

Table S4

	Query id	Database match id	percentage identity	align length	evaluate	pathway	product domain class
PKS	MAG.005-P10260_5_0_825_1205	EpoD_Q9L8C7_4mod	59		382	8,00E-125 epothilone	modular
PKS	MAG.005-P13942_1_3_544_938	AveA2_Q9S0R7_3mod	43		430	6,00E-79 avermectin	modular
PKS	MAG.005-P25347_1_20_40_457	EpoE_Q9L8C6_1mod	61		422	2,00E-143 epothilone	modular
PKS	MAG.005-P3213_4_11_18_463	LnMJ_AF484556_2T	39		453	2,00E-82 leinamycin	trans
PKS	MAG.005-P32468_3_8_1429_1842	EpoA_Q9L8C9_mod	52		429	2,00E-107 epothilone	modular
PKS	MAG.005-P40732_4_7_363_832	ArsA_Azotobacter_PUFA	46		468	3,00E-92 alkylresorcinol	PUFA
PKS	MAG.005-P63942_2_40_31_452	EpoA_Q9L8C9_mod	57		427	4,00E-113 epothilone	modular
hgls-PK	MAG.005-P72308_4_33_12_468	PfaA_Shewanella_PUFA	55		458	1,00E-137 polyunsaturated	fatty acid PUFA
hgls-PK	MAG.005-P13690_4_1_23_454	PfaC_Shewanella_PUFA	43		253	6,00E-49 polyunsaturated	fatty acid PUFA
hgls-PK	MAG.005-P34834_2_30_750_1185	ArsA_Azotobacter_PUFA	52		451	9,00E-99 alkylresorcinol	fatty acid PUFA
PKS	MAG.032-P16732_4_11_24_471	LnMJ_AF484556_4T	45		453	3,00E-109 leinamycin	trans
PKS-NRPS	MAG.032-P44098_3_0_1_275	EpoC_Q9L8C8_H	62		274	1,00E-100 epothilone	hybridKS
PKS-NRPS	MAG.032-P55014_5_1_14_441	EpoC_Q9L8C8_H	57		428	1,00E-151 epothilone	hybridKS
PKS-NRPS	MAG.032-P40879_3_0_24_458	yersi_YP_070123_H	60		435	2,00E-159 yersiniabactin	hybridKS
NRPS	MAG.032-P16732_6_8_74_376	bleom9_C2_cyc	44		298	5,00E-63 bleomycin	cyc
NRPS	MAG.032-P20996_2_0_1059_1362	yersi2_C1_cyc	56		296	1,00E-82 yersiniabactin	cyc
NRPS	MAG.032-P40879_1_0_664_965	yersi1_C2_cyc	49		293	1,00E-60 yersiniabactin	cyc
NRPS	MAG.032-P60072_4_1_109_408	yersi1_C1_cyc	52		294	1,00E-82 yersiniabactin	cyc
NRPS	MAG.032-P64469_1_0_80_381	bleom9_C3_cyc	45		294	7,00E-61 bleomycin	cyc