

1 Type I Polyketide synthases

1.0.1 Cluster 9

Gene	BLAST hit	Accession no.	Species	Score	E-value
g2445	hypothetical protein	GAD93348.1	<i>B. spectabilis</i>	94.4	1e-20
g2446	Cell wall glucanase	XP_013328261.1	<i>R. emersonii</i>	700	0.0
g2447	hypothetical protein	XP_013328259.1	<i>R. emersonii</i>	545	0.0
g2448	Polyketide synthase	XP_013328257.1	<i>R. emersonii</i>	603	0.0
g2449	Enoyl reductase (acyl carrier protein)	XP_013328256.1	<i>R. emersonii</i>	4130	0.0
g2450	Polyketide synthase	XP_013331718.1	<i>R. emersonii</i>	2979	0.0
g2451	Polyketide synthase	XP_013331718.1	<i>R. emersonii</i>	353	8e-110
g2452	Kinesin family protein	XP_013331717.1	<i>R. emersonii</i>	1647	0.0
g2453	hypothetical protein	XP_013331716.1	<i>R. emersonii</i>	262	3e-88
g2454	hypothetical protein	OXN11489.1	<i>A. turcosus</i>	355	1e-122
g2455	Cyclic nucleotide-binding domain protein	XP_013331714.1	<i>R. emersonii</i>	1581	0.0
g2456	hypothetical protein	XP_013331713.1	<i>R. emersonii</i>	570	0.0

Table 1: Cluster 9 top BLAST hits

Gene	pHMM hit	smCOG	MiBiG hit	Species
g2448	PP-binding	Thioesterase SMCOG1004	Terrein	<i>A. terreus</i>
g2449	PKS_KS	Beta-Ketoacyl synthase SMCOG1022	Squalestatin S1	<i>Phoma sp.</i>
	PKS_AT			
	Adh_short			
g2449	PP-binding	Beta-Ketoacyl synthase SMCOG1022	Grayanic acid	<i>Cladonia grayi</i>
	PKS_AT			
	Iterative KS			
g2455		Transcription Regulator SMCOG1133		

Table 2: Cluster 9 pHMM hits, smCOG hits and known BGC homology (MiBig)

1.0.2 Cluster 12

Gene	BLAST hit	Accession no.	Species	Score	E-value
g3688	Amino acid transporter	XP_013324126.1	<i>R. emersonii</i>	1102	0.0
g3689	hypothetical protein	XP_020121917.1	<i>T. atrovirens</i>	679	0.0
g3690	hypothetical protein	XP_013329987.1	<i>R. emersonii</i>	380	5e-129
g3691	Serine hydrolase	KXG50575.1	<i>P. griseofulvum</i>	219	1e-67
g3692	hypothetical protein	XP_013329985.1	<i>R. emersonii</i>	225	5e-70
g3693	Lovastatin nonaketide synthase	XP_013329984.1	<i>R. emersonii</i>	4252	0.0
g3694	Cytochrome P450 alkane hydroxylase	XP_013329983.1	<i>R. emersonii</i>	1046	0.0
g3695	RNA-directed RNA polymerase	XP_013329982.1	<i>R. emersonii</i>	2122	0.0
g3696	Clock controlled protein	XP_013329981.1	<i>R. emersonii</i>	757	0.0
g3697	hypothetical protein	XP_013329980.1	<i>R. emersonii</i>	125	1e-31
g3698	Carbonyl reductase	XP_013329979.1	<i>R. emersonii</i>	566	0.0

Table 3: Cluster 12 top BLAST hits

Gene	pHMM hit	smCOG	MiBiG hit	Species
g3688		phenylalanine specific permease SMCOG1038	Dothistromin	<i>Mycosphaerella pini</i>
g3693	PKS_KS	Beta-Ketoacyl synthase SMCOG1022	Fusaric acid	<i>Fusarium verticillioides</i>
	PKS_AT			
	Adh_short			
g3694	p450	Cytochrome p450 SMCOG1034	Fusaridione A	<i>Fusarium heterosporum</i>
g3698		short chain dehydrogenase/reductase (SDR)	Aeruginosin	<i>Microcystis aeruginosa</i>

Table 4: Cluster 12 pHMM hits, smCOG hits, known BGC homology (MiBiG)

1.0.3 Cluster 15

Gene	BLAST hit	Accession no.	Species	Score	E-value
g4161	Beta-glucosidase	XP_013323191.1	<i>R. emersonii</i>	1516	0.0
g4162	Ubiquitinyl hydrolase 1	XP_013323194.1	<i>R. emersonii</i>	2274	0.0
g4163	3-methyl-2-oxobutanoate dehydrogenase kinase	XP_013323195.1	<i>R. emersonii</i>	888	0.0
g4164	Lovastatin nonaketide synthase	XP_013323196.1	<i>R. emersonii</i>	4947	0.0
g4165	hypothetical protein	XP_022583449.1	<i>P. zonata</i>	130	1e-37
g4166	N/A	N/A	N/A	N/A	N/A

Table 5: Cluster 15 top BLAST hits

Gene	pHMM hit	smCOG	MiBiG hit	Species
g4164	PP-binding	Beta-Ketoacyl synthase SMCOG1022	Squalestatin S1	<i>Phoma sp</i>
	PKS_AT			
	iterative KS			
	adh_short			

Table 6: Cluster 15 pHMM hits, smCOG hits, known BGC homology (MiBiG)

1.0.4 Cluster 17

Gene	BLAST hit	Accession no.	Species	Score	E-value
g4274	hypothetical protein	OXV11967.1	<i>E. granulosus</i>	229	1e-72
g4275	flap endonuclease	CRG83000.1	<i>T. islandicus</i>	721	0.0
g4276	Fungal specific transcription factor	XP_013331423.1	<i>R. emersonii</i>	1298	0.0
g4277	hypothetical protein	CRG91162.1	<i>T. islandicus</i>	319	3e-102
g4278	Maltose phosphorylase	XP_013331425.1	<i>R. emersonii</i>	1882	0.0
g4279	hypothetical protein	XP_013331426.1	<i>R. emersonii</i>	952	0.0
g4280	hypothetical protein	XP_013331427.1	<i>R. emersonii</i>	499	1e-176
g4281	Lovastatin nonaketide synthase	XP_013331428.1	<i>R. emersonii</i>	5179	0.0
g4282	NAD(P)H oxidase	XP_013331429.1	<i>R. emersonii</i>	1152	0.0
g4283	Glutaryl-CoA dehydrogenase	XP_013331430.1	<i>R. emersonii</i>	806	0.0
g4284	hypothetical protein	KUM61315.1	<i>P. freii</i>	308	7e-106
g4285	Glyoxalase family protein	XP_013331432.1	<i>R. emersonii</i>	747	0.0
g4286	RNA processing protein Emg1	XP_013331433.1	<i>R. emersonii</i>	512	0.0
g4287	hypothetical protein	XP_013331434.1	<i>R. emersonii</i>	774	0.0

Table 7: Cluster 17 top BLAST hits

Gene	pHMM hit	smCOG	MiBiG hit	Species
g4279	p450	Cytochrome p450 SMCOG1034	Botrydial	<i>Botrytis cinerea</i>
g4281	PP-binding	Beta-Ketoacyl synthase SMCOG1022	Alternapyrone	<i>Alternaria solani</i>
	PKS_AT			
	iterative KS			
	adh_short			
g4283		acyl-CoA hydrogenase	Zwittermycin A	<i>Bacillus cereus</i>

Table 8: Cluster 17 pHMM hits, smCOG hits, known BGC homology (MiBiG)

1.0.5 Cluster 20

Gene	BLAST hit	Accession no.	Species	Score	E-value
g4888	hypothetical protein	OJJ08167.1	<i>A. versicolor</i>	590	0.0
g4889	Beta-lactamase	XP_007779066.1	<i>C. apollinis</i>	679	0.0
g4890	hypothetical protein	OQD73893.1	<i>P. decumbens</i>	610	0.0
g4891	hypothetical protein	OQD73938.1	<i>P. decumbens</i>	615	0.0
g4892	hypothetical protein	OJJ08171.1	<i>A. versicolor</i>	1789	0.0
g4893	FAD-binding domain containing protein	XP_025492900.1	<i>A. uvarum</i>	902	0.0
g4894	cytochrome P450	RAK78080.1	<i>A. fijiensis</i>	674	0.0
g4895	hypothetical protein	OJJ08174.1	<i>A. versicolor</i>	839	0.0
g4896	putative Polyketide synthase	XP_025437739.1	<i>A. fijiensis</i>	4842	0.0
g4897	hypothetical protein	OQD73972.1	<i>P. decumbens</i>	900	0.0
g4898	hypothetical protein	OQD73953.1	<i>P. decumbens</i>	603	0.0

Table 9: Cluster 20 top BLAST hits

Gene	pHMM hit	smCOG	MiBiG hit	Species
g4888		crotonyl-CoA reductase / alcohol dehydrogenase SMCOG1028	Betaenone C Betaenone A	<i>Phoma betae</i>
g4889		Beta-lactamase SMCOG1053	Lovastatin	<i>Aspergillus terreus</i>
g4890		short chain dehydrogenase \reductase (SDR) SMCOG1001	Betaenone C Betaenone A	<i>Phoma betae</i>
g4891		methyltransferase SMCOG1089	Squalestatin S1	<i>Phoma sp.</i>
g4892	p450	Cytochrome P450 SMCOG1034	Fumonisin	<i>Fusarium oxysporum</i>
g4893		FAD linked oxidase domain protein	Betaenone C Betaenone A	<i>Phoma betae</i>
g4894	p450	Cytochrome P450 SMCOG1034	Pyripyropene	<i>Aspergillus fumigatus</i>
g4896	PP-binding	Beta-ketoacyl synthase SMCOG1022	Betaenone A Betaenone B	<i>Phoma betae</i>
	PKS_AT			
	iterative KS			
	adh_short			
	NAD_binding			
g4897		Drug resistance transporter EmrB/QacA SMCOG1005	Lovastatin	<i>Aspergillus terreus</i>

Table 10: Cluster 20 pHMM hits, smCOG hits, known BGC homology (MiBiG)

1.0.6 Cluster 21

Gene	BLAST hit	Accession no.	Species	Score	E-value
g5133	Pyridine nucleotide disulfide oxidoreductase	XP_013329826.1	<i>R. emersonii</i>	1094	0.0
g5134	hypothetical protein	OJJ35311.1	<i>A. wentii</i>	740	0.0
g5135	hypothetical protein	XP_013329823.1	<i>R. emersonii</i>	254	9e-83
g5136	PKS-NRPS protein	XP_008603175.1	<i>B. bassiana</i>	2927	0.0
g5137	hypothetical protein	OBT75938.1	<i>Pseudogymnoascus sp.</i>	501	3e-175
g5138	Zn(II)2-Cys6 binuclear cluster domain-like protein	PNY25474.1	<i>T. capitatum</i>	234	9e-66
g5139	Phenylacetate 2-hydroxylase	XP_013329822.1	<i>R. emersonii</i>	975	0.0

Table 11: Cluster 21 top BLAST hits

Gene	pHMM hit	smCOG	MiBiG hit	Species
g5134		major facilitator transporter SMCOG1106	Communesin	<i>Penicillium expansum</i>
g5135		putative carboxymuconolactone decarboxylase SMCOG1298		
g5136	PP-binding	Beta-ketoacyl synthase SMCOG1022	Cytochalasin	<i>Aspergillus clavatus</i>
	PKS_AT			
	iterative KS			
	adh_short			
g5137		crotonyl-CoA reductase / alcohol dehydrogenase SMCOG1028	Equisetin	<i>Fusarium heterosporum</i>
g5139	p450	Cytochrome P450 SMCOG1034	Lovastatin	<i>Aspergillus terreus</i>

Table 12: Cluster 21 pHMM hits, smCOG hits, known BGC homology (MiBiG)

1.0.7 Cluster 26

Gene	BLAST hit	Accession no.	Species	Score	E-value
g6601	hypothetical protein	XP_013323428.1	<i>R. emersonii</i>	185	2e-54
g6602	transcription factor Cys6	XP_013329851.1	<i>R. emersonii</i>	1400	0.0
g6603	O-methyltransferase	XP_013329850.1	<i>R. emersonii</i>	684	0.0
g6604	O-methyltransferase	XP_013329850.1	<i>R. emersonii</i>	392	3e-128
g6605	hypothetical protein	XP_013329849.1	<i>R. emersonii</i>	533	0.0
g6606	Cytochrome P450	XP_007785430.1	<i>R. emersonii</i>	671	0.0
g6607	Monoxygenase	XP_013329847.1	<i>R. emersonii</i>	863	0.0
g6608	hypothetical protein	XP_013329846.1	<i>R. emersonii</i>	259	4e-87
g6609	6-deoxyerythronolide-B synthase	XP_013329845.1	<i>R. emersonii</i>	4081	0.0
g6610	hypothetical protein	XP_013329844.1	<i>R. emersonii</i>	520	0.0
g6611	Cytochrome P450	PQE05307.1	<i>Rutstroemia sp.</i>	687	0.0
g6612	hypothetical protein	XP_013329842.1	<i>R. emersonii</i>	688	0.0
g6613	Extracellular cell wall glucanase	XP_013329840.1	<i>R. emersonii</i>	554	0.0

Table 13: Cluster 26 top BLAST hits

Gene	pHMM hit	smCOG	MiBiG hit	Species
g6603		O-methyltransferase SMCOG1042	Aflatoxin	<i>Aspergillus oryzae</i>
g6606	p450	Cytochrome P450 SMCOG1034	Aflatoxin	<i>Aspergillus nomius</i>
g6609	PP-binding	Beta-ketoacyl synthase SMCOG1022	Naphthopyrone	<i>Aspergillus nidulans</i>
	PKS_AT			
	iterative KS			
g6611	p450	Cytochrome P450 SMCOG1034	Yanuthone D	<i>Aspergillus niger</i>
g6612		O-methyltransferase SMCOG1042	Grayanic acid	<i>Cladonia grayi</i>

Table 14: Cluster 26 pHMM hits, smCOG hits, known BGC homology (MiBiG)

1.0.8 Cluster 27

Gene	BLAST hit	Accession no.	Species	Score	E-value
g6638	Disease resistance protein	XP_013323199.1	<i>R. emersonii</i>	302	6e-102
g6639	Ulp1 protease	XP_013323200.1	<i>R. emersonii</i>	1979	0.0
g6640	Ulp1 protease	XP_013323200.1	<i>R. emersonii</i>	718	0.0
g6641	Serine-aspartate repeat containing protein	XP_013323201.1	<i>T. islandicus</i>	562	6e-175
g6642	Uncharacterized protein	XP_013326236.1	<i>R. emersonii</i>	962	0.0
g6643	hypothetical protein	XP_013326235.1	<i>R. emersonii</i>	1405	0.0
g6644	6-deoxyerythronolide-B synthase	XP_013326234.1	<i>R. emersonii</i>	4099	0.0
g6645	Multicopper oxidase	XP_013326233.1	<i>R. emersonii</i>	1109	0.0
g6646	SH3 domain protein (CyK3)	XP_013326232.1	<i>R. emersonii</i>	2011	0.0
g6647	Exopolyphosphatase	XP_013326231.1	<i>R. emersonii</i>	888	0.0

Table 15: Cluster 27 top BLAST hits

Gene	pHMM hit	smCOG	MiBiG hit	Species
g6644	PP-binding	Beta-ketoacyl synthase	Naphthopyrone	Aspergillus nidulans
	PKS_AT			
	iterative KS			
	PF12967			

Table 16: Cluster 27 pHMM hits, smCOG hits, known BGC homology (MiBiG)

1.0.9 Cluster 28

Gene	BLAST hit	Accession no.	Species	Score	E-value
g6920	hypothetical protein	KFA80026.1	<i>S. chartarum</i>	122	2e-30
g6921	cytochrome p450	ORY66548.1	<i>P. vexata</i>	82.8	2e-15
g6922	hypothetical protein	KXL41576.1	<i>A. richmondensis</i>	831	0.0
g6923	Methyltransferase	PQE15806.1	<i>Rutstroemia sp.</i>	365	5e-125
g6924	hypothetical protein	OXS11770.1	<i>A. thermomutatus</i>	332	6e-109
g6925	putative Polyketide synthase	XP_025468994.1	<i>A. sclerotioniger</i>	3320	0.0
g6926	Ankyrin repeat containing domain	OOO09208.1	<i>A. oryzae</i>	425	5e-133
g6927	hypothetical protein	XP_013314938.1	<i>E. xenobiotica</i>	253	2e-82

Table 17: Cluster 28 top BLAST hits

Gene	pHMM hit	smCOG	MiBiG hit	Species
g6921	p450	Cytochrome P450 SMCOG1034		
g6925	PP-binding	Beta-ketoacyl synthase SMCOG1022	Alternapyrone	<i>Alternaria solani</i>
	PKS_AT			
	PKS_KS			
	iterative KS			
g6926		Cytochrome P450 SMCOG1034	Penitrem	<i>Penicillium simplicissimum</i>

Table 18: Cluster 28 pHMM hits, smCOG hits, known BGC homology (MiBiG)

1.0.10 Cluster 29

Gene	BLAST hit	Accession no.	Species	Score	E-value
g7062	Glucose transporter	KKP06396.1	<i>T. harzianum</i>	232	1e-72
g7063	hypothetical protein	XP_013324719.1	<i>R. emersonii</i>	585	2e-15
g7064	hypothetical protein	XP_020124735.1	<i>T. atrovirens</i>	193	4e-57
g7065	FAD binding domain	OCK75290.1	<i>L. palustris</i>	884	0.0
g7066	Type I iterative Polyketide synthase	XP_018134599.1	<i>P. verrucosus</i>	3667	0.0
g7067	Oxidoreductase	KUI53239.1	<i>Valsa mali</i> var.	6777	0.0

Table 19: Cluster 29 top BLAST hits

Gene	pHMM hit	smCOG	MiBiG hit	Species
g7062		sugar transport unit SMCOG1169		
g7063		short-chain dehydrogenase/reductase SDR	Cystomanamides	<i>Cystobacter fuscus</i>
g7065		monooxygenase FAD binding SMCOG1050	Rebeccamycin	<i>Lechevalieria aerocolonigenes</i>
g7066	PP-binding	Beta-ketoacyl synthase SMCOG1022	Fusarubin	<i>Fusarium fujikuroi</i>
	PKS_AT			
	PKS_KS			
	NAD-binding			

Table 20: Cluster 29 pHMM hits, smCOG hits, known BGC homology (MiBiG)

1.0.11 Cluster 30

Gene	BLAST hit	Accession no.	Species	Score	E-value
g7133	fatty acid hydroxylase	GAD95728.1	<i>B. spectabilis</i>	623	0.0
g7134	RNA splicing factor	XP_013330719.1	<i>R. emersonii</i>	839	0.0
g7135	hypothetical protein	XP_013330718.1	<i>R. emersonii</i>	946	0.0
g7136	hypothetical protein	XP_013330717.1	<i>R. emersonii</i>	451	3e-157
g7137	hypothetical protein	XP_013330716.1	<i>R. emersonii</i>	276	8e-93
g7138	hypothetical protein	XP_013330715.1	<i>R. emersonii</i>	553	0.0
g7139	Polyketide synthase	XP_013330714.1	<i>R. emersonii</i>	4249	0.0
g7140	sterigmatocystin O-methyltransferase	XP_013330713.1	<i>R. emersonii</i>	789	0.0

Table 21: Cluster 30 top BLAST hits

Gene	pHMM hit	smCOG	MiBiG hit	Species
g7138		short chain dehydrogenase/ reductase (SDR) SMCOG1001	Charteusin	<i>Streptomyces chartreusis</i>
g7139	PP-binding	Beta-ketoacyl synthase SMCOG1022	Cercosporin	<i>Cercospora nicotianae</i>
	PKS_AT			
	iterative KS			
	PF12697			
g7140		O-methyltransferase SMCOG1042	Fusarubin	<i>Fusarium fujikuroi</i>

Table 22: Cluster 30 pHMM hits, smCOG hits, known BGC homology (MiBiG)

1.0.12 Cluster 34

Gene	BLAST hit	Accession no.	Species	Score	E-value
g7133	fatty acid hydroxylase	GAD95728.1	<i>B. spectabilis</i>	623	0.0
g7134	RNA splicing factor	XP_013330719.1	<i>R. emersonii</i>	839	0.0
g7135	hypothetical protein	XP_013330718.1	<i>R. emersonii</i>	946	0.0
g7136	hypothetical protein	XP_013330717.1	<i>R. emersonii</i>	451	3e-157
g7137	hypothetical protein	XP_013330716.1	<i>R. emersonii</i>	276	8e-93
g7138	hypothetical protein	XP_013330715.1	<i>R. emersonii</i>	553	0.0
g7139	Polyketide synthase	XP_013330714.1	<i>R. emersonii</i>	4249	0.0
g7140	sterigmatocystin O-methyltransferase	XP_013330713.1	<i>R. emersonii</i>	789	0.0

Table 23: Cluster 34 top BLAST hits

Gene	pHMM hit	smCOG	MiBiG hit	Species
g7572		Glutathione-S transferase SMCOG1193	Emercillin	<i>Aspergillus nidulans</i>
g7575	AMP-binding	AMP dependent synthetase SMCOG1002	Emercillin	<i>Aspergillus nidulans</i>
	AMP-binding			
g7577	PP-binding	SMCOG1002 synthase SMCOG1022	Emercillin	<i>Aspergillus nidulans</i>
	PKS_AT			
	iterative KS			
g7578		Metallo-beta- lactamase protein SMCOG1170	Emercillin	<i>Aspergillus nidulans</i>

Table 24: Cluster 34 pHMM hits, smCOG hits, known BGC homology (MiBiG)

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2.0.1 Cluster 5

Gene	BLAST hit	Accession no.	Species	Score	E-value
g1839	Adenylyl cyclase	XP_013329907.1	<i>R. emersonii</i>	452	3e-155
g1840	PfkB carbohydrate kinase	XP_013329908.1	<i>R. emersonii</i>	788	0.0
g1841	hypothetical protein	XP_001268985.1	<i>A. clavatus</i>	163	7e-51
g1842	Ribonuclease III	XP_013329909.1	<i>R. emersonii</i>	787	0.0
g1843	PBSP domain	XP_013329910.1	<i>R. emersonii</i>	565	0.0
g1844	hypothetical protein	XP_013329911.1	<i>R. emersonii</i>	2407	0.0
g1845	Nonribosomal siderophore peptide synthase	XP_013329912.1	<i>R. emersonii</i>	8833	0.0
g1846	hypothetical protein	XP_013329913.1	<i>R. emersonii</i>	1194	0.0
g1847	hypothetical protein	XP_013329914.1	<i>R. emersonii</i>	877	0.0
g1848	ABC transporter	XP_013329915.1	<i>R. emersonii</i>	2538	0.0
g1849	Rho GTPase activator	XP_013329916.1	<i>R. emersonii</i>	1817	0.0
g1450	hypothetical protein	XP_013329917.1	<i>R. emersonii</i>	638	0.0

Table 25: Cluster 5 top BLAST hits

Gene	pHMM hit	smCOG	MiBiG hit	Species
g1840		PfkB domain protein SMCOG1276		
g1845	Condensation	AMP-dependent synthetase SMCOG1002	Epichloenin	<i>Epichloe festucae</i>
	PP-binding			
	AMP-binding			
g1846	AMP-binding	AMP-dependent synthetase SMCOG1002	Fengycin	<i>Bacillus amyloliquefaciens</i>
g1847		putative siderophore biosynthesis protein SMCOG1203	Cupriachelin	<i>Ralstonia eutropha</i>
g1848		ABC transporter related protein SMCOG1288	Sirodesmin	<i>Leptosphaeria maculans.</i>

Table 26: Cluster 5 pHMM hits, smCOG hits, known BGC homology (MiBiG)

2.0.2 Cluster 6

Gene	BLAST hit	Accession no.	Species	Score	E-value
g1943	hypothetical protein	XP_013332566.1	<i>R. emersonii</i>	1277	0.0
g1944	UV-damaged DNA binding protein	XP_013332567.1	<i>R. emersonii</i>	2216	0.0
g1945	hypothetical protein	XP_013332568.1	<i>R. emersonii</i>	1244	0.0
g1946	hypothetical protein	OJJ37726.1	<i>A. wentii</i>	546	0.0
g1947	Cell morphogenesis protein (PAG1)	XP_013326831.1	<i>R. emersonii</i>	5255	0.0
g1948	NADPH-hemoprotein reductase	XP_013325989.1	<i>R. emersonii</i>	1397	0.0

Table 27: Cluster 6 top BLAST hits

Gene	pHMM hit	smCOG	MiBiG hit	Species
g1945	Condensation	AMP-dependent synthetase SMCOG1002	fumiquinazolines	<i>Aspergillus fumigatus</i>
	PP-binding			
	AMP-binding			
g1946		3-hydroxyisobutyrate dehydrogenase SMCOG1100	meilingmycin	<i>Streptomyces nanchangensis</i>

Table 28: Cluster 6 pHMM hits, smCOG hits, known BGC homology (MiBiG)

2.0.3 Cluster 7

Gene	BLAST hit	Accession no.	Species	Score	E-value
g1979	hypothetical protein	XP_013327491.1	<i>R. emersonii</i>	360	5e-119
g1980	hypothetical protein	CRG90445.1	<i>T. islandicus</i>	548	0.0
g1981	Cytochrome b5	PLN77449.1	<i>A. taichungensis</i>	161	4e-50
g1982	mRNA splicing factor RNA helicase	XP_013327492.1	<i>R. emersonii</i>	2198	0.0
g1983	Protein kinase	XP_013327493.1	<i>R. emersonii</i>	1936	0.0
g1984	N-(5-amino-5-carboxypentanoyl)-L-cysteinyl-D-valine synthase	XP_013327495.1	<i>R. emersonii</i>	9455	0.0
g1985	hypothetical protein	XP_013327496.1	<i>R. emersonii</i>	853	0.0
g1986	Palmitoyltransferase	XP_013327497.1	<i>R. emersonii</i>	1358	0.0
g1987	Cyclin-dependent proetin kinase	XP_013327498.1	<i>R. emersonii</i>	562	0.0
g1988	hypothetical protein	XP_013327499.1	<i>R. emersonii</i>	582	0.0
g1989	hypothetical protein	XP_013324144.1	<i>R. emersonii</i>	983	0.0

Table 29: Cluster 7 top BLAST hits

Gene	pHMM hit	smCOG	MiBiG hit	Species
g1983	PKinase	serine/threonine protein kinase SMCOG1033		
g1984	Condensation	AMP-dependent synthetase SMCOG1002	Epichloenin	<i>Epichloe festucae</i>
	PP-binding			
	AMP-binding			
g1985		lysine/ornithine N-monooxygenase SMCOG1080	Cupriachelin	<i>Ralstonia eutropha</i>
g1989		cysteine synthase SMCOG1081	Lipopolysaccharide	<i>Xanthomonas campestris</i>

Table 30: Cluster 7 pHMM hits, smCOG hits, known BGC homology (MiBiG)

2.0.4 Cluster 13

Gene	BLAST hit	Accession no.	Species	Score	E-value
g3718	MFS quinate transporter	XP_013331539.1	<i>R. emersonii</i>	184	2e-53
g3719	Phenylalanine racemase	XP_013331540.1	<i>R. emerosnii</i>	14667	0.0
g3720	2-alkenal reductase	XP_013331541.1	<i>R. emersonii</i>	2769	0.0
g3721	hypothetical protein	XP_013331542.1	<i>R. emersonii</i>	266	5e-87
g3722	CCCH zing finger	XP_013331543.1	<i>R. emersonii</i>	884	0.0
g3723	DNA-directed RNA polymerase III	GAD92677.1	<i>B. spectabilis</i>	358	1e-124
g3724	Cystathione gamma-lyase	XP_013331544.1	<i>R. emersonii</i>	814	0.0

Table 31: Cluster 13 top BLAST hits

Gene	pHMM hit	smCOG	MiBiG hit	Species
g3719	Condensation	AMP-dependent synthetase SMCOG1002	Fungisporin	<i>Penicillium rubens</i>
	PP-binding			
	AMP-binding			
g3720		ABC transporter related protein SMCOG1288	Leucinostatins	<i>Purpureocillium lilacinum</i>
g3724	DegT_DnrJ_EryC1	O-succinylhomoserine sulfhydrylase SMCOG1168	Lipopolysaccharide	<i>Xanthomonas campestris</i>

Table 32: Cluster 13 pHMM hits, smCOG hits, known BGC homology (MiBiG)

Gene	BLAST hit	Accession no.	Species	Score	E-value
g6066	NRPS	OBT60533.1	<i>Pseudogymnoascus sp.</i>	3599	0.0
g6067	G protein-coupled receptor	XP_013329617.1	<i>R. emersonii</i>	743	0.0
g6068	hypothetical protein	XP_013329619.1	<i>R. emersonii</i>	188	2e-58
g6069	hypothetical protein	XP_013332105.1	<i>R. emersonii</i>	323	6e-112
g6070	Oxidoreductase 2OG-Fe(II)	XP_013332106.1	<i>R. emersonii</i>	1195	0.0
g6071	hypothetical protein	XP_013332107.1	<i>R. emersonii</i>	868	0.0
g6072	O-acetylhomoserine (Thiol)-lyase	XP_013332108.1	<i>R. emersonii</i>	558	0.0

Table 33: Cluster 25 top BLAST hits

2.0.5 Cluster 25

Gene	pHMM hit	smCOG	MiBiG hit	Species
g6066	Condensation	AMP-dependent synthetase SMCOG1002	Verlamelin	<i>Lecanicillium sp.</i>
	PP-binding			
	AMP-binding			
g6070	PF12697	alpha/beta hydrolase fold protein SMCOG1036	Pneumocandin	<i>Glarea lozoyensis</i>
	PF00561			
g6071		major facilitator superfamily transporter SMCOG1106		
g6072	DegT_DnrJ_EryC1	O-succinylhomoserine sulphydrylase SMCOG1168	Fusaric acid	Fusarium verticilloides

Table 34: Cluster 25 pHMM hits, smCOG hits, known BGC homology (MiBiG)

3 Terpene Cyclases

3.0.1 Cluster 2

Gene	BLAST hit	Accession no.	Species	Score	E-value
g176	Cysteien-tRNA synthetase	XP_001274092.1	<i>A. clavatus</i>	1382	0.0
g177	Transaldolase	XP_013327314.1	<i>R. emerosnii</i>	504	1e-178
g178	PQ loop repeat	XP_013327313.1	<i>R. emersonii</i>	655	2e-58
g179	SGT1 + CS domain	XP_013327312.1	<i>R. emersonii</i>	891	6e-112
g180	Lanosterol synthase	XP_013327311.1	<i>R. emersonii</i>	1515	0.0
g181	hypothetical protein	XP_013327310.1	<i>R. emersonii</i>	292	4e-95
g182	Ubiquitin-ligase	XP_013327309.1	<i>R. emersonii</i>	343	1e-119
g183	hypothetical protein	XP_013327308.1	<i>R. emersonii</i>	934	0.0
g184	Chronological lifespan protein 2 precursor	XP_013327307.1	<i>R. emersonii</i>	237	5e-79
g185	hypothetical protein	XP_013327306.1	<i>R. emersonii</i>	406	7e-141

Table 35: Cluster 2 top BLAST hits

Gene	pHMM hit	smCOG	MiBiG hit	Species
g180	Terpene cyclase		Clavaric Acid	<i>Hypholoma sublateritium</i>

Table 36: Cluster 2 pHMM hits, smCOG hits, known BGC homology (MiBiG)

3.0.2 Cluster 4

Gene	BLAST hit	Accession no.	Species	Score	E-value
g1049	DNA-directed polymerase	GAD96339.1	<i>B. spectabilis</i>	914	0.0
g1050	hypothetical protein	XP_013330117.1	<i>R. emerosnii</i>	1014	0.0
g1051	DNA J domain	XP_013330116.1	<i>R. emersonii</i>	903	0.0
g1052	Squalene synthase	XP_013330115.1	<i>R. emersonii</i>	873	0.0
g1053	hypothetical protein	RAO65178.1	<i>T. amestolkiae</i>	287	2e-96
g1054	hypothetical protein	XP_013330113.1	<i>R. emersonii</i>	149	4e-95
g1055	hypothetical protein	OOF94898.1	<i>A. carbonarius</i>	175	2e-53

Table 37: Cluster 4 top BLAST hits

Gene	pHMM hit	smCOG	MiBiG hit	Species
g1052	phytoene synthase		Squalestatin	<i>Phoma sp.</i>

Table 38: Cluster 4 pHMM hits, smCOG hits, known BGC homology (MiBiG)

3.0.3 Cluster 10

Gene	BLAST hit	Accession no.	Species	Score	E-value
g2851	MFS transporter	XP_013332210.1	<i>R. emersonii</i>	1672	0.0
g2852	Allergen ASP F7	GAD99797.1	<i>B. spectabilis</i>	196	2e-58
g2853	Terpene Synthase	XP_013324630.1	<i>R. emersonii</i>	637	0.0
g2854	hypothetical protein	XP_013324631.1	<i>R. emersonii</i>	308	2e-102
g2855	Ribonuclease-diphosphate reductase	XP_013324632.1	<i>R. emersonii</i>	1795	0.0

Table 39: Cluster 10 top BLAST hits

Gene	pHMM hit	smCOG	MiBiG hit	Species
g2851		major facilitator transporter SMCOG1106		
g2853	Terpene synthase C	Terpene synthase/cyclase metal-binding domain protein SMCOG1052		

Table 40: Cluster 10 pHMM hits, smCOG hits, known BGC homology (MiBiG)

3.0.4 Cluster 14

Gene	BLAST hit	Accession no.	Species	Score	E-value
g3910	DUF543 domain	XP_013326174.1	<i>R. emersonii</i>	152	3e-46
g3911	Copper activated transcription factor	XP_013326173.1	<i>B. spectabilis</i>	924	0.0
g3912	Mitochondrial outer membrane protein	XP_002146237.1	<i>T. marneffeii</i>	441	4e-153
g3913	hypothetical protein	XP_013326171.1	<i>R. emersonii</i>	420	3e-145
g3914	Cell division control protein	XP_013326170.1	<i>R. emersonii</i>	564	0.0
g3915	Dimethylallyltranstransferase	XP_013326169.1	<i>R. emersonii</i>	701	0.0
g3916	hypothetical protein	XP_013326168.1	<i>R. emersonii</i>	139	3e-37
g3917	hypothetical protein	KEY76747.1	<i>A. fumigatus</i>	354	3e-121
g3918	predicted protein	GAD98384.1	<i>B. spectabilis</i>	280	5e-89

Table 41: Cluster 14 top BLAST hits

Gene	pHMM hit	smCOG	MiBiG hit	Species
g3913		methyltransferase SMCOG1089		
g3915	fung_ggps	Polyprenyl synthase SMCOG1182	Aflatrem	<i>Aspergillus flavus</i>
	fung_ggps2			

Table 42: Cluster 14 pHMM hits, smCOG hits, known BGC homology (MiBiG)

3.0.5 Cluster 22

Gene	BLAST hit	Accession no.	Species	Score	E-value
g5372	hypothetical protein	XP_015404725.1	<i>A. nomius</i>	295	1e-93
g5373	hypothetical protein	XP_013327864.1	<i>R. emersonii</i>	896	0.0
g5374	Ran-interacting protein	XP_013327865.1	<i>R. emersonii</i>	437	8e-155
g5375	SprT metallopeptidase	XP_013327866.1	<i>R. emersonii</i>	1063	3e-121

Table 43: Cluster 22 pHMM hits, smCOG hits, known BGC homology (MiBiG)

Gene	pHMM hit	smCOG	MiBiG hit	Species
g5372	Terpene synthase C	Terpene synthase/cyclase metal-binding domain protein SMC0G1052	Botrydial	<i>Botrytis cinerea</i>

Table 44: Cluster 22 pHMM hits, smCOG hits, known BGC homology (MiBiG)

4 DMATs (Indole)

4.0.1 Cluster 23

Gene	BLAST hit	Accession no.	Species	Score	E-value
g5523	hypothetical protein	XP_013322741.1	<i>R. emersonii</i>	319	6e-104
g5524	beta-calactosidase	KFG84136.1	<i>M. anisopliae</i>	653	0.0
g5525	7-dimethylallyltryptophan synthase	XP_013327865.1	<i>R. emersonii</i>	775	0.0
g5526	Nitrogen assimilation transcription factor	XP_013322737.1	<i>R. emersonii</i>	1168	0.0
g5527	Adolase	XP_001397356.1	<i>A. niger</i>	531	0.0
g5528	Quinone oxidoreductase	XP_025403059.1	<i>A. heteromorphus</i>	540	0.0
g5529	2-pyrone-4,6-dicarboxylate lactonase	XP_013330163.1	<i>R. emersonii</i>	573	0.0
g5530	hypothetical protein	XP_013330164.1	<i>R. emersonii</i>	130	1e-33

Table 45: Cluster 23 top BLAST hits

Gene	pHMM hit	smCOG	MiBiG hit	Species
g5372	Terpene synthase C	Terpene synthase/cyclase metal-binding domain protein SMC0G1052	Botrydial	<i>Botrytis cinerea</i>

Table 46: Cluster 23 pHMM hits, smCOG hits, known BGC homology (MiBiG)

5 PKS-NRPS Hybrids

5.0.1 Cluster 3

Gene	BLAST hit	Accession no.	Species	Score	E-value
g762	PH domain	XP_013330940.1	<i>R. emersonii</i>	1832	0.0
g763	Signal peptidase I	XP_013330939.1	<i>R. emersonii</i>	432	3e-150
g764	LRP16 family protein	XP_013330938.1	<i>R. emersonii</i>	535	0.0
g765	GNAT N-acetyltransferase	XP_013330937.1	<i>R. emersonii</i>	296	5e-99
g766	von Willebrand domain	XP_013330936.1	<i>R. emersonii</i>	1481	0.0
g767	Hybrid NRPS/PKS	XP_013324710.1	<i>R. emersonii</i>	6320	0.0
g768	cytochrome p450 monooxygenase	XP_013324711.1	<i>R. emersonii</i>	1049	0.0
g769	Alcohol Dehydrogenase	XP_013324712.1	<i>R. emersonii</i>	639	0.0
g770	Solid-state culture protein	XP_013330980.1	<i>R. emersonii</i>	432	7e-149
g771	HET domain	XP_013323138.1	<i>R. emersonii</i>	1216	0.0
g772	Fungal specific transcription factor	XP_013323136.1	<i>R. emersonii</i>	1462	0.0
g773	ATP-binding cassette multidrug transporter	XP_013323135.1	<i>R. eemrsonii</i>	3008	0.0

Table 47: Cluster 3 top BLAST hits

Gene	pHMM hit	smCOG	MiBiG hit	Species
g767	Condensation	Beta-ketoacyl synthase SMCOG1022	Cytochalasin	<i>Aspergillus clavatus</i>
	PP-binding			
	AMP-binding			
	PKS_AT			
	iterative KS			
	adh_short			
	NAD-binding			
g768	p450	Cytochrome P450 SMCOG1034	Bassianolide	<i>Beauveria bassiana</i>
g769		crotonyl-CoA reductase / alcohol dehydrogenase SMCOG1028	Lovastatin	<i>Aspergillus terreus</i>
g773		ABC transporter ATP-binding protein SMCOG1000	Patulin	<i>Penicillium expansum</i>

Table 48: Cluster 3 pHMM hits, smCOG hits, known BGC homology (MiBiG)

5.0.2 Cluster 16

Gene	BLAST hit	Accession no.	Species	Score	E-value
g4203	hypothetical protein	XP_001389467.2	<i>A. niger</i>	1025	0.0
g4204	hypothetical protein	XP_013331297.1	<i>R. emersonii</i>	698	0.0
g4205	translation initiation factor subunit eIF2B-gamma	XP_013331296.1	<i>R. emersonii</i>	1201	0.0
g4206	hypothetical protein	XP_013331295.1	<i>R. emersonii</i>	707	0.0
g4207	Polyketide synthase	XP_013330927.1	<i>R. emersonii</i>	7583	0.0
g4208	hypothetical protein	XP_013330928.1	<i>R. emersonii</i>	629	0.0
g4209	O-methyltransferase	XP_013330929.1	<i>R. emersonii</i>	768	0.0
g4210	hypothetical protein	KIM92880.1	<i>O. maius</i>	677	0.0
g4211	uncharacterized protein	XP_013326761.1	<i>R. emersonii</i>	1051	7e-149
g4212	Fungal specific transcription factor	XP_013326762.1	<i>R. emersonii</i>	1305	0.0
g4213	hypothetical protein	XP_013326763.1	<i>R. emersonii</i>	863	0.0

Table 49: Cluster 16 top BLAST hits

Gene	pHMM hit	smCOG	MiBiG hit	Species
g4205				
g4207	Condensation	Beta-ketoacyl synthase SMCOG1022	Cytochalasin	<i>Aspergillus clavatus</i>
	PP-binding			
	AMP-binding			
	PKS_AT		Pneumocandin	<i>Glarea lozoyensis</i>
	iterative KS adh_short			
g4209			Fusaric acid	<i>Fusarium verticilloides</i>
g4210	p450	Cytochrome P450 SMCOG1034	Bassianolide	<i>Beauveria bassiana</i>
g4211		crotonyl-CoA reductase / alcohol dehydrogenase SMCOG1028	Lovastatin	<i>Aspergillus terreus</i>
g773		ABC transporter ATP-binding protein SMCOG1000	Patulin	<i>Penicillium expansum</i>

Table 50: Cluster 16 pHMM hits, smCOG hits, known BGC homology (MiBiG)

5.0.3 Cluster 32

No BLAST hits were returned for cluster 32.

Gene	pHMM hit	smCOG	MiBiG hit	Species
g5372	Terpene synthase C	Terpene synthase/cyclase metal-binding domain protein SMCOG1052	Botrydial	<i>Botrytis cinerea</i>

Table 51: Cluster 32 pHMM hits, smCOG hits, known BGC homology (MiBiG)

6 Other

6.0.1 Cluster 1

Gene	BLAST hit	Accession no.	Species	Score	E-value
g124	hypothetical protein	PGH37011.1	<i>E. crescens</i>	239	7e-71
g125	Ribonuclease	XP_013327337.1	<i>R. emersonii</i>	647	0.0
g126	Mannosyltransferase	XP_013327334.1	<i>R. emersonii</i>	1522	0.0
g127	hypothetical protein	XP_013327333.1	<i>R. emersonii</i>	613	0.0
g128	MFS transporter	XP_013327332.1	<i>R. emersonii</i>	909	0.0
g129	putative NRPS	XP_013327331.1	<i>R. emersonii</i>	990	0.0
g130	Cytoplasmic dynein 1	CRG92160.1	<i>T. islandicus</i>	1150	0.0
g131	hypothetical protein	OXS07106.1	<i>A. thermomutatus</i>	150	2e-45
g132	COP9 signalosome	XP_013327329.1	<i>R. emersonii</i>	458	8e-161
g133	dolichyl-diphosphooligosaccharide-protein-glycosyltransferase	CRG92163.1	<i>T. islandicus</i>	1328	0.0
g134	Oxidoreductase	XP_013327327.1	<i>R. emersonii</i>	482	3e-170
g135	hypothetical protein	RAO72425.1	<i>T. amestolkiae</i>	135	9e-37
g136	hypothetical protein	XP_013327324.1	<i>R. emersonii</i>	430	1e-148

Table 52: Cluster 1 top BLAST hits

Gene	pHMM hit	smCOG	MiBiG hit	Species
g125		methyltransferase SMCOG1089	Nivalenol	<i>Fusarium sporotrichioides</i>
g128		major facilitator transporter SMCOG1106	Herboxidiene	<i>Streptomyces chromofuscus</i>
g129	PP-binding	Cytochrome P450 SMCOG1034	Bassianolide	<i>Beauveria bassiana</i>
	AMP-binding			
	PF12697			
g134	adh_short	short-chain dehydrogenase/reductase SDR SMCOG1034	Citrinin	<i>Monascus ruber</i>
	polysacc_synth_2			

Table 53: Cluster 1 pHMM hits, smCOG hits and known BGC homology (MiBiG)

6.0.2 Cluster 8

Gene	BLAST hit	Accession no.	Species	Score	E-value
g2122	Histone Acetyltransferase	XP_013328144.1	<i>R. emersonii</i>	2203	0.0
g2123	Ser/Threonine kinase	XP_013328145.1	<i>R. emersonii</i>	1037	0.0
g2124	Peptidyl Isomerase	XP_013328146.1	<i>R. emersonii</i>	740	0.0
g2125	DNA damage repair Mus42	XP_013328147.1	<i>R. emersonii</i>	2048	0.0
g2126	L-aminoadipate-semialdehyde dehydrogenase	XP_013328148.1	<i>R. emersonii</i>	1947	0.0
g2127	C6 transcription factor	XP_002340816.1	<i>T. stipitatus</i>	939	0.0
g2128	hypothetical protein	CRG84517.1	<i>T. islandicus</i>	57	2e-06
g2129	C6 finger domain	XP_013328151.1	<i>R. emersonii</i>	211	1e-67
g2130	RNA helicase	XP_013328153.1	<i>R. emersonii</i>	1340	0.0
g2131	tRNA methyltransfrase	XP_013328154.1	<i>R. emersonii</i>	750	0.0

Table 54: Cluster 8 top BLAST hits

Gene	pHMM hit	smCOG	MiBiG hit	Species
g2123	Pkinase	serine/threonine protein kinase SMCOG1030		
g2126	PP-binding	AMP-dependent synthetase and ligase SMCOG1002	LL-Z1272	<i>Stachybotrys bisbyi</i>
	AMP-binding			
	NAD-binding			

Table 55: Cluster 8 pHMM hits, smCOG hits, known BGC homology (MiBiG)

Gene	BLAST hit	Accession no.	Species	Score	E-value
g3291	Plasma membrane fusion protein	XP_013327121.1	<i>R. emersonii</i>	1396	0.0
g3292	Xanthine dehydrogenase	XP_013327122.1	<i>R. emersonii</i>	2761	0.0
g3293	hypothetical protein	XP_013327123.1	<i>R. emersonii</i>	1153	0.0
g3294	L-aminoadipate-semialdehyde dehydrogenase	XP_013327124.1	<i>R. emersonii</i>	2803	0.0
g3295	hypothetical protein	XP_013327125.1	<i>R. emersonii</i>	633	0.0
g3296	hypothetical protein	XP_013327126.1	<i>R. emersonii</i>	2293	0.0
g3297	HMG box transcriptional regulator	XP_013327127.1	<i>R. emersonii</i>	1221	0.0
g3298	hypothetical protein	XP_013327128.1	<i>R. emersonii</i>	582	0.0
g3299	40s ribosomal protein	XP_013327129.1	<i>R. emersonii</i>	465	2e-165

Table 56: Cluster 11 top BLAST hits

6.0.3 Cluster 11

Gene	pHMM hit	smCOG	MiBiG hit	Species
g3292		aldehyde oxidase and xanthine dehydrogenase SMCOG1293		
g3294	PP-binding	condensation domain-containing protein SMCOG1127	Nostocyclopeptide	<i>Nostoc sp.</i>
	AMP-binding			
	NAD-binding			

Table 57: Cluster 11 pHMM hits, smCOG hits, known BGC homology (MiBiG)

6.0.4 Cluster 18

Gene	BLAST hit	Accession no.	Species	Score	E-value
g4401	hypothetical protein	XP_013329605.1	<i>R. emersonii</i>	847	0.0
g4402	hypothetical protein	XP_013329606.1	<i>R. emersonii</i>	2761	0.0
g4403	Isocrate dehydrogenase NADP(+)	XP_013329607.1	<i>R. emersonii</i>	914	0.0
g4404	C1 tetrahydrofolate synthase	XP_013329608.1	<i>R. emersonii</i>	3479	0.0
g4405	hypothetical protein	XP_013329609.1	<i>R. emersonii</i>	633	0.0
g4406	hypothetical protein	XP_013329610.1	<i>R. emersonii</i>	556	0.0
g4407	translation initiation factor 3 subunit 2i	XP_002488027.1	<i>T. stipitatus</i>	662	0.0
g4408	Multiprotein-bridging factor 1	XP_013323547.1	<i>R. emersonii</i>	304	2e-104
g4409	SH3 domain protein	XP_013323546.1	<i>R. emersonii</i>	400	1e-139
g4410	hypothetical protein	XP_013323545.1	<i>R. emersonii</i>	573	0.0

Table 58: Cluster 18 top BLAST hits

Gene	pHMM hit	smCOG	MiBiG hit	Species
g4401		mandelate racemase/ muconate lactonizing enzyme SMCOG1268		
g4404	PP-binding AMP-binding	AMP-dependent synthetase / ligase SMCOG1002	Terrequinone	<i>Aspergillus nidulans</i>

Table 59: Cluster 18 pHMM hits, smCOG hits, known BGC homology (MiBiG)

6.1 Cluster 19

Gene	BLAST hit	Accession no.	Species	Score	E-value
g4552	Pc16g11810	XP_002561482.1	<i>P. rubens</i>	92.8	3e-19
g4553	hypothetical protein	XP_013331025.1	<i>R. emersonii</i>	943	0.0
g4554	hypothetical protein	XP_013331024.1	<i>R. emersonii</i>	627	0.0
g4555	hypothetical protein	XP_013331023.1	<i>R. emersonii</i>	1926	0.0
g4556	glycoside hydrolase	OCK99381.1	<i>C. geophilum</i>	863	0.0
g4557	hypothetical protein	XP_013329610.1	<i>R. emersonii</i>	556	0.0
g4558	trichothecene efflux pump	AUB51322.1	<i>T. hypoxylon</i>	662	0.0
g4559	Cyclohexane monooxygenase	XP_013331019.1	<i>R. emersonii</i>	1006	0.0

Table 60: Cluster 19 top BLAST hits

Gene	pHMM hit	smCOG	MiBiG hit	Species
g4553		major facilitator transporter SMCOG1106	Diazepinomicin	<i>Micromonospora sp.</i>
g4554	PP-binding	AMP-dependent synthetase / ligase SMCOG1002	Fusaric Acid	<i>Fusarium verticillioides</i>
	AMP-binding			
	NAD-binding			

Table 61: Cluster 19 pHMM hits, smCOG hits, known BGC homology (MiBiG)

6.1.1 Cluster 24

Gene	BLAST hit	Accession no.	Species	Score	E-value
g6011	Pc16g11810	XP_002561482.1	<i>P. rubens</i>	92.8	3e-19
g6012	hypothetical protein	XP_013331025.1	<i>R. emersonii</i>	943	0.0
g6013	hypothetical protein	XP_013331024.1	<i>R. emersonii</i>	627	0.0
g6014	hypothetical protein	XP_013331023.1	<i>R. emersonii</i>	1926	0.0
g6015	glycoside hydrolase	OCK99381.1	<i>C. geophilum</i>	863	0.0
g6016	hypothetical protein	XP_013329610.1	<i>R. emersonii</i>	556	0.0
g6017	trichothecene efflux pump	AUB51322.1	<i>T. hypoxylon</i>	662	0.0
g6018	Cyclohexane monooxygenase	XP_013331019.1	<i>R. emersonii</i>	1006	0.0

Table 62: Cluster 24 top BLAST hits

Gene	pHMM hit	smCOG	MiBiG hit	Species
g6012	p450	Cytochrome P450 SMCOG1034	Leucinostatin A	<i>Purpureocillium lilacinum</i>
g6013	Pkinase	serine/threonine protein kinase SMCOG1030		
g6017	AMP-binding	AMP-dependent synthetase and ligase SMCOG1002	Ochratoxin A	<i>Penicillium nordicum</i>
	NAD-binding			
	PP-binding			
g6018		transketolase SMCOG1204	Sch47554	<i>Streptomyces sp.</i>

Table 63: Cluster 24 pHMM hits, smCOG hits, known BGC homology (MiBiG)

6.1.2 Cluster 31

Gene	BLAST hit	Accession no.	Species	Score	E-value
g7177	NRPS	XP_013326109.1	<i>R. emersonii</i>	996	0.0
g7178	hypothetical protein	XP_013331405.1	<i>R. emersonii</i>	68.9	3e-11
g7179	Flavin-containing monooxygenase	XP_013331401.1	<i>R. emersonii</i>	910	0.0
g7180	MFS sugar transporter	XP_013331399.1	<i>R. emersonii</i>	1041	0.0
g7181	hypothetical protein	XP_013331398.1	<i>C. geophilum</i>	619	0.0

Table 64: Cluster 31 top BLAST hits

Gene	pHMM hit	smCOG	MiBiG hit	Species
g7177	AMP-binding	AMP-dependent synthetase and ligase SMCOG1002	Myxalamid	<i>Stigmatella aurantiaca</i>
	NAD-binding			
	PP-binding			
g7180		sugar transport protein SMCOG1169	Sordarin	<i>Sordaria araneosa</i>

Table 65: Cluster 31 pHMM hits, smCOG hits, known BGC homology (MiBiG)

6.1.3 Cluster 33

Gene	BLAST hit	Accession no.	Species	Score	E-value
g7516	serine/threonine kinase	XP_013324275.1	<i>R. emersonii</i>	893	0.0
g7517	Chromosome segregation protein SudA	XP_013329273.1	<i>R. emersonii</i>	2211	0.0
g7518	hypothetical protein	XP_013329274.1	<i>R. emersonii</i>	376	8e-131
g7519	Cytochrome-b5 reductase	XP_013329275.1	<i>R. emersonii</i>	621	0.0
g7520	hypothetical protein	XP_013329276.1	<i>R. emersonii</i>	651	0.0
g7521	Arginine-tRNA ligase	XP_013329277.1	<i>R. emersonii</i>	1313	0.0
g7522	hypothetical protein	XP_013329278.1	<i>R. emersonii</i>	323	3e-107
g7523	hypothetical protein	XP_013329279.1	<i>R. emersonii</i>	589	0.0
g7524	NRPS-like enzyme	XP_013329282.1	<i>R. emersonii</i>	1654	0.0
g7525	HET-s/LopB domain	XP_002148962.1	<i>T. marneffei</i>	258	9e-81

Table 66: Cluster 33 top BLAST hits

Gene	pHMM hit	smCOG	MiBiG hit	Species
g7524	AMP-binding	AMP-dependent synthetase and ligase SMCOG1002	Fusaric Acid	<i>Fusarium verticillioides</i>
	NAD-binding			

Table 67: Cluster 33 pHMM hits, smCOG hits, known BGC homology (MiBiG)

Gene	BLAST hit	Accession no.	Species	Score	E-value
g8345	NRPS	XP_013326109.1	<i>R. emersonii</i>	2055	0.0
g8346	hypothetical protein	XP_013326108.1	<i>R. emersonii</i>	405	7e-142

Table 68: Cluster 35 top BLAST hits

Gene	pHMM hit	smCOG	MiBiG hit	Species
g8345	AMP-binding	AMP-dependent synthetase and ligase SMCOG1002	4,4'-piperazine- 2,5-diyl-dimethyl- bis-phenol	<i>Aspergillus flavus</i>
	NAD-binding			
	PP-binding			

Table 69: Cluster 35 pHMM hits, smCOG hits, known BGC homology (MiBiG)

6.1.4 Cluster 35