUL_2003	chorismate pyruvate-lyase
78	133	2216250	+	GTGGCCGAACGGTTGCG	pks15/1	MUL_2005	polyketide synthase Pks15/1
79	305	2228469	+	GTGGCTCAACGGTGGCT	-	MUL_2009	methyltransferase
75	67	2230104	+	GTGTCACACCGTTGAA	mas	MUL_2010	multifunctional mycocerosic acid synthase membrane-associated Mas
78	354	2240002	-	ACGGCAAGATCATTGCC	drrB	MUL_2013	daunorubicin-DIM-transport integral membrane protein ABC transporter DrrB
76	153	2240793	-	CTGGCGCGGTCGTTCCC	drrA	MUL_2014	daunorubicin-DIM-transport ATP-binding protein ABC transporter DrrA
77	288	2240928	-	TTGGCAATGCCGGTGCG	drrA	MUL_2014	daunorubicin-DIM-transport ATP-binding protein ABC transporter DrrA
84	178	2245274	-	GTGACACTGATTTTGA	ppsE	MUL_2015	phenolphthiocerol synthesis type-I polyketide synthase PpsE
80	247	2250769	-	ATGGCCCTCGAGTTGCG	ppsD	MUL_2016	phenolphthiocerol synthesis type-I polyketide synthase PpsD
82	34	2257161	-	TTGGAACAGCTTCGCA	ppsC	MUL_2017	phenolphthiocerol synthesis type-I polyketide synthase PpsC
76	121	2266630	-	GTGGCCGACGTCGTGCT	ppsA	MUL_2019	phenolphthiocerol synthesis type-I polyketide synthase PpsA

3 NRPS 2921595-2959529

Score	Distance		Strand	Sequence	Gene	Synonym	Protein Name
	From ORF	N					
79	76	2921519	+	TCGGCACGATAATTCCT	-	MUL_2620	hypothetical protein
80	216	2929670	-	ATGTGCGGGCATTGCT	-	MUL_2625	hypothetical protein
81	92	2930909	-	CTGGCGCAGACCGTGCA	fadE25	MUL_2626	acyl-CoA dehydrogenase FadE25
75	87	2934800	-	GTCGCGCGGGATTGCC	birA	MUL_2631	bifunctional protein BirA
76	286	2952542	-	GTGGCAGACCTGCGGCT	sigF	MUL_2640	RNA polymerase sigma factor SigF
83	205	2953689	-	GTGGCACGGCGCCGCT	usfY	MUL_2642	hypothetical protein

4 NRPS/PKS 4029686-4059363

Score	Distance		Strand	Sequence	Gene	Synonym	Protein Name
	From ORF	N					
76	385	4033562	-	TTGGACTACGGCTTGCT	mbtB	MUL_3632	phenylloxazoline synthase MbtB non-ribosomal peptide synthetase
75	397	4038148	-	CTGGCCCCACCGCTGCC	mbtF	MUL_3633	MbtF
75	61	4042974	+	GTTGAATGGCTGTTGCG	-	MUL_3635	hypothetical protein
76	245	4044260	+	CTGGCACTTCGCGTGAT	mbtC	MUL_3637	polyketide synthase MbtC
76	56	4050456	-	ATGGCAACGCTATTACC	mbtG	MUL_3640	lysine-N-oxygenase MbtG short-chain membrane-associated
80	31	4053325	+	ATCGCAGGCTCATTGCA	-	MUL_3643	dehydrogenase acyl-[acyl-carrier protein] desaturase
75	317	4057245	-	CTGGCTCGGCAGCGGCA	desA1_1	MUL_3646	DesA1_1

5	NRPS	4833556-4838804						
6	NRPS	5377263-5405727						
		Distance						
	Score	From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
	77	255	5378620	+	ACGGCACCAGCACTGCT	-	MUL_4854	oxidoreductase
	75	467	5379274	+	CTGGCCAAGGTTTGGA	-	MUL_4855	hypothetical protein
	84	398	5391216	-	TCGGCCCGGATATTGCT	-	MUL_4861	hypothetical protein
	83	199	5396076	-	ATGGCAATGACGTTGCG	-	MUL_4867	hypothetical protein
7	PKS	5523988-5532849						

NC_006361.1 Nocardia farcinica IFM 10152, complete genome

1	PKS	184410-208907						
		Distance						
	Score	From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
	78	160	207612	+	GTGGCGCCGTCGGTGCT	-	nfa1980	hypothetical protein
2	NRPS	742402-783087						
		Distance						
	Score	From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
	78	5	782060	+	GTGGCACGCGTGCCGCG	-	nfa7210	putative esterase
3	NRPS/PKS	809229-843740						
		Distance						
	Score	From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
	75	426	815841	-	GTGGGCCAACAACTGCT	-	nfa7550	putative ATP-dependent protease
	78	324	816789	-	CTGGCCTGGGCGGTGCT	amiE	nfa7560	acylamide amidohydrolase
	78	239	820253	-	TTGGCGCAACACGTGCG	-	nfa7600	hypothetical protein
	80	307	820321	-	CTGGCGAGCCAGTTGCC	-	nfa7600	hypothetical protein
	76	231	827277	+	CTGGCCGAGCGGATGCT	nbtD	nfa7660	putative non-ribosomal peptide synthetase
	76	64	837122	+	CTGGCCGAGCTGTGGCA	nbtF	nfa7680	putative non-ribosomal peptide synthetase
4	NRPS	1219367-1235955						
		Distance						
	Score	From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
	77	475	1218892	+	CTGGCCCGTTGCTGCG	-	nfa11040	hypothetical protein
5	NRPS	2965856-2985159						
6	PKS	3189119-3223839						
		Distance						
	Score	From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
	76	247	3191679	-	CTGGCGCTGGTGCTGCG	-	nfa30090	putative iron-sulfur oxidoreductase
	75	103	3193577	-	CTAGCGCGCGGATTGCG	-	nfa30110	putative monooxygenase
	75	380	3193854	-	GTGGCATCCTGGTGCC	-	nfa30110	putative monooxygenase
	76	406	3195498	-	CTGGGGCAGTGATTGCG	-	nfa30120	acyl-CoA synthetase
	75	62	3198518	+	CCGGCAAGCGCATGCT	-	nfa30170	hypothetical protein
	76	56	3202150	+	ATTGCTGGAATATTGCT	-	nfa30220	putative sigma factor
	75	459	3212616	-	CTGGCGGACCAACTGCT	-	nfa30250	putative polyketide synthase
	76	221	3220860	-	CTGGACTTCTGTTGCT	-	nfa30320	hypothetical protein
7	NRPS	3297940-3312573						
		Distance						
	Score	From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name

78	179	3299108	-	GTGGCCGGGACCGTGCA	-	nfa31160	putative ABC transporter ATP-binding protein
77	296	3299225	-	CTGGCGCGGGACTTCCG	-	nfa31160	putative ABC transporter ATP-binding protein
8	PKS 4478704-4491458						
	Distance						
Score	From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
76	338	4489377	-	ATGGCACAGGTGGCGCC	-	nfa43240	putative polyketide synthase
77	493	4491951	-	CCGGCAACGCACTTGCC	-	nfa43260	putative transporter
9	NRPS 5244714-5291138						
10	NRPS 5318160-5361768						
11	PKS 5919882-5934805						
	Distance						
Score	From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
80	97	5923205	+	GCGGCACGTGAGCTGCT	-	nfa55870	hypothetical protein
79	153	5926963	-	GTGGCACGACCGTGCCA	-	nfa55900	long-chain-fatty-acid--CoA ligase
78	189	5926962	+	ATGGCACGGTCGTGCCA	-	nfa55910	putative dioxygenase

NC_009142.1 Saccharopolyspora erythraea NRRL 2338, complete genome

1	PKS 14813-51921						
	Distance						
Score	From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
81	175	15677	-	TTGGCCGGGCCGTTGCG	-	SACE_0012	TetR family transcriptional regulator
76	129	49054	+	GCGGCCCGGCTCTTCT	-	SACE_0029	RNA polymerase sigma factor
2	PKS 778214-832825						
	Distance						
Score	From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
76	328	783452	-	CTGGCGCTACGGTGCA	eryCIV	SACE_0716	eryCIV NDP-6-deoxyhexose 3,4-dehydratase
76	128	784712	-	CTGGCACAGGTGATCCG	eryBVI	SACE_0717	NDP-4-keto-6-deoxy-glucose 2,3-dehydratase
77	362	787113	-	GTGGCACGACGGCGGCG	eryBV	SACE_0719	6-DEB TDP-mycarosyl glycosyltransferase
81	224	831762	-	GAGGTACGGCTTGCA	ermE	SACE_0733	N-6-aminoadenine-N-methyltransferase,erythromycin resistance
3	NRPS 1436967-1445722						
4	PKS 2528343-2549947						
	Distance						
Score	From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
76	242	2528101	+	GTGGACCGGCAGTTGGT	cmtC	SACE_2339	trehalose corynomocolyl transferase C
5	PKS 2795362-2818679						
	Distance						
Score	From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
76	132	2798967	-	TCGGCACGCGACTTGGG	-	SACE_2592	glucose-methanol-choline oxidoreductase
80	116	2800190	-	CTGGCGCACCGGGTGCT	-	SACE_2593	glycopeptide antibiotics resistance protein
6	NRPS/PKS 2838066-2886848						

Score	Distance		Strand	Sequence	Gene	Synonym	Protein Name
	From ORF	N					
81	433	2844648	-	GTGGCGCAGGTGCTGCA	-	SACE_2619	non-ribosomal peptide synthetase
79	322	2855647	-	GAGGCACTGCGCCTGCT	-	SACE_2627	isopentenyl-diphosphate delta-isomerase II 2
77	316	2883545	-	GTGGCGCTGGCGCTGCA	-	SACE_2635	major facilitator superfamily transporter phthalate permease
7	NRPS	2944491-2974637					
Score	Distance		Strand	Sequence	Gene	Synonym	Protein Name
From ORF	N						
75	112	2962692	+	GTGGAACGCGCCGCGCA	-	SACE_2698	putative regulatory protein
76	63	2974297	+	GTGGCACGCGCGCGCC	-	SACE_2709	hypothetical protein
8	PKS	3127652-3157229					
Score	Distance		Strand	Sequence	Gene	Synonym	Protein Name
From ORF	N						
76	284	3131486	-	TCGGCACGGTGTTCGCC	rifI	SACE_2867	aminoquinolate/shikimate dehydrogenase
79	195	3138945	+	GTGCCATTCCGGTTGCT	-	SACE_2875	modular polyketide synthase
77	158	3138982	+	CAGGCATCGAGTTGCG	-	SACE_2875	modular polyketide synthase
78	428	3151884	+	CTGGCGCACGTGTTCT	mhpA	SACE_2877	3-(3-hydroxyphenyl)propionate hydroxylase
77	240	3152072	+	CTGGCACGGCCTCTACC	mhpA	SACE_2877	3-(3-hydroxyphenyl)propionate hydroxylase
9	NRPS	3301269-3308199					
Score	Distance		Strand	Sequence	Gene	Synonym	Protein Name
From ORF	N						
77	55	3307140	+	ACGGCGCGGATCGTGCT	-	SACE_3016	SyrP-like protein
10	NRPS	3326161-3344964					
Score	Distance		Strand	Sequence	Gene	Synonym	Protein Name
From ORF	N						
85	242	3325919	+	GTGGCCAGGCGTTGCT	-	SACE_3033	putative peptide monooxygenase
11	PKS	4545937-4616845					
Score	Distance		Strand	Sequence	Gene	Synonym	Protein Name
From ORF	N						
75	59	4554457	+	TTGACTAGAGTGTGCT	-	SACE_4130	hypothetical protein
78	290	4559173	+	ATGGCCTCGCGTTGCC	-	SACE_4132	acyl carrier protein
86	49	4563179	+	TGGGCACCGCCCTTGCT	-	SACE_4135	MaoC-like dehydratase
80	259	4572145	-	CTGGCCGGCACCTGCT	-	SACE_4138	type I PKS modular polyketide synthas
78	417	4588385	-	GTGGAACAGGCCTTCCA	-	SACE_4139	type I modular polyketide synthase
75	146	4612861	-	GTGGCGCTGCGCTGCC	-	SACE_4142	cytochrome P450 monooxygenase
75	251	4612966	-	CTGGCTCGGATGGAGCT	-	SACE_4142	cytochrome P450 monooxygenase
83	27	4614155	-	ATGGCAGGGAAGTTCCT	-	SACE_4143	cytochrome P450 monooxygenase
12	NRPS	4759004-4809694					
Score	Distance		Strand	Sequence	Gene	Synonym	Protein Name
From ORF	N						
78	475	4772132	-	CTGGCCCGGGCGCTGCG	-	SACE_4285	AMP-dependent synthetase and ligase

	76	498	4772155	-	GTGGCGCGCTGCTGGCC	-	SACE_4285	AMP-dependent synthetase and ligase
13	PKS	4821866-4828194						
14	PKS	4992823-5006652						
	Score	Distance From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
	75	183	4996606	-	GTGGACCGCCCGGTGCA	-	SACE_4472	NAD-dependent epimerase/dehydratase
	79	82	4997888	-	GTGGCGCTGAAGCTGCT	qor	SACE_4474	quinone oxidoreductase
15	PKS	5102367-5117363						
	Score	Distance From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
	79	327	5106524	+	CTGCGACGCGCCTGCA	-	SACE_4566	hypothetical protein
	78	359	5112790	+	GTGCCGCAACGTTTGCT	pteA1	SACE_4574	modular polyketide synthase
16	PKS	5932907-5941187						
	Score	Distance From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
	78	213	5933803	+	CGGCCACGCCGTTGCA	chlB1	SACE_5308	iterative type I polyketide synthase
17	PKS	6225358-6248235						
	Score	Distance From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
	78	287	6239374	-	TCGGCACCGCTCTCCA	-	SACE_5540	3-oxoacyl (acyl carrier protein) synthase III

NC_009380.1 *Salinispora tropica* CNB-440, complete genome

1	PKS	671414-679577						
	Score	Distance From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
	75	214	671873	+	TTGGAACGAAACGAGCT	-	Strop_0597	hypothetical protein
	83	374	672939	+	ATGGCTGGCACGTTGCT	-	Strop_0598	beta-ketoacyl synthase
2	NRPS/PKS	144505-1172682						
	Score	Distance From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
	79	296	1150310	-	CTGGCATGCCTCCGGCA	-	Strop_1020	MbtH domain-containing protein
	82	296	1164400	+	GTGGCATGGCCTATGCC	-	Strop_1028	hypothetical protein
	76	157	1164539	+	CTGGCCGGCCGATCGCT	-	Strop_1028	hypothetical protein
	78	220	1165260	+	CTGCCACGGCTGCTGCC	-	Strop_1029	cyclase family protein
	81	438	1167460	-	CTGGCACAGATAGCGCT	-	Strop_1030	regulatory protein, LuxR
3	PKS	2502319-2520690						
	Score	Distance From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
	76	33	2505275	-	TGGGCACAAAGCCTGCG	-	Strop_2212	TAP domain-containing protein
	75	447	2507023	-	GCGGCACCCTGTTGAT	-	Strop_2213	hypothetical protein
	78	480	2513894	-	ATGGGACTGACCTCGCT	-	Strop_2220	hypothetical protein
	83	411	2514406	+	CTGGTAGAGCAGTTGCA	-	Strop_2222	dTDP-glucose 4,6-dehydratase
	75	1	2517088	+	TGGGCACGGTCCGGCA	-	Strop_2224	beta-ketoacyl synthase
	76	463	2519253	+	GCGGCCGCCCCGTTGCT	-	Strop_2227	hypothetical protein
4	PKS	2795012-2816666						
	Score	Distance From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name

75	433	2798754	-	CTGGTCGAACTCTTGCG	-	Strop_2487	dehydrogenase, E1 component AMP-dependent synthetase and ligase
76	124	2804213	-	GAGGCCGACCTGTTGCT	-	Strop_2492	beta-ketoacyl synthase
81	84	2805809	-	CTGGCCTGGCTTGTGCA	-	Strop_2494	antibiotic biosynthesis monooxygenase
80	205	2809136	-	GTGGCCACCGTGTGCT	-	Strop_2498	cupin 2 domain-containing protein
77	357	2812320	-	GTGGCCGAGATCCTGCA	-	Strop_2501	acetyl-CoA carboxylase, biotin carboxyl carrier protein
77	112	2814752	-	CTGGCCGACCTGGTGCC	-	Strop_2504	

5 NRPS/PKS 2956815-2996840

Score	Distance		Strand	Sequence	Gene	Synonym	Protein Name
	From ORF	N					
78	393	2974666	-	TTGGCCGAGCTCTGGCC	-	Strop_2648	methyltransferase type 12
80	85	2977211	-	CTGGCACCCGCGTGCC	-	Strop_2650	ABC transporter related binding-protein-dependent transport systems inner membrane component
75	466	2979339	-	CTGGCGTTGACCCTGCA	-	Strop_2652	hypothetical protein
77	150	2996990	-	TTGGCCAAGCAAGTGCT	-	Strop_2659	

6 PKS 3020222-3042851

Score	Distance		Strand	Sequence	Gene	Synonym	Protein Name
	From ORF	N					
76	204	3023263	-	GTGGCCTGGTTCTGGCC	-	Strop_2686	alpha amylase, catalytic region helix-turn-helix domain-containing protein
75	322	3025145	-	TTGGCATGTGGTGCCT	-	Strop_2688	hypothetical protein
75	330	3026030	-	GCGGCACCGCGTTGTT	-	Strop_2689	hypothetical protein
76	207	3027623	-	ACGGCCCTCTCGTGCT	-	Strop_2691	hypothetical protein flavin reductase domain-containing protein
81	377	3031869	-	TTGGCAGGGCCGGTGCC	-	Strop_2695	beta-ketoacyl synthase
77	192	3037925	-	CTGGCGTGGCCTCGCA	-	Strop_2697	hypothetical protein
76	235	3043086	-	ATGGCACGGGTGTTCTC	-	Strop_2701	

7 NRPS/PKS 3112454-3249126

Score	Distance		Strand	Sequence	Gene	Synonym	Protein Name
	From ORF	N					
75	422	3116359	+	ACGGCATGAGCGTCGCA	-	Strop_2766	regulatory protein, TetR
75	117	3141159	-	CTGGTCCGGCTGGTGCC	-	Strop_2770	cytochrome P450
80	282	3142490	+	CTGGCCCGACCGTGCG	-	Strop_2772	aminotransferase, class I and II
76	440	3143585	+	CTGGCCGGCCGATGCA	-	Strop_2773	hypothetical protein
76	344	3143681	+	GTGGCCGGCGCCGTGCA	-	Strop_2773	hypothetical protein AMP-dependent synthetase and ligase
77	410	3144589	+	TTGGCCGACGGCTGCG	-	Strop_2774	beta-ketoacyl synthase
79	25	3160851	-	CTGGCAACGAGTTTGGT	-	Strop_2778	acyl transferase domain-containing protein
85	327	3165966	-	CTGGCCCGCACCTGCT	-	Strop_2779	hypothetical protein
76	471	3188122	-	GCGGCACGCCGATCGCC	-	Strop_2785	AMP-dependent synthetase and ligase
77	312	3190952	-	AGGGCAAGCGGATTGCC	-	Strop_2787	alpha/beta hydrolase fold
75	112	3193950	-	CTGGCCGCGACCTGCT	-	Strop_2791	alpha/beta hydrolase fold
75	303	3194141	-	CTGGCCGACCCGCTGCT	-	Strop_2791	beta-ketoacyl synthase
78	427	3198676	-	TTGGCACTCTCATGGCC	-	Strop_2795	phosphopantetheine-binding
78	168	3198676	-	TTGGCACTCTCATGGCC	-	Strop_2796	phosphopantetheine-binding
79	373	3198881	-	GCGGCACTGCTCTGGCT	-	Strop_2796	phosphopantetheine-binding
75	470	3198978	-	CGGGAACGAGCCCTGCT	-	Strop_2796	L-carnitine dehydratase/bile acid- inducible protein F
75	370	3201972	-	CAGGCACGGCTGCGGCA	-	Strop_2800	AMP-dependent synthetase and ligase
76	7	3203132	+	CTGGCACTCTGGAGGCT	-	Strop_2803	

78	466	3212075	+	CTGGCGCTGGAGGTGCT	-	Strop_2809	hypothetical protein
78	205	3222961	-	CGGGCACTGCGGGTGCT	-	Strop_2817	thioesterase
75	410	3224293	-	GTGGCTCGACTGGTACT	-	Strop_2818	thiazolinylyl imide reductase
78	126	3241571	-	GCGCCACAGGACTTGCT	-	Strop_2825	cytochrome P450

8 PKS 3475927-3510099

9 NRPS 4996301-5013814

Score	Distance		Strand	Sequence	Gene	Synonym	Protein Name
	From ORF	N					
80	426	4997797	-	GTGGCCCCGCTCTTCT	-	Strop_4414	methyltransferase type 12 amino acid adenylation domain-containing protein
84	166	5003350	-	ATGGCCCGCGCGTTGCG	-	Strop_4416	containing protein
79	496	5009133	-	CTGGCCCGCGGCTGCG	-	Strop_4419	kynurenine 3-monooxygenase

NC_003155.4 *Streptomyces avermitilis* MA-4680, complete genome

1 PKS 113361-118594

2 PKS 486648-567017

Score	Distance		Strand	Sequence	Gene	Synonym	Protein Name
	From ORF	N					
76	157	490476	-	TTGGCAAGAAAGCGGCA	pteF	SAV_409	LuxR family transcriptional regulator
77	370	567387	-	CTGGCCGAGATTTTCGCA	pteA1	SAV_419	modular polyketide synthase

3 NRPS 751402-762285

4 NRPS/PKS 991484-1042269

Score	Distance		Strand	Sequence	Gene	Synonym	Protein Name
	From ORF	N					
75	136	992855	-	CGGGTGCGTCTGTTGCT	cyp4	SAV_838	cytochrome P450
77	39	1002360	-	CTGGCCCGCGGTTGGC	-	SAV_845	modular polyketide synthase
75	51	1021253	-	CTGGCACACAAAGAGCG	nrps7-8	SAV_855	non-ribosomal peptide synthetase
76	223	1022254	-	TTGGCCGAGGACGTGCT	-	SAV_856	thioesterase
87	293	1024835	+	CTGGCACGGCCCTTCCA	nrps7-10	SAV_859	non-ribosomal peptide synthetase
81	433	1026118	+	TTGGCCGCGGGCGTGCA	nrps7-11	SAV_860	non-ribosomal peptide synthetase
79	488	1036207	+	GTGGCAGGCGAACTGCC	-	SAV_867	ABC transporter ATP-binding protein

5 PKS 1132045-1212960

Score	Distance		Strand	Sequence	Gene	Synonym	Protein Name
	From ORF	N					
75	76	1168427	+	ATGGCACCGCACCCGCC	aveC	SAV_940	AveC
75	111	1208710	-	CAGGCCCGCACCTGCT	aveBV	SAV_949	dTDP-4-keto-6-deoxyhexose 3,5-epimerase
76	410	1212380	-	ACGGCCCGGATACTGCA	aveBVIII	SAV_952	dTDP-4-keto-6-deoxy-L-hexose 2,3-reductase
77	281	1211927	+	GGAGCACTGCTGTTGCT	aveG	SAV_953	thioesterase
75	114	1212094	+	GTGGGACACGGGCTGCC	aveG	SAV_953	thioesterase

6 PKS 1549424-1554224

7 PKS 1893266-1913284

Score	Distance		Strand	Sequence	Gene	Synonym	Protein Name
	From ORF	N					
78	263	1910520	-	GCGGTACGCCAGTTGCC	pks2-2	SAV_1551	modular polyketide synthase
76	443	1912725	-	CTGGCCCTCTTGTGCG	pks2-3	SAV_1552	non-ribosomal peptide synthetase
76	354	1912250	+	CTGGTGCAGGCGTGCT	-	SAV_1553	methyltransferase

8	PKS	2773878-2784841						
9	PKS	2877941-2894413						
10	PKS	2896543-2914291						
		Distance						
	Score	From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
	81	339	2904983	-	CTGGCACCGCTCACGCT	-	SAV_2378	polyketide oxidase/hydroxylase
	75	296	2906293	+	ACGGCCCGCCCGCTGCT	-	SAV_2381	TetR family transcriptional regulator
11	PKS	3477658-3493243						
		Distance						
	Score	From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
	77	112	3491806	-	CTGGCCCTGTTCTGCC	-	SAV_2846	hypothetical protein
	75	159	3492602	-	GAGGCACCCCTTCTGCG	-	SAV_2847	hypothetical protein
	77	210	3493453	-	ACGGCCAGCACCTTGCT	-	SAV_2849	hypothetical protein
12	PKS	3534525-3634592						
		Distance						
	Score	From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
	77	17	3630164	-	ATGGCGCGGCTCGCGCA	olmRII	SAV_2901	LuxR family transcriptional regulator
13	NRPS	3930306-3937493						
14	NRPS	3980213-3994940						
		Distance						
	Score	From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
	76	11	3985530	-	CTGGAAGGTACCGTGCA	nrps1-1	SAV_3197	non-ribosomal peptide synthetase
	77	263	3989602	-	CGGGCACGGGACTGGCC	nrps1-2	SAV_3198	non-ribosomal peptide synthetase
15	NRPS	4494250-4540450						
		Distance						
	Score	From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
	79	266	4496242	-	CTGGCGCAGATCCTGCC	pptA4	SAV_3637	phosphopantetheinyl transferase
	83	421	4500418	-	CTGGCCCGGAACTGCT	-	SAV_3641	ornithine carbamoyltransferase
	80	163	4516448	-	CTGGCACGCCGAGGGCA	nrps2-2	SAV_3643	non-ribosomal peptide synthetase
	76	214	4521073	-	GCGGCACAGCTGTTCCC	cysK2	SAV_3648	cysteine synthase
	77	416	4521275	-	CTGGCGCAGCTCGCC	cysK2	SAV_3648	cysteine synthase
	76	211	4523419	-	CTGGCCAGGCTGCTGCG	fadE25	SAV_3650	acyl-CoA dehydrogenase
	75	154	4528046	-	GTGGCCAAGGAGATGCT	-	SAV_3652	isomerase
	75	388	4536085	-	ATGGCGCTGCGGGTGCG	-	SAV_3661	hypothetical protein
16	PKS	8553602-8561604						
		Distance						
	Score	From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
	75	252	8560553	-	CTGGCCCGGACCGAGCT	-	SAV_7185	UDP-glucose:sterol glucosyltransferase
17	PKS	8776963-8789766						

NC_003888.3 *Streptomyces coelicolor* A3(2), complete genome

1	PKS	104989-119654						
---	-----	---------------	--	--	--	--	--	--

2	NRPS	513989-526783
3	PKS	1335793-1343779
4	NRPS	3543335-3585724
5	PKS	5508078-5508078
6	PKS	6432566-6465258
7	PKS	6895193-6961810
8	NRPS	7106284-7116513
9	PKS	7590412-7602007
10	NRPS	8506283-8523749

NC_010572.1 Streptomyces griseus subsp. griseus NBRC 13350, complete genome

1	PKS	294490-307047						
2	NRPS	480685-538065						
		Distance						
	Score	From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
	80	142	535949	-	CTGGCCCCGGTGCTGCT	-	SGR_453	iron ABC transporter
	75	367	536174	-	CTGGCCCGCCGCTGAA	-	SGR_453	iron ABC transporter
3	NRPS	659688-691515						
		Distance						
	Score	From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
	80	48	664691	+	GTGGCGTGCCTTCTGCA	-	SGR_578	putative SyrP-like protein
	76	167	676251	+	CTGGCCCGGCTGGAGCT	-	SGR_583	putative NRPS
	82	298	685576	-	CTGGCCCGCCTCTGCT	-	SGR_588	hypothetical protein
4	PKS	704021-717508						
		Distance						
	Score	From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
	76	480	703541	+	GTGCGACGGCGTTGCC	tebC	SGR_604	putative enediyne biosynthesis protein
	76	474	704168	+	AGGGCACCCGAGGTGCT	unbL1	SGR_605	putative enediyne biosynthesis protein
	79	329	708297	+	GTGGCACGCCAGTGGA	unbU	SGR_608	putative enediyne biosynthesis protein
5	NRPS	762595-774309						
6	PKS	937762-968455						
		Distance						
	Score	From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
	78	299	940053	+	CTGCCACAGCCGATGCA	-	SGR_803	putative large multi-functional protein
	81	130	956182	-	CTGGCACGGCAGCTCCA	-	SGR_813	putative FAD-dependent oxidoreductase
7	NRPS	1044652-1071469						
		Distance						
	Score	From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
	75	294	1046802	-	GGGGCACGCACATCGCC	-	SGR_890	hypothetical protein
	75	437	1060513	-	CTGGCTCACCGGATGCG	-	SGR_896	putative O-methyltransferase
8	NRPS/PKS	2924650-2941895						

Score	Distance		Strand	Sequence	Gene	Synonym	Protein Name
	From ORF	N					
75	374	2930023	+	ATGGTGCGGCAGTTGGA	-	SGR_2485	putative NRPS
75	470	2935806	+	ATGGCCATGTGCTGCC	-	SGR_2486	putative aminopeptidase 2
78	400	2937233	+	ATGGCGCAGCGGTGCA	-	SGR_2487	putative thioesterase

9 NRPS 3048501-3074603

10 NRPS 3762124-3830096

11 PKS 7102079-7171428

Score	Distance		Strand	Sequence	Gene	Synonym	Protein Name
	From ORF	N					
76	362	7161653	+	TCGGCAGCTCGGTGCC	pks1-7	SGR_6083	putative type-I PKS

12 PKS 7286041-7354154

13 PKS 7551740-7619551

Score	Distance		Strand	Sequence	Gene	Synonym	Protein Name
	From ORF	N					
83	426	7551314	+	CTGGCAGGGCAGTTGGA	-	SGR_6359	hypothetical protein
78	256	7570469	-	CTGGGACTGTCTCGCT	-	SGR_6360	hypothetical protein
75	422	7574873	-	GTGGCCGACGTAGTGCA	-	SGR_6365	hypothetical protein
76	266	7596949	-	CTGGCCGGGCACCTGCG	pks3-3	SGR_6371	putative type-I PKS
81	244	7619795	-	GTGGCCAGCGGTGCA	pks3-1	SGR_6373	putative type-I PKS

14 NRPS 8011976-8029693

Score	Distance		Strand	Sequence	Gene	Synonym	Protein Name
	From ORF	N					
81	164	8012818	+	GCGGCAGATCCGTGCA	-	SGR_6714	putative ABC-type Fe3+-siderophore transporter substrate-binding protein
85	326	8015602	+	CTGGCCGGCTGGTGCT	-	SGR_6716	putative NRPS
77	424	8030117	-	CTGGCACATCGGTGCT	-	SGR_6718	putative esterase

15 NRPS 8049140-8065069

16 PKS 8100042-8154770

Score	Distance		Strand	Sequence	Gene	Synonym	Protein Name
	From ORF	N					
78	30	8100012	+	CGGGCAGAGTCTTGCG	pks4-1	SGR_6776	putative NRPS-type-I PKS fusion protein
77	383	8110593	+	TTCGCACGGACGGTGCG	pks4-2	SGR_6777	putative type-I PKS
75	269	8124572	+	TTCGGACGCATCGTGCT	-	SGR_6780	putative malonyl-CoA:ACP transacylase

NC_003228.3 Bacteroides fragilis NCTC 9343, complete genome

1 NRPS 3294535-3306572

2 NRPS 3635663-3639879

Score	Distance		Strand	Sequence	Gene	Synonym	Protein Name
	From ORF	N					
75	357	3638482	+	GCGGCCGACAGCTTGCT	-	BF3118	hypothetical protein

NC_005125.1 Gloeobacter violaceus PCC 7421, complete genome

1 PKS 2057662-2100787

Score	Distance		Strand	Sequence	Gene	Synonym	Protein Name
	From ORF	N					
76	304	2064191	-	ATGGTCCGCATCTTCT	-	gll1939	cyclopropane-fatty-acyl-phospholipid synthase

83	457	2064344	-	CTGGCCCCGAGATCTGCT	-	gll1939	cyclopropane-fatty-acyl-phospholipid synthase
77	280	2065156	-	ATGGCCCAAGTTGTGGCC	-	gll1940	fatty acid desaturase
77	423	2072927	-	GCGGCCCTGGGGTTGCT	-	gll1946	fatty acid desaturase
81	329	2073836	-	GTGGGGCGGCTTTTGCC	-	gll1947	fatty acid desaturase
75	166	2078085	-	CCGGCAGCACTCTGCA	-	gll1950	long-chain fatty-acid-CoA ligase
76	219	2078138	-	ATGGCTTCGCACTCGCT	-	gll1950	long-chain fatty-acid-CoA ligase
77	466	2078385	-	GGGGCGCACCCCTTGCG	-	gll1950	long-chain fatty-acid-CoA ligase
81	411	2079094	-	CTGGAGCGCTGTTTGCA	-	gll1951	phosphopantetheinyltransferase family protein
76	461	2088597	-	GTGGCTGGACAGTTGAT	-	gll1954	polyketide synthase
76	146	2088597	-	GTGGCTGGACAGTTGAT	-	gll1955	polyketide synthase
75	317	2088768	-	ATGGCCCTGATCTTTCG	-	gll1955	polyketide synthase
75	277	2094691	-	CTGGACCAGTTGCTGCA	-	gll1957	glycolipid synthase

2 PKS 2999221-3029646

Score	Distance From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
77	396	2998825	+	CTGGCACCAGAAACGCT	-	glr2821	WD repeat-containing protein
81	288	3009343	-	CTGGCGGGCCTTTGCG	-	gll2826	hypothetical protein
77	307	3010641	-	ACGGGACATGATTGCT	-	gll2827	hypothetical protein
80	157	3014822	-	CAGGCGCTGATCTTGCT	-	gll2829	polyketide synthase
79	450	3023483	-	GTGGCACAGACCGTCCT	-	gll2836	alcohol dehydrogenase
79	174	3023483	-	GTGGCACAGACCGTCCT	-	gsl2837	hypothetical protein

3 PKS 3033832-3050434

Score	Distance From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
75	221	3040466	+	CTGGCGCAGTGTGAG	-	glr2850	thioesterase
79	41	3040646	+	CTGGCAACTCGGTGCA	-	glr2850	thioesterase
78	393	3048049	+	GTGGCCCGTCCGATGCC	-	glr2859	oxidoreductase

4 PKS 4421532-4440489

Score	Distance From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
75	215	4422391	-	CTGGAAAGTCCATCGCT	-	gll4219	hypothetical protein
83	331	4422933	-	CTGGCCGAGGATTGCT	-	gll4220	hypothetical protein
75	154	4431563	-	CTGGTAGGCCCATGCG	-	gll4225	glycolipid synthase

NC_010296.1 Microcystis aeruginosa NIES-843, complete genome

1 NRPS/PKS 2507861-2539146

Score	Distance From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
77	38	2518358	+	TGGGCGCAAGCCTTGCG	-	MAE_27820	amino acid adenylation short-chain
78	118	2526583	+	TGGGCGCGAGCATTGCG	-	MAE_27860	dehydrogenase/reductase
79	235	2537743	+	GTGGCATCGGTTGTGCG	-	MAE_27910	hypothetical protein

2 NRPS/PKS 3486436-3541027

Score	Distance From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
79	340	3528001	+	GTGGCAATTGCTCTGCA	mcyF	MAE_38620	McyF protein
79	114	3540068	+	ATGGCAATATTCTGCA	mcyJ	MAE_38660	McyJ protein

3 NRPS 5194435-5220124

Score	Distance From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
75	130	5208380	-	TTGGCATGGTATTCTCA	-	MAE_56550	hypothetical protein

80	148	5209406	-	TTGGCTCGACCGTTTCT	-	MAE_56560	bacilysin biosynthesis protein BacA-like protein
80	198	5209456	-	ATGGCTTAGACCTTGCC	-	MAE_56560	bacilysin biosynthesis protein BacA-like protein

4 843, complete genome 5519975-5552181 Type: NRPS

NC_010628.1 Nostoc punctiforme PCC 73102, complete genome

1	PKS	56243-74142						
Score	Distance From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name	
81	379	58235	-	GTGGCAATATAATTGCC	-	Npun_R0038	short-chain dehydrogenase/reductase SDR polyketide synthase thioester	
79	405	60343	-	TTCGCAAAACTATTGCT	-	Npun_R0039	reductase subunit HglB	
76	291	68964	-	ATGGCCCAAAGTTTCA	-	Npun_R0042	KR	
2	PKS	1549256-1571247						
3	PKS	2521301-2548634						
4	NRPS/PKS	2648282-2708401						
Score	Distance From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name	
75	183	2660116	-	TTGTCATAGACATTGCC	-	Npun_R2175	KR	
79	484	2664987	-	ATGGCAGGTATAATGCC	-	Npun_R2178	WD-40 repeat-containing protein	
76	206	2704134	+	GTGATACAGTAATTGCA	-	Npun_F2186	alcohol dehydrogenase	
81	362	2705124	+	CAGGCATTCTATTGCT	-	Npun_F2187	pyrroline-5-carboxylate reductase	
5	NRPS	3054973-3081156						
Score	Distance From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name	
76	50	3055694	+	TGGGCAAGGATATAGCA	-	Npun_F2460	amino acid adenylation domain-containing protein	
76	93	3065615	+	GTGACTCAAGAGTTGCT	-	Npun_F2462	amino acid adenylation domain-containing protein	
6	NRPS/PKS	3722118-3780010						
7	NRPS/PKS	3899401-3958883						
Score	Distance From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name	
75	191	3899210	+	TTCACACGTATGTTGCT	-	Npun_F3155	hypothetical protein	
86	415	3925855	+	ATGGCGTGAATTTTGCT	-	Npun_F3168	hypothetical protein	
76	296	3950844	+	GTGGCTAGGGTCTGCG	-	Npun_F3173	amino acid adenylation domain-containing protein	
75	148	3950992	+	AAGGCCCTAGTATTGCC	-	Npun_F3173	amino acid adenylation domain-containing protein	
75	54	3955358	+	TAGGAAGATAATTGCT	-	Npun_F3174	isoprenylcysteine carboxyl methyltransferase	
8	PKS	4180429-4210477						
Score	Distance From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name	
75	482	4181756	-	CTGGAACATTTATTGCT	-	Npun_R3355	thioesterase	
75	474	4185955	+	TTGTCAGGAGGTTGCC	-	Npun_F3359	beta-ketoacyl synthase	
76	364	4186065	+	CTGGCTAGAGAAATGCT	-	Npun_F3359	beta-ketoacyl synthase	

	83	221	4201954	+	ATGGCAGTGATATTGCC	-	Npun_F3363	short-chain dehydrogenase/reductase SDR, HetN
9	NRPS/PKS		4256267-4330313					
	Score	Distance From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
	81	468	4259675	-	ATGGCAAGAGTTTTGTA	-	Npun_R3419	thioesterase
	81	165	4259675	-	ATGGCAAGAGTTTTGTA	-	Npun_R3420	MbtH domain-containing protein
	76	491	4260403	-	ATTGCACGAGGCTTCT	-	Npun_R3421	hypothetical protein
	77	499	4280094	-	ACGGCCCGACTGTAGCT	-	Npun_R3429	condensation domain-containing protein
	76	482	4286311	-	TTGGATCGCGCATCGCT	-	Npun_R3430	beta-ketoacyl synthase
	75	239	4307280	-	ATGGCTCTCTTATTGAA	-	Npun_R3436	amino acid adenylation domain-containing protein
	78	331	4307372	-	TTGGCATCCAGCTTGTT	-	Npun_R3436	amino acid adenylation domain-containing protein
	81	358	4321256	-	ATGGCAGCACTTGTGCA	-	Npun_R3448	taurine catabolism dioxygenase TauD/TfdA
10	NRPS/PKS		8150738-8167006					

NC_008536.1 *Solibacter usitatus* Ellin6076, complete genome

1	PKS		2480784-2494608					
	Score	Distance From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
	80	22	2489341	+	CTGGCCGGGAGATTGCG	-	Acid_1973	beta-ketoacyl synthase
	77	463	2493837	+	ACGGCAGACCCATTGCC	-	Acid_1974	putative acyl carrier protein
2	PKS		3884932-3895290					
	Score	Distance From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
	75	213	3885870	-	GTGGATCGAGTTTCGCT	-	Acid_3076	4'-phosphopantetheinyl transferase
	78	300	3885957	-	ATGGCACCGCGCTGAT	-	Acid_3076	4'-phosphopantetheinyl transferase
	77	50	3893616	-	CGGGCAGCCGCTTGAG	-	Acid_3077	beta-ketoacyl synthase

NC_009674.1 *Bacillus cereus* subsp. *cytotoxis* NVH 391-98, complete genome

1	NRPS		417602-429629					
	Score	Distance From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
	80	491	422474	+	CTGGTAGAGGATTTGCA	-	Bcer98_0368	amino acid adenylation domain-containing protein
2	NRPS		1197549-1205485					
	Score	Distance From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
	77	484	1198103	+	ACGTCACGAGGTTTGCA	-	Bcer98_1088	2-nitropropane dioxygenase NPD
3	NRPS		1853248-1878954					
	Score	Distance From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
	76	310	1855588	+	TTGGAGCGTCTTTGGCT	-	Bcer98_1744	AMP-dependent synthetase and ligase
	80	293	1856961	+	TAGGCGCTGGTGTGCT	-	Bcer98_1745	hypothetical protein
4	PKS		3245067-3256221					

5	PKS	1781906-1859783						
Score	Distance From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name	
77	130	1785974	+	CCGGCACCTTAGCTGCT	pksE	BSU17120	enzyme involved in polyketide synthesis	
81	446	1791566	+	CTGCCACAGATATTGCC	pksI	BSU17170	polyketide biosynthesis enoyl-CoA hydratase	

6	NRPS	1949682-2002351						
Score	Distance From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name	
81	138	1956312	-	GTGGAACGGATGCTGCG	yngI	BSU18250	AMP-binding domain protein	
82	303	1956477	-	CTGGCACGGCAAATGGT	yngI	BSU18250	AMP-binding domain protein	
79	340	1957700	-	CGGGCACTGCTCTTGTT	yngJ	BSU18260	acyl-CoA dehydrogenase, short-chain specific	
76	263	1960350	-	ATGGAAGCGCCTGCG	yngL	BSU18290	putative integral inner membrane protein	
77	161	1975017	-	ATTGAACACTTTTGCT	ppsD	BSU18310	plipastatin synthetase	

7	NRPS	3280519-3297919						
Score	Distance From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name	
75	391	3290651	-	GTGGCACCTGTCCAGCG	dhbE	BSU31980	2,3-dihydroxybenzoate-AMP ligase	
82	299	3291784	-	TTGGCCTTGAGCTTGCA	dhbC	BSU31990	isochorismate synthase DhbC	
78	267	3296537	-	CAGGCACAGCGACTGCC	yuiF	BSU32040	amino acid transporter	
80	328	3296598	-	ATGGCAGGAACGTTTCT	yuiF	BSU32040	amino acid transporter	

8	NRPS	3952275-3958482						
Score	Distance From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name	
78	347	3957044	+	ATGGCACCGCCTATGGT	ywaA	BSU38550	branched-chain amino acid aminotransferase	

NC_003030.1 Clostridium acetobutylicum ATCC 824, complete genome

1	PKS	3529432-3534819						
---	-----	-----------------	--	--	--	--	--	--

NC_009706.1 Clostridium kluveri DSM 555, complete genome

1	NRPS	1554646-1602560						
Score	Distance From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name	
75	321	1564208	+	CTCGAATGGATATTGCT	-	CKL_1507	NRPS cyclization domain containing protein	
77	233	1578681	+	GAGGCATAGAACATGCA	-	CKL_1515	hypothetical protein	

2	NRPS/PKS	1818097-1833491						
---	----------	-----------------	--	--	--	--	--	--

3	NRPS/PKS	2414655-2426709						
Score	Distance From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name	
76	361	2419626	-	TTGATACAGTTTTTGCA	-	CKL_2354	nonribosomal peptide synthetase	

NC_008497.1 Lactobacillus brevis ATCC 367, complete genome

1	NRPS	1293616-1300116						
Score	Distance From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name	
75	122	1297040	-	GTGCAACTGTTGTTGCA	-	LVIS_1323	D-alanyl transfer protein	

81	491	1300607	-	GGGGCACCACGGTTGCG	-	LVIS_1327	D-Ala-teichoic acid biosynthesis protein (putative)
----	-----	---------	---	-------------------	---	-----------	---

NC_002973.6 *Listeria monocytogenes* str. 4b F2365, complete genome

1	NRPS	1002948-1007380
----------	------	-----------------

NC_002952.2 *Staphylococcus aureus* subsp. *aureus* MRSA252, complete genome

1	NRPS	198393-206225						
	Score	Distance From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
	81	487	197906	+	CTAGCATGCTTGTGCT	-	SAR0180	putative non-ribosomal peptide synthetase

NC_003063.2 *Agrobacterium tumefaciens* str. C58 chromosome linear, complete sequence

1	NRPS	74687-80557						
	Score	Distance From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
	78	121	79699	-	ATGGCTGCTCGGTTGCT	-	Atu3073	aspartate racemase
	83	322	80879	-	CCGGCAGCGGCTCGCT	-	Atu3074	short chain dehydrogenase
2	NRPS/PKS	716058-769035						
	Score	Distance From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
	78	463	729910	-	CTGGTCCGGATTCGCT	-	Atu3673	siderophore biosynthesis protein
	78	187	729910	-	CTGGTCCGGATTCGCT	-	Atu3674	hypothetical protein
	85	425	734796	+	ATGGCACGCTACTGGCG	-	Atu3677	polyketide synthase, siderophore biosynthesis protein
	75	293	734928	+	GCGGCGGTTTCTCGCT	-	Atu3677	polyketide synthase, siderophore biosynthesis protein
	75	28	737448	+	ATGCAAGGCTTCTTGCA	-	Atu3680	putative siderophore biosynthesis protein
	80	62	742445	+	ATGGCAGCGCTTTGAT	-	Atu3682	non-ribosomal peptide synthetase, siderophore biosynthesis protein
	86	328	765024	+	TTGGCACGGATGTCGCC	fecD	Atu3690	ABC transporter, membrane spanning protein (iron (III) dicitrate)
	79	247	765105	+	CCGGCAGCGCGTTGCA	fecD	Atu3690	ABC transporter, membrane spanning protein (iron (III) dicitrate)
	75	470	767004	+	CTGGCGCCCAGGTGCC	-	Atu3692	sigma factor

NC_012988.1 *Methylobacterium extorquens* DM4, complete genome

1	PKS	2613383-2622159
----------	-----	-----------------

NC_012988.1 *Methylobacterium extorquens* DM4, complete genome

1	NRPS	4859328-4866323
----------	------	-----------------

rquens DM4, complete genome 5649466-5678659 Type: NRPS

	Score	Distance From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
--	-------	-------------------	---	--------	----------	------	---------	--------------

86	134	5649332	+	CAGGCACAGGCTTTGCT	-	METDI5670	putative UDP-N-acetyl-D-mannosaminuronic acid dehydrogenase
77	53	5653547	+	ATGGCGCCCGTCTTCT	-	METDI5674	putative glycosyl transferase
75	105	5662917	-	CCGGCAACCACCTTGCC	-	METDI5678	hypothetical protein
75	46	5667529	-	ATGGCAGGTCCGCCGCT	-	METDI5683	hypothetical protein
75	148	5675379	-	CTGGCACCGCGCTTCGA	murE	METDI5688	UDP-N-acetylmuramoylalanyl-D-glutamate--2, 6-diaminopimelate ligase
75	355	5677962	-	TTGGTGCGCGGCTGCA	-	METDI5690	hypothetical protein

NC_003296.1 Ralstonia solanacearum GMI1000 plasmid pGMI1000MP, complete sequence

1	NRPS/PKS	782247-820777						
		Distance						
	Score	From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
	76	194	802722	+	CTGGCCGAACCTCTGGCA	RSp0642	RS05859	peptide synthetase protein
2	NRPS	1782597-1797233						
		Distance						
	Score	From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
	76	13	1787443	+	CTCCCACCGCTTTTGCA	RSp1421	RS03121	hypothetical protein
3	NRPS/PKS	1945814-1979076						
		Distance						
	Score	From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
	79	452	1949544	-	GTCGCACGCGATCTGCA	tISRso15	RSp1547	ISRSO15-transposase protein
	83	50	1950406	-	GTGGCAGTTCATGCG	RSp1549	RS02105	hypothetical protein
	82	103	1951581	-	CCGGCATTGCTTTTGCA	RSp1551	RS02107	hypothetical protein
	80	248	1951726	-	GTGGCGCTGCTGGTGCA	RSp1551	RS02107	hypothetical protein
	75	279	1957715	+	GTGGGATGGGATATGCC	hexR	RSp1556	putative transcription regulation repressor HEXR transcription regulator protein
	75	60	1957934	+	GCGGCCCCGCGCTTGCC	hexR	RSp1556	putative transcription regulation repressor HEXR transcription regulator protein
	77	289	1960873	-	GCGGCACTGGGCTGCA	pgl	RSp1558	6-phosphogluconolactonase oxidoreductase protein
	77	106	1962311	+	GAGGCACGCAATTCGCG	edd	RSp1560	phosphogluconate dehydratase
	78	135	1964859	-	CGGGCATCGTTGTTGCG	RSp1561	RS02117	hypothetical protein
	80	247	1964633	+	ATGGCGCGGATGGTGCC	RSp1562	RS02118	hypothetical protein
	77	139	1965305	+	TGCGCATGGATTTTGCA	RSp1563	RS02119	hypothetical protein
	75	312	1974525	-	CTGGAATGGCGTTAGCG	RSp1571	RS02127	transcriptional regulator transcription regulator protein

NC_008095.1 Myxococcus xanthus DK 1622, complete genome

1	NRPS	1488859-1520119						
		Distance						
	Score	From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
	82	476	1490324	+	GTGGCGCGGCCCTTGAA	-	MXAN_1276	glutamate-cysteine ligase family 2 protein
	77	461	1497379	-	TCTGGAACGCTGCAGAGGGG	-	MXAN_1281	hypothetical protein
	75	1	1500305	+	AGGGCAAGGCATTCCA	-	MXAN_1284	2-isopropylmalate synthase/homocitrate synthase family protein

75	159	1503794	+	TTGGACCGCTCGTGCG	abcA	MXAN_1286	ABC transporter permease/ATP-binding protein
75	63	1503890	+	TTGGCGCGGAAGGCGCA	abcA	MXAN_1286	ABC transporter permease/ATP-binding protein
76	304	1505775	+	CATTGCCCGCCCTGCTGCTG	-	MXAN_1287	hypothetical protein
78	233	1505846	+	GAGGCCAACTGTTGCG	-	MXAN_1287	hypothetical protein
77	252	1517769	-	CCCTGGCACGTGACGTGTCAA	-	MXAN_1291	non-ribosomal peptide synthetase
79	252	1517769	-	CCCTGGCACGTGACGTGTCA	-	MXAN_1291	non-ribosomal peptide synthetase
80	250	1517767	-	CTGGCACGTGACGTGTT	-	MXAN_1291	non-ribosomal peptide synthetase
76	460	1517977	-	GTGGTGCGGCGGATGCA	-	MXAN_1291	non-ribosomal peptide synthetase
76	455	1518967	-	GCTGGCGCGGAGGAAGTGAAG	-	MXAN_1292	hypothetical protein
75	300	1520419	-	ACCGGTACACAGTTGGTGGCG	hemG	MXAN_1293	protoporphyrinogen oxidase
76	336	1520455	-	GGAGACCGGCGTTGTGATG	hemG	MXAN_1293	protoporphyrinogen oxidase

2 NRPS 1832662-1910318

Score	Distance From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
75	298	1834249	-	GTGGCACGTCGCTGGTG	-	MXAN_1560	class I aminotransferase
79	84	1836766	-	TCTGGCACGGTGACTGCTAAGC	ahpC	MXAN_1564	alkyl hydroperoxide reductase C
89	85	1836767	-	TTCTGGCACGGTGACTGCTAAG	ahpC	MXAN_1564	alkyl hydroperoxide reductase C
89	83	1836765	-	CTGGCACGGTGACTGCT	ahpC	MXAN_1564	alkyl hydroperoxide reductase C
88	85	1836767	-	TTCTGGCACGGTGACTGCTAAG	ahpC	MXAN_1564	alkyl hydroperoxide reductase C
77	420	1841516	-	CGCTGGCGCGGTTGCTGCGCAT	-	MXAN_1567	urea amidolyase-like protein
79	420	1841516	-	CGCTGGCGCGGTTGCTGCGCA	-	MXAN_1567	urea amidolyase-like protein
80	418	1841514	-	CTGGCGCGGTTGCTGCG	-	MXAN_1567	urea amidolyase-like protein
76	61	1842452	-	GGCTGGCACGCCAGCGTCTCCG	-	MXAN_1568	LamB/YcsF family/allophanate hydrolase family protein
78	61	1842452	-	GGCTGGCACGCCAGCGTCTCC	-	MXAN_1568	LamB/YcsF family/allophanate hydrolase family protein
75	461	1842852	-	AGCTGCCACGCGCTGGCGCG	-	MXAN_1568	LamB/YcsF family/allophanate hydrolase family protein
76	293	1844083	+	ATGACTCGACGCTTGCG	-	MXAN_1570	class V aminotransferase
75	376	1847137	+	GCTGGCCTCCAGGTGGTGACG	-	MXAN_1573	AMP-binding domain protein
77	227	1849786	-	CCTGGCGCGCCGGGGTGAAG	-	MXAN_1574	TfoX domain-containing protein
75	60	1854462	-	CACGGCGCAGCGCTTGCTAAGG	-	MXAN_1578	metallo-beta-lactamase family protein
75	61	1854463	-	CCACGGCGCAGCGCTTGCTAAG	-	MXAN_1578	metallo-beta-lactamase family protein
81	59	1854461	-	ACGGCGCAGCGCTTGCT	-	MXAN_1578	metallo-beta-lactamase family protein
76	104	1854518	+	GGGGCGCAATCCTTGCG	-	MXAN_1579	hypothetical protein
77	75	1854547	+	GGGGCGCAGGTCTTGCG	-	MXAN_1579	hypothetical protein
80	180	1860605	-	AAGTGGCGCGCCGCTGCTTGG	-	MXAN_1584	hypothetical protein
80	180	1860605	-	AAGTGGCGCGCCGCTGCTTGG	-	MXAN_1584	hypothetical protein
84	178	1860603	-	GTGGCGCGCCGCTGCT	-	MXAN_1584	hypothetical protein
75	146	1861734	+	GTGGGACATCCGGTGCG	-	MXAN_1587	hypothetical protein
76	130	1866438	-	GGAGGCACGCCACGCTGGAA	-	MXAN_1590	putative para-aminobenzoate synthase, component I
75	190	1871142	-	CCTGCTCTGCAGGAGCTGAAG	-	MXAN_1592	hypothetical protein

75	203	1871155	-	GGCTGGAAGTGGACCTGCTCTG	-	MXAN_1592	hypothetical protein
77	203	1871155	-	GGCTGGAAGTGGACCTGCTCT	-	MXAN_1592	hypothetical protein
78	130	1875006	-	CATGGCACGGGGGACGAAGAGG	-	MXAN_1595	hypothetical protein
75	428	1875304	-	GGAGGATGACCGGCTGCTGATG	-	MXAN_1595	hypothetical protein
76	277	1877522	+	GGTGGCCAGCCGGGCGGACG	-	MXAN_1599	putative methyltransferase
75	44	1877755	+	GTGGTGCCGCTGCTGCT	-	MXAN_1599	putative methyltransferase
75	398	1878919	+	GGAGGCCCGCTCCGAGCTGTGG	-	MXAN_1600	class I aminotransferase
79	267	1879050	+	GGCTGGCTCGGGCGTTGCGTCC	-	MXAN_1600	class I aminotransferase
85	270	1879047	+	CTGGCTCGGGCGTTGCG	-	MXAN_1600	class I aminotransferase
80	268	1879049	+	GGCTGGCTCGGGCGTTGCGTC	-	MXAN_1600	class I aminotransferase
79	398	1881868	-	GTGGCCCGGGCACTGCG	-	MXAN_1601	fatty acid desaturase family protein putative non-ribosomal peptide
76	297	1883277	+	GTGGCCTGGGTGGTGCC	-	MXAN_1603	synthetase
78	262	1889174	+	TGCTGGAAGGGTGCCTGCTGGG	-	MXAN_1605	putative permease
79	263	1889173	+	TGCTGGAAGGGTGCCTGCTGG	-	MXAN_1605	putative permease
78	265	1889171	+	CTGGAAGGGTGCCTGCTGCT	-	MXAN_1605	putative permease
75	256	1890469	+	GGTGGCCCGCTTCATGCTGGAG	-	MXAN_1606	hypothetical protein
75	260	1890465	+	GTGGCCCGCTTCATGCT	-	MXAN_1606	hypothetical protein
75	294	1910612	-	GTAGGAACGCACGACCTCAAG	-	MXAN_1608	hypothetical protein

3 NRPS/PKS 3251570-3266656

4 PKS 4029025-4040172

Score	Distance From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
76	178	4029404	+	GCTGGTCCACATCATGCTCGAG	-	MXAN_3460	Gfo/Idh/MocA family oxidoreductase
76	182	4029400	+	CTGGTCCACATCATGCT	-	MXAN_3460	Gfo/Idh/MocA family oxidoreductase

5 NRPS/PKS 4220394-4350875

Score	Distance From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
75	319	4254532	-	ATGGCGGAAGAGCTGCT	-	MXAN_3627	hypothetical protein
75	398	4255390	-	ACTGCCACGCCAGCAGCTCGGG	-	MXAN_3628	thioesterase non-ribosomal peptide biosynthesis
75	399	4255391	-	AACTGCCACGCCAGCAGCTCG	-	MXAN_3628	thioesterase
75	308	4259689	-	CTGGCGGACATCTGGCA	-	MXAN_3630	polyketide synthase type I
75	287	4264309	-	GAAGGAACAGCTGTTGCGCATG	-	MXAN_3631	polyketide synthase type I
78	286	4264308	-	AAGGAACAGCTGTTGCG	-	MXAN_3631	polyketide synthase type I
76	211	4284118	+	AAGGCGTGCGCATTGCT	-	MXAN_3635	non-ribosomal peptide synthase/polyketide synthase
77	32	4334952	+	CTGGTACTTCGAGTGCA	-	MXAN_3638	M19 family peptidase
76	311	4347401	-	GTGGAAAACCATCTGCT	-	MXAN_3644	isochorismatase
75	268	4351143	-	GTGGCACGCGAAATCCC	-	MXAN_3647	2,3-dihydroxybenzoate-2,3- dehydrogenase

6 PKS 4498820-4544105

Score	Distance From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
76	284	4498536	+	TTGAGACGGAGATTGCG	-	MXAN_3778	DnaK family protein

7 PKS 4729983-4809194

Score	Distance From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
75	337	4731192	-	CGTGGGCCGGTCCGGCTCAAG	-	MXAN_3931	hypothetical protein
76	73	4740097	-	TCAGACACGCCATCGCTGATC	-	MXAN_3932	polyketide synthase
75	90	4740114	-	CTTGAAAACCGGTTGCTCAGA	-	MXAN_3932	polyketide synthase
75	103	4755572	-	AGGTGGTACTTCGCTTACTCG	-	MXAN_3933	mixed type I polyketide synthase - peptide synthetase

76	101	4755570	-	GTGGTACTTCGCTTACT	-	MXAN_3933	mixed type I polyketide synthase - peptide synthetase	
75	428	4784222	-	ATTGGCTCGCGTCTGGCTGCGC	-	MXAN_3935	non-ribosomal peptide synthase/polyketide synthase Ta1	
77	221	4784015	-	TGCTGGCACGAACCCTGGGCG	-	MXAN_3935	non-ribosomal peptide synthase/polyketide synthase Ta1	
82	427	4784221	-	TTGGCTCGCGTCTGGCT	-	MXAN_3935	non-ribosomal peptide synthase/polyketide synthase Ta1	
78	219	4784013	-	CTGGCACGAACCCTGGG	-	MXAN_3935	non-ribosomal peptide synthase/polyketide synthase Ta1	
75	315	4784109	-	TTGGCGCTGAGCGTGCC	-	MXAN_3935	non-ribosomal peptide synthase/polyketide synthase Ta1	
78	333	4790662	-	GTTGGTCCGCCGGCGGTGGAG	-	MXAN_3936	polyketide synthase	
75	155	4797857	-	GCTGTCGCTCGTGACGCTCAAG	-	MXAN_3938	polyketide synthase	
76	245	4800766	-	GGCTGGCTCTGCAACTGCGCAG	-	MXAN_3941	polyketide beta-ketoacyl:acyl carrier protein synthase	
76	245	4800766	-	GGCTGGCTCTGCAACTGCGCA	-	MXAN_3941	polyketide beta-ketoacyl:acyl carrier protein synthase	
75	243	4800764	-	CTGGCTCTGCAACTGCG	-	MXAN_3941	polyketide beta-ketoacyl:acyl carrier protein synthase	
77	318	4804366	-	GTGGCGCATGCCTTTCT	-	MXAN_3943	cytochrome P450 family protein	
77	97	4805951	-	CCTGGACAGCCTGCGGCTGCAG	taF	MXAN_3945	polyketide TA biosynthesis protein TaF	
76	464	4806318	-	CCTGTCGCGCGTGGTGTGGAC	taF	MXAN_3945	polyketide TA biosynthesis protein TaF	
76	220	4806318	-	CCTGTCGCGCGTGGTGTGGAC	-	MXAN_3946	putative acyl carrier protein	
8	NRPS/PKS		4875470-4906976					
		Distance						
	Score	From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
	79	135	4900530	-	CTGCCCGCAGGTTGCA	-	MXAN_4001	non-ribosomal peptide synthase/polyketide synthase
	75	470	4906209	-	AGGGCACGGCCCGTGAT	-	MXAN_4002	nonribosomal peptide synthetase
9	NRPS/PKS		4996865-5026357					
10	NRPS/PKS		5252320-5298262					
		Distance						
	Score	From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
	76	350	5253698	+	GCTGGAGCGCGTGTCTGGCC	-	MXAN_4290	putative thioesterase
	77	352	5253696	+	TGCTGGAGCGCGTGTCTGG	-	MXAN_4290	putative thioesterase
	76	354	5253694	+	CTGGAGCGCGTGTCTGCT	-	MXAN_4290	putative thioesterase
	76	132	5263568	-	ATGTCGCCGTGCTTGCA	-	MXAN_4295	patatin-like phospholipase family protein
	77	150	5267893	-	AGCTGGGAGTGGACCTGCTCA	-	MXAN_4296	non-ribosomal peptide synthetase
	77	379	5279177	-	GATGCGTCGGCAGTTGCTGATG	-	MXAN_4298	polyketide synthase type I
	80	178	5287908	-	ATGGCGCTCGAGTTGCG	-	MXAN_4299	non-ribosomal peptide synthase/polyketide synthase
	77	183	5292178	-	CGCTGGCGAAGCGGCTGTGT	-	MXAN_4300	polyketide synthase type I
	76	181	5292176	-	CTGGCGAAGCGGCTGTCT	-	MXAN_4300	polyketide synthase type I
11	PKS		5407416-5440677					
12	NRPS/PKS		5444807-5471033					

Score	Distance From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
75	182	5448069	+	CCTGGACGACCGGTTGGTGCTG	-	MXAN_4413	hypothetical protein
78	328	5468596	+	CCTGGGCCACGGATTGCTGCGC	-	MXAN_4416	cephalosporin hydroxylase family protein
79	332	5468592	+	CTGGGCCACGGATTGCT	-	MXAN_4416	cephalosporin hydroxylase family protein

13 NRPS/PKS 5600883-5653548

Score	Distance From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
75	259	5612126	-	ATGGCGCTGGAGCTGCG	-	MXAN_4526	polyketide synthase type I
78	373	5612240	-	ATGGCGCTGCTGTTGGA	-	MXAN_4526	polyketide synthase type I
81	466	5612333	-	GTGGCAGGGCAGGTGCG	-	MXAN_4526	polyketide synthase type I
75	170	5627582	-	CTGGCTGAACAACCTGCA	-	MXAN_4527	polyketide synthase
79	187	5653735	-	GTGGCACAAGCTGCGCT	-	MXAN_4532	non-ribosomal peptide synthase

14 NRPS 5735538-5780049

Score	Distance From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
75	39	5755794	+	CAATGGAACGGCGCATCCTCC	-	MXAN_4598	non-ribosomal peptide synthase
75	41	5755792	+	ATGGAACGGCGCATCCT	-	MXAN_4598	non-ribosomal peptide synthase
75	485	5759989	+	CCTGGGCTACGGGGTGTGCGC	-	MXAN_4599	M28 family peptidase radical SAM domain-containing protein
75	493	5765386	-	GGTGGCCTGGGCGTCGGTGGCG	-	MXAN_4600	radical SAM domain-containing protein
75	40	5764933	-	GCGGTAAAGTCTTTGCT	-	MXAN_4600	protein
78	237	5774788	+	CCTGGCCCGTCTGGAGCTCCAG	-	MXAN_4602	hypothetical protein
75	241	5774784	+	CTGGCCCGTCTGGAGCT	-	MXAN_4602	hypothetical protein
76	62	5777754	+	ATGTCGCTCGACTTGCT	-	MXAN_4604	hypothetical protein

NC_010162.1 Sorangium cellulosum 'So ce 56', complete genome

1	PKS	488146-499710					
2	PKS	1150403-1167578					
		Distance					
	Score	From ORF	N	Strand	Sequence	Gene	Synonym
	76	300	1150103	+	CTGGCCTGCGCGTCGCT	-	sce0818
	75	299	1151780	+	ATGGCGCTGATCTCCG	-	sce0819
							Protein Name
							putative dioxygenase
							polyketide synthase
3	NRPS	3204860-3216562					
4	PKS	4376667-4461851					
		Distance					
	Score	From ORF	N	Strand	Sequence	Gene	Synonym
	84	488	4376179	+	CTGGCAGGATATCTGCT	-	sce3188
	77	52	4440389	+	CTGGGGCGGATCTCGCT	-	sce3193
							Protein Name
							polyketide synthase
							polyketide synthase
5	PKS	5761328-5853706					
6	PKS	6867494-6856887					
7	PKS	9402480-9513516					
		Distance					
	Score	From ORF	N	Strand	Sequence	Gene	Synonym
	81	172	9407529	-	TCGGCAGGCTGCCTGCA	-	sce6747
	90	68	9411437	-	GTGGCGCGCCGCTTGCT	-	sce6751
	75	485	9425010	-	GTGGCGCGCGGCTGCC	-	sce6759
	75	4	9436354	+	ATGGCAGGAGGGGTGAT	-	sce6766
							Protein Name
							hypothetical protein
							hypothetical protein
							hypothetical protein
							putative secreted protein

81	80	9440680	-	CGGGCACGGGCGCTGCT	-	sce6770	hypothetical protein
80	438	9441038	-	AGGGCATGATCGTTGCC	-	sce6770	hypothetical protein
77	38	9452036	-	GCGGTACACCCCTTGCG	-	sce6780	hypothetical protein
75	93	9452091	-	GAGGCGCGGGGATGCT	-	sce6780	hypothetical protein
81	344	9452342	-	CTGGCTCGAGGCTGCA	-	sce6780	hypothetical protein
75	212	9452057	+	GCGGCCGCCGCTGCT	-	sce6781	TetR family transcriptional regulator
77	479	9456589	+	ACGGCACGCGACGTGCG	-	sce6785	hypothetical protein
77	260	9460836	+	CTGGCACGGGCGAGCT	-	sce6787	hypothetical protein
78	361	9466227	-	CTGGCGCTCGATCTGCT	-	sce6792	hypothetical protein
77	107	9470202	-	TTCGCATGGCTGTTGGA	-	sce6797	hypothetical protein
75	293	9479287	-	ATGGTTCTTCTCGCT	-	sce6805	hypothetical protein
77	345	9497084	-	GTGGATCGAGTCATGCT	-	sce6819	hypothetical protein

8 NRPS/PKS 11424644-11529102

Score	Distance		Strand	Sequence	Gene	Synonym	Protein Name
	From ORF	N					
81	427	11427264	-	GGGGCACGATCGCTGCT	-	sce8207	sigma-54 dependent transcriptional regulator
84	42	11432421	-	CTGGCATCCCTCGTCTGCT	-	sce8210	putative DNA helicase
75	419	11456144	+	AGGGCGCGGGCTGCTGCA	-	sce8233	hypothetical protein
82	43	11458261	+	AGGGCACGGCTCTTGGGA	-	sce8234	hypothetical protein
76	173	11460728	+	GTGGCCGACGTCTGCT	yfbL2	sce8235	putative aminopeptidases
75	388	11472575	+	GTGGCGGCTCCCCGCT	-	sce8244	putative protein phosphatase
75	371	11475747	-	GAGGCCAGCTCGTGCA	-	sce8246	CobW/P47K family protein

NC_002163.1 Campylobacter jejuni subsp. jejuni NCTC 11168, complete genome

1 NRPS 1236809-1238584

NC_000913.2 Escherichia coli str. K-12 substr. MG1655, complete genome

1 NRPS 608682-631222

Score	Distance		Strand	Sequence	Gene	Synonym	Protein Name
	From ORF	N					
78	373	612792	+	ATCGCACCGTGGTTGCC	ybdZ	b4511	conserved protein
80	361	619783	-	CTGGTACGCCGATGCG	fepC	b0588	iron-enterobactin transporter subunit
79	153	620564	-	CCGTCAGCTACTTCTGCT	fepG	b0589	iron-enterobactin transporter subunit
79	138	621385	+	CGGGCACGGCAATGGCG	entS	b0591	enterobactin exporter, iron-regulated
76	428	624161	-	TGGGCGCAAGTGTGCC	fepB	b0592	iron-enterobactin transporter subunit
79	291	625002	+	CTGGCCTGTCTGCTGCA	entE	b0594	2,3-dihydroxybenzoate-AMP ligase component of enterobactin synthase multienzyme complex

NC_002942.5 Legionella pneumophila subsp. pneumophila str. Philadelphia 1, complete genome

1 NRPS/PKS 2166115-2171151

2 NRPS/PKS 2442757-2470485

NC_002516.2 Pseudomonas aeruginosa PAO1, complete genome

1 NRPS 2532669-2549458

Score	Distance		Strand	Sequence	Gene	Synonym	Protein Name
	From ORF	N					
90	276	2539319	-	CTGGCCGGGCTTGCT	-	PA2302	non-ribosomal peptide synthetase

79	154	2545100	-	ATGGCGCTGCTGTTGGT	-	PA2305	non-ribosomal peptide synthetase
83	8	2545667	-	ATGGAACGAATGTCGCT	-	PA2306	hypothetical protein
84	55	2547555	-	CTGGCAGGACTATTCT	-	PA2308	ABC transporter ATP-binding protein

2	NRPS	2636517-2687178						
	Score	Distance From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
	75	125	2640910	+	ACGGCACTGTCCTCCA	fpvR	PA2388	FpvR
	80	88	2651219	+	CTGGCGCCGAGCCTGCT	pvdO	PA2395	PvdO
	75	140	2653197	-	CTTCCACGTAATGCA	pvdF	PA2396	pyoverdine synthetase F
	77	421	2665565	-	CTGGCGCGGATGCCGCT	pvdD	PA2399	pyoverdine synthetase D
	77	479	2672108	-	CTGGCGCGGATGCCGCT	pvdJ	PA2400	PvdJ

3	NRPS	4724639-4746551						
	Score	Distance From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
	81	393	4727194	-	CTGGCTCGCGGGCTGCT	fptA	PA4221	Fe(III)-pyochelin outer membrane receptor precursor
	78	265	4728882	-	CCGGCGAGCCTGTTGCT	-	PA4222	ABC transporter ATP-binding protein
	80	286	4728903	-	CTGGCCGTGCGCTGCT	-	PA4222	ABC transporter ATP-binding protein
	75	43	4731415	-	CTGGCGCAATCCTTGTC	pchG	PA4224	pyochelin biosynthetic protein PchG
	75	16	4736814	-	CTGGAAGAGGGCGTGCT	pchF	PA4225	pyochelin synthetase
	81	64	4736862	-	CTTGCCCGCACTTGCA	pchF	PA4225	pyochelin synthetase
	77	465	4741576	-	CTGGTCGGCGCCTTGCA	pchE	PA4226	dihydroaeruginic acid synthetase

NC_002947.3 Pseudomonas putida KT2440, complete genome

1	NRPS	4767855-4798662						
	Score	Distance From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
	79	278	4795256	-	TTGGCGCCGAAGGTGCA	-	PP_4222	syrP protein, putative
	77	431	4795409	-	ATGGGGCAGCGGTTGCG	-	PP_4222	syrP protein, putative
	80	413	4796855	-	ATGGGCCAGGCATTGCT	-	PP_4223	diaminobutyrate--2-oxoglutarate aminotransferase
2	NRPS	4818235-4832793						
	Score	Distance From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
	76	122	4832915	-	TTGGCCAGTGGCCTGCT	-	PP_4245	siderophore biosynthesis protein, putative

NC_004578.1 Pseudomonas syringae pv. tomato str. DC3000, complete genome

1	NRPS	2307009-2356936						
	Score	Distance From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
	81	315	2306694	+	ATGGAATTCACCTTGCT	-	PSPTO_2134	pyoverdine synthetase, thioesterase component
	76	381	2322147	+	CTGGTCGGTCATTGCA	-	PSPTO_2137	MbtH-like protein
	78	274	2324978	-	CCGGCGCCGAAATTGCT	-	PSPTO_2139	cation ABC transporter, permease protein
	80	491	2327813	-	CTGGCACAAAGTGGCGCT	-	PSPTO_2143	hypothetical protein

	75	384	2330265	+	CTGGA AACGACGTGCT	-	PSPTO_2147	pyoverdine sidechain peptide synthetase I, epsilon-Lys module
	77	389	2333571	+	CCGACACACTGTTGCT	-	PSPTO_2148	pyoverdine sidechain peptide synthetase II, D-Asp-L-Thr component
2	NRPS/PKS		2863432-2890634					
	Score	Distance From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
	76	322	2868091	-	TTGGCGCGGGTGCCGCA	-	PSPTO_2593	multidrug resistance protein, AcrA/AcrE family
	79	78	2872757	-	GTGGCCAGGCTCTGGCA	irp4	PSPTO_2598	yersiniabactin synthetase, thioesterase component
	81	235	2873968	-	CTGGCGCAACTCGCA	irp3	PSPTO_2599	yersiniabactin synthetase, thiazolanyl reductase component
	80	112	2884576	-	CTGGCGCGGCACTTGAG	-	PSPTO_2601	hypothetical protein
	78	384	2884848	-	CTGGCGCTGACGTGGCT	-	PSPTO_2601	hypothetical protein
	75	89	2890723	-	CAGGCTCGGA ACTGGCA	-	PSPTO_2602	yersiniabactin non-ribosomal peptide synthetase
3	NRPS		3151815-3185293					
	Score	Distance From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
	76	472	3152407	+	TTGATACGGCTGATGCT	syfA	PSPTO_2829	non-ribosomal peptide synthetase SyfA
4	NRPS		5087432-5106501					
	Score	Distance From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
	76	440	5088005	+	CTGGCAGCCTGGTTCT	-	PSPTO_4518	non-ribosomal peptide synthetase, initiating component
5	PKS		5282597-5304804					
	Score	Distance From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
	75	23	5284944	+	CTGGTCCGCAAGTCGCT	cfa3	PSPTO_4683	coronafacic acid beta-ketoacyl synthetase component
	75	194	5286445	+	CTGCCAGGCCA ACTGCT	cfa5	PSPTO_4685	coronafacic acid synthetase, ligase component
6	NRPS		5313602-5327197					

NC_003198.1 Salmonella enterica subsp. enterica serovar Typhi str. CT18, complete genome

1	NRPS		624926-644794					
	Score	Distance From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
	82	483	640548	-	CTGGCGCAATTTCTGCT	fepB	STY0638	iron-enterobactin transporter periplasmic binding protein
	79	288	641267	+	CTGGCCTGTCTGCTGCA	entE	STY0640	enterobactin synthase subunit E

NC_004347.1 Shewanella oneidensis MR-1, complete genome

1	PKS		1670313-1686159					
	Score	Distance From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
	78	441	1676645	-	ATAGCATGAGTATTGCC	-	SO_1599	beta keto-acyl synthase

NC_003143.1 *Yersinia pestis* CO92, complete genome

1		NRPS		839849-856936				
Score	Distance	From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
79		186	841919	-	CGGGCACTATTGCTGCT	-	YPO0774	hypothetical protein
81		353	857289	-	ATGGCCCCCGCCTGCT	-	YPO0778	putative siderophore biosynthesis protein
2		NRPS/PKS		2140840-2169669				
Score	Distance	From ORF	N	Strand	Sequence	Gene	Synonym	Protein Name
82		239	2145615	-	CTGGCGCGACTGCTGCG	irp4	YPO1908	yersiniabactin biosynthetic protein YbtT
75		486	2166571	+	ATGACACGCTGCTGGCG	irp8	YPO1915	putative signal transducer
83		441	2167924	+	CTGGCCGGCGGATTGCT	ybtS	YPO1916	salicylate synthase Irp9
79		96	2168269	+	GGGGCATTACGTTGCT	ybtS	YPO1916	salicylate synthase Irp9