Bacterial Death and TRADD-N domains help define novel apoptosis and immunity mechanisms shared by prokaryotes and metazoans

Figure 2-Source data 1

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1. Source data. Gene neighborhoods and domain architectures of the bacterial Death-like domain 3 (bDLD3)

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
ADE14635.1	<-NTP_transferase<-?||?→?→||<-?||HKD→ TIR+bDLD3→ *bDLD3+nSTAND1+FGS*→	TIR+bDLD3	799	Nhal_1492	Gammaproteobacteria	Nitrosococcus halophilus Nc 4	protein of unknown function DUF323 [Nitrosococcus halophilus Nc 4].	GCA_000024725.1
ADE14636.1	*bDLD3→		246	Nhal_1493	Gammaproteobacteria	Nitrosococcus halophilus Nc 4	TIR protein [Nitrosococcus halophilus Nc 4].	GCA_000024725.1
AMV23994.1	<-HEPN<-?||?→?→ bDLD3→*?*→ *McrA-NTD+HNH2*→*?*→||<-*?*||*?*→*?*→*?*→ *PNPase+TRADDN+CASPASE+bDLD3*→ APATPase+TPR+TPR→	bDLD3	816	VT84_06335	Planctomycetes	Gemmata sp. SH-PL17	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase [Gemmata sp. SH-PL17].	GCA_001610855.1
AMV24002.1	*bDLD3→		518	VT84_06375	Planctomycetes	Gemmata sp. SH-PL17	hypothetical protein VT84_06375 [Gemmata sp. SH-PL17].	GCA_001610855.1
APA97850.1	<-SIG+NPCBM<-TM+TM+TM+TM||PNPase+bDLD3→ *bDLD3+NPCBM*→ TM+NPCBM→||<-LD-peptidase<-?<-HD||?→ GNTR-HTH→	PNPase+bDLD3	349	mtnN	Actinobacteria	Nocardia seriolae	Adenosylhomocysteine nucleosidase [Nocardia seriolae].	GCA_001865855.1
APA97851.1	*bDLD3→		217	NS506_03802	Actinobacteria	Nocardia seriolae	hypothetical protein NS506_03802 [Nocardia seriolae].	GCA_001865855.1
BAW07945.1	<-SIG+NPCBM||?→ PNPase+bDLD3*→ bDLD3+NPCBM→ TM+NPCBM→||<-LD-peptidase<-?<-HD||?→ GNTR-HTH→	PNPase+bDLD3	245	NSERUTF1_4813	Actinobacteria	Nocardia seriolae	conserved hypothetical protein [Nocardia seriolae].	GCA_002356035.1
BAY07541.1	Uma2→||<-?<-?||EAD9+CASPASE+bDLD3*→ APATPase+BetaPropeller→?→?→||<-?<-?||Pkinase→	EAD9+CASPASE+bDLD3	391	NIES2098_06580	Cyanobacteria	Calothrix sp. NIES-2098	hypothetical protein NIES2098_06580 [Calothrix sp. NIES-2098].	GCA_002368175.1
ETW99001.1	bDLD3+nSTAND1+FGS*→	bDLD3+nSTAND1+FGS	783	ETSY1_16630	Nitrospinae/Tectomicrobia group	Candidatus Entotheonella factor	hypothetical protein ETSY1_16630 [Candidatus Entotheonella factor].	GCA_000522425.1
ETW99008.1	bDLD3+NACHT*→	bDLD3+NACHT	326	ETSY1_16605	Nitrospinae/Tectomicrobia group	Candidatus Entotheonella factor	hypothetical protein ETSY1_16605 [Candidatus Entotheonella factor].	GCA_000522425.1
ETX07101.1	TIR→ bDLD3*→||<-FGS	bDLD3	125	ETSY2_13175	Nitrospinae/Tectomicrobia group	Candidatus Entotheonella gemina	hypothetical protein ETSY2_13175 [Candidatus Entotheonella gemina].	GCA_000522445.1
ETX07918.1	bDLD3+NACHT+FGS*→	bDLD3+NACHT+FGS	922	ETSY2_08400	Nitrospinae/Tectomicrobia group	Candidatus Entotheonella gemina	hypothetical protein ETSY2_08400 [Candidatus Entotheonella gemina].	GCA_000522445.1
GAX40011.1	SIG+CASPASE→?→||<-?||?→||<-?||?→ CASPASE+bDLD3*→ APATPase+BetaPropeller→||<-?<-?||Calcineurin→ Calcineurin→||<-BetaPropeller<-DNAJ+TPR	CASPASE+bDLD3	292	NIES4075_09730	Cyanobacteria	Tolypothrix sp. NIES-4075	hypothetical protein NIES4075_09730 [Tolypothrix sp. NIES-4075].	GCA_002218085.1
HID99200.1	Trypsin+bDLD3→ *bDLD3+iSTAND*→ MoxR-AAA→	Trypsin+bDLD3	390	EYP59_02780	Gammaproteobacteria	Thiotrichaceae bacterium	TPA: hypothetical protein EYP59_02780 [Thiotrichaceae bacterium].	-
HID99201.1	*bDLD3→		317	EYP59_02785	Gammaproteobacteria	Thiotrichaceae bacterium	TPA: serine protease [Thiotrichaceae bacterium].	-
HIE01287.1	bDLD3→ *bDLD3+ClpABC*→	bDLD3	679	EYP59_13525	Gammaproteobacteria	Thiotrichaceae bacterium	TPA: AAA family ATPase, partial [Thiotrichaceae bacterium].	-
HIE01288.1	*bDLD3→		232	EYP59_13530	Gammaproteobacteria	Thiotrichaceae bacterium	TPA: hypothetical protein EYP59_13530 [Thiotrichaceae bacterium].	-
NER21298.1	<-HAD||?→ PNPase+bDLD3*→	PNPase+bDLD3	346	F6J96_11435	Cyanobacteria	Symploca sp. SIO1C2	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase [Symploca sp. SIO1C2].	-
NES00173.1	PNPase+bDLD3→ bDLD3*→	bDLD3	58	F6J86_41320	Cyanobacteria	Symploca sp. SIO1B1	hypothetical protein F6J86_41320 [Symploca sp. SIO1B1].	-
NES19675.1	bDLD3→ *bDLD3+APATPase+TPR*→	bDLD3	911	F6K41_12275	Cyanobacteria	Symploca sp. SIO3E6	hypothetical protein F6K41_12275 [Symploca sp. SIO3E6].	-
NES19676.1	bDLD3*→	bDLD3	72	F6K41_12280	Cyanobacteria	Symploca sp. SIO3E6	hypothetical protein F6K41_12280, partial [Symploca sp. SIO3E6].	-

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
NET43317.1	Trypco2→ TCAD4+CASPASE+bDLD3→ *SIG+bDLD3+APATPase*→||<-?||?→||<-?<-?<-?<-?<-Pkinase	TCAD4+CASPASE+bDLD3	537	F6K15_16045	Cyanobacteria	Okeania sp. SIO2B3	CHAT domain-containing protein [Okeania sp. SIO2B3].	-
NET43318.1	SIG+bDLD3+APATPase*→	SIG+bDLD3+APATPase	241	F6K15_16050	Cyanobacteria	Okeania sp. SIO2B3	hypothetical protein F6K15_16050 [Okeania sp. SIO2B3].	-
NET60851.1	PNPase+bDLD3→ *bDLD3+FGS*→||<-HAD	PNPase+bDLD3	361	F6K47_33365	Cyanobacteria	Symploca sp. SIO2E6	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase [Symploca sp. SIO2E6].	-
NET60852.1	bDLD3+FGS*→	bDLD3+FGS	414	F6K47_33370	Cyanobacteria	Symploca sp. SIO2E6	formylglycine-generating enzyme family protein [Symploca sp. SIO2E6].	-
NJL79331.1	PNPase+bDLD3*→ TM+TM+TM+TM→||<-PSE<-PSE<-PsaD	PNPase+bDLD3	392	HC917_11650	Cyanobacteria	Richelia sp. SM2_1_7	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase [Richelia sp. SM2_1_7].	-
NJM20757.1	SIG+Band_7→||<-?||?→?→?→?→ PNPase+bDLD3*→ TM+TM+TM+TM→||<-PSE<-?<-PsaD	PNPase+bDLD3	687	HC907_19595	Cyanobacteria	Richelia sp. SM1_7_0	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase [Richelia sp. SM1_7_0].	-
NJN10092.1	<-PP2C+TM||?→ SIG+Band_7→||<-?||?→?→?→ PNPase+bDLD3*→ TM+TM+TM+TM→||<-PSE<-?<-PsaD	PNPase+bDLD3	687	HC815_19700	Cyanobacteria	Richelia sp. RM1_1_1	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase [Richelia sp. RM1_1_1].	-
NJO29889.1	SIG+Band_7→||<-?||?→?→?→?→?→ PNPase+bDLD3*→ TM+TM+TM+TM→||<-PSE<-PSE<-PsaD	PNPase+bDLD3	560	HC874_21920	Cyanobacteria	Richelia sp. SL_2_1	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase [Richelia sp. SL_2_1].	-
NJS15985.1	PNPase+bDLD3*→	PNPase+bDLD3	359	HC787_01195	Cyanobacteria	Nostocaceae cyanobacterium CSU_2_110	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase [Nostocaceae cyanobacterium CSU_2_110].	-
OUL27313.1	<-TPR+nSTAND1+BetaPropeller<-AAA_22||EAD9+CASPASE+bDLD3*→ PSE→ APATPase+BetaPropeller→ CASPASE→?→||<-CASPASE+GUN4<-CASPASE	EAD9+CASPASE+bDLD3	391	BV378_11875	Cyanobacteria	Nostoc sp. RF31YmG	hypothetical protein BV378_11875 [Nostoc sp. RF31Y].	GCA_002155185.1
OUL31312.1	Uma2→||<-?<-?<-?<-?<-TPR+nSTAND1+BetaPropeller<-AAA_22||EAD9+CASPASE+bDLD3*→ APATPase+BetaPropeller→	EAD9+CASPASE+bDLD3	398	BV372_20335	Cyanobacteria	Nostoc sp. T09	hypothetical protein BV372_20335 [Nostoc sp. T09].	GCA_002154695.1
OUL35760.1	EAD9+CASPASE+bDLD3*→ PSE→ APATPase+BetaPropeller→||<-?||?→ RelE-ParE→?→?→ RelE-ParE→	EAD9+CASPASE+bDLD3	391	BV375_01415	Cyanobacteria	Nostoc sp. 106C	hypothetical protein BV375_01415 [Nostoc sp. 106C].	GCA_002154725.1
PKW31742.1	Pkinase+bDLD3*→||<-TPR+TPR+Caspase<-vWA-L+TM+CASPASE<-VWA<-MoxR-AAA<-bDLD3+iSTAND2<-?||TCAD9+Pkinase+bDLD3→	Pkinase+bDLD3	501	CLT72_1056	Actinobacteria	Micromonospora sp. CNZ309	hypothetical protein CLT72_1056 [Micromonospora sp. CNZ309].	GCA_002846525.1
RKZ54270.1	CASPASE+APATPase+bDLD3→ *bDLD3+EAD2+Pkinase+TM+TM+TM+TM+TM+TM+TM*→	CASPASE+APATPase+bDLD3	663	DRR00_01560	Gammaproteobacteria	Gammaproteobacteria bacterium	hypothetical protein DRR00_01560 [Gammaproteobacteria bacterium].	GCA_003645185.1
RKZ54271.1	bDLD3+EAD2+Pkinase+TM+TM+TM+TM+TM+TM+TM*→	bDLD3+EAD2+Pkinase+TM+TM+TM+TM+TM+TM+TM	935	DRR00_01565	Gammaproteobacteria	Gammaproteobacteria bacterium	hypothetical protein DRR00_01565 [Gammaproteobacteria bacterium].	GCA_003645185.1
RYZ09240.1	EAD5+CASPASE+bDLD3*→	EAD5+CASPASE+bDLD3	775	EOO73_05625	Deltaproteobacteria	Myxococcales bacterium	caspase family protein [Myxococcales bacterium].	GCA_004193285.1
RZU04509.1	Pkinase+bDLD3*→ bDLD3+TPR→?→?→||<-?||?→||<-?<-BACTERIALFRINGE+TM+TM	Pkinase+bDLD3	594	EV371_0866	Actinobacteria	Plantactinospora sp. CNZ321	hypothetical protein EV371_0866 [Plantactinospora sp. CNZ321].	GCA_004217235.1
SFL94903.1	<-SIG+HAD<-?<-KAP-NTPase||TIR+bDLD3*→ bDLD3+nSTAND1+FGS→||<-?<-NACHT+FGS<-ABhydrolase+bDLD3<-?<-?||LexA-protease→	TIR+bDLD3	254	SAMN05421863_1007111	Betaproteobacteria	Nitrosomonas communis	TIR domain-containing protein [Nitrosomonas communis].	GCA_900114745.1
SPT51846.1	SIG+TM+TM+NACHT+APATPase+TPR+TPR+TPR→||<-?<-?||?→?→?→?→ SIG+bDLD3*→	SIG+bDLD3	301	NCTC11373_02572	Actinobacteria	Actinomadura madurae	Uncharacterised protein [Actinomadura madurae].	GCA_900445005.1
TVR58388.1	TIR+bDLD3→ *bDLD3+nSTAND1+FGS*→?→||<-NACHT+FGS	TIR+bDLD3	802	EA420_17215	Gammaproteobacteria	Candidatus Competibacteraceae bacterium	hypothetical protein EA420_17215 [Candidatus Competibacteraceae bacterium].	GCA_007695245.1
TVR58389.1	TIR+bDLD3*→	TIR+bDLD3	268	EA420_17220	Gammaproteobacteria	Candidatus Competibacteraceae bacterium	toll/interleukin-1 receptor domain-containing protein [Candidatus Competibacteraceae bacterium].	GCA_007695245.1
WP_009738298.1	bDLD3+NACHT+BetaPropeller→ *TPR+TPR+Caspase→||<-Pkinase+bDLD3*	bDLD3+NACHT+BetaPropeller	1268	FRAQA3DRAFT_RS06645	Actinobacteria	Frankia sp. QA3	AAA family ATPase [Frankia sp. QA3].	GCF_000262465.1
WP_009738300.1	Pkinase+bDLD3*→	Pkinase+bDLD3	513	FRAQA3DRAFT_RS06655	Actinobacteria	Frankia sp. QA3	hypothetical protein [Frankia sp. QA3].	GCF_000262465.1

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
WP_030438849.1	PNPase+bDLD3→ *bDLD3+TM→*||<-?<-?<-?<-?<-ACYC	PNPase+bDLD3	254	IH26_RS0125970	Actinobacteria	Actinoplanes subtropicus	hypothetical protein [Actinoplanes subtropicus].	GCF_000721705.1
WP_033090725.1	<-SIG+NPCBM<-TM+TM+TM+TM||?→?→ PNPase+bDLD3→ *bDLD3+NPCBM→* TM+NPCBM→||<-LD-peptidase<-?<-HD||?→ GNTR-HTH→	PNPase+bDLD3	279	NSERUTF1_RS23480	Actinobacteria	Nocardia seriolae	hypothetical protein [Nocardia seriolae].	GCF_002356035.1
WP_038072636.1	PNPase+bDLD3*→ TM+TM+TM+TM→ PSE→||<-?<-?<-PsaD	PNPase+bDLD3	672	HC643_RS13555	Cyanobacteria	Tolypothrix bouteillei	hypothetical protein [Tolypothrix bouteillei].	GCF_000760695.4
WP_044290893.1	<-TCAD10<-?<-?||?→||<-?||?→ bDLD3+APATPase*→ APATPase+BetaPropeller→	bDLD3+APATPase	327	RIV7116_RS11765	Cyanobacteria	Rivularia sp. PCC 7116	hypothetical protein [Rivularia sp. PCC 7116].	GCF_000316665.1
WP_051808508.1	PNPase+bDLD3*→	PNPase+bDLD3	394	IH26_RS0125965	Actinobacteria	Actinoplanes subtropicus	hypothetical protein [Actinoplanes subtropicus].	GCF_000721705.1
WP_051809451.1	PNPase+bDLD3*→	PNPase+bDLD3	413	IH26_RS0141600	Actinobacteria	Actinoplanes subtropicus	hypothetical protein [Actinoplanes subtropicus].	GCF_000721705.1
WP_052086955.1	bDLD3+NPCBM*→	bDLD3+NPCBM	241	NSERUTF1_RS23475	Actinobacteria	Nocardia seriolae	NPCBM/NEW2 domain-containing protein [Nocardia seriolae].	GCF_002356035.1
WP_063628695.1	CASPASE+bDLD3*→ APATPase+BetaPropeller→||<-?||?→ Calcineurin→?→ Calcineurin→	CASPASE+bDLD3	292	TOL9009_RS39910	Cyanobacteria	[Scytonema hofmanni] UTEX B 1581	CHAT domain-containing protein [[Scytonema hofmanni] UTEX B 1581].	GCF_000582685.1
WP_074904183.1	<-LexA-protease||?→?→ ABhydrolase+bDLD3→ *NACHT+FGS→||<-bDLD3+nSTAND1+FGS*<-TIR+bDLD3*	ABhydrolase+bDLD3	363	BM122_RS04970	Betaproteobacteria	Nitrosomonas communis	hypothetical protein [Nitrosomonas communis].	GCF_900114745.1
WP_074904186.1	SIG+bDLD3+nSTAND1+FGS*→	SIG+bDLD3+nSTAND1+FGS	823	BM122_RS04980	Betaproteobacteria	Nitrosomonas communis	SUMF1/EgtB/PvdO family nonheme iron enzyme [Nitrosomonas communis].	GCF_900114745.1
WP_074904188.1	TIR+bDLD3*→	TIR+bDLD3	277	BM122_RS04985	Betaproteobacteria	Nitrosomonas communis	TIR domain-containing protein [Nitrosomonas communis].	GCF_900114745.1
WP_081986291.1	PNPase+bDLD3*→ bDLD3+NPCBM→ TM+NPCBM→||<-LD-peptidase<-?<-HD||?→ GNTR-HTH→	PNPase+bDLD3	285	GL308_RS29360	Actinobacteria	Nocardia seriolae	hypothetical protein [Nocardia seriolae].	GCF_003667075.1
WP_082062736.1	<-SIG+NPCBM<-TM+TM+TM+TM||PNPase+bDLD3*→ bDLD3+NPCBM→ TM+NPCBM→||<-PSE<-?<-HD||?→ GNTR-HTH→	PNPase+bDLD3	397	AOQ36_RS28625	Actinobacteria	Nocardia seriolae	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase [Nocardia seriolae].	GCF_000583715.2
WP_086688304.1	Uma2→||<-?<-?<-?<-?<-TPR+nSTAND1+BetaPropeller<-AAA_22||CASPASE+bDLD3*→	CASPASE+bDLD3	288	BV372_RS20170	Cyanobacteria	Nostoc sp. T09	CHAT domain-containing protein [Nostoc sp. T09].	GCF_002154695.1
WP_086756477.1	CASPASE+bDLD3*→ APATPase+BetaPropeller→||<-?||?→ RelE-ParE→?→?→ RelE-ParE→	CASPASE+bDLD3	303	BV375_RS01380	Cyanobacteria	Nostoc sp. 106C	CHAT domain-containing protein [Nostoc sp. 106C].	GCF_002154725.1
WP_086834185.1	<-TPR+nSTAND1+BetaPropeller<-AAA_22||CASPASE+bDLD3*→ APATPase+BetaPropeller→ CASPASE→?→||<-CASPASE+GUN4<-CASPASE<-?<-CASPASE	CASPASE+bDLD3	325	BV378_RS11765	Cyanobacteria	Nostoc sp. RF31YmG	CHAT domain-containing protein [Nostoc sp. RF31YmG].	GCF_002155185.1
WP_089718394.1	TIR+bDLD3→ *bDLD3+nSTAND1+FGS→*	TIR+bDLD3	798	FLV43_RS07510	Nitrospinae/Tectomicrobia group	Candidatus Entotheonella palauensis	SUMF1/EgtB/PvdO family nonheme iron enzyme [Candidatus Entotheonella palauensis].	GCF_900079105.1
WP_089718395.1	TIR+bDLD3*→	TIR+bDLD3	256	FLV43_RS07515	Nitrospinae/Tectomicrobia group	Candidatus Entotheonella palauensis	TIR domain-containing protein [Candidatus Entotheonella palauensis].	GCF_900079105.1
WP_089941919.1	TIR+bDLD3*→||<-NACHT+FGS<-FxSC	TIR+bDLD3	239	FLV42_RS28560	Nitrospinae/Tectomicrobia group	Candidatus Entotheonella palauensis	toll/interleukin-1 receptor domain-containing protein [Candidatus Entotheonella palauensis].	GCF_900079095.1
WP_091254464.1	NUDIX→?→?→ PNPase+bDLD3*→	PNPase+bDLD3	438	GA0070216_RS32615	Actinobacteria	Micromonospora matsumotoense	hypothetical protein [Micromonospora matsumotoense].	GCF_900091525.1
WP_096595110.1	Uma2→||<-?<-?||CASPASE+bDLD3*→ APATPase+BetaPropeller→	CASPASE+bDLD3	288	CA733_RS03310	Cyanobacteria	Calothrix sp. NIES-2098	CHAT domain-containing protein [Calothrix sp. NIES-2098].	GCF_002368175.1
WP_096656445.1	<-PP2C+TM||?→ SIG+Band_7→||<-?||?→?→?→ PNPase+bDLD3*→ TM+TM+TM+TM→?→||<-PsaD	PNPase+bDLD3	687	CA729_RS14610	Cyanobacteria	Calothrix parasitica	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase [Calothrix parasitica].	GCF_002368095.1
WP_096691054.1	PNPase+bDLD3*→?→||<-?<-PsaD	PNPase+bDLD3	679	CDC41_RS35135	Cyanobacteria	unclassified Calothrix	MULTISPECIES: hypothetical protein [unclassified Calothrix].	GCF_002368455.1
WP_102152967.1	SIG+CASPASE+bDLD3+APATPase+BetaPropeller*→	SIG+CASPASE+bDLD3+APATPase+BetaPropeller	955	CEN39_RS27445	Cyanobacteria	Fischerella thermalis	hypothetical protein [Fischerella thermalis].	GCF_002870785.1
WP_128137951.1	bDLD3→*?→||<-?<-bDLD3*	bDLD3	246	DRA43_RS16270	Actinobacteria	Micromonospora chalcea	hypothetical protein [Micromonospora chalcea].	GCF_003298855.1

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
WP_128137954.1	bDLD3*→	bDLD3	161	DRA43_RS16285	Actinobacteria	Micromonospora chalcea	hypothetical protein [Micromonospora chalcea].	GCF_003298855.1
WP_130460897.1	Pkinase+bDLD3→ *bDLD3+TPR*→?→?→?→||<-?<-BACTERIALFRINGE+TM+TM	Pkinase+bDLD3	509	EV371_RS04300	Actinobacteria	Plantactinospora sp. CNZ321	hypothetical protein [Plantactinospora sp. CNZ321].	GCF_004217235.1
WP_130460898.1	bDLD3+TPR*→	bDLD3+TPR	351	EV371_RS04305	Actinobacteria	Plantactinospora sp. CNZ321	tetratricopeptide repeat protein [Plantactinospora sp. CNZ321].	GCF_004217235.1
WP_130472516.1	PNPase+bDLD3→ *bDLD3*→	PNPase+bDLD3	374	EJP87_RS14170	Alphaproteobacteria	Candidatus Magnetaquicoccus inordinatus	hypothetical protein [Candidatus Magnetaquicoccus inordinatus].	GCF_004217665.1
WP_130472517.1	bDLD3*→	bDLD3	703	EJP87_RS14175	Alphaproteobacteria	Candidatus Magnetaquicoccus inordinatus	hypothetical protein [Candidatus Magnetaquicoccus inordinatus].	GCF_004217665.1
WP_143309823.1	TIR→ TIR+bDLD3*→	TIR+bDLD3	180	FLV42_RS32380	Nitrospinae/Tectomicrobia group	Candidatus Entotheonella palauensis	hypothetical protein [Candidatus Entotheonella palauensis].	GCF_900079095.1
WP_144082196.1	Pkinase+bDLD3→*//<-TPR+TPR+Caspase<-vWA-L+TM+CASPASE<-VWA<-MoxR-AAA<-bDLD3+iSTAND2<-*?||TCAD9+Pkinase+bDLD3*→||<-?||?→||<-?||?→ GNTR-HTH→	Pkinase+bDLD3	334	CLT72_RS05190	Actinobacteria	Micromonospora sp. CNZ309	hypothetical protein [Micromonospora sp. CNZ309].	GCF_002846525.1
WP_144082198.1	TCAD9+Pkinase+bDLD3*→	TCAD9+Pkinase+bDLD3	532	CLT72_RS05200	Actinobacteria	Micromonospora sp. CNZ309	hypothetical protein [Micromonospora sp. CNZ309].	GCF_002846525.1
WP_146877386.1	APATPase+TPR+TPR+TPR→||<-?||?→?→?→ Pkinase+bDLD3→ *SIG+bDLD3+MgtE_N*→	Pkinase+bDLD3	326	DTB52_RS46895	Actinobacteria	Actinomadura madurae	hypothetical protein [Actinomadura madurae].	GCF_900445005.1
WP_146877388.1	SIG+bDLD3+MgtE_N*→	SIG+bDLD3+MgtE_N	535	DTB52_RS46900	Actinobacteria	Actinomadura madurae	hypothetical protein [Actinomadura madurae].	GCF_900445005.1
WP_147207373.1	PNPase+bDLD3*→ bDLD3+NPCBM→ TM+NPCBM→||<-LD-peptidase<-?<-HD||?→ GNTR-HTH→	PNPase+bDLD3	281	NS2_RS30205	Actinobacteria	Nocardia seriolae	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase, partial [Nocardia seriolae].	GCF_007990715.1
WP_154788099.1	<-TM+TM+TM+TM||PNPase+bDLD3→ *bDLD3+APATPase*→ TPR→ TPR→	PNPase+bDLD3	350	GLP40_RS12945	Actinobacteria	Nocardia sp. CT2-14	hypothetical protein [Nocardia sp. CT2-14].	GCF_009708175.1
WP_154788100.1	bDLD3+APATPase*→	bDLD3+APATPase	500	GLP40_RS12950	Actinobacteria	Nocardia sp. CT2-14	hypothetical protein [Nocardia sp. CT2-14].	GCF_009708175.1
WP_157437393.1	PNPase+bDLD3*→	PNPase+bDLD3	405	-	Actinobacteria	Actinoplanes subtropicus	hypothetical protein [Actinoplanes subtropicus].	-
WP_158241970.1	SIG+bDLD3*→	SIG+bDLD3	379	CLT72_RS05165	Actinobacteria	Micromonospora sp. CNZ309	hypothetical protein [Micromonospora sp. CNZ309].	GCF_002846525.1
WP_158660795.1	<-SIG+NPCBM<-TM+TM+TM+TM||PNPase+bDLD3→ bDLD3+NPCBM*→ TM+NPCBM→||<-LD-peptidase<-?<-HD||?→ GNTR-HTH→	bDLD3+NPCBM	227	NS506_RS18405	Actinobacteria	Nocardia seriolae	NPCBM/NEW2 domain-containing protein [Nocardia seriolae].	GCF_001865855.1
WP_167727085.1	CASPASE+bDLD3*→ APATPase+BetaPropeller→	CASPASE+bDLD3	290	HCG51_RS32855	Cyanobacteria	Tolypothrix sp. PCC 7910	CHAT domain-containing protein [Tolypothrix sp. PCC 7910].	GCF_011769525.1

2. Source data. Gene neighborhoods and domain architectures of the iSTAND2 systems

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
APR86273.1	Calcineurin+EAD8→ EAD2?+iSTAND2*→ MoxR→ vWA→ vWA-L+SLOG+PNPase→	EAD2?+iSTAND2	314	A7982_11622	deltaproteobacteria	Minicystis rosea	Hypothetical protein A7982_11622 [Minicystis rosea].	GCA_001931535.1
ARV63238.1	EAD1+iSTAND2*→	EAD1+iSTAND2	333	BZZ01_25840	cyanobacteria	Nostocales cyanobacterium HT-58-2	hypothetical protein BZZ01_25840 [Nostocales cyanobacterium HT-58-2].	GCA_002163975.1
EFC83428.1	<-EAD1+TIR||EAD1+iSTAND2*→ MoxR→ vWA→ vWA-L+EAD1+EAD1+cNMP_cyclase→	EAD1+iSTAND2	371	FrEUN1fDRAFT_3426	actinobacteria	Frankia sp. EUN1f	hypothetical protein FrEUN1fDRAFT_3426 [Frankia sp. EUN1f].	GCA_000177675.1
GAK57647.1	TIR+iSTAND2*→ MoxR→	TIR+iSTAND2	388	U27_04614	bacteria	Candidatus Vecturithrix granuli	methyltransferase type 11 [Candidatus Vecturithrix granuli].	GCA_000739535.1
GAK60733.1	TIR+iSTAND2*→	TIR+iSTAND2	382	U27_00631	bacteria	Candidatus Vecturithrix granuli	TIR protein [Candidatus Vecturithrix granuli].	GCA_000739535.1
PZN29457.1	EAD5+EAD7→ EAD8+iSTAND2*→ MoxR→	EAD8+iSTAND2	345	DIU80_09340	chloroflexi	Chloroflexi bacterium	hypothetical protein DIU80_09340 [Chloroflexi bacterium].	GCA_003242165.1
WP_006101837.1	EAD8+iSTAND2*→ MoxR→ vWA→ PSE→	EAD8+iSTAND2	375	-	cyanobacteria	Coleofasciculus chthonoplastes	hypothetical protein [Coleofasciculus chthonoplastes].	GCF_000155555.1
WP_011611104.1	??+iSTAND2*→ MoxR→	??+iSTAND2	357	-	cyanobacteria	Trichodesmium erythraeum	hypothetical protein [Trichodesmium erythraeum].	GCF_000014265.1
WP_015179963.1	Trypsin→ EAD1+iSTAND2*→ MoxR→ vWA→ vWA-L+HTH→	EAD1+iSTAND2	352	-	cyanobacteria	Crinalium epipsammum	hypothetical protein [Crinalium epipsammum].	GCF_000317495.1
WP_023806061.1	EAD5+Trypsin→??+iSTAND2*→ MoxR→ vWA→ vWA-L+REC+HNH+CASPASE→	??+iSTAND2	340	-	alphaproteobacteria	Mesorhizobium sp. L2C089B000	hypothetical protein [Mesorhizobium sp. L2C089B000].	GCF_000502355.1
WP_024968615.1	EAD8+Trypsin_2→?→ EAD8+iSTAND2*→ MoxR→ Uma2→ vWA→ HD+RelA_SpoT+TGS+ACT	EAD8+iSTAND2	387	-	cyanobacteria	Microcystis aeruginosa	hypothetical protein [Microcystis aeruginosa].	GCF_000599945.1
WP_033364276.1	Trypco1→ Trypsin+iSTAND2*→ MoxR→ vWA→ vWA-L+FtsK+FtsK+FtsK+FtsK+FtsK+FtsK→	Trypsin+iSTAND2	417	-	actinobacteria	Dactylosporangium aurantiacum	trypsin-like peptidase domain-containing protein [Dactylosporangium aurantiacum].	GCF_000716715.1
WP_038071878.1	EAD1+iSTAND2*→	EAD1+iSTAND2	200	-	cyanobacteria	Tolypothrix bouteillei	hypothetical protein [Tolypothrix bouteillei].	-
WP_073635979.1	EAD1+iSTAND2*→ MoxR→ vWA→ vWA-L+TIR+GUN4→	EAD1+iSTAND2	334	-	cyanobacteria	Scytonema sp. HK-05	hypothetical protein [Scytonema sp. HK-05].	GCF_002368235.1
WP_073644499.1	??+iSTAND2*→ MoxR→ vWA→ vWA-L+HTH→	??+iSTAND2	291	-	cyanobacteria	Nostoc calcicola	hypothetical protein, partial [Nostoc calcicola].	GCF_001904715.1
WP_077000516.1	EAD1+Trypsin→ EAD1+iSTAND2*→ MoxR→ vWA→ vWA-L+STAND+HEATs+PUA+MPTase(inactive)	EAD1+iSTAND2	320	-	betaproteobacteria	Variovorax sp. KK3	hypothetical protein [Variovorax sp. KK3].	GCF_001984055.1
WP_086923325.1	EAD1+Trypsin→ EAD1+iSTAND2*→ MoxR→ vWA→ vWA-L+STAND+HEATs+PUA+MPTase(inactive)→	EAD1+iSTAND2	320	-	betaproteobacteria	Variovorax sp. JS1663	hypothetical protein [Variovorax sp. JS1663].	GCF_002157355.1
WP_091114990.1	EAD1+Trypsin→ EAD1+iSTAND2*→ MoxR→ vWA→ vWA-L+subtilase	EAD1+iSTAND2	305	-	actinobacteria	Geodermatophilus dictyosporus	hypothetical protein [Geodermatophilus dictyosporus].	GCF_900115505.1
WP_092544601.1	EAD1+Trypsin→ EAD1+iSTAND2*→ MoxR→ vWA→ PSE→	EAD1+iSTAND2	321	-	actinobacteria	Actinoplanes derwentensis	hypothetical protein [Actinoplanes derwentensis].	GCF_900104725.1
WP_101409760.1	bDLD3+iSTAND2*→	bDLD3+iSTAND2	310	-	actinobacteria	Micromonospora sp. CNZ309	hypothetical protein [Micromonospora sp. CNZ309].	-
WP_103920108.1	EAD1+Trypsin→?→??+iSTAND2*→ MoxR→ vWA→ ParD→ ParE→	??+iSTAND2	329	-	gammaproteobacteria	Thiotrichales bacterium HS_08	hypothetical protein [Thiotrichales bacterium HS_08].	GCF_900099115.1
WP_111653783.1	EAD1+iSTAND2*→	EAD1+iSTAND2	292	-	actinobacteria	Actinoplanes lutulentus	hypothetical protein [Actinoplanes lutulentus].	-
WP_114085439.1	EAD1+iSTAND2*→ MoxR→ vWA→ pentapeptides+TIR+EAD1+CASPASE	EAD1+iSTAND2	348	-	cyanobacteria	Nostoc sp. ATCC 53789	hypothetical protein [Nostoc sp. ATCC 53789].	GCF_009873495.1
WP_118164052.1	EAD8+Trypsin_2→?→ EAD8→ iSTAND2*→ MoxR→ vWA→ vWA-L+??	iSTAND2	223	-	cyanobacteria	Nostoc sphaeroides	hypothetical protein [Nostoc sphaeroides].	GCF_003443655.1

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
WP_127507280.1	<-EAD5+Trypsin<-?||EAD2?+iSTAND2*→ MoxR→ vWA→ vWA-L+Trypsin+STAND→	EAD2?+iSTAND2	348	-	actinobacteria	Actinoplanes sp. LAM7112	hypothetical protein [Actinoplanes sp. LAM7112].	GCF_003999975.1

3. Source data. Gene neighborhoods and domain architectures of the TERNS3 systems

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
AGZ40701.1	TIR+TERNS3-N+TERNS3*→ MoxR→||<-?||vWA→ vWA-L+??+a/b_hydrolase→ SLATT+SLATT→	TIR+TERNS3-N+TERNS3	413	AFR_12075	actinobacteria	Actinoplanes friuliensis DSM 7358	hypothetical protein AFR_12075 [Actinoplanes friuliensis DSM 7358].	GCA_000494755.1
AIS01002.1	bcl2?+TERNS3-N+TERNS3*→	bcl2?+TERNS3-N+TERNS3	294	SGLAU_25320	actinobacteria	Streptomyces glaucescens	hypothetical protein SGLAU_25320 [Streptomyces glaucescens].	GCA_000761215.1
EXG79871.1	TIR+TERNS3-N_TERNS3*→ MoxR→ vWA→	TIR+TERNS3-N_TERNS3	390	CryarDRAFT_0921	actinobacteria	Cryptosporangium arvum DSM 44712	hypothetical protein CryarDRAFT_0921 [Cryptosporangium arvum DSM 44712].	GCA_000585375.1
EXI90101.1	TIR+TERNS3-N+TERNS3*→ MoxR→	TIR+TERNS3-N+TERNS3	420	AW11_01135	betaproteobacteria	Candidatus Accumulibacter sp. BA-93	hypothetical protein AW11_01135 [Candidatus Accumulibacter sp. BA-93].	GCA_000585075.1
HAO80527.1	TIR+TERNS3-N_TERNS3*→ MoxR→	TIR+TERNS3-N_TERNS3	445	DCQ92_16470	verrucomicrobia	Verrucomicrobia subdivision 3 bacterium	TPA: hypothetical protein DCQ92_16470 [Verrucomicrobia subdivision 3 bacterium].	GCA_003455565.1
HBL29163.1	CASPASE+TIR+TERNS3-N+TERNS3*→ MoxR→ vWA→	CASPASE+TIR+TERNS3-N+TERNS3	690	DD490_20220	acidobacteria	Acidobacteria bacterium	TPA: hypothetical protein DD490_20220 [Acidobacteria bacterium].	GCA_003504885.1
KDN76873.1	SLATT+SLATT→ TIR+TERNS3-N+TERNS3*→ MoxR→ vWA→ vWA-L+?+CASPASE→	TIR+TERNS3-N+TERNS3	422	DF19_14140	actinobacteria	Streptomyces olindensis	hypothetical protein DF19_14140 [Streptomyces olindensis].	GCA_000696115.1
KFB69572.1	TIR+TERNS3-N+TERNS3*→ MoxR→ vWA→ vWA-L+TIR+FGS_fold→	TIR+TERNS3-N+TERNS3	443	CAPSK01_000631	betaproteobacteria	Candidatus Accumulibacter sp. SK-01	hypothetical protein CAPSK01_000631 [Candidatus Accumulibacter sp. SK-01].	GCA_000584955.2
KFB72205.1	TIR+TERNS3-N+TERNS3*→ MoxR→ vWA→ vWA-L+TIR+FGS_fold→	TIR+TERNS3-N+TERNS3	443	AW09_002623	betaproteobacteria	Candidatus Accumulibacter sp. BA-91	hypothetical protein AW09_002623 [Candidatus Accumulibacter sp. BA-91].	GCA_000585035.2
KNZ33320.1	TIR+TERNS3-N+TERNS3*→ MoxR→ vWA→	TIR+TERNS3-N+TERNS3	444	AD742_06935	betaproteobacteria	Methylibium sp. NZG	hypothetical protein AD742_06935 [Methylibium sp. NZG].	GCA_001263235.1
KQP26499.1	TIR+TERNS3-N+TERNS3*→ MoxR→ vWA→	TIR+TERNS3-N+TERNS3	369	ASF25_21095	alphaproteobacteria	Methylobacterium sp. Leaf100	hypothetical protein ASF25_21095 [Methylobacterium sp. Leaf100].	GCA_001422845.1
KUI28159.1	TIR+TERNS3-N+TERNS3*→	TIR+TERNS3-N+TERNS3	467	AU195_20580	actinobacteria	Mycobacterium sp. IS-1496	hypothetical protein AU195_20580 [Mycobacterium sp. IS-1496].	GCA_001499995.1
KUM86142.1	TIR+TERNS3-N+TERNS3*→ MoxR→ vWA→ vWA-L+??+S1+S1+S1+S1→?→ SLOG→	TIR+TERNS3-N+TERNS3	463	AQI94_24265	actinobacteria	Streptomyces pseudovenezuelae	hypothetical protein AQI94_24265 [Streptomyces pseudovenezuelae].	GCA_001513955.1
KYF52375.1	trypsin+TERNS3-N+TERNS3*→ MoxR→	trypsin+TERNS3-N+TERNS3	503	BE04_07830	deltaproteobacteria	Sorangium cellulosum	hypothetical protein BE04_07830 [Sorangium cellulosum].	GCA_001589195.1
NEM04743.1	TIR+TERNS3-N_TERNS3*→	TIR+TERNS3-N_TERNS3	444	GCU54_01715	actinobacteria	Geodermatophilus normandii	toll/interleukin-1 receptor domain-containing protein [Geodermatophilus normandii].	-
NMQ07203.1	TIR+TERNS3-N+TERNS3*→ MoxR→ vWA→ vWA-L+TIR+FGS_fold→?→ TIR+TIR+TIR+SLOG→	TIR+TERNS3-N+TERNS3	468	E4Q08_19150	betaproteobacteria	Candidatus Accumulibacter phosphatis	TIR domain-containing protein [Candidatus Accumulibacter phosphatis].	-

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
NMQ29341.1	TIR+TERNS3-N+TERNS3*→ MoxR→ vWA→ vWA-L+TIR+FGS_fold→	TIR+TERNS3-N+TERNS3	460	E4Q23_17175	betaproteobacteria	Candidatus Accumulibacter phosphatis	TIR domain-containing protein [Candidatus Accumulibacter phosphatis].	-
OPC80455.1	TIR+TERNS3-N+TERNS3*→ SLATT+SLATT→	TIR+TERNS3-N+TERNS3	582	B4N89_05385	actinobacteria	Embleya scabrispora	hypothetical protein B4N89_05385 [Embleya scabrispora].	GCA_002024165.1
PSK62948.1	TIR+TERNS3-N+TERNS3*→ MoxR→ vWA→ vWA-L+??+S1+S1+S1+OST-HTH→	TIR+TERNS3-N+TERNS3	452	B0E53_05125	actinobacteria	Micromonospora sp. MH33	hypothetical protein B0E53_05125 [Micromonospora sp. MH33].	GCA_003013775.1
PTH87452.1	TIR+TERNS3-N+TERNS3*→ MoxR→ vWA→ vWA-L+??+S1+S1+S1+S1→?→ SLOG→	TIR+TERNS3-N+TERNS3	463	C9J60_19135	actinobacteria	Streptomyces sp. A244	hypothetical protein C9J60_19135 [Streptomyces sp. A244].	GCA_003041235.1
PUB76299.1	TIR+TERNS3-N+TERNS3*→ MoxR→	TIR+TERNS3-N+TERNS3	446	DBP03_04880	gammaproteobacteria	gamma proteobacterium symbiont of Ctena orbiculata	hypothetical protein DBP03_04880 [gamma proteobacterium symbiont of Ctena orbiculata].	GCA_003058495.1
PZN81550.1	TIR+TERNS3-N+TERNS3*→ MoxR→ vWA→ vWA-L+TIR+FGS_fold→	TIR+TERNS3-N+TERNS3	413	DM484_08310	gammaproteobacteria	Candidatus Methyloumidiphilus alinensis	hypothetical protein DM484_08310 [Candidatus Methyloumidiphilus alinensis].	GCA_003242955.1
RIK40644.1	TIR+TERNS3-N+TERNS3*→	TIR+TERNS3-N+TERNS3	425	DCC55_14310	chloroflexi	Chloroflexi bacterium	hypothetical protein DCC55_14310 [Chloroflexi bacterium].	GCA_003577005.1
RLJ15768.1	TIR+TERNS3-N+TERNS3*→ MoxR→	TIR+TERNS3-N+TERNS3	445	DJ030_18025	bacteria	bacterium endosymbiont of Escarpia laminata	hypothetical protein DJ030_18025 [bacterium endosymbiont of Escarpia laminata].	GCA_003660225.1
RSO09108.1	SLATT+SLATT→ TIR+TERNS3-N+TERNS3*→ MoxR→ vWA→ vWA-L+?+CASPASE→	TIR+TERNS3-N+TERNS3	420	DMH26_01890	actinobacteria	Streptomyces sp. WAC 05379	hypothetical protein DMH26_01890 [Streptomyces sp. WAC 05379].	GCA_003947555.1
RZL40587.1	TIR+TERNS3-N+TERNS3*→ MoxR→ vWA+vWA-L+??+VipA+VipB→	TIR+TERNS3-N+TERNS3	416	EOP35_00425	betaproteobacteria	Rubrivivax sp.	TIR domain-containing protein [Rubrivivax sp.].	GCA_004211235.1
SDH38921.1	TIR+TERNS3-N+TERNS3*→ MoxR→ vWA→ vWA-L+??+S1+S1+S1+OST-HTH→	TIR+TERNS3-N+TERNS3	446	SAMN05216553_120150	actinobacteria	Lechevalieria fradiae	TIR domain-containing protein [Lechevalieria fradiae].	GCA_900100955.1
TMC21179.1	PNPase+TIR→?→ TRANSGLUTAMINASE+TIR+TERNS3-N+TERNS3*→ MoxR→ vWA→ vWA-L+TPRs+PNPase+TIR→	TRANSGLUTAMINASE+TIR+TERNS3-N+TERNS3	672	E6J34_10390	chloroflexi	Chloroflexi bacterium	hypothetical protein E6J34_10390 [Chloroflexi bacterium].	GCA_005879655.1
VFJ73521.1	TIR+TERNS3-N+TERNS3*→ MoxR→	TIR+TERNS3-N+TERNS3	427	BECKFW1821C_GA0114237_105219	gammaproteobacteria	Candidatus Kentron sp. FW	TIR domain-containing protein [Candidatus Kentron sp. FW].	-
WP_003954434.1	SLATT+SLATT→?→ MoxR→ vWA→ vWA-L+Betapropeller+TIM_barrel_glycosyl_hydrolase→ TIR+TERNS3-N+TERNS3*→	TIR+TERNS3-N+TERNS3	415	-	actinobacteria	Streptomyces clavuligerus	toll/interleukin-1 receptor domain-containing protein [Streptomyces clavuligerus].	GCF_000163875.1
WP_003959455.1	TIR+TERNS3-N+TERNS3*→ MoxR→ vWA→	TIR+TERNS3-N+TERNS3	434	-	actinobacteria	Streptomyces clavuligerus	toll/interleukin-1 receptor domain-containing protein [Streptomyces clavuligerus].	GCF_000163875.1
WP_005160854.1	SLATT+SLATT→ TIR+TERNS3-N_TERNS3*→ MoxR→ vWA→ vWA-L+STAND+TPRs→	TIR+TERNS3-N_TERNS3	431	-	actinobacteria	Amycolatopsis azurea	toll/interleukin-1 receptor domain-containing protein [Amycolatopsis azurea].	GCF_000340415.1
WP_006140008.1	MoxR→ vWA→ vWA-L+Betapropeller+TIM_barrel_glycosyl_hydrolase→ TIR+TERNS3-N+TERNS3*→||<-ParA-Soj_NTPase+TIR+STAND+TPRs	TIR+TERNS3-N+TERNS3	406	-	actinobacteria	Streptomyces	MULTISPECIES: toll/interleukin-1 receptor domain-containing protein [Streptomyces].	GCF_000204605.1
WP_009737883.1	E2+EAD1?→ EAD1+TERNS3-N+TERNS3*→ MoxR→ vWA→ vWA-L+Tir+Pkinase→ EAD1+fvmYukDl-Nterm+Ub→||<-E1+ZnR?	EAD1+TERNS3-N+TERNS3	372	-	actinobacteria	Frankia sp. QA3	hypothetical protein [Frankia sp. QA3].	GCF_000262465.1
WP_015037308.1	SLATT+SLATT→?→ MoxR→ vWA→ vWA-L+Betapropeller+TIM_barrel_glycosyl_hydrolase→ TIR+TERNS3-N+TERNS3*→	TIR+TERNS3-N+TERNS3	422	-	actinobacteria	Streptomyces	MULTISPECIES: toll/interleukin-1 receptor domain-containing protein [Streptomyces].	GCF_000253235.1
WP_029084398.1	TIR+TERNS3-N+TERNS3*→ MoxR→ vWA→	TIR+TERNS3-N+TERNS3	414	-	alphaproteobacteria	Bradyrhizobium sp. th.b2	toll/interleukin-1 receptor domain-containing protein [Bradyrhizobium sp. th.b2].	GCF_000426785.1

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
WP_030935396.1	SLATT+SLATT→ TIR+TERNS3-N+TERNS3*→ MoxR→ vWA→ vWA-L+TIR+STAND+TPRs→ TIR+STAND+TPRs→	TIR+TERNS3-N+TERNS3	418	-	actinobacteria	Streptomyces sp. NRRL S-646	toll/interleukin-1 receptor domain-containing protein [Streptomyces sp. NRRL S-646].	GCF_000720765.1
WP_053636820.1	TIR+TERNS3-N+TERNS3*→ MoxR→	TIR+TERNS3-N+TERNS3	427	-	actinobacteria	Streptomyces sp. XY152	toll/interleukin-1 receptor domain-containing protein [Streptomyces sp. XY152].	GCF_001279455.1
WP_058554423.1	TIR+TERNS3-N+TERNS3*→ MoxR→ vWA→ vWA-L+TIR+FGS_fold→	TIR+TERNS3-N+TERNS3	447	-	gammaproteobacteria	Thiohalocapsa sp. ML1	toll/interleukin-1 receptor domain-containing protein [Thiohalocapsa sp. ML1].	GCF_001469165.1
WP_062724228.1	TIR+TERNS3-N+TERNS3*→ MoxR→ vWA→ vWA-L+??+CASPASE+a/b_hydrolase→	TIR+TERNS3-N+TERNS3	410	-	actinobacteria	Streptomyces caeruleatus	toll/interleukin-1 receptor domain-containing protein [Streptomyces caeruleatus].	GCF_001514235.1
WP_067167006.1	vWA→ vWA-L+Betapropeller+TIM_barrel_glycosyl_hydrolase→ TIR+TERNS3-N+TERNS3*→	TIR+TERNS3-N+TERNS3	421	-	actinobacteria	Streptomyces sp. ERV7	toll/interleukin-1 receptor domain-containing protein [Streptomyces sp. ERV7].	GCF_001653515.1
WP_067805560.1	TIR+TERNS3-N+TERNS3*→ MoxR→ vWA→ vWA-L+??+S1+S1+S1→	TIR+TERNS3-N+TERNS3	469	-	actinobacteria	Nocardia beijingensis	toll/interleukin-1 receptor domain-containing protein [Nocardia beijingensis].	GCF_001612785.1
WP_070017317.1	MoxR→ vWA→ vWA-L+Betapropeller+TIM_barrel_glycosyl_hydrolase→ TIR+TERNS3-N+TERNS3*→	TIR+TERNS3-N+TERNS3	413	-	actinobacteria	Streptomyces nanshensis	toll/interleukin-1 receptor domain-containing protein [Streptomyces nanshensis].	GCF_001751255.1
WP_074954915.1	TIR+TERNS3-N+TERNS3*→ MoxR→	TIR+TERNS3-N+TERNS3	410	-	deltaproteobacteria	Myxococcus fulvus	toll/interleukin-1 receptor domain-containing protein [Myxococcus fulvus].	GCF_007991095.1
WP_077058200.1	<-SLATT+SLATT||?→ MoxR→ vWA→ vWA-L+Betapropeller+TIM_barrel_glycosyl_hydrolase→ TIR+TERNS3-N+TERNS3*→	TIR+TERNS3-N+TERNS3	436	-	actinobacteria	Streptomyces sp. MP131-18	toll/interleukin-1 receptor domain-containing protein [Streptomyces sp. MP131-18].	GCF_001984575.1
WP_078922055.1	TIR+TERNS3-N+TERNS3*→ MoxR→ vWA→ vWA-L+ZnR+GAF+REC(inactive?)+TIR→	TIR+TERNS3-N+TERNS3	406	-	gammaproteobacteria	Thiothrix eikelboomii	toll/interleukin-1 receptor domain-containing protein [Thiothrix eikelboomii].	GCF_900167255.1
WP_079308407.1	MoxR→ vWA→ vWA-L+Betapropeller+TIM_barrel_glycosyl_hydrolase→ TIR+TERNS3-N+TERNS3*→	TIR+TERNS3-N+TERNS3	416	-	actinobacteria	Streptomyces sp. GKU 895	toll/interleukin-1 receptor domain-containing protein [Streptomyces sp. GKU 895].	GCF_002027195.1
WP_086569346.1	TIR+TERNS3-N+TERNS3*→	TIR+TERNS3-N+TERNS3	428	-	actinobacteria	Streptomyces alboverticillatus	toll/interleukin-1 receptor domain-containing protein [Streptomyces alboverticillatus].	GCF_002150845.1
WP_086575434.1	TIR+TERNS3-N+TERNS3*→ MoxR→	TIR+TERNS3-N+TERNS3	444	-	actinobacteria	Streptomyces alboverticillatus	toll/interleukin-1 receptor domain-containing protein [Streptomyces alboverticillatus].	-
WP_093784682.1	vWA-L+Betapropeller+TIM_barrel_glycosyl_hydrolase→ TIR+TERNS3-N+TERNS3*→||<-ParA-Soj_NTPase+TIR+STAND+TPRs	TIR+TERNS3-N+TERNS3	407	-	actinobacteria	Streptomyces guanduensis	toll/interleukin-1 receptor domain-containing protein [Streptomyces guanduensis].	GCF_900103985.1
WP_093909564.1	TIR+TERNS3-N+TERNS3*→ MoxR→ vWA→ vWA-L+??+CASPASE+a/b_hydrolase→	TIR+TERNS3-N+TERNS3	410	-	actinobacteria	Streptomyces sp. cf386	toll/interleukin-1 receptor domain-containing protein [Streptomyces sp. cf386].	GCF_900103585.1
WP_109500779.1	TIR+TERNS3-N+TERNS3*→ MoxR→ vWA→	TIR+TERNS3-N+TERNS3	573	-	actinobacteria	Streptomyces sp. Act143	toll/interleukin-1 receptor domain-containing protein [Streptomyces sp. Act143].	GCF_003143935.1
WP_109888160.1	SLATT+SLATT→ TIR+TERNS3-N+TERNS3*→ MoxR→	TIR+TERNS3-N+TERNS3	423	-	actinobacteria	Streptomyces sp. NEAU-S7GS2	toll/interleukin-1 receptor domain-containing protein [Streptomyces sp. NEAU-S7GS2].	GCF_003173275.1

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
WP_111601039.1	MoxR→ vWA→ vWA-L+Betapropeller+TIM_barrel_glycosyl_hydrolase→ TIR+TERNS3-N+TERNS3*→	TIR+TERNS3-N+TERNS3	417	-	actinobacteria	Streptomyces sp. Amel2xB2	toll/interleukin-1 receptor domain-containing protein [Streptomyces sp. Amel2xB2].	GCF_003259355.1
WP_114029261.1	TIR+TERNS3-N+TERNS3*→ MoxR→ vWA→ vWA-L+??+S1+S1+S1→	TIR+TERNS3-N+TERNS3	456	-	actinobacteria	Sphaerisporangium album	toll/interleukin-1 receptor domain-containing protein [Sphaerisporangium album].	GCF_003323745.1
WP_120606365.1	TIR+TERNS3-N+TERNS3*→ MoxR→	TIR+TERNS3-N+TERNS3	410	-	deltaproteobacteria	Corallococcus sp. CA043D	toll/interleukin-1 receptor domain-containing protein [Corallococcus sp. CA043D].	GCF_003611695.1
WP_121007100.1	SLATT+SLATT→ TIR+TERNS3-N+TERNS3*→ MoxR→ vWA→ vWA-L+STAND+TPRs→	TIR+TERNS3-N+TERNS3	404	-	actinobacteria	Saccharothrix australiensis	toll/interleukin-1 receptor domain-containing protein [Saccharothrix australiensis].	GCF_003634935.1
WP_128963913.1	TIR+TERNS3-N+TERNS3*→ MoxR→ vWA→ vWA-L+CASPASE+TPRs	TIR+TERNS3-N+TERNS3	417	-	alphaproteobacteria	Bradyrhizobium guangdongense	TIR domain-containing protein [Bradyrhizobium guangdongense].	GCF_004114975.1
WP_132123911.1	TIR+TERNS3-N_TERNS3*→ MoxR→ vWA→ vWA-L+STAND+TPRs→	TIR+TERNS3-N_TERNS3	423	-	actinobacteria	Actinocrispum wychmicini	toll/interleukin-1 receptor domain-containing protein [Actinocrispum wychmicini].	GCF_004345645.1
WP_133291404.1	TIR+TERNS3-N+TERNS3*→ MoxR→ vWA→ vWA+vWA-L+??+VipA+VipB→	TIR+TERNS3-N+TERNS3	412	-	alphaproteobacteria	Dankookia rubra	toll/interleukin-1 receptor domain-containing protein [Dankookia rubra].	GCF_004355005.1
WP_141296792.1	TIR+TERNS3-N+TERNS3*→	TIR+TERNS3-N+TERNS3	572	-	actinobacteria	Streptomyces gardneri	TIR domain-containing protein [Streptomyces gardneri].	-
WP_141982648.1	TIR+TERNS3-N_TERNS3*→ MoxR→ vWA→ vWA-L+STAND+TPRs→	TIR+TERNS3-N_TERNS3	423	-	actinobacteria	Saccharothrix saharensis	TIR domain-containing protein [Saccharothrix saharensis].	GCF_006716745.1
WP_143049943.1	TIR+TERNS3-N+TERNS3*→ MoxR→	TIR+TERNS3-N+TERNS3	427	-	actinobacteria	Asanoa ishikariensis	toll/interleukin-1 receptor domain-containing protein [Asanoa ishikariensis].	GCF_900107455.1
WP_146519555.1	TIR+TERNS3-N+TERNS3*→ MoxR→ vWA+vWA-L+??+VipA+VipB→	TIR+TERNS3-N+TERNS3	417	-	planctomycetes	Planctomycetes bacterium Pla52n	TIR domain-containing protein [Planctomycetes bacterium Pla52n].	GCF_007860045.1
WP_146520106.1	TIR+TERNS3-N+TERNS3*→ MoxR→ vWA→ vWA-L+??+S1+??+S1+??→	TIR+TERNS3-N+TERNS3	616	-	planctomycetes	Planctomycetes bacterium Pla52n	TIR domain-containing protein [Planctomycetes bacterium Pla52n].	GCF_007860045.1
WP_149224808.1	TIR+TERNS3-N+TERNS3*→ MoxR→ vWA+vWA-L+??+Calcineurin+??+REase→	TIR+TERNS3-N+TERNS3	407	-	alphaproteobacteria	Azospirillum sp. B21	TIR domain-containing protein [Azospirillum sp. B21].	GCF_008364825.1
WP_150234755.1	SLATT+SLATT→ TIR+TERNS3-N+TERNS3*→ MoxR→ vWA→ vWA-L+?+CASPASE→	TIR+TERNS3-N+TERNS3	423	-	actinobacteria	Streptomyces filamentosus	TIR domain-containing protein [Streptomyces filamentosus].	-
WP_153453600.1	SLATT+SLATT→ TIR+TERNS3-N+TERNS3*→ MoxR→ vWA→ vWA-L+TIR+STAND+TPRs→ TIR+STAND+TPRs→ TIR+STAND+TPRs→	TIR+TERNS3-N+TERNS3	424	-	actinobacteria	Streptomyces sp. RB5	TIR domain-containing protein [Streptomyces sp. RB5].	GCF_009604385.1
WP_157858102.1	TIR+TERNS3-N+TERNS3*→ MoxR→ vWA→ vWA-L+??+CASPASE+a/b_hydrolase→	TIR+TERNS3-N+TERNS3	414	-	actinobacteria	Streptomyces durhamensis	TIR domain-containing protein [Streptomyces durhamensis].	GCF_000725475.1
WP_158088688.1	SLATT+SLATT→ TIR+TERNS3-N+TERNS3*→ MoxR→ vWA→ vWA-L?+Trypsin+STAND+TPRs→	TIR+TERNS3-N+TERNS3	419	-	actinobacteria	Thermoactinospora rubra	TIR domain-containing protein [Thermoactinospora rubra].	GCF_002093975.1
WP_158625805.1	TIR+TERNS3-N+TERNS3*→ MoxR→	TIR+TERNS3-N+TERNS3	409	-	deltaproteobacteria	Corallococcus carmarthensis	TIR domain-containing protein [Corallococcus carmarthensis].	GCF_003611695.1
WP_158626622.1	<-TIR+TIR+TIR+SLOG||?→?→ TIR+TERNS3-N+TERNS3*→ MoxR→ vWA→ vWA-L+TIR+STAND+TPRs→	TIR+TERNS3-N+TERNS3	413	-	deltaproteobacteria	Corallococcus interemptor	TIR domain-containing protein [Corallococcus interemptor].	GCF_003668875.1
WP_158997559.1	TIR+TERNS3-N+TERNS3*→ MoxR→ vWA→ vWA-L?+STAND+TPRs→	TIR+TERNS3-N+TERNS3	440	-	actinobacteria	Streptomyces aureus	TIR domain-containing protein [Streptomyces aureus].	GCF_000725495.1
WP_159049469.1	TIR+TERNS3-N+TERNS3*→ MoxR→ vWA→ vWA-L?+TIR+STAND+TPRs→	TIR+TERNS3-N+TERNS3	435	-	actinobacteria	Streptomyces sp. NRRL WC-3618	TIR domain-containing protein [Streptomyces sp. NRRL WC-3618].	GCF_001280005.1
WP_159688556.1	TIR+TERNS3-N+TERNS3*→ MoxR→ vWA→ vWA-L+CASPASE+a/b_hydrolase+TIR→	TIR+TERNS3-N+TERNS3	438	-	betaproteobacteria	Azoarcus sp. HKLI-1	TIR domain-containing protein [Azoarcus sp. HKLI-1].	GCF_009800965.1

acc	**operon**	**architecture**	**len**	**gen.name**	**taxend**	**species**	**defline**	**gca**
WP_164008272.1	TIR+TERNS3-N+TERNS3*→ MoxR→	TIR+TERNS3-N+TERNS3	402	-	deltaproteobacteria	Pyxidicoccus sp. AB060A	TIR domain-containing protein [Pyxidicoccus sp. AB060A].	GCF_010894435.1
WP_168498259.1	vWA→ vWA-L+Betapropeller+TIM_barrel_glycosyl_hydrolase→ TIR+TERNS3-N+TERNS3*→	TIR+TERNS3-N+TERNS3	417	-	actinobacteria	Streptomyces sp. RLB1-33	TIR domain-containing protein [Streptomyces sp. RLB1-33].	GCF_012273535.1
WP_169849771.1	TIR+TERNS3-N+TERNS3*→ MoxR→	TIR+TERNS3-N+TERNS3	403	-	deltaproteobacteria	Corallococcus exiguus	TIR domain-containing protein [Corallococcus exiguus].	GCF_012985275.1
WP_170164844.1	TIR+TERNS3-N+TERNS3*→ MoxR→ vWA→ vWA-L+TIR+FGS_fold→	TIR+TERNS3-N+TERNS3	416	-	gammaproteobacteria	Thiocapsa rosea	toll/interleukin-1 receptor domain-containing protein [Thiocapsa rosea].	GCF_003634315.1

4. Source data. Gene neighborhoods and domain architectures of the bacterial NPCBM domain described in this study

acc	**operon**	**architecture**	**len**	**gen.name**	**taxend**	**species**	**defline**	**gca**
APA97851.1	<-SIG+NPCBM<-?||PNPase+bDLD3→ bDLD3+NPCBM*→ DUF1707-SHOCT-bihelical+TM+NPCBM→||<-LD-peptidase	bDLD3+NPCBM	217	NS506_03802	actinobacteria	Nocardia seriolae	hypothetical protein NS506_03802 [Nocardia seriolae].	GCA_001865855.1
ATE54357.1	HTH+APATPase+TPR→?→ TIR+SWACOS→ SIG+TIR+APATPase+TPR+TPR+TPR→?→ TIR+NPCBM*→	TIR+NPCBM	345	CNX65_14540	actinobacteria	Actinosynnema pretiosum	hypothetical protein CNX65_14540 [Actinosynnema pretiosum].	GCA_002354875.1
OLO83644.1	NPCBM*→	NPCBM	151	BKH12_07845	actinobacteria	Actinomyces naeslundii	hypothetical protein BKH12_07845 [Actinomyces naeslundii].	GCA_001937595.1
ONF63682.1	TIR+NPCBM*→	TIR+NPCBM	322	AVR91_0232695	actinobacteria	Amycolatopsis keratiniphila subsp. keratiniphila	hypothetical protein AVR91_0232695 [Amycolatopsis keratiniphila subsp. keratiniphila].	GCA_001620365.2
QFU87533.1	TIR+NPCBM*→||<-?<-?<-AAA<-TIR+Pkinase	TIR+NPCBM	325	YIM_11700	actinobacteria	Amycolatopsis sp. YIM 10	SEFIR domain protein [Amycolatopsis sp. YIM 10].	-
RLK54954.1	TIR+NPCBM*→	TIR+NPCBM	326	CLV68_5345	actinobacteria	Actinokineospora cianjurensis	SEFIR domain-containing protein [Actinokineospora cianjurensis].	GCA_003663795.1
RSD09590.1	<-AAA?<-?<-ParA+TIR+pIdsmall1<-TIR||TIR+NPCBM*→	TIR+NPCBM	433	EIY87_41985	actinobacteria	Amycolatopsis sp. GLM-1	TIR domain-containing protein [Amycolatopsis sp. GLM-1].	GCA_003937945.1
RSM57848.1	TIR+NPCBM*→||<-SIGMA-HTH	TIR+NPCBM	327	DMH03_26220	actinobacteria	Amycolatopsis sp. WAC 01376	hypothetical protein DMH03_26220 [Amycolatopsis sp. WAC 01376].	GCA_003947415.1
RSM82716.1	TIR+NPCBM*→||<-SIGMA-HTH	TIR+NPCBM	327	DL991_05030	actinobacteria	Amycolatopsis sp. WAC 01375	hypothetical protein DL991_05030 [Amycolatopsis sp. WAC 01375].	GCA_003947325.1
RSN39203.1	<-TIR<-AAA?<-?<-ParA+TIR+pIdsmall1<-TIR||TIR+NPCBM*→	TIR+NPCBM	343	DMC64_39445	actinobacteria	Amycolatopsis sp. WAC 04197	hypothetical protein DMC64_39445 [Amycolatopsis sp. WAC 04197].	GCA_003947475.1
RSN62459.1	TIR+NPCBM*→||<-SIGMA-HTH	TIR+NPCBM	327	DMH01_07185	actinobacteria	Amycolatopsis sp. WAC 04182	hypothetical protein DMH01_07185 [Amycolatopsis sp. WAC 04182].	GCA_003947465.1
SCF21250.1	SIG+NPCBM*→	SIG+NPCBM	246	GA0070563_106214	actinobacteria	Micromonospora carbonacea	NPCBM/NEW2 domain-containing protein [Micromonospora carbonacea].	GCA_900091535.1
SDD51526.1	TIR+NPCBM*→	TIR+NPCBM	295	SAMN05216174_11273	actinobacteria	Alloactinosynnema iranicum	NPCBM/NEW2 domain-containing protein [Alloactinosynnema iranicum].	GCA_900101685.1
SDI31347.1	TIR+NPCBM*→	TIR+NPCBM	292	SAMN05421871_10490	actinobacteria	Alloactinosynnema album	NPCBM/NEW2 domain-containing protein [Alloactinosynnema album].	GCA_900099755.1
SDW33810.1	TIR+NPCBM*→||<-SIGMA-HTH	TIR+NPCBM	318	SAMN05421504_101304	actinobacteria	Amycolatopsis xylanica	NPCBM/NEW2 domain-containing protein [Amycolatopsis xylanica].	GCA_900107045.1
SER09138.1	TIR+NPCBM*→	TIR+NPCBM	326	SAMN04487818_101553	actinobacteria	Actinokineospora terrae	NPCBM/NEW2 domain-containing protein [Actinokineospora terrae].	GCA_900111175.1
SES13392.1	<-TIR<-Pkinase+PASTA+NPCBM||TIR+NPCBM*→?→||<-?<-?<-?||SIG+Phytase-like→	TIR+NPCBM	369	SAMN04488000_116167	actinobacteria	Lentzea albida	NPCBM/NEW2 domain-containing protein [Lentzea albida].	GCA_900111005.1
WP_003100488.1	TIR+NPCBM*→||<-Pkinase+PASTA+NPCBM	TIR+NPCBM	330	H480_RS44040	actinobacteria	Amycolatopsis vancoresmycina	TIR domain-containing protein [Amycolatopsis vancoresmycina].	GCF_000388135.1
WP_004558432.1	TIR+NPCBM*→||<-?<-PSE||DeoR→	TIR+NPCBM	323	H480_RS29455	actinobacteria	Amycolatopsis vancoresmycina	TIR domain-containing protein [Amycolatopsis vancoresmycina].	GCF_000388135.1
WP_018681508.1	TIR+NPCBM*→	TIR+NPCBM	320	C503_RS0107190	actinobacteria	Actinokineospora enzanensis	TIR domain-containing protein [Actinokineospora enzanensis].	GCF_000374445.1
WP_019932839.1	<-HTH+APATPase+TPR||?→?→ TPR+TM+TM→ TIR+NPCBM*→ DUF1707-SHOCT-bihelical+TM+NPCBM→	TIR+NPCBM	369	G361_RS0140320	actinobacteria	Nocardia sp. BMG111209	TIR domain-containing protein [Nocardia sp. BMG111209].	GCF_000381925.1

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
WP_026425923.1	TIR+NPCBM*→	TIR+NPCBM	324	H504_RS0130665	actinobacteria	Actinokineospora inagensis	TIR domain-containing protein [Actinokineospora inagensis].	GCF_000482865.1
WP_043787644.1	TIR+NPCBM*→||<-?||DeoR→	TIR+NPCBM	323	DV20_RS35395	actinobacteria	Amycolatopsis rifamycinica	TIR domain-containing protein [Amycolatopsis rifamycinica].	GCF_000695625.1
WP_043833411.1	TIR+NPCBM*→	TIR+NPCBM	317	L943_RS22200	actinobacteria	Amycolatopsis orientalis	TIR domain-containing protein [Amycolatopsis orientalis].	GCF_000411995.1
WP_051173847.1	TIR+NPCBM*→	TIR+NPCBM	311	L324_RS40905	actinobacteria	Amycolatopsis orientalis	TIR domain-containing protein [Amycolatopsis orientalis].	GCF_000478275.1
WP_051729748.1	TIR+NPCBM*→	TIR+NPCBM	317	IF70_RS45275	actinobacteria	Streptomyces sp. NRRL F-3213	TIR domain-containing protein [Streptomyces sp. NRRL F-3213].	GCF_000720075.1
WP_051913277.1	TIR+NPCBM*→||<-?<-?<-HTH+APATPase+TPR	TIR+NPCBM	297	KALB_RS43740	actinobacteria	Kutzneria albida	TIR domain-containing protein [Kutzneria albida].	GCF_000525635.1
WP_051972565.1	TIR+NPCBM*→	TIR+NPCBM	311	AJAP_RS42550	actinobacteria	Amycolatopsis japonica	TIR domain-containing protein [Amycolatopsis japonica].	GCF_000732925.1
WP_052086955.1	PNPase+bDLD3→ bDLD3+NPCBM*→?→||<-LD-peptidase	bDLD3+NPCBM	241	FH09_RS38115	actinobacteria	Nocardia seriolae	NPCBM/NEW2 domain-containing protein [Nocardia seriolae].	GCF_002356035.1
WP_052120938.1	TIR+NPCBM*→	TIR+NPCBM	311	ED92_RS41465	actinobacteria	Amycolatopsis sp. MJM2582	TIR domain-containing protein [Amycolatopsis sp. MJM2582].	GCF_000754115.1
WP_053738304.1	<-TIR+SWACOS||TIR+NPCBM*→	TIR+NPCBM	313	ADL03_RS37120	actinobacteria	Nocardia sp. NRRL S-836	TIR domain-containing protein [Nocardia sp. NRRL S-836].	GCF_001279525.1
WP_059080926.1	SIG+NPCBM*→	SIG+NPCBM	249	AV118_RS18065	actinobacteria	Streptomyces scabiei	hypothetical protein [Streptomyces scabiei].	GCF_001485125.1
WP_060884640.1	SIG+NPCBM*→	SIG+NPCBM	249	AW217_RS20820	actinobacteria	Streptomyces	MULTISPECIES: hypothetical protein [Streptomyces].	GCF_001550315.1
WP_063021686.1	TIR+NPCBM*→	TIR+NPCBM	365	NNI01S_RS20285	actinobacteria	Nocardia niwae	TIR domain-containing protein [Nocardia niwae].	GCF_001613465.1
WP_063271509.1	TIR+NPCBM*→	TIR+NPCBM	311	AVR91_RS32695	actinobacteria	Amycolatopsis keratiniphila	TIR domain-containing protein [Amycolatopsis keratiniphila].	GCF_001620365.2
WP_065912847.1	TIR+NPCBM*→||<-SIGMA-HTH<-?<-?||TIR+APATPase+TPR→ Pkinase+PASTA+NPCBM→	TIR+NPCBM	311	SD37_RS16400	actinobacteria	Amycolatopsis orientalis	TIR domain-containing protein [Amycolatopsis orientalis].	GCF_000943515.2
WP_065917610.1	<-TIR+SWACOS||TIR+NPCBM*→	TIR+NPCBM	313	BBK82_RS27620	actinobacteria	Lentzea guizhouensis	TIR domain-containing protein [Lentzea guizhouensis].	GCF_001701025.1
WP_067504284.1	TIR+NPCBM*→ DUF1707-SHOCT-bihelical+TM+NPCBM→	TIR+NPCBM	354	DFR74_RS01985	actinobacteria	Nocardia puris	TIR domain-containing protein [Nocardia puris].	GCF_001613185.1
WP_067576374.1	TIR+NPCBM*→	TIR+NPCBM	317	BM362_RS43075	actinobacteria	Amycolatopsis	MULTISPECIES: TIR domain-containing protein [Amycolatopsis].	GCF_900115345.1
WP_072027654.1	TIR+NPCBM*→	TIR+NPCBM	311	BS330_RS33980	actinobacteria	Amycolatopsis keratiniphila	TIR domain-containing protein [Amycolatopsis keratiniphila].	GCF_900105855.1
WP_072480469.1	TIR+NPCBM*→	TIR+NPCBM	313	BT341_RS36010	actinobacteria	Amycolatopsis australiensis	TIR domain-containing protein [Amycolatopsis australiensis].	GCF_900119165.1
WP_073842247.1	TIR+NPCBM*→	TIR+NPCBM	311	AMK34_RS00365	actinobacteria	Amycolatopsis sp. CB00013	TIR domain-containing protein [Amycolatopsis sp. CB00013].	GCF_001905755.1
WP_075973728.1	TIR+NPCBM*→	TIR+NPCBM	321	BJP25_RS05870	actinobacteria	Actinokineospora bangkokensis	TIR domain-containing protein [Actinokineospora bangkokensis].	GCF_001940455.1
WP_076994098.1	TIR+NPCBM*→	TIR+NPCBM	319	ALI144C_RS48690	actinobacteria	Actinosynnema sp. ALI-1.44	TIR domain-containing protein [Actinosynnema sp. ALI-1.44].	GCF_001984155.1
WP_081378834.1	TM+NPCBM*→	TM+NPCBM	241	BKH12_RS13860	actinobacteria	Actinomyces naeslundii	NPCBM/NEW2 domain-containing protein [Actinomyces naeslundii].	GCF_001937595.1
WP_083302693.1	SIG+NPCBM*→	SIG+NPCBM	248	GA0070563_RS15405	actinobacteria	Micromonospora carbonacea	NPCBM/NEW2 domain-containing protein [Micromonospora carbonacea].	GCF_900091535.1

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
WP_083946854.1	SIG+NPCM→*	*	237	-	actinobacteria	Actinomadura latina	NPCBM/NEW2 domain-containing protein [Actinomadura latina].	-
WP_084466056.1	TIR+NPCBM*→	TIR+NPCBM	351	NC5_RS29410	actinobacteria	Nocardia salmonicida	TIR domain-containing protein [Nocardia salmonicida].	GCF_001612865.1
WP_084468436.1	TIR+NPCM→*	*	386	-	actinobacteria	Actinokineospora inagensis	TIR domain-containing protein [Actinokineospora inagensis].	-
WP_084476879.1	TIR+NPCM→*	*	418	-	actinobacteria	Actinokineospora enzanensis	TIR domain-containing protein [Actinokineospora enzanensis].	-
WP_084477357.1	TIR+NPCBM*→	TIR+NPCBM	368	C503_RS45000	actinobacteria	Actinokineospora enzanensis	TIR domain-containing protein [Actinokineospora enzanensis].	GCF_000374445.1
WP_086672996.1	TIR+NPCBM*→||<-?<-?||DeoR→	TIR+NPCBM	324	CCN36_RS07390	actinobacteria	Amycolatopsis pretoriensis	NPCBM/NEW2 domain-containing protein [Amycolatopsis pretoriensis].	GCF_900107925.1
WP_086838076.1	TIR+NPCBM*→||<-Pkinase+PASTA+NPCBM	TIR+NPCBM	334	CCN39_RS01920	actinobacteria	Amycolatopsis kentuckyensis	TIR domain-containing protein [Amycolatopsis kentuckyensis].	GCF_002155975.1
WP_086857686.1	TIR+NPCBM*→||<-?||?→ ABhydrolase→	TIR+NPCBM	324	CCN50_RS10835	actinobacteria	Amycolatopsis lexingtonensis	TIR domain-containing protein [Amycolatopsis lexingtonensis].	GCF_002156005.1
WP_086858461.1	HTH+APATPase+TPR→ TIR+NPCBM*→	TIR+NPCBM	333	CCN50_RS15120	actinobacteria	Amycolatopsis lexingtonensis	TIR domain-containing protein [Amycolatopsis lexingtonensis].	GCF_002156005.1
WP_089922416.1	<-TIR<-Pkinase+PASTA+NPCBM||TIR+NPCBM*→?→||<-?<-?<-?||SIG+Phytase-like→	TIR+NPCBM	400	BMY74_RS32975	actinobacteria	Lentzea albida	TIR domain-containing protein [Lentzea albida].	GCF_900111005.1
WP_091285568.1	TIR+NPCBM*→||<-SIGMA-HTH	TIR+NPCBM	332	BLV57_RS01490	actinobacteria	Amycolatopsis xylanica	TIR domain-containing protein [Amycolatopsis xylanica].	GCF_900107045.1
WP_091312295.1	TIR+NPCBM*→||<-?||DeoR→?→?→?→?→ TPRs+TM+TM→	TIR+NPCBM	324	BLW76_RS27015	actinobacteria	Amycolatopsis tolypomycina	TIR domain-containing protein [Amycolatopsis tolypomycina].	GCF_900105945.1
WP_091377330.1	<-AAA?<-?||TIR+NPCBM*→	TIR+NPCBM	406	BLR56_RS14460	actinobacteria	Alloactinosynnema album	TIR domain-containing protein [Alloactinosynnema album].	GCF_900099755.1
WP_091509601.1	TIR+NPCBM*→	TIR+NPCBM	307	BMZ92_RS19550	actinobacteria	Amycolatopsis sacchari	TIR domain-containing protein [Amycolatopsis sacchari].	GCF_900114035.1
WP_091597157.1	TIR+NPCM→*	*	338	-	actinobacteria	Amycolatopsis lurida	TIR domain-containing protein [Amycolatopsis lurida].	-
WP_092774771.1	<-AAA?<-?<-ParA+TIR+pIdsmall1<-TIR||TIR+NPCBM*→	TIR+NPCBM	370	BMY07_RS02730	actinobacteria	Actinokineospora terrae	TIR domain-containing protein [Actinokineospora terrae].	GCF_900111175.1
WP_096492220.1	TIR+NPCBM*→	TIR+NPCBM	321	CNX65_RS08180	actinobacteria	Actinosynnema pretiosum	TIR domain-containing protein [Actinosynnema pretiosum].	GCF_002354875.1
WP_101607037.1	TIR+NPCBM*→||<-SIGMA-HTH	TIR+NPCBM	311	BKN51_RS08135	actinobacteria	Amycolatopsis sp. BJA-103	TIR domain-containing protein [Amycolatopsis sp. BJA-103].	GCF_002849735.1
WP_103339180.1	TIR+NPCBM*→||<-?||DeoR→	TIR+NPCBM	324	C2L58_RS20385	actinobacteria	Amycolatopsis sp. CA-126428	TIR domain-containing protein [Amycolatopsis sp. CA-126428].	GCF_002904335.1
WP_103349374.1	TIR+NPCBM*→||<-Pkinase+PASTA+NPCBM	TIR+NPCBM	330	C2L59_RS10725	actinobacteria	Amycolatopsis sp. CA-128772	TIR domain-containing protein [Amycolatopsis sp. CA-128772].	GCF_002904295.1
WP_103354377.1	TIR+NPCBM*→||<-?||?→ HTH+APATPase+TPR→||<-?||?→ ABhydrolase→	TIR+NPCBM	324	C2L59_RS37045	actinobacteria	Amycolatopsis sp. CA-128772	NPCBM/NEW2 domain-containing protein [Amycolatopsis sp. CA-128772].	GCF_002904295.1
WP_116202815.1	HTH+APATPase+TPR→ TIR+NPCBM*→	TIR+NPCBM	332	D0D37_RS23965	actinobacteria	Amycolatopsis circi	TIR domain-containing protein [Amycolatopsis circi].	GCF_003385235.1
WP_116206775.1	<-ParA+TIR+pIdsmall1<-TIR||TIR+NPCBM*→	TIR+NPCBM	302	D0D37_RS45550	actinobacteria	Amycolatopsis circi	TIR domain-containing protein, partial [Amycolatopsis circi].	GCF_003385235.1
WP_118945693.1	TIR+NPCBM*→	TIR+NPCBM	321	APASM_RS08545	actinobacteria	Actinosynnema pretiosum	TIR domain-containing protein [Actinosynnema pretiosum].	GCF_003516205.1
WP_121393603.1	TIR+NPCM→*	*	374	-	actinobacteria	Actinokineospora cianjurensis	TIR domain-containing protein [Actinokineospora cianjurensis].	-
WP_121434386.1	SIG+NPCBM*→||<-MACRODOMAIN	SIG+NPCBM	236	BZB76_2536	actinobacteria	Actinomadura pelletieri	NPCBM/NEW2 domain-containing protein [Actinomadura pelletieri].	-

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
WP_125313210.1	HTH+APATPase+TPR→ TIR+NPCBM*→	TIR+NPCBM	333	EIY87_RS30160	actinobacteria	Amycolatopsis sp. GLM-1	TIR domain-containing protein [Amycolatopsis sp. GLM-1].	GCF_003937945.1
WP_125687207.1	TIR+NPCBM*→	TIR+NPCBM	311	DMC61_RS04995	actinobacteria	Amycolatopsis sp. WAC 04169	TIR domain-containing protein [Amycolatopsis sp. WAC 04169].	GCF_003947535.1
WP_132047124.1	AbiJ-NTD3+HEPN→||<-?<-AbiJ-NTD2<-?||SIG+NPCBM*→	SIG+NPCBM	233	EDF27_RS02545	actinobacteria	Curtobacterium sp. PhB136	NPCBM/NEW2 domain-containing protein [Curtobacterium sp. PhB136].	GCF_004346855.1
WP_132121932.1	TIR+NPCBM*→||<-TIR+APATPase+TPR<-HTH+APATPase+TPR	TIR+NPCBM	320	EV192_RS31600	actinobacteria	Actinocrispum wychmicini	TIR domain-containing protein [Actinocrispum wychmicini].	GCF_004345645.1
WP_132396057.1	SIG+NPCBM*→	SIG+NPCBM	248	E1258_RS01390	actinobacteria	Micromonospora sp. KC207	hypothetical protein [Micromonospora sp. KC207].	GCF_004348615.1
WP_134666532.1	TIR+NPCM→*	*	401	-	actinobacteria	Amycolatopsis sp. CFH S0078	TIR domain-containing protein [Amycolatopsis sp. CFH S0078].	-
WP_134731967.1	TIR+NPCM→*	*	401	-	actinobacteria	Amycolatopsis sp. CFH S0261	TIR domain-containing protein [Amycolatopsis sp. CFH S0261].	-
WP_134736094.1	TIR+NPCM→*	*	401	-	actinobacteria	Amycolatopsis sp. CFH S0740	TIR domain-containing protein [Amycolatopsis sp. CFH S0740].	-
WP_139190910.1	<-AAA?<-?||TIR+NPCBM*→	TIR+NPCBM	428	BLS56_RS22670	actinobacteria	Alloactinosynnema iranicum	TIR domain-containing protein [Alloactinosynnema iranicum].	GCF_900101685.1
WP_145934223.1	<-AAA?<-?<-ParA+TIR+pIdsmall1<-TIR||TIR+NPCBM*→	TIR+NPCBM	318	FNH07_RS09925	actinobacteria	Amycolatopsis bartoniae	TIR domain-containing protein [Amycolatopsis bartoniae].	GCF_007713755.1
WP_146108413.1	TIR+NPCBM*→	TIR+NPCBM	324	CLV40_RS36380	actinobacteria	Actinokineospora auranticolor	TIR domain-containing protein [Actinokineospora auranticolor].	GCF_002934265.1
WP_153029663.1	TIR+NPCBM*→	TIR+NPCBM	314	YIM_RS07645	actinobacteria	Amycolatopsis sp. YIM 10	TIR domain-containing protein [Amycolatopsis sp. YIM 10].	GCF_009429145.1
WP_153030365.1	<-AAA?<-?<-ParA+TIR+pIdsmall1<-TIR||TIR+NPCBM*→||<-?<-?<-AAA<-TIR+Pkinase||SIG+TIR→	TIR+NPCBM	341	YIM_RS11635	actinobacteria	Amycolatopsis sp. YIM 10	TIR domain-containing protein [Amycolatopsis sp. YIM 10].	GCF_009429145.1
WP_153804578.1	<-HTH+APATPase+TPR||?→?→ TPR+TM+TM→ TIR+NPCBM*→ DUF1707-SHOCT-bihelical+TM+NPCBM→	TIR+NPCBM	348	GFY24_RS09395	actinobacteria	Nocardia sp. SYP-A9097	TIR domain-containing protein [Nocardia sp. SYP-A9097].	GCF_009649815.1
WP_154760338.1	<-AAA?<-?<-ParA+TIR+pIdsmall1<-TIR||TIR+NPCBM*→	TIR+NPCBM	380	GKO32_30380	actinobacteria	Amycolatopsis pithecelloba	TIR domain-containing protein [Amycolatopsis pithecelloba].	-
WP_155543819.1	TIR+NPCBM*→||<-?<-?<-?||DeoR→	TIR+NPCBM	324	AA23TX_RS18915	actinobacteria	Amycolatopsis sp. A23	TIR domain-containing protein [Amycolatopsis sp. A23].	GCF_902497555.1
WP_156077140.1	HTH+APATPase+TPR→?→ TIR+SWACOS→?→ TIR+NPCBM*→	TIR+NPCBM	345	OQ02_RS41080	actinobacteria	Saccharothrix sp. NRRL B-16314	TIR domain-containing protein [Saccharothrix sp. NRRL B-16314].	GCF_000716595.1
WP_156753285.1	<-AAA?<-?<-ParA+TIR+pIdsmall1<-TIR||TIR+NPCBM*→	TIR+NPCBM	409	GCL84_RS00345	actinobacteria	Actinokineospora sp. TRM65233	TIR domain-containing protein [Actinokineospora sp. TRM65233].	GCF_009745975.1
WP_157767649.1	SIG+TIR+APATPase+TPR+TPR+TPR→?→ TIR+NPCBM*→	TIR+NPCBM	338	CNX65_RS14535	actinobacteria	Actinosynnema pretiosum	TIR domain-containing protein [Actinosynnema pretiosum].	GCF_002354875.1
WP_158005434.1	TIR+NPCBM*→||<-SIGMA-HTH	TIR+NPCBM	311	BLW75_RS08360	actinobacteria	Amycolatopsis lurida	TIR domain-containing protein [Amycolatopsis lurida].	GCF_900105055.1
WP_158104517.1	TIR+NPCBM*→||<-?||DeoR→?→?→?→?→ TPRs+TM+TM→	TIR+NPCBM	323	CCN39_RS17180	actinobacteria	Amycolatopsis kentuckyensis	TIR domain-containing protein [Amycolatopsis kentuckyensis].	GCF_002155975.1
WP_158242545.1	TIR+NPCBM*→	TIR+NPCBM	322	ATK30_RS34520	actinobacteria	Amycolatopsis niigatensis	TIR domain-containing protein [Amycolatopsis niigatensis].	GCF_002846615.1
WP_158632605.1	TIR+NPCBM*→||<-SIGMA-HTH	TIR+NPCBM	311	DL990_RS12775	actinobacteria	unclassified Amycolatopsis	MULTISPECIES: TIR domain-containing protein [unclassified Amycolatopsis].	GCF_003947325.1
WP_158633124.1	TIR+NPCBM*→||<-SIGMA-HTH	TIR+NPCBM	311	DMH03_RS26290	actinobacteria	Amycolatopsis sp. WAC 01376	TIR domain-containing protein [Amycolatopsis sp. WAC 01376].	GCF_003947415.1
WP_158633195.1	TIR+NPCBM*→||<-SIGMA-HTH	TIR+NPCBM	311	DMH01_RS07200	actinobacteria	Amycolatopsis sp. WAC 04182	TIR domain-containing protein [Amycolatopsis sp. WAC 04182].	GCF_003947465.1

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
WP_158634321.1	TIR+NPCBM*→	TIR+NPCBM	311	DMC64_RS39520	actinobacteria	Amycolatopsis sp. WAC 04197	TIR domain-containing protein [Amycolatopsis sp. WAC 04197].	GCF_003947475.1
WP_158641456.1	TIR+NPCBM*→	TIR+NPCBM	323	EIY87_RS41990	actinobacteria	Amycolatopsis sp. GLM-1	TIR domain-containing protein [Amycolatopsis sp. GLM-1].	GCF_003937945.1
WP_158660795.1	<-SIG+NPCBM<-?||PNPase+bDLD3→ bDLD3+NPCBM*→ DUF1707-SHOCT-bihelical+TM+NPCBM→||<-LD-peptidase	bDLD3+NPCBM	227	NS506_RS18405	actinobacteria	Nocardia seriolae	NPCBM/NEW2 domain-containing protein [Nocardia seriolae].	GCF_001865855.1
WP_160694349.1	TIR+NPCBM*→	TIR+NPCBM	333	GTY80_RS02520	actinobacteria	Amycolatopsis sp. SID8362	NPCBM/NEW2 domain-containing protein [Amycolatopsis sp. SID8362].	GCF_010550475.1
WP_160695878.1	<-ParA+TIR+pIdsmall1<-TIR||TIR+NPCBM*→	TIR+NPCBM	323	GTY80_RS10210	actinobacteria	Amycolatopsis sp. SID8362	TIR domain-containing protein [Amycolatopsis sp. SID8362].	GCF_010550475.1
WP_162945306.1	HTH+APATPase+TPR→?→ TIR+SWACOS→ SIG+TIR+APATPase+TPR+TPR+TPR→?→ TIR+NPCBM*→	TIR+NPCBM	334	APASM_RS15040	actinobacteria	Actinosynnema pretiosum	TIR domain-containing protein [Actinosynnema pretiosum].	GCF_003516205.1
WP_166054137.1	TIR+NPCBM*→	TIR+NPCBM	358	G7043_RS41275	actinobacteria	Lentzea sp. NEAU-D13	TIR domain-containing protein [Lentzea sp. NEAU-D13].	GCF_011067745.1
WP_166459784.1	TIR+NPCBM*→	TIR+NPCBM	312	GKO32_RS30390	actinobacteria	Amycolatopsis pithecelloba	TIR domain-containing protein [Amycolatopsis pithecelloba].	GCF_009707865.1
WP_166658167.1	<-AAA?<-?||TIR+NPCBM*→	TIR+NPCBM	333	C8E96_RS30065	actinobacteria	Alloactinosynnema album	TIR domain-containing protein [Alloactinosynnema album].	GCF_004362515.1
WP_167754290.1	TIR+NPCBM*→	TIR+NPCBM	317	EIZ44_RS27085	actinobacteria	Amycolatopsis sp. CFH S0261	TIR domain-containing protein [Amycolatopsis sp. CFH S0261].	GCF_004522235.1
WP_167756625.1	TIR+NPCBM*→	TIR+NPCBM	317	EIZ45_RS33520	actinobacteria	Amycolatopsis sp. CFH S0740	TIR domain-containing protein [Amycolatopsis sp. CFH S0740].	GCF_004522315.1
WP_167757025.1	TIR+NPCBM*→	TIR+NPCBM	317	EIZ40_RS28840	actinobacteria	Amycolatopsis sp. CFH S0078	TIR domain-containing protein [Amycolatopsis sp. CFH S0078].	GCF_004522265.1
WP_168444669.1	GDSL+YEATS→||<-?||?→ CASPASE→ HTH+APATPase+TPR→?→ TIR+APATPase+TPR→ SIG+NPCBM*→	SIG+NPCBM	234	AL2_RS24450	actinobacteria	Actinomadura latina	NPCBM/NEW2 domain-containing protein [Actinomadura latina].	GCF_001552195.1
WP_170180607.1	SIG+NPCBM*→||<-MACRODOMAIN	SIG+NPCBM	213	BZB76_RS12335	actinobacteria	Actinomadura pelletieri	NPCBM/NEW2 domain-containing protein [Actinomadura pelletieri].	GCF_003634705.1
WP_170224594.1	TIR+NPCBM*→	TIR+NPCBM	316	CLV68_RS26440	actinobacteria	Actinokineospora cianjurensis	TIR domain-containing protein [Actinokineospora cianjurensis].	GCF_003663795.1

5. Source data. Gene neighborhoods and domain architectures of the FGS domains described in this study

acc	**operon**	**architecture**	**len**	**gen.name**	**taxend**	**species**	**defline**	**gca**
ABX05873.1	BACTERIALFRINGE→ BetaPropeller→||<-?||?→?→ NACHT+FGS*→	NACHT+FGS	957	Haur_3236	chloroflexi	Herpetosiphon aurantiacus DSM 785	protein of unknown function DUF323 [Herpetosiphon aurantiacus DSM 785].	GCA_000018565.1
AEQ20336.1	Pkinase+FHA→ SIGMA-HTH→?→ DrHyd+nSTAND1+FGS*→||<-RVT<-TIR+FGS<-TIR+nSTAND1+FGS	DrHyd+nSTAND1+FGS	947	THIMO_RS13755	bacteria	uncultured bacterium EC5	formylglycine-generating sulfatase-like enzyme [uncultured bacterium EC5].	-
AGA91585.1	<-ABhydrolase<-?<-?<-?<-?||TIR+nSTAND1+FGS*→||<-SIG+SWC3<-TIR+nSTAND1+FGS	TIR+nSTAND1+FGS	891	Thimo_2887	gammaproteobacteria	Thioflavicoccus mobilis 8321	hypothetical protein Thimo_2887 [Thioflavicoccus mobilis 8321].	GCA_000327045.1
ASF47990.1	<-SIG+TM+TM+TM<-?||TIR+NACHT→ SIG+FGS*→	SIG+FGS	257	CEK71_19030	gammaproteobacteria	Methylovulum psychrotolerans	hypothetical protein CEK71_19030 [Methylovulum psychrotolerans].	GCA_002209385.1
AUB79799.1	FGS*→||<-?<-CASPASE	FGS	289	THSYN_01695	gammaproteobacteria	Candidatus Thiodictyon syntrophicum	hypothetical protein THSYN_01695 [Candidatus Thiodictyon syntrophicum].	GCA_002813775.1
AUB81902.1	EAD8→ nSTAND1→ FGS*→?→?→?→||<-FGS	FGS	294	THSYN_13670	gammaproteobacteria	Candidatus Thiodictyon syntrophicum	hypothetical protein THSYN_13670 [Candidatus Thiodictyon syntrophicum].	GCA_002813775.1
CAB1059904.1	<-REC<-?||?→ CNMP→ CNMP→ KAP-NTPase→ KAP-NTPase+FGS*→||<-?<-?<-Cluster455_2clades<-?<-?||REC+ACYC→||<-LRP-HTH	KAP-NTPase+FGS	540	D1BOALGB6SA_4669	deltaproteobacteria	Olavius sp. associated proteobacterium Delta 1	hypothetical protein D1BOALGB6SA_4669 [Olavius sp. associated proteobacterium Delta 1].	-
CAB1065856.1	KAP-NTPase+FGS*→	KAP-NTPase+FGS	661	D1BOALGB6SA_10655	deltaproteobacteria	Olavius sp. associated proteobacterium Delta 1	hypothetical protein D1BOALGB6SA_10655 [Olavius sp. associated proteobacterium Delta 1].	-
CBH39249.1	<-N-OB<-?||Calcineurin+NACHT+FGS*→?→?→||<-?<-?<-LittleFinger	Calcineurin+NACHT+FGS	1107	BSM_27270	archaea	uncultured archaeon	hypothetical protein, calcineurin-like phosphoesterase, NACHT domain, and DUF323 family [uncultured archaeon].	-
CUS31463.1	DrHyd+nSTAND1+FGS*→	DrHyd+nSTAND1+FGS	911	COMA1_10121	nitrospirae	Candidatus Nitrospira nitrosa	Sigma 54 interacting domain protein [Candidatus Nitrospira nitrosa].	GCA_001458735.1
ETW99001.1	bDLD3+nSTAND1+FGS*→	bDLD3+nSTAND1+FGS	783	ETSY1_16630	nitrospinae/tectomicrobia group	Candidatus Entotheonella factor	hypothetical protein ETSY1_16630 [Candidatus Entotheonella factor].	GCA_000522425.1
EXI66627.1	LRP-HTH→?→ YBAK→||<-?<-?<-?<-?||EAD8+nSTAND1+FGS*→	EAD8+nSTAND1+FGS	826	pkn1_3	betaproteobacteria	Candidatus Accumulibacter sp. SK-12	Serine/threonine-protein kinase pkn1 [Candidatus Accumulibacter sp. SK-12].	GCA_000585015.1
EXI69278.1	SIG+TM+TM+TM+TM+TM+TM+TM+TM→||<-Patatin||?→||<-?||?→||<-?||TIR+nSTAND1+FGS*→	TIR+nSTAND1+FGS	762	pkn1_1	betaproteobacteria	Candidatus Accumulibacter sp. SK-12	Serine/threonine-protein kinase pkn1 [Candidatus Accumulibacter sp. SK-12].	GCA_000585015.1

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
EXI70483.1	EAD8+nSTAND1+FGS*→	EAD8+nSTAND1+FGS	824	pkn1_6	betaproteobacteria	Candidatus Accumulibacter sp. SK-11	Serine/threonine-protein kinase pkn1 [Candidatus Accumulibacter sp. SK-11].	GCA_000584995.1
EXI75672.1	SWC3→||<-?<-?||?→ FGS*→	FGS	248	pkn1_2	betaproteobacteria	Candidatus Accumulibacter sp. SK-11	Serine/threonine-protein kinase pkn1 [Candidatus Accumulibacter sp. SK-11].	GCA_000584995.1
EXI76855.1	SIG+TM+TM+TM+TM+TM+TM+TM+TM→||<-Patatin||?→||<-?||?→||<-?||nSTAND1+FGS*→||<-fvmYukDl-Nterm	nSTAND1+FGS	765	pkn1_1	betaproteobacteria	Candidatus Accumulibacter sp. SK-11	Serine/threonine-protein kinase pkn1 [Candidatus Accumulibacter sp. SK-11].	GCA_000584995.1
EXI82219.1	<-CNMP+CRP-HTH||FAD-NAD-dep-oxidoreductase→?→||<-?<-?<-?<-ABhydrolase||nSTAND1+FGS*→||<-?<-SIG+CACHE+TM+PAS+PAS+GGDEF+EAL<-?||?→?→ ABC-ATPase→	nSTAND1+FGS	784	pkn1_4	betaproteobacteria	Candidatus Accumulibacter sp. BA-92	Serine/threonine-protein kinase pkn1 [Candidatus Accumulibacter sp. BA-92].	GCA_000585055.1
EXI89946.1	nSTAND1→ nSTAND1+FGS*→	nSTAND1+FGS	409	pkn1	betaproteobacteria	Candidatus Accumulibacter sp. BA-94	Serine/threonine-protein kinase pkn1 [Candidatus Accumulibacter sp. BA-94].	GCA_000585095.1
EXI90315.1	<-CNMP+CRP-HTH||FAD-NAD-dep-oxidoreductase→?→||<-?<-?<-?<-ABhydrolase||TIR+nSTAND1+FGS*→||<-ABHYDROLASE<-SIG+CACHE+TM+PAS+PAS+GGDEF+EAL<-?||?→ ABC-ATPase→	TIR+nSTAND1+FGS	778	pkn1_1	betaproteobacteria	Candidatus Accumulibacter sp. BA-93	Serine/threonine-protein kinase pkn1 [Candidatus Accumulibacter sp. BA-93].	GCA_000585075.1
GAK51596.1	FGS*→ Four-helical-protein→	FGS	347	U14_02841	bacteria	Candidatus Moduliflexus flocculans	hypothetical protein U14_02841 [Candidatus Moduliflexus flocculans].	GCA_000739515.1
GAK55793.1	SIG+TM+TM+TM+TM+TM+TM+TM+TM+TM→?→ ABC-ATPase→ ABC-ATPase→ NACHT+FGS*→	NACHT+FGS	1007	U27_02752	bacteria	Candidatus Vecturithrix granuli	hypothetical protein U27_02752 [Candidatus Vecturithrix granuli].	GCA_000739535.1
GAK57663.1	TIR+NACHT+FGS*→ MED26C→?→||<-ABC-ATPase	TIR+NACHT+FGS	1091	U27_04630	bacteria	Candidatus Vecturithrix granuli	hypothetical protein U27_04630 [Candidatus Vecturithrix granuli].	GCA_000739535.1
GAK60834.1	SIG+TM+TM+TM+TM+TM→?→?→ REase→ TIR+NACHT+FGS*→||<-?<-?<-?<-?<-?<-?||GNTR-HTH→	TIR+NACHT+FGS	1098	U27_00732	bacteria	Candidatus Vecturithrix granuli	signal transduction protein [Candidatus Vecturithrix granuli].	GCA_000739535.1
GDY22761.1	NACHT+FGS*→	NACHT+FGS	859	LBMAG56_41080	verrucomicrobia	Verrucomicrobia bacterium	hypothetical protein LBMAG56_41080 [Verrucomicrobia bacterium].	-
HAW49373.1	REase+NACHT+FGS*→	REase+NACHT+FGS	821	DCX16_00245	bacteria	bacterium	TPA: hypothetical protein DCX16_00245 [bacterium].	GCA_003498085.1
HAY28136.1	nSTAND1-C+FGS*→||<-RVT	nSTAND1-C+FGS	564	DCY47_11690	betaproteobacteria	Candidatus Accumulibacter sp.	TPA: hypothetical protein DCY47_11690, partial [Candidatus Accumulibacter sp.].	GCA_003487685.1
HBW50062.1	BACTERIALFRINGE→ BetaPropeller→||<-?||?→?→ NACHT+FGS*→	NACHT+FGS	961	DEF47_09155	chloroflexi	Herpetosiphon sp.	TPA: hypothetical protein DEF47_09155 [Herpetosiphon sp.].	GCA_003512625.1
HBY06356.1	<-ABC-ATPase<-LRP-HTH||SIG+TM+TM+TM→?→?→?→ KAP-NTPase→ SIG+KAP-NTPase+FGS*→ KAP-NTPase→	SIG+KAP-NTPase+FGS	655	DEH22_00650	chloroflexi	Chloroflexi bacterium	TPA: hypothetical protein DEH22_00650 [Chloroflexi bacterium].	GCA_003512075.1
HBY99326.1	FGS*→	FGS	244	DEP84_36210	chloroflexi	Chloroflexi bacterium	TPA: hypothetical protein DEP84_36210 [Chloroflexi bacterium].	GCA_003520455.1
HCB49403.1	NACHT+FGS*→	NACHT+FGS	568	DEP47_07750	chloroflexi	Chloroflexi bacterium	TPA: hypothetical protein DEP47_07750 [Chloroflexi bacterium].	GCA_003519205.1

acc	**operon**	**architecture**	**len**	**gen.name**	**taxend**	**species**	**defline**	**gca**
HCQ00349.1	FGS*→	FGS	230	DIT99_06480	bacteria	Candidatus Latescibacteria bacterium	TPA: formylglycine-generating enzyme family protein [Candidatus Latescibacteria bacterium].	GCA_003533805.1
HCS89156.1	FGS*→||<-Trypsin<-Trypco1	FGS	269	DIW77_03590	gammaproteobacteria	Chromatiaceae bacterium	TPA: hypothetical protein DIW77_03590 [Chromatiaceae bacterium].	GCA_003525925.1
HCS89670.1	FGS*→||<-Four-helical-protein||RVT→	FGS	269	DIW77_06290	gammaproteobacteria	Chromatiaceae bacterium	TPA: hypothetical protein DIW77_06290 [Chromatiaceae bacterium].	GCA_003525925.1
HCZ14308.1	FGS*→||<-RVT||Four-helical-protein→||<-SIG+FGS	FGS	328	DHV85_06865	betaproteobacteria	Candidatus Accumulibacter sp.	TPA: hypothetical protein DHV85_06865 [Candidatus Accumulibacter sp.].	GCA_003538495.1
HCZ17485.1	<-ABhydrolase<-?||nSTAND1+FGS*→||<-SIG+CACHE+TM+PAS+PAS+GGDEF+EAL	nSTAND1+FGS	833	DHV85_23525	betaproteobacteria	Candidatus Accumulibacter sp.	TPA: hypothetical protein DHV85_23525 [Candidatus Accumulibacter sp.].	GCA_003538495.1
HDP89132.1	NACHT+FGS*→	NACHT+FGS	860	ENN42_04130	gammaproteobacteria	Thioalkalivibrio sp.	TPA: NACHT domain-containing protein [Thioalkalivibrio sp.].	-
HDQ70913.1	TM+NACHT+FGS*→	TM+NACHT+FGS	1091	ENN19_02320	chloroflexi	Chloroflexi bacterium	TPA: NACHT domain-containing protein [Chloroflexi bacterium].	-
HDQ71358.1	FGS→ *Four-helical-protein→ FGS→ RVT→ NACHT+FGS→*	FGS	210	ENN19_04585	chloroflexi	Chloroflexi bacterium	TPA: hypothetical protein ENN19_04585, partial [Chloroflexi bacterium].	-
HDQ71362.1	NACHT+FGS*→	NACHT+FGS	951	ENN19_04605	chloroflexi	Chloroflexi bacterium	TPA: hypothetical protein ENN19_04605 [Chloroflexi bacterium].	-
HDU42372.1	TIR+FGS*→?→ Eukglutathionesyn-ATPgrasp→	TIR+FGS	438	ENQ67_02445	chloroflexi	Chloroflexi bacterium	TPA: TIR domain-containing protein [Chloroflexi bacterium].	-
HDU42685.1	TIR+FGS*→||<-TIMbarrel	TIR+FGS	376	ENQ67_04025	chloroflexi	Chloroflexi bacterium	TPA: TIR domain-containing protein [Chloroflexi bacterium].	-
HDU45349.1	SWC3→ SWC3→ FGS*→	FGS	293	ENQ67_17585	chloroflexi	Chloroflexi bacterium	TPA: hypothetical protein ENQ67_17585 [Chloroflexi bacterium].	-
HDW29972.1	ABhydrolase→?→||<-?||TIR+FGS*→?→?→?→?→?→ SIR2→	TIR+FGS	403	ENQ61_08065	chloroflexi	Chloroflexi bacterium	TPA: TIR domain-containing protein [Chloroflexi bacterium].	-
HDX49653.1	KAP-NTPase+FGS*→	KAP-NTPase+FGS	750	ENQ23_11400	chloroflexi	Chloroflexi bacterium	TPA: hypothetical protein ENQ23_11400 [Chloroflexi bacterium].	-
HDY04216.1	<-SIG+TM+TM+TM+TM+TM+TM+TM+TM+TM<-?||?→?→?→?→?→ START+FGS*→?→?→?→?→?→ MoxR-AAA→	START+FGS	371	ENQ01_08530	chloroflexi	Chloroflexi bacterium	TPA: hypothetical protein ENQ01_08530 [Chloroflexi bacterium].	-
HEC22740.1	NACHT+FGS*→	NACHT+FGS	981	ENI95_07470	chloroflexi	Chloroflexi bacterium	TPA: NACHT domain-containing protein [Chloroflexi bacterium].	-
HET90350.1	KAP-NTPase+FGS*→||<-?<-?<-?<-TPR+TPR+TPR+TPR	KAP-NTPase+FGS	776	ENN99_06380	chloroflexi	Chloroflexi bacterium	TPA: hypothetical protein ENN99_06380 [Chloroflexi bacterium].	-
HET91868.1	NACHT+FGS*→	NACHT+FGS	1053	ENN99_14185	chloroflexi	Chloroflexi bacterium	TPA: NACHT domain-containing protein [Chloroflexi bacterium].	-

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HEU31392.1	NACHT+FGS*→ Four-helical-protein→ RVT→	NACHT+FGS	452	ENQ60_07770	bacteria	bacterium	TPA: formylglycine-generating enzyme family protein [bacterium].	-
HEY85774.1	CASPASE+FGS*→ RVT→ Four-helical-protein→	CASPASE+FGS	599	G4N96_11770	chloroflexi	Chloroflexi bacterium	TPA: SUMF1/EgtB/PvdO family nonheme iron enzyme [Chloroflexi bacterium].	-
HFG28526.1	NACHT→ NACHT+FGS*→ SIG+SWC3→ RVT→||<-?||?→?→?→ SIGMA-HTH→	NACHT+FGS	437	ENS73_16885	verrucomicrobia	Verrucomicrobia subdivision 3 bacterium	TPA: hypothetical protein ENS73_16885 [Verrucomicrobia subdivision 3 bacterium].	-
HFI29792.1	NACHT+FGS*→ FURR-HTH→	NACHT+FGS	761	ENS47_13485	chloroflexi	Chloroflexi bacterium	TPA: NACHT domain-containing protein, partial [Chloroflexi bacterium].	-
HGH57499.1	KAP-NTPase+FGS*→	KAP-NTPase+FGS	750	ENV55_04065	chloroflexi	Chloroflexi bacterium	TPA: hypothetical protein ENV55_04065 [Chloroflexi bacterium].	-
HGH59410.1	FGS*→	FGS	299	ENV55_14010	chloroflexi	Chloroflexi bacterium	TPA: formylglycine-generating enzyme family protein [Chloroflexi bacterium].	-
HGV26478.1	NACHT+FGS*→ SIG+SWC3→?→?→||<-?<-?<-SIG+PTSIIB-sorb	NACHT+FGS	1042	ENS93_08620	chloroflexi	Chloroflexi bacterium	TPA: NACHT domain-containing protein [Chloroflexi bacterium].	-
HGV28164.1	bDLD1+NACHT+FGS→?→?→ KAP-NTPase+FGS*→?→?→?→?→ SIG+TPR+TPR+TPR→	KAP-NTPase+FGS	742	ENS93_17300	chloroflexi	Chloroflexi bacterium	TPA: hypothetical protein ENS93_17300 [Chloroflexi bacterium].	-
HGY49632.1	EAD7+TIR+FGS*→	EAD7+TIR+FGS	580	ENR34_13005	chloroflexi	Anaerolineae bacterium	TPA: TIR domain-containing protein [Anaerolineae bacterium].	-
HGY52758.1	FGS*→	FGS	228	ENR34_29005	chloroflexi	Anaerolineae bacterium	TPA: formylglycine-generating enzyme family protein [Anaerolineae bacterium].	-
HHF60465.1	ZNR+NACHT+FGS→ *CASPASE*→ *NACHT*→ *FGS*→	ZNR+NACHT+FGS	925	ENL51_05545	acidobacteria	Candidatus Solibacter sp.	TPA: NACHT domain-containing protein [Candidatus Solibacter sp.].	-
HHF60468.1	FGS*→	FGS	344	ENL51_05560	acidobacteria	Candidatus Solibacter sp.	TPA: hypothetical protein ENL51_05560 [Candidatus Solibacter sp.].	-
HHH41247.1	NACHT+FGS*→ SIG+SWC3→	NACHT+FGS	1027	ENK56_04500	chloroflexi	Chloroflexi bacterium	TPA: NACHT domain-containing protein [Chloroflexi bacterium].	-
HHR86634.1	NACHT+FGS*→	NACHT+FGS	996	ENL64_01430	chloroflexi	Anaerolineae bacterium	TPA: NACHT domain-containing protein [Anaerolineae bacterium].	-
HHW76671.1	SIG+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM→ ABC-ATPase→ TIR+nSTAND1+FGS*→||<-MED24<-?||FGS→ REase→ RVT→||<-FGS	TIR+nSTAND1+FGS	754	GX399_06480	gammaproteobacteria	Xanthomonadaceae bacterium	TPA: SUMF1/EgtB/PvdO family nonheme iron enzyme [Xanthomonadaceae bacterium].	-
HHW77288.1	NACHT+FGS*→	NACHT+FGS	827	GX399_09735	gammaproteobacteria	Xanthomonadaceae bacterium	TPA: SUMF1/EgtB/PvdO family nonheme iron enzyme [Xanthomonadaceae bacterium].	-
HHZ92662.1	FGS*→	FGS	236	EYN65_19595	bacteria	Candidatus Poribacteria bacterium	TPA: formylglycine-generating enzyme family protein [Candidatus Poribacteria bacterium].	-

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HIC91070.1	FGS*→	FGS	259	EYP21_03210	deltaproteobacteria	Syntrophaceae bacterium	TPA: hypothetical protein EYP21_03210 [Syntrophaceae bacterium].	-
HID19936.1	NACHT+FGS*→	NACHT+FGS	740	EYP28_03210	euryarchaeota	Methanophagales archaeon	TPA: NACHT domain-containing protein [Methanophagales archaeon].	-
HID51452.1	<-PIN<-?||SIG+KAP-NTPase+FGS*→	SIG+KAP-NTPase+FGS	847	EYP41_05380	chloroflexi	Anaerolineae bacterium	TPA: hypothetical protein EYP41_05380 [Anaerolineae bacterium].	-
HID51956.1	NACHT+FGS*→	NACHT+FGS	383	EYP41_07970	chloroflexi	Anaerolineae bacterium	TPA: hypothetical protein EYP41_07970, partial [Anaerolineae bacterium].	-
HID52846.1	EAD7+NACHT+FGS*→	EAD7+NACHT+FGS	964	EYP41_12530	chloroflexi	Anaerolineae bacterium	TPA: NACHT domain-containing protein [Anaerolineae bacterium].	-
HID54715.1	FGS→?→ NACHT+FGS*→	NACHT+FGS	985	EYP41_22100	chloroflexi	Anaerolineae bacterium	TPA: NACHT domain-containing protein, partial [Anaerolineae bacterium].	-
HIE28389.1	SIG+Trypsin+PDZ+PDZ→ SIG+FGS*→	SIG+FGS	524	EYP66_14005	bacteria	Candidatus Poribacteria bacterium	TPA: PEGA domain-containing protein [Candidatus Poribacteria bacterium].	-
HIE38682.1	KAP-NTPase+FGS*→	KAP-NTPase+FGS	769	EYP77_06385	chloroflexi	Anaerolineae bacterium	TPA: hypothetical protein EYP77_06385 [Anaerolineae bacterium].	-
KAA3641003.1	TIMbarrel→?→ EAD8+Trypsin→ DADA-Ligase→?→ Cluster323_2clades→?→ EAD8+NACHT+FGS*→	EAD8+NACHT+FGS	1039	DWQ02_01180	bacteroidetes	Bacteroidetes bacterium	hypothetical protein DWQ02_01180 [Bacteroidetes bacterium].	-
KAB2859035.1	TIR+FGS*→	TIR+FGS	340	F9K46_11255	chloroflexi	Anaerolineae bacterium	formylglycine-generating enzyme family protein, partial [Anaerolineae bacterium].	-
KAB2893788.1	TIR→ ParA-Soj-PloopNTPase+TIR+NACHT+FGS*→||<-?<-?||?→||<-?<-?<-?<-SF2-DUF3427A+LPD33	ParA-Soj-PloopNTPase+TIR+NACHT+FGS	1177	F9K28_07510	bacteroidetes	Bacteriodetes bacterium	SUMF1/EgtB/PvdO family nonheme iron enzyme [Bacteriodetes bacterium].	-
KAB2903680.1	FGS*→?→||<-VWA+FHA<-?<-?<-ABC-ATPase<-ABC-ATPase	FGS	280	F9K27_12805	chloroflexi	Anaerolineae bacterium	formylglycine-generating enzyme family protein [Anaerolineae bacterium].	-
KAB2903832.1	TIR+FGS*→	TIR+FGS	549	F9K27_11930	chloroflexi	Anaerolineae bacterium	SUMF1/EgtB/PvdO family nonheme iron enzyme [Anaerolineae bacterium].	-
KAB2904272.1	TIR+FGS→ *TIR+FGS*→||<-?||ABhydrolase→	TIR+FGS	523	F9K27_09315	chloroflexi	Anaerolineae bacterium	SUMF1/EgtB/PvdO family nonheme iron enzyme [Anaerolineae bacterium].	-
KAB2904273.1	TIR+FGS*→	TIR+FGS	421	F9K27_09320	chloroflexi	Anaerolineae bacterium	SUMF1/EgtB/PvdO family nonheme iron enzyme [Anaerolineae bacterium].	-
KAB2905607.1	DrHyd+NACHT+FGS→ NUDIX→?→?→ TIR+NACHT+FGS*→ NUDIX→	TIR+NACHT+FGS	902	F9K27_02420	chloroflexi	Anaerolineae bacterium	SUMF1/EgtB/PvdO family nonheme iron enzyme [Anaerolineae bacterium].	-
KAF0106945.1	nSTAND1+Pentapeptide→ KAP-NTPase+FGS*→	KAP-NTPase+FGS	727	FD146_2055	chloroflexi	Anaerolineaceae bacterium	hypothetical protein FD146_2055 [Anaerolineaceae bacterium].	-

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
KFB67876.1	TIR+NACHT→ FGS*→	FGS	279	pkn1_17	betaproteobacteria	Candidatus Accumulibacter sp. SK-01	Serine/threonine-protein kinase pkn1 [Candidatus Accumulibacter sp. SK-01].	GCA_000584955.2
KFB69575.1	TIR→ MoxR-AAA→ MED26C→ vWA-L+FGS*→	vWA-L+FGS	808	pkn1_4	betaproteobacteria	Candidatus Accumulibacter sp. SK-01	Serine/threonine-protein kinase pkn1 [Candidatus Accumulibacter sp. SK-01].	GCA_000584955.2
KFB72199.1	ABC-ATPase→||<-?<-?||?→?→ SIG+FGS→*//<-Four-helical-protein//RVT→//<-FGS*<-MED26C<-MoxR-AAA<-TIR	SIG+FGS	194	egtB_1	betaproteobacteria	Candidatus Accumulibacter sp. BA-91	Iron(II)-dependent oxidoreductase EgtB [Candidatus Accumulibacter sp. BA-91].	GCA_000585035.2
KFB72202.1	FGS*→	FGS	826	pkn1_7	betaproteobacteria	Candidatus Accumulibacter sp. BA-91	Serine/threonine-protein kinase pkn1 [Candidatus Accumulibacter sp. BA-91].	GCA_000585035.2
KFB75278.1	NACHT+FGS*→||<-DrHyd+NACHT+FGS<-?||?→?→?→?→ MoxR-AAA→	NACHT+FGS	959	pkn1_15	betaproteobacteria	Candidatus Accumulibacter sp. SK-02	Serine/threonine-protein kinase pkn1 [Candidatus Accumulibacter sp. SK-02].	GCA_000584975.2
KFB77125.1	SIG+drhyd→ FGS*→	FGS	250	pkn1_7	betaproteobacteria	Candidatus Accumulibacter sp. SK-02	Serine/threonine-protein kinase pkn1 [Candidatus Accumulibacter sp. SK-02].	GCA_000584975.2
KFB77789.1	TIR→ MoxR-AAA→ MED26C→ vWA-L+FGS→*//<-RVT//Four-helical-protein→//<-FGS*<-?<-SIG+SWC3||?→||<-nSTAND1+TM+TPR+TPR<-?||?→ REase→	vWA-L+FGS	789	pkn1_3	betaproteobacteria	Candidatus Accumulibacter sp. SK-02	Serine/threonine-protein kinase pkn1 [Candidatus Accumulibacter sp. SK-02].	GCA_000584975.2
KFB77792.1	FGS*→	FGS	300	pkn1_4	betaproteobacteria	Candidatus Accumulibacter sp. SK-02	Serine/threonine-protein kinase pkn1 [Candidatus Accumulibacter sp. SK-02].	GCA_000584975.2
KKO20907.1	NACHT+FGS*→	NACHT+FGS	635	BROFUL_00364	planctomycetes	Candidatus Brocadia fulgida	hypothetical protein BROFUL_00364 [Candidatus Brocadia fulgida].	GCA_000987375.1
KPA14107.1	DrHyd+nSTAND1+FGS*→	DrHyd+nSTAND1+FGS	1037	MHK_005707	deltaproteobacteria	Candidatus Magnetomorum sp. HK-1	signal transduction protein [Candidatus Magnetomorum sp. HK-1].	GCA_001292585.1
KXK13840.1	TIR+NACHT+TCAD10+TCAD10→ TIR+FGS*→||<-TRANSGLUTAMINASE	TIR+FGS	530	UZ15_CFX003003227	chloroflexi	Chloroflexi bacterium OLB15	serine/threonine protein kinase [Chloroflexi bacterium OLB15].	GCA_001567085.1
KXK49058.1	SIG+TM+TM+TM+TM+TM→?→||<-?<-?<-?<-?||FGS*→||<-ABhydrolase||?→||<-?||?→?→ ABC-ATPase→	FGS	253	UZ13_03331	chloroflexi	Chloroflexi bacterium OLB13	serine/threonine protein kinase [Chloroflexi bacterium OLB13].	GCA_001567485.1
MAF11603.1	SIG+FGS*→	SIG+FGS	549	CMK11_14230	bacteria	Candidatus Poribacteria bacterium	hypothetical protein CMK11_14230 [Candidatus Poribacteria bacterium].	GCA_002687025.1
MAS33641.1	SAM-methylase→?→?→?→?→ TIR+NACHT+FGS*→	TIR+NACHT+FGS	1028	CL610_06530	chloroflexi	Anaerolineaceae bacterium	hypothetical protein CL610_06530 [Anaerolineaceae bacterium].	GCA_002702065.1
MAS34537.1	TIR+FGS*→||<-?<-?||?→?→?→?→ Cluster323_2clades→	TIR+FGS	498	CL610_11050	chloroflexi	Anaerolineaceae bacterium	hypothetical protein CL610_11050 [Anaerolineaceae bacterium].	GCA_002702065.1
MAS34702.1	ABC-ATPase→?→?→?→ FHA+FHA+TIR→ FGS*→	FGS	304	CL610_11890	chloroflexi	Anaerolineaceae bacterium	hypothetical protein CL610_11890 [Anaerolineaceae bacterium].	GCA_002702065.1
MAS35610.1	FURR-HTH→||<-?<-?<-?<-?||?→||<-?||TIR+FGS*→?→?→ TIR+APATPase→||<-?<-?<-PSE<-?||TIR+TPR+TPR+TPR+TPR→	TIR+FGS	528	CL610_16485	chloroflexi	Anaerolineaceae bacterium	hypothetical protein CL610_16485 [Anaerolineaceae bacterium].	GCA_002702065.1

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MAS36115.1	TIR+NACHT+TCAD10+TCAD10→ TIR+FGS*→	TIR+FGS	531	CL610_19065	chloroflexi	Anaerolineaceae bacterium	hypothetical protein CL610_19065 [Anaerolineaceae bacterium].	GCA_002702065.1
MAS36626.1	TIR+FGS*→||<-?<-?||?→?→||<-?<-TIR	TIR+FGS	403	CL610_21660	chloroflexi	Anaerolineaceae bacterium	hypothetical protein CL610_21660 [Anaerolineaceae bacterium].	GCA_002702065.1
MAT95609.1	MED26C→?→ NACHT+FGS*→ RVT→ Four-helical-protein→?→?→ MED24→ ABC-ATPase→	NACHT+FGS	965	CL608_00455	chloroflexi	Anaerolineaceae bacterium	hypothetical protein CL608_00455 [Anaerolineaceae bacterium].	GCA_002699125.1
MAU09406.1	<-ABC-ATPase<-?||TIR+FGS*→	TIR+FGS	395	CL607_06270	chloroflexi	Anaerolineaceae bacterium	hypothetical protein CL607_06270 [Anaerolineaceae bacterium].	GCA_002699585.1
MAU10918.1	TIR+FGS*→||<-?<-TIMbarrel	TIR+FGS	485	CL607_13935	chloroflexi	Anaerolineaceae bacterium	hypothetical protein CL607_13935 [Anaerolineaceae bacterium].	GCA_002699585.1
MAU11412.1	ABhydrolase→||<-?<-?<-?||?→ TIR+NACHT+TCAD10+TCAD10→ TIR+FGS*→	TIR+FGS	543	CL607_16440	chloroflexi	Anaerolineaceae bacterium	hypothetical protein CL607_16440 [Anaerolineaceae bacterium].	GCA_002699585.1
MQM29574.1	FGS→//*<-FGS*	FGS	689	CRU78_03095	betaproteobacteria	Candidatus Accumulibacter phosphatis	hypothetical protein CRU78_03095, partial [Candidatus Accumulibacter phosphatis].	GCA_009467885.1
MQM29575.1	FGS*→	FGS	253	CRU78_03100	betaproteobacteria	Candidatus Accumulibacter phosphatis	hypothetical protein CRU78_03100 [Candidatus Accumulibacter phosphatis].	GCA_009467885.1
MQM29634.1	<-CNMP+CRP-HTH||FAD-NAD-dep-oxidoreductase→?→||<-?<-?<-?<-ABhydrolase||nSTAND1+FGS*→||<-SIG+CACHE+TM+PAS+PAS+GGDEF+EAL	nSTAND1+FGS	753	CRU78_03420	betaproteobacteria	Candidatus Accumulibacter phosphatis	hypothetical protein CRU78_03420 [Candidatus Accumulibacter phosphatis].	GCA_009467885.1
MQM32166.1	EAD8+nSTAND1+FGS*→	EAD8+nSTAND1+FGS	832	CRU78_17325	betaproteobacteria	Candidatus Accumulibacter phosphatis	hypothetical protein CRU78_17325 [Candidatus Accumulibacter phosphatis].	GCA_009467885.1
MQM33262.1	<-CNMP+CRP-HTH||FAD-NAD-dep-oxidoreductase→?→||<-?<-?<-?<-ABhydrolase||TIR+nSTAND1+FGS*→||<-ABHYDROLASE<-SIG+CACHE+TM+PAS+PAS+GGDEF+EAL<-?||?→ ABC-ATPase→	TIR+nSTAND1+FGS	779	CRU72_02110	betaproteobacteria	Candidatus Accumulibacter phosphatis	hypothetical protein CRU72_02110 [Candidatus Accumulibacter phosphatis].	GCA_009467855.1
MSP13386.1	TPR→?→?→||<-ICP8OBfold<-MED26C||?→ TPR→ EAD10+NACHT+FGS*→||<-ABhydrolase	EAD10+NACHT+FGS	858	EXR62_10580	chloroflexi	Chloroflexi bacterium	NACHT domain-containing protein [Chloroflexi bacterium].	GCA_009692745.1
MSP38253.1	DrHyd+nSTAND1+FGS*→	DrHyd+nSTAND1+FGS	889	EXR70_07155	deltaproteobacteria	Deltaproteobacteria bacterium	DUF4062 domain-containing protein [Deltaproteobacteria bacterium].	GCA_009692615.1
MXV93275.1	TCAD10→ TIR+FGS*→	TIR+FGS	544	F4Z94_07615	chloroflexi	Chloroflexi bacterium	SUMF1/EgtB/PvdO family nonheme iron enzyme [Chloroflexi bacterium].	-
MYD08867.1	SIG+TM+TM+TM+TM+TM+TM+TM+TM+TM→?→ ABC-ATPase→ ABC-ATPase→?→||<-SIG+TM+TM+TM+TM+TM+TM+TM+TM||TIR+NACHT+TCAD10→ TIR+FGS*→	TIR+FGS	570	F4X02_02375	chloroflexi	Chloroflexi bacterium	SUMF1/EgtB/PvdO family nonheme iron enzyme [Chloroflexi bacterium].	-
MYH66053.1	SIG+TM+TM+TM+TM+TM+TM+TM+TM+TM→?→ ABC-ATPase→ ABC-ATPase→?→||<-SIG+TM+TM+TM+TM+TM+TM+TM+TM||TIR+NACHT+TCAD10→ TIR+FGS*→	TIR+FGS	544	F4136_10500	chloroflexi	Chloroflexi bacterium	SUMF1/EgtB/PvdO family nonheme iron enzyme [Chloroflexi bacterium].	-
NAS88359.1	Beta-helix+Beta-helix+Beta-helix+ABhydrolase→?→ Calcineurin+NACHT+FGS*→||<-?<-tRNA<-?<-?||?→||<-?<-ParA-Soj-PloopNTPase	Calcineurin+NACHT+FGS	1124	C4E24_01245	euryarchaeota	ANME-1 cluster archaeon AG-394-G21	hypothetical protein C4E24_01245 [ANME-1 cluster archaeon AG-394-G21].	-

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
NAT10007.1	Beta-helix+Beta-helix+Beta-helix+ABhydrolase→?→ Calcineurin+NACHT+FGS*→||<-?<-tRNA<-?<-?||?→||<-?<-ParA-Soj-PloopNTPase	Calcineurin+NACHT+FGS	1123	C4E22_00360	euryarchaeota	ANME-1 cluster archaeon AG-394-G06	hypothetical protein C4E22_00360 [ANME-1 cluster archaeon AG-394-G06].	-
NBO65033.1	NACHT+FGS*→?→||<-Four-helical-protein||RVT→	NACHT+FGS	795	EBU88_09360	acidobacteria	Acidobacteria bacterium	NACHT domain-containing protein, partial [Acidobacteria bacterium].	-
NBO66226.1	FGS*→	FGS	269	EBU88_15525	acidobacteria	Acidobacteria bacterium	hypothetical protein EBU88_15525, partial [Acidobacteria bacterium].	-
NCA69346.1	SWC3→ SIG+NACHT+FGS*→||<-NACHT+FGS<-CASPASE+TCAD1+TCAD2<-?<-REase	SIG+NACHT+FGS	1164	EOM91_04440	bacteroidetes	Sphingobacteriia bacterium	NACHT domain-containing protein [Sphingobacteriia bacterium].	GCA_009928635.1
NCC35438.1	FGS*→	FGS	488	EOM24_26010	chloroflexi	Chloroflexia bacterium	hypothetical protein EOM24_26010, partial [Chloroflexia bacterium].	GCA_009929835.1
NCC37506.1	FGS*→	FGS	334	EOM24_36670	chloroflexi	Chloroflexia bacterium	formylglycine-generating enzyme family protein, partial [Chloroflexia bacterium].	GCA_009929835.1
NDD63295.1	TIR→ NACHT+FGS*→	NACHT+FGS	819	EBZ36_04855	acidobacteria	Acidobacteria bacterium	NACHT domain-containing protein [Acidobacteria bacterium].	-
NDD65503.1	FGS*→	FGS	316	EBZ36_16240	acidobacteria	Acidobacteria bacterium	hypothetical protein EBZ36_16240, partial [Acidobacteria bacterium].	-
NDD65920.1	FGS*→	FGS	346	EBZ36_18380	acidobacteria	Acidobacteria bacterium	formylglycine-generating enzyme family protein, partial [Acidobacteria bacterium].	-
NDJ33386.1	Pkinase+TCAD10+FGS*→	Pkinase+TCAD10+FGS	476	GYB64_01830	chloroflexi	Chloroflexi bacterium	SUMF1/EgtB/PvdO family nonheme iron enzyme, partial [Chloroflexi bacterium].	-
NDJ36083.1	<-ABhydrolase<-?||?→ TRANSGLUTAMINASE→ FGS*→	FGS	316	GYB64_15620	chloroflexi	Chloroflexi bacterium	formylglycine-generating enzyme family protein [Chloroflexi bacterium].	-
NDJ51790.1	DrHyd+nSTAND1+FGS*→	DrHyd+nSTAND1+FGS	1023	GYB68_01745	chloroflexi	Chloroflexi bacterium	SUMF1/EgtB/PvdO family nonheme iron enzyme [Chloroflexi bacterium].	-
NDJ54987.1	NACHT+FGS*→	NACHT+FGS	957	GYB68_18090	chloroflexi	Chloroflexi bacterium	SUMF1/EgtB/PvdO family nonheme iron enzyme [Chloroflexi bacterium].	-
NDJ55381.1	TIR+FGS*→	TIR+FGS	372	GYB68_20100	chloroflexi	Chloroflexi bacterium	formylglycine-generating enzyme family protein, partial [Chloroflexi bacterium].	-
NDJ62967.1	Pkinase+NACHT+FGS*→	Pkinase+NACHT+FGS	1135	GYB67_17740	chloroflexi	Chloroflexi bacterium	SUMF1/EgtB/PvdO family nonheme iron enzyme, partial [Chloroflexi bacterium].	-
NDJ74926.1	TIR+FGS*→ FGS→	TIR+FGS	407	GYB65_01595	chloroflexi	Chloroflexi bacterium	SUMF1/EgtB/PvdO family nonheme iron enzyme [Chloroflexi bacterium].	-
NDJ77993.1	DrHyd+nSTAND1+FGS*→	DrHyd+nSTAND1+FGS	919	GYB65_17215	chloroflexi	Chloroflexi bacterium	SUMF1/EgtB/PvdO family nonheme iron enzyme [Chloroflexi bacterium].	-

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NDJ78043.1	FGS*→?→?→?→?→?→||<-BLBD	FGS	497	GYB65_17470	chloroflexi	Chloroflexi bacterium	formylglycine-generating enzyme family protein, partial [Chloroflexi bacterium].	-
NDJ79077.1	FGS*→ Four-helical-protein→||<-?<-MED26C	FGS	315	GYB65_22730	chloroflexi	Chloroflexi bacterium	formylglycine-generating enzyme family protein, partial [Chloroflexi bacterium].	-
NDJ84742.1	TIR+FGS*→?→||<-?<-?||?→?→||<-?||REC→	TIR+FGS	401	GYB66_02545	chloroflexi	Chloroflexi bacterium	SUMF1/EgtB/PvdO family nonheme iron enzyme [Chloroflexi bacterium].	-
NDJ86912.1	TIR+FGS*→	TIR+FGS	571	GYB66_13605	chloroflexi	Chloroflexi bacterium	SUMF1/EgtB/PvdO family nonheme iron enzyme [Chloroflexi bacterium].	-
NEP63621.1	nSTAND1-C+FGS*→||<-EAD1+FGS	nSTAND1-C+FGS	517	F6K31_43145	cyanobacteria	Symploca sp. SIO2G7	formylglycine-generating enzyme family protein [Symploca sp. SIO2G7].	-
NET36060.1	ACYC→ nSTAND1+FGS*→	nSTAND1+FGS	814	F6K19_29210	cyanobacteria	Cyanothece sp. SIO1E1	SUMF1/EgtB/PvdO family nonheme iron enzyme [Cyanothece sp. SIO1E1].	-
NGZ09817.1	FGS*→	FGS	148	CV088_10590	nitrospirae	Nitrospira sp. LK70	hypothetical protein CV088_10590 [Nitrospira sp. LK70].	-
NGZ10364.1	TIR+FGS*→?→||<-?<-?||?→?→ SIG+TM+HAMP+HISKIN→ SIG+Trypsin+PDZ+PDZ→	TIR+FGS	401	CV088_13405	nitrospirae	Nitrospira sp. LK70	TIR domain-containing protein [Nitrospira sp. LK70].	-
NGZ10802.1	DrHyd+iSTAND→ MoxR-AAA→ SIG+VWA→||<-?||TIR+TIR+FGS*→	TIR+TIR+FGS	593	CV088_15685	nitrospirae	Nitrospira sp. LK70	TIR domain-containing protein [Nitrospira sp. LK70].	-
NGZ11578.1	SWC3→||<-?<-?||DrHyd+nSTAND1+FGS*→ Four-helical-protein→?→?→ FGS→	DrHyd+nSTAND1+FGS	880	CV088_19770	nitrospirae	Nitrospira sp. LK70	DUF4062 domain-containing protein [Nitrospira sp. LK70].	-
NIA29268.1	RVT→ DrHyd→ NACHT+FGS*→ Four-helical-protein→	NACHT+FGS	707	GWP06_05045	actinobacteria	Actinobacteria bacterium	SUMF1/EgtB/PvdO family nonheme iron enzyme [Actinobacteria bacterium].	-
NIA30537.1	NACHT+FGS*→?→?→ TM+TM+TM+TM+TM+TM+TM→	NACHT+FGS	847	GWP06_11575	actinobacteria	Actinobacteria bacterium	SUMF1/EgtB/PvdO family nonheme iron enzyme, partial [Actinobacteria bacterium].	-
NIM11161.1	NACHT+FGS*→?→ Four-helical-protein→ RVT→ FGS→ Calcineurin→	NACHT+FGS	519	GTO81_04210	bacteria	Candidatus Aminicenantes bacterium	SUMF1/EgtB/PvdO family nonheme iron enzyme, partial [Candidatus Aminicenantes bacterium].	-
NIM14207.1	Calcineurin→ NACHT+FGS*→	NACHT+FGS	752	GTO81_19680	bacteria	Candidatus Aminicenantes bacterium	SUMF1/EgtB/PvdO family nonheme iron enzyme [Candidatus Aminicenantes bacterium].	-
NIM14242.1	NACHT+FGS*→	NACHT+FGS	438	GTO81_19860	bacteria	Candidatus Aminicenantes bacterium	SUMF1/EgtB/PvdO family nonheme iron enzyme, partial [Candidatus Aminicenantes bacterium].	-
NIM15894.1	SWC3→?→ Calcineurin+NACHT+FGS*→	Calcineurin+NACHT+FGS	1153	GTO81_28290	bacteria	Candidatus Aminicenantes bacterium	SUMF1/EgtB/PvdO family nonheme iron enzyme [Candidatus Aminicenantes bacterium].	-

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NIM16827.1	Calcineurin→ NACHT+FGS*→?→?→?→||<-Cluster235_2clades||?→ Eukglutathionesyn-ATPgrasp→	NACHT+FGS	835	GTO81_32990	bacteria	Candidatus Aminicenantes bacterium	SUMF1/EgtB/PvdO family nonheme iron enzyme [Candidatus Aminicenantes bacterium].	-
NIM17712.1	NACHT+FGS→||<-?||Calcineurin+NACHT+FGS*→?→?→||<-?||SIG+TM→	Calcineurin+NACHT+FGS	1126	GTO81_37510	bacteria	Candidatus Aminicenantes bacterium	SUMF1/EgtB/PvdO family nonheme iron enzyme [Candidatus Aminicenantes bacterium].	-
NIM97201.1	NACHT+FGS*→	NACHT+FGS	753	GTO24_03660	bacteria	candidate division Zixibacteria bacterium	SUMF1/EgtB/PvdO family nonheme iron enzyme, partial [candidate division Zixibacteria bacterium].	-
NIO69120.1	NACHT+FGS*→?→ RVT→ Four-helical-protein→ DrHyd→	NACHT+FGS	666	GTN71_08815	chloroflexi	Anaerolineae bacterium	SUMF1/EgtB/PvdO family nonheme iron enzyme, partial [Anaerolineae bacterium].	-
NIO69566.1	KAP-NTPase+FGS*→	KAP-NTPase+FGS	725	GTN71_11185	chloroflexi	Anaerolineae bacterium	SUMF1/EgtB/PvdO family nonheme iron enzyme, partial [Anaerolineae bacterium].	-
NIO69816.1	KAP-NTPase+FGS*→ REase→	KAP-NTPase+FGS	741	GTN71_12500	chloroflexi	Anaerolineae bacterium	SUMF1/EgtB/PvdO family nonheme iron enzyme [Anaerolineae bacterium].	-
NIO71404.1	TIR+FGS*→	TIR+FGS	394	GTN71_20820	chloroflexi	Anaerolineae bacterium	SUMF1/EgtB/PvdO family nonheme iron enzyme, partial [Anaerolineae bacterium].	-
NIP46832.1	ACYC+NACHT+FGS*→	ACYC+NACHT+FGS	944	GWO29_10605	gammaproteobacteria	Gammaproteobacteria bacterium	SUMF1/EgtB/PvdO family nonheme iron enzyme [Gammaproteobacteria bacterium].	-
NIP84022.1	FGS*→	FGS	268	GTO03_00060	planctomycetes	Planctomycetales bacterium	SUMF1/EgtB/PvdO family nonheme iron enzyme, partial [Planctomycetales bacterium].	-
NIW94495.1	KAP-NTPase→ FGS*→	FGS	314	GWN20_16860	planctomycetes	Phycisphaerae bacterium	SUMF1/EgtB/PvdO family nonheme iron enzyme [Phycisphaerae bacterium].	-
NJD06933.1	DrHyd+iSTAND→ MoxR-AAA→ SIG+VWA→ vWA-L+TIR+DrHyd+FGS*→	vWA-L+TIR+DrHyd+FGS	905	FIA97_10615	gammaproteobacteria	Methylococcaceae bacterium	DUF4062 domain-containing protein [Methylococcaceae bacterium].	-
NJL17799.1	FGS*→	FGS	337	HC938_11975	nitrospirae	Nitrospira sp.	formylglycine-generating enzyme family protein, partial [Nitrospira sp.].	-
NJL55027.1	TIR→ NACHT+FGS→ *PSE*→ *Four-helical-protein*→ *TIR+FGS*→	NACHT+FGS	859	HC928_07430	bacteria	bacterium	SUMF1/EgtB/PvdO family nonheme iron enzyme [bacterium].	-
NJL55029.1	TIR+FGS*→	TIR+FGS	428	HC928_07445	bacteria	bacterium	SUMF1/EgtB/PvdO family nonheme iron enzyme [bacterium].	-
NJL55119.1	TIR→ NACHT+FGS*→	NACHT+FGS	721	HC928_07980	bacteria	bacterium	formylglycine-generating enzyme family protein [bacterium].	-
NJL55722.1	TIR+FGS*→	TIR+FGS	402	HC928_11325	bacteria	bacterium	SUMF1/EgtB/PvdO family nonheme iron enzyme [bacterium].	-

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
NJL93048.1	<-TIMbarrel<-?<-?<-?||FGS*→	FGS	308	HC915_04650	chloroflexi	Anaerolineae bacterium	formylglycine-generating enzyme family protein [Anaerolineae bacterium].	-
NJL95335.1	FGS*→?→?→?→||<-SIG+TM+HAMP+HISKIN	FGS	212	HC915_17250	chloroflexi	Anaerolineae bacterium	formylglycine-generating enzyme family protein, partial [Anaerolineae bacterium].	-
NJN82052.1	FGS*→	FGS	310	HC802_07060	chloroflexi	Caldilineaceae bacterium	formylglycine-generating enzyme family protein [Caldilineaceae bacterium].	-
NJN93303.1	NACHT+FGS*→	NACHT+FGS	695	HC875_04045	chloroflexi	Anaerolineales bacterium	SUMF1/EgtB/PvdO family nonheme iron enzyme [Anaerolineales bacterium].	-
NJN94208.1	FGS*→||<-?<-?<-PSE||?→ PSE→?→?→||<-PSE<-YBAK	FGS	242	HC875_09015	chloroflexi	Anaerolineales bacterium	formylglycine-generating enzyme family protein [Anaerolineales bacterium].	-
NJN98786.1	NACHT+FGS*→ FGS→	NACHT+FGS	463	HC875_34180	chloroflexi	Anaerolineales bacterium	SUMF1/EgtB/PvdO family nonheme iron enzyme [Anaerolineales bacterium].	-
NJN99601.1	NACHT→?→ FGS*→	FGS	264	HC875_38615	chloroflexi	Anaerolineales bacterium	formylglycine-generating enzyme family protein [Anaerolineales bacterium].	-
NJP06778.1	VWA+FGS*→||<-PSE<-PSE<-?<-tRNA||SbcC+SbcC→	VWA+FGS	782	HC837_14760	chloroflexi	Chloroflexaceae bacterium	SUMF1/EgtB/PvdO family nonheme iron enzyme [Chloroflexaceae bacterium].	-
NJP06949.1	<-FGS||?→?→?→?→?→ Pkinase+FGS*→	Pkinase+FGS	514	HC837_15690	chloroflexi	Chloroflexaceae bacterium	SUMF1/EgtB/PvdO family nonheme iron enzyme [Chloroflexaceae bacterium].	-
NJP07891.1	FGS*→	FGS	408	HC837_20850	chloroflexi	Chloroflexaceae bacterium	formylglycine-generating enzyme family protein [Chloroflexaceae bacterium].	-
NKB76742.1	<-Four-helical-protein||RVT→ DrHyd→ NACHT+FGS*→||<-?<-SIG+TM+TM+TM+TM+TM+TM+TM+TM<-PAS+HISKIN+REC<-?<-REC+ACYC	NACHT+FGS	610	GKR96_06745	gammaproteobacteria	Gammaproteobacteria bacterium	SUMF1/EgtB/PvdO family nonheme iron enzyme [Gammaproteobacteria bacterium].	-
NKQ37578.1	NACHT+FGS*→?→?→||<-?<-ABC-ATPase<-?||?→||<-LittleFinger	NACHT+FGS	946	HF973_18435	chloroflexi	Chloroflexi bacterium	SUMF1/EgtB/PvdO family nonheme iron enzyme [Chloroflexi bacterium].	-
NLE52136.1	FGS*→||<-RVT	FGS	304	GX613_12100	chloroflexi	Chloroflexi bacterium	formylglycine-generating enzyme family protein, partial [Chloroflexi bacterium].	-
NLF75470.1	TIR+TM+NACHT+7xTM+FGS*→?→||<-ABhydrolase<-ABhydrolase<-?<-ABhydrolase<-?||wHTH-4stranded+TPRs+nSTAND1+TM+BetaPropeller→	TIR+TM+NACHT+7xTM+FGS	1172	GX573_07210	chloroflexi	Chloroflexi bacterium	SUMF1/EgtB/PvdO family nonheme iron enzyme [Chloroflexi bacterium].	-
NLF75680.1	SWC3→?→?→?→?→ TIR+NACHT+FGS*→	TIR+NACHT+FGS	818	GX573_08280	chloroflexi	Chloroflexi bacterium	SUMF1/EgtB/PvdO family nonheme iron enzyme [Chloroflexi bacterium].	-
NLF77023.1	<-TIR+APATPase+BetaPropeller||?→?→ TIR→?→||<-PSE||FGS*→	FGS	224	GX573_15095	chloroflexi	Chloroflexi bacterium	formylglycine-generating enzyme family protein, partial [Chloroflexi bacterium].	-
NLF78373.1	DrHyd+nSTAND1+FGS*→	DrHyd+nSTAND1+FGS	972	GX573_21985	chloroflexi	Chloroflexi bacterium	SUMF1/EgtB/PvdO family nonheme iron enzyme [Chloroflexi bacterium].	-

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NLF78947.1	FGS*→	FGS	250	GX573_24915	chloroflexi	Chloroflexi bacterium	formylglycine-generating enzyme family protein [Chloroflexi bacterium].	-
NLF78951.1	TIR+FGS*→	TIR+FGS	508	GX573_24935	chloroflexi	Chloroflexi bacterium	SUMF1/EgtB/PvdO family nonheme iron enzyme, partial [Chloroflexi bacterium].	-
NLF78992.1	TIR+NACHT+FGS→*?→ DrHyd+nSTAND1+FGS→*	TIR+NACHT+FGS	993	GX573_25145	chloroflexi	Chloroflexi bacterium	SUMF1/EgtB/PvdO family nonheme iron enzyme [Chloroflexi bacterium].	-
NLF78994.1	TIR+NACHT+FGS*→	TIR+NACHT+FGS	923	GX573_25155	chloroflexi	Chloroflexi bacterium	SUMF1/EgtB/PvdO family nonheme iron enzyme [Chloroflexi bacterium].	-
NLS76118.1	FGS→ CASPASE+TCAD1+TCAD2→ NACHT+FGS→ NACHT+FGS*→	NACHT+FGS	1049	GXY76_02550	chloroflexi	Chloroflexi bacterium	SUMF1/EgtB/PvdO family nonheme iron enzyme [Chloroflexi bacterium].	-
NLX11872.1	<-DrHyd<-?<-?||FGS*→	FGS	250	GXY36_19670	chloroflexi	Chloroflexi bacterium	formylglycine-generating enzyme family protein [Chloroflexi bacterium].	-
NMB90542.1	TPR→?→ FGS*→	FGS	276	GYA17_19435	chloroflexi	Chloroflexi bacterium	formylglycine-generating enzyme family protein [Chloroflexi bacterium].	-
NMC02153.1	FGS*→	FGS	221	GYA30_07250	chloroflexi	Chloroflexi bacterium	formylglycine-generating enzyme family protein, partial [Chloroflexi bacterium].	-
NMC03023.1	NACHT+FGS*→	NACHT+FGS	839	GYA30_11700	chloroflexi	Chloroflexi bacterium	SUMF1/EgtB/PvdO family nonheme iron enzyme, partial [Chloroflexi bacterium].	-
NMC11372.1	TPR→?→ FGS*→?→?→?→?→?→?→ SIG+TM→	FGS	262	GYA34_00645	chloroflexi	Chloroflexi bacterium	formylglycine-generating enzyme family protein [Chloroflexi bacterium].	-
NMQ05699.1	FGS*→||<-TRANSGLUTAMINASE||?→||<-?||PSE→?→||<-Patatin	FGS	259	E4Q08_10675	betaproteobacteria	Candidatus Accumulibacter phosphatis	hypothetical protein E4Q08_10675 [Candidatus Accumulibacter phosphatis].	-
NMQ07713.1	TIR→ MoxR-AAA→ MED26C→ SIG+FGS*→||<-RVT||Four-helical-protein→||<-SIG+FGS<-?<-?<-ABC-ATPase	SIG+FGS	803	E4Q08_21970	betaproteobacteria	Candidatus Accumulibacter phosphatis	hypothetical protein E4Q08_21970 [Candidatus Accumulibacter phosphatis].	-
NMQ07738.1	<-BLBD<-?||?→?→||<-?<-PSE<-?<-?||TIR+nSTAND1+FGS*→ FGS→||<-Four-helical-protein||RVT→||<-TIR+FGS<-?<-RVT	TIR+nSTAND1+FGS	955	E4Q08_22105	betaproteobacteria	Candidatus Accumulibacter phosphatis	TIR domain-containing protein [Candidatus Accumulibacter phosphatis].	-
NNJ84960.1	FGS*→	FGS	333	HKP13_08525	gammaproteobacteria	Gammaproteobacteria bacterium	SUMF1/EgtB/PvdO family nonheme iron enzyme [Gammaproteobacteria bacterium].	-
NNK95096.1	NACHT+FGS*→	NACHT+FGS	471	HKP41_12165	deltaproteobacteria	Desulfobacterales bacterium	formylglycine-generating enzyme family protein, partial [Desulfobacterales bacterium].	-
OAI48271.1	EAD1+nSTAND1+FGS*→?→ EAD1+Trypsin→||<-?||?→?→ VWA→	EAD1+nSTAND1+FGS	770	AYO44_07515	planctomycetes	Planctomycetaceae bacterium SCGC AG-212-F19	hypothetical protein AYO44_07515 [Planctomycetaceae bacterium SCGC AG-212-F19].	GCA_001644415.1

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OGO38189.1	<-ABhydrolase<-?<-?<-PSE<-PSE<-TIMbarrel||?→||<-?<-?||FGS*→	FGS	282	A2W35_08715	chloroflexi	Chloroflexi bacterium RBG_16_57_11	hypothetical protein A2W35_08715 [Chloroflexi bacterium RBG_16_57_11].	GCA_001795165.1
OGO41187.1	SIG+TM+NACHT+FGS*→	SIG+TM+NACHT+FGS	973	A2W36_01705	chloroflexi	Chloroflexi bacterium RBG_16_58_14	hypothetical protein A2W36_01705 [Chloroflexi bacterium RBG_16_58_14].	GCA_001796915.1
OIO90464.1	PIN→?→?→?→ CASPASE+FGS*→	CASPASE+FGS	501	AUK03_12910	chloroflexi	Anaerolineae bacterium CG2_30_64_16	hypothetical protein AUK03_12910 [Anaerolineae bacterium CG2_30_64_16].	GCA_001871755.1
OQA20201.1	NACHT+FGS*→	NACHT+FGS	1059	pkn1_2	chloroflexi	Chloroflexi bacterium ADurb.Bin360	Serine/threonine-protein kinase pkn1 [Chloroflexi bacterium ADurb.Bin360].	GCA_002068755.1
OQA95056.1	NACHT+FGS*→	NACHT+FGS	891	pkn1_5	chloroflexi	Chloroflexi bacterium ADurb.Bin222	Serine/threonine-protein kinase pkn1 [Chloroflexi bacterium ADurb.Bin222].	GCA_002069935.1
OQA95154.1	FGS*→?→ RVT→ Four-helical-protein→	FGS	256	pkn1_4	chloroflexi	Chloroflexi bacterium ADurb.Bin222	Serine/threonine-protein kinase pkn1 [Chloroflexi bacterium ADurb.Bin222].	GCA_002069935.1
OQB01206.1	<-SIG+TPR+TPR+TPR<-?<-?<-?||FGS*→	FGS	260	pkn1_3	chloroflexi	Chloroflexi bacterium ADurb.Bin222	Serine/threonine-protein kinase pkn1 [Chloroflexi bacterium ADurb.Bin222].	GCA_002069935.1
OQB02365.1	TM→?→?→ EAD7→?→?→?→ ZNR+NACHT+FGS*→ RVT→	ZNR+NACHT+FGS	965	egtB	chloroflexi	Chloroflexi bacterium ADurb.Bin222	Iron(II)-dependent oxidoreductase EgtB [Chloroflexi bacterium ADurb.Bin222].	GCA_002069935.1
OQW81078.1	ABC-ATPase→ DrHyd+nSTAND1+FGS*→	DrHyd+nSTAND1+FGS	908	BVN30_11975	proteobacteria	Proteobacteria bacterium ST_bin16	hypothetical protein BVN30_11975 [Proteobacteria bacterium ST_bin16].	GCA_002083595.1
OQX00845.1	TIR+NACHT+FGS*→	TIR+NACHT+FGS	954	BWK73_47570	gammaproteobacteria	Thiothrix lacustris	hypothetical protein BWK73_47570 [Thiothrix lacustris].	GCA_002083875.1
OQX02689.1	TIR+FGS*→||<-RVT	TIR+FGS	455	BWK73_41905	gammaproteobacteria	Thiothrix lacustris	hypothetical protein BWK73_41905 [Thiothrix lacustris].	GCA_002083875.1
OQX03012.1	FGS→ SIG+TM+NACHT+FGS*→ RVT→ Four-helical-protein→	SIG+TM+NACHT+FGS	959	BWK73_40840	gammaproteobacteria	Thiothrix lacustris	hypothetical protein BWK73_40840 [Thiothrix lacustris].	GCA_002083875.1
OQX05770.1	TIR+NACHT+FGS*→?→ MED26C→ ABhydrolase→	TIR+NACHT+FGS	934	BWK73_32675	gammaproteobacteria	Thiothrix lacustris	hypothetical protein BWK73_32675 [Thiothrix lacustris].	GCA_002083875.1
OQX14334.1	<-PAS+HISKIN+REC||?→||<-?||?→||<-?||?→||<-?||TIR+FGS*→||<-?||?→?→||<-PAS+HISKIN+REC	TIR+FGS	427	BWK73_09810	gammaproteobacteria	Thiothrix lacustris	hypothetical protein BWK73_09810 [Thiothrix lacustris].	GCA_002083875.1
OQY20877.1	ZNR+NACHT→ ZNR+NACHT+FGS*→	ZNR+NACHT+FGS	991	B6I35_09750	chloroflexi	Anaerolineaceae bacterium 4572_32.2	hypothetical protein B6I35_09750 [Anaerolineaceae bacterium 4572_32.2].	GCA_002084625.1
OQY22096.1	KAP-NTPase+FGS*→||<-?<-?<-PSE<-TPR+TPR+TPR+TPR	KAP-NTPase+FGS	762	B6I35_06850	chloroflexi	Anaerolineaceae bacterium 4572_32.2	hypothetical protein B6I35_06850 [Anaerolineaceae bacterium 4572_32.2].	GCA_002084625.1
OQY80126.1	FGS*→||<-ABhydrolase	FGS	253	B6D42_13475	chloroflexi	Anaerolineae bacterium UTCFX5	hypothetical protein B6D42_13475 [Anaerolineae bacterium UTCFX5].	GCA_002050245.1

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OQY84655.1	NACHT+FGS*→	NACHT+FGS	1052	B6D41_15310	chloroflexi	Chloroflexi bacterium UTCFX4	hypothetical protein B6D41_15310 [Chloroflexi bacterium UTCFX4].	GCA_002050085.1
OQY90620.1	ABC-ATPase→ ABC-ATPase→?→?→?→?→ KAP-NTPase+FGS*→||<-?||?→ SWC3→	KAP-NTPase+FGS	730	B6D38_02510	chloroflexi	Anaerolineae bacterium UTCFX1	hypothetical protein B6D38_02510 [Anaerolineae bacterium UTCFX1].	GCA_002050275.1
OQY94544.1	<-LexA-HTH+LexA-protease<-?||SIG+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM→?→ SIG+NACHT+FGS*→ SIG+SWC3→	SIG+NACHT+FGS	1100	B6D41_06985	chloroflexi	Chloroflexi bacterium UTCFX4	hypothetical protein B6D41_06985 [Chloroflexi bacterium UTCFX4].	GCA_002050085.1
OQZ00200.1	NACHT+FGS*→ Four-helical-protein→ RVT→	NACHT+FGS	612	B6D41_00255	chloroflexi	Chloroflexi bacterium UTCFX4	hypothetical protein B6D41_00255, partial [Chloroflexi bacterium UTCFX4].	GCA_002050085.1
OQZ00584.1	SIG+DrHyd+VirB11+NACHT+FGS*→?→||<-ICP8OBfold<-MED26C	SIG+DrHyd+VirB11+NACHT+FGS	983	B6D35_06300	planctomycetes	Candidatus Brocadia sp. UTAMX2	hypothetical protein B6D35_06300 [Candidatus Brocadia sp. UTAMX2].	GCA_002050315.1
PDW00941.1	MNS-STAND+FGS*→ KAP-NTPase→	MNS-STAND+FGS	742	A9Q02_21485	chloroflexi	Candidatus Chloroploca asiatica	hypothetical protein A9Q02_21485 [Candidatus Chloroploca asiatica].	GCA_002532075.1
PDW01800.1	MNS-STAND+FGS*→	MNS-STAND+FGS	619	CJ255_17210	chloroflexi	Candidatus Viridilinea mediisalina	hypothetical protein CJ255_17210 [Candidatus Viridilinea mediisalina].	GCA_002532535.1
PID85266.1	NACHT+FGS*→ RVT→ Four-helical-protein→ EAD1+Trypsin→	NACHT+FGS	946	CSB13_08890	chloroflexi	Chloroflexi bacterium	hypothetical protein CSB13_08890 [Chloroflexi bacterium].	GCA_002746795.1
PIE33434.1	<-Cluster366_2clades<-?||?→?→?→?→ NACHT+FGS*→	NACHT+FGS	750	CSA56_11545	bacteria	candidate division KSB3 bacterium	hypothetical protein CSA56_11545 [candidate division KSB3 bacterium].	GCA_002748445.1
PIE79716.1	NACHT+FGS→*?*→ *NACHT+FGS*→?→ SIG+TM+HAMP+HISKIN→	NACHT+FGS	370	CSA11_10845	chloroflexi	Chloroflexi bacterium	hypothetical protein CSA11_10845, partial [Chloroflexi bacterium].	GCA_002748985.1
PIE79718.1	NACHT+FGS*→	NACHT+FGS	1071	CSA11_10855	chloroflexi	Chloroflexi bacterium	hypothetical protein CSA11_10855 [Chloroflexi bacterium].	GCA_002748985.1
PJF20835.1	TIR+FGS*→	TIR+FGS	353	CUN56_14160	chloroflexi	Candidatus Thermofonsia Clade 2 bacterium	hypothetical protein CUN56_14160 [Candidatus Thermofonsia Clade 2 bacterium].	GCA_002794505.1
PJF23219.1	TIR+FGS*→	TIR+FGS	490	CUN56_01990	chloroflexi	Candidatus Thermofonsia Clade 2 bacterium	hypothetical protein CUN56_01990 [Candidatus Thermofonsia Clade 2 bacterium].	GCA_002794505.1
PJF28084.1	TCAD10→ TIR+FGS*→	TIR+FGS	506	CUN53_01595	chloroflexi	Candidatus Thermofonsia Clade 2 bacterium	hypothetical protein CUN53_01595 [Candidatus Thermofonsia Clade 2 bacterium].	GCA_002794695.1
PJF28825.1	TIR+FGS*→	TIR+FGS	500	CUN52_11490	chloroflexi	Candidatus Thermofonsia Clade 2 bacterium	hypothetical protein CUN52_11490 [Candidatus Thermofonsia Clade 2 bacterium].	GCA_002794515.1

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PJF29540.1	DrHyd→ nSTAND1+FGS*→	nSTAND1+FGS	718	CUN52_07865	chloroflexi	Candidatus Thermofonsia Clade 2 bacterium	hypothetical protein CUN52_07865 [Candidatus Thermofonsia Clade 2 bacterium].	GCA_002794515.1
PJF30051.1	TIR+FGS*→	TIR+FGS	445	CUN52_05275	chloroflexi	Candidatus Thermofonsia Clade 2 bacterium	hypothetical protein CUN52_05275, partial [Candidatus Thermofonsia Clade 2 bacterium].	GCA_002794515.1
PJF30836.1	TIR+FGS*→	TIR+FGS	513	CUN51_06530	chloroflexi	Candidatus Thermofonsia Clade 1 bacterium	hypothetical protein CUN51_06530 [Candidatus Thermofonsia Clade 1 bacterium].	GCA_002794705.1
PJF31663.1	<-ABhydrolase||DrHyd+nSTAND1+FGS*→	DrHyd+nSTAND1+FGS	1006	CUN52_02370	chloroflexi	Candidatus Thermofonsia Clade 2 bacterium	hypothetical protein CUN52_02370 [Candidatus Thermofonsia Clade 2 bacterium].	GCA_002794515.1
PJF37172.1	TIR+FGS*→	TIR+FGS	525	CUN49_01770	chloroflexi	Candidatus Thermofonsia Clade 1 bacterium	hypothetical protein CUN49_01770 [Candidatus Thermofonsia Clade 1 bacterium].	GCA_002794555.1
PJF43622.1	TIR+FGS*→	TIR+FGS	486	CUN55_08140	chloroflexi	Candidatus Thermofonsia Clade 2 bacterium	hypothetical protein CUN55_08140, partial [Candidatus Thermofonsia Clade 2 bacterium].	GCA_002794585.1
PJF44139.1	FGS*→	FGS	376	CUN55_05530	chloroflexi	Candidatus Thermofonsia Clade 2 bacterium	hypothetical protein CUN55_05530 [Candidatus Thermofonsia Clade 2 bacterium].	GCA_002794585.1
PUB73139.1	ABHYDROLASE→?→?→ drhyd+NACHT+FGS*→||<-?<-?<-SIG+CACHE+TM+PAS+PAS+GGDEF+EAL<-?||?→?→||<-CBS	drhyd+NACHT+FGS	1022	DBO99_20690	gammaproteobacteria	gamma proteobacterium symbiont of Ctena orbiculata	hypothetical protein DBO99_20690 [gamma proteobacterium symbiont of Ctena orbiculata].	GCA_003058485.1
PUB73261.1	ABHYDROLASE→?→?→ drhyd+NACHT+FGS*→||<-?<-?<-SIG+CACHE+TM+PAS+PAS+GGDEF+EAL	drhyd+NACHT+FGS	1022	DBP03_13830	gammaproteobacteria	gamma proteobacterium symbiont of Ctena orbiculata	hypothetical protein DBP03_13830 [gamma proteobacterium symbiont of Ctena orbiculata].	GCA_003058495.1
PUB76292.1	TIR+nSTAND1+FGS→ *FGS*→ FGS→||<-RVT<-?<-TIR+FGS*<-MoxR-AAA<-TIR<-TIR+TCAD2	TIR+nSTAND1+FGS	913	DBP03_04845	gammaproteobacteria	gamma proteobacterium symbiont of Ctena orbiculata	hypothetical protein DBP03_04845 [gamma proteobacterium symbiont of Ctena orbiculata].	GCA_003058495.1
PUB76293.1	FGS*→	FGS	255	DBP03_04850	gammaproteobacteria	gamma proteobacterium symbiont of Ctena orbiculata	hypothetical protein DBP03_04850 [gamma proteobacterium symbiont of Ctena orbiculata].	GCA_003058495.1
PUB76297.1	TIR+FGS*→	TIR+FGS	961	DBP03_04870	gammaproteobacteria	gamma proteobacterium symbiont of Ctena orbiculata	hypothetical protein DBP03_04870 [gamma proteobacterium symbiont of Ctena orbiculata].	GCA_003058495.1
PWB73128.1	nSTAND1-C+FGS*→||<-RVT||Four-helical-protein→||<-FGS	nSTAND1-C+FGS	467	C3F07_10390	chloroflexi	Anaerolineales bacterium	hypothetical protein C3F07_10390, partial [Anaerolineales bacterium].	GCA_003105325.1

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PWH19196.1	TPR→?→ FGS*→	FGS	269	DDG59_03890	chloroflexi	Anaerolineae bacterium	formylglycine-generating enzyme family protein [Anaerolineae bacterium].	GCA_003130835.1
PYR00059.1	drhyd+NACHT+FGS*→?→ ORF6N→ VWA→	drhyd+NACHT+FGS	998	DMF96_04700	acidobacteria	Acidobacteria bacterium	hypothetical protein DMF96_04700 [Acidobacteria bacterium].	GCA_003222505.1
PYR17830.1	SIG+HISKIN+REC→?→ drhyd+NACHT+FGS*→?→ ORF6N→ VWA→	drhyd+NACHT+FGS	998	DMF94_22285	acidobacteria	Acidobacteria bacterium	hypothetical protein DMF94_22285 [Acidobacteria bacterium].	GCA_003222535.1
PYR41523.1	drhyd+NACHT+FGS*→?→ ORF6N→ VWA→	drhyd+NACHT+FGS	858	DMF95_30835	acidobacteria	Acidobacteria bacterium	hypothetical protein DMF95_30835, partial [Acidobacteria bacterium].	GCA_003223755.1
PZN49102.1	TIR+FGS*→	TIR+FGS	519	DIU68_20660	chloroflexi	Chloroflexi bacterium	hypothetical protein DIU68_20660 [Chloroflexi bacterium].	GCA_003242205.1
PZN54847.1	ABC-ATPase→?→||<-Cluster235_2clades<-?<-SIG+TM+TM+TM+TM+TM<-?||FGS*→	FGS	254	DIU68_09635	chloroflexi	Chloroflexi bacterium	hypothetical protein DIU68_09635 [Chloroflexi bacterium].	GCA_003242205.1
PZN71605.1	FGS*→||<-RVT	FGS	215	DM484_25995	gammaproteobacteria	Candidatus Methyloumidiphilus alinensis	hypothetical protein DM484_25995, partial [Candidatus Methyloumidiphilus alinensis].	GCA_003242955.1
PZN73048.1	nSTAND1-C+FGS*→	nSTAND1-C+FGS	478	DM484_23385	gammaproteobacteria	Candidatus Methyloumidiphilus alinensis	hypothetical protein DM484_23385, partial [Candidatus Methyloumidiphilus alinensis].	GCA_003242955.1
PZN74864.1	CASPASE+NACHT+FGS*→?→ Trypco1→	CASPASE+NACHT+FGS	1074	DM484_20170	gammaproteobacteria	Candidatus Methyloumidiphilus alinensis	hypothetical protein DM484_20170 [Candidatus Methyloumidiphilus alinensis].	GCA_003242955.1
PZN74977.1	NACHT+FGS*→||<-?<-Four-helical-protein||RVT→||<-NACHT+FGS<-?<-TIR<-DrHyd	NACHT+FGS	914	DM484_19825	gammaproteobacteria	Candidatus Methyloumidiphilus alinensis	hypothetical protein DM484_19825 [Candidatus Methyloumidiphilus alinensis].	GCA_003242955.1
PZN77746.1	DrHyd+nSTAND1+FGS*→	DrHyd+nSTAND1+FGS	1041	DM484_14085	gammaproteobacteria	Candidatus Methyloumidiphilus alinensis	hypothetical protein DM484_14085 [Candidatus Methyloumidiphilus alinensis].	GCA_003242955.1
PZN84786.1	<-SAM-methylase<-?<-?||?→?→?→ drhyd+NACHT+FGS*→	drhyd+NACHT+FGS	1034	DM484_02145	gammaproteobacteria	Candidatus Methyloumidiphilus alinensis	hypothetical protein DM484_02145 [Candidatus Methyloumidiphilus alinensis].	GCA_003242955.1
RCK71670.1	TPR→?→ FGS*→||<-?<-?<-?<-?||?→?→ SIG+TM+TM+TM+TM+TM+TM+TM+TM→	FGS	269	ANABAC_1196	chloroflexi	Anaerolineae bacterium	serine/threonine kinase [Anaerolineae bacterium].	GCA_003327455.1
RCV64808.1	TIR→ ParA-Soj-PloopNTPase+TIR+NACHT+FGS→*?→ Calcineurin+NACHT+FGS*→?→?→?→?→?→||<-?||LRP-HTH→	ParA-Soj-PloopNTPase+TIR+NACHT+FGS	1130	C5S53_06925	euryarchaeota	Methanophagales archaeon	Formylglycine-generating enzyme [Methanophagales archaeon].	GCA_003336485.1
RCV64810.1	ParA-Soj-PloopNTPase+TIR+NACHT+FGS*→	ParA-Soj-PloopNTPase+TIR+NACHT+FGS	1273	C5S53_06935	euryarchaeota	Methanophagales archaeon	Formylglycine-generating enzyme [Methanophagales archaeon].	GCA_003336485.1
RDE49756.1	TIR+nSTAND1+FGS*→||<-?<-?||?→?→ KAP-NTPase→	TIR+nSTAND1+FGS	1034	DVS81_14945	betaproteobacteria	Candidatus Accumulibacter phosphatis	TIR domain-containing protein [Candidatus Accumulibacter phosphatis].	GCA_003332265.1
RDE50257.1	TIR+NACHT+FGS*→||<-?<-FGS	TIR+NACHT+FGS	962	DVS81_12365	betaproteobacteria	Candidatus Accumulibacter phosphatis	TIR domain-containing protein [Candidatus Accumulibacter phosphatis].	GCA_003332265.1

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RDE50357.1	FAD-NAD-dep-oxidoreductase→?→||<-?<-?<-?<-ABhydrolase||?→ nSTAND1+FGS*→||<-SIG+CACHE+TM+PAS+PAS+GGDEF+EAL<-?||?→||<-PIN	nSTAND1+FGS	753	DVS81_11680	betaproteobacteria	Candidatus Accumulibacter phosphatis	hypothetical protein DVS81_11680 [Candidatus Accumulibacter phosphatis].	GCA_003332265.1
RDE51785.1	EAD8+nSTAND1+FGS*→ EAD8+TIR+NACHT+FGS→	EAD8+nSTAND1+FGS	830	DVS81_03940	betaproteobacteria	Candidatus Accumulibacter phosphatis	hypothetical protein DVS81_03940 [Candidatus Accumulibacter phosphatis].	GCA_003332265.1
RIK31324.1	KAP-NTPase+FGS*→||<-?<-ICP8OBfold<-MED26C	KAP-NTPase+FGS	831	DCC56_03825	chloroflexi	Anaerolineae bacterium	hypothetical protein DCC56_03825 [Anaerolineae bacterium].	GCA_003577395.1
RIK35349.1	NACHT+FGS*→	NACHT+FGS	973	DCC55_30565	chloroflexi	Chloroflexi bacterium	hypothetical protein DCC55_30565 [Chloroflexi bacterium].	GCA_003577005.1
RIL10952.1	EAD8→?→ EAD8→ KAP-NTPase+FGS*→ TIR→||<-?||ACYC+APATPase+TPR→||<-?||?→||<-ACYC+NACHT+FGS	KAP-NTPase+FGS	836	DCC79_06390	bacteria	bacterium	hypothetical protein DCC79_06390 [bacterium].	GCA_003576755.1
RIL11051.1	EAD8+NACHT+FGS*→||<-EAD8+NACHT+FGS	EAD8+NACHT+FGS	967	DCC79_06090	bacteria	bacterium	hypothetical protein DCC79_06090 [bacterium].	GCA_003576755.1
RIL11755.1	FGS→||<-?<-?||?→ PSE→ PSE→?→ TIR+NACHT+FGS→ *FGS→||<-Four-helical-protein||RVT→||<-DrHyd+nSTAND1+FGS*||?→?→ ABhydrolase+ABhydrolase+CASPASE+TPR-S→	TIR+NACHT+FGS	995	DCC79_03775	bacteria	bacterium	hypothetical protein DCC79_03775 [bacterium].	GCA_003576755.1
RIL11759.1	DrHyd+nSTAND1+FGS*→	DrHyd+nSTAND1+FGS	944	DCC79_03795	bacteria	bacterium	hypothetical protein DCC79_03795 [bacterium].	GCA_003576755.1
RKU24994.1	HSP70→ FGS→ DNAJ+FGS*→	DNAJ+FGS	445	C6499_15805	bacteria	Candidatus Poribacteria bacterium	hypothetical protein C6499_15805 [Candidatus Poribacteria bacterium].	GCA_003635255.1
RLC59981.1	ABC-ATPase→?→ KAP-NTPase+FGS*→	KAP-NTPase+FGS	780	DRI80_11660	chloroflexi	Chloroflexi bacterium	hypothetical protein DRI80_11660 [Chloroflexi bacterium].	GCA_003647875.1
RLC64729.1	<-Cluster366_2clades<-?<-?||ACYC+ACYC+SWACOS+TPR+TPR+TPR→?→?→?→ KAP-NTPase+FGS*→	KAP-NTPase+FGS	778	DRI80_00630	chloroflexi	Chloroflexi bacterium	hypothetical protein DRI80_00630 [Chloroflexi bacterium].	GCA_003647875.1
RLC71356.1	NACHT+FGS*→ Four-helical-protein→	NACHT+FGS	843	DRI81_17855	chloroflexi	Chloroflexi bacterium	hypothetical protein DRI81_17855, partial [Chloroflexi bacterium].	GCA_003648025.1
RLC71990.1	FGS*→	FGS	341	DRI81_16965	chloroflexi	Chloroflexi bacterium	hypothetical protein DRI81_16965 [Chloroflexi bacterium].	GCA_003648025.1
RLC79416.1	KAP-NTPase+FGS*→||<-?<-?<-?<-TPR+TPR+TPR+TPR	KAP-NTPase+FGS	762	DRI81_05360	chloroflexi	Chloroflexi bacterium	hypothetical protein DRI81_05360 [Chloroflexi bacterium].	GCA_003648025.1
RLC80321.1	ZNR+NACHT+FGS*→ Four-helical-protein→ RVT→ SIG+SWC3→	ZNR+NACHT+FGS	945	DRJ03_21950	chloroflexi	Chloroflexi bacterium	hypothetical protein DRJ03_21950 [Chloroflexi bacterium].	GCA_003648075.1
RLC85952.1	FGS*→||<-?<-?<-?<-TPR+TPR+TPR+TPR	FGS	288	DRJ03_10225	chloroflexi	Chloroflexi bacterium	DNA-binding protein [Chloroflexi bacterium].	GCA_003648075.1
RLD03540.1	NACHT+FGS*→ TIR+TCAD2→	NACHT+FGS	911	DRI56_12305	chloroflexi	Chloroflexi bacterium	hypothetical protein DRI56_12305 [Chloroflexi bacterium].	GCA_003648195.1
RLJ15771.1	<-Cluster393_2clades<-Pentapeptide||?→ TIR→ MoxR-AAA→||<-?||SIG+FGS*→||<-?<-PSE<-?<-Cluster187_2clades<-?<-HSP70<-?<-IES1	SIG+FGS	788	DJ030_18040	bacteria	bacterium endosymbiont of Escarpia laminata	hypothetical protein DJ030_18040 [bacterium endosymbiont of Escarpia laminata].	GCA_003660225.1

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RLJ21529.1	MalT→ Cluster440_2clades→ SIG+RFC-AAA→?→ SIG+TM+TM+TM+TM→ SIG+TM+HAMP→?→ drhyd+NACHT+FGS*→	drhyd+NACHT+FGS	953	DJ031_02685	bacteria	bacterium endosymbiont of Escarpia laminata	hypothetical protein DJ031_02685 [bacterium endosymbiont of Escarpia laminata].	GCA_003660235.1
RLJ22000.1	SIG+FGS*→||<-?<-Cluster187_2clades<-?<-HSP70<-?<-IES1	SIG+FGS	788	DJ031_01870	bacteria	bacterium endosymbiont of Escarpia laminata	hypothetical protein DJ031_01870 [bacterium endosymbiont of Escarpia laminata].	GCA_003660235.1
RLT41139.1	NACHT+FGS*→ RVT→ Four-helical-protein→	NACHT+FGS	1064	DWI57_07410	chloroflexi	Chloroflexi bacterium	NACHT domain-containing protein [Chloroflexi bacterium].	GCA_003670625.1
RLW71008.1	TIR→ TIR+FGS→ SIG+FGS*→	SIG+FGS	146	B6D71_04250	gammaproteobacteria	gamma proteobacterium symbiont of Stewartia floridana	hypothetical protein B6D71_04250, partial [gamma proteobacterium symbiont of Stewartia floridana].	GCA_003676185.1
RME02281.1	NACHT+FGS*→	NACHT+FGS	853	D6816_11190	bacteroidetes	Bacteroidetes bacterium	NACHT domain-containing protein, partial [Bacteroidetes bacterium].	GCA_003694615.1
RME06715.1	FGS*→	FGS	309	D6816_07410	bacteroidetes	Bacteroidetes bacterium	hypothetical protein D6816_07410 [Bacteroidetes bacterium].	GCA_003694615.1
RME41053.1	NACHT+FGS*→	NACHT+FGS	885	D6796_16335	chloroflexi	Caldilineae bacterium	NACHT domain-containing protein, partial [Caldilineae bacterium].	GCA_003695385.1
RMF51509.1	TIR+FGS*→	TIR+FGS	471	D6749_07615	chloroflexi	Chloroflexi bacterium	TIR domain-containing protein [Chloroflexi bacterium].	GCA_003695215.1
RMF78466.1	TIR+NACHT+TCAD10+TCAD10→ TIR+FGS*→	TIR+FGS	519	D6737_14645	chloroflexi	Chloroflexi bacterium	TIR domain-containing protein [Chloroflexi bacterium].	GCA_003695675.1
RMG71792.1	TIR→ EAD8+TIR+NACHT+FGS*→ FGS→	EAD8+TIR+NACHT+FGS	1095	D6711_14505	chloroflexi	Chloroflexi bacterium	TIR domain-containing protein [Chloroflexi bacterium].	GCA_003696565.1
RMG75601.1	TIR+FGS*→	TIR+FGS	463	D6711_06165	chloroflexi	Chloroflexi bacterium	TIR domain-containing protein [Chloroflexi bacterium].	GCA_003696565.1
RMG81795.1	TIR+FGS*→	TIR+FGS	524	D6712_15685	chloroflexi	Chloroflexi bacterium	TIR domain-containing protein [Chloroflexi bacterium].	GCA_003696545.1
RNC70126.1	<-ABhydrolase+ABhydrolase+CASPASE+TPR-S<-TIR+APATPase<-?||DrHyd+nSTAND1+FGS*→ DrHyd+NACHT+FGS→||<-?||?→?→?→ TRD+TRD→ SF2-DUF3427A+LPD33→	DrHyd+nSTAND1+FGS	908	ED859_06590	deltaproteobacteria	Desulfuromonadales bacterium	DUF4062 domain-containing protein [Desulfuromonadales bacterium].	GCA_003712145.1
RPH58975.1	NACHT+FGS*→	NACHT+FGS	477	EHM81_09025	chloroflexi	Chloroflexi bacterium	hypothetical protein EHM81_09025, partial [Chloroflexi bacterium].	GCA_003818555.1
RPI90984.1	FGS*→	FGS	257	EHM40_16975	chloroflexi	Chloroflexi bacterium	hypothetical protein EHM40_16975 [Chloroflexi bacterium].	GCA_003820075.1
RPJ19812.1	NACHT+FGS*→	NACHT+FGS	400	EHM35_20270	planctomycetes	Planctomycetaceae bacterium	hypothetical protein EHM35_20270 [Planctomycetaceae bacterium].	GCA_003820145.1
RPJ25004.1	FGS*→	FGS	258	EHM33_15980	chloroflexi	Chloroflexi bacterium	hypothetical protein EHM33_15980 [Chloroflexi bacterium].	GCA_003820175.1
RQW03777.1	FGS*→ Four-helical-protein→ FGS→	FGS	342	EH223_08950	bacteria	candidate division KSB1 bacterium	formylglycine-generating enzyme family protein, partial [candidate division KSB1 bacterium].	GCA_003854975.1

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RQW04566.1	SIG+TM+TM+NACHT+TCAD10+FGS→ DrHyd+NACHT+FGS*→ DrHyd→	DrHyd+NACHT+FGS	977	EH223_07060	bacteria	candidate division KSB1 bacterium	DUF4062 domain-containing protein [candidate division KSB1 bacterium].	GCA_003854975.1
RQW05893.1	TM+NACHT+FGS*→ Four-helical-protein→ FGS→	TM+NACHT+FGS	922	EH223_03525	bacteria	candidate division KSB1 bacterium	NACHT domain-containing protein [candidate division KSB1 bacterium].	GCA_003854975.1
RRR65524.1	SIG+NACHT+FGS*→?→?→?→ KAP-NTPase→	SIG+NACHT+FGS	1077	EI684_22890	chloroflexi	Candidatus Viridilinea halotolerans	hypothetical protein EI684_22890 [Candidatus Viridilinea halotolerans].	GCA_003934145.1
RRR69407.1	iSTAND→?→?→ MoxR-AAA→ SIG+VWA→ vWA-L+MNS-STAND+FGS*→	vWA-L+MNS-STAND+FGS	920	EI684_15695	chloroflexi	Candidatus Viridilinea halotolerans	hypothetical protein EI684_15695 [Candidatus Viridilinea halotolerans].	GCA_003934145.1
RRR73738.1	VWA+NACHT+FGS*→	VWA+NACHT+FGS	1417	EI684_08395	chloroflexi	Candidatus Viridilinea halotolerans	NACHT domain-containing protein [Candidatus Viridilinea halotolerans].	GCA_003934145.1
RRR76062.1	MNS-STAND+FGS→ *MNS-STAND+FGS*→ Four-helical-protein→	MNS-STAND+FGS	605	EI684_03590	chloroflexi	Candidatus Viridilinea halotolerans	hypothetical protein EI684_03590 [Candidatus Viridilinea halotolerans].	GCA_003934145.1
RRR76063.1	MNS-STAND+EAD9+FGS*→	MNS-STAND+EAD9+FGS	715	EI684_03595	chloroflexi	Candidatus Viridilinea halotolerans	hypothetical protein EI684_03595 [Candidatus Viridilinea halotolerans].	GCA_003934145.1
RRS32393.1	<-Cluster393_2clades<-Pentapeptide||TIR→ MED26C→ vWA-L+FGS*→||<-Cluster187_2clades<-?<-HSP70<-?<-IES1	vWA-L+FGS	797	OI74_11720	gammaproteobacteria	Gammaproteobacteria bacterium (ex Lamellibrachia satsuma)	hypothetical protein OI74_11720 [Gammaproteobacteria bacterium (ex Lamellibrachia satsuma)].	GCA_003934985.1
RRS33515.1	SIG+TM+TM+TM+TM+TM→?→?→?→?→ TIR→?→ NACHT+FGS*→||<-?<-SIG+TM+HAMP<-SIG+TM+TM+TM+TM<-?<-SIG+RFC-AAA<-Cluster440_2clades<-MalT	NACHT+FGS	526	OI74_07790	gammaproteobacteria	Gammaproteobacteria bacterium (ex Lamellibrachia satsuma)	hypothetical protein OI74_07790 [Gammaproteobacteria bacterium (ex Lamellibrachia satsuma)].	GCA_003934985.1
RZB36777.1	<-TM<-?||?→||<-?||?→ SIG+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM→||<-?||KAP-NTPase+FGS*→ Four-helical-protein→ NACHT+FGS→||<-?<-?<-?<-LexA-HTH+LexA-protease	KAP-NTPase+FGS	658	SRB2_01856	deltaproteobacteria	Desulfobacteraceae bacterium Eth-SRB2	hypothetical protein SRB2_01856 [Desulfobacteraceae bacterium Eth-SRB2].	GCA_004193595.1
TAH46387.1	PIN→ TIR+NACHT+FGS*→	TIR+NACHT+FGS	956	EYC67_09120	betaproteobacteria	Betaproteobacteria bacterium	TIR domain-containing protein [Betaproteobacteria bacterium].	GCA_004295105.1
TAH48128.1	<-ABhydrolase||NACHT+FGS*→ ABC-ATPase→?→?→||<-PIN	NACHT+FGS	1067	EYC68_22510	chloroflexi	Chloroflexi bacterium	NACHT domain-containing protein [Chloroflexi bacterium].	GCA_004295045.1
TAH51040.1	TIR+FGS*→?→||<-?||?→ N-OB→	TIR+FGS	430	EYC68_12490	chloroflexi	Chloroflexi bacterium	TIR domain-containing protein [Chloroflexi bacterium].	GCA_004295045.1
TAN48986.1	SIG+TM+NACHT+FGS*→	SIG+TM+NACHT+FGS	961	EPN21_13470	gammaproteobacteria	Methylococcaceae bacterium	NACHT domain-containing protein [Methylococcaceae bacterium].	GCA_004299145.1
TEU10577.1	FGS*→?→||<-?<-?<-?<-TIR+TM+FGS	FGS	301	E3J21_25805	chloroflexi	Anaerolineales bacterium	formylglycine-generating enzyme family protein [Anaerolineales bacterium].	GCA_004377365.1
TEU11372.1	Pkinase+FGS*→	Pkinase+FGS	972	E3J25_08125	chloroflexi	Anaerolineales bacterium	hypothetical protein E3J25_08125 [Anaerolineales bacterium].	GCA_004377265.1

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TEU12777.1	FGS*→	FGS	245	E3J21_20265	chloroflexi	Anaerolineales bacterium	formylglycine-generating enzyme family protein [Anaerolineales bacterium].	GCA_004377365.1
TEU17403.1	FGS*→	FGS	293	E3J21_08455	chloroflexi	Anaerolineales bacterium	formylglycine-generating enzyme family protein [Anaerolineales bacterium].	GCA_004377365.1
TEU18290.1	<-RADICAL-SAM<-?<-?||?→?→ Pkinase+Pkinase+FGS*→	Pkinase+Pkinase+FGS	869	E3J21_06280	chloroflexi	Anaerolineales bacterium	hypothetical protein E3J21_06280 [Anaerolineales bacterium].	GCA_004377365.1
THI85089.1	<-SIG+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM<-?<-FURR-HTH||?→||<-?||?→?→ DrHyd+nSTAND1+FGS*→||<-TIR+TM+BetaPropeller||CASPASE→ CASPASE+TPR-S→	DrHyd+nSTAND1+FGS	886	CAF41_012685	nitrospirae	Nitrospira sp. CG24A	DUF4062 domain-containing protein [Nitrospira sp. CG24A].	GCA_002869925.2
THI90736.1	TIR+FGS→ DrHyd+nSTAND1+FGS*→	DrHyd+nSTAND1+FGS	877	CAF41_002995	nitrospirae	Nitrospira sp. CG24A	DUF4062 domain-containing protein [Nitrospira sp. CG24A].	GCA_002869925.2
TKB61807.1	nSTAND1+FGS*→	nSTAND1+FGS	646	E8D48_09975	nitrospirae	Nitrospira sp.	formylglycine-generating enzyme family protein [Nitrospira sp.].	GCA_005116895.1
TKB62458.1	TPR→?→?→?→?→||<-?||?→ PSE→ DrHyd+nSTAND1+FGS*→	DrHyd+nSTAND1+FGS	879	E8D49_01790	nitrospirae	Nitrospira sp.	DUF4062 domain-containing protein [Nitrospira sp.].	GCA_005116885.1
TKB70058.1	DrHyd+nSTAND1+FGS*→ Four-helical-protein→	DrHyd+nSTAND1+FGS	900	E8D52_03140	nitrospirae	Nitrospira sp.	DUF4062 domain-containing protein [Nitrospira sp.].	GCA_005116745.1
TKB79855.1	DrHyd+nSTAND1+FGS*→	DrHyd+nSTAND1+FGS	892	E8D42_00345	nitrospirae	Nitrospira sp.	DUF4062 domain-containing protein [Nitrospira sp.].	GCA_005116955.1
TKB89607.1	TPR→?→?→?→?→||<-?||?→ DrHyd+nSTAND1+FGS*→	DrHyd+nSTAND1+FGS	870	E8D41_13485	nitrospirae	Nitrospira sp.	DUF4062 domain-containing protein [Nitrospira sp.].	GCA_005116945.1
TKB92435.1	<-TIR||CASPASE→ FGS→?→ FGS*→ CASPASE+TPR-S→	FGS	279	E8D41_06385	nitrospirae	Nitrospira sp.	formylglycine-generating enzyme family protein [Nitrospira sp.].	GCA_005116945.1
TKJ29986.1	NACHT+FGS*→ KAP-NTPase+FGS→	NACHT+FGS	1038	CEE40_06785	chloroflexi	Chloroflexi bacterium B3_Chlor	hypothetical protein CEE40_06785 [Chloroflexi bacterium B3_Chlor].	GCA_005223035.1
TLD45545.1	<-PAS+HISKIN+REC||?→||<-?||?→ DrHyd+iSTAND→ MoxR-AAA→ SIG+VWA→ vWA-L+TIR+DrHyd+FGS*→	vWA-L+TIR+DrHyd+FGS	896	pkn1_9	betaproteobacteria	Candidatus Accumulibacter sp.	Serine/threonine-protein kinase pkn1 [Candidatus Accumulibacter sp.].	GCA_005524045.1
TLD45954.1	EAD8+DrHyd+nSTAND1+FGS*→||<-RVT||Four-helical-protein→||<-FGS<-TIR+NACHT+FGS	EAD8+DrHyd+nSTAND1+FGS	1062	pkn1_8	betaproteobacteria	Candidatus Accumulibacter sp.	Serine/threonine-protein kinase pkn1 [Candidatus Accumulibacter sp.].	GCA_005524045.1
TLD46242.1	SIG+TM+TM+TM+TM+TM+TM+TM+TM→||<-Patatin||?→||<-?||?→||<-?||nSTAND1+FGS*→	nSTAND1+FGS	764	pkn1_4	betaproteobacteria	Candidatus Accumulibacter sp.	Serine/threonine-protein kinase pkn1 [Candidatus Accumulibacter sp.].	GCA_005524045.1
TLD46403.1	TIR+NACHT+FGS*→	TIR+NACHT+FGS	991	pkn1_3	betaproteobacteria	Candidatus Accumulibacter sp.	Serine/threonine-protein kinase pkn1 [Candidatus Accumulibacter sp.].	GCA_005524045.1
TMQ74907.1	SIG+drhyd→ FGS*→	FGS	250	ACCUM_2481	betaproteobacteria	Candidatus Accumulibacter phosphatis	protein of unknown function DUF323 [Candidatus Accumulibacter phosphatis].	GCA_005889575.1
TSA11332.1	KAP-NTPase+FGS*→	KAP-NTPase+FGS	535	D4R73_04040	deltaproteobacteria	Deltaproteobacteria bacterium	hypothetical protein D4R73_04040 [Deltaproteobacteria bacterium].	GCA_007280345.1
TVR19569.1	TRD+TRD→?→ SWC3→ SF2-DUF3427A+LPD33→ DrHyd+nSTAND1+FGS*→	DrHyd+nSTAND1+FGS	963	EA396_12385	chloroflexi	Anaerolineaceae bacterium	hypothetical protein EA396_12385 [Anaerolineaceae bacterium].	GCA_007693385.1

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TVR20270.1	DrHyd+nSTAND1+FGS*→	DrHyd+nSTAND1+FGS	925	EA396_10895	chloroflexi	Anaerolineaceae bacterium	hypothetical protein EA396_10895, partial [Anaerolineaceae bacterium].	GCA_007693385.1
TVR25455.1	NACHT+FGS*→	NACHT+FGS	1003	EA396_00070	chloroflexi	Anaerolineaceae bacterium	TIR domain-containing protein [Anaerolineaceae bacterium].	GCA_007693385.1
TVR58137.1	<-SWC3<-FGS||?→ NACHT+FGS*→	NACHT+FGS	935	EA420_17850	gammaproteobacteria	Candidatus Competibacteraceae bacterium	NACHT domain-containing protein [Candidatus Competibacteraceae bacterium].	GCA_007695245.1
TVR58388.1	TIR+bDLD3→ bDLD3+nSTAND1+FGS*→?→||<-NACHT+FGS	bDLD3+nSTAND1+FGS	802	EA420_17215	gammaproteobacteria	Candidatus Competibacteraceae bacterium	hypothetical protein EA420_17215 [Candidatus Competibacteraceae bacterium].	GCA_007695245.1
TXG93317.1	TIR+BetaPropeller+BetaPropeller→ TIR+NACHT+FGS*→ TIR+NACHT→	TIR+NACHT+FGS	974	E6R15_09770	betaproteobacteria	Zoogloea sp.	TIR domain-containing protein [Zoogloea sp.].	-
TXH27877.1	FGS*→||<-?<-?||ABhydrolase→	FGS	242	E6Q99_02970	elusimicrobia	Elusimicrobia bacterium	hypothetical protein E6Q99_02970, partial [Elusimicrobia bacterium].	-
TXI20020.1	DrHyd+nSTAND1+FGS*→	DrHyd+nSTAND1+FGS	896	E6Q62_02620	betaproteobacteria	Nitrosomonas sp.	DUF4062 domain-containing protein [Nitrosomonas sp.].	-
VEN74385.1	SIG+PTSIIB-sorb→?→ NACHT+FGS→*?*→ *KAP-NTPase+FGS*→?→?→||<-?<-?<-?<-?||?→ NACHT+FGS*→?→?→ MED26C→	NACHT+FGS	898	EPICR_30322	deltaproteobacteria	uncultured Desulfobacteraceae bacterium	Signal transduction protein [uncultured Desulfobacteraceae bacterium].	GCA_900659855.1
VEN74387.1	KAP-NTPase+FGS*→	KAP-NTPase+FGS	669	EPICR_30324	deltaproteobacteria	uncultured Desulfobacteraceae bacterium	conserved hypothetical protein [uncultured Desulfobacteraceae bacterium].	GCA_900659855.1
VEN74395.1	TM+NACHT+FGS*→	TM+NACHT+FGS	1024	EPICR_30332	deltaproteobacteria	uncultured Desulfobacteraceae bacterium	hypothetical protein EPICR_30332 [uncultured Desulfobacteraceae bacterium].	GCA_900659855.1
WP_002710120.1	TIR+NACHT→?→?→?→ FGS*→ ABhydrolase+ABhydrolase+CASPASE+TPR-S→	FGS	266	THINI_RS24560	gammaproteobacteria	Thiothrix nivea	SUMF1/EgtB/PvdO family nonheme iron enzyme [Thiothrix nivea].	GCF_000260135.1
WP_006563305.1	MED26C→?→?→?→?→?→?→ MNS-STAND+FGS*→ KAP-NTPase→	MNS-STAND+FGS	646	OSCT_RS18055	chloroflexi	Oscillochloris trichoides	formylglycine-generating enzyme family protein [Oscillochloris trichoides].	GCF_000152145.1
WP_007042322.1	DrHyd+nSTAND1+FGS*→||<-PSE<-NACHT+FGS	DrHyd+nSTAND1+FGS	892	THIDR-DRAFT_RS24020	gammaproteobacteria	Thiorhodococcus drewsii	SUMF1/EgtB/PvdO family nonheme iron enzyme [Thiorhodococcus drewsii].	GCF_000224065.1
WP_013032524.1	TIR+bDLD3→ bDLD3+nSTAND1+FGS*→||<-?<-Four-helical-protein||RVT→	bDLD3+nSTAND1+FGS	799	NHAL_RS07270	gammaproteobacteria	Nitrosococcus halophilus	SUMF1/EgtB/PvdO family nonheme iron enzyme [Nitrosococcus halophilus].	GCF_000024725.1
WP_013964922.1	SIG+CACHE+TM+PAS+PAS+GGDEF+EAL→?→?→?→?→ TIR+NACHT+FGS*→	TIR+NACHT+FGS	954	NIT79A3_RS03700	betaproteobacteria	Nitrosomonas sp. Is79A3	SUMF1/EgtB/PvdO family nonheme iron enzyme [Nitrosomonas sp. Is79A3].	GCF_000219585.1
WP_013967247.1	DrHyd+nSTAND1+FGS*→	DrHyd+nSTAND1+FGS	932	NIT79A3_RS16330	betaproteobacteria	Nitrosomonas sp. Is79A3	SUMF1/EgtB/PvdO family nonheme iron enzyme [Nitrosomonas sp. Is79A3].	GCF_000219585.1
WP_015766782.1	<-CNMP+CRP-HTH||FAD-NAD-dep-oxidoreductase→?→||<-?<-?<-?<-?||nSTAND1+FGS*→||<-?<-ABHYDROLASE	nSTAND1+FGS	844	CAP2UW1_RS11490	betaproteobacteria	Candidatus Accumulibacter phosphatis	SUMF1/EgtB/PvdO family nonheme iron enzyme [Candidatus Accumulibacter phosphatis].	GCF_000024165.1

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WP_015766797.1	EAD8+TIR+NACHT+FGS*→||<-RVT<-?<-EAD8+TIR+ABhydrolase	EAD8+TIR+NACHT+FGS	1092	CAP2UW1_RS23785	betaproteobacteria	Candidatus Accumulibacter phosphatis	SUMF1/EgtB/PvdO family nonheme iron enzyme [Candidatus Accumulibacter phosphatis].	GCF_000024165.1
WP_020502879.1	NACHT+FGS*→	NACHT+FGS	728	-	gammaproteobacteria	Lamprocystis purpurea	SUMF1/EgtB/PvdO family nonheme iron enzyme [Lamprocystis purpurea].	-
WP_020504760.1	EAD8+nSTAND1+FGS*→	EAD8+nSTAND1+FGS	925	A39O_RS0111260	gammaproteobacteria	Lamprocystis purpurea	SUMF1/EgtB/PvdO family nonheme iron enzyme [Lamprocystis purpurea].	GCF_000379525.1
WP_026199145.1	EAD8+nSTAND1+FGS*→||<-Trypsin+EAD8<-Trypco1	EAD8+nSTAND1+FGS	868	A39O_RS36165	gammaproteobacteria	Lamprocystis purpurea	SUMF1/EgtB/PvdO family nonheme iron enzyme [Lamprocystis purpurea].	GCF_000379525.1
WP_026199412.1	nSTAND1+FGS*→	nSTAND1+FGS	833	A39O_RS0114350	gammaproteobacteria	Lamprocystis purpurea	SUMF1/EgtB/PvdO family nonheme iron enzyme [Lamprocystis purpurea].	GCF_000379525.1
WP_028314253.1	Calcineurin+NACHT+FGS*→||<-MED26C	Calcineurin+NACHT+FGS	1101	G491_RS0108205	deltaproteobacteria	Desulfatibacillum aliphaticivorans	SUMF1/EgtB/PvdO family nonheme iron enzyme [Desulfatibacillum aliphaticivorans].	GCF_000429905.1
WP_028315860.1	Calcineurin+NACHT+FGS*→	Calcineurin+NACHT+FGS	1088	G491_RS0120200	deltaproteobacteria	Desulfatibacillum aliphaticivorans	SUMF1/EgtB/PvdO family nonheme iron enzyme [Desulfatibacillum aliphaticivorans].	GCF_000429905.1
WP_046850450.1	<-ADP_ribosyl_GH<-?<-?<-?||DrHyd+nSTAND1+FGS*→?→||<-nSTAND1<-?<-PSE<-SIG+nSTAND1<-TIR	DrHyd+nSTAND1+FGS	868	AAW31_RS12305	betaproteobacteria	Nitrosomonas communis	SUMF1/EgtB/PvdO family nonheme iron enzyme [Nitrosomonas communis].	GCF_001007935.1
WP_052347676.1	nSTAND1+FGS*→	nSTAND1+FGS	515	D779_RS20855	gammaproteobacteria	Imhoffiella purpurea	formylglycine-generating enzyme family protein [Imhoffiella purpurea].	GCF_000585215.1
WP_052515241.1	KAP-NTPase+FGS*→ Four-helical-protein→ RVT→ Calcineurin+NACHT+FGS→	KAP-NTPase+FGS	689	X474_RS14675	deltaproteobacteria	Dethiosulfatarculus sandiegensis	SUMF1/EgtB/PvdO family nonheme iron enzyme [Dethiosulfatarculus sandiegensis].	GCF_000931935.2
WP_054534535.1	BACTERIALFRINGE→ BetaPropeller→||<-?||?→?→ NACHT+FGS*→	NACHT+FGS	957	SE18_RS11130	chloroflexi	Herpetosiphon geysericola	SUMF1/EgtB/PvdO family nonheme iron enzyme [Herpetosiphon geysericola].	GCF_001306135.1
WP_058554345.1	nSTAND1+FGS*→||<-SIG+CACHE+TM+PAS+PAS+GGDEF+EAL||?→||<-?||SIR2→	nSTAND1+FGS	820	ML01_RS05180	gammaproteobacteria	Thiohalocapsa sp. ML1	SUMF1/EgtB/PvdO family nonheme iron enzyme [Thiohalocapsa sp. ML1].	GCF_001469165.1
WP_058554420.1	TIR→ MoxR-AAA→ MED26C→ FGS*→?→||<-?<-FGS||?→?→ TIR→ EAD1+fvmYukDl-Nterm→	FGS	857	ML01_RS05595	gammaproteobacteria	Thiohalocapsa sp. ML1	SUMF1/EgtB/PvdO family nonheme iron enzyme [Thiohalocapsa sp. ML1].	GCF_001469165.1
WP_058557121.1	EAD8→ EAD8+nSTAND1+FGS*→?→?→ RVT→	EAD8+nSTAND1+FGS	964	ML01_RS19795	gammaproteobacteria	Thiohalocapsa sp. ML1	SUMF1/EgtB/PvdO family nonheme iron enzyme [Thiohalocapsa sp. ML1].	GCF_001469165.1
WP_073644744.1	TIR+nSTAND1+FGS*→||<-EAD1+FGS<-EAD1+Trypsin	TIR+nSTAND1+FGS	931	FACHB389_RS31975	cyanobacteria	Nostoc calcicola	SUMF1/EgtB/PvdO family nonheme iron enzyme [Nostoc calcicola].	GCF_001904715.1
WP_074904186.1	TIR+bDLD3→ bDLD3+nSTAND1+FGS*→||<-NACHT+FGS<-ABhydrolase+bDLD3	bDLD3+nSTAND1+FGS	823	BM122_RS04980	betaproteobacteria	Nitrosomonas communis	SUMF1/EgtB/PvdO family nonheme iron enzyme [Nitrosomonas communis].	GCF_900114745.1

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WP_074906405.1	<-ADP_ribosyl_GH<-?<-?<-?||DrHyd+nSTAND1+FGS*→ FGS→ PSE→?→||<-?<-?<-?<-SWC3	DrHyd+nSTAND1+FGS	824	BM122_RS14970	betaproteobacteria	Nitrosomonas communis	SUMF1/EgtB/PvdO family nonheme iron enzyme [Nitrosomonas communis].	GCF_900114745.1
WP_078922991.1	TIR+NACHT+FGS*→	TIR+NACHT+FGS	961	B5D50_RS12585	gammaproteobacteria	Thiothrix eikelboomii	SUMF1/EgtB/PvdO family nonheme iron enzyme [Thiothrix eikelboomii].	GCF_900167255.1
WP_081485890.1	FGS*→	FGS	285	-	gammaproteobacteria	Thiothrix nivea	SUMF1/EgtB/PvdO family nonheme iron enzyme [Thiothrix nivea].	-
WP_083884749.1	<-ABhydrolase<-?<-?<-?<-?||TIR+nSTAND1+FGS*→||<-RVT<-SIG+SWC3<-FGS<-TIR+nSTAND1+FGS	TIR+nSTAND1+FGS	974	THIMO_RS13755	gammaproteobacteria	Thioflavicoccus mobilis	SUMF1/EgtB/PvdO family nonheme iron enzyme [Thioflavicoccus mobilis].	GCF_000327045.1
WP_084511416.1	Calcineurin+NACHT+FGS*→	Calcineurin+NACHT+FGS	1109	-	deltaproteobacteria	Desulfatibacillum aliphaticivorans	SUMF1/EgtB/PvdO family nonheme iron enzyme [Desulfatibacillum aliphaticivorans].	-
WP_088618636.1	DrHyd+NACHT+FGS*→?→||<-FGS<-?||?→||<-RADICAL-SAM	DrHyd+NACHT+FGS	1016	CEK71_RS06560	gammaproteobacteria	Methylovulum psychrotolerans	SUMF1/EgtB/PvdO family nonheme iron enzyme [Methylovulum psychrotolerans].	GCF_002209385.1
WP_089718394.1	TIR+bDLD3→ bDLD3+nSTAND1+FGS*→	bDLD3+nSTAND1+FGS	798	FLV43_RS07510	nitrospinae/tectomicrobia group	Candidatus Entotheonella palauensis	SUMF1/EgtB/PvdO family nonheme iron enzyme [Candidatus Entotheonella palauensis].	GCF_900079105.1
WP_089936193.1	ABC-ATPase→ ABC-ATPase→ drhyd+nSTAND1+FGS*→	drhyd+nSTAND1+FGS	929	FLV42_RS11295	nitrospinae/tectomicrobia group	Candidatus Entotheonella palauensis	SUMF1/EgtB/PvdO family nonheme iron enzyme [Candidatus Entotheonella palauensis].	GCF_900079095.1
WP_090322194.1	DrHyd→ nSTAND1→ FGS*→	FGS	263	BMY41_RS13900	betaproteobacteria	Nitrosomonas oligotropha	formylglycine-generating enzyme family protein [Nitrosomonas oligotropha].	GCF_900106555.1
WP_090742272.1	DrHyd+nSTAND1+FGS*→	DrHyd+nSTAND1+FGS	914	COMA1_RS00565	nitrospirae	Candidatus Nitrospira nitrosa	SUMF1/EgtB/PvdO family nonheme iron enzyme [Candidatus Nitrospira nitrosa].	GCF_001458735.1
WP_095042164.1	NACHT+FGS*→	NACHT+FGS	1092	CFX0092_RS03310	chloroflexi	Candidatus Promineofilum breve	SUMF1/EgtB/PvdO family nonheme iron enzyme [Candidatus Promineofilum breve].	GCF_900066015.1
WP_095043336.1	<-MED26C||?→?→||<-?<-?||EAD7+TIR+FGS*→||<-ABhydrolase||?→ Cluster455_2clades→||<-ABhydrolase<-?||?→ MED26C→	EAD7+TIR+FGS	604	CFX0092_RS09700	chloroflexi	Candidatus Promineofilum breve	SUMF1/EgtB/PvdO family nonheme iron enzyme [Candidatus Promineofilum breve].	GCF_900066015.1
WP_097644514.1	CASPASE+EAD2→ EAD2→?→ MoxR-AAA→ SIG+VWA→ vWA-L+MNS-STAND+FGS*→	vWA-L+MNS-STAND+FGS	917	CJ255_RS12915	chloroflexi	Candidatus Viridilinea mediisalina	SUMF1/EgtB/PvdO family nonheme iron enzyme [Candidatus Viridilinea mediisalina].	GCF_002532535.1
WP_097646022.1	MNS-STAND+FGS→//*<-?<-?//FGS*→	MNS-STAND+FGS	331	CJ255_RS20935	chloroflexi	Candidatus Viridilinea mediisalina	formylglycine-generating enzyme family protein [Candidatus Viridilinea mediisalina].	GCF_002532535.1

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WP_097646178.1	FGS*→	FGS	273	CJ255_RS21825	chloroflexi	Candidatus Viridilinea mediisalina	SUMF1/EgtB/PvdO family nonheme iron enzyme [Candidatus Viridilinea mediisalina].	GCF_002532535.1
WP_097650659.1	MNS-STAND+FGS*→ KAP-NTPase→	MNS-STAND+FGS	798	A9Q02_RS01775	chloroflexi	Candidatus Chloroploca asiatica	SUMF1/EgtB/PvdO family nonheme iron enzyme [Candidatus Chloroploca asiatica].	GCF_002532075.1
WP_097650736.1	MNS-STAND+FGS*→ KAP-NTPase→	MNS-STAND+FGS	677	A9Q02_RS02220	chloroflexi	Candidatus Chloroploca asiatica	SUMF1/EgtB/PvdO family nonheme iron enzyme [Candidatus Chloroploca asiatica].	GCF_002532075.1
WP_097651198.1	Eukglutathionesyn-ATPgrasp→?→?→||<-?<-?<-?<-?||MNS-STAND+FGS*→ EAD2→||<-?||ABhydrolase→	MNS-STAND+FGS	748	A9Q02_RS04675	chloroflexi	Candidatus Chloroploca asiatica	SUMF1/EgtB/PvdO family nonheme iron enzyme [Candidatus Chloroploca asiatica].	GCF_002532075.1
WP_100918361.1	nSTAND1+FGS*→	nSTAND1+FGS	825	THSYN_RS06160	gammaproteobacteria	Candidatus Thiodictyon syntrophicum	SUMF1/EgtB/PvdO family nonheme iron enzyme [Candidatus Thiodictyon syntrophicum].	GCF_002813775.1
WP_100921702.1	<-HSP70<-?<-?||?→ SbcC+SbcC→?→||<-?||PSE→ FGS→//*<-SIG+SWC3<-TIR+FGS*<-TIR<-FURR-HTH	FGS	290	THSYN_RS26100	gammaproteobacteria	Candidatus Thiodictyon syntrophicum	SUMF1/EgtB/PvdO family nonheme iron enzyme [Candidatus Thiodictyon syntrophicum].	GCF_002813775.1
WP_100921704.1	TIR+FGS*→	TIR+FGS	408	THSYN_RS26110	gammaproteobacteria	Candidatus Thiodictyon syntrophicum	SUMF1/EgtB/PvdO family nonheme iron enzyme [Candidatus Thiodictyon syntrophicum].	GCF_002813775.1
WP_103975510.1	SIG+drhyd+NACHT+FGS*→?→?→?→ SIG+TM+TM+TM→	SIG+drhyd+NACHT+FGS	920	AADEFJLK_RS19975	gammaproteobacteria	Methylovulum psychrotolerans	SUMF1/EgtB/PvdO family nonheme iron enzyme [Methylovulum psychrotolerans].	GCF_002923755.1
WP_106247884.1	DrHyd+nSTAND1+FGS*→	DrHyd+nSTAND1+FGS	937	bacteria>actinobacteria	Allonocardiopsis opalescens	-	1361040121	-
WP_107803916.1	DrHyd+nSTAND1→ SIG+FGS*→	SIG+FGS	232	C8R26_RS11925	betaproteobacteria	Nitrosomonas oligotropha	SUMF1/EgtB/PvdO family nonheme iron enzyme [Nitrosomonas oligotropha].	GCF_003050805.1
WP_109821479.1	SIG+CACHE+TM+PAS+PAS+GGDEF+EAL→||<-?||?→?→?→?→?→ TIR+NACHT+FGS*→||<-?||?→||<-?<-?||GNTR-HTH→	TIR+NACHT+FGS	932	DKT75_RS00505	gammaproteobacteria	Leucothrix arctica	SUMF1/EgtB/PvdO family nonheme iron enzyme [Leucothrix arctica].	GCF_003172895.1
WP_109838176.1	<-SIG+CACHE+TM+PAS+PAS+GGDEF+EAL<-SIG+CACHE+TM+PAS+PAS+GGDEF+EAL<-?||TIR+NACHT+FGS→//*<-RVT*//*Four-helical-protein*→//*<-?<-TIR+NACHT+FGS*<-?||?→||<-?||SWC3→	TIR+NACHT+FGS	935	DKW60_RS13450	gammaproteobacteria	Leucothrix pacifica	SUMF1/EgtB/PvdO family nonheme iron enzyme [Leucothrix pacifica].	GCF_003172875.1
WP_109838180.1	TIR+NACHT+FGS*→	TIR+NACHT+FGS	1009	DKW60_RS13470	gammaproteobacteria	Leucothrix pacifica	SUMF1/EgtB/PvdO family nonheme iron enzyme [Leucothrix pacifica].	GCF_003172875.1
WP_113718124.1	CASPASE+FGS*→	CASPASE+FGS	581	bacteria>actinobacteria	Arthrobacter dokdonellae	-	1428153431	-
WP_117400917.1	<-TIMbarrel||?→?→?→ EAD8+Trypsin→ DADA-Ligase→ EAD2+NACHT+FGS*→	EAD2+NACHT+FGS	982	D0T12_RS19005	actinobacteria	Actinomadura sp. LHW52907	SUMF1/EgtB/PvdO family nonheme iron enzyme [Actinomadura sp. LHW52907].	GCF_003432485.1

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WP_120798715.1	TIR+nSTAND1+FGS*→	TIR+nSTAND1+FGS	943	-	gammaproteobacteria	Thiocapsa rosea	SUMF1/EgtB/PvdO family nonheme iron enzyme [Thiocapsa rosea].	-
WP_120798722.1	TIR+nSTAND1+FGS→ *PSE→?→ TIR+TCAD2→ ABhydrolase+ABhydrolase+CASPASE+TPR-S→ TIR→ MoxR-AAA→ MED26C→ vWA-L+TIR+FGS→*||<-DrHyd<-TM+TM+TM+TM+TM+TM<-TIR+LDcluster2	TIR+nSTAND1+FGS	887	BDD21_RS20395	gammaproteobacteria	Thiocapsa rosea	SUMF1/EgtB/PvdO family nonheme iron enzyme [Thiocapsa rosea].	GCF_003634315.1
WP_121435660.1	<-TIMbarrel||?→?→?→ EAD8+Trypsin→ DADA-Ligase→ NACHT+FGS*→	NACHT+FGS	978	BZB76_RS18480	actinobacteria	Actinomadura pelletieri	SUMF1/EgtB/PvdO family nonheme iron enzyme [Actinomadura pelletieri].	GCF_003634705.1
WP_124681989.1	MNS-STAND+FGS*→	MNS-STAND+FGS	639	CJ255_RS17220	chloroflexi	Candidatus Viridilinea mediisalina	formylglycine-generating enzyme family protein [Candidatus Viridilinea mediisalina].	GCF_002532535.1
WP_129630085.1	MNS-STAND+FGS*→ KAP-NTPase→||<-?||?→ FAD-NAD-dep-oxidoreductase→	MNS-STAND+FGS	723	EKD03_RS09875	chloroflexi	Candidatus Oscillochloris fontis	SUMF1/EgtB/PvdO family nonheme iron enzyme [Candidatus Oscillochloris fontis].	GCF_004138135.1
WP_129675764.1	<-EAD2+CASPASE||CASPASE+EAD2→?→?→ EAD2+iSTAND→ MoxR-AAA→ SIG+VWA→ vWA-L+MNS-STAND+FGS*→||<-?||EAD2+SAVED→	vWA-L+MNS-STAND+FGS	910	EKD05_RS18730	chloroflexi	Candidatus Chloroploca sp. Khr17	SUMF1/EgtB/PvdO family nonheme iron enzyme [Candidatus Chloroploca sp. Khr17].	GCF_004138165.1
WP_129676117.1	<-ABC-ATPase<-?||?→||<-?<-?<-SIG+HISKIN+REC<-?||MNS-STAND+FGS*→	MNS-STAND+FGS	771	EKD05_RS19365	chloroflexi	Candidatus Chloroploca sp. Khr17	SUMF1/EgtB/PvdO family nonheme iron enzyme [Candidatus Chloroploca sp. Khr17].	GCF_004138165.1
WP_129680571.1	TIR+NACHT+FGS*→||<-?<-?<-?<-TM+TM+TM+TM+TM+TM+TM<-?||SIG+TM+HAMP+HISKIN→	TIR+NACHT+FGS	1113	EKD04_RS05935	chloroflexi	Chloroflexales bacterium ZM16-3	SUMF1/EgtB/PvdO family nonheme iron enzyme [Chloroflexales bacterium ZM16-3].	GCF_004138175.2
WP_129682868.1	ABhydrolase→||<-?||?→ CNMP+CRP-HTH→?→ Pkinase+FHA→?→ Pkinase+FHA+TM+TM+FGS*→	Pkinase+FHA+TM+TM+FGS	994	EKD04_RS11830	chloroflexi	Chloroflexales bacterium ZM16-3	SUMF1/EgtB/PvdO family nonheme iron enzyme [Chloroflexales bacterium ZM16-3].	GCF_004138175.2
WP_133117020.1	MNS-STAND+FGS*→	MNS-STAND+FGS	468	CJ255_RS20920	chloroflexi	Candidatus Viridilinea mediisalina	formylglycine-generating enzyme family protein, partial [Candidatus Viridilinea mediisalina].	GCF_002532535.1
WP_135477535.1	MNS-STAND+FGS*→ KAP-NTPase→	MNS-STAND+FGS	671	EYB53_RS07210	chloroflexi	Candidatus Chloroploca sp. M-50	SUMF1/EgtB/PvdO family nonheme iron enzyme [Candidatus Chloroploca sp. M-50].	GCF_004762035.1
WP_135478271.1	MNS-STAND+FGS→*?→?→ MNS-STAND+FGS*→ KAP-NTPase→	MNS-STAND+FGS	749	EYB53_RS11155	chloroflexi	Candidatus Chloroploca sp. M-50	SUMF1/EgtB/PvdO family nonheme iron enzyme [Candidatus Chloroploca sp. M-50].	GCF_004762035.1
WP_135478274.1	MNS-STAND+EAD9+FGS*→	MNS-STAND+EAD9+FGS	726	bacteria>chloroflexi	Candidatus Chloroploca sp. M-50	-	1610950059	-
WP_135480949.1	<-CASPASE<-EAD2||CASPASE+EAD2→ EAD2+iSTAND→ MoxR-AAA→ SIG+VWA→ vWA-L+MNS-STAND+FGS*→||<-?||EAD2+SAVED→||<-?||?→||<-?<-SIG+TM+HAMP+HISKIN	vWA-L+MNS-STAND+FGS	865	EYB53_RS21460	chloroflexi	Candidatus Chloroploca sp. M-50	SUMF1/EgtB/PvdO family nonheme iron enzyme [Candidatus Chloroploca sp. M-50].	GCF_004762035.1

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WP_135481914.1	FGS*→	FGS	498	bacteria>chloroflexi	Candidatus Chloroploca sp. M-50	-	1610955746	-
WP_138678219.1	NACHT+FGS*→||<-DrHyd+NACHT+FGS<-?||?→?→?→?→ MoxR-AAA→	NACHT+FGS	959	ACCUM_RS11740	betaproteobacteria	Candidatus Accumulibacter phosphatis	SUMF1/EgtB/PvdO family nonheme iron enzyme [Candidatus Accumulibacter phosphatis].	GCF_005889575.1
WP_138678880.1	FGS*→	FGS	336	-	betaproteobacteria	Candidatus Accumulibacter phosphatis	SUMF1/EgtB/PvdO family nonheme iron enzyme [Candidatus Accumulibacter phosphatis] .	-
WP_138678883.1	nSTAND1+TM+TPR+TPR→||<-?||SIG+SWC3→?→ FGS→*//<-RVT//Four-helical-protein→//<-?<-FGS*<-MED26C	FGS	785	ACCUM_RS18245	betaproteobacteria	Candidatus Accumulibacter phosphatis	SUMF1/EgtB/PvdO family nonheme iron enzyme [Candidatus Accumulibacter phosphatis].	GCF_005889575.1
WP_138679000.1	SIG+drhyd→ FGS*→	FGS	273	ACCUM_RS19505	betaproteobacteria	Candidatus Accumulibacter phosphatis	SUMF1/EgtB/PvdO family nonheme iron enzyme [Candidatus Accumulibacter phosphatis].	GCF_005889575.1
WP_141354765.1	TIR+nSTAND1+FGS*→	TIR+nSTAND1+FGS	1034	-	betaproteobacteria	Zoogloea ramigera	SUMF1/EgtB/PvdO family nonheme iron enzyme [Zoogloea ramigera].	-
WP_141354768.1	TIR+NACHT+FGS→*//<-DrHyd//TM+TM+TM+TM+TM+TM→//<-TIR+nSTAND1+FGS*	TIR+NACHT+FGS	1005	ZRA01_RS18100	betaproteobacteria	Zoogloea ramigera	SUMF1/EgtB/PvdO family nonheme iron enzyme [Zoogloea ramigera].	GCF_006539865.1
WP_141508656.1	FGS*→	FGS	438	A9Q02_RS01600	chloroflexi	Candidatus Chloroploca asiatica	SUMF1/EgtB/PvdO family nonheme iron enzyme, partial [Candidatus Chloroploca asiatica].	GCF_002532075.1
WP_144412951.1	<-ADP_ribosyl_GH<-?<-?<-?||PSE→ nSTAND1+FGS*→?→||<-nSTAND1<-PSE<-SIG+nSTAND1<-TIR	nSTAND1+FGS	811	BCL69_RS09525	betaproteobacteria	Nitrosomonas communis	SUMF1/EgtB/PvdO family nonheme iron enzyme [Nitrosomonas communis].	GCF_008124795.1
WP_155247659.1	Trypco1→ SIG+Trypsin+NACHT+FGS*→	SIG+Trypsin+NACHT+FGS	1057	K382_RS0113985	gammaproteobacteria	Teredinibacter turnerae	SUMF1/EgtB/PvdO family nonheme iron enzyme [Teredinibacter turnerae].	GCF_000426805.1
WP_155312115.1	NACHT+FGS→ Calcineurin+NACHT+FGS→?→?→ NACHT+FGS→?→ PSE→?→ NACHT+FGS*→?→||<-?||?→?→ ABC-ATPase→	NACHT+FGS	527	GN112_RS21635	deltaproteobacteria	Desulfosarcina ovata	SUMF1/EgtB/PvdO family nonheme iron enzyme [Desulfosarcina ovata].	GCF_009689005.1
WP_155342158.1	DrHyd+nSTAND1+FGS*→	DrHyd+nSTAND1+FGS	889	Acor_RS41020	actinobacteria	Acrocarpospora corrugata	SUMF1/EgtB/PvdO family nonheme iron enzyme, partial [Acrocarpospora corrugata].	GCF_009687845.1
WP_156427941.1	NACHT+FGS*→	NACHT+FGS	859	ML01_RS23445	gammaproteobacteria	Thiohalocapsa sp. ML1	SUMF1/EgtB/PvdO family nonheme iron enzyme, partial [Thiohalocapsa sp. ML1].	GCF_001469165.1
WP_156428023.1	NACHT+FGS*→	NACHT+FGS	942	ML01_RS26210	gammaproteobacteria	Thiohalocapsa sp. ML1	SUMF1/EgtB/PvdO family nonheme iron enzyme, partial [Thiohalocapsa sp. ML1].	GCF_001469165.1
WP_157468427.1	Calcineurin+NACHT+FGS*→	Calcineurin+NACHT+FGS	1121	-	deltaproteobacteria	Desulfatibacillum aliphaticivorans	SUMF1/EgtB/PvdO family nonheme iron enzyme [Desulfatibacillum aliphaticivorans].	-

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WP_157633685.1	NACHT+FGS*→	NACHT+FGS	720	THIMO_RS07195	gammaproteobacteria	Thioflavicoccus mobilis	SUMF1/EgtB/PvdO family nonheme iron enzyme [Thioflavicoccus mobilis].	GCF_000327045.1
WP_157679426.1	<-SIG+TM+TM+TM<-?||TIR+NACHT→ SIG+FGS*→	SIG+FGS	279	CEK71_RS19030	gammaproteobacteria	Methylovulum psychrotolerans	SUMF1/EgtB/PvdO family nonheme iron enzyme [Methylovulum psychrotolerans].	GCF_002209385.1
WP_157817391.1	FGS*→||<-?<-CASPASE	FGS	207	THSYN_RS01715	gammaproteobacteria	Candidatus Thiodictyon syntrophicum	SUMF1/EgtB/PvdO family nonheme iron enzyme [Candidatus Thiodictyon syntrophicum].	GCF_002813775.1
WP_157817655.1	EAD8→ nSTAND1→ FGS*→?→?→?→||<-FGS	FGS	267	THSYN_RS13780	gammaproteobacteria	Candidatus Thiodictyon syntrophicum	SUMF1/EgtB/PvdO family nonheme iron enzyme [Candidatus Thiodictyon syntrophicum].	GCF_002813775.1
WP_159693692.1	SWC3→?→?→?→?→?→?→ DrHyd+nSTAND1+FGS*→||<-CASPASE	DrHyd+nSTAND1+FGS	981	GQB03_RS21575	betaproteobacteria	Azoarcus sp. HKLI-1	SUMF1/EgtB/PvdO family nonheme iron enzyme [Azoarcus sp. HKLI-1].	GCF_009800965.1
WP_164689583.1	BACTERIALFRINGE→ BetaPropeller→||<-?||?→?→ NACHT+FGS*→	NACHT+FGS	960	C5S61_RS17250	chloroflexi	Herpetosiphon llansteffanensis	SUMF1/EgtB/PvdO family nonheme iron enzyme [Herpetosiphon llansteffanensis].	GCF_003205875.1
WP_165360989.1	FGS*→ KAP-NTPase→	FGS	232	EKD05_RS25290	chloroflexi	Candidatus Chloroploca sp. Khr17	SUMF1/EgtB/PvdO family nonheme iron enzyme, partial [Candidatus Chloroploca sp. Khr17].	GCF_004138165.1
WP_167857354.1	MNS-STAND+EAD9+FGS*→	MNS-STAND+EAD9+FGS	719	EYB53_RS11170	chloroflexi	Candidatus Chloroploca sp. M-50	SUMF1/EgtB/PvdO family nonheme iron enzyme [Candidatus Chloroploca sp. M-50].	GCF_004762035.1
WP_167857593.1	VWA→?→?→?→?→ FGS*→	FGS	490	EYB53_RS23920	chloroflexi	Candidatus Chloroploca sp. M-50	SUMF1/EgtB/PvdO family nonheme iron enzyme [Candidatus Chloroploca sp. M-50].	GCF_004762035.1
WP_167857622.1	FGS*→ VWA→	FGS	240	EYB53_RS25075	chloroflexi	Candidatus Chloroploca sp. M-50	SUMF1/EgtB/PvdO family nonheme iron enzyme, partial [Candidatus Chloroploca sp. M-50].	GCF_004762035.1
WP_169065694.1	nSTAND1+FGS*→||<-?||PSE→ CBS→	nSTAND1+FGS	617	E4Q23_RS05470	betaproteobacteria	Candidatus Accumulibacter phosphatis	SUMF1/EgtB/PvdO family nonheme iron enzyme [Candidatus Accumulibacter phosphatis].	GCF_012939955.1
WP_169066177.1	<-CNMP+CRP-HTH||FAD-NAD-dep-oxidoreductase→?→||<-?<-?<-PSE<-ABhydrolase||TIR+nSTAND1+FGS*→?→||<-PIN	TIR+nSTAND1+FGS	776	E4Q23_RS08160	betaproteobacteria	Candidatus Accumulibacter phosphatis	SUMF1/EgtB/PvdO family nonheme iron enzyme [Candidatus Accumulibacter phosphatis].	GCF_012939955.1
WP_169067799.1	FGS→//*<-FGS*<-MED26C<-MoxR-AAA<-TIR||SIG+TM+TM+TM+TM+TM+TM+TM+TM→?→||<-ABhydrolase	FGS	253	E4Q23_RS17320	betaproteobacteria	Candidatus Accumulibacter phosphatis	SUMF1/EgtB/PvdO family nonheme iron enzyme [Candidatus Accumulibacter phosphatis].	GCF_012939955.1

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WP_169067800.1	FGS*→	FGS	808	E4Q23_RS17325	betaproteobacteria	Candidatus Accumulibacter phosphatis	SUMF1/EgtB/PvdO family nonheme iron enzyme [Candidatus Accumulibacter phosphatis].	GCF_012939955.1
WP_169070388.1	FGS*→||<-TRANSGLUTAMINASE||?→||<-?||PSE→?→||<-Patatin	FGS	242	E4Q08_RS10725	betaproteobacteria	Candidatus Accumulibacter phosphatis	SUMF1/EgtB/PvdO family nonheme iron enzyme [Candidatus Accumulibacter phosphatis].	GCF_012940005.1
WP_169071960.1	ABC-ATPase→?→?→ SIG+FGS→*||<-Four-helical-protein||RVT→||<-SIG+FGS*<-MED26C<-MoxR-AAA<-TIR	SIG+FGS	194	E4Q08_RS22030	betaproteobacteria	Candidatus Accumulibacter phosphatis	SUMF1/EgtB/PvdO family nonheme iron enzyme [Candidatus Accumulibacter phosphatis].	GCF_012940005.1
WP_169071963.1	FGS*→	FGS	825	E4Q08_RS22045	betaproteobacteria	Candidatus Accumulibacter phosphatis	SUMF1/EgtB/PvdO family nonheme iron enzyme [Candidatus Accumulibacter phosphatis].	GCF_012940005.1
WP_169071986.1	<-BLBD<-?||?→?→||<-?<-PSE<-?<-?||TIR+nSTAND1+FGS*→ FGS→||<-Four-helical-protein||RVT→||<-TIR+FGS<-?<-RVT	TIR+nSTAND1+FGS	934	E4Q08_RS22180	betaproteobacteria	Candidatus Accumulibacter phosphatis	SUMF1/EgtB/PvdO family nonheme iron enzyme [Candidatus Accumulibacter phosphatis].	GCF_012940005.1
WP_170141027.1	DrHyd+nSTAND1+FGS*→	DrHyd+nSTAND1+FGS	920	CLV72_RS18670	actinobacteria	Allonocardiopsis opalescens	SUMF1/EgtB/PvdO family nonheme iron enzyme [Allonocardiopsis opalescens].	GCF_003002095.1
WP_170164843.1	TIR+nSTAND1+FGS*→	TIR+nSTAND1+FGS	939	BDD21_RS20355	gammaproteobacteria	Thiocapsa rosea	SUMF1/EgtB/PvdO family nonheme iron enzyme [Thiocapsa rosea].	GCF_003634315.1
WP_170183022.1	TIR+nSTAND1+FGS*→	TIR+nSTAND1+FGS	893	ZRA01_RS18085	betaproteobacteria	Zoogloea ramigera	SUMF1/EgtB/PvdO family nonheme iron enzyme [Zoogloea ramigera].	GCF_006539865.1
WP_171047426.1	FGS*→	FGS	233	ACCUM_RS18225	betaproteobacteria	Candidatus Accumulibacter phosphatis	SUMF1/EgtB/PvdO family nonheme iron enzyme [Candidatus Accumulibacter phosphatis].	GCF_005889575.1

6. Source data. Gene neighborhoods and domain architectures of the bacterial and prophage/phage SPRY domain

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
ACF52192.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→ Phage-tail-tape→	SPRY+X	655	Smal_2491	Gammaproteobacteria	Stenotrophomonas maltophilia R551-3	hypothetical protein Smal_2491 [Stenotrophomonas maltophilia R551-3].	GCA_000020665.1
ASA22786.1	SUN→ SPRY+SUN*→ SUN→ Laminin_G_3→ Disaggr_repeat→ Phage_holin_4_1→	SPRY+SUN	358	B9T62_19455	Firmicutes	Paenibacillus donghaensis	hypothetical protein B9T62_19455 [Paenibacillus donghaensis].	GCA_002192415.1
CAA2107092.1	TM+PhageMin_Tail→?→?→?→?→ SPRY*→	SPRY	456	VVAX_04063	Betaproteobacteria	Variovorax paradoxus	hypothetical protein VVAX_04063 [Variovorax paradoxus].	-
CAA2108205.1	TM+PhageMin_Tail→?→?→?→?→ SPRY*→	SPRY	455	VVAX_04716	Betaproteobacteria	Variovorax paradoxus	hypothetical protein VVAX_04716 [Variovorax paradoxus].	-
EJP76868.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→ Phage-tail-tape→ ConA-repeats→	SPRY+X	658	A1OC_01671	Gammaproteobacteria	Stenotrophomonas maltophilia Ab55555	hypothetical protein A1OC_01671 [Stenotrophomonas maltophilia Ab55555].	GCA_000287935.1
HAG44903.1	SPRY*→ SPRY→ SUN→	SPRY	249	DCL31_18225	Firmicutes	Clostridium sp.	TPA: hypothetical protein DCL31_18225 [Clostridium sp.].	GCA_003451415.1
HAU79614.1	Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→||<-?||?→?→?→ Phage-tail-tape→	SPRY+X	655	DCW96_02920	Gammaproteobacteria	Stenotrophomonas sp.	TPA: hypothetical protein DCW96_02920 [Stenotrophomonas sp.].	GCA_003484865.1
HBC50726.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY*→	SPRY	169	DC051_05805	Gammaproteobacteria	Stenotrophomonas maltophilia	TPA: hypothetical protein DC051_05805, partial [Stenotrophomonas maltophilia].	GCA_003487985.1
HBJ00556.1	SPRY*→ SUN→	SPRY	221	DDY89_06200	Firmicutes	Lysinibacillus sp.	TPA: hypothetical protein DDY89_06200, partial [Lysinibacillus sp.].	GCA_003507435.1
HBJ00935.1	SPRY*→	SPRY	146	DDY89_08865	Firmicutes	Lysinibacillus sp.	TPA: hypothetical protein DDY89_08865, partial [Lysinibacillus sp.].	GCA_003507435.1

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
HBS54551.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→ Phage-tail-tape→ ConA-repeats→	SPRY+X	655	DEA38_02315	Gammaproteobacteria	Stenotrophomonas sp.	TPA: hypothetical protein DEA38_02315 [Stenotrophomonas sp.].	GCA_003510825.1
HBT70779.1	DISCOIDIN→ SUN→ SPRY*→	SPRY	169	DEB37_00445	Firmicutes	Lysinibacillus sp.	TPA: hypothetical protein DEB37_00445, partial [Lysinibacillus sp.].	GCA_003510425.1
HDO36693.1	Cluster187_2clades→?→ Cluster187_2clades→?→ SPRY+SPRY*→	SPRY+SPRY	913	ENH07_10435	Nitrospirae	Nitrospirae bacterium	TPA: hypothetical protein ENH07_10435 [Nitrospirae bacterium].	GCA_011041165.1
HHG11560.1	SPRY+LisH*→	SPRY+LisH	821	ENL98_17835	unclassified Bacteria	bacterium	TPA: hypothetical protein ENL98_17835 [bacterium].	GCA_011373825.1
HHG11879.1	SIG+SPRY*→	SIG+SPRY	553	ENL98_19440	unclassified Bacteria	bacterium	TPA: hypothetical protein ENL98_19440 [bacterium].	GCA_011373825.1
KAB2901287.1	SPRY*→	SPRY	854	F9K31_02560	Gammaproteobacteria	Dokdonella sp.	hypothetical protein F9K31_02560 [Dokdonella sp.].	GCA_008933665.1
KAF6631785.1	<-Polbetant||ACET→ Cupin_2→ ABhydrolase→||<-?<-DUF2935||SIG+SPRY*→	SIG+SPRY	323	H6F38_13125	Firmicutes	Paenibacillus sp. EKM208P	hypothetical protein H6F38_13125 [Paenibacillus sp. EKM208P].	GCA_011066295.1
KGM23936.1	DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→?→ Phage-tail-tape→ ConA-repeats→	SPRY+X	657	LI87_0109275	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein LI87_0109275 [Stenotrophomonas maltophilia].	GCA_000758465.1
KHS06610.1	Phage-tail-tape→?→?→?→?→ SPRY+X*→?→ DAM→	SPRY+X	658	RM61_15205	Gammaproteobacteria	Xanthomonas phaseoli pv. phaseoli	hypothetical protein RM61_15205 [Xanthomonas phaseoli pv. phaseoli].	GCA_000807875.2
KKW33547.1	SIG+SPRY*→	SIG+SPRY	838	UY79_C0020G0005	Bacteria	Parcubacteria group bacterium GW2011_GWA2_53_21	Filamentous hemagglutinin-like protein [Parcubacteria group bacterium GW2011_GWA2_53_21].	GCA_001004625.1
KOS00949.1	SPRY*→	SPRY	155	AM598_20185	Firmicutes	Paenibacillus polymyxa	hypothetical protein AM598_20185, partial [Paenibacillus polymyxa].	GCA_001277855.1
KZT13763.1	SPRY*→?→?→?→ DAM→	SPRY	449	A1D30_21880	Betaproteobacteria	Acidovorax sp. GW101-3H11	hypothetical protein A1D30_21880 [Acidovorax sp. GW101-3H11].	GCA_001633105.1
MAE42393.1	SIG+TM+TM+IG*→	SIG+TM+TM+IG	1722	CMO93_01365	DPANN group	Candidatus Woesearchaeota archaeon	hypothetical protein CMO93_01365, partial [Candidatus Woesearchaeota archaeon].	GCA_002686855.1

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
MAH29320.1	Laminin_G_3+SPRY*→ Cluster74_6clades→	Laminin_G_3+SPRY	903	CL959_01385	Euryarchaeota	Euryarchaeota archaeon	hypothetical protein CL959_01385 [Euryarchaeota archaeon].	GCA_002689085.1
MAL42735.1	SPRY*→?→ Cluster388_2clades→	SPRY	473	CME98_01825	Alphaproteobacteria	Hyphomonas sp.	hypothetical protein CME98_01825 [Hyphomonas sp.].	GCA_002692925.1
MAN64718.1	LamG→ Laminin_G_3+SPRY*→ Cluster74_6clades→ Cluster153_2clades→	Laminin_G_3+SPRY	671	CMI60_22525	Alphaproteobacteria	Parvibaculum sp.	hypothetical protein CMI60_22525 [Parvibaculum sp.].	GCA_002695905.1
MAT11680.1	Phage_T7_tail→ Cluster93_5clades→ Laminin_G_3+Laminin_G_3+SPRY*→ Cluster74_6clades→	Laminin_G_3+Laminin_G_3+SPRY	921	CMM02_11805	Planctomycetes	Rhodopirellula sp.	hypothetical protein CMM02_11805 [Rhodopirellula sp.].	GCA_002698965.1
MAU75364.1	Laminin_G_3+SPRY*→ Cluster74_6clades→	Laminin_G_3+SPRY	630	CL831_00645	Bacteroidetes	Crocinitomicaceae bacterium	hypothetical protein CL831_00645 [Crocinitomicaceae bacterium].	GCA_002700285.1
MBA0297283.1	Phage-tail-tape→ ConA-repeats→?→ SPRY+X*→?→?→?→?→ SIG+TM+TM+TM+TM+TM+TM+TM+TM→ ABC-ATPase→	SPRY+X	604	D7Y24_02420	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein D7Y24_02420 [Stenotrophomonas maltophilia].	GCA_013463875.1
MBA0313726.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY*→	SPRY	249	D7Y33_22370	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein D7Y33_22370, partial [Stenotrophomonas maltophilia].	GCA_013464125.1
MBA0313748.1	SPRY*→	SPRY	249	D7Y33_22510	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein D7Y33_22510, partial [Stenotrophomonas maltophilia].	GCA_013464125.1
MBA0421339.1	Phage-tail-tape→ ConA-repeats→?→ SPRY+X*→?→?→?→?→?→?→||<-Ribonuc_L-PSP	SPRY+X	604	D7Y22_10225	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein D7Y22_10225 [Stenotrophomonas maltophilia].	GCA_013463895.1
MBB5530851.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→ Phage-tail-tape→ ConA-repeats→ ConA→?→||<-SRAP	SPRY+X	657	GGD72_001629	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein GGD72_001629 [Stenotrophomonas maltophilia].	GCA_014200115.1
MBC17709.1	Phage_T7_tail→ SUN+SPRY*→ Phage_tail_APC→	SUN+SPRY	749	CL942_11735	Deltaproteobacteria	Desulfovibrio sp.	hypothetical protein CL942_11735 [Desulfovibrio sp.].	GCA_002711645.1
MBO71803.1	Cluster310_2clades→?→?→?→ Cluster359_2clades→ Laminin_G_3+SPRY+SPRY*→	Laminin_G_3+SPRY+SPRY	973	CL508_05750	Actinobacteria	Actinobacteria bacterium	hypothetical protein CL508_05750, partial [Actinobacteria bacterium].	GCA_002724835.1
MPS35004.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→ Phage-tail-tape→?→?→ Cluster201_3clades→	SPRY+X	652	E2593_06880	Gammaproteobacteria	Stenotrophomonas sp.	hypothetical protein E2593_06880 [Stenotrophomonas sp.].	GCA_009360425.1
NBO27128.1	Laminin_G_3+SPRY*→ Cluster366_2clades→	Laminin_G_3+SPRY	547	EBU96_10150	Actinobacteria	Actinobacteria bacterium	hypothetical protein EBU96_10150 [Actinobacteria bacterium].	GCA_009918685.1

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
NBO39260.1	IG+IG+IG+LEVANB+SPRY*→	IG+IG+IG+LEVANB+SPRY	2486	EBU99_11835	unclassified Bacteria	bacterium	hypothetical protein EBU99_11835, partial [bacterium].	GCA_009918675.1
NBQ97491.1	Laminin_G_3+SPRY*→?→ Cluster358_2clades→	Laminin_G_3+SPRY	447	EBU12_04555	Actinobacteria	Microbacteriaceae bacterium	hypothetical protein EBU12_04555 [Microbacteriaceae bacterium].	GCA_009920365.1
NBR26007.1	SPRY*→	SPRY	290	EBU08_19945	Actinobacteria	Micrococcales bacterium	hypothetical protein EBU08_19945, partial [Micrococcales bacterium].	GCA_009920425.1
NBR26025.1	Laminin_G_3+SPRY*→	Laminin_G_3+SPRY	450	EBU08_20035	Actinobacteria	Micrococcales bacterium	hypothetical protein EBU08_20035, partial [Micrococcales bacterium].	GCA_009920425.1
NBS68787.1	Laminin_G_3+SPRY*→?→?→ Cluster153_2clades→	Laminin_G_3+SPRY	775	EBT31_07700	unclassified Bacteria	bacterium	hypothetical protein EBT31_07700 [bacterium].	GCA_009921885.1
NBS71002.1	Laminin_G_3+SPRY*→	Laminin_G_3+SPRY	470	EBT31_19160	unclassified Bacteria	bacterium	hypothetical protein EBT31_19160, partial [bacterium].	GCA_009921885.1
NBS80068.1	Laminin_G_3+SPRY*→	Laminin_G_3+SPRY	347	EBS57_09835	unclassified Bacteria	bacterium	hypothetical protein EBS57_09835 [bacterium].	GCA_009923095.1
NBT48002.1	Laminin_G_3+SPRY*→	Laminin_G_3+SPRY	734	EBT07_09340	Actinobacteria	Actinobacteria bacterium	hypothetical protein EBT07_09340, partial [Actinobacteria bacterium].	GCA_009922275.1
NBT76477.1	Laminin_G_3+SPRY*→ Cluster74_6clades→	Laminin_G_3+SPRY	576	EBT15_11040	Betaproteobacteria	Betaproteobacteria bacterium	hypothetical protein EBT15_11040, partial [Betaproteobacteria bacterium].	GCA_009922135.1
NBU64721.1	Cluster359_2clades→?→ Laminin_G_3+SPRY*→	Laminin_G_3+SPRY	351	EBS29_09505	Chloroflexi	Chloroflexia bacterium	hypothetical protein EBS29_09505, partial [Chloroflexia bacterium].	GCA_009923655.1
NBU69993.1	Laminin_G_3+SPRY+Laminin_G_3*→	Laminin_G_3+SPRY+Laminin_G_3	937	EBS53_00865	Bacteroidetes	Bacteroidetes bacterium	hypothetical protein EBS53_00865 [Bacteroidetes bacterium].	GCA_009923185.1
NBU73444.1	Laminin_G_3+SPRY*→	Laminin_G_3+SPRY	374	EBS53_18720	Bacteroidetes	Bacteroidetes bacterium	hypothetical protein EBS53_18720, partial [Bacteroidetes bacterium].	GCA_009923185.1
NBW17394.1	Laminin_G_3+SPRY*→ Cluster214_3clades→	Laminin_G_3+SPRY	581	EBR82_56380	Alphaproteobacteria	Caulobacteraceae bacterium	hypothetical protein EBR82_56380, partial [Caulobacteraceae bacterium].	GCA_009924585.1
NBW17505.1	Laminin_G_3+SPRY*→	Laminin_G_3+SPRY	764	EBR82_56945	Alphaproteobacteria	Caulobacteraceae bacterium	hypothetical protein EBR82_56945, partial [Caulobacteraceae bacterium].	GCA_009924585.1

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
NBW18892.1	Laminin_G_3+SPRY*→	Laminin_G_3+SPRY	722	EBR82_64050	Alphaproteobacteria	Caulobacteraceae bacterium	hypothetical protein EBR82_64050, partial [Caulobacteraceae bacterium].	GCA_009924585.1
NBW20101.1	SPRY*→	SPRY	400	EBR82_70235	Alphaproteobacteria	Caulobacteraceae bacterium	hypothetical protein EBR82_70235, partial [Caulobacteraceae bacterium].	GCA_009924585.1
NBW20127.1	Laminin_G_3+SPRY*→	Laminin_G_3+SPRY	498	EBR82_70370	Alphaproteobacteria	Caulobacteraceae bacterium	hypothetical protein EBR82_70370, partial [Caulobacteraceae bacterium].	GCA_009924585.1
NBW20301.1	Laminin_G_3+SPRY*→	Laminin_G_3+SPRY	508	EBR82_71270	Alphaproteobacteria	Caulobacteraceae bacterium	hypothetical protein EBR82_71270 [Caulobacteraceae bacterium].	GCA_009924585.1
NBW20891.1	Laminin_G_3+SPRY*→	Laminin_G_3+SPRY	494	EBR82_74310	Alphaproteobacteria	Caulobacteraceae bacterium	hypothetical protein EBR82_74310, partial [Caulobacteraceae bacterium].	GCA_009924585.1
NBW21054.1	Laminin_G_3+SPRY*→	Laminin_G_3+SPRY	448	EBR82_75135	Alphaproteobacteria	Caulobacteraceae bacterium	hypothetical protein EBR82_75135, partial [Caulobacteraceae bacterium].	GCA_009924585.1
NBW21679.1	SPRY*→	SPRY	285	EBR82_78355	Alphaproteobacteria	Caulobacteraceae bacterium	hypothetical protein EBR82_78355, partial [Caulobacteraceae bacterium].	GCA_009924585.1
NBW22642.1	SPRY*→	SPRY	394	EBR82_83325	Alphaproteobacteria	Caulobacteraceae bacterium	hypothetical protein EBR82_83325, partial [Caulobacteraceae bacterium].	GCA_009924585.1
NBW23811.1	Laminin_G_3+SPRY*→	Laminin_G_3+SPRY	335	EBR82_89280	Alphaproteobacteria	Caulobacteraceae bacterium	hypothetical protein EBR82_89280, partial [Caulobacteraceae bacterium].	GCA_009924585.1
NBX81523.1	Laminin_G_3+SPRY*→	Laminin_G_3+SPRY	455	EBQ90_00310	unclassified Bacteria	bacterium	hypothetical protein EBQ90_00310, partial [bacterium].	GCA_009927045.1
NBX88437.1	SPRY*→	SPRY	317	EBQ97_07980	Bacteroidetes	Bacteroidetes bacterium	hypothetical protein EBQ97_07980, partial [Bacteroidetes bacterium].	GCA_009926925.1
NDA10477.1	Laminin_G_3+SPRY*→ Cluster214_3clades→	Laminin_G_3+SPRY	692	EBZ07_06485	Verrucomicrobia	Verrucomicrobia bacterium	hypothetical protein EBZ07_06485, partial [Verrucomicrobia bacterium].	GCA_010025475.1
NDB59170.1	Cluster201_3clades→?→?→?→ LamG→ SPRY+TM*→?→ Cluster366_2clades→	SPRY+TM	300	EB001_12060	unclassified Bacteria	bacterium	hypothetical protein EB001_12060 [bacterium].	GCA_010026765.1

acc	**operon**	**architecture**	**len**	**gen.name**	**taxend**	**species**	**defline**	**gca**
NDB60922.1	Laminin_G_3+SPRY*→	Laminin_G_3+SPRY	799	EB001_21125	unclassified Bacteria	bacterium	hypothetical protein EB001_21125 [bacterium].	GCA_010026765.1
NDC49301.1	Cluster93_5clades→ Laminin_G_3+SPRY*→ Cluster214_3clades→	Laminin_G_3+SPRY	803	EBZ61_09545	Actinobacteria	Micrococcales bacterium	hypothetical protein EBZ61_09545 [Micrococcales bacterium].	GCA_010027415.1
NDC57204.1	SIG+SPRY*→	SIG+SPRY	239	EBZ69_10460	Alphaproteobacteria	Alphaproteobacteria bacterium	hypothetical protein EBZ69_10460, partial [Alphaproteobacteria bacterium].	GCA_010027225.1
NDD55753.1	Laminin_G_3+SPRY*→	Laminin_G_3+SPRY	430	EBZ39_18125	unclassified Bacteria	bacterium	hypothetical protein EBZ39_18125, partial [bacterium].	GCA_010027825.1
NDD86023.1	SPRY*→	SPRY	370	EBZ38_17325	unclassified Bacteria	bacterium	hypothetical protein EBZ38_17325, partial [bacterium].	GCA_010027835.1
NDG32417.1	Laminin_G_3+SPRY*→	Laminin_G_3+SPRY	801	EB118_20375	unclassified Bacteria	bacterium	hypothetical protein EB118_20375, partial [bacterium].	GCA_010031135.1
NEU24684.1	HTH_20→||<-PSE<-Polbetant<-Polbetant||ACET→ Cupin_2→||<-?||SIG+SPRY*→	SIG+SPRY	355	G3M74_00590	Firmicutes	Paenibacillus polymyxa	hypothetical protein G3M74_00590 [Paenibacillus polymyxa].	GCA_010692785.1
NEZ74825.1	Cluster171_2clades→?→?→ Cluster216_2clades→?→?→ PSE→ SUN→ SPRY*→ SUN→ TM→ Cluster104_2clades→?→?→35exo→ Cluster112_2clades→	SPRY	447	EXM56_05600	Firmicutes	Clostridium botulinum	cell adhesion protein [Clostridium botulinum].	GCA_011010615.1
NFM46879.1	Cluster171_2clades→?→?→ Cluster143_2clades→?→?→ PSE→ SUN→ SPRY*→ SUN→ TM→ Cluster104_2clades→?→?→35exo→ Cluster112_2clades→	SPRY	447	FDB72_12170	Firmicutes	Clostridium botulinum	cell adhesion protein [Clostridium botulinum].	GCA_011017125.1
NFM77397.1	Cluster216_2clades→?→?→?→ SUN→ SPRY*→ SUN→ TM→ Cluster104_2clades→?→?→35exo→ Cluster112_2clades→	SPRY	448	FDC04_00825	Firmicutes	Clostridium botulinum	cell adhesion protein [Clostridium botulinum].	GCA_011017715.1
NIT14181.1	Cluster165_3clades→?→?→ Cluster303_2clades→ SIG+HORMA→ Cluster138_2clades→ Cluster138_2clades→ SPRY*→ ThuA-GATase→	SPRY	831	GTN99_08085	Bacteria	Candidatus Dadabacteria bacterium	hypothetical protein GTN99_08085 [Candidatus Dadabacteria bacterium].	GCA_011772905.1
NSB16447.1	SPRY+Big_2*→ TM→	SPRY+Big_2	376	BCD95_004706	Firmicutes	Clostridium beijerinckii	uncharacterized protein YjdB [Clostridium beijerinckii].	GCA_013297045.1
NUH63603.1	HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY*→	SPRY	353	HUF69_20240	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein HUF69_20240, partial [Stenotrophomonas maltophilia].	GCA_013345715.1
OBU49329.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→	SPRY+X	657	A9K69_19720	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein A9K69_19720 [Stenotrophomonas maltophilia].	GCA_001676445.1

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
ODV27998.1	SPRY*→	SPRY	1123	ABT19_00375	Gammaproteobacteria	Rhodanobacter sp. SCN 68-63	hypothetical protein ABT19_00375 [Rhodanobacter sp. SCN 68-63].	GCA_001725485.1
OEU67544.1	Cluster138_2clades→?→?→ SPRY*→ Cluster135_2clades→?→ ThuA-GATase→	SPRY	483	BA863_12330	Deltaproteobacteria	Desulfovibrio sp. S3730MH75	hypothetical protein BA863_12330 [Desulfovibrio sp. S3730MH75].	GCA_001750915.1
OEU68515.1	SIG+PTX*→	SIG+PTX	1668	BBJ57_07495	Deltaproteobacteria	Desulfobacterales bacterium PC51MH44	hypothetical protein BBJ57_07495 [Desulfobacterales bacterium PC51MH44].	GCA_001751165.1
OEU69113.1	SPRY*→ Cluster135_2clades→?→?→ ThuA-GATase→	SPRY	436	BA863_04090	Deltaproteobacteria	Desulfovibrio sp. S3730MH75	hypothetical protein BA863_04090 [Desulfovibrio sp. S3730MH75].	GCA_001750915.1
OUW13744.1	Laminin_G_3+Laminin_G_3+SPRY*→ Cluster74_6clades→ Cluster388_2clades→	Laminin_G_3+Laminin_G_3+SPRY	1163	CBD24_02790	Euryarchaeota	Euryarchaeota archaeon TMED164	hypothetical protein CBD24_02790 [Euryarchaeota archaeon TMED164].	GCA_002170935.1
OYV39756.1	SPRY*→	SPRY	137	B7Z80_06345	Alphaproteobacteria	Rhodospirillales bacterium 20-64-7	hypothetical protein B7Z80_06345 [Rhodospirillales bacterium 20-64-7].	GCA_002255195.1
PJO52612.1	Phage-tail-tape→ ConA-repeats→?→ SPRY+X*→?→?→?→?→?→||<-Ribonuc_L-PSP	SPRY+X	604	CR156_10635	Gammaproteobacteria	Stenotrophomonas lactitubi	hypothetical protein CR156_10635 [Stenotrophomonas lactitubi].	GCA_002803515.1
PKQ92730.1	SUN→ SUN→ SUN→ SPRY+SUN*→ Laminin_G_3→ Disaggr_repeat→	SPRY+SUN	425	CXK86_01005	Firmicutes	Paenibacillus sp. BGI2013	hypothetical protein CXK86_01005 [Paenibacillus sp. BGI2013].	GCA_002843485.1
PPC99495.1	Cluster368_2clades→?→?→ Cluster201_3clades→ TM+TM→ Laminin_G_3+SPRY*→?→?→||<-?<-?<-REC+OmpR-HTH	Laminin_G_3+SPRY	541	CTY35_04040	Betaproteobacteria	Methylotenera sp.	hypothetical protein CTY35_04040 [Methylotenera sp.].	GCA_002928435.1
PPD25805.1	SPRY*→	SPRY	389	CTY21_14065	Gammaproteobacteria	Methylomonas sp.	hypothetical protein CTY21_14065, partial [Methylomonas sp.].	GCA_002928935.1
QDL55294.1	Phage-tail_3+FN3→ Cluster93_5clades→ Laminin_G_3+SPRY*→?→?→||<-?<-REC+OmpR-HTH	Laminin_G_3+SPRY	544	EXZ61_14585	Betaproteobacteria	Rhodoferax sediminis	hypothetical protein EXZ61_14585 [Rhodoferax sediminis].	GCA_006974105.1
QDY47412.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→?→?→ Phage-tail-tape→ ConA-repeats→	SPRY+X	657	DUW70_02065	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein DUW70_02065 [Stenotrophomonas maltophilia].	GCA_007833655.1
QDY50235.1	Phage-tail-tape→ ConA-repeats→?→ SPRY+X*→	SPRY+X	604	DUW70_17765	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein DUW70_17765 [Stenotrophomonas maltophilia].	GCA_007833655.1

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<tr><th>acc</th><th>operon</th><th>architecture</th><th>len</th><th>gen.name</th><th>taxend</th><th>species</th><th>defline</th><th>gca</th></tr>
<tr><td>QDY50408.1</td><td>Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→||<-?||?→ Phage-tail-tape→ ConA-repeats→</td><td>SPRY+X</td><td>655</td><td>DUW70_18735</td><td>Gammaproteobacteria</td><td>Stenotrophomonas maltophilia</td><td>hypothetical protein DUW70_18735 [Stenotrophomonas maltophilia].</td><td>GCA_007833655.1</td></tr>
<tr><td>QGG50745.1</td><td>SUN→ SUN→ SPRY+SUN*→ SUN→ Laminin_G_3→ Disaggr_repeat→?→?→ Phage_holin_1→</td><td>SPRY+SUN</td><td>444</td><td>GDS87_07165</td><td>Firmicutes</td><td>Lysinibacillus pakistanensis</td><td>hypothetical protein GDS87_07165 [Lysinibacillus pakistanensis].</td><td>GCA_009649975.1</td></tr>
<tr><td>QIO87716.1</td><td>Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→?→ Phage_TTP_11→?→ SPRY*→?→?→||<-SRAP</td><td>SPRY</td><td>278</td><td>G9274_001401</td><td>Gammaproteobacteria</td><td>Stenotrophomonas rhizophila</td><td>hypothetical protein G9274_001401 [Stenotrophomonas rhizophila].</td><td>GCA_011604605.1</td></tr>
<tr><td>RCK36140.1</td><td>Baseplate_J→ SPRY*→</td><td>SPRY</td><td>575</td><td>TH9_05700</td><td>Alphaproteobacteria</td><td>Thalassospira xiamenensis</td><td>hypothetical protein TH9_05700 [Thalassospira xiamenensis].</td><td>GCA_003326725.1</td></tr>
<tr><td>REJ66078.1</td><td>JAB+NLPC→?→ Phage-tail_3→ Cluster93_5clades→ Laminin_G_3+SPRY*→ Cluster74_6clades→</td><td>Laminin_G_3+SPRY</td><td>1115</td><td>DWQ28_08310</td><td>Proteobacteria</td><td>Proteobacteria bacterium</td><td>hypothetical protein DWQ28_08310 [Proteobacteria bacterium].</td><td>GCA_003388625.1</td></tr>
<tr><td>REK63903.1</td><td>Phage_tail_APC→ TM+TM→ Laminin_G_3+SPRY*→ Cluster74_6clades→?→?→ Phage_tail_APC→</td><td>Laminin_G_3+SPRY</td><td>797</td><td>DWQ49_02055</td><td>Bacteroidetes</td><td>Bacteroidetes bacterium</td><td>hypothetical protein DWQ49_02055 [Bacteroidetes bacterium].</td><td>GCA_003389155.1</td></tr>
<tr><td>RLC76825.1</td><td>Cluster187_2clades→ SPRY*→ Cluster135_2clades→</td><td>SPRY</td><td>515</td><td>DRJ03_27900</td><td>Chloroflexi</td><td>Chloroflexi bacterium</td><td>hypothetical protein DRJ03_27900 [Chloroflexi bacterium].</td><td>GCA_003648075.1</td></tr>
<tr><td>RPI56186.1</td><td>Cluster138_2clades→?→?→ SPRY*→ Cluster135_2clades→</td><td>SPRY</td><td>495</td><td>EHM49_00895</td><td>Deltaproteobacteria</td><td>Deltaproteobacteria bacterium</td><td>hypothetical protein EHM49_00895 [Deltaproteobacteria bacterium].</td><td>GCA_003819885.1</td></tr>
<tr><td>RRY03816.1</td><td>SPRY*→?→ Phage_lysozyme→</td><td>SPRY</td><td>771</td><td>EGJ58_22195</td><td>Alphaproteobacteria</td><td>Ochrobactrum anthropi</td><td>hypothetical protein EGJ58_22195 [Ochrobactrum anthropi].</td><td>GCA_003937425.1</td></tr>
<tr><td>RYG67597.1</td><td>fn3+SPRY*→</td><td>fn3+SPRY</td><td>1230</td><td>EON64_07085</td><td>Archaea</td><td>archaeon</td><td>hypothetical protein EON64_07085 [archaeon].</td><td>GCA_004145555.1</td></tr>
<tr><td>RYH32433.1</td><td>SF2-helicase+SPRY*→</td><td>SF2-helicase+SPRY</td><td>535</td><td>EON65_00615</td><td>Archaea</td><td>archaeon</td><td>DEAD/DEAH box helicase [archaeon].</td><td>GCA_004146225.1</td></tr>
<tr><td>RYY37588.1</td><td>SPRY*→</td><td>SPRY</td><td>952</td><td>EON62_01040</td><td>Archaea</td><td>archaeon</td><td>hypothetical protein EON62_01040, partial [archaeon].</td><td>GCA_004173375.1</td></tr>
<tr><td>RYY72402.1</td><td>SPRY*→</td><td>SPRY</td><td>164</td><td>EON63_20910</td><td>Archaea</td><td>archaeon</td><td>hypothetical protein EON63_20910 [archaeon].</td><td>GCA_004173275.1</td></tr>
<tr><td>TDL67967.1</td><td>SUN→ SUN→ SPRY+SUN*→ Laminin_G_3→ Disaggr_repeat→</td><td>SPRY+SUN</td><td>425</td><td>E2R58_01745</td><td>Firmicutes</td><td>Paenibacillus amylolyticus</td><td>hypothetical protein E2R58_01745 [Paenibacillus amylolyticus].</td><td>GCA_004358835.1</td></tr>
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TSC88001.1	Laminin_G_3+Laminin_G_3+Laminin_G_3+Laminin_G_3→?→?→?→?→ SPRY+SUN*→ Laminin_G_3+Laminin_G_3+Laminin_G_3+Laminin_G_3→	SPRY+SUN	607	G01um10145_950	Bacteria	Microgenomates group bacterium Gr01-1014_5	hypothetical protein G01um10145_950 [Microgenomates group bacterium Gr01-1014_5].	GCA_007376395.1
VUI62768.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→ Phage-tail-tape→	SPRY+X	655	GCPJBBEJ_01199	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein GCPJBBEJ_01199 [Stenotrophomonas maltophilia].	GCA_902156415.1
VUJ81145.1	Phage-tail-tape→ ConA-repeats→?→ SPRY+X*→?→?→?→?→ SIG+TM+TM+TM+TM+TM+TM+TM+TM→ ABC-ATPase→	SPRY+X	604	IEEHEPME_02021	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein IEEHEPME_02021 [Stenotrophomonas maltophilia].	GCA_902156595.1
VUL57431.1	Terminase_LS→ SPRY*→?→||<-?||SIG+TM+TM+TM+TM+ABC-ATPase→	SPRY	217	LBGBLGGB_01284	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein LBGBLGGB_01284 [Stenotrophomonas maltophilia].	GCA_902156925.1
VUL62146.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→?→ Phage-tail-tape→	SPRY+X	657	CCANPDJD_00380	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein CCANPDJD_00380 [Stenotrophomonas maltophilia].	GCA_902157015.1
VUL75017.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→?→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→?→ Phage-tail-tape→	SPRY+X	655	GEILPBKL_02464	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein GEILPBKL_02464 [Stenotrophomonas maltophilia].	GCA_902156945.1
VUM07479.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→?→ Phage-tail-tape→ ConA-repeats→?→?→ SRAP→	SPRY+X	657	IKOGNNCB_02002	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein IKOGNNCB_02002 [Stenotrophomonas maltophilia].	GCA_902157055.1
VUM45402.1	ConA-repeats→?→ SPRY+X*→	SPRY+X	604	FMOPOFGM_00942	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein FMOPOFGM_00942 [Stenotrophomonas maltophilia].	GCA_902157105.1
VUM59055.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→?→ Phage-tail-tape→ ConA-repeats→	SPRY+X	657	FMOPOFGM_03099	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein FMOPOFGM_03099 [Stenotrophomonas maltophilia].	GCA_902157105.1
VUN16325.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→||<-?||?→?→ Phage-tail-tape→ ConA-repeats→	SPRY+X	657	CPDIOOCO_00061	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein CPDIOOCO_00061 [Stenotrophomonas maltophilia].	GCA_902157315.1
VUN62462.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→?→ Phage-tail-tape→ ConA-repeats→ ConA→	SPRY+X	655	FHOPGADK_00135	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein FHOPGADK_00135 [Stenotrophomonas maltophilia].	GCA_902157435.1
VUN67178.1	Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→?→ SPRY+X*→||<-?||?→ Phage-tail-tape→	SPRY+X	601	JLECIBJP_00444	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein JLECIBJP_00444 [Stenotrophomonas maltophilia].	GCA_902157425.1

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VUN71522.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→ Phage-tail-tape→ ConA-repeats→?→?→ SRAP→	SPRY+X	655	IJMOMJOI_00888	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein IJMOMJOI_00888 [Stenotrophomonas maltophilia].	GCA_902157415.1
VUO23348.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→?→ Phage-tail-tape→?→?→?→||<-SRAP	SPRY+X	656	JBIDJGIM_02130	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein JBIDJGIM_02130 [Stenotrophomonas maltophilia].	GCA_902157545.1
VUO59656.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→?→ Phage-tail-tape→ ConA-repeats→?→?→||<-SRAP	SPRY+X	655	CMGNCPHI_00882	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein CMGNCPHI_00882 [Stenotrophomonas maltophilia].	GCA_902157585.1
VUP11864.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→?→ Phage-tail-tape→	SPRY+X	658	ECEFJIBE_02107	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein ECEFJIBE_02107 [Stenotrophomonas maltophilia].	GCA_902157845.1
VUP33787.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→?→ Phage-tail-tape→	SPRY+X	657	ECEFJIBE_03296	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein ECEFJIBE_03296 [Stenotrophomonas maltophilia].	GCA_902157845.1
VUP45028.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→?→ Phage-tail-tape→ ConA-repeats→?→?→ SRAP→	SPRY+X	657	KEFPIIEB_04064	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein KEFPIIEB_04064 [Stenotrophomonas maltophilia].	GCA_902157865.1
VUP91253.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→||<-?||?→?→ Phage-tail-tape→ ConA-repeats→	SPRY+X	657	BLDAJIEI_03531	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein BLDAJIEI_03531 [Stenotrophomonas maltophilia].	GCA_902157935.1
VUP99062.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→?→ Phage-tail-tape→	SPRY+X	655	BIEDFHEJ_01659	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein BIEDFHEJ_01659 [Stenotrophomonas maltophilia].	GCA_902157995.1
VUQ06316.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→?→ Phage-tail-tape→	SPRY+X	655	JPICFAGD_01619	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein JPICFAGD_01619 [Stenotrophomonas maltophilia].	GCA_902158065.1
VUQ08603.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→||<-?||?→ Phage-tail-tape→ ConA-repeats→	SPRY+X	655	MKCCKLKB_01148	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein MKCCKLKB_01148 [Stenotrophomonas maltophilia].	GCA_902158105.1
VUQ16634.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→||<-?||?→ Phage-tail-tape→	SPRY+X	657	DOOMHBAD_02908	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein DOOMHBAD_02908 [Stenotrophomonas maltophilia].	GCA_902158025.1
VUR39033.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→?→ Phage-tail-tape→ ConA-repeats→?→?→ SRAP→	SPRY+X	657	JHKEGKPK_04271	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein JHKEGKPK_04271 [Stenotrophomonas maltophilia].	GCA_902158305.1
VUR45784.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→?→ Phage-tail-tape→ ConA-repeats→?→?→||<-SRAP	SPRY+X	657	PGEAMFKH_03207	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein PGEAMFKH_03207 [Stenotrophomonas maltophilia].	GCA_902158325.1

acc	**operon**	**architecture**	**len**	**gen.name**	**taxend**	**species**	**defline**	**gca**
VUR81206.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→?→ Phage-tail-tape→ ConA-repeats→ ConA→?→||<-SRAP	SPRY+X	655	GMKOKIBD_01185	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein GMKOKIBD_01185 [Stenotrophomonas maltophilia].	GCA_902158475.1
WP_007428531.1	<-ABhydrolase<-?||SIG+SPRY→ *SIG+SPRY*→ SUN→||<-?<-Glycos_transf_2<-?||SUN→	SIG+SPRY	322	WG8_RS02665	Firmicutes	Paenibacillus sp. Aloe-11	hypothetical protein [Paenibacillus sp. Aloe-11].	GCF_000245715.1
WP_010076376.1	<-SIG+IG<-?||SPRY+Big_2→ *SPRY+Big_2*→||<-ACET	SPRY+Big_2	292	CLOCEL_RS05090	Firmicutes	Clostridium cellulovorans	Ig-like domain-containing protein [Clostridium cellulovorans].	GCF_000145275.1
WP_013308530.1	HTH_20→||<-ABhydrolase<-Polbetant||ACET→ Cupin_2→||<-DUF2935||SIG+SPRY*→||<-?||?→||<-Glycos_transf_2	SIG+SPRY	346	PPE_RS02405	Firmicutes	Paenibacillus polymyxa	hypothetical protein [Paenibacillus polymyxa].	GCF_000146875.3
WP_013513300.1	Phage_T7_tail→ SPRY*→ Phage_tail_APC→	SPRY	528	DAES_RS01675	Deltaproteobacteria	Pseudodesulfovibrio aespoeensis	SPla/RYanodine receptor SPRY domain-containing protein [Pseudodesulfovibrio aespoeensis].	GCF_000176915.2
WP_019226907.1	SIG+SPRY*→	SIG+SPRY	378	BN359_RS15990	Firmicutes	Dehalobacter	MULTISPECIES: hypothetical protein [Dehalobacter].	GCF_000309295.1
WP_019639008.1	SPRY+SUN→ *SUN+SPRY*→ Laminin_G_3→ Disaggr_repeat→ Phage_holin_4_1→	SPRY+SUN	411	G358_RS0119880	Firmicutes	Paenibacillus fonticola	hypothetical protein [Paenibacillus fonticola].	GCF_000381905.1
WP_019639009.1	-	-	413	G358_RS0119885	Firmicutes	Paenibacillus fonticola	discoidin domain-containing protein [Paenibacillus fonticola].	GCF_000381905.1
WP_019687775.1	SUN→ SPRY+Glyco_hydro_106*→ Laminin_G_3→ Disaggr_repeat→ Phage_holin_4_1→	SPRY+Glyco_hydro_106	403	H7A89_RS14065	Firmicutes	Paenibacillus polymyxa	hypothetical protein [Paenibacillus polymyxa].	GCF_903797665.1
WP_020591223.1	Phage_T7_tail→ SPRY*→	SPRY	1351	B152_RS0104640	Alphaproteobacteria	Kiloniella laminariae	hypothetical protein [Kiloniella laminariae].	GCF_000374005.1
WP_021132610.1	SPRY*→ Phage_tail_APC→	SPRY	746	K678_RS11425	Alphaproteobacteria	Phaeospirillum fulvum	hypothetical protein [Phaeospirillum fulvum].	GCF_000442515.1
WP_021203812.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→?→ Phage-tail-tape→ ConA-repeats→?→?→||<-SRAP	SPRY+X	657	L681_RS129520	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_000455685.1
WP_023986763.1	<-Trypsin<-ABhydrolase<-Polbetant||ACET→ Cupin_2→ ABhydrolase→||<-DUF2935||SIG+SPRY*→||<-PSE||?→ SIG+SPRY→ PSE→||<-Glycos_transf_2	SIG+SPRY	331	X809_RS02170	Firmicutes	Paenibacillus polymyxa	hypothetical protein [Paenibacillus polymyxa].	GCF_000507205.3
WP_024956478.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→ SPRY+X*→?→?→ Phage-tail-tape→	SPRY+X	657	BMR86_RS03335	Gammaproteobacteria	Stenotrophomonas	MULTISPECIES: hypothetical protein [Stenotrophomonas].	GCF_001591205.1
WP_025116403.1	SPRY→*?*→ *SPRY+SUN*→	SPRY	559	U863_RS0116605	Firmicutes	Lysinibacillus fusiformis	discoidin domain-containing protein [Lysinibacillus fusiformis].	GCF_000633275.1

acc	**operon**	**architecture**	**len**	**gen.name**	**taxend**	**species**	**defline**	**gca**
WP_025116405.1	-	-	396	U863_RS0116615	Firmicutes	Lysinibacillus fusiformis	hypothetical protein [Lysinibacillus fusiformis].	GCF_000633275.1
WP_025219035.1	SUN→ SPRY*→ SUN→ SPRY→ Laminin_G_3→ Disaggr_repeat→?→?→ Phage_holin_1→	SPRY	281	T479_RS06935	Firmicutes	Lysinibacillus varians	hypothetical protein [Lysinibacillus varians].	GCF_000600105.1
WP_025363879.1	HTH_20→||<-Trypsin<-ABhydrolase||ACET→||<-DUF2935<-?||SIG+SPRY*→	SIG+SPRY	332	LK13_RS15595	Firmicutes	Paenibacillus polymyxa	hypothetical protein [Paenibacillus polymyxa].	GCF_000597985.1
WP_025676232.1	HTH_20→||<-Trypsin<-ABhydrolase||ACET→||<-DUF2935<-?||SIG+SPRY*→	SIG+SPRY	327	L695_RS0111830	Firmicutes	Paenibacillus polymyxa	hypothetical protein [Paenibacillus polymyxa].	GCF_000520795.1
WP_025682581.1	HTH_20→||<-?||?→||<-DUF2935<-?||SIG+SPRY*→||<-PSE||SUN→||<-?||?→||<-?<-?<-Phage_holin_4_1	SIG+SPRY	332	L696_RS0104535	Firmicutes	Paenibacillus maysiensis	hypothetical protein [Paenibacillus maysiensis].	GCF_000520815.1
WP_025716755.1	HTH_20→||<-ABhydrolase<-?||SIG+SPRY*→	SIG+SPRY	314	L693_RS0107595	Firmicutes	Paenibacillus sp. 1-18	hypothetical protein [Paenibacillus sp. 1-18].	GCF_000520755.1
WP_025721904.1	HTH_20→||<-Trypsin<-ABhydrolase<-Polbetant||ACET→ Cupin_2→||<-DUF2935||SIG+SPRY*→	SIG+SPRY	218	L694_RS0112470	Firmicutes	Paenibacillus polymyxa	hypothetical protein, partial [Paenibacillus polymyxa].	GCF_000520775.1
WP_028541175.1	<-ABhydrolase<-Polbetant||ACET→ Cupin_2→ ABhydrolase→||<-DUF2935<-?||SIG+SPRY*→||<-?||?→ SIG+SPRY→||<-Glycos_transf_2	SIG+SPRY	320	BM358_RS15270	Firmicutes	unclassified Paenibacillus	MULTISPECIES: hypothetical protein [unclassified Paenibacillus].	GCF_900116035.1
WP_028562231.1	SPRY+SUN*→ SUN→ Laminin_G_3→ Disaggr_repeat→	SPRY+SUN	414	H583_RS35510	Firmicutes	Paenibacillus pinihumi	hypothetical protein [Paenibacillus pinihumi].	GCF_000422505.1
WP_029516016.1	<-ABhydrolase<-Polbetant||ACET→ Cupin_2→ ABhydrolase→||<-DUF2935||SUN→ SIG+SPRY*→?→||<-Glycos_transf_2	SIG+SPRY	322	B439_RS0108145	Firmicutes	Paenibacillus polymyxa	hypothetical protein [Paenibacillus polymyxa].	GCF_000463565.1
WP_029518099.1	SUN→ SUN*→ Laminin_G_3→ Disaggr_repeat→	SUN	403	B439_RS0121250	Firmicutes	Paenibacillus polymyxa	hypothetical protein [Paenibacillus polymyxa].	GCF_000463565.1
WP_031462749.1	HTH_20→||<-Trypsin<-ABhydrolase||ACET→||<-DUF2935<-?||SIG+SPRY*→	SIG+SPRY	308	FC01_RS0115670	Firmicutes	Paenibacillus polymyxa	hypothetical protein [Paenibacillus polymyxa].	GCF_000735775.1
WP_033066158.1	Cluster143_2clades→?→?→?→ SUN→ SPRY*→ PSE→ PSE→ SUN→ TM→ Cluster104_2clades→?→?→35exo→ Cluster112_2clades→	SPRY	447	N496_RS05195	Firmicutes	Clostridium botulinum	cell adhesion protein [Clostridium botulinum].	GCF_000710995.1
WP_036124491.1	SUN→ SUN→?→ SUN→ SUN→ SPRY*→ SUN→ Laminin_G_3→ Disaggr_repeat→?→?→ Phage_holin_1→	SPRY	257	HR49_RS16910	Firmicutes	Lysinibacillus	MULTISPECIES: hypothetical protein [Lysinibacillus].	GCF_000724775.3
WP_036147628.1	SUN→ SPRY+SUN→ *SPRY+SUN*→ SUN→ SUN→ SUN→ Laminin_G_3→ Disaggr_repeat→	SPRY+SUN	414	KQ41_RS11015	Firmicutes	Lysinibacillus fusiformis	discoidin domain-containing protein [Lysinibacillus fusiformis].	GCF_000755455.1
WP_036147629.1	-	-	433	KQ41_RS11020	Firmicutes	Lysinibacillus fusiformis	discoidin domain-containing protein [Lysinibacillus fusiformis].	GCF_000755455.1

acc	**operon**	**architecture**	**len**	**gen.name**	**taxend**	**species**	**defline**	**gca**
WP_036669882.1	SUN→ SPRY+SUN→ *SPRY+SUN*→ Laminin_G_3→ Disaggr_repeat→	SPRY+SUN	395	C161_RS09450	Firmicutes	Paenibacillus sp. FSL R5-192	hypothetical protein [Paenibacillus sp. FSL R5-192].	GCF_000517845.1
WP_040102262.1	HTH_20→||<-Trypsin<-ABhydrolase||ACET→||<-DUF2935<-?||SIG+SPRY*→	SIG+SPRY	319	RE92_RS09150	Firmicutes	Paenibacillus polymyxa	hypothetical protein [Paenibacillus polymyxa].	GCF_000819665.1
WP_044646514.1	<-DUF2935||?→||<-?||SIG+SPRY*→	SIG+SPRY	326	QD47_RS12890	Firmicutes	Paenibacillus terrae	hypothetical protein [Paenibacillus terrae].	GCF_000943545.1
WP_044648488.1	SIG+SPRY*→||<-?<-?<-?<-?<-?<-Phage_holin_4_1	SIG+SPRY	327	QD47_RS23995	Firmicutes	Paenibacillus terrae	hypothetical protein [Paenibacillus terrae].	GCF_000943545.1
WP_044787083.1	HTH_20→||<-Trypsin<-ABhydrolase||ACET→||<-DUF2935<-?||SIG+SPRY*→	SIG+SPRY	357	DS866_RS12660	Firmicutes	Paenibacillus polymyxa	hypothetical protein [Paenibacillus polymyxa].	GCF_000943535.1
WP_046501577.1	Phage_T7_tail→ SPRY*→	SPRY	1158	WH95_RS00475	Alphaproteobacteria	Kiloniella litopenaei	hypothetical protein [Kiloniella litopenaei].	GCF_000982415.1
WP_048035679.1	SUN→ SUN→ SPRY*→?→?→?→||<-?<-?<-?<-ABC-ATPase	SPRY	890	AB432_RS03735	Firmicutes	Brevibacillus brevis	hypothetical protein [Brevibacillus brevis].	GCF_001039275.2
WP_049431026.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→ SPRY+X*→||<-?||?→?→ Phage-tail-tape→ ConA-repeats→	SPRY+X	657	G5A48_RS10580	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_001069295.1
WP_049432438.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→?→ Phage-tail-tape→ ConA-repeats→	SPRY+X	655	A7X76_RS05335	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_001070785.1
WP_049448603.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→ Phage-tail-tape→ ConA-repeats→	SPRY+X	657	ADH94_RS22020	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_001071475.1
WP_049450667.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→ Phage-tail-tape→?→?→?→||<-SRAP	SPRY+X	656	EGS96_RS20790	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_001071195.1
WP_049454514.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→?→ Phage-tail-tape→ ConA-repeats→?→?→||<-SRAP	SPRY+X	658	ADF89_RS18240	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_001069005.1
WP_049459324.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→?→ Phage-tail-tape→ ConA-repeats→	SPRY+X	657	ADM04_RS16360	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_001074705.1
WP_049736558.1	SUN→ Laminin_G_3+SPRY*→	Laminin_G_3+SPRY	822	BRE01_RS08970	Firmicutes	Brevibacillus reuszeri	hypothetical protein [Brevibacillus reuszeri].	GCF_006540225.1
WP_051447145.1	SUN→ SPRY+SUN→ *SUN*→ *SPRY+SUN*→ Laminin_G_3→ Disaggr_repeat→	SPRY+SUN	421	C170_RS30045	Firmicutes	Paenibacillus sp. FSL H7-689	discoidin domain-containing protein [Paenibacillus sp. FSL H7-689].	GCF_000517905.1
WP_051447146.1	-	-	399	C170_RS30050	Firmicutes	Paenibacillus sp. FSL H7-689	discoidin domain-containing protein [Paenibacillus sp. FSL H7-689].	GCF_000517905.1
WP_051449672.1	-	-	402	C161_RS31475	Firmicutes	Paenibacillus sp. FSL R5-192	hypothetical protein [Paenibacillus sp. FSL R5-192].	GCF_000517845.1
WP_051626263.1	<-REC+OmpR-HTH<-?<-OBfold<-?<-?||?→||<-?||SIG+SPRY*→	SIG+SPRY	653	EP01_RS18270	Oligoflexia	Bdellovibrio bacteriovorus	hypothetical protein [Bdellovibrio bacteriovorus].	GCF_000691605.1

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
WP_052310845.1	-	-	229	WG8_RS02660	Firmicutes	Paenibacillus sp. Aloe-11	hypothetical protein, partial [Paenibacillus sp. Aloe-11].	GCF_000245715.1
WP_053324515.1	<-ABhydrolase<-Polbetant||ACET→ Cupin_2→ ABhydrolase→||<-DUF2935<-?||SIG+SPRY→*//<-PSE//?*→ *SIG+SPRY*→||<-Glycos_transf_2	SIG+SPRY	373	BK119_RS14050	Firmicutes	Paenibacillus	MULTISPECIES: hypothetical protein [Paenibacillus].	GCF_001922145.1
WP_053324516.1	<-ABhydrolase<-Polbetant||ACET→ Cupin_2→ ABhydrolase→||<-DUF2935<-?||SIG+SPRY*→?→ SIG+SPRY→ PSE→||<-Glycos_transf_2	SIG+SPRY	328	ABE82_RS02500	Firmicutes	Paenibacillus peoriae	hypothetical protein [Paenibacillus peoriae].	GCF_001272655.2
WP_053497216.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→?→ Phage-tail-tape→ ConA-repeats→ ConA→?→||<-SRAP	SPRY+X	655	ABW42_RS03390	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_001276345.1
WP_053519524.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→ Phage-tail-tape→ ConA-repeats→	SPRY+X	655	ABW43_RS14405	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_001276355.1
WP_053595626.1	SUN→ SPRY+SUN*→ SUN→ SUN→ Laminin_G_3→ Disaggr_repeat→	SPRY+SUN	413	AN161_RS17530	Firmicutes	Lysinibacillus sp. FJAT-14222	discoidin domain-containing protein [Lysinibacillus sp. FJAT-14222].	GCF_001278875.1
WP_054136806.1	<-SIG+IG<-?||?→?→?→||<-?<-?||SUN+SPRY*→	SUN+SPRY	466	IP80_RS13885	Betaproteobacteria	unclassified Betaproteobacteria	MULTISPECIES: tautomerase family protein [unclassified Betaproteobacteria].	GCF_001295865.1
WP_054704414.1	SPRY+TM*→ SUN→ SUN→ Laminin_G_3→ Disaggr_repeat→	SPRY+TM	211	JCM16419_RS00705	Firmicutes	Paenibacillus pinihumi	hypothetical protein [Paenibacillus pinihumi].	GCF_001312305.1
WP_058710989.1	HTH_20→||<-Trypsin<-ABhydrolase||ACET→||<-DUF2935<-PSE||SIG+SPRY*→	SIG+SPRY	306	NS115_RS07620	Firmicutes	Paenibacillus	MULTISPECIES: hypothetical protein [Paenibacillus].	GCF_002872435.1
WP_058830612.1	HTH_20→||<-Trypsin<-ABhydrolase||ACET→||<-DUF2935<-?||SIG+SPRY*→	SIG+SPRY	339	AVK83_RS16520	Firmicutes	Paenibacillus polymyxa	hypothetical protein [Paenibacillus polymyxa].	GCF_001481575.1
WP_058981995.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→?→?→ Phage-tail-tape→ ConA-repeats→	SPRY+X	657	BN1263_RS14155	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_001499715.1
WP_059064521.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→ Phage-tail-tape→ ConA-repeats→?→ SRAP→	SPRY+X	655	AV528_RS10010	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_001499755.1
WP_063211944.1	HTH_20→||<-ABhydrolase<-?||ACET→ Cupin_2→ SIG+SPRY*→	SIG+SPRY	337	AV545_RS14475	Firmicutes	Paenibacillus jamilae	hypothetical protein [Paenibacillus jamilae].	GCF_001619755.1
WP_064201871.1	SPRY*→?→?→?→||<-?<-?<-?<-ABC-ATPase	SPRY	894	A4S11_RS18990	Firmicutes	Brevibacillus brevis	hypothetical protein [Brevibacillus brevis].	GCF_001649505.1
WP_064796708.1	HTH_20→||<-ABhydrolase<-Polbetant||ACET→ Cupin_2→||<-?||SIG+SPRY*→	SIG+SPRY	314	A9P44_RS12255	Firmicutes	Paenibacillus polymyxa	hypothetical protein [Paenibacillus polymyxa].	GCF_001663585.1
WP_065179322.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→ Phage-tail-tape→	SPRY+X	655	A9K70_RS20570	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_001676395.1
WP_065181897.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→||<-?||?→?→ Phage-tail-tape→ ConA-repeats→	SPRY+X	655	A9K56_RS08050	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_001676315.1

acc	**operon**	**architecture**	**len**	**gen.name**	**taxend**	**species**	**defline**	**gca**
WP_065200553.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→||<-?||?→?→?→ Phage-tail-tape→ ConA-repeats→ ConA→	SPRY+X	655	A9K58_RS17510	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_001676385.1
WP_068434738.1	Cluster93_5clades→ Laminin_G_3+SPRY*→?→?→?→||<-?<-Cluster297_2clades<-EMAP	Laminin_G_3+SPRY	467	XM1_RS14675	Alphaproteobacteria	Magnetospirillum sp. XM-1	hypothetical protein [Magnetospirillum sp. XM-1].	GCF_001511835.1
WP_068499071.1	<-SUN<-?<-?||SIG+SPRY*→	SIG+SPRY	378	BAZ21_RS08685	Firmicutes	Paenibacillus kribbensis	hypothetical protein [Paenibacillus kribbensis].	GCF_001705305.1
WP_068504121.1	<-ABhydrolase||?→||<-?||SIG+SPRY*→||<-PSE||SUN→	SIG+SPRY	308	BAZ21_RS19160	Firmicutes	Paenibacillus kribbensis	hypothetical protein [Paenibacillus kribbensis].	GCF_001705305.1
WP_068940847.1	SUN→ SPRY+SUN→ *SPRY*→ Disaggr_repeat→	SPRY+SUN	698	A7312_RS18605	Firmicutes	Paenibacillus polymyxa	hypothetical protein [Paenibacillus polymyxa].	GCF_001707685.1
WP_068940849.1	-	-	419	A7312_RS18610	Firmicutes	Paenibacillus polymyxa	hypothetical protein [Paenibacillus polymyxa].	GCF_001707685.1
WP_068941209.1	-	-	320	BK119_RS14035	Firmicutes	Paenibacillus	MULTISPECIES: hypothetical protein [Paenibacillus].	GCF_001922145.1
WP_069010793.1	HTH_20→||<-ABhydrolase<-Polbetant||ACET→ Cupin_2→ ABhydrolase→||<-DUF2935||SIG+SPRY*→?→||<-Glycos_transf_2	SIG+SPRY	346	A7311_RS06950	Firmicutes	Paenibacillus polymyxa	hypothetical protein [Paenibacillus polymyxa].	GCF_001709075.1
WP_069481585.1	SUN+SPRY→*?→?→?→ SUN→ SPRY+SUN→*	SUN+SPRY	559	BG258_RS12185	Firmicutes	Lysinibacillus fusiformis	discoidin domain-containing protein [Lysinibacillus fusiformis].	GCF_001726065.1
WP_069481589.1	-	-	403	BG258_RS12205	Firmicutes	Lysinibacillus fusiformis	hypothetical protein [Lysinibacillus fusiformis].	GCF_001726065.1
WP_071558628.1	<-SUN||SIG+SPRY*→||<-?<-?<-?<-?<-?<-Phage_holin_4_1	SIG+SPRY	334	CG775_RS21655	Firmicutes	Paenibacillus polymyxa	hypothetical protein [Paenibacillus polymyxa].	GCF_001874425.3
WP_071639359.1	HTH_20→||<-ABhydrolase<-Polbetant||ACET→ Cupin_2→ ABhydrolase→||<-DUF2935||SIG+SPRY→*?→ SIG+SPRY→* PSE→||<-Glycos_transf_2	SIG+SPRY	373	PPYC1_RS02475	Firmicutes	Paenibacillus polymyxa	hypothetical protein [Paenibacillus polymyxa].	GCF_001874405.2
WP_071639361.1	-	-	323	PPYC1_RS02485	Firmicutes	Paenibacillus polymyxa	hypothetical protein [Paenibacillus polymyxa].	GCF_001874405.2
WP_072733996.1	SUN→ SUN→ SUN→ TM+SPRY+SUN→ *SPRY*→ Disaggr_repeat→	TM+SPRY+SUN	708	BUA17_RS14040	Firmicutes	Paenibacillus sp. ov031	hypothetical protein [Paenibacillus sp. ov031].	GCF_900143165.1
WP_072733997.1	-	-	422	BUA17_RS14045	Firmicutes	Paenibacillus sp. ov031	discoidin domain-containing protein [Paenibacillus sp. ov031].	GCF_900143165.1
WP_075141582.1	Cluster216_2clades→?→?→?→ SUN→ SPRY*→ PSE→ SUN→ SUN→ TM→ Cluster104_2clades→?→?→35exo→	SPRY	447	RSJ3_RS04310	Firmicutes	Clostridium botulinum	cell adhesion protein [Clostridium botulinum].	GCF_001921965.1
WP_076158833.1	<-ABhydrolase<-Polbetant||ACET→ Cupin_2→ ABhydrolase→||<-DUF2935||SIG+SPRY*→||<-PSE||?→ PSE→||<-Glycos_transf_2	SIG+SPRY	301	BK134_RS12705	Firmicutes	Paenibacillus peoriae	hypothetical protein [Paenibacillus peoriae].	GCF_001956115.1

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
WP_076172386.1	Cluster171_2clades→?→?→ Cluster143_2clades→?→?→ PSE→ SUN→ SPRY*→ SUN→ TM→ Cluster104_2clades→?→?→35exo→ Cluster112_2clades→	SPRY	465	N487_RS14900	Firmicutes	Clostridium botulinum	cell adhesion protein [Clostridium botulinum].	GCF_000710975.1
WP_076252374.1	SUN→ SPRY+SUN*→ SUN→ SUN→ Laminin_G_3→ Disaggr_repeat→	SPRY+SUN	403	BK136_RS15140	Firmicutes	Paenibacillus amylolyticus	hypothetical protein [Paenibacillus amylolyticus].	GCF_001956175.1
WP_076265166.1	<-ABhydrolase<-Polbetant||ACET→ Cupin_2→ ABhydrolase→||<-DUF2935<-?||SIG+SPRY*→||<-?||?→ SIG+SPRY→||<-Glycos_transf_2	SIG+SPRY	320	BK143_RS19680	Firmicutes	Paenibacillus peoriae	hypothetical protein [Paenibacillus peoriae].	GCF_001956225.1
WP_076293278.1	HTH_20→||<-PSE<-ABhydrolase<-Polbetant||ACET→ Cupin_2→ ABhydrolase→||<-DUF2935||SIG+SPRY*→||<-?||?→ PSE→||<-Glycos_transf_2	SIG+SPRY	326	BK135_RS10440	Firmicutes	Paenibacillus peoriae	hypothetical protein [Paenibacillus peoriae].	GCF_001956155.1
WP_076295423.1	<-ABhydrolase<-Polbetant||ACET→ Cupin_2→ ABhydrolase→||<-DUF2935<-?||SIG+SPRY→*||<-?||?→ SIG+SPRY*→||<-Glycos_transf_2	SIG+SPRY	331	BK145_RS14470	Firmicutes	Paenibacillus peoriae	hypothetical protein [Paenibacillus peoriae].	GCF_001956235.1
WP_076318343.1	SUN→ SUN→ SUN→ SPRY+SUN*→ Laminin_G_3→ Disaggr_repeat→	SPRY+SUN	412	BK124_RS08255	Firmicutes	Paenibacillus amylolyticus	hypothetical protein [Paenibacillus amylolyticus].	GCF_001955995.1
WP_076327021.1	SUN→ SPRY+SUN*→ SUN→ Laminin_G_3→ Disaggr_repeat→	SPRY+SUN	414	BK129_RS03095	Firmicutes	Paenibacillus amylolyticus	discoidin domain-containing protein [Paenibacillus amylolyticus].	GCF_001956035.1
WP_079564340.1	SUN→ SPRY+SUN→ *SUN→ SUN→ SPRY+SUN*→ SUN→ SUN→ SUN→	SPRY+SUN	485	B5X66_RS24790	Firmicutes	unclassified Lysinibacillus	MULTISPECIES: hypothetical protein [unclassified Lysinibacillus].	GCF_900167885.1
WP_079564349.1	-	-	413	B5X66_RS24805	Firmicutes	unclassified Lysinibacillus	MULTISPECIES: discoidin domain-containing protein [unclassified Lysinibacillus].	GCF_900167885.1
WP_079564406.1	SUN→ SUN→ SUN→ SPRY+SUN*→?→ SUN→ SUN→ SUN→ SUN→ SUN→	SPRY+SUN	389	B5X66_RS24915	Firmicutes	unclassified Lysinibacillus	MULTISPECIES: discoidin domain-containing protein [unclassified Lysinibacillus].	GCF_900167885.1
WP_080291782.1	DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→?→ Phage-tail-tape→ ConA-repeats→	SPRY+X	655	LI87_RS0109275	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_000758465.1
WP_080639352.1	RHS_repeat+RHS_repeat+RHS_repeat+RHS_repeat+Laminin_G_3+SPRY*→?→?→ PSE→ PSE→35exo→	RHS_repeat+RHS_repeat+RHS_repeat+RHS_repeat+Laminin_G_3+SPRY	2000	YUK_RS0107305	Gammaproteobacteria	Teredinibacter turnerae	hypothetical protein [Teredinibacter turnerae].	GCF_000379165.1
WP_080974705.1	Cluster143_2clades→?→?→?→?→?→ SPRY→ SPRY*→ PSE→ TM→ Cluster104_2clades→	SPRY	311	ADC50_RS20320	Firmicutes	Clostridium sporogenes	hypothetical protein [Clostridium sporogenes].	GCF_001058825.1
WP_081280966.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→?→ Phage-tail-tape→	SPRY+X	655	A9K69_RS19730	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_001676445.1
WP_084315242.1	SIG+TM+TM+TM+TM+TM+TM+TM+TM→ SIG+TM+TM+TM+TM+TM+TM+TM+TM→ ABC-ATPase→ SIG+TM+TM+TM+TM+ABC-ATPase→||<-?||?→ SPRY+Big_2*→?→?→ ACET→	SPRY+Big_2	535	BR69_RS21395	Firmicutes	Clostridium hydrogeniformans	Ig domain-containing protein [Clostridium hydrogeniformans].	GCF_000686705.1
WP_084575678.1	EMAP→ Cluster297_2clades→?→?→?→ SIG+SPRY*→?→?→?→?→?→ SIG+METHYLASE→	SIG+SPRY	349	B9A22_RS10460	Firmicutes	Sporomusa malonica	hypothetical protein [Sporomusa malonica].	GCF_900176355.1

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WP_085321805.1	Cluster171_2clades→?→?→ Cluster143_2clades→?→?→ PSE→ SUN→ SPRY*→ SUN→ TM→ Cluster104_2clades→?→?→35exo→ Cluster112_2clades→	SPRY	447	B2M06_RS15395	Firmicutes	Clostridium botulinum	cell adhesion protein [Clostridium botulinum].	GCF_002866045.1
WP_085899262.1	Phage_T7_tail→ SPRY*→	SPRY	1359	BKB51_RS01170	Alphaproteobacteria	Kiloniella majae	hypothetical protein [Kiloniella majae].	GCF_002118315.1
WP_087445183.1	SUN→ SPRY+SUN*→ SUN→ Laminin_G_3→ Disaggr_repeat→ Phage_holin_4_1→?→ SIG+ConA+beta-propeller→	SPRY+SUN	430	FLT43_09110	Firmicutes	Paenibacillus thiaminolyticus	hypothetical protein [Paenibacillus thiaminolyticus].	-
WP_087803178.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→?→ Phage-tail-tape→ ConA-repeats→?→?→||<-SRAP	SPRY+X	657	B7H27_RS11730	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_002189565.1
WP_088432438.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→?→ Phage-tail-tape→ ConA-repeats→	SPRY+X	658	CEE60_RS02675	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_002205165.1
WP_089986629.1	SUN→ SPRY+SUN*→ DISCOIDIN→ SUN→ SUN→ SUN→ Laminin_G_3→ Disaggr_repeat→	SPRY+SUN	433	BLP61_RS17210	Firmicutes	Lysinibacillus fusiformis	discoidin domain-containing protein [Lysinibacillus fusiformis].	GCF_900102355.1
WP_090738921.1	<-SUN<-?<-PSE||SIG+SPRY*→	SIG+SPRY	373	BN1546_RS23290	Firmicutes	Paenibacillus sp. Mc5Re-14	hypothetical protein [Paenibacillus sp. Mc5Re-14].	GCF_001049835.1
WP_090920079.1	SUN→ SUN→ SPRY+SUN*→ Laminin_G_3→ Disaggr_repeat→	SPRY+SUN	412	BLQ13_RS12675	Firmicutes	Paenibacillus polysaccharolyticus	discoidin domain-containing protein [Paenibacillus polysaccharolyticus].	GCF_900102085.1
WP_092074738.1	SPRY+Big_2*→	SPRY+Big_2	341	HSX37_RS17715	Firmicutes	Dendrosporobacter quercicolus	Ig-like domain-containing protein [Dendrosporobacter quercicolus].	GCF_900104455.1
WP_093534303.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→?→ Phage-tail-tape→	SPRY+X	655	BQ2375_RS10775	Gammaproteobacteria	Stenotrophomonas rhizophila	hypothetical protein [Stenotrophomonas rhizophila].	GCF_900095765.1
WP_094156505.1	<-ABhydrolase<-?||SIG+SPRY→ *SIG+SPRY*→ SUN→||<-PSE<-Glycos_transf_2	SIG+SPRY	358	B4V02_RS22570	Firmicutes	Paenibacillus kribbensis	hypothetical protein [Paenibacillus kribbensis].	GCF_002240415.1
WP_094936690.1	SUN→ SPRY+SUN*→ SUN→ Laminin_G_3→ Disaggr_repeat→	SPRY+SUN	423	CA599_RS04535	Firmicutes	Paenibacillus taichungensis	discoidin domain-containing protein [Paenibacillus taichungensis].	GCF_002264305.1
WP_095523199.1	Cluster180_2clades→?→?→ Cluster242_2clades→?→?→?→ VWA+Phage-tail_3+SPRY*→?→?→ DAM→	VWA+Phage-tail_3+SPRY	1093	BSR46_RS01740	Betaproteobacteria	Candidatus Dactylopiibacterium carminicum	VWA domain-containing protein [Candidatus Dactylopiibacterium carminicum].	GCF_002284975.1
WP_095529535.1	Cluster180_2clades→?→?→ Cluster242_2clades→?→?→?→ VWA+Phage-tail_3+SPRY*→?→?→ DAM→	VWA+Phage-tail_3+SPRY	1093	CGU28_RS03090	Betaproteobacteria	Candidatus Dactylopiibacterium carminicum	VWA domain-containing protein [Candidatus Dactylopiibacterium carminicum].	GCF_002284935.1

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WP_097012028.1	Phage_T7_tail→ SUN+SPRY*→ Phage_tail_APC→	SUN+SPRY	749	DPRO_RS10715	Deltaproteobacteria	Pseudodesulfovibrio profundus	hypothetical protein [Pseudodesulfovibrio profundus].	GCF_900217235.1
WP_097053084.1	SPRY*→	SPRY	749	CRO34_RS20720	Alphaproteobacteria	Thalassospira xiamenensis	hypothetical protein [Thalassospira xiamenensis].	GCF_900217835.1
WP_099470440.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→?→ Phage-tail-tape→ ConA-repeats→?→?→ SRAP→	SPRY+X	657	BRB94_RS07965	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_002739365.1
WP_099473308.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→?→ Phage-tail-tape→ ConA-repeats→?→?→ SRAP→	SPRY+X	657	BRB96_RS16380	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_002739315.1
WP_099475740.1	Phage_TAC_13→?→ SPRY+X*→?→ Phage-tail-tape→?→?→?→ SRAP→	SPRY+X	657	BRB49_RS05320	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_002739555.1
WP_099491760.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→?→ Phage-tail-tape→ ConA-repeats→?→?→||<-SRAP	SPRY+X	657	BRB88_RS10470	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_002739275.1
WP_099494832.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→ Phage-tail-tape→ ConA-repeats→ ConA→	SPRY+X	655	BRC08_RS17670	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_002739465.1
WP_099529564.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ PSE→ SPRY+X*→?→ Phage-tail-tape→ ConA-repeats→	SPRY+X	657	BRB33_RS00490	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_002738715.1
WP_099539415.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→ Phage-tail-tape→ ConA-repeats→	SPRY+X	657	BRB39_RS15215	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_002738665.1
WP_099539896.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→ Phage-tail-tape→	SPRY+X	656	BRB48_RS14865	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_002738885.1
WP_099553167.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→?→ Phage-tail-tape→ ConA-repeats→?→?→||<-SRAP	SPRY+X	657	BRC04_RS15490	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_002739455.1
WP_099605638.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→ Phage-tail-tape→ ConA-repeats→?→?→||<-SRAP	SPRY+X	657	BRC06_RS15605	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_002740185.1
WP_099654222.1	SPRY*→	SPRY	991	BJV55_RS14285	Gammaproteobacteria	Rhodanobacter sp. TND4EH1	hypothetical protein [Rhodanobacter sp. TND4EH1].	GCF_002749725.1
WP_099854778.1	SUN→ SPRY+SUN*→ SUN→ SUN→ SUN→ Laminin_G_3→ Disaggr_repeat→	SPRY+SUN	425	CS562_RS07475	Firmicutes	Paenibacillus sp. LK1	discoidin domain-containing protein [Paenibacillus sp. LK1].	GCF_002750415.1
WP_099858289.1	SPRY+SUN*→ SUN→ Laminin_G_3→ Disaggr_repeat→ Phage_holin_4_1→	SPRY+SUN	410	CS562_RS22615	Firmicutes	Paenibacillus sp. LK1	hypothetical protein [Paenibacillus sp. LK1].	GCF_002750415.1
WP_100317531.1	Phage-tail-tape→?→?→ SPRY+X*→?→ DAM→	SPRY+X	655	CO615_RS10755	Gammaproteobacteria	Xanthomonadaceae bacterium NML75-0749	hypothetical protein [Xanthomonadaceae bacterium NML75-0749].	GCF_002798185.1

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WP_100438259.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→?→ Phage-tail-tape→ ConA-repeats→	SPRY+X	658	B9Y60_RS06960	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_002799135.1
WP_100443561.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→ Phage-tail-tape→ ConA-repeats→	SPRY+X	657	B9Y57_RS09005	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_002798925.1
WP_100474847.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→?→ Phage-tail-tape→	SPRY+X	657	B9Y82_RS18595	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_002799155.1
WP_102039859.1	Glyco_hydro_16+SPRY*→	Glyco_hydro_16+SPRY	1003	CXF86_RS19745	Gammaproteobacteria	Shewanella sp. GutCb	DUF1833 family protein [Shewanella sp. GutCb].	GCF_002836135.1
WP_102945666.1	Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→ Phage-tail-tape→	SPRY+X	655	C2U58_RS09715	Gammaproteobacteria	Stenotrophomonas sp. VV52	hypothetical protein [Stenotrophomonas sp. VV52].	GCF_002893095.1
WP_103046829.1	<-Trypsin<-ABhydrolase<-Polbetant||ACET→ Cupin_2→||<-DUF2935<-?||SIG+SPRY*→	SIG+SPRY	326	C1T21_RS00825	Firmicutes	Paenibacillus sp. F4	hypothetical protein [Paenibacillus sp. F4].	GCF_002894905.1
WP_103744628.1	-	-	320	CG775_RS10930	Firmicutes	Paenibacillus polymyxa	hypothetical protein [Paenibacillus polymyxa].	GCF_002916985.1
WP_103977131.1	SUN→ SUN→ SUN→ SUN+SPRY*→ Disaggr_repeat→?→?→ Phage_holin_1→	SUN+SPRY	980	LYSIN_RS10210	Firmicutes	Lysinibacillus sphaericus	hypothetical protein [Lysinibacillus sphaericus].	GCF_002923795.1
WP_104497237.1	HTH_20→||<-ABhydrolase<-Polbetant||ACET→ Cupin_2→||<-DUF2935||SIG+SPRY*→||<-?||?→||<-Glycos_transf_2	SIG+SPRY	332	C5G87_RS19490	Firmicutes	Paenibacillus peoriae	hypothetical protein [Paenibacillus peoriae].	GCF_002937395.1
WP_105407850.1	SUN→ SPRY+SUN*→ SUN→ Laminin_G_3→ Disaggr_repeat→	SPRY+SUN	419	C0Q44_RS13525	Firmicutes	Paenibacillus sp. PCH8	hypothetical protein [Paenibacillus sp. PCH8].	GCF_002968835.1
WP_106549337.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→ SPRY+X*→||<-?||?→ Phage-tail-tape→ ConA-repeats→	SPRY+X	657	CV100_RS06160	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_003015035.1
WP_106891819.1	SPRY*→?→?→ DAM→	SPRY	820	C7S18_RS12140	Gammaproteobacteria	Ahniella affigens	hypothetical protein [Ahniella affigens].	GCF_003015185.1
WP_107951039.1	SUN→ SPRY+SUN→ *SPRY+SUN*→ SUN→ SUN→ Laminin_G_3→ Disaggr_repeat→?→?→ Phage_holin_1→	SPRY+SUN	435	C9J32_RS17875	Firmicutes	Lysinibacillus parviboronicapiens	discoidin domain-containing protein [Lysinibacillus parviboronicapiens].	GCF_003049605.1
WP_107951040.1	-	-	411	C9J32_RS17880	Firmicutes	Lysinibacillus parviboronicapiens	discoidin domain-containing protein [Lysinibacillus parviboronicapiens].	GCF_003049605.1
WP_107981750.1	SPRY*→	SPRY	401	B5V90_RS01965	Firmicutes	Bacillus sporothermodurans	hypothetical protein [Bacillus sporothermodurans].	GCF_003055065.1
WP_108753440.1	Phage_H_T_join→ HK97-gp10_like→ DUF3168→||<-?||Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→?→ Phage-tail-tape→ ConA-repeats→ ConA→?→||<-SRAP	SPRY+X	657	C1933_RS11930	Gammaproteobacteria	Stenotrophomonas sp. ZAC14D2_NAIMI4_6	hypothetical protein [Stenotrophomonas sp. ZAC14D2_NAIMI4_6].	GCF_003086875.1
WP_108762304.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→?→ Phage-tail-tape→ ConA-repeats→ ConA→	SPRY+X	657	C1932_RS11845	Gammaproteobacteria	Stenotrophomonas sp. YAU14D1_LEIMI4_1	hypothetical protein [Stenotrophomonas sp. YAU14D1_LEIMI4_1].	GCF_003086815.1

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WP_108767941.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→?→ Phage-tail-tape→ ConA-repeats→?→||<-SRAP	SPRY+X	655	C1925_RS05020	Gammaproteobacteria	Stenotrophomonas sp. SAU14A_NAIMI4_5	hypothetical protein [Stenotrophomonas sp. SAU14A_NAIMI4_5].	GCF_003086795.1
WP_109073515.1	SIG+SPRY*→ Phage_tail_APC→?→ Phage_lysozyme→	SIG+SPRY	399	TSH20_RS03980	Alphaproteobacteria	unclassified Azospirillum	MULTISPECIES: hypothetical protein [unclassified Azospirillum].	GCF_003115945.1
WP_109150419.1	SIG+SPRY*→ Phage_tail_APC→ Phage_lysozyme→ Cluster368_2clades→	SIG+SPRY	399	TSO5_RS04345	Alphaproteobacteria	Azospirillum sp. TSO5	hypothetical protein [Azospirillum sp. TSO5].	GCF_003116065.1
WP_109813956.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→||<-?||?→?→ Phage-tail-tape→ ConA-repeats→	SPRY+X	657	DKY64_RS04935	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_003172845.1
WP_110895171.1	-	-	698	HUB98_RS06520	Firmicutes	Paenibacillus barcinonensis	hypothetical protein [Paenibacillus barcinonensis].	GCF_013347305.1
WP_110932422.1	SPRY+SUN*→ SUN→ Laminin_G_3→ Disaggr_repeat→ Phage_holin_4_1→	SPRY+SUN	419	CZ379_RS15410	Firmicutes	Paenibacillus bouchesdurhonensis	hypothetical protein [Paenibacillus bouchesdurhonensis].	GCF_900155685.1
WP_111008118.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→?→ Phage-tail-tape→ ConA-repeats→ ConA→	SPRY+X	655	A7X97_RS14925	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_003244875.1
WP_111096871.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→?→ Phage-tail-tape→ ConA-repeats→ ConA→?→||<-SRAP	SPRY+X	655	A7X84_RS18825	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_003244495.1
WP_111113613.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→ Phage-tail-tape→ ConA-repeats→ ConA→?→ SRAP→	SPRY+X	655	A7X83_RS21130	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_003244775.1
WP_111118812.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→?→ Phage-tail-tape→ ConA-repeats→?→?→||<-SRAP	SPRY+X	657	A7X74_RS15970	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_003244465.1
WP_111176598.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→ Phage-tail-tape→ ConA-repeats→?→||<-SRAP	SPRY+X	655	A7X87_RS07275	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_003244795.1
WP_111187870.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→ SPRY+X*→?→ Phage-tail-tape→ ConA-repeats→?→?→ SRAP→	SPRY+X	657	A7X60_RS00295	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_003244645.1
WP_111203746.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→?→ Phage-tail-tape→ ConA-repeats→?→?→ SRAP→	SPRY+X	657	A7X75_RS09430	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_003244735.1
WP_117310047.1	Phage_H_T_join→ HK97-gp10_like→ DUF3168→||<-?||Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→ Phage-tail-tape→ ConA-repeats→?→ SRAP→	SPRY+X	655	D0Y85_RS07625	Gammaproteobacteria	Stenotrophomonas sp. G4	hypothetical protein [Stenotrophomonas sp. G4].	GCF_003428825.1
WP_119554390.1	SPRY*→	SPRY	674	D3H34_RS15355	Betaproteobacteria	Acidovorax cavernicola	hypothetical protein [Acidovorax cavernicola].	GCF_003581445.1
WP_119798183.1	SUN→ SUN→?→ SPRY*→ Disaggr_repeat→?→ Phage_holin_4_1→	SPRY	707	D3P07_RS00690	Firmicutes	Paenibacillus sp. 1011MAR3C5	hypothetical protein [Paenibacillus sp. 1011MAR3C5].	GCF_003591485.1
WP_120033984.1	SPRY*→?→?→ Phage_holin_1→	SPRY	411	CJ483_RS08545	Firmicutes	Bacillus sp. PK3_68	hypothetical protein [Bacillus sp. PK3_68].	GCF_003600835.1

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WP_120225163.1	Cluster165_3clades→?→||<-?||?→?→ SPRY*→	SPRY	554	CLY44_RS11090	Alphaproteobacteria	Thalassospira sp. DSM 26710	hypothetical protein [Thalassospira sp. DSM 26710].	GCF_003610215.1
WP_120497558.1	Phage_T7_tail→ SPRY*→	SPRY	1175	D9A03_RS12780	Alphaproteobacteria	Kiloniella sp. EL199	hypothetical protein [Kiloniella sp. EL199].	GCF_900313065.1
WP_120498928.1	<-ACET||?→?→?→?→?→?→ Beta-Roll+Beta-Roll+Beta-Roll+Beta-Roll+BetaPropeller+Beta-Roll+CADHERIN+Beta-Roll+CADHERIN+Beta-Roll+Beta-Roll+BetaPropeller+Beta-Roll*→	Beta-Roll+Beta-Roll+Beta-Roll+Beta-Roll+BetaPropeller+Beta-Roll+CADHERIN+Beta-Roll+CADHERIN+Beta-Roll+Beta-Roll+BetaPropeller+Beta-Roll	4942	D9A03_RS19645	Alphaproteobacteria	Kiloniella sp. EL199	hypothetical protein [Kiloniella sp. EL199].	GCF_900313065.1
WP_121219693.1	SPRY+CARDB*→	SPRY+CARDB	601	BCL74_RS10110	Alphaproteobacteria	Oceanibaculum indicum	hypothetical protein [Oceanibaculum indicum].	GCF_003633955.1
WP_122906669.1	SUN→ SPRY+SUN*→ Laminin_G_3→ Disaggr_repeat→?→?→ Phage_holin→	SPRY+SUN	424	EDM57_RS21100	Firmicutes	Brevibacillus gelatini	discoidin domain-containing protein [Brevibacillus gelatini].	GCF_003710935.1
WP_123769372.1	Phage-tail-tape→?→?→?→?→ SPRY+X*→?→ DAM→?→||<-?||?→||<-Redoxin	SPRY+X	660	EDC50_RS05235	Gammaproteobacteria	Vulcaniibacterium tengchongense	hypothetical protein [Vulcaniibacterium tengchongense].	GCF_003814555.1
WP_123796746.1	HTH_20→||<-Trypsin<-ABhydrolase||ACET→||<-DUF2935<-?||SIG+SPRY*→	SIG+SPRY	332	EG487_RS02750	Firmicutes	Paenibacillus polymyxa	hypothetical protein [Paenibacillus polymyxa].	GCF_003813765.1
WP_123958466.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→ Phage-tail-tape→ ConA-repeats→	SPRY+X	657	EGY09_RS07240	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_003812985.1
WP_124116383.1	SUN→ SPRY+SUN→ *SPRY*→ Disaggr_repeat→ Phage_holin_4_1→	SPRY+SUN	707	EDO6_RS18680	Firmicutes	Paenibacillus xylanexedens	hypothetical protein [Paenibacillus xylanexedens].	GCF_003833245.1
WP_124116384.1	-	-	413	EDO6_RS18685	Firmicutes	Paenibacillus xylanexedens	discoidin domain-containing protein [Paenibacillus xylanexedens].	GCF_003833245.1
WP_124650057.1	Arm-DNA-bind_3+SPRY*→	Arm-DNA-bind_3+SPRY	469	DIE19_RS04180	Betaproteobacteria	Burkholderia sp. Bp9126	integrase arm-type DNA-binding domain-containing protein [Burkholderia sp. Bp9126].	GCF_003853715.1
WP_125335565.1	SPRY*→?→ Phage_lysozyme→	SPRY	816	EGJ58_RS22040	Alphaproteobacteria	Ochrobactrum anthropi	hypothetical protein [Ochrobactrum anthropi].	GCF_003937425.1
WP_129381357.1	SUN→ SPRY+SUN→ *SPRY+SUN*→ Laminin_G_3→ Disaggr_repeat→ Phage_holin_4_1→	SPRY+SUN	423	EBB07_RS29185	Firmicutes	Paenibacillaceae bacterium	hypothetical protein [Paenibacillaceae bacterium].	GCF_004134985.1
WP_129381358.1	-	-	415	EBB07_RS29190	Firmicutes	Paenibacillaceae bacterium	hypothetical protein [Paenibacillaceae bacterium].	GCF_004134985.1
WP_130767937.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→ Phage-tail-tape→ ConA-repeats→ ConA→?→ PSE→||<-?||SRAP→	SPRY+X	655	STNY_RS04735	Gammaproteobacteria	Stenotrophomonas sp. Y	hypothetical protein [Stenotrophomonas sp. Y].	GCF_004306035.1
WP_134709562.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→?→ Phage-tail-tape→ ConA-repeats→ ConA→	SPRY+X	655	EUA01_RS04295	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_004522395.1

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WP_134729602.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→?→ Phage-tail-tape→ ConA-repeats→?→?→||<-SRAP	SPRY+X	657	EUA00_RS03030	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_004522355.1
WP_136006293.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→ Phage-tail-tape→	SPRY+X	656	E5352_RS15345	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_004794075.1
WP_136702221.1	SPRY*→ Phage_tail_APC→	SPRY	539	E6C67_RS08475	Alphaproteobacteria	Azospirillum sp. TSA2s	hypothetical protein [Azospirillum sp. TSA2s].	GCF_004923315.1
WP_136702953.1	SPRY*→?→?→ Cluster153_2clades→	SPRY	708	E6C67_RS14155	Alphaproteobacteria	Azospirillum sp. TSA2s	hypothetical protein [Azospirillum sp. TSA2s].	GCF_004923315.1
WP_137222083.1	Redoxin→||<-tRNA<-?||?→||<-tRNA<-tRNA<-tRNA||?→?→ SIG+SPRY+Cohesin*→	SIG+SPRY+Cohesin	509	PaeCFBP13512_RS06670	Firmicutes	Paenibacillus sp. CFBP13512	hypothetical protein [Paenibacillus sp. CFBP13512].	GCF_005233705.1
WP_140785213.1	SPRY+Laminin_G_3*→	SPRY+Laminin_G_3	473	FJ417_RS24630	Alphaproteobacteria	Mesorhizobium sp. B3-1-7	hypothetical protein [Mesorhizobium sp. B3-1-7].	GCF_006439385.1
WP_140977547.1	SPRY+Clostridium_P47+TM+TM+TM*→	SPRY+Clostridium_P47+TM+TM+TM	750	C2U70_RS08460	Alphaproteobacteria	Bradyrhizobium guangdongense	TULIP family P47-like protein [Bradyrhizobium guangdongense].	GCF_006483445.1
WP_144787026.1	SUN→ SUN→ SUN→ SUN→ SUN→ SPRY+SUN*→ SUN→ Laminin_G_3→ Disaggr_repeat→?→?→ Phage_holin_1→	SPRY+SUN	427	FS727_RS01315	Firmicutes	Lysinibacillus fusiformis	discoidin domain-containing protein [Lysinibacillus fusiformis].	GCF_007678325.1
WP_145413289.1	SUN→ SUN→ SPRY+SUN*→ Laminin_G_3→ Disaggr_repeat→ Phage_holin_4_1→	SPRY+SUN	411	FS823_RS10960	Firmicutes	Paenibacillus xylanexedens	discoidin domain-containing protein [Paenibacillus xylanexedens].	GCF_007679855.1
WP_145958251.1	Phage-tail-tape→ PSE→?→?→?→ SPRY+X*→?→ DAM→	SPRY+X	658	C0575_RS17020	Gammaproteobacteria	Xanthomonas	MULTISPECIES: hypothetical protein [Xanthomonas].	GCF_002759275.1
WP_147429703.1	<-REC+OmpR-HTH<-?<-?<-?<-?||RHS_repeat+RHS_repeat+RHS_repeat+IG+SPRY+SPRY*→	RHS_repeat+RHS_repeat+RHS_repeat+IG+SPRY+SPRY	1116	K256_RS17555	Gammaproteobacteria	Alteromonadaceae bacterium 2052S.S.stab0a.01	hypothetical protein [Alteromonadaceae bacterium 2052S.S.stab0a.01].	GCF_003634075.1
WP_149425237.1	TM+TM→ Laminin_G_3+SPRY*→ Cluster358_2clades→?→?→ Phage_holin→?→?→||<-SRAP	Laminin_G_3+SPRY	714	OTERR_RS06755	Betaproteobacteria	Oryzomicrobium terrae	hypothetical protein [Oryzomicrobium terrae].	GCF_008274805.1
WP_151150764.1	Phage_T7_tail→ SPRY*→ Phage_tail_APC→	SPRY	494	F8A88_RS08730	Deltaproteobacteria	Desulfovibrio senegalensis	hypothetical protein [Desulfovibrio senegalensis].	GCF_008830225.1
WP_152380319.1	HTH_20→||<-ABhydrolase<-?||SIG+SPRY*→	SIG+SPRY	377	GCU48_RS13350	Firmicutes	Paenibacillus brasilensis	hypothetical protein [Paenibacillus brasilensis].	GCF_009363115.1
WP_152906267.1	Phage-tail-tape→ ConA-repeats→?→ SPRY+X*→?→ PSE→||<-?||REC+OmpR-HTH→	SPRY+X	633	ADI69_RS15035	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_001073045.1
WP_153164331.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→ Phage-tail-tape→?→?→?→||<-SRAP	SPRY+X	656	GDJ08_RS03810	Gammaproteobacteria	Stenotrophomonas sp. CPCC 101271	hypothetical protein [Stenotrophomonas sp. CPCC 101271].	GCF_009467805.1

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WP_153794576.1	SIG+SPRY*→	SIG+SPRY	333	BJH92_RS10685	Firmicutes	Paenibacillus polymyxa	hypothetical protein [Paenibacillus polymyxa].	GCF_009650715.1
WP_154081143.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→?→ Phage-tail-tape→	SPRY+X	655	B861_RS0208195	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_000295735.1
WP_154263126.1	Phage-tail-tape→ ConA-repeats→?→ SPRY+X*→	SPRY+X	655	FEO89_RS08390	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_009676565.1
WP_154352257.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→?→ Phage-tail-tape→ ConA-repeats→	SPRY+X	657	FEO88_RS08425	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_009676585.1
WP_154965920.1	SIG+SPRY*→?→||<-?<-PSE<-PSE<-?<-?<-?<-Phage_holin	SIG+SPRY	346	F1386_RS02215	Firmicutes	Paenibacillus azotifigens	hypothetical protein [Paenibacillus azotifigens].	GCF_008635805.1
WP_156830543.1	Cluster180_2clades→?→?→?→?→?→?→ SPRY*→	SPRY	830	METMA_RS27135	Gammaproteobacteria	Methylobacter marinus	hypothetical protein [Methylobacter marinus].	GCF_000383855.1
WP_157628481.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→ Phage-tail-tape→	SPRY+X	657	SMAL_RS12680	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_000020665.1
WP_157793929.1	SUN→ SPRY+SUN*→ SUN→ Laminin_G_3→ Disaggr_repeat→ Phage_holin_4_1→	SPRY+SUN	409	B9T62_RS19340	Firmicutes	Paenibacillus donghaensis	discoidin domain-containing protein [Paenibacillus donghaensis].	GCF_002192415.1
WP_158702666.1	SUN→ SPRY+SUN*→	SPRY+SUN	405	C8268_RS03870	Firmicutes	Paenibacillus sp. Marseille-P3787	discoidin domain-containing protein [Paenibacillus sp. Marseille-P3787].	GCF_900289175.1
WP_159054946.1	OBfold→?→?→||<-?||?→ ConA-repeats→?→ SPRY+X*→	SPRY+X	655	C9J74_RS07540	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_003030985.1
WP_160788604.1	HTH_20→||<-PSE<-ABhydrolase<-Polbetant||ACET→ Cupin_2→ ABhydrolase→||<-DUF2935||SIG+SPRY*→?→ PSE→||<-Glycos_transf_2	SIG+SPRY	338	GRP75_RS03415	Firmicutes	Paenibacillus sp. OT2-17	hypothetical protein [Paenibacillus sp. OT2-17].	GCF_009827695.1
WP_161771818.1	Phage_TAC_13→?→ SPRY+X*→?→?→ Phage-tail-tape→	SPRY+X	657	AR275_RS25795	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_001506105.1
WP_162174107.1	Cluster165_3clades→?→?→ Cluster303_2clades→?→?→ TM+TM→ SPRY*→?→?→?→?→?→?→ SIG+HORMA→	SPRY	125	HMCN_RS19520	Betaproteobacteria	Herminiimonas sp. CN	hypothetical protein [Herminiimonas sp. CN].	GCF_000622895.1
WP_162407361.1	Phage-tail-tape→?→?→ SUN→ SPRY+X*→?→||<-?||DAM→	SPRY+X	654	CSC62_RS14285	Gammaproteobacteria	Pseudoxanthomonas jiangsuensis	hypothetical protein [Pseudoxanthomonas jiangsuensis].	GCF_010093185.1
WP_162815241.1	SPRY*→	SPRY	219	DOU47_RS11710	Actinobacteria	Microbacterium arborescens	hypothetical protein [Microbacterium arborescens].	GCF_003339645.1
WP_163369807.1	SPRY*→	SPRY	262	G7B23_RS04230	Gammaproteobacteria	Endozoicomonas acroporae	hypothetical protein [Endozoicomonas acroporae].	GCF_010994325.1

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WP_163387923.1	SPRY*→	SPRY	262	EO230_RS13880	Gammaproteobacteria	Endozoicomonas acroporae	hypothetical protein [Endozoicomonas acroporae].	GCF_010994335.1
WP_163679668.1	Laminin_G_3+SPRY+SPRY*→	Laminin_G_3+SPRY+SPRY	704	G4223_RS11800	Alphaproteobacteria	Magnetospirillum aberrantis	hypothetical protein [Magnetospirillum aberrantis].	GCF_011022235.1
WP_164136018.1	Phage_H_T_join→ HK97-gp10_like→ DUF3168→?→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→?→ Phage-tail-tape→ ConA-repeats→ ConA→	SPRY+X	657	G4995_RS01655	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_010604725.1
WP_164170835.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→ Phage-tail-tape→ ConA-repeats→	SPRY+X	657	G5A21_RS04165	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_010605085.1
WP_164171533.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→?→ Phage-tail-tape→ ConA-repeats→?→?→ SRAP→	SPRY+X	657	G5A20_RS11530	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_010607635.1
WP_164186354.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→?→ Phage-tail-tape→ ConA-repeats→?→?→ SRAP→	SPRY+X	657	G4996_RS10295	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_010608865.1
WP_164222458.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→||<-?||?→?→ Phage-tail-tape→ ConA-repeats→	SPRY+X	658	G5A44_RS14400	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_010608905.1
WP_164227274.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→ Phage-tail-tape→ ConA-repeats→?→?→||<-PSE||?→ SRAP→	SPRY+X	658	G5A23_RS09720	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_010605135.1
WP_164262535.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→?→ Phage-tail-tape→ ConA-repeats→?→||<-SRAP	SPRY+X	655	G5A42_RS09935	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_010609005.1
WP_164272506.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→?→ Phage-tail-tape→ ConA-repeats→ ConA→?→||<-SRAP	SPRY+X	657	G4G00_RS08180	Gammaproteobacteria	Stenotrophomonas sp. B1-1	hypothetical protein [Stenotrophomonas sp. B1-1].	GCF_010894375.1
WP_164283369.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→ Phage-tail-tape→ ConA-repeats→ ConA→?→||<-SRAP	SPRY+X	655	GJV38_RS08100	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_010994225.1
WP_164687941.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→?→ Phage-tail-tape→ ConA-repeats→ ConA→?→||<-SRAP	SPRY+X	655	G5C63_RS04670	Gammaproteobacteria	Stenotrophomonas pavanii	hypothetical protein [Stenotrophomonas pavanii].	GCF_011043715.1
WP_164776353.1	SUN→ SPRY+SUN*→ SUN→ Laminin_G_3→ Disaggr_repeat→ Phage_holin_4_1→?→ SIG+ConA+beta-propeller→	SPRY+SUN	423	FLT43_RS09110	Firmicutes	Paenibacillus thiaminolyticus	hypothetical protein [Paenibacillus thiaminolyticus].	GCF_004001005.1
WP_164965245.1	HTH_20→||<-Trypsin<-ABhydrolase||ACET→||<-DUF2935<-?||SIG+SPRY*→	SIG+SPRY	369	G9G57_RS16175	Firmicutes	Paenibacillus sp. EKM211P	hypothetical protein [Paenibacillus sp. EKM211P].	GCF_011066175.1
WP_165083476.1	HTH_20→||<-Trypsin<-ABhydrolase||ACET→||<-DUF2935<-?||SIG+SPRY*→	SIG+SPRY	312	G9G64_RS19615	Firmicutes	unclassified Paenibacillus	MULTISPECIES: hypothetical protein [unclassified Paenibacillus].	GCF_011066085.1
WP_165148029.1	HTH_20→||<-ABhydrolase<-Polbetant||ACET→ Cupin_2→ ABhydrolase→||<-DUF2935||SIG+SPRY*→?→||<-Glycos_transf_2	SIG+SPRY	345	G9G52_RS14675	Firmicutes	unclassified Paenibacillus	MULTISPECIES: hypothetical protein [unclassified Paenibacillus].	GCF_011066155.1

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WP_165178844.1	HTH_20→||<-ABhydrolase<-Polbetant||ACET→ Cupin_2→||<-DUF2935||SIG+SPRY*→	SIG+SPRY	330	G9G54_RS16165	Firmicutes	Paenibacillus sp. EKM212P	hypothetical protein [Paenibacillus sp. EKM212P].	GCF_011066115.1
WP_165980135.1	SUN→ SUN→ SPRY+SUN*→ Laminin_G_3→ Disaggr_repeat→	SPRY+SUN	412	E2R58_RS01745	Firmicutes	Paenibacillus amylolyticus	hypothetical protein [Paenibacillus amylolyticus].	GCF_004358835.1
WP_167440979.1	HTH_20→||<-Trypsin<-ABhydrolase||ACET→||<-DUF2935<-?||SIG+SPRY*→	SIG+SPRY	332	HFD99_RS19285	Firmicutes	Paenibacillus sp. EKM301P	hypothetical protein [Paenibacillus sp. EKM301P].	GCF_011800295.1
WP_168180444.1	SPRY+SUN*→ SUN→ SUN→ Laminin_G_3→ Disaggr_repeat→ Phage_holin_4_1→	SPRY+SUN	417	HRG14_RS16580	Firmicutes	Paenibacillus dendritiformis	hypothetical protein [Paenibacillus dendritiformis].	GCF_012272915.1
WP_168224778.1	Phage-tail_3+FN3→ Cluster93_5clades→ Laminin_G_3+SPRY*→?→?→||<-?<-REC+OmpR-HTH	Laminin_G_3+SPRY	442	EXZ61_RS14580	Betaproteobacteria	Rhodoferax sediminis	hypothetical protein [Rhodoferax sediminis].	GCF_006974105.1
WP_168759630.1	Phage_H_T_join→ HK97-gp10_like→ DUF3168→?→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→ Phage-tail-tape→ ConA-repeats→?→?→||<-PSE||?→ SRAP→	SPRY+X	655	HGN30_RS14120	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_012647025.1
WP_170142066.1	Phage-tail_3→?→ SPRY*→?→?→?→?→?→ DAM→	SPRY	223	DFQ59_RS06730	Gammaproteobacteria	Thioalbus denitrificans	hypothetical protein [Thioalbus denitrificans].	GCF_003337735.1
WP_171365214.1	SUN→ SUN→?→ DISCOIDIN→ SUN→ SPRY+SUN*→ SUN→ Laminin_G_3→ Disaggr_repeat→?→?→ Phage_holin_1→	SPRY+SUN	425	HL291_RS06145	Firmicutes	Lysinibacillus fusiformis	discoidin domain-containing protein [Lysinibacillus fusiformis].	GCF_013112215.1
WP_180361703.1	SUN→ SUN→ SUN→ SPRY+SUN*→ Laminin_G_3→ Disaggr_repeat→	SPRY+SUN	412	CXK86_RS01005	Firmicutes	Paenibacillus sp. BGI2013	hypothetical protein [Paenibacillus sp. BGI2013].	GCF_002843485.1
WP_180832871.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→?→ Phage-tail-tape→ ConA-repeats→?→?→||<-SRAP	SPRY+X	657	D7U76_RS15765	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_013463655.1
WP_180835450.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→ Phage-tail-tape→?→?→?→||<-PSE||?→||<-SRAP	SPRY+X	657	D7U87_RS15230	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_013463795.1
WP_180837803.1	Phage-tail-tape→ ConA-repeats→?→ SPRY+X*→?→?→?→?→?→?→||<-Ribonuc_L-PSP	SPRY+X	633	D7Y22_RS10130	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_013463895.1
WP_180844236.1	Phage-tail-tape→ ConA-repeats→?→ SPRY+X*→?→?→?→?→ SIG+TM+TM+TM+TM+TM+TM+TM+TM→ ABC-ATPase→	SPRY+X	655	D7Y24_RS02400	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_013463875.1
WP_180874375.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→?→ Phage-tail-tape→ ConA-repeats→?→?→||<-SRAP	SPRY+X	657	D7Y39_RS15850	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_013464195.1
WP_180877176.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→?→ Phage-tail-tape→ ConA-repeats→?→?→||<-SRAP	SPRY+X	657	D7U95_RS06530	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_013463605.1
WP_180890353.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→?→ Phage-tail-tape→ ConA-repeats→?→?→||<-SRAP	SPRY+X	658	D7Y45_RS11625	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_013464305.1
WP_182068260.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→?→ Phage-tail-tape→ ConA-repeats→ ConA→	SPRY+X	655	H7A80_RS13755	Gammaproteobacteria	Stenotrophomonas pavanii	hypothetical protein [Stenotrophomonas pavanii].	GCF_903970895.1

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
WP_182680994.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→?→ Phage-tail-tape→ ConA-repeats→?→?→||<-SRAP	SPRY+X	657	H4O10_RS07755	Gammaproteobacteria	Stenotrophomonas sp. I18B00994	hypothetical protein [Stenotrophomonas sp. I18B00994].	GCF_014145825.1
WP_182852413.1	Cluster242_2clades→?→ PSE→?→ SPRY*→	SPRY	255	H7K70_RS11535	Gammaproteobacteria	Pseudomonas otitidis	hypothetical protein [Pseudomonas otitidis].	GCF_014161995.1
WP_183080221.1	Phage_connect_1→ Phage_H_T_join→ HK97-gp10_like→ DUF3168→ Phage_TTP_11→ Phage_TAC_13→?→ SPRY+X*→?→?→ Phage-tail-tape→ ConA-repeats→?→?→ SRAP→	SPRY+X	657	C7543_RS14050	Gammaproteobacteria	Stenotrophomonas sp. CF319	hypothetical protein [Stenotrophomonas sp. CF319].	GCF_003633905.1

7. Source data. Gene neighborhoods and domain architectures of TPR-GREAB-C-PIN systems

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
-	-	-	NA	NA	NA	NA	NA	GCF_016236915.1
AAQ66293.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1140	PG_1202	Bacteroidetes	Porphyromonas gingivalis W83	hypothetical protein PG_1202 [Porphyromonas gingivalis W83].	GCA_000007585.1
ABA73572.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1113	Pfl01_1829	Gammaproteobacteria	Pseudomonas fluorescens Pf0-1	hypothetical protein Pfl01_1829 [Pseudomonas fluorescens Pf0-1].	GCA_000012445.1
ABP70317.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1188	Rsph17025_1421	Alphaproteobacteria	Rhodobacter sphaeroides ATCC 17025	hypothetical protein Rsph17025_1421 [Rhodobacter sphaeroides ATCC 17025].	GCA_000016405.1
ACB93983.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1100	Bind_0329	Alphaproteobacteria	Beijerinckia indica subsp. indica ATCC 9039	Tetratricopeptide TPR_2 repeat protein [Beijerinckia indica subsp. indica ATCC 9039].	GCA_000019845.1
ACQ93407.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1069	Tola_1798	Gammaproteobacteria	Tolumonas auensis DSM 9187	hypothetical protein Tola_1798 [Tolumonas auensis DSM 9187].	GCA_000023065.1
ADX44119.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1383	Acav_0193	Betaproteobacteria	Acidovorax avenae subsp. avenae ATCC 19860	hypothetical protein Acav_0193 [Acidovorax avenae subsp. avenae ATCC 19860].	GCA_000176855.2
AFD27801.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1286	DGo_PC0009	Deinococci	Deinococcus gobiensis I-0	hypothetical protein DGo_PC0009 (plasmid) [Deinococcus gobiensis I-0].	GCA_000252445.1
AFJ56694.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1321	PflA506_2672	Gammaproteobacteria	Pseudomonas fluorescens A506	tetratricopeptide repeat protein [Pseudomonas fluorescens A506].	GCA_000262325.2
AGO88322.1	REase+TPR+GreAB-C+PIN*→?→?→ Calcineurin→ Calcineurin→?→ Calcineurin→	REase+TPR+GreAB-C+PIN	1344	MOC_1p0084	Alphaproteobacteria	Methylobacterium oryzae CBMB20	Tetratricopeptide TPR_2 repeat protein (plasmid) [Methylobacterium oryzae CBMB20].	-
AHC85672.1	HetE-N1→ TPR+TPR+GreAB-C+PIN*→	TPR+TPR+GreAB-C+PIN	1114	X969_07375	Gammaproteobacteria	Pseudomonas monteilii SB3078	hypothetical protein X969_07375 [Pseudomonas monteilii SB3078].	GCA_000510285.1
AHG89833.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1325	J421_2296	Gemmatimonadetes	Gemmatirosa kalamazoonesis	hypothetical protein J421_2296 [Gemmatirosa kalamazoonesis].	GCA_000522985.1
AHZ68657.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1527	OU5_1578	Gammaproteobacteria	Pseudomonas mandelii JR-1	hypothetical protein OU5_1578 [Pseudomonas mandelii JR-1].	GCA_000257545.3
AIO22452.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1474	DM41_7691	Betaproteobacteria	Burkholderia cepacia ATCC 25416	tetratricopeptide repeat family protein (plasmid) [Burkholderia cepacia ATCC 25416].	GCA_003546465.1
AJG23424.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1348	RR42_s1836	Betaproteobacteria	Cupriavidus basilensis	hypothetical protein RR42_s1836 [Cupriavidus basilensis].	GCA_000832305.1
AJG25013.1	NACHT→ REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1361	RR42_s3437	Betaproteobacteria	Cupriavidus basilensis	hypothetical protein RR42_s3437 [Cupriavidus basilensis].	GCA_000832305.1
ALA80840.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	706	VN11_01310	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein VN11_01310 [Stenotrophomonas maltophilia].	GCA_001274595.1
ALK23663.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1346	APZ15_37705	Betaproteobacteria	Burkholderia cepacia ATCC 25416	hypothetical protein APZ15_37705 (plasmid) [Burkholderia cepacia ATCC 25416].	GCA_001411495.1
ALY84300.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	808	HV95_15440	Gammaproteobacteria	Pseudomonas aeruginosa	hypothetical protein HV95_15440 [Pseudomonas aeruginosa].	GCA_001516225.1
AMM82949.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1090	AW43_10865	Gammaproteobacteria	Pasteurella multocida subsp. multocida PMTB2.1	hypothetical protein AW43_10865 [Pasteurella multocida subsp. multocida PMTB2.1].	GCA_001578435.2
ANP41882.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1247	K529_013985	Alphaproteobacteria	Epibacterium mobile F1926	hypothetical protein K529_013985 [Epibacterium mobile F1926].	GCA_000376545.2
AOE80004.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	962	A7318_15795	Gammaproteobacteria	Pseudomonas lurida	hypothetical protein A7318_15795 [Pseudomonas lurida].	GCA_001708485.1

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APP29939.1	REase+TPR+GreAB-C+PIN*→||||<-?||HTH→	REase+TPR+GreAB-C+PIN	1216	AUO97_03535	Gammaproteobacteria	Acinetobacter baumannii	hypothetical protein AUO97_03535 [Acinetobacter baumannii].	GCA_001593425.2
APT35017.1	REase+TPR+GreAB-C+PIN*→?→?→ Calcineurin→ Calcineurin→?→ Calcineurin→	REase+TPR+GreAB-C+PIN	1340	MCBMB27_05726	Alphaproteobacteria	Methylobacterium phyllosphaerae	hypothetical protein MCBMB27_05726 (plasmid) [Methylobacterium phyllosphaerae].	GCA_001936175.1
APV35618.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1211	BEN76_06135	Gammaproteobacteria	Acinetobacter soli	hypothetical protein BEN76_06135 [Acinetobacter soli].	GCA_001953195.1
ARP63802.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1328	A9K65_010750	Alphaproteobacteria	Mesorhizobium sp. WSM1497	hypothetical protein A9K65_010750 [Mesorhizobium sp. WSM1497].	GCA_001672455.2
ARS41908.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1265	CA265_20515	Bacteroidetes	Sphingobacteriaceae bacterium GW460-11-11-14-LB5	hypothetical protein CA265_20515 [Sphingobacteriaceae bacterium GW460-11-11-14-LB5].	GCA_002151545.1
AWD09427.1	HetE-N1→?→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	512	C7D56_14785	Gammaproteobacteria	Salmonella enterica subsp. enterica serovar Corvallis	hypothetical protein C7D56_14785 [Salmonella enterica subsp. enterica serovar Corvallis].	GCA_003071545.1
AXQ72363.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1090	AWY89_05050	Gammaproteobacteria	Pasteurella multocida subsp. multocida	hypothetical protein AWY89_05050 [Pasteurella multocida subsp. multocida].	GCA_003428945.1
AXW62973.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1325	CJO94_14695	Betaproteobacteria	Ralstonia solanacearum	hypothetical protein CJO94_14695 [Ralstonia solanacearum].	GCA_003515385.1
AYG03885.1	X+PIN*→	X+PIN	1170	D7I44_10295	Actinobacteria	Gryllotalpicola protaetiae	hypothetical protein D7I44_10295 [Gryllotalpicola protaetiae].	GCA_003627055.1
BAE85210.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1306	DSY3421	Firmicutes	Desulfitobacterium hafniense Y51	hypothetical protein DSY3421 [Desulfitobacterium hafniense Y51].	GCA_000010045.1
BBD03377.1	REase+TPR→ TPR→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	656	YGS_C2P1391	Alphaproteobacteria	Sphingobium sp. YG1	hypothetical protein YGS_C2P1391 [Sphingobium sp. YG1].	GCA_003609795.1
BBZ79150.1	TPR+PIN*→	TPR+PIN	1186	MANY_44870	Actinobacteria	Mycolicibacterium anyangense	hypothetical protein MANY_44870 [Mycolicibacterium anyangense].	GCA_010731855.1
BBZ91069.1	PIN*→	PIN	190	F07S3_09020	Alphaproteobacteria	Bradyrhizobium diazoefficiens	hypothetical protein F07S3_09020 [Bradyrhizobium diazoefficiens].	GCA_014163475.1
CAA9240899.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1079	AVDCRST_MAG77-1676	environmental samples	uncultured Chloroflexi bacterium	MAG: hypothetical protein AVDCRST_MAG77-1676 [uncultured Chloroflexi bacterium].	GCA_902805635.1
CAB3809090.1	PIN*→	PIN	270	LMG28138_06082	Betaproteobacteria	Pararobbsia alpina	hypothetical protein LMG28138_06082 [Pararobbsia alpina].	GCA_902859895.1
CAC9458388.1	TPR+GreAB-C+PIN*→?→||||<-PSE||PSE→ PSE→?→ PSE→ PSE→ PSE→?→?→ TPR→	TPR+GreAB-C+PIN	1164	SMARSOXL104_LOCUS2140	environmental samples	uncultured Gammaproteobacteria bacterium	hypothetical protein [uncultured Gammaproteobacteria bacterium].	GCA_903813475.1
CAC9474194.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1164	SMARSOXL102_LOCUS3344	environmental samples	uncultured Gammaproteobacteria bacterium	hypothetical protein [uncultured Gammaproteobacteria bacterium].	GCA_903813445.1
CAC9479061.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	677	SMARSOXL51_LOCUS3828	environmental samples	uncultured Gammaproteobacteria bacterium	hypothetical protein [uncultured Gammaproteobacteria bacterium].	GCA_903813485.1
CAD79080.1	TRD+TRD→?→?→ REase+SNF2→?→ TM+TM+TPR+GreAB-C+PIN*→	TM+TM+TPR+GreAB-C+PIN	1274	RB11367	Planctomycetes	Rhodopirellula baltica SH 1	hypothetical protein RB11367 [Rhodopirellula baltica SH 1].	GCA_000196115.1
CAE7733776.1	IMS+HHH+GreAB+AraC-HTH+AraC-HTH*→	IMS+HHH+GreAB+AraC-HTH+AraC-HTH	771	dinB	Alveolata	Symbiodinium microadriaticum	dinB [Symbiodinium microadriaticum].	GCA_905231925.1
CAG37728.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1114	DP2999	Deltaproteobacteria	Desulfotalea psychrophila LSv54	unknown protein [Desulfotalea psychrophila LSv54].	GCA_000025945.1
CCD86698.1	REase+TPR+TPR+GreAB-C+PIN*→	REase+TPR+TPR+GreAB-C+PIN	1326	BRAO285_2000017	Alphaproteobacteria	Bradyrhizobium sp. ORS 285	conserved hypothetical protein [Bradyrhizobium sp. ORS 285].	GCA_000239755.2
CDF45779.1	X+PIN*→?→?→ CITB-HTH+LexA-protease→	X+PIN	1212	BN450_02242	environmental samples	Roseburia sp. CAG:100	uncharacterized protein BN450_02242 [Roseburia sp. CAG:100].	GCA_000436955.1
CDH20863.1	HetE-N1→ TPR+GreAB-C+PIN*→ TPR+GreAB-C+PIN→	TPR+GreAB-C+PIN	846	XBKQ1_2810009	Gammaproteobacteria	Xenorhabdus bovienii str. kraussei Quebec	conserved hypothetical protein [Xenorhabdus bovienii str. kraussei Quebec].	GCA_000736555.1
CEL29322.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1486	SRM1_02673	Gammaproteobacteria	Pseudomonas fluorescens	hypothetical protein SRM1_02673 [Pseudomonas fluorescens].	GCA_000827755.2

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
CFK79862.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1327	ERS012324_00072	Betaproteobacteria	Burkholderia pseudomallei	Uncharacterised protein [Burkholderia pseudomallei].	GCA_001327015.1
CGG41859.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1147	ERS020510_00033	Firmicutes	Streptococcus pneumoniae	putative PEP-CTERM system TPR-repeat lipoprotein [Streptococcus pneumoniae].	GCA_001339955.1
CNG28227.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1094	ERS137937_00749	Gammaproteobacteria	Yersinia enterocolitica	Uncharacterised protein [Yersinia enterocolitica].	GCA_001160345.1
COE44409.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1147	ERS020529_01064	Firmicutes	Streptococcus pneumoniae	putative PEP-CTERM system TPR-repeat lipoprotein [Streptococcus pneumoniae].	GCA_002889635.1
CRI57148.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1419	CCOS191_2612	Gammaproteobacteria	Pseudomonas sp. CCOS 191	hypothetical protein CCOS191_2612 [Pseudomonas sp. CCOS 191].	GCA_001007005.1
CTR52279.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1093	ERS085432_03851	Gammaproteobacteria	Escherichia coli	Uncharacterised protein [Escherichia coli].	GCA_001277455.1
CTU76757.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1093	ERS085409_04356	Gammaproteobacteria	Escherichia coli	Uncharacterised protein [Escherichia coli].	GCA_001284445.1
EAA6823230.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	839	DRV62_14440	Gammaproteobacteria	Salmonella enterica subsp. enterica serovar Corvallis	hypothetical protein DRV62_14440, partial [Salmonella enterica subsp. enterica serovar Corvallis].	GCA_004191475.1
EAA7528536.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	997	WB97_04605	Gammaproteobacteria	Salmonella enterica subsp. enterica	hypothetical protein WB97_04605, partial [Salmonella enterica subsp. enterica].	GCA_004218105.1
EAB9718450.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1094	EBD60_05220	Gammaproteobacteria	Escherichia coli	hypothetical protein EBD60_05220 [Escherichia coli].	GCA_004268345.1
EAC0684623.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1117	ECA66_22430	Gammaproteobacteria	Salmonella enterica subsp. enterica serovar Molade	hypothetical protein ECA66_22430 [Salmonella enterica subsp. enterica serovar Molade].	GCA_004273605.1
EAM8584006.1	HetE-N1→ TPR+GreAB-C+PIN*→?→||||<-Trypsin	TPR+GreAB-C+PIN	1121	BET14_04310	Gammaproteobacteria	Salmonella enterica	hypothetical protein BET14_04310 [Salmonella enterica].	GCA_005437065.1
EAM9325916.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1106	DPR23_14355	Gammaproteobacteria	Salmonella enterica	hypothetical protein DPR23_14355 [Salmonella enterica].	GCA_005440115.1
EAN1748525.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1107	D8T88_07580	Gammaproteobacteria	Salmonella enterica	hypothetical protein D8T88_07580 [Salmonella enterica].	GCA_005450625.1
EAO3021897.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	727	E3A68_19440	Gammaproteobacteria	Salmonella enterica	hypothetical protein E3A68_19440, partial [Salmonella enterica].	GCA_005498265.1
EAO5192492.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	867	E7928_13885	Gammaproteobacteria	Salmonella enterica	hypothetical protein E7928_13885, partial [Salmonella enterica].	GCA_005509025.1
EAO9608739.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	776	BH019_23310	Gammaproteobacteria	Salmonella enterica	hypothetical protein BH019_23310, partial [Salmonella enterica].	GCA_005533575.1
EAR5961962.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1101	ES925_14455	Gammaproteobacteria	Salmonella enterica	hypothetical protein ES925_14455 [Salmonella enterica].	GCA_005654255.1
EAR6368406.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1117	EU234_19825	Gammaproteobacteria	Salmonella enterica	hypothetical protein EU234_19825 [Salmonella enterica].	GCA_005655905.1
EAS2553591.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	590	DMT50_24325	Gammaproteobacteria	Salmonella enterica	hypothetical protein DMT50_24325, partial [Salmonella enterica].	GCA_005679955.1
EAS5437941.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	985	D8Z11_24970	Gammaproteobacteria	Salmonella enterica	hypothetical protein D8Z11_24970 [Salmonella enterica].	GCA_005692135.1
EAT5893226.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1106	E3L72_21800	Gammaproteobacteria	Salmonella enterica	hypothetical protein E3L72_21800 [Salmonella enterica].	GCA_005737135.1
EAT6283696.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	843	E5797_05930	Gammaproteobacteria	Salmonella enterica	hypothetical protein E5797_05930, partial [Salmonella enterica].	GCA_005739275.1
EAV44914.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1295	SIAM614_12903	Alphaproteobacteria	Labrenzia aggregata IAM 12614	hypothetical protein SIAM614_12903 [Labrenzia aggregata IAM 12614].	GCA_000168975.1
EAW0681535.1	HetE-N1→ TPR+GreAB-C+PIN+TM+TM*→	TPR+GreAB-C+PIN+TM+TM	1106	AIB54_02885	Gammaproteobacteria	Salmonella enterica	hypothetical protein AIB54_02885 [Salmonella enterica].	GCA_005896365.1
EAW0902300.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	638	B2H02_24145	Gammaproteobacteria	Salmonella enterica	hypothetical protein B2H02_24145, partial [Salmonella enterica].	GCA_005898285.1
EAY5481430.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	858	MB58_12360	Gammaproteobacteria	Salmonella enterica	hypothetical protein MB58_12360, partial [Salmonella enterica].	GCA_006012385.1

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EBD0849223.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	970	FHN97_07895	Gammaproteobacteria	Salmonella enterica	hypothetical protein FHN97_07895, partial [Salmonella enterica].	GCA_006217605.1
EBD3738487.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1107	CRZ11_10865	Gammaproteobacteria	Salmonella enterica	hypothetical protein CRZ11_10865 [Salmonella enterica].	GCA_006248335.1
EBD8181391.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	606	C6600_23545	Gammaproteobacteria	Salmonella enterica	hypothetical protein C6600_23545 [Salmonella enterica].	GCA_006268595.1
EBF2432475.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	986	DKG18_08085	Gammaproteobacteria	Salmonella enterica	hypothetical protein DKG18_08085, partial [Salmonella enterica].	GCA_006332345.1
EBF2786917.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	738	C2240_24885	Gammaproteobacteria	Salmonella enterica subsp. enterica serovar Corvallis	hypothetical protein C2240_24885, partial [Salmonella enterica subsp. enterica serovar Corvallis].	GCA_006331745.1
EBF4219990.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	702	FH403_17525	Gammaproteobacteria	Salmonella enterica	hypothetical protein FH403_17525, partial [Salmonella enterica].	GCA_006342775.1
EBG7115752.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	822	FJA42_18775	Gammaproteobacteria	Salmonella enterica	hypothetical protein FJA42_18775, partial [Salmonella enterica].	GCA_006457615.1
EBI5135933.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	642	DQO15_25245	Gammaproteobacteria	Salmonella enterica	hypothetical protein DQO15_25245, partial [Salmonella enterica].	GCA_006559185.1
EBI9233829.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	670	DLA64_23180	Gammaproteobacteria	Salmonella enterica	hypothetical protein DLA64_23180, partial [Salmonella enterica].	GCA_006576485.1
EBI9496533.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	749	DLP94_24755	Gammaproteobacteria	Salmonella enterica	hypothetical protein DLP94_24755, partial [Salmonella enterica].	GCA_006578745.1
EBK5150964.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	786	DON25_22080	Gammaproteobacteria	Salmonella enterica	hypothetical protein DON25_22080, partial [Salmonella enterica].	GCA_006645025.1
EBL0898297.1	HetE-N1→ TPR+GreAB-C+PIN*→?→||||<-Trypsin	TPR+GreAB-C+PIN	1121	D0R07_07295	Gammaproteobacteria	Salmonella enterica	hypothetical protein D0R07_07295 [Salmonella enterica].	GCA_006670825.1
EBM3541219.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1117	DYJ09_14310	Gammaproteobacteria	Salmonella enterica	hypothetical protein DYJ09_14310 [Salmonella enterica].	GCA_006729905.1
EBM4506587.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	652	DZ654_25740	Gammaproteobacteria	Salmonella enterica	hypothetical protein DZ654_25740, partial [Salmonella enterica].	GCA_006730405.1
EBM4858227.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	648	D0R05_25725	Gammaproteobacteria	Salmonella enterica	hypothetical protein D0R05_25725, partial [Salmonella enterica].	GCA_006733825.1
EBM6537845.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1028	D2U20_21570	Gammaproteobacteria	Salmonella enterica	hypothetical protein D2U20_21570, partial [Salmonella enterica].	GCA_006740525.1
EBO1039185.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	643	D3T71_25030	Gammaproteobacteria	Salmonella enterica	hypothetical protein D3T71_25030, partial [Salmonella enterica].	GCA_006805285.1
EBQ9134585.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	707	DK746_24010	Gammaproteobacteria	Salmonella enterica subsp. enterica serovar Corvallis	hypothetical protein DK746_24010, partial [Salmonella enterica subsp. enterica serovar Corvallis].	GCA_006932075.1
EBR0236973.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	757	DNV25_24155	Gammaproteobacteria	Salmonella enterica subsp. enterica serovar Corvallis	hypothetical protein DNV25_24155, partial [Salmonella enterica subsp. enterica serovar Corvallis].	GCA_006936135.1
EBS1151706.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1007	D6P66_23730	Gammaproteobacteria	Salmonella enterica subsp. enterica serovar Corvallis	hypothetical protein D6P66_23730 [Salmonella enterica subsp. enterica serovar Corvallis].	GCA_006989745.1
EBS2228649.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	684	DRL12_24325	Gammaproteobacteria	Salmonella enterica subsp. enterica serovar Corvallis	hypothetical protein DRL12_24325, partial [Salmonella enterica subsp. enterica serovar Corvallis].	GCA_006993385.1
EBS6357254.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	999	D4E88_23815	Gammaproteobacteria	Salmonella enterica subsp. enterica serovar Albany	hypothetical protein D4E88_23815, partial [Salmonella enterica subsp. enterica serovar Albany].	GCA_007016725.1
EBU7006421.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	620	DKU11_24275	Gammaproteobacteria	Salmonella enterica subsp. enterica serovar Kintambo	hypothetical protein DKU11_24275, partial [Salmonella enterica subsp. enterica serovar Kintambo].	GCA_007139165.1

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EBU7167144.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1106	DKU92_07615	Gammaproteobacteria	Salmonella enterica subsp. enterica serovar Stockholm	hypothetical protein DKU92_07615 [Salmonella enterica subsp. enterica serovar Stockholm].	GCA_007140245.1
EBV1256929.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	719	DNW25_24775	Gammaproteobacteria	Salmonella enterica subsp. enterica serovar Corvallis	hypothetical protein DNW25_24775, partial [Salmonella enterica subsp. enterica serovar Corvallis].	GCA_007158045.1
EBV2191014.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1106	DN155_01500	Gammaproteobacteria	Salmonella enterica subsp. enterica serovar Afula	hypothetical protein DN155_01500 [Salmonella enterica subsp. enterica serovar Afula].	GCA_007161245.1
EBV8290347.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	704	AUE34_22015	Gammaproteobacteria	Salmonella enterica subsp. arizonae serovar 18:z4,z23:-	hypothetical protein AUE34_22015, partial [Salmonella enterica subsp. arizonae serovar 18:z4,z23:-].	GCA_007188075.1
EBV8290357.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	385	AUE34_22090	Gammaproteobacteria	Salmonella enterica subsp. arizonae serovar 18:z4,z23:-	hypothetical protein AUE34_22090, partial [Salmonella enterica subsp. arizonae serovar 18:z4,z23:-].	GCA_007188075.1
EBV8849078.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1000	AUA06_21700	Gammaproteobacteria	Salmonella enterica subsp. arizonae serovar 18:z4,z23:-	hypothetical protein AUA06_21700, partial [Salmonella enterica subsp. arizonae serovar 18:z4,z23:-].	GCA_007190395.1
EBV8917369.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	688	ASH63_21975	Gammaproteobacteria	Salmonella enterica subsp. arizonae serovar 18:z4,z23:-	hypothetical protein ASH63_21975, partial [Salmonella enterica subsp. arizonae serovar 18:z4,z23:-].	GCA_007194415.1
EBV9159081.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	620	ASA02_25470	Gammaproteobacteria	Salmonella enterica subsp. enterica serovar Alachua	hypothetical protein ASA02_25470, partial [Salmonella enterica subsp. enterica serovar Alachua].	GCA_007191635.1
EBV9391419.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	665	AUA09_21865	Gammaproteobacteria	Salmonella enterica subsp. arizonae serovar 18:z4,z23:-	hypothetical protein AUA09_21865, partial [Salmonella enterica subsp. arizonae serovar 18:z4,z23:-].	GCA_007194695.1
EBV9454977.1	TPR+GreAB-C*→	TPR+GreAB-C	257	AUA11_22355	Gammaproteobacteria	Salmonella enterica subsp. arizonae serovar 18:z4,z23:-	hypothetical protein AUA11_22355, partial [Salmonella enterica subsp. arizonae serovar 18:z4,z23:-].	GCA_007193095.1
EBV9865076.1	TPR+GreAB-C*→	TPR+GreAB-C	371	AUA58_21825	Gammaproteobacteria	Salmonella enterica subsp. arizonae serovar 18:z4,z23:-	hypothetical protein AUA58_21825, partial [Salmonella enterica subsp. arizonae serovar 18:z4,z23:-].	GCA_007194715.1
EBV9897412.1	TPR+GreAB-C*→	TPR+GreAB-C	379	AUA59_22385	Gammaproteobacteria	Salmonella enterica subsp. arizonae serovar 18:z4,z23:-	hypothetical protein AUA59_22385, partial [Salmonella enterica subsp. arizonae serovar 18:z4,z23:-].	GCA_007194855.1
EBW0217976.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1107	AUA78_22040	Gammaproteobacteria	Salmonella enterica subsp. arizonae serovar 18:z4,z23:-	hypothetical protein AUA78_22040 [Salmonella enterica subsp. arizonae serovar 18:z4,z23:-].	GCA_007204575.1
EBW0231167.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	990	AUA77_22025	Gammaproteobacteria	Salmonella enterica subsp. arizonae serovar 18:z4,z23:-	hypothetical protein AUA77_22025, partial [Salmonella enterica subsp. arizonae serovar 18:z4,z23:-].	GCA_007204595.1
EBW0678507.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	861	AR803_21985	Gammaproteobacteria	Salmonella enterica subsp. arizonae serovar 18:z4,z23:-	hypothetical protein AR803_21985, partial [Salmonella enterica subsp. arizonae serovar 18:z4,z23:-].	GCA_007197055.1
EBW5988048.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	813	AUB18_21995	Gammaproteobacteria	Salmonella enterica subsp. arizonae serovar 18:z4,z23:-	hypothetical protein AUB18_21995, partial [Salmonella enterica subsp. arizonae serovar 18:z4,z23:-].	GCA_007217995.1
EBW8169800.1	TPR+GreAB-C*→	TPR+GreAB-C	283	AUB36_22265	Gammaproteobacteria	Salmonella enterica subsp. arizonae serovar 18:z4,z23:-	hypothetical protein AUB36_22265, partial [Salmonella enterica subsp. arizonae serovar 18:z4,z23:-].	GCA_007226835.1
EBW9751630.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1106	DQR71_22645	Gammaproteobacteria	Salmonella enterica subsp. enterica serovar Kingston	hypothetical protein DQR71_22645 [Salmonella enterica subsp. enterica serovar Kingston].	GCA_007234155.1

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EBX0426906.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	864	DP854_08040	Gammaproteobacteria	Salmonella enterica subsp. enterica serovar Corvallis	hypothetical protein DP854_08040, partial [Salmonella enterica subsp. enterica serovar Corvallis].	GCA_007237735.1
EBX5460983.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	817	DSN29_17980	Gammaproteobacteria	Salmonella enterica subsp. enterica serovar Corvallis	hypothetical protein DSN29_17980, partial [Salmonella enterica subsp. enterica serovar Corvallis].	GCA_007257955.1
EBX5569113.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1106	DSN37_03170	Gammaproteobacteria	Salmonella enterica subsp. enterica serovar Kuessel	hypothetical protein DSN37_03170 [Salmonella enterica subsp. enterica serovar Kuessel].	GCA_007259425.1
EBX6009347.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1021	DSR61_24855	Gammaproteobacteria	Salmonella enterica subsp. enterica serovar Corvallis	hypothetical protein DSR61_24855, partial [Salmonella enterica subsp. enterica serovar Corvallis].	GCA_007258725.1
EBY0196060.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	991	DUP89_08940	Gammaproteobacteria	Salmonella enterica subsp. enterica serovar Corvallis	hypothetical protein DUP89_08940, partial [Salmonella enterica subsp. enterica serovar Corvallis].	GCA_007275795.1
EBY1533788.1	HetE-N1→?→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	775	DTD21_03800	Gammaproteobacteria	Salmonella enterica subsp. enterica serovar Mgulani	hypothetical protein DTD21_03800 [Salmonella enterica subsp. enterica serovar Mgulani].	GCA_007282305.1
EBY3547778.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	781	D4F04_22510	Gammaproteobacteria	Salmonella enterica subsp. enterica serovar Corvallis	hypothetical protein D4F04_22510, partial [Salmonella enterica subsp. enterica serovar Corvallis].	GCA_007290715.1
ECB7917957.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	841	E1365_23450	Gammaproteobacteria	Salmonella enterica subsp. enterica serovar Corvallis	hypothetical protein E1365_23450, partial [Salmonella enterica subsp. enterica serovar Corvallis].	GCA_007440385.1
ECC0701089.1	HetE-N1→?→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	815	FMV45_11650	Gammaproteobacteria	Salmonella enterica subsp. enterica serovar Mgulani	hypothetical protein FMV45_11650 [Salmonella enterica subsp. enterica serovar Mgulani].	GCA_007457195.1
ECC3303083.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	878	ACP91_22675	Gammaproteobacteria	Salmonella enterica subsp. arizonae	hypothetical protein ACP91_22675, partial [Salmonella enterica subsp. arizonae].	GCA_007472415.1
ECC9297450.1	TPR+GreAB-C+PIN*→?→||||<-Trypsin	TPR+GreAB-C+PIN	1011	DRF02_24595	Gammaproteobacteria	Salmonella enterica subsp. salamae	hypothetical protein DRF02_24595 [Salmonella enterica subsp. salamae].	GCA_007500125.1
ECE0143412.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	625	NC53_22885	Gammaproteobacteria	Salmonella enterica subsp. arizonae	hypothetical protein NC53_22885, partial [Salmonella enterica subsp. arizonae].	GCA_007547655.1
ECE0541238.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	879	ACK19_22505	Gammaproteobacteria	Salmonella enterica subsp. arizonae	hypothetical protein ACK19_22505, partial [Salmonella enterica subsp. arizonae].	GCA_007549055.1
ECE0545534.1	TPR+GreAB-C*→	TPR+GreAB-C	384	ACK84_23000	Gammaproteobacteria	Salmonella enterica subsp. arizonae	hypothetical protein ACK84_23000, partial [Salmonella enterica subsp. arizonae].	GCA_007549175.1
ECE0554408.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	669	ACK35_22635	Gammaproteobacteria	Salmonella enterica subsp. arizonae	hypothetical protein ACK35_22635, partial [Salmonella enterica subsp. arizonae].	GCA_007549195.1
ECE0554409.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	428	ACK35_22640	Gammaproteobacteria	Salmonella enterica subsp. arizonae	hypothetical protein ACK35_22640, partial [Salmonella enterica subsp. arizonae].	GCA_007549195.1
ECE1015908.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1116	AHY48_24995	Gammaproteobacteria	Salmonella enterica subsp. enterica	hypothetical protein AHY48_24995 [Salmonella enterica subsp. enterica].	GCA_007551035.1
ECF6862263.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	985	C702_18880	Gammaproteobacteria	Salmonella enterica subsp. enterica serovar Labadi	hypothetical protein C702_18880 [Salmonella enterica subsp. enterica serovar Labadi].	GCA_007627255.1
ECF7216075.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	985	ACL93_22670	Gammaproteobacteria	Salmonella enterica subsp. arizonae	hypothetical protein ACL93_22670, partial [Salmonella enterica subsp. arizonae].	GCA_007627105.1
ECF7535990.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	866	AF553_23825	Gammaproteobacteria	Salmonella enterica subsp. enterica	hypothetical protein AF553_23825, partial [Salmonella enterica subsp. enterica].	GCA_007629935.1
ECG8314709.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	967	E1871_22275	Gammaproteobacteria	Salmonella enterica subsp. enterica serovar Mgulani	hypothetical protein E1871_22275 [Salmonella enterica subsp. enterica serovar Mgulani].	GCA_007694365.1
ECH7956768.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	731	SW47_20185	Gammaproteobacteria	Salmonella enterica subsp. enterica	hypothetical protein SW47_20185, partial [Salmonella enterica subsp. enterica].	GCA_007742835.1
ECH9260474.1	HetE-N1→ TPR+GreAB-C+PIN→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	654	YR28_14840	Gammaproteobacteria	Salmonella enterica subsp. enterica	hypothetical protein YR28_14840 [Salmonella enterica subsp. enterica].	GCA_007749495.1

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ECI0362610.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	969	ACK10_22270	Gammaproteobacteria	Salmonella enterica subsp. arizonae	hypothetical protein ACK10_22270, partial [Salmonella enterica subsp. arizonae].	GCA_007755195.1
ECI0389037.1	TPR+GreAB-C*→	TPR+GreAB-C	376	ACL48_23155	Gammaproteobacteria	Salmonella enterica subsp. arizonae	hypothetical protein ACL48_23155, partial [Salmonella enterica subsp. arizonae].	GCA_007754635.1
ECI1216662.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	836	AF582_21855	Gammaproteobacteria	Salmonella enterica subsp. arizonae	hypothetical protein AF582_21855, partial [Salmonella enterica subsp. arizonae].	GCA_007758765.1
ECI5614625.1	HetE-N1→?→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	655	AHW94_03505	Gammaproteobacteria	Salmonella enterica subsp. enterica	hypothetical protein AHW94_03505, partial [Salmonella enterica subsp. enterica].	GCA_007777085.1
ECM8537065.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1117	YI35_19225	Gammaproteobacteria	Salmonella enterica subsp. enterica serovar Corvallis	hypothetical protein YI35_19225 [Salmonella enterica subsp. enterica serovar Corvallis].	GCA_008050935.1
ECS4963358.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	874	A9T74_22060	Gammaproteobacteria	Salmonella enterica subsp. arizonae serovar 18:z4,z23:-	hypothetical protein A9T74_22060, partial [Salmonella enterica subsp. arizonae serovar 18:z4,z23:-].	GCA_008426085.1
ECS5089259.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	688	A9T03_21360	Gammaproteobacteria	Salmonella enterica subsp. arizonae serovar 18:z4,z23:-	hypothetical protein A9T03_21360, partial [Salmonella enterica subsp. arizonae serovar 18:z4,z23:-].	GCA_008426245.1
ECS5722565.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	763	BEE21_21925	Gammaproteobacteria	Salmonella enterica	hypothetical protein BEE21_21925, partial [Salmonella enterica].	GCA_008427725.1
ECS7544753.1	HetE-N1→ TPR+GreAB-C+PIN*→?→||||<-Trypsin	TPR+GreAB-C+PIN	1121	CI474_11845	Gammaproteobacteria	Salmonella enterica subsp. enterica serovar Denver	hypothetical protein CI474_11845 [Salmonella enterica subsp. enterica serovar Denver].	GCA_008435705.1
ECU7350952.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	816	A9S02_22180	Gammaproteobacteria	Salmonella enterica subsp. enterica serovar Kentucky	hypothetical protein A9S02_22180, partial [Salmonella enterica subsp. enterica serovar Kentucky].	GCA_008522685.1
ECV0014755.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	672	C9G23_25520	Gammaproteobacteria	Salmonella enterica	hypothetical protein C9G23_25520 [Salmonella enterica].	GCA_008534115.1
ECX3800078.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	647	F6B58_20445	Gammaproteobacteria	Salmonella enterica	hypothetical protein F6B58_20445, partial [Salmonella enterica].	GCA_008659475.1
ECY0836069.1	MarR-HTH→||||<-PSE||PSE→||||<-?||?→?→||||<-?||?→ HetE-N1→ TPR+GreAB-C+PIN*→?→||||<-Trypsin	TPR+GreAB-C+PIN	1121	F6Y43_14905	Gammaproteobacteria	Salmonella enterica subsp. enterica	hypothetical protein F6Y43_14905 [Salmonella enterica subsp. enterica].	GCA_008716255.1
ECY8988972.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1117	F7L41_18095	Gammaproteobacteria	Salmonella enterica	hypothetical protein F7L41_18095 [Salmonella enterica].	GCA_008760695.1
ECZ2850292.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	736	F7T15_22920	Gammaproteobacteria	Salmonella enterica	hypothetical protein F7T15_22920, partial [Salmonella enterica].	GCA_008785865.1
EDA5083812.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	861	F9F62_19420	Gammaproteobacteria	Salmonella enterica	hypothetical protein F9F62_19420, partial [Salmonella enterica].	GCA_008860845.1
EDB4036569.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	810	A6J23_15240	Gammaproteobacteria	Salmonella enterica	hypothetical protein A6J23_15240, partial [Salmonella enterica].	GCA_008904195.1
EDB4763898.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	985	A8H08_23565	Gammaproteobacteria	Salmonella enterica subsp. enterica serovar Corvallis	hypothetical protein A8H08_23565 [Salmonella enterica subsp. enterica serovar Corvallis].	GCA_008907365.1
EDB6166846.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	994	BBD73_10015	Gammaproteobacteria	Salmonella enterica subsp. enterica serovar Corvallis	hypothetical protein BBD73_10015, partial [Salmonella enterica subsp. enterica serovar Corvallis].	GCA_008914005.1
EDN4259744.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	840	Y652_004461	Gammaproteobacteria	Salmonella enterica subsp. enterica	hypothetical protein Y652_004461, partial [Salmonella enterica subsp. enterica].	GCA_009997765.1
EDO1617810.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	838	CVA64_22730	Gammaproteobacteria	Salmonella enterica subsp. enterica serovar Molade	hypothetical protein CVA64_22730, partial [Salmonella enterica subsp. enterica serovar Molade].	GCA_010125745.1
EDP8916875.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	775	ZT80_004634	Gammaproteobacteria	Salmonella enterica subsp. enterica serovar Chailey	hypothetical protein ZT80_004634, partial [Salmonella enterica subsp. enterica serovar Chailey].	GCA_010369345.1

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EDP9779517.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	844	A9223_002456	Gammaproteobacteria	Salmonella enterica subsp. enterica serovar Alachua	hypothetical protein A9223_002456, partial [Salmonella enterica subsp. enterica serovar Alachua].	GCA_010373825.1
EDR2934822.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	754	KS39_001997	Gammaproteobacteria	Salmonella enterica subsp. enterica serovar Ruiru	hypothetical protein KS39_001997, partial [Salmonella enterica subsp. enterica serovar Ruiru].	GCA_010439595.1
EDR3921234.1	<-HTH<-?<-PSE||HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1101	BWC65_003323	Gammaproteobacteria	Salmonella enterica	hypothetical protein BWC65_003323 [Salmonella enterica].	GCA_010444135.1
EDR7156767.1	HetE-N1→ TPR+GreAB-C+PIN→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	457	GRJ98_004481	Gammaproteobacteria	Salmonella enterica	hypothetical protein GRJ98_004481 [Salmonella enterica].	GCA_010460165.1
EDR9691108.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	644	CSL67_004218	Gammaproteobacteria	Salmonella enterica subsp. arizonae	hypothetical protein CSL67_004218 [Salmonella enterica subsp. arizonae].	GCA_010471185.1
EDT9803200.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	828	GQ119_004456	Gammaproteobacteria	Salmonella enterica	hypothetical protein GQ119_004456, partial [Salmonella enterica].	GCA_010569565.1
EDU6324669.1	HetE-N1→ TPR+GreAB-C+PIN*→?→||||<-Trypsin	TPR+GreAB-C+PIN	1121	CAE39_004078	Gammaproteobacteria	Salmonella enterica subsp. enterica serovar Edinburgh	hypothetical protein CAE39_004078 [Salmonella enterica subsp. enterica serovar Edinburgh].	GCA_010619425.1
EDV9361828.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	870	QG02_001683	Gammaproteobacteria	Salmonella enterica subsp. enterica	hypothetical protein QG02_001683, partial [Salmonella enterica subsp. enterica].	GCA_010676285.1
EDW0654491.1	<-HTH<-?<-?||HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1106	JU54_004053	Gammaproteobacteria	Salmonella enterica subsp. enterica serovar Weslaco	hypothetical protein JU54_004053 [Salmonella enterica subsp. enterica serovar Weslaco].	GCA_010695505.1
EDW1854316.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1107	S887_003116	Gammaproteobacteria	Salmonella enterica subsp. diarizonae	hypothetical protein S887_003116 [Salmonella enterica subsp. diarizonae].	GCA_010701205.1
EDW7381411.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	838	CJF03_003360	Gammaproteobacteria	Salmonella enterica subsp. enterica serovar Alachua	hypothetical protein CJF03_003360, partial [Salmonella enterica subsp. enterica serovar Alachua].	GCA_010728605.1
EDX0815680.1	MarR-HTH→||||<-PSE||PSE→||||<-?||?→?→||||<-?||?→ HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1047	GTA77_003301	Gammaproteobacteria	Salmonella enterica subsp. enterica	hypothetical protein GTA77_003301, partial [Salmonella enterica subsp. enterica].	GCA_010745015.1
EDY1906151.1	MarR-HTH→||||<-PSE||PSE→||||<-?||?→?→||||<-?||?→ HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1043	GTA76_003216	Gammaproteobacteria	Salmonella enterica subsp. enterica	hypothetical protein GTA76_003216, partial [Salmonella enterica subsp. enterica].	GCA_010803285.1
EDY7338112.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	873	GRN59_004759	Gammaproteobacteria	Salmonella enterica subsp. enterica serovar Alachua	hypothetical protein GRN59_004759, partial [Salmonella enterica subsp. enterica serovar Alachua].	GCA_010827805.1
EDZ6443278.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	813	GOH01_21475	Gammaproteobacteria	Salmonella enterica	hypothetical protein GOH01_21475, partial [Salmonella enterica].	GCA_010859905.1
EED4174297.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	944	S577_12620	Gammaproteobacteria	Salmonella enterica subsp. enterica serovar Rubislaw	hypothetical protein S577_12620, partial [Salmonella enterica subsp. enterica serovar Rubislaw].	GCA_011083145.1
EEG2646873.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1117	GXG13_10075	Gammaproteobacteria	Salmonella enterica	hypothetical protein GXG13_10075 [Salmonella enterica].	GCA_011218655.1
EEH6562392.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	561	G9D83_004649	Gammaproteobacteria	Salmonella enterica	hypothetical protein G9D83_004649, partial [Salmonella enterica].	GCA_011296115.1
EEH8607740.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	751	GXG09_15375	Gammaproteobacteria	Salmonella enterica	hypothetical protein GXG09_15375, partial [Salmonella enterica].	GCA_011310075.1
EEI7790049.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1003	G7421_004640	Gammaproteobacteria	Salmonella enterica	hypothetical protein G7421_004640, partial [Salmonella enterica].	GCA_011384105.1
EEJ3916542.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	931	C1D58_004804	Gammaproteobacteria	Salmonella enterica subsp. enterica serovar Waral	hypothetical protein C1D58_004804, partial [Salmonella enterica subsp. enterica serovar Waral].	GCA_011421105.1
EEJ8590178.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1106	YR33_002856	Gammaproteobacteria	Salmonella enterica subsp. enterica	hypothetical protein YR33_002856 [Salmonella enterica subsp. enterica].	GCA_011444435.1

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EEM3099552.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	837	C7106_19315	Gammaproteobacteria	Salmonella enterica subsp. enterica serovar Corvallis	hypothetical protein C7106_19315, partial [Salmonella enterica subsp. enterica serovar Corvallis].	GCA_011562745.1
EEN9063089.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1003	G5014_004598	Gammaproteobacteria	Salmonella enterica subsp. enterica	hypothetical protein G5014_004598, partial [Salmonella enterica subsp. enterica].	GCA_011642815.1
EEO4791769.1	GreAB-C*→	GreAB-C	475	GCV36_004805	Gammaproteobacteria	Salmonella enterica	hypothetical protein GCV36_004805, partial [Salmonella enterica].	GCA_011672825.1
EEP6626700.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1098	HB923_004453	Gammaproteobacteria	Salmonella enterica	hypothetical protein HB923_004453, partial [Salmonella enterica].	GCA_011737335.1
EEQ0870631.1	GreAB-C*→	GreAB-C	401	HC115_004664	Gammaproteobacteria	Salmonella enterica subsp. enterica serovar Corvallis	hypothetical protein HC115_004664, partial [Salmonella enterica subsp. enterica serovar Corvallis].	GCA_011766905.1
EER8058271.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1094	F0645_003838	Gammaproteobacteria	Escherichia coli	hypothetical protein F0645_003838 [Escherichia coli].	GCA_011871345.1
EES4613658.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1094	EZQ25_003302	Gammaproteobacteria	Escherichia coli	hypothetical protein EZQ25_003302 [Escherichia coli].	GCA_011897605.1
EEU6346619.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	663	HES36_004810	Gammaproteobacteria	Salmonella enterica	hypothetical protein HES36_004810, partial [Salmonella enterica].	GCA_011985205.1
EEU8409948.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	733	HDI19_004538	Gammaproteobacteria	Salmonella enterica	hypothetical protein HDI19_004538, partial [Salmonella enterica].	GCA_012002765.1
EEU8431734.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	770	HDI14_004564	Gammaproteobacteria	Salmonella enterica	hypothetical protein HDI14_004564, partial [Salmonella enterica].	GCA_012002965.1
EEU8450206.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	686	HDI09_004415	Gammaproteobacteria	Salmonella enterica	hypothetical protein HDI09_004415, partial [Salmonella enterica].	GCA_012003165.1
EEU8461067.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	777	HDI12_003619	Gammaproteobacteria	Salmonella enterica	hypothetical protein HDI12_003619, partial [Salmonella enterica].	GCA_012003025.1
EEU8472241.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	832	HDI08_003001	Gammaproteobacteria	Salmonella enterica	hypothetical protein HDI08_003001, partial [Salmonella enterica].	GCA_012003185.1
EEU8646489.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	746	HDI02_002414	Gammaproteobacteria	Salmonella enterica	hypothetical protein HDI02_002414, partial [Salmonella enterica].	GCA_012004065.1
EEV5892122.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1094	ELJ91_00185	Gammaproteobacteria	Escherichia coli	hypothetical protein ELJ91_00185 [Escherichia coli].	GCA_012046565.1
EEW2250301.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	649	D9F29_22745	Gammaproteobacteria	Escherichia coli	hypothetical protein D9F29_22745, partial [Escherichia coli].	GCA_012074905.1
EEW6232025.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1025	D7V76_23725	Gammaproteobacteria	Escherichia coli	hypothetical protein D7V76_23725, partial [Escherichia coli].	GCA_012087875.1
EEZ4464859.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1009	DED50_002664	Gammaproteobacteria	Escherichia coli	hypothetical protein DED50_002664, partial [Escherichia coli].	GCA_012207825.1
EFA5448049.1	GreAB-C*→	GreAB-C	270	EZF43_26870	Gammaproteobacteria	Escherichia coli	hypothetical protein EZF43_26870, partial [Escherichia coli].	GCA_012252965.1
EFB4141030.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	803	C0X77_005316	Gammaproteobacteria	Escherichia coli O88:H1	hypothetical protein C0X77_005316, partial [Escherichia coli O88:H1].	GCA_012307025.1
EFB7592548.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	871	E4J78_25685	Gammaproteobacteria	Escherichia coli	hypothetical protein E4J78_25685, partial [Escherichia coli].	GCA_012318985.1
EFD6843528.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	785	HG348_004580	Gammaproteobacteria	Salmonella enterica subsp. enterica serovar Corvallis	hypothetical protein HG348_004580, partial [Salmonella enterica subsp. enterica serovar Corvallis].	GCA_012407905.1
EFD8840406.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	342	CO273_005362	Gammaproteobacteria	Escherichia coli	hypothetical protein CO273_005362, partial [Escherichia coli].	GCA_012416985.1
EFE7110517.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	631	GCY86_26975	Gammaproteobacteria	Escherichia coli	hypothetical protein GCY86_26975, partial [Escherichia coli].	GCA_012449745.1

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EFE7435055.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	917	F9S89_16525	Gammaproteobacteria	Escherichia coli	hypothetical protein F9S89_16525, partial [Escherichia coli].	GCA_012452135.1
EFE7908555.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1007	F3644_26165	Gammaproteobacteria	Escherichia coli	hypothetical protein F3644_26165, partial [Escherichia coli].	GCA_012454005.1
EFF2139424.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	639	B9T00_004906	Gammaproteobacteria	Escherichia coli	hypothetical protein B9T00_004906, partial [Escherichia coli].	GCA_012475085.1
EFG3018646.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	644	BOZ88_000259	Gammaproteobacteria	Escherichia coli	hypothetical protein BOZ88_000259, partial [Escherichia coli].	GCA_012551215.1
EFG6909290.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	747	BMM73_004701	Gammaproteobacteria	Escherichia coli	hypothetical protein BMM73_004701, partial [Escherichia coli].	GCA_012567505.1
EFH5729117.1	GreAB-C*→	GreAB-C	499	GPH08_24725	Gammaproteobacteria	Escherichia coli	hypothetical protein GPH08_24725, partial [Escherichia coli].	GCA_012607235.1
EFK2051151.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1094	A8650_000222	Gammaproteobacteria	Escherichia coli	hypothetical protein A8650_000222 [Escherichia coli].	GCA_012745335.1
EFK2630094.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1094	A8611_000403	Gammaproteobacteria	Escherichia coli	hypothetical protein A8611_000403 [Escherichia coli].	GCA_012750705.1
EFK4277858.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1094	A8W36_000742	Gammaproteobacteria	Escherichia coli	hypothetical protein A8W36_000742 [Escherichia coli].	GCA_012757595.1
EFK5336626.1	GreAB-C*→	GreAB-C	296	G5Y50_005070	Gammaproteobacteria	Escherichia coli	hypothetical protein G5Y50_005070, partial [Escherichia coli].	GCA_012762195.1
EFM2410662.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1064	HCP88_003534	Gammaproteobacteria	Escherichia coli	hypothetical protein HCP88_003534, partial [Escherichia coli].	GCA_012855135.1
EFM6245585.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1094	G8G69_000691	Gammaproteobacteria	Escherichia coli	hypothetical protein G8G69_000691 [Escherichia coli].	GCA_012890895.1
EFN7425919.1	HetE-N1→ HetE-N1+TPR+GreAB-C+PIN*→	HetE-N1+TPR+GreAB-C+PIN	1094	EHR20_13780	Gammaproteobacteria	Escherichia coli	hypothetical protein EHR20_13780 [Escherichia coli].	GCA_013040925.1
EFO0890621.1	GreAB-C*→	GreAB-C	328	DYJ49_27190	Gammaproteobacteria	Escherichia coli	hypothetical protein DYJ49_27190, partial [Escherichia coli].	GCA_013061045.1
EFO1176558.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1073	DW520_17505	Gammaproteobacteria	Escherichia coli	hypothetical protein DW520_17505, partial [Escherichia coli].	GCA_013062025.1
EFS2240967.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1094	GTJ56_01995	Gammaproteobacteria	Shigella sonnei	hypothetical protein GTJ56_01995 [Shigella sonnei].	GCA_013627075.1
EFT8083545.1	<-HTH<-PSE||HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1107	HVC06_002423	Gammaproteobacteria	Salmonella enterica	hypothetical protein HVC06_002423 [Salmonella enterica].	GCA_013717865.1
EFU7164914.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1012	HTZ39_004610	Gammaproteobacteria	Escherichia coli	hypothetical protein HTZ39_004610, partial [Escherichia coli].	GCA_013766175.1
EFW2864166.1	TPR+GreAB-C*→	TPR+GreAB-C	440	H3T30_004508	Gammaproteobacteria	Salmonella enterica	hypothetical protein H3T30_004508, partial [Salmonella enterica].	GCA_013859415.1
EFZ7349264.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1094	A8I24_003489	Gammaproteobacteria	Shigella sonnei	hypothetical protein A8I24_003489 [Shigella sonnei].	GCA_014033075.1
EGB9339943.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	694	H8Q22_004544	Gammaproteobacteria	Salmonella enterica	hypothetical protein H8Q22_004544, partial [Salmonella enterica].	GCA_014249275.1
EGF6340579.1	GreAB-C*→	GreAB-C	417	IBT07_004591	Gammaproteobacteria	Salmonella enterica subsp. enterica serovar Molade	hypothetical protein IBT07_004591, partial [Salmonella enterica subsp. enterica serovar Molade].	GCA_014515725.1
EGG4494193.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	990	HKL61_004648	Gammaproteobacteria	Salmonella enterica	hypothetical protein HKL61_004648, partial [Salmonella enterica].	GCA_014566815.1
EGG4638401.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	777	HKL37_003624	Gammaproteobacteria	Salmonella enterica	hypothetical protein HKL37_003624, partial [Salmonella enterica].	GCA_014566995.1
EGG4725781.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	855	HKE56_003805	Gammaproteobacteria	Salmonella enterica	hypothetical protein HKE56_003805, partial [Salmonella enterica].	GCA_014566275.1

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<tr><td>EGS2470077.1</td><td>HetE-N1→ TPR+GreAB-C+PIN*→</td><td>TPR+GreAB-C+PIN</td><td>1117</td><td>I8K59_003334</td><td>Gammaproteobacteria</td><td>Salmonella enterica</td><td>hypothetical protein I8K59_003334 [Salmonella enterica].</td><td>GCA_015867645.1</td></tr>
<tr><td>EGS6048781.1</td><td>HetE-N1→ TPR+GreAB-C+PIN*→</td><td>TPR+GreAB-C+PIN</td><td>998</td><td>I4Y87_004789</td><td>Gammaproteobacteria</td><td>Salmonella enterica subsp. enterica serovar Alachua</td><td>hypothetical protein I4Y87_004789, partial [Salmonella enterica subsp. enterica serovar Alachua].</td><td>GCA_015906765.1</td></tr>
<tr><td>EGT0637485.1</td><td>GreAB-C*→</td><td>GreAB-C</td><td>478</td><td>JAG24_004773</td><td>Gammaproteobacteria</td><td>Citrobacter freundii</td><td>hypothetical protein JAG24_004773, partial [Citrobacter freundii].</td><td>GCA_015943305.1</td></tr>
<tr><td>EGT3640898.1</td><td>TPR+GreAB-C+PIN*→</td><td>TPR+GreAB-C+PIN</td><td>1067</td><td>DFW15_03700</td><td>Firmicutes</td><td>Clostridioides difficile</td><td>hypothetical protein DFW15_03700 [Clostridioides difficile].</td><td>GCA_016071215.1</td></tr>
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<tr><td>EHA1126835.1</td><td>HetE-N1→ TPR+GreAB-C+PIN*→</td><td>TPR+GreAB-C+PIN</td><td>1114</td><td>FG475_17175</td><td>Gammaproteobacteria</td><td>Vibrio navarrensis</td><td>hypothetical protein FG475_17175 [Vibrio navarrensis].</td><td>GCA_016611225.1</td></tr>
<tr><td>EHB5819355.1</td><td>HetE-N1→ TPR+GreAB-C+PIN*→</td><td>TPR+GreAB-C+PIN</td><td>1106</td><td>JXL86_002072</td><td>-</td><td>Enterobacter hormaechei</td><td>hypothetical protein JXL86_002072 [Enterobacter hormaechei].</td><td>GCA_016985635.1</td></tr>
<tr><td>EHB7585965.1</td><td>HetE-N1→ TPR+GreAB-C+PIN*→</td><td>TPR+GreAB-C+PIN</td><td>759</td><td>JV429_000621</td><td>Gammaproteobacteria</td><td>Escherichia coli</td><td>hypothetical protein JV429_000621, partial [Escherichia coli].</td><td>GCA_017003995.1</td></tr>
<tr><td>EHB7691780.1</td><td>TPR+GreAB-C+PIN*→</td><td>TPR+GreAB-C+PIN</td><td>745</td><td>JV466_004427</td><td>Gammaproteobacteria</td><td>Escherichia coli</td><td>hypothetical protein JV466_004427, partial [Escherichia coli].</td><td>GCA_017004675.1</td></tr>
<tr><td>EHC1615065.1</td><td>TPR+GreAB-C+PIN*→</td><td>TPR+GreAB-C+PIN</td><td>732</td><td>JT622_005238</td><td>Gammaproteobacteria</td><td>Escherichia coli</td><td>hypothetical protein JT622_005238, partial [Escherichia coli].</td><td>GCA_017029715.1</td></tr>
<tr><td>EHD4655635.1</td><td>HetE-N1→ TPR+GreAB-C+PIN*→</td><td>TPR+GreAB-C+PIN</td><td>807</td><td>JRB69_003203</td><td>Gammaproteobacteria</td><td>Salmonella enterica</td><td>hypothetical protein JRB69_003203, partial [Salmonella enterica].</td><td>GCA_017143955.1</td></tr>
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EHD4703897.1	GreAB-C*→	GreAB-C	419	JRB68_004676	Gammaproteobacteria	Salmonella enterica	hypothetical protein JRB68_004676, partial [Salmonella enterica].	GCA_017144295.1
EHD5811550.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	628	JQZ13_004415	Gammaproteobacteria	Escherichia coli	hypothetical protein JQZ13_004415, partial [Escherichia coli].	GCA_017158335.1
EHD6029608.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1085	JQ325_002365	Gammaproteobacteria	Vibrio parahaemolyticus	hypothetical protein JQ325_002365 [Vibrio parahaemolyticus].	GCA_017160295.1
EHF0016324.1	?*→	?	690	IFX66_005031	Gammaproteobacteria	Escherichia coli	hypothetical protein IFX66_005031, partial [Escherichia coli].	GCA_017278275.1
EHG1523212.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1001	J1L78_003684	Gammaproteobacteria	Salmonella enterica subsp. enterica serovar Corvallis	hypothetical protein J1L78_003684, partial [Salmonella enterica subsp. enterica serovar Corvallis].	GCA_017373035.1
EHG6154572.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1094	J5T29_002362	Gammaproteobacteria	Escherichia fergusonii	hypothetical protein J5T29_002362 [Escherichia fergusonii].	GCA_017528445.1
EHG8446233.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1106	J6D68_002379	Gammaproteobacteria	Salmonella enterica subsp. enterica	hypothetical protein J6D68_002379 [Salmonella enterica subsp. enterica].	GCA_017573985.1
EHH5222655.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	630	J6876_004216	Gammaproteobacteria	Escherichia coli	hypothetical protein J6876_004216, partial [Escherichia coli].	GCA_017685995.1
EHH5972888.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1039	J8O14_004858	Gammaproteobacteria	Salmonella enterica subsp. enterica serovar Alachua	hypothetical protein J8O14_004858, partial [Salmonella enterica subsp. enterica serovar Alachua].	GCA_017690295.1
EHH6676921.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1094	J6H48_001187	Gammaproteobacteria	Escherichia coli	hypothetical protein J6H48_001187 [Escherichia coli].	GCA_017723775.1
EHH7564006.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1015	J5J30_004554	Gammaproteobacteria	Escherichia coli	hypothetical protein J5J30_004554, partial [Escherichia coli].	GCA_017727775.1
EHH7810630.1	GreAB-C*→	GreAB-C	318	J5B41_005221	Gammaproteobacteria	Escherichia coli	hypothetical protein J5B41_005221, partial [Escherichia coli].	GCA_017733975.1
EHI0937798.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	636	J1A00_004749	Gammaproteobacteria	Escherichia coli	hypothetical protein J1A00_004749, partial [Escherichia coli].	GCA_017780845.1
EHI2008363.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	694	J9U59_004724	Gammaproteobacteria	Salmonella enterica	hypothetical protein J9U59_004724, partial [Salmonella enterica].	GCA_017791685.1
EHI3384480.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	747	J9U04_004755	Gammaproteobacteria	Salmonella enterica	hypothetical protein J9U04_004755, partial [Salmonella enterica].	GCA_017798465.1
EHI3712656.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	723	J9T76_004561	Gammaproteobacteria	Salmonella enterica	hypothetical protein J9T76_004561, partial [Salmonella enterica].	GCA_017800075.1
EHI5184709.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	999	J9014_004542	Gammaproteobacteria	Salmonella enterica	hypothetical protein J9014_004542, partial [Salmonella enterica].	GCA_017806615.1
EHI6070991.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	984	J9J70_003931	Gammaproteobacteria	Salmonella enterica	hypothetical protein J9J70_003931, partial [Salmonella enterica].	GCA_017810795.1
EHI8244355.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	784	J9M94_004032	Gammaproteobacteria	Salmonella enterica	hypothetical protein J9M94_004032, partial [Salmonella enterica].	GCA_017828575.1
EHI9713257.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	735	J9T07_004736	Gammaproteobacteria	Salmonella enterica	hypothetical protein J9T07_004736, partial [Salmonella enterica].	GCA_017836875.1
EHJ6284301.1	<-HTH<-?<-PSE||HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1106	KAM53_001182	Gammaproteobacteria	Salmonella enterica	hypothetical protein KAM53_001182 [Salmonella enterica].	GCA_017922215.1
EHJ8153220.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	707	KB264_004740	Gammaproteobacteria	Escherichia coli	hypothetical protein KB264_004740, partial [Escherichia coli].	GCA_017943665.1
EHJ9993052.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1085	KB972_002278	Gammaproteobacteria	Vibrio parahaemolyticus	hypothetical protein KB972_002278 [Vibrio parahaemolyticus].	GCA_017968025.1
EHK2882579.1	HetE-N1→ HetE-N1+TPR+GreAB-C+PIN*→	HetE-N1+TPR+GreAB-C+PIN	1091	J7H88_002175	Gammaproteobacteria	Vibrio parahaemolyticus	hypothetical protein J7H88_002175 [Vibrio parahaemolyticus].	GCA_018017275.1
EHL5831134.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1117	KEB97_001561	Gammaproteobacteria	Salmonella enterica	hypothetical protein KEB97_001561 [Salmonella enterica].	GCA_018132225.1

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EKD28835.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1282	ACD_79C00188G0006	environmental samples	uncultured bacterium	MAG: hypothetical protein ACD_79C00188G0006 [uncultured bacterium].	GCA_000299275.1
EKM26807.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1091	VCHENC03_4410	Gammaproteobacteria	Vibrio sp. HENC-03	hypothetical protein VCHENC03_4410 [Vibrio sp. HENC-03].	GCA_000305755.2
ENE18425.1	GreAB-C*→	GreAB-C	334	ECP03047993_5652	Gammaproteobacteria	Escherichia coli P0304799.3	hypothetical protein ECP03047993_5652, partial [Escherichia coli P0304799.3].	GCA_000357685.2
ENV19736.1	HetE-N1→?→?→ GreAB-C+PIN*→	GreAB-C+PIN	553	F963_04374	Gammaproteobacteria	Acinetobacter bereziniae NIPH 3	hypothetical protein F963_04374 [Acinetobacter bereziniae NIPH 3].	GCA_000368505.1
EOS47428.1	HNH→?→?→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1071	C809_02304	Firmicutes	Lachnospiraceae bacterium MD335	hypothetical protein C809_02304 [Lachnospiraceae bacterium MD335].	GCA_000403335.2
ERS81691.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	480	Q672_10295	Gammaproteobacteria	Marinobacter sp. EVN1	hypothetical protein Q672_10295 [Marinobacter sp. EVN1].	GCA_000475375.1
ERU60319.1	DOC+HTH→ REase+TOPC→?→ HetE-N1→ HetE-N1+TPR+GreAB-C+PIN*→	HetE-N1+TPR+GreAB-C+PIN	1126	Q088_04776	Gammaproteobacteria	Pseudomonas aeruginosa C41	hypothetical protein Q088_04776 [Pseudomonas aeruginosa C41].	GCA_000480455.1
ETK41841.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1486	H098_09645	Gammaproteobacteria	Pseudomonas fluorescens FH5	hypothetical protein H098_09645 [Pseudomonas fluorescens FH5].	GCA_000511155.2
EWS54147.1	REase+TPR→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1054	X551_03051	Betaproteobacteria	Methylibium sp. T29	hypothetical protein X551_03051 [Methylibium sp. T29].	GCA_000576205.1
EXI84113.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1363	AW11_03978	Betaproteobacteria	Candidatus Accumulibacter sp. BA-93	MAG: hypothetical protein AW11_03978 [Candidatus Accumulibacter sp. BA-93].	GCA_000585075.1
EXU80592.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1391	AX13_15135	Betaproteobacteria	Comamonas aquatica DA1877	hypothetical protein AX13_15135 [Comamonas aquatica DA1877].	GCA_000590985.1
GAC55419.1	TPR+PIN*→	TPR+PIN	1183	GOAMI_53_00020	Actinobacteria	Gordonia amicalis NBRC 100051 = JCM 11271	hypothetical protein GOAMI_53_00020 [Gordonia amicalis NBRC 100051 = JCM 11271].	GCA_000332995.1
GAF05793.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	524	JCM21142_104546	Bacteroidetes	Saccharicrinis fermentans DSM 9555 = JCM 21142	hypothetical protein JCM21142_104546 [Saccharicrinis fermentans DSM 9555 = JCM 21142].	GCA_000583675.1
GBF59066.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1327	bepA_7	Alphaproteobacteria	Candidatus Phycosocius bacilliformis	beta-barrel assembly-enhancing protease [Candidatus Phycosocius bacilliformis].	GCA_003112735.1
GBH08795.1	HetE-N1→||||<-?||HetE-N1+TPR+GreAB-C+PIN→||||<-?<-?||TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	953	KPSA1_02176	Gammaproteobacteria	Pseudomonas syringae pv. actinidiae	ATP-dependent exoDNAse beta subunit [Pseudomonas syringae pv. actinidiae].	GCA_003202975.1
GBH17945.1	REase+TPR+GreAB-C+PIN*→?→ REase+nSTAND3→ REase+nSTAND3→	REase+TPR+GreAB-C+PIN	1491	KPSA3_03922	Gammaproteobacteria	Pseudomonas syringae pv. actinidiae	Tetratricopeptide repeat [Pseudomonas syringae pv. actinidiae].	GCA_003202995.1
GBU16512.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1107	AwMethylo_07270	Alphaproteobacteria	Methylobacterium sp.	hypothetical protein AwMethylo_07270 [Methylobacterium sp.].	GCA_003864615.1
GCL65539.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1455	AQPW35_46200	Betaproteobacteria	Aquabacterium pictum	hypothetical protein AQPW35_46200 [Aquabacterium pictum].	GCA_005403045.1
GCM29814.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	622	ExPECSC050_01644	Gammaproteobacteria	Escherichia coli	hypothetical protein ExPECSC050_01644 [Escherichia coli].	GCA_005383045.1
GFJ77328.1	TM+TPR+PIN*→ REase→	TM+TPR+PIN	1362	Phou_015080	Actinobacteria	Phytohabitans houttuyneae	hypothetical protein Phou_015080 [Phytohabitans houttuyneae].	GCA_011764425.1
GGJ71040.1	TPR+PIN*→	TPR+PIN	1223	GCM10012282_79870	Actinobacteria	Streptomyces lacrimifluminis	hypothetical protein GCM10012282_79870 [Streptomyces lacrimifluminis].	GCA_014646095.1
GGK48292.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1120	GCM10009103_48460	Gammaproteobacteria	Pseudomonas koreensis	hypothetical protein GCM10009103_48460 [Pseudomonas koreensis].	GCA_014646955.1
GGR17482.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1357	GCM10008957_32760	Deinococci	Deinococcus ruber	hypothetical protein GCM10008957_32760 [Deinococcus ruber].	GCA_014648095.1
GGZ02836.1	HetE-N1→?→ GreAB-C*→	GreAB-C	451	GCM10007169_19550	Gammaproteobacteria	Shewanella fodinae	hypothetical protein GCM10007169_19550 [Shewanella fodinae].	GCA_014651955.1
GHB08256.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1025	GCM10007107_21780	Gammaproteobacteria	Shewanella indica	hypothetical protein GCM10007107_21780 [Shewanella indica].	GCA_014652115.1

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GIE51569.1	TPR+PIN→?→?→ PIN*→||||<-?<-?||AbiJ-NTD3+REase→	PIN	177	Ani05nite_51030	Actinobacteria	Actinoplanes nipponensis	hypothetical protein Ani05nite_51030 [Actinoplanes nipponensis].	GCA_016862275.1
GIG67348.1	TM+TPR+PIN*→	TM+TPR+PIN	1072	Pen01_36430	Actinobacteria	Phytomonospora endophytica	hypothetical protein Pen01_36430 [Phytomonospora endophytica].	GCA_016862855.1
GIJ10564.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1377	Van01_37780	Actinobacteria	Micromonospora andamanensis	hypothetical protein Van01_37780 [Micromonospora andamanensis].	GCA_016863495.1
GIM80122.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1253	Aau02nite_89080	Actinobacteria	Actinoplanes auranticolor	hypothetical protein Aau02nite_89080 [Actinoplanes auranticolor].	GCA_018332655.1
GIM97804.1	TPR+PIN*→	TPR+PIN	1137	Ato02nite_095970	Actinobacteria	Actinoplanes toevensis	hypothetical protein Ato02nite_095970 [Actinoplanes toevensis].	GCA_018332695.1
HAF5476147.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1117	G8A91_001303	Gammaproteobacteria	Salmonella enterica	TPA: hypothetical protein G8A91_001303 [Salmonella enterica].	GCA_011304215.1
HAH9826030.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	986	HIF24_22945	Gammaproteobacteria	Escherichia coli	TPA: hypothetical protein HIF24_22945, partial [Escherichia coli].	GCA_012753875.1
HAK4911912.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1117	H2B38_003821	Gammaproteobacteria	Salmonella enterica	TPA: hypothetical protein H2B38_003821 [Salmonella enterica].	GCA_013572415.1
HAK9873068.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1028	H3L74_004566	Gammaproteobacteria	Escherichia coli	TPA: hypothetical protein H3L74_004566, partial [Escherichia coli].	GCA_013794255.1
HAL9130497.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1094	H7U58_003240	Gammaproteobacteria	Escherichia coli	TPA: hypothetical protein H7U58_003240 [Escherichia coli].	GCA_014184975.1
HAL9453557.1	GreAB-C*→	GreAB-C	337	H7V29_005028	Gammaproteobacteria	Escherichia coli	TPA: hypothetical protein H7V29_005028, partial [Escherichia coli].	GCA_014186535.1
HAM4053647.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1094	IBV36_002404	Gammaproteobacteria	Escherichia coli	TPA: hypothetical protein IBV36_002404 [Escherichia coli].	GCA_014461175.1
HAM8943229.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	618	IDX96_004717	Gammaproteobacteria	Escherichia coli	TPA: hypothetical protein IDX96_004717, partial [Escherichia coli].	GCA_014571125.1
HAM8943373.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	474	IDX96_004882	Gammaproteobacteria	Escherichia coli	TPA: hypothetical protein IDX96_004882, partial [Escherichia coli].	GCA_014571125.1
HAM8966916.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1094	IDX85_003830	Gammaproteobacteria	Escherichia coli	TPA: hypothetical protein IDX85_003830 [Escherichia coli].	GCA_014573095.1
HAM8991159.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1094	IDX80_003853	Gammaproteobacteria	Escherichia coli	TPA: hypothetical protein IDX80_003853 [Escherichia coli].	GCA_014573135.1
HAN3697638.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1050	IE973_004718	Gammaproteobacteria	Escherichia coli	TPA: hypothetical protein IE973_004718, partial [Escherichia coli].	GCA_014687295.1
HAN4834938.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1094	IFD90_003495	Gammaproteobacteria	Escherichia coli	TPA: hypothetical protein IFD90_003495 [Escherichia coli].	GCA_014683685.1
HAN6118733.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1094	IFZ61_002838	Gammaproteobacteria	Escherichia coli	TPA: hypothetical protein IFZ61_002838 [Escherichia coli].	GCA_014708655.1
HAN7634134.1	GreAB-C*→	GreAB-C	447	IF647_005249	Gammaproteobacteria	Escherichia coli	TPA: hypothetical protein IF647_005249, partial [Escherichia coli].	GCA_014724455.1
HAO1938999.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1094	IHJ42_000411	Gammaproteobacteria	Escherichia coli	TPA: hypothetical protein IHJ42_000411 [Escherichia coli].	GCA_014815885.1
HAS1413650.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	845	I4D28_09180	Gammaproteobacteria	Enterobacter hormaechei	TPA: hypothetical protein I4D28_09180 [Enterobacter hormaechei].	-
HAT2286137.1	HetE-N1→ TPR+GreAB-C+PIN+TM+TM*→	TPR+GreAB-C+PIN+TM+TM	1106	I8156_002891	Gammaproteobacteria	Citrobacter freundii	TPA: hypothetical protein I8156_002891 [Citrobacter freundii].	GCA_015897485.1
HAT3687084.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	958	I8574_002665	Gammaproteobacteria	Citrobacter freundii	TPA: hypothetical protein I8574_002665, partial [Citrobacter freundii].	GCA_015902705.1
HAT3994325.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1131	I9Y74_003743	Bacteroidetes	Elizabethkingia anophelis	TPA: hypothetical protein I9Y74_003743 [Elizabethkingia anophelis].	GCA_015930145.1
HAT8488811.1	HetE-N1→ HetE-N1+TPR+GreAB-C+PIN*→	HetE-N1+TPR+GreAB-C+PIN	1088	I7187_21710	Gammaproteobacteria	Vibrio vulnificus	TPA: hypothetical protein I7187_21710 [Vibrio vulnificus].	GCA_015968635.1

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HAU8300026.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1130	I7159_21955	Gammaproteobacteria	Vibrio vulnificus	TPA: hypothetical protein I7159_21955 [Vibrio vulnificus].	GCA_016110185.1
HAU9261412.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1094	JEX66_004253	Gammaproteobacteria	Escherichia coli	TPA: hypothetical protein JEX66_004253 [Escherichia coli].	GCA_016116905.1
HAV13598.1	GreAB*→	GreAB	620	DCX06_08945	Verrucomicrobia	Opitutae bacterium	MAG TPA: transcription elongation factor GreAB [Opitutae bacterium].	GCA_003485085.1
HAV1378302.1	HetE-N1→ NACHT+GreAB-C+PIN*→	NACHT+GreAB-C+PIN	1085	JG804_003376	Gammaproteobacteria	Vibrio parahaemolyticus	TPA: hypothetical protein JG804_003376 [Vibrio parahaemolyticus].	GCA_016429865.1
HAV1873259.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	742	JG951_004564	Gammaproteobacteria	Enterobacter hormaechei subsp. steigerwaltii	TPA: hypothetical protein JG951_004564, partial [Enterobacter hormaechei subsp. steigerwaltii].	GCA_016431145.1
HAV7695504.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1094	JK751_001166	Gammaproteobacteria	Escherichia coli	TPA: hypothetical protein JK751_001166 [Escherichia coli].	GCA_016656125.1
HAV9376548.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	575	JLF84_000973	Gammaproteobacteria	Escherichia coli	TPA: hypothetical protein JLF84_000973 [Escherichia coli].	GCA_016665225.1
HAW2926691.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1094	JLR28_003506	Gammaproteobacteria	Escherichia coli	TPA: hypothetical protein JLR28_003506 [Escherichia coli].	GCA_016681635.1
HAW5283885.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1094	JLY51_001282	Gammaproteobacteria	Escherichia coli	TPA: hypothetical protein JLY51_001282 [Escherichia coli].	GCA_016693495.1
HAW6997627.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1250	JIR16_12805	Gammaproteobacteria	Acinetobacter baumannii	TPA: hypothetical protein JIR16_12805 [Acinetobacter baumannii].	GCA_016844125.1
HAY34439.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1108	DCY06_09910	Bacteroidetes	Bacteroidetes bacterium	MAG TPA: hypothetical protein DCY06_09910 [Bacteroidetes bacterium].	GCA_003486905.1
HBA3776861.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1117	J5F89_004850	Gammaproteobacteria	Escherichia coli	TPA: hypothetical protein J5F89_004850 [Escherichia coli].	GCA_017730375.1
HBC0128974.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	661	JES91_004961	Gammaproteobacteria	Salmonella enterica subsp. enterica	TPA: hypothetical protein JES91_004961, partial [Salmonella enterica subsp. enterica].	GCA_018032925.1
HBC3987585.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1130	KD867_004179	Gammaproteobacteria	Vibrio parahaemolyticus	TPA: hypothetical protein KD867_004179 [Vibrio parahaemolyticus].	GCA_018126825.1
HBJ33554.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	857	DDZ51_02100	Planctomycetes	Planctomycetaceae bacterium	MAG TPA: hypothetical protein DDZ51_02100, partial [Planctomycetaceae bacterium].	GCA_003506095.1
HBX77020.1	X+PIN*→	X+PIN	940	DEG43_05200	Actinobacteria	Acidimicrobiaceae bacterium	MAG TPA: hypothetical protein DEG43_05200 [Acidimicrobiaceae bacterium].	GCA_003514205.1
HCD05045.1	HetE-N1→?→ TPR+GreAB-C+PIN*→||||<-REase+UvrD	TPR+GreAB-C+PIN	841	DEQ60_06940	Gammaproteobacteria	Methylophaga sp.	MAG TPA: hypothetical protein DEQ60_06940, partial [Methylophaga sp.].	GCA_003517125.1
HCG03150.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1325	DEV93_21745	Chloroflexi	Chloroflexi bacterium	MAG TPA: hypothetical protein DEV93_21745 [Chloroflexi bacterium].	GCA_003530725.1
HCN10799.1	HTH→?→?→?→?→?→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1128	DIS75_00410	Bacteroidetes	Chryseobacterium sp.	MAG TPA: hypothetical protein DIS75_00410 [Chryseobacterium sp.].	GCA_003536155.1
HEE61010.1	GreAB*→	GreAB	217	ENP71_13075	Chloroflexi	Chloroflexi bacterium	MAG TPA: transcription elongation factor GreA [Chloroflexi bacterium].	GCA_011051445.1
HEN27530.1	PIN*→	PIN	194	ENQ77_02470	Bacteria	candidate division WOR-3 bacterium	MAG TPA: RNA ligase partner protein [candidate division WOR-3 bacterium].	GCA_011046955.1
HFX16357.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1269	ENW10_10035	unclassified Bacteria	bacterium	MAG TPA: hypothetical protein ENW10_10035 [bacterium].	GCA_011334465.1
HGB35656.1	PIN*→	PIN	194	ENV38_01955	Bacteria	candidate division WOR-3 bacterium	MAG TPA: RNA ligase partner protein [candidate division WOR-3 bacterium].	GCA_011338235.1
HGZ37950.1	Calcineurin+TPR+GreAB-C+PIN*→	Calcineurin+TPR+GreAB-C+PIN	1423	ENR19_05950	Nitrospirae	Nitrospirae bacterium	MAG TPA: hypothetical protein ENR19_05950, partial [Nitrospirae bacterium].	GCA_011331925.1
HHC78382.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1134	ENK46_00760	Bacteroidetes	Flavobacteriia bacterium	MAG TPA: hypothetical protein ENK46_00760 [Flavobacteriia bacterium].	GCA_011330545.1
HIB63801.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1486	EYO33_01435	Planctomycetes	Phycisphaerales bacterium	MAG TPA: hypothetical protein EYO33_01435 [Phycisphaerales bacterium].	GCA_012964585.1

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HIP26815.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1038	EYG80_04080	Bacteroidetes	Flavobacteriaceae bacterium	MAG TPA: tetratricopeptide repeat protein [Flavobacteriaceae bacterium].	GCA_015662995.1
KAA0086698.1	TPR+PIN*→	TPR+PIN	1159	CIW52_01945	Actinobacteria	Mycolicibacterium sp. P9-64	hypothetical protein CIW52_01945 [Mycolicibacterium sp. P9-64].	GCA_008329605.1
KAB1070169.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	641	F6X53_30340	Alphaproteobacteria	Methylobacterium soli	tetratricopeptide repeat protein [Methylobacterium soli].	GCA_008806385.1
KCZ93824.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1142	HJO_00570	Alphaproteobacteria	Hyphomonas johnsonii MHS-2	hypothetical protein HJO_00570 [Hyphomonas johnsonii MHS-2].	GCA_000685275.1
KGF68042.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1283	LL06_18825	Alphaproteobacteria	Hoeflea sp. BAL378	hypothetical protein LL06_18825 [Hoeflea sp. BAL378].	GCA_000759435.1
KGM47444.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1329	ATO9_17580	Alphaproteobacteria	Pseudooceanicola atlanticus	hypothetical protein ATO9_17580 [Pseudooceanicola atlanticus].	GCA_000768315.1
KGS12485.1	GreAB-C+PIN*→	GreAB-C+PIN	509	OA77_21590	Gammaproteobacteria	Pseudomonas coronafaciens	hypothetical protein OA77_21590, partial [Pseudomonas coronafaciens].	GCA_000773135.1
KHO23731.1	X+PIN*→	X+PIN	762	QQ44_16085	Actinobacteria	Mycolicibacterium setense	hypothetical protein QQ44_16085 [Mycolicibacterium setense].	GCA_000805375.1
KIF65994.1	REase+TPR+TPR+GreAB-C+PIN*→	REase+TPR+TPR+GreAB-C+PIN	1274	HY68_38205	Actinobacteria	Streptomyces sp. AcH 505	hypothetical protein HY68_38205 [Streptomyces sp. AcH 505].	GCA_000818175.1
KIU53353.1	REase+TPR+TPR+GreAB-C+PIN*→	REase+TPR+TPR+GreAB-C+PIN	1254	QU41_01355	Alphaproteobacteria	Bradyrhizobium elkanii	hypothetical protein QU41_01355 [Bradyrhizobium elkanii].	GCA_000878305.1
KJS28984.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1318	VR64_22320	Deltaproteobacteria	Desulfatitalea sp. BRH_c12	MAG: hypothetical protein VR64_22320 [Desulfatitalea sp. BRH_c12].	GCA_000961655.1
KOY46643.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1085	ACX03_05530	Gammaproteobacteria	Vibrio parahaemolyticus	hypothetical protein ACX03_05530 [Vibrio parahaemolyticus].	GCA_001280625.1
KPC32725.1	PIN*→	PIN	407	ABJ99_1577	Gammaproteobacteria	Pseudomonas syringae pv. cilantro	Tetratricopeptide repeat protein [Pseudomonas syringae pv. cilantro].	GCA_001293775.1
KPH04186.1	GreAB-C+PIN*→	GreAB-C+PIN	532	AOG23_34735	Alphaproteobacteria	Rhizobium acidisoli	hypothetical protein AOG23_34735 [Rhizobium acidisoli].	GCA_001297245.1
KPW31206.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1491	ALO87_03437	Gammaproteobacteria	Pseudomonas syringae pv. apii	Uncharacterized protein ALO87_03437 [Pseudomonas syringae pv. apii].	GCA_001401385.1
KPW71831.1	PIN*→	PIN	419	ALO76_102575	Gammaproteobacteria	Pseudomonas syringae pv. coriandricola	hypothetical protein ALO76_102575 [Pseudomonas syringae pv. coriandricola].	GCA_001400185.1
KPX07181.1	REase→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	882	ALO74_05417	Gammaproteobacteria	Pseudomonas syringae pv. cunninghamiae	Uncharacterized protein ALO74_05417, partial [Pseudomonas syringae pv. cunninghamiae].	GCA_001400795.1
KQR06792.1	TPR+PIN*→	TPR+PIN	1157	ASF74_05425	Actinobacteria	Arthrobacter sp. Leaf145	hypothetical protein ASF74_05425 [Arthrobacter sp. Leaf145].	GCA_001423565.1
KQY47975.1	HTH+PNPase+TPR+GreAB-C+PIN*→	HTH+PNPase+TPR+GreAB-C+PIN	1492	ASD18_12170	Actinobacteria	Cellulomonas sp. Root137	hypothetical protein ASD18_12170 [Cellulomonas sp. Root137].	GCA_001426725.1
KRK09263.1	X+PIN*→	X+PIN	1209	FD11_GL001067	Firmicutes	Lactobacillus pobuzihii E100301 = KCTC 13174	hypothetical protein FD11_GL001067 [Lactobacillus pobuzihii E100301 = KCTC 13174].	GCA_001433815.1
KSV64106.1	REase+TPR+TPR+GreAB-C+PIN*→	REase+TPR+TPR+GreAB-C+PIN	1352	N182_36590	Alphaproteobacteria	Sinorhizobium sp. GL2	hypothetical protein N182_36590 [Sinorhizobium sp. GL2].	GCA_001461715.1
KTR52035.1	PIN*→	PIN	473	NS359_08065	Actinobacteria	Curtobacterium oceanosedimentum	hypothetical protein NS359_08065 [Curtobacterium oceanosedimentum].	GCA_001476135.1
KVD10066.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1276	WI81_28275	Betaproteobacteria	Burkholderia ubonensis	hypothetical protein WI81_28275 [Burkholderia ubonensis].	GCA_001523425.1
KVK86408.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1305	WJ44_35230	Betaproteobacteria	Burkholderia ubonensis	hypothetical protein WJ44_35230 [Burkholderia ubonensis].	GCA_001526225.1
KVP54755.1	PIN*→	PIN	270	WJ90_06090	Betaproteobacteria	Burkholderia ubonensis	hypothetical protein WJ90_06090 [Burkholderia ubonensis].	GCA_001527145.1
KVR94766.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1283	WK29_06535	Betaproteobacteria	Burkholderia vietnamiensis	hypothetical protein WK29_06535 [Burkholderia vietnamiensis].	GCA_001528565.1

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KVS41438.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1273	WK37_19925	Betaproteobacteria	Burkholderia ubonensis	hypothetical protein WK37_19925 [Burkholderia ubonensis].	GCA_001529725.1
KWO74502.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1308	WM31_08005	Betaproteobacteria	Burkholderia ubonensis	hypothetical protein WM31_08005 [Burkholderia ubonensis].	GCA_001534425.1
KWW10220.1	HetE-N1→ TPR+GreAB-C+PIN→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	695	VM82_06380	Gammaproteobacteria	Pasteurella multocida	hypothetical protein VM82_06380 [Pasteurella multocida].	GCA_001542975.1
KXC04457.1	X+PIN*→?→ Calcineurin→	X+PIN	1058	MhomT_16215	Actinobacteria	Microbacterium hominis	hypothetical protein MhomT_16215 [Microbacterium hominis].	GCA_001553805.1
KXF54879.1	HTH+PNPase+TPR+GreAB-C+PIN*→	HTH+PNPase+TPR+GreAB-C+PIN	1496	AXA44_39745	Actinobacteria	Rhodococcus sp. SC4	hypothetical protein AXA44_39745 [Rhodococcus sp. SC4].	GCA_001555475.1
KYK33744.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1243	AYK18_14685	Euryarchaeota	Theionarchaea archaeon DG-70	MAG: hypothetical protein AYK18_14685 [Theionarchaea archaeon DG-70].	GCA_001595795.1
KZM34260.1	X+PIN*→	X+PIN	802	OJAG_30920	Actinobacteria	Oerskovia enterophila	hypothetical protein OJAG_30920 [Oerskovia enterophila].	GCA_001624335.1
KZM57325.1	TPR+PIN*→	TPR+PIN	1172	A3Q36_16940	Firmicutes	Geobacillus stearothermophilus	hypothetical protein A3Q36_16940 [Geobacillus stearothermophilus].	GCA_001624615.1
MAK67575.1	HetE-N1→ TPR+GreAB-C+PIN*→||||<-REase+UvrD	TPR+GreAB-C+PIN	1111	CMH19_11360	Gammaproteobacteria	Methylophaga sp.	MAG: hypothetical protein CMH19_11360 [Methylophaga sp.].	GCA_002692615.1
MAK82682.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1322	CMJ17_12550	Alphaproteobacteria	Phenylobacterium sp.	MAG: hypothetical protein CMJ17_12550 [Phenylobacterium sp.].	GCA_002693985.1
MAM61427.1	REase+TOPC→||||<-?||REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1313	CMH11_08050	Alphaproteobacteria	Maritimibacter sp.	MAG: hypothetical protein CMH11_08050 [Maritimibacter sp.].	GCA_002695005.1
MAQ47157.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	928	CL812_15115	Alphaproteobacteria	Actibacterium sp.	MAG: hypothetical protein CL812_15115 [Actibacterium sp.].	GCA_002701285.1
MAX35781.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1254	CME33_04335	Planctomycetes	Gimesia sp.	MAG: hypothetical protein CME33_04335 [Gimesia sp.].	GCA_002706765.1
MAX78311.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1318	CMN12_16605	Alphaproteobacteria	Roseobacter sp.	MAG: hypothetical protein CMN12_16605 [Roseobacter sp.].	GCA_002706785.1
MBA2669970.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	581	H0U67_06335	Gemmatimonadetes	Gemmatimonadetes bacterium	MAG: hypothetical protein H0U67_06335 [Gemmatimonadetes bacterium].	GCA_013697765.1
MBA3005285.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1285	FP810_01590	Deltaproteobacteria	Desulfocapsa sp.	MAG: hypothetical protein FP810_01590 [Desulfocapsa sp.].	GCA_013792135.1
MBA3178888.1	HetE-N1→ TPR+GreAB-C+PIN*→?→||||<-Trypsin	TPR+GreAB-C+PIN	1121	CBX59_021210	Gammaproteobacteria	Salmonella enterica	hypothetical protein CBX59_021210 [Salmonella enterica].	GCA_006112745.2
MBA3341438.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1397	H0T48_06340	Gemmatimonadetes	Gemmatimonadaceae bacterium	MAG: hypothetical protein H0T48_06340 [Gemmatimonadaceae bacterium].	GCA_013813715.1
MBA3557151.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	877	H0W30_00995	Gemmatimonadetes	Gemmatimonadaceae bacterium	MAG: hypothetical protein H0W30_00995 [Gemmatimonadaceae bacterium].	GCA_013817545.1
MBA3619565.1	REase→ PIN*→	PIN	572	H0W56_08245	Actinobacteria	Acidothermales bacterium	MAG: hypothetical protein H0W56_08245, partial [Acidothermales bacterium].	GCA_013817005.1
MBA3973802.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1263	C0504_06240	Acidobacteria	Candidatus Solibacter sp.	MAG: hypothetical protein C0504_06240 [Candidatus Solibacter sp.].	GCA_013822245.1
MBA4090929.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1315	C0494_10085	Alphaproteobacteria	Sphingobium sp.	MAG: hypothetical protein C0494_10085 [Sphingobium sp.].	GCA_013822485.1
MBA4148880.1	TPR+PIN*→	TPR+PIN	1103	H0X66_12260	Verrucomicrobia	Verrucomicrobia bacterium	MAG: hypothetical protein H0X66_12260 [Verrucomicrobia bacterium].	GCA_013820875.1
MBB1073428.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1321	HUU62_03265	Betaproteobacteria	Rhodoferax jenense	DUF4365 domain-containing protein [Rhodoferax jenense].	GCA_014145235.1
MBB1121889.1	DOC+HTH→ REase+TOPC→ HetE-N1→?→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	992	H4983_26725	Gammaproteobacteria	Pseudomonas aeruginosa	hypothetical protein H4983_26725 [Pseudomonas aeruginosa].	GCA_014145725.1
MBB4577222.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1268	GGE58_005472	Alphaproteobacteria	Rhizobium lentis	tetratricopeptide (TPR) repeat protein [Rhizobium lentis].	GCA_014198785.1

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MBB5991665.1	REase→ TPR+GreAB-C+PIN*→?→?→ HNH→	TPR+GreAB-C+PIN	1242	HNP04_003690	Gammaproteobacteria	Pseudomonas viridiflava	tetratricopeptide (TPR) repeat protein/transcription elongation GreA/GreB family factor [Pseudomonas viridiflava].	GCA_014204055.1
MBB6509406.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	780	F4695_002763	Alphaproteobacteria	Rhizobium soli	putative nucleic acid-binding protein [Rhizobium soli].	GCA_014207075.1
MBB9310955.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	575	FSF17_011690	Gammaproteobacteria	Escherichia coli	hypothetical protein FSF17_011690 [Escherichia coli].	GCA_012385615.2
MBC6414865.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1326	GDA46_00495	Oligoflexia	Bdellovibrionales bacterium	MAG: hypothetical protein GDA46_00495 [Bdellovibrionales bacterium].	GCA_014323935.1
MBC70602.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1253	CL492_17300	Gammaproteobacteria	Acinetobacter sp.	MAG: hypothetical protein CL492_17300 [Acinetobacter sp.].	GCA_002711945.1
MBC7145404.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1332	H5U24_08360	Alphaproteobacteria	Thioclava marina	MAG: hypothetical protein H5U24_08360 [Thioclava marina].	GCA_014359625.1
MBC7391182.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1270	H7329_18405	Verrucomicrobia	Cytophagales bacterium	MAG: tetratricopeptide repeat protein [Opitutaceae bacterium].	GCA_014376535.1
MBC74230.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1131	CMH47_18575	Bacteroidetes	Muricauda sp.	MAG: hypothetical protein CMH47_18575 [Muricauda sp.].	GCA_002711825.1
MBD0373736.1	TPR+GreAB-C*→	TPR+GreAB-C	885	ICV60_23090	Acidobacteria	Pyrinomonadaceae bacterium	MAG: tetratricopeptide repeat protein, partial [Pyrinomonadaceae bacterium].	GCA_014534425.1
MBD3293793.1	TPR+PIN*→	TPR+PIN	1505	GF393_12790	Armatimonadetes	Armatimonadia bacterium	MAG: hypothetical protein GF393_12790 [Armatimonadia bacterium].	GCA_014728405.1
MBD3811358.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1374	IE917_03935	Betaproteobacteria	Betaproteobacteria bacterium	MAG: hypothetical protein IE917_03935 [Betaproteobacteria bacterium].	GCA_014764035.1
MBD8566197.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1235	IFU01_18215	Betaproteobacteria	Oxalobacteraceae sp. CFBP 8763	hypothetical protein IFU01_18215 [Oxalobacteraceae sp. CFBP 8763].	GCA_014841525.1
MBD8722144.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1511	IFT43_02050	Betaproteobacteria	Oxalobacteraceae sp. CFBP 13708	hypothetical protein IFT43_02050 [Oxalobacteraceae sp. CFBP 13708].	GCA_014842315.1
MBE2259083.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1335	IAE88_09505	Alphaproteobacteria	Rhodobacteraceae bacterium	MAG: hypothetical protein IAE88_09505 [Rhodobacteraceae bacterium].	GCA_014879755.1
MBE3996728.1	HetE-N1→?→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	910	HJ133_08285	Gammaproteobacteria	Vibrio parahaemolyticus	hypothetical protein HJ133_08285 [Vibrio parahaemolyticus].	GCA_014919735.1
MBE7465263.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1253	HS116_17430	Planctomycetes	Planctomycetes bacterium	MAG: hypothetical protein HS116_17430 [Planctomycetes bacterium].	GCA_015075375.1
MBE8523541.1	TPR+PIN*→	TPR+PIN	1310	ILP97_39665	Actinobacteria	Amycolatopsis sp. H6(2020)	hypothetical protein ILP97_39665 [Amycolatopsis sp. H6(2020)].	GCA_015163035.1
MBE8960063.1	GreAB-C*→	GreAB-C	307	IH766_22715	Gammaproteobacteria	Escherichia coli	hypothetical protein IH766_22715, partial [Escherichia coli].	GCA_015206795.1
MBE9468467.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1221	IMY72_09155	Bacteroidetes	Bacteroidetes bacterium	MAG: hypothetical protein IMY72_09155 [Bacteroidetes bacterium].	GCA_015222055.1
MBF0231519.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1223	HQK65_00575	Deltaproteobacteria	Desulfamplus sp.	MAG: hypothetical protein HQK65_00575 [Desulfamplus sp.].	GCA_015231525.1
MBF0529118.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	678	HQK55_07585	Deltaproteobacteria	Deltaproteobacteria bacterium	MAG: hypothetical protein HQK55_07585 [Deltaproteobacteria bacterium].	GCA_015233515.1
MBF3699451.1	TPR+GreAB-C+PIN*→||||<-HTH+HTH	TPR+GreAB-C+PIN	872	ISF48_14710	Betaproteobacteria	Burkholderia pseudomallei	hypothetical protein ISF48_14710 [Burkholderia pseudomallei].	GCA_015319855.1
MBF3842067.1	TPR+GreAB-C+PIN*→||||<-HTH+HTH	TPR+GreAB-C+PIN	872	ISF68_21105	Betaproteobacteria	Burkholderia pseudomallei	hypothetical protein ISF68_21105 [Burkholderia pseudomallei].	GCA_015320325.1
MBF4269202.1	TPR+GreAB-C*→	TPR+GreAB-C	686	EAY71_20240	Gammaproteobacteria	Vibrio anguillarum	hypothetical protein EAY71_20240, partial [Vibrio anguillarum].	GCA_015343035.1
MBF9243682.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1438	I4I80_05390	Gammaproteobacteria	Pseudomonas syringae pv. tomato	hypothetical protein I4I80_05390 [Pseudomonas syringae pv. tomato].	GCA_015694365.1

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MBF9246381.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1320	I4I80_19980	Gammaproteobacteria	Pseudomonas syringae pv. tomato	DUF4365 domain-containing protein [Pseudomonas syringae pv. tomato].	GCA_015694365.1
MBG2992436.1	PAIREDC-HTH→ PSE→ HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1092	I4607_12420	Gammaproteobacteria	Proteus mirabilis	hypothetical protein I4607_12420 [Proteus mirabilis].	GCA_015723275.1
MBG6040926.1	PAIREDC-HTH→ PSE→ HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1092	I5F94_05610	Gammaproteobacteria	Proteus mirabilis	hypothetical protein I5F94_05610 [Proteus mirabilis].	GCA_015740165.1
MBG6251627.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1140	I5I20_11010	Gammaproteobacteria	Pseudomonas aeruginosa	hypothetical protein I5I20_11010 [Pseudomonas aeruginosa].	GCA_015762745.1
MBG7090225.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1170	I5G28_04925	Gammaproteobacteria	Pseudomonas aeruginosa	hypothetical protein I5G28_04925 [Pseudomonas aeruginosa].	GCA_015765435.1
MBH04121.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1338	CMP08_08385	Gammaproteobacteria	Xanthomonadales bacterium	MAG: hypothetical protein CMP08_08385 [Xanthomonadales bacterium].	GCA_002715985.1
MBH1476826.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1243	I5U61_05170	Gammaproteobacteria	Stenotrophomonas maltophilia	CDC27 family protein [Stenotrophomonas maltophilia].	GCA_015997065.1
MBH7847781.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1071	I6A75_20240	Firmicutes	Clostridioides difficile	hypothetical protein I6A75_20240 [Clostridioides difficile].	GCA_016052935.1
MBI1182363.1	REase+TPR+TPR+GreAB-C+PIN*→	REase+TPR+TPR+GreAB-C+PIN	1295	GC201_17615	Alphaproteobacteria	Alphaproteobacteria bacterium	MAG: hypothetical protein GC201_17615 [Alphaproteobacteria bacterium].	GCA_016124315.1
MBI1904375.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1292	HYS13_25040	Planctomycetes	Planctomycetia bacterium	MAG: hypothetical protein HYS13_25040 [Planctomycetia bacterium].	GCA_016177915.1
MBI3888209.1	TPR+PIN*→	TPR+PIN	1190	HY311_00230	Bacteria	Candidatus Nomurabacteria bacterium	MAG: tetratricopeptide repeat protein [Candidatus Nomurabacteria bacterium].	GCA_016199805.1
MBI4633825.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1294	HY742_08030	Deltaproteobacteria	Deltaproteobacteria bacterium	MAG: hypothetical protein HY742_08030 [Deltaproteobacteria bacterium].	GCA_016209105.1
MBI4696055.1	Cas_Cas1→ REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1313	HY749_18755	Gammaproteobacteria	Gammaproteobacteria bacterium	MAG: DUF4365 domain-containing protein [Gammaproteobacteria bacterium].	GCA_016209015.1
MBI4846278.1	TM+SIR2+TPR+PIN+PIN+TM*→	TM+SIR2+TPR+PIN+PIN+TM	2304	HY810_07390	PVC group	Candidatus Omnitrophica bacterium	MAG: SIR2 family protein [Candidatus Omnitrophica bacterium].	GCA_016213925.1
MBI5207389.1	HTH+REase+PIN*→	HTH+REase+PIN	808	HY934_06310	Bacteria	Candidatus Firestonebacteria bacterium	MAG: helix-turn-helix domain-containing protein [Candidatus Firestonebacteria bacterium].	GCA_016212735.1
MBI5354508.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1282	HZB50_17850	Chloroflexi	Chloroflexi bacterium	MAG: hypothetical protein HZB50_17850 [Chloroflexi bacterium].	GCA_016219545.1
MBI5356660.1	TPR+PIN*→||||<-?<-?||HTH→	TPR+PIN	1074	HZB78_03530	Bacteria	Candidatus Collierbacteria bacterium	MAG: hypothetical protein HZB78_03530 [Candidatus Collierbacteria bacterium].	GCA_016219325.1
MBI5458930.1	HEPN→ REase+SNF2→ REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1256	HY987_04275	Euryarchaeota	Methanobacterium sp.	MAG: hypothetical protein HY987_04275 [Methanobacterium sp.].	GCA_016217785.1
MBI5516335.1	GreAB*→	GreAB	172	HY909_21300	Deltaproteobacteria	Deltaproteobacteria bacterium	MAG: GreA/GreB family elongation factor [Deltaproteobacteria bacterium].	GCA_016218725.1
MBI5711428.1	GreAB*→	GreAB	903	HZC42_14175	Bacteria	Candidatus Eisenbacteria bacterium	MAG: GreA/GreB family elongation factor [Candidatus Eisenbacteria bacterium].	GCA_016223045.1
MBI5910925.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1318	HY848_13355	Betaproteobacteria	Betaproteobacteria bacterium	MAG: hypothetical protein HY848_13355 [Betaproteobacteria bacterium].	GCA_016234705.1
MBI5925874.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1369	HY836_09780	Betaproteobacteria	Aquabacterium sp.	MAG: hypothetical protein HY836_09780 [Aquabacterium sp.].	GCA_016234775.1
MBI6873434.1	TPR+PIN*→	TPR+PIN	1232	I6U51_12055	Firmicutes	Clostridium aciditolerans	hypothetical protein I6U51_12055 [Clostridium aciditolerans].	GCA_016316925.1
MBJ3588954.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	924	JGC49_23910	Gammaproteobacteria	Salmonella enterica subsp. enterica serovar London	hypothetical protein JGC49_23910, partial [Salmonella enterica subsp. enterica serovar London].	GCA_016412075.1
MBJ7510055.1	REase+TPR+TPR+GreAB-C+PIN*→?→ HNH→	REase+TPR+TPR+GreAB-C+PIN	1324	JHC97_02180	Alphaproteobacteria	Brevundimonas sp.	MAG: hypothetical protein JHC97_02180 [Brevundimonas sp.].	GCA_016463795.1

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MBK4592903.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	444	JJQ23_24565	Gammaproteobacteria	Enterobacter hormaechei	hypothetical protein JJQ23_24565, partial [Enterobacter hormaechei].	GCA_016633275.1
MBK4660580.1	TPR+GreAB-C*→	TPR+GreAB-C	362	JJQ36_24785	Gammaproteobacteria	Enterobacter hormaechei	hypothetical protein JJQ36_24785, partial [Enterobacter hormaechei].	GCA_016633665.1
MBK4769022.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1118	FT726_04985	Gammaproteobacteria	Pantoea sp. Morm	MAG: hypothetical protein FT726_04985 [Pantoea sp. Morm].	GCA_016643525.1
MBK5650341.1	REase+TPR+TPR+GreAB-C+PIN*→	REase+TPR+TPR+GreAB-C+PIN	1254	I4N50_01815	Alphaproteobacteria	Rhizobium sp.	MAG: hypothetical protein I4N50_01815, partial [Rhizobium sp.].	GCA_016652855.1
MBK7033605.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	852	IPH49_10150	Ignavibacteriae	Ignavibacteria bacterium	MAG: hypothetical protein IPH49_10150 [Ignavibacteria bacterium].	GCA_016708405.1
MBK7130254.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1238	IPH66_12960	Bacteroidetes	Crocinitomicaceae bacterium	MAG: hypothetical protein IPH66_12960 [Crocinitomicaceae bacterium].	GCA_016708105.1
MBK7149038.1	TPR+GreAB-C+PIN*→?→?→?→ TRD+TRD→	TPR+GreAB-C+PIN	1255	IPH78_09510	Bacteroidetes	Bacteroidetes bacterium	MAG: tetratricopeptide repeat protein [Bacteroidetes bacterium].	GCA_016707905.1
MBK7953772.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1351	IPK02_07330	Betaproteobacteria	Candidatus Accumulibacter sp.	MAG: hypothetical protein IPK02_07330 [Candidatus Accumulibacter sp.].	GCA_016713625.1
MBK8138001.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	749	IPK52_19665	Chloroflexi	Chloroflexi bacterium	MAG: hypothetical protein IPK52_19665 [Chloroflexi bacterium].	GCA_016712885.1
MBK8143858.1	TPR+PIN*→	TPR+PIN	641	IPK62_02070	Bacteroidetes	Bacteroidetes bacterium	MAG: hypothetical protein IPK62_02070 [Bacteroidetes bacterium].	GCA_016712665.1
MBK8927388.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1238	IPM74_16180	Bacteroidetes	Crocinitomicaceae bacterium	MAG: hypothetical protein IPM74_16180 [Crocinitomicaceae bacterium].	GCA_016720025.1
MBK9927324.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1144	IPP66_18800	Chloroflexi	Anaerolineales bacterium	MAG: tetratricopeptide repeat protein [Anaerolineales bacterium].	GCA_016721115.1
MBL0869327.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1510	IBJ18_01985	Planctomycetes	Phycisphaerales bacterium	MAG: SIR2 family protein [Phycisphaerales bacterium].	GCA_016741915.1
MBL0919126.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1320	IBJ14_10515	Betaproteobacteria	Hydrogenophaga sp.	MAG: DUF4365 domain-containing protein [Hydrogenophaga sp.].	GCA_016741995.1
MBL1279106.1	TPR+PIN*→	TPR+PIN	1234	COA33_002470	Bacteroidetes	Fluviicola sp.	MAG: hypothetical protein COA33_002470 [Fluviicola sp.].	GCA_002734065.2
MBL4609540.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1114	JKY58_02600	Gammaproteobacteria	Pseudomonas sp.	MAG: hypothetical protein JKY58_02600 [Pseudomonas sp.].	GCA_016763285.1
MBL7760873.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1264	JNK08_09270	Bacteroidetes	Sediminibacterium sp.	MAG: hypothetical protein JNK08_09270 [Sediminibacterium sp.].	GCA_016786865.1
MBL7768787.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1258	JNK20_07425	Bacteroidetes	Flavipsychrobacter sp.	MAG: hypothetical protein JNK20_07425 [Flavipsychrobacter sp.].	GCA_016787265.1
MBL7772244.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1151	JNM95_05270	Bacteroidetes	Chitinophagaceae bacterium	MAG: hypothetical protein JNM95_05270 [Chitinophagaceae bacterium].	GCA_016787065.1
MBL7856049.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1173	JNM57_00050	Bacteroidetes	Cyclobacteriaceae bacterium	MAG: hypothetical protein JNM57_00050 [Cyclobacteriaceae bacterium].	GCA_016787565.1
MBL8263961.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1239	JNM58_16225	Gammaproteobacteria	Xanthomonadaceae bacterium	MAG: hypothetical protein JNM58_16225 [Xanthomonadaceae bacterium].	GCA_016789405.1
MBL8602392.1	<-SIG+SM-MscS<-?<-?||GreAB*→	GreAB	172	JNK72_10760	Deltaproteobacteria	Myxococcales bacterium	MAG: GreA/GreB family elongation factor [Myxococcales bacterium].	GCA_016792845.1
MBL8821106.1	REase→?→ REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1262	JNJ77_00865	Planctomycetes	Planctomycetia bacterium	MAG: hypothetical protein JNJ77_00865 [Planctomycetia bacterium].	GCA_016795155.1
MBL8873833.1	MNS+TPR+PIN*→	MNS+TPR+PIN	2502	JNK90_28920	Planctomycetes	Planctomycetaceae bacterium	MAG: tetratricopeptide repeat protein [Planctomycetaceae bacterium].	GCA_016792705.1
MBL8874044.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1287	JNK90_29995	Planctomycetes	Planctomycetaceae bacterium	MAG: hypothetical protein JNK90_29995 [Planctomycetaceae bacterium].	GCA_016792705.1
MBL9102506.1	Calcineurin+TPR+GreAB-C+PIN*→	Calcineurin+TPR+GreAB-C+PIN	1429	JNL82_16210	Deltaproteobacteria	Myxococcales bacterium	MAG: metallophosphoesterase [Myxococcales bacterium].	GCA_016793465.1

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MBM0224540.1	TPR+PIN*→	TPR+PIN	990	JNW87_02235	Actinobacteria	Micromonospora sp. ATA51	hypothetical protein JNW87_02235 [Micromonospora sp. ATA51].	GCA_016802855.1
MBM0258116.1	TM+TPR+PIN*→	TM+TPR+PIN	1165	JNW89_16135	Actinobacteria	Micromonospora sp. 4G55	hypothetical protein JNW89_16135 [Micromonospora sp. 4G55].	GCA_016803375.1
MBM4070384.1	TPR+GreAB-C*→	TPR+GreAB-C	409	FJ271_15725	Planctomycetes	Planctomycetes bacterium	MAG: hypothetical protein FJ271_15725 [Planctomycetes bacterium].	GCA_016873095.1
MBM4845996.1	HetE-N1→ HetE-N1+TPR+GreAB-C+PIN*→	HetE-N1+TPR+GreAB-C+PIN	1091	HYO58_20990	Gammaproteobacteria	Vibrio parahaemolyticus	hypothetical protein HYO58_20990 [Vibrio parahaemolyticus].	GCA_016876175.1
MBN1214554.1	TPR+PIN*→	TPR+PIN	1151	JXA99_03840	Asgard group	Candidatus Lokiarchaeota archaeon	MAG: hypothetical protein JXA99_03840 [Candidatus Lokiarchaeota archaeon].	GCA_016926735.1
MBN1453691.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1287	JW963_21935	Chloroflexi	Anaerolineales bacterium	MAG: hypothetical protein JW963_21935 [Anaerolineales bacterium].	GCA_016928525.1
MBN2019675.1	TPR+PIN*→	TPR+PIN	1063	JW749_05560	Planctomycetes	Sedimentisphaerales bacterium	MAG: tetratricopeptide repeat protein [Sedimentisphaerales bacterium].	GCA_016932095.1
MBN2455312.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	958	JXB29_02055	Planctomycetes	Sedimentisphaerales bacterium	MAG: hypothetical protein JXB29_02055 [Sedimentisphaerales bacterium].	GCA_016935195.1
MBN4052768.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1150	JYU07_00650	Chloroflexi	Roseiflexus sp. AH-315-K22	hypothetical protein JYU07_00650, partial [Roseiflexus sp. AH-315-K22].	GCA_017114345.1
MBN5297052.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1090	JY477_14370	Gammaproteobacteria	Serratia marcescens	hypothetical protein JY477_14370 [Serratia marcescens].	GCA_017152845.1
MBN8213566.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1240	J0M09_11660	Gammaproteobacteria	Xanthomonadales bacterium	MAG: hypothetical protein J0M09_11660 [Xanthomonadales bacterium].	GCA_017302135.1
MBN8506452.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1310	J0L58_18450	Betaproteobacteria	Burkholderiales bacterium	MAG: DUF4365 domain-containing protein [Burkholderiales bacterium].	GCA_017302655.1
MBN8549455.1	<-HNH<-?<-?||?→||||<-?||?→?→ REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1254	J0M12_09085	Deltaproteobacteria	Deltaproteobacteria bacterium	MAG: hypothetical protein J0M12_09085 [Deltaproteobacteria bacterium].	GCA_017302875.1
MBN8618419.1	TPR+PIN*→	TPR+PIN	1277	J0L63_05915	Chloroflexi	Anaerolineae bacterium	MAG: hypothetical protein J0L63_05915 [Anaerolineae bacterium].	GCA_017303775.1
MBN8865737.1	TPR+GreAB-C+PIN*→||||<-REase	TPR+GreAB-C+PIN	435	J0H92_20355	Bacteroidetes	Sphingobacteriales bacterium	MAG: hypothetical protein J0H92_20355 [Sphingobacteriales bacterium].	GCA_017304765.1
MBN8904954.1	TPR+GreAB-C+PIN*→ REase→	TPR+GreAB-C+PIN	679	J0H57_28395	Alphaproteobacteria	Rhodospirillales bacterium	MAG: hypothetical protein J0H57_28395, partial [Rhodospirillales bacterium].	GCA_017305035.1
MBN8956855.1	REase+TPR+TPR+GreAB-C+PIN*→	REase+TPR+TPR+GreAB-C+PIN	1322	J0H17_09800	Alphaproteobacteria	Rhizobiales bacterium	MAG: GreA/GreB family elongation factor [Rhizobiales bacterium].	GCA_017304555.1
MBN8979284.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1129	J0I08_22735	Alphaproteobacteria	Rhizobiales bacterium	MAG: hypothetical protein J0I08_22735 [Rhizobiales bacterium].	GCA_017305555.1
MBN9409395.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1520	J0H69_09625	Betaproteobacteria	Burkholderiales bacterium	MAG: hypothetical protein J0H69_09625 [Burkholderiales bacterium].	GCA_017307855.1
MBN9598737.1	TIR→?→?→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1117	J0G28_03540	Alphaproteobacteria	Afipia sp.	MAG: hypothetical protein J0G28_03540 [Afipia sp.].	GCA_017308625.1
MBO1224632.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1279	JYX80_09380	Planctomycetes	Candidatus Scalindua sediminis	MAG: hypothetical protein JYX80_09380 [Candidatus Scalindua sediminis].	GCA_017368835.1
MBO5183033.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1061	J6B64_01405	Firmicutes	Bacilli bacterium	MAG: hypothetical protein J6B64_01405 [Bacilli bacterium].	GCA_017623135.1
MBO5920175.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	507	J6Q34_06770	Bacteroidetes	Bacteroidales bacterium	MAG: hypothetical protein J6Q34_06770, partial [Bacteroidales bacterium].	GCA_017631435.1
MBO6496597.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1166	JJ978_13575	Bacteroidetes	Roseivirga sp.	MAG: hypothetical protein JJ978_13575 [Roseivirga sp.].	GCA_017640405.1
MBO6761342.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1095	JJ909_10290	Bacteroidetes	Roseivirga sp.	MAG: hypothetical protein JJ909_10290, partial [Roseivirga sp.].	GCA_017643085.1
MBO7636147.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1171	J6S89_06175	Bacteroidetes	Paludibacteraceae bacterium	MAG: hypothetical protein J6S89_06175 [Paludibacteraceae bacterium].	GCA_017651825.1

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MBP8894107.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	985	KBH09_17290	Bacteroidetes	Saprospiraceae bacterium	MAG: hypothetical protein KBH09_17290 [Saprospiraceae bacterium].	GCA_018055665.1
MBR7522021.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1105	KC233_15980	Gammaproteobacteria	Pseudomonas juntendi	hypothetical protein KC233_15980 [Pseudomonas juntendi].	GCA_018138545.1
MHJ03184.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	523	EEN62_25195	Gammaproteobacteria	Salmonella enterica	hypothetical protein EEN62_25195 [Salmonella enterica].	GCA_003786665.1
MKC77438.1	TPR+GreAB-C+PIN*→?→||||<-Trypsin	TPR+GreAB-C+PIN	1057	D1800_22940	Gammaproteobacteria	Salmonella enterica subsp. enterica serovar Denver	hypothetical protein D1800_22940, partial [Salmonella enterica subsp. enterica serovar Denver].	GCA_003891855.1
MPS34312.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1237	E2593_03230	Gammaproteobacteria	Stenotrophomonas sp.	MAG: hypothetical protein E2593_03230 [Stenotrophomonas sp.].	GCA_009360425.1
MSW50706.1	TPR+PIN*→	TPR+PIN	1289	F2817_07440	Actinobacteria	Actinobacteria bacterium	MAG: hypothetical protein F2817_07440 [Actinobacteria bacterium].	GCA_009699505.1
MTI67851.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1274	FH753_14795	Firmicutes	Firmicutes bacterium	MAG: hypothetical protein FH753_14795 [Firmicutes bacterium].	GCA_009711765.1
MVM42293.1	-	-	400	GO730_39050	Bacteroidetes	Spirosoma sp. HMF3257	hypothetical protein GO730_39050 [Spirosoma sp. HMF3257].	GCA_009754885.1
MXP30641.1	REase→?→ REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1265	GRI94_02255	Alphaproteobacteria	Parerythrobacter jejuensis	hypothetical protein GRI94_02255 [Parerythrobacter jejuensis].	GCA_009827995.1
MXW27298.1	REase+TPR+GREAB-C+PIN*→	REase+TPR+GREAB-C+PIN	1302	F4Z80_00100	Chloroflexi	Chloroflexi bacterium	MAG: hypothetical protein F4Z80_00100 [Chloroflexi bacterium].	GCA_009835825.1
MXX46821.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1267	F4Z38_00735	Chloroflexi	Chloroflexi bacterium	MAG: tetratricopeptide repeat protein [Chloroflexi bacterium].	GCA_009836695.1
MXX90812.1	SFI-Helicase+REase+TPR+GreAB-C+PIN*→	SFI-Helicase+REase+TPR+GreAB-C+PIN	1846	F4Y68_16490	Alphaproteobacteria	Boseongicola sp. SB0665_bin_10	MAG: DUF4011 domain-containing protein [Boseongicola sp. SB0665_bin_10].	GCA_009838075.1
MXX91940.1	GreAB*→?→?→ DAGKIN→	GreAB	297	F4Y63_00605	Chloroflexi	Chloroflexi bacterium	MAG: transcription elongation factor GreA [Chloroflexi bacterium].	GCA_009838175.1
MXX97366.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1278	F4Y64_07095	Bacteroidetes	Rhodothermaceae bacterium	MAG: hypothetical protein F4Y64_07095 [Rhodothermaceae bacterium].	GCA_009838195.1
MXZ48148.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1281	F4Z13_02660	Bacteria	Candidatus Dadabacteria bacterium	MAG: hypothetical protein F4Z13_02660 [Candidatus Dadabacteria bacterium].	GCA_009837205.1
MXZ55165.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1297	F4Z14_03240	Gammaproteobacteria	Gammaproteobacteria bacterium	MAG: hypothetical protein F4Z14_03240 [Gammaproteobacteria bacterium].	GCA_009837185.1
MXZ61096.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1297	F4Z12_09585	Acidobacteria	Acidobacteria bacterium	MAG: hypothetical protein F4Z12_09585 [Acidobacteria bacterium].	GCA_009837215.1
MYA00894.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1267	F4Y35_03835	Chloroflexi	Chloroflexi bacterium	MAG: tetratricopeptide repeat protein [Chloroflexi bacterium].	GCA_009838735.1
MYA68860.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1308	F4Y19_01960	Bacteria	Candidatus Poribacteria bacterium	MAG: tetratricopeptide repeat protein [Candidatus Poribacteria bacterium].	GCA_009839085.1
MYB15443.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1263	F4X41_00185	Chloroflexi	Chloroflexi bacterium	MAG: hypothetical protein F4X41_00185 [Chloroflexi bacterium].	GCA_009840625.1
MYB42498.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1283	F4X76_09995	Chloroflexi	Chloroflexi bacterium	MAG: tetratricopeptide repeat protein [Chloroflexi bacterium].	GCA_009839925.1
MYB43588.1	TPR+PIN*→	TPR+PIN	1200	F4X74_01405	Actinobacteria	Acidimicrobiia bacterium	MAG: hypothetical protein F4X74_01405 [Acidimicrobiia bacterium].	GCA_009839965.1
MYB75895.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1300	F4X83_02110	Chloroflexi	Chloroflexi bacterium	MAG: hypothetical protein F4X83_02110 [Chloroflexi bacterium].	GCA_009839775.1
MYC64541.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1258	F4X16_17195	Chloroflexi	Caldilineaceae bacterium SB0661_bin_34	MAG: tetratricopeptide repeat protein [Caldilineaceae bacterium SB0661_bin_34].	GCA_009841145.1
MYD93275.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1302	F4Y02_06215	Chloroflexi	Chloroflexi bacterium	MAG: hypothetical protein F4Y02_06215 [Chloroflexi bacterium].	GCA_009839425.1

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MYE61432.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	638	F4235_05210	Bacteria	Candidatus Dadabacteria bacterium	MAG: GreA/GreB family elongation factor [Candidatus Dadabacteria bacterium].	GCA_009841925.1
MYF79095.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	716	F4180_04215	Chloroflexi	Chloroflexi bacterium	MAG: tetratricopeptide repeat protein, partial [Chloroflexi bacterium].	GCA_009843025.1
MYH48359.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1248	F4151_02205	Gammaproteobacteria	Gammaproteobacteria bacterium	MAG: hypothetical protein F4151_02205 [Gammaproteobacteria bacterium].	GCA_009843625.1
MYK18704.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	911	F4055_11145	Bacteria	Candidatus Poribacteria bacterium	MAG: tetratricopeptide repeat protein, partial [Candidatus Poribacteria bacterium].	GCA_009845505.1
MYK96751.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	470	F4009_22610	Bacteria	Candidatus Poribacteria bacterium	MAG: hypothetical protein F4009_22610 [Candidatus Poribacteria bacterium].	GCA_009846415.1
NAT27530.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	692	CVE22_06655	Gammaproteobacteria	Pseudomonas syringae pv. actinidiae	hypothetical protein CVE22_06655, partial [Pseudomonas syringae pv. actinidiae].	GCA_009903115.1
NBW14976.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1102	EBR82_43945	Alphaproteobacteria	Caulobacteraceae bacterium	MAG: hypothetical protein EBR82_43945, partial [Caulobacteraceae bacterium].	GCA_009924585.1
NCC04365.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1308	EOM37_10050	Proteobacteria	Proteobacteria bacterium	MAG: tetratricopeptide repeat protein [Proteobacteria bacterium].	GCA_009929575.1
NCN59296.1	<-CITB-HTH+LexA-protease||TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1274	GW940_05255	Bacteria	Candidatus Microgenomates bacterium	MAG: hypothetical protein GW940_05255 [Candidatus Microgenomates bacterium].	GCA_009992065.1
NCO24709.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	415	GW897_06315	unclassified Bacteria	bacterium	MAG: hypothetical protein GW897_06315 [bacterium].	GCA_009992775.1
NEZ58684.1	TPR+TPR→ TPR+TPR→ TPR+TPR→ TPR+TPR→ TPR+TPR→ TPR→ TPR→ PNPase+TPR+GreAB-C+PIN*→?→||||<-TPR+TPR	PNPase+TPR+GreAB-C+PIN	1392	DXZ20_24195	Cyanobacteria	Leptolyngbyaceae cyanobacterium CCMR0081	hypothetical protein DXZ20_24195 [Leptolyngbyaceae cyanobacterium CCMR0081].	GCA_011009555.1
NEZ64367.1	TPR+TPR→ TPR+TPR→ TPR+TPR→ TPR+TPR→ TPR+TPR→ TPR+TPR→ PNPase+TPR+GreAB-C+PIN*→?→||||<-TPR+TPR<-TPR+TPR<-?<-TIR	PNPase+TPR+GreAB-C+PIN	1392	D0962_16475	Cyanobacteria	Leptolyngbyaceae cyanobacterium CCMR0082	hypothetical protein D0962_16475 [Leptolyngbyaceae cyanobacterium CCMR0082].	GCA_011009535.1
NHI06604.1	PIN*→	PIN	211	STPH2_1967	Actinobacteria	Streptomyces sp. KO7888	hypothetical protein STPH2_1967 [Streptomyces sp. KO7888].	GCA_011317205.1
NHK99992.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	911	G7087_16540	Betaproteobacteria	Rubrivivax benzoatilyticus	hypothetical protein G7087_16540 [Rubrivivax benzoatilyticus].	GCA_011365705.1
NJN11600.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	298	HC815_27960	Cyanobacteria	Richelia sp. RM1_1_1	MAG: hypothetical protein HC815_27960 [Richelia sp. RM1_1_1].	GCA_012032385.1
NJO54209.1	REase+TPR+TPR+GreAB-C+PIN*→	REase+TPR+TPR+GreAB-C+PIN	1338	HC829_04580	Bacteroidetes	Bacteroidales bacterium	MAG: hypothetical protein HC829_04580 [Bacteroidales bacterium].	GCA_012033435.1
NKI94745.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1340	FHT26_002685	Betaproteobacteria	Rhizobacter sp. SG703	tetratricopeptide (TPR) repeat protein [Rhizobacter sp. SG703].	GCA_012275445.1
NLD36189.1	REase+TPR+PIN*→	REase+TPR+PIN	1360	GX654_04895	Deltaproteobacteria	Desulfatiglans sp.	MAG: tetratricopeptide repeat protein [Desulfatiglans sp.].	GCA_012513605.1
NLD38959.1	TPR+PIN*→	TPR+PIN	1143	GX654_19035	Deltaproteobacteria	Desulfatiglans sp.	MAG: tetratricopeptide repeat protein [Desulfatiglans sp.].	GCA_012513605.1
NLD90744.1	PNPase+TPR+GreAB-C+PIN*→	PNPase+TPR+GreAB-C+PIN	1613	GX634_10460	Lentisphaerae	Lentisphaerae bacterium	MAG: hypothetical protein GX634_10460 [Lentisphaerae bacterium].	GCA_012514035.1
NLE27049.1	SIR2+TPR+GreAB-C+PIN*→	SIR2+TPR+GreAB-C+PIN	1448	GX625_17245	Firmicutes	Clostridiaceae bacterium	MAG: hypothetical protein GX625_17245 [Clostridiaceae bacterium].	GCA_012514215.1
NLE28033.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	758	GX625_22395	Firmicutes	Clostridiaceae bacterium	MAG: hypothetical protein GX625_22395, partial [Clostridiaceae bacterium].	GCA_012514215.1
NLG15547.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1341	GX561_15255	Lentisphaerae	Lentisphaerae bacterium	MAG: hypothetical protein GX561_15255 [Lentisphaerae bacterium].	GCA_012515425.1
NLX50682.1	REase+TPR+GreAB-C+PIN*→ PSE→?→?→ REase+SNF2→	REase+TPR+GreAB-C+PIN	1299	GXY72_01105	Deltaproteobacteria	Deltaproteobacteria bacterium	MAG: hypothetical protein GXY72_01105 [Deltaproteobacteria bacterium].	GCA_012729055.1
NMQ30291.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1072	E4Q23_22545	Betaproteobacteria	Candidatus Accumulibacter phosphatis	hypothetical protein E4Q23_22545, partial [Candidatus Accumulibacter phosphatis].	GCA_012939955.1
NOT34484.1	GreAB*→	GreAB	904	HOP12_09975	Bacteria	Candidatus Eisenbacteria bacterium	MAG: hypothetical protein HOP12_09975 [Candidatus Eisenbacteria bacterium].	GCA_013140805.1

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NOU31123.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	536	HOO96_24755	Deltaproteobacteria	Polyangiaceae bacterium	MAG: hypothetical protein HOO96_24755 [Polyangiaceae bacterium].	GCA_013141295.1
NQE54029.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1291	lapB_1	Euryarchaeota	ANME-1 cluster archaeon GoMg3.2	Lipopolysaccharide assembly protein B [ANME-1 cluster archaeon GoMg3.2].	GCA_013180565.1
NQV22738.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1245	HQ518_00080	Planctomycetes	Rhodopirellula sp.	MAG: hypothetical protein HQ518_00080 [Rhodopirellula sp.].	GCA_013203845.1
NQY79025.1	TPR+PIN*→	TPR+PIN	1272	HRT47_01810	Terrabacteria group	Candidatus Caenarcaniphilales bacterium	MAG: hypothetical protein HRT47_01810 [Candidatus Caenarcaniphilales bacterium].	GCA_013216135.1
NQZ35237.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1069	HRT58_06210	Bacteroidetes	Crocinitomicaceae bacterium	MAG: hypothetical protein HRT58_06210 [Crocinitomicaceae bacterium].	GCA_013214785.1
NQZ40471.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1088	HRT96_10385	Gammaproteobacteria	Moritella sp.	MAG: hypothetical protein HRT96_10385 [Moritella sp.].	GCA_013215705.1
NSZ07544.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1180	G6M14_14320	Alphaproteobacteria	Agrobacterium tumefaciens	hypothetical protein G6M14_14320 [Agrobacterium tumefaciens].	GCA_013318315.1
NTV22000.1	TPR+PIN*→	TPR+PIN	942	HGB03_00315	Bacteria	Candidatus Yonathbacteria bacterium	MAG: hypothetical protein HGB03_00315 [Candidatus Yonathbacteria bacterium].	GCA_013334825.1
NTW26872.1	REase→ REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1310	HGA36_00950	Bacteria	Candidatus Moranbacteria bacterium	MAG: hypothetical protein HGA36_00950 [Candidatus Moranbacteria bacterium].	GCA_013336225.1
NTZ52560.1	HetE-N1→?→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	513	FCH32_20020	Gammaproteobacteria	Citrobacter gillenii	hypothetical protein FCH32_20020 [Citrobacter gillenii].	GCA_013337685.1
NWE92806.1	PIN*→	PIN	344	HX893_32300	Gammaproteobacteria	Pseudomonas reactans	hypothetical protein HX893_32300, partial [Pseudomonas reactans].	GCA_013386215.1
NWO07476.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1130	HLX50_17830	Gammaproteobacteria	Alteromonadaceae bacterium	MAG: hypothetical protein HLX50_17830 [Alteromonadaceae bacterium].	GCA_013393545.1
OBH13398.1	X+PIN*→	X+PIN	755	A5695_13915	Actinobacteria	Mycobacterium sp. E1747	hypothetical protein A5695_13915 [Mycobacterium sp. E1747].	GCA_001667775.1
OBR53101.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1277	A6456_09045	Betaproteobacteria	Paraburkholderia tropica	hypothetical protein A6456_09045 [Paraburkholderia tropica].	GCA_001673675.1
OCX17561.1	REase+TPR+TPR+GreAB-C+PIN*→	REase+TPR+TPR+GreAB-C+PIN	1207	QV13_12440	Alphaproteobacteria	Mesorhizobium hungaricum	hypothetical protein QV13_12440 [Mesorhizobium hungaricum].	GCA_001705425.1
ODM45291.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1187	A9320_11670	Alphaproteobacteria	Ruegeria sp. PBVC088	hypothetical protein A9320_11670 [Ruegeria sp. PBVC088].	GCA_001717995.1
ODS63626.1	GreAB-C+PIN*→	GreAB-C+PIN	516	ABS37_11570	Betaproteobacteria	Acidovorax sp. SCN 65-108	MAG: hypothetical protein ABS37_11570 [Acidovorax sp. SCN 65-108].	GCA_001724055.1
ODT73806.1	REase+TPR+TPR+GreAB-C+PIN*→	REase+TPR+TPR+GreAB-C+PIN	1296	ABS76_38455	Alphaproteobacteria	Pelagibacterium sp. SCN 64-44	MAG: hypothetical protein ABS76_38455 [Pelagibacterium sp. SCN 64-44].	GCA_001724955.1
OEJ21925.1	REase+PIN*→	REase+PIN	1260	AR457_38995	Actinobacteria	Streptomyces agglomeratus	hypothetical protein AR457_38995 [Streptomyces agglomeratus].	GCA_001746465.1
OFX87846.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1236	A2X00_15495	Bacteroidetes	Bacteroidetes bacterium GWE2_32_14	MAG: hypothetical protein A2X00_15495 [Bacteroidetes bacterium GWE2_32_14].	GCA_001768405.1
OFY15991.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1237	A2X02_04985	Bacteroidetes	Bacteroidetes bacterium GWF2_29_10	MAG: hypothetical protein A2X02_04985 [Bacteroidetes bacterium GWF2_29_10].	GCA_001768555.1
OGC02499.1	PIN*→	PIN	178	A2V82_02050	Bacteria	candidate division KSB1 bacterium RBG_16_48_16	MAG: hypothetical protein A2V82_02050 [candidate division KSB1 bacterium RBG_16_48_16].	GCA_001771235.1
OGH88116.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1191	A3J93_00010	Bacteria	Candidatus Magasanikbacteria bacterium RIFOXYC2_FULL_42_28	MAG: hypothetical protein A3J93_00010 [Candidatus Magasanikbacteria bacterium RIFOXYC2_FULL_42_28].	GCA_001784435.1
OGI36016.1	TRD+TRD→?→?→?→ TPR+PIN*→	TPR+PIN	1186	A2259_01680	Bacteria	Candidatus Moranbacteria bacterium RIFOXYA2_FULL_43_15	MAG: hypothetical protein A2259_01680 [Candidatus Moranbacteria bacterium RIFOXYA2_FULL_43_15].	GCA_001784835.1

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OGS08035.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1270	A2270_03040	Elusimicrobia	Elusimicrobia bacterium RIFOXYA12_FULL_51_18	MAG: hypothetical protein A2270_03040 [Elusimicrobia bacterium RIFOXYA12_FULL_51_18].	GCA_001800245.1
OGU66359.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1303	A2W30_02620	Ignavibacteriae	Ignavibacteria bacterium RBG_16_36_9	MAG: hypothetical protein A2W30_02620 [Ignavibacteria bacterium RBG_16_36_9].	GCA_001802895.1
OGU77131.1	PIN*→	PIN	573	A2W11_11280	Ignavibacteriae	Ignavibacteria bacterium RBG_16_35_7	MAG: hypothetical protein A2W11_11280 [Ignavibacteria bacterium RBG_16_35_7].	GCA_001802885.1
OIP66815.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	402	AUK42_07760	Bacteria	Candidatus Atribacteria bacterium CG2_30_33_13	MAG: hypothetical protein AUK42_07760 [Candidatus Atribacteria bacterium CG2_30_33_13].	GCA_001873345.1
OJV65414.1	HetE-N1→ HetE-N1+TPR+GreAB-C+PIN*→	HetE-N1+TPR+GreAB-C+PIN	1117	BGO35_21125	Betaproteobacteria	Burkholderiales bacterium 64-34	MAG: hypothetical protein BGO35_21125 [Burkholderiales bacterium 64-34].	GCA_001897585.1
OJW35018.1	TPR+GreAB-C+PIN*→||||<-REase	TPR+GreAB-C+PIN	1246	BGO54_02365	Bacteroidetes	Sphingobacteriales bacterium 46-32	MAG: hypothetical protein BGO54_02365 [Sphingobacteriales bacterium 46-32].	GCA_001898485.1
OJW61617.1	TIR→?→?→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1114	BGO65_09490	Alphaproteobacteria	Afipia sp. 64-13	MAG: hypothetical protein BGO65_09490 [Afipia sp. 64-13].	GCA_001897755.1
OMR67119.1	TPR+GreAB-C+PIN*→||||<-HTH+HTH	TPR+GreAB-C+PIN	879	AQ727_25970	Betaproteobacteria	Burkholderia pseudomallei	hypothetical protein AQ727_25970 [Burkholderia pseudomallei].	GCA_001976575.1
OSN14318.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1486	BV340_04459	Gammaproteobacteria	Pseudomonas syringae pv. actinidiae	hypothetical protein BV340_04459 [Pseudomonas syringae pv. actinidiae].	GCA_002111665.1
OSN30099.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1336	BV342_05184	Gammaproteobacteria	Pseudomonas syringae pv. actinidiae	hypothetical protein BV342_05184 [Pseudomonas syringae pv. actinidiae].	GCA_002111745.1
OUC14796.1	TPR+TPR+PNPase→ PNPase+TPR+GreAB-C+PIN*→	PNPase+TPR+GreAB-C+PIN	1396	B0A82_10750	Cyanobacteria	Alkalinema sp. CACIAM 70d	MAG: hypothetical protein B0A82_10750 [Alkalinema sp. CACIAM 70d].	GCA_002148405.1
OUR78422.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1191	A9Q83_07770	Alphaproteobacteria	Alphaproteobacteria bacterium 46_93_T64	hypothetical protein A9Q83_07770 [Alphaproteobacteria bacterium 46_93_T64].	GCA_002163135.1
OWZ89184.1	REase+TPR+TPR+GreAB-C+PIN*→	REase+TPR+TPR+GreAB-C+PIN	1352	B9J07_34245	Alphaproteobacteria	Sinorhizobium sp. LM21	hypothetical protein B9J07_34245 [Sinorhizobium sp. LM21].	GCA_002216665.1
OYD66813.1	REase+TPR+GreAB-C+PIN*→?→ Trypsin→	REase+TPR+GreAB-C+PIN	1243	BDB13_0310	Actinobacteria	Rhodococcus sp. OK302	uncharacterized protein DUF4365 [Rhodococcus sp. OK302].	GCA_002245895.1
OYW86349.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	629	B7Z22_06790	Alphaproteobacteria	Hyphomonas sp. 32-62-5	MAG: hypothetical protein B7Z22_06790, partial [Hyphomonas sp. 32-62-5].	GCA_002280065.1
OYX15563.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1211	B7Z15_00100	Alphaproteobacteria	Rhizobiales bacterium 32-66-8	MAG: hypothetical protein B7Z15_00100 [Rhizobiales bacterium 32-66-8].	GCA_002280205.1
OZB15488.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1294	B7X53_11340	Alphaproteobacteria	Hyphomonas sp. 34-62-18	MAG: hypothetical protein B7X53_11340 [Hyphomonas sp. 34-62-18].	GCA_002282565.1
PBC66280.1	X+PIN*→	X+PIN	685	BX265_8343	Actinobacteria	Streptomyces sp. TLI_235	hypothetical protein BX265_8343 [Streptomyces sp. TLI_235].	GCA_002300355.1
PCJ29538.1	REase+TPR+PIN*→	REase+TPR+PIN	1292	COA99_19375	Gammaproteobacteria	Moraxellaceae bacterium	MAG: hypothetical protein COA99_19375 [Moraxellaceae bacterium].	GCA_002402125.1
PDQ17661.1	REase+TPR+TPR+GreAB-C+PIN*→	REase+TPR+TPR+GreAB-C+PIN	1265	CN311_28810	Alphaproteobacteria	Mesorhizobium sanjuanii	hypothetical protein CN311_28810 [Mesorhizobium sanjuanii].	GCA_002529485.1
PGS40120.1	TPR+PIN*→	TPR+PIN	1006	COC58_18130	Firmicutes	Bacillus cereus	hypothetical protein COC58_18130 [Bacillus cereus].	GCA_002577165.1
PIG41510.1	TPR+PIN*→	TPR+PIN	1214	CLZ78_0083	Actinobacteria	Streptomyces sp. 61	hypothetical protein CLZ78_0083 [Streptomyces sp. 61].	GCA_002754535.1
PIP62053.1	<-CITB-HTH+LexA-protease||TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1272	COW99_00715	Bacteria	Candidatus Roizmanbacteria bacterium CG22_combo_CG10-13_8_21_14_all_38_20	MAG: hypothetical protein COW99_00715 [Candidatus Roizmanbacteria bacterium CG22_combo_CG10-13_8_21_14_all_38_20].	GCA_002786635.1
PIU06549.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1132	COT56_09580	Alphaproteobacteria	Methylobacterium sp. CG09_land_8_20_14_0_10_71_15	MAG: hypothetical protein COT56_09580 [Methylobacterium sp. CG09_land_8_20_14_0_10_71_15].	GCA_002778835.1

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PKM50370.1	TPR+PIN*→	TPR+PIN	1214	CVV02_11355	Firmicutes	Firmicutes bacterium HGW-Firmicutes-7	MAG: hypothetical protein CVV02_11355 [Firmicutes bacterium HGW-Firmicutes-7].	GCA_002841375.1
PKN75416.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1116	CVU49_03915	FCB group	Candidatus Cloacimonetes bacterium HGW-Cloacimonetes-2	MAG: hypothetical protein CVU49_03915 [Candidatus Cloacimonetes bacterium HGW-Cloacimonetes-2].	GCA_002842035.1
PKO82710.1	HetE-N1→ HetE-N1+TPR+GreAB-C+PIN*→	HetE-N1+TPR+GreAB-C+PIN	1126	CVU19_00260	Betaproteobacteria	Betaproteobacteria bacterium HGW-Betaproteobacteria-13	MAG: hypothetical protein CVU19_00260 [Betaproteobacteria bacterium HGW-Betaproteobacteria-13].	GCA_002842325.1
PLP59030.1	REase+TPR+TPR+GreAB-C+PIN*→	REase+TPR+TPR+GreAB-C+PIN	1226	CYK37_11065	Alphaproteobacteria	Mesorhizobium loti	hypothetical protein CYK37_11065 [Mesorhizobium loti].	GCA_002858745.1
PLX86308.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1333	C0617_01645	Deltaproteobacteria	Desulfuromonas sp.	MAG: hypothetical protein C0617_01645 [Desulfuromonas sp.].	GCA_002868845.1
PLY41243.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1106	CSZ94_17070	Betaproteobacteria	Janthinobacterium sp. ROICE36	hypothetical protein CSZ94_17070 [Janthinobacterium sp. ROICE36].	GCA_002869965.1
PMJ73057.1	HetE-N1→?→ GreAB-C*→	GreAB-C	461	BCU23_16040	Gammaproteobacteria	Vibrio splendidus	hypothetical protein BCU23_16040 [Vibrio splendidus].	GCA_002877525.1
POU10505.1	PIN*→	PIN	385	C3420_16980	Gammaproteobacteria	Acinetobacter sp. ACNIH3	hypothetical protein C3420_16980 [Acinetobacter sp. ACNIH3].	GCA_002918965.1
PQZ99140.1	TPR+PIN*→	TPR+PIN	932	CQ019_16410	Actinobacteria	Arthrobacter sp. MYb229	hypothetical protein CQ019_16410 [Arthrobacter sp. MYb229].	GCA_002975405.1
PRY64434.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1090	B0H98_10595	Gammaproteobacteria	Halomonas songnenensis	hypothetical protein B0H98_10595 [Halomonas songnenensis].	GCA_003002925.1
PSL26440.1	HNH+TPR+GreAB-C+PIN*→	HNH+TPR+GreAB-C+PIN	1234	CLV42_111154	Bacteroidetes	Chitinophaga ginsengisoli	HNH endonuclease [Chitinophaga ginsengisoli].	GCA_003014595.1
PTH81074.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	851	DAA48_11040	Gammaproteobacteria	Aeromonas veronii	hypothetical protein DAA48_11040 [Aeromonas veronii].	GCA_003036425.1
PTL60251.1	X+PIN*→	X+PIN	1319	C7Y72_11685	Actinobacteria	Conexibacter sp. Seoho-28	hypothetical protein C7Y72_11685 [Conexibacter sp. Seoho-28].	GCA_003044185.1
PTX57421.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1184	C8N43_2089	Alphaproteobacteria	Litoreibacter ponti	hypothetical protein C8N43_2089 [Litoreibacter ponti].	GCA_003054285.1
PWM31885.1	GreAB*→	GreAB	675	DBX55_01895	Verrucomicrobia	Verrucomicrobia bacterium	MAG: transcription elongation factor GreAB [Verrucomicrobia bacterium].	GCA_003343565.1
PWM77364.1	NACHT→?→ X+PIN*→ HTH→	X+PIN	733	DBY32_08445	Firmicutes	Phascolarctobacterium sp.	MAG: hypothetical protein DBY32_08445 [Phascolarctobacterium sp.].	GCA_003150755.1
PWM80532.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1185	DBY41_05620	Firmicutes	Clostridium sp.	MAG: hypothetical protein DBY41_05620 [Clostridium sp.].	GCA_003150745.1
PZR80846.1	BirA-HTH→ HEPN→ REase+TPR+TPR+GreAB-C+PIN*→	REase+TPR+TPR+GreAB-C+PIN	1131	DI537_39015	Gammaproteobacteria	Pseudomonas stutzeri	MAG: hypothetical protein DI537_39015, partial [Pseudomonas stutzeri].	GCA_003243385.1
PZR82088.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1139	DI537_37240	Gammaproteobacteria	Pseudomonas stutzeri	MAG: hypothetical protein DI537_37240 [Pseudomonas stutzeri].	GCA_003243385.1
PZU06315.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1323	DI605_19340	Alphaproteobacteria	Sphingomonas sp.	MAG: hypothetical protein DI605_19340 [Sphingomonas sp.].	GCA_003248515.1
PZU12119.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	859	DI622_15520	Bacteroidetes	Chryseobacterium sp.	MAG: hypothetical protein DI622_15520, partial [Chryseobacterium sp.].	GCA_003248465.1
QDS92471.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1250	FF011L_12140	Planctomycetes	Planctomycetes bacterium FF011L	hypothetical protein FF011L_12140 [Planctomycetes bacterium FF011L].	GCA_007741495.1
QDT50511.1	REase+TPR+GreAB-C+PIN→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	495	Pan258_45900	Planctomycetes	Symmachiella dynata	hypothetical protein Pan258_45900 [Symmachiella dynata].	GCA_007744975.1
QDV12361.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1246	CA51_22440	Planctomycetes	Rosistilla oblonga	Tetratricopeptide repeat protein [Rosistilla oblonga].	GCA_007751715.1
QDV84971.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	954	TBK1r_39230	Planctomycetes	Planctomycetes bacterium TBK1r	hypothetical protein TBK1r_39230 [Planctomycetes bacterium TBK1r].	GCA_007753675.1

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QFS96076.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1184	FIV06_01510	Alphaproteobacteria	Labrenzia sp. THAF191b	hypothetical protein FIV06_01510 [Labrenzia sp. THAF191b].	GCA_009363315.1
QHB84489.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1094	GIS01_21340	Gammaproteobacteria	Aeromonas veronii	hypothetical protein GIS01_21340 [Aeromonas veronii].	GCA_009833025.1
QIC10441.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1069	PmVP161_2026	Gammaproteobacteria	Pasteurella multocida	hypothetical protein PmVP161_2026 [Pasteurella multocida].	GCA_011390865.1
QND19257.1	REase+TPR+TPR+GreAB-C+PIN*→	REase+TPR+TPR+GreAB-C+PIN	1348	HB774_02700	Alphaproteobacteria	Rhizobium leguminosarum bv. viciae	hypothetical protein HB774_02700 [Rhizobium leguminosarum bv. viciae].	GCA_014189655.1
QPL52208.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1130	I3X05_08770	Gammaproteobacteria	Vibrio navarrensis	hypothetical protein I3X05_08770 [Vibrio navarrensis].	GCA_015767675.1
QQO85647.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1089	D7032_21665	Gammaproteobacteria	Shewanella algae	hypothetical protein D7032_21665 [Shewanella algae].	-
QQR55448.1	X+PIN*→	X+PIN	1237	IPG41_02740	Bacteria	Candidatus Peregrinibacteria bacterium	MAG: hypothetical protein IPG41_02740 [Candidatus Peregrinibacteria bacterium].	GCA_016699145.1
RAZ30556.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1208	DO944_13495	Actinobacteria	Microbacterium sp. SMR1	hypothetical protein DO944_13495 [Microbacterium sp. SMR1].	GCA_003289625.1
RBN51622.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1135	DR980_00180	Bacteroidetes	Flavobacterium psychrolimnae	hypothetical protein DR980_00180 [Flavobacterium psychrolimnae].	GCA_003312425.1
RBP77372.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1175	DFO80_1601	Alphaproteobacteria	Rhodobacter sp. 140A	hypothetical protein DFO80_1601, partial [Rhodobacter sp. 140A].	GCA_003315475.1
RCI79301.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	630	DNK03_13895	Alphaproteobacteria	Brucella anthropi	hypothetical protein DNK03_13895 [Brucella anthropi].	GCA_003325675.1
REJ78752.1	TPR+GreAB-C+PIN*→||||<-?<-?<-?<-REase+SNF2	TPR+GreAB-C+PIN	1257	DWQ32_08270	Acidobacteria	Acidobacteria bacterium	MAG: hypothetical protein DWQ32_08270 [Acidobacteria bacterium].	GCA_003385635.1
REJ87566.1	TPR+PIN*→	TPR+PIN	2085	DWQ34_24785	Planctomycetes	Planctomycetes bacterium	MAG: hypothetical protein DWQ34_24785 [Planctomycetes bacterium].	GCA_003388575.1
RGJ64387.1	X+PIN*→ HTH→?→?→ HTH→	X+PIN	1176	DXD50_08885	Firmicutes	Dorea formicigenerans	hypothetical protein DXD50_08885 [Dorea formicigenerans].	GCA_003437395.1
RGN88412.1	X+PIN*→ HTH→?→?→ HTH→	X+PIN	1176	DXB36_13695	Firmicutes	Dorea formicigenerans	hypothetical protein DXB36_13695 [Dorea formicigenerans].	GCA_003439255.1
RGR97298.1	TM+TM+TPR+PIN*→	TM+TM+TPR+PIN	1206	DWY20_07060	Bacteroidetes	Phocaeicola coprocola	hypothetical protein DWY20_07060 [Phocaeicola coprocola].	GCA_003458565.1
RGS66838.1	X+PIN*→ HTH→?→?→ HTH→	X+PIN	766	DWX78_14950	Firmicutes	Dorea formicigenerans	hypothetical protein DWX78_14950 [Dorea formicigenerans].	GCA_003458845.1
RGY02630.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	410	DXA56_15985	Firmicutes	Blautia obeum	hypothetical protein DXA56_15985 [Blautia obeum].	GCA_003463085.1
RGZ63692.1	Mbetalac→ Trypsin→?→ TPR+PIN*→	TPR+PIN	1371	DW979_12370	Firmicutes	Eubacterium sp. AM49-13BH	hypothetical protein DW979_12370, partial [Eubacterium sp. AM49-13BH].	GCA_003464165.1
RHN14952.1	X+PIN*→ HTH→?→?→ HTH→	X+PIN	1175	DWZ24_11335	Firmicutes	Dorea formicigenerans	hypothetical protein DWZ24_11335 [Dorea formicigenerans].	GCA_003475555.1
RHV44852.1	X+PIN*→	X+PIN	1229	DXB47_09745	Firmicutes	Firmicutes bacterium OM04-13BH	hypothetical protein DXB47_09745 [Firmicutes bacterium OM04-13BH].	GCA_003481745.1
RHZ93582.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	924	D1920_20895	Alphaproteobacteria	Rhodopseudomonas palustris	hypothetical protein D1920_20895 [Rhodopseudomonas palustris].	GCA_003547145.1
RJT21930.1	TPR+GreAB-C*→	TPR+GreAB-C	282	D5I55_15915	Alphaproteobacteria	Aestuariisphingobium litorale	hypothetical protein D5I55_15915 [Aestuariisphingobium litorale].	GCA_003602075.1
RKE07817.1	TPR+PIN*→	TPR+PIN	806	C8E86_2653	Actinobacteria	Catellatospora citrea	hypothetical protein C8E86_2653 [Catellatospora citrea].	GCA_003610235.1
RKG98095.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	461	D7X32_30660	Deltaproteobacteria	Corallococcus carmarthensis	hypothetical protein D7X32_30660 [Corallococcus carmarthensis].	GCA_003611695.1
RKS06034.1	TPR+PIN*→ PAIREDC-HTH→	TPR+PIN	1209	DFP74_1655	Actinobacteria	Nocardiopsis sp. Huas11	hypothetical protein DFP74_1655 [Nocardiopsis sp. Huas11].	GCA_003634495.1

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RKU09109.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1315	C6502_13840	Bacteria	Candidatus Poribacteria bacterium	MAG: hypothetical protein C6502_13840 [Candidatus Poribacteria bacterium].	GCA_003635265.1
RKW53732.1	X+PIN*→	X+PIN	1207	D8H95_11955	Firmicutes	Lachnospiraceae bacterium	MAG: hypothetical protein D8H95_11955 [Lachnospiraceae bacterium].	GCA_003640285.1
RKY60125.1	PIN*→	PIN	174	DRP94_01435	FCB group	Candidatus Latescibacteria bacterium	MAG: DUF3368 domain-containing protein [Candidatus Latescibacteria bacterium].	GCA_003645885.1
RMB87410.1	TPR+PIN*→	TPR+PIN	746	CTZ28_00010	Actinobacteria	Streptomyces shenzhenensis	hypothetical protein CTZ28_00010 [Streptomyces shenzhenensis].	GCA_003688995.1
RMQ50424.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1489	ALQ04_05433	Gammaproteobacteria	Pseudomonas cichorii	hypothetical protein ALQ04_05433 [Pseudomonas cichorii].	GCA_003700275.1
RMV01228.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1486	ALP20_200053	Gammaproteobacteria	Pseudomonas coronafaciens pv. coronafaciens	hypothetical protein ALP20_200053 [Pseudomonas coronafaciens pv. coronafaciens].	GCA_003702885.1
RMV06369.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	904	ALP17_05452	Gammaproteobacteria	Pseudomonas savastanoi	hypothetical protein ALP17_05452 [Pseudomonas savastanoi].	GCA_003702965.1
RMV08832.1	REase→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	881	ALP16_05399	Gammaproteobacteria	Pseudomonas savastanoi	hypothetical protein ALP16_05399, partial [Pseudomonas savastanoi].	GCA_003702985.1
RNA68542.1	<-REase||TPR+PIN*→	TPR+PIN	999	EBO34_00790	Firmicutes	Bacillus sp. KQ-3	hypothetical protein EBO34_00790 [Bacillus sp. KQ-3].	GCA_003710255.1
RND30553.1	HetE-N1→ HetE-N1+TPR+GreAB-C+PIN*→	HetE-N1+TPR+GreAB-C+PIN	1088	EC575_19215	Gammaproteobacteria	Vibrio cholerae	hypothetical protein EC575_19215 [Vibrio cholerae].	GCA_003712005.1
ROZ42670.1	HTH+PNPase+TPR+GreAB-C+PIN*→	HTH+PNPase+TPR+GreAB-C+PIN	1571	EEB13_29810	Actinobacteria	Rhodococcus sp. WS3	hypothetical protein EEB13_29810 [Rhodococcus sp. WS3].	GCA_003797085.1
RPV62916.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	808	IPC830_03545	Gammaproteobacteria	Pseudomonas aeruginosa	hypothetical protein IPC830_03545 [Pseudomonas aeruginosa].	GCA_003836445.1
RPX47920.1	DOC+HTH→ REase+TOPC→?→ HetE-N1→ HetE-N1+TPR+GreAB-C+PIN*→	HetE-N1+TPR+GreAB-C+PIN	1126	IPC713_13275	Gammaproteobacteria	Pseudomonas aeruginosa	hypothetical protein IPC713_13275 [Pseudomonas aeruginosa].	GCA_003836815.1
RQR65213.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1346	DIE12_31765	Betaproteobacteria	Burkholderia sp. Bp9015	tetratricopeptide repeat protein [Burkholderia sp. Bp9015].	GCA_003853505.1
RQY09920.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1135	DF117_34925	Betaproteobacteria	Burkholderia stagnalis	tetratricopeptide repeat protein [Burkholderia stagnalis].	GCA_003857615.1
RSM21562.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	851	C5B76_20720	Gammaproteobacteria	Aeromonas salmonicida	hypothetical protein C5B76_20720 [Aeromonas salmonicida].	GCA_003947355.1
RSM25744.1	MNS-Npun2340+TPR+GreAB-C+PIN*→	MNS-Npun2340+TPR+GreAB-C+PIN	851	C5B77_18585	Gammaproteobacteria	Aeromonas salmonicida	hypothetical protein C5B77_18585 [Aeromonas salmonicida].	GCA_003947375.1
RWE64146.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1329	EOS62_30690	Alphaproteobacteria	Mesorhizobium sp.	MAG: hypothetical protein EOS62_30690 [Mesorhizobium sp.].	GCA_004018195.1
RWI50090.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1328	EOR16_31040	Alphaproteobacteria	Mesorhizobium sp.	MAG: hypothetical protein EOR16_31040 [Mesorhizobium sp.].	GCA_004019035.1
RWN29279.1	REase+TPR+TPR+GreAB-C+PIN*→	REase+TPR+TPR+GreAB-C+PIN	1333	EOR95_21980	Alphaproteobacteria	Mesorhizobium sp.	MAG: hypothetical protein EOR95_21980 [Mesorhizobium sp.].	GCA_004020785.1
RWN66659.1	REase+TPR+TPR+GreAB-C+PIN*→	REase+TPR+TPR+GreAB-C+PIN	1333	EOR99_16025	Alphaproteobacteria	Mesorhizobium sp.	MAG: hypothetical protein EOR99_16025 [Mesorhizobium sp.].	GCA_004020565.1
RWQ61473.1	REase+TPR+TPR+GreAB-C+PIN*→	REase+TPR+TPR+GreAB-C+PIN	1333	EOS86_33015	Alphaproteobacteria	Mesorhizobium sp.	MAG: hypothetical protein EOS86_33015 [Mesorhizobium sp.].	GCA_004021745.1
RWQ70448.1	REase+TPR+TPR+GreAB-C+PIN*→	REase+TPR+TPR+GreAB-C+PIN	1002	EOS85_27065	Alphaproteobacteria	Mesorhizobium sp.	MAG: hypothetical protein EOS85_27065 [Mesorhizobium sp.].	GCA_004021925.1
RWU17258.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1447	DM813_28290	Gammaproteobacteria	Pseudomonas alkylphenolica	hypothetical protein DM813_28290 [Pseudomonas alkylphenolica].	GCA_004025535.1
RXH58244.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1185	GRAN_1554	Acidobacteria	Granulicella sibirica	hypothetical protein GRAN_1554 [Granulicella sibirica].	GCA_004115155.1
RXK05389.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1249	CRU97_08585	Epsilonproteobacteria	Halarcobacter bivalviorum	hypothetical protein CRU97_08585 [Halarcobacter bivalviorum].	GCA_004116705.1

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RXO70745.1	HetE-N1→?→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	686	D0516_07920	Gammaproteobacteria	Salmonella enterica	hypothetical protein D0516_07920 [Salmonella enterica].	GCA_004120835.1
RYE55646.1	PIN*→	PIN	344	EOP48_09765	Bacteroidetes	Sphingobacteriales bacterium	MAG: hypothetical protein EOP48_09765 [Sphingobacteriales bacterium].	GCA_004144425.1
RYG99407.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1330	EON58_04040	Alphaproteobacteria	Alphaproteobacteria bacterium	MAG: hypothetical protein EON58_04040 [Alphaproteobacteria bacterium].	GCA_004145575.1
RYX84272.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1192	EON83_11290	unclassified Bacteria	bacterium	MAG: hypothetical protein EON83_11290 [bacterium].	GCA_004172935.1
RYY90115.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1333	EOO15_03925	Bacteroidetes	Chitinophagaceae bacterium	MAG: hypothetical protein EOO15_03925 [Chitinophagaceae bacterium].	GCA_004173495.1
RZJ58585.1	TPR+PIN*→	TPR+PIN	1309	EOO55_00010	Bacteroidetes	Hymenobacter sp.	MAG: hypothetical protein EOO55_00010 [Hymenobacter sp.].	GCA_004211105.1
RZJ92304.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1267	EOO20_02310	Bacteroidetes	Chryseobacterium sp.	MAG: hypothetical protein EOO20_02310 [Chryseobacterium sp.].	GCA_004210875.1
RZJ92386.1	REase+nSTAND3→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1237	EOO20_01975	Bacteroidetes	Chryseobacterium sp.	MAG: tetratricopeptide repeat protein [Chryseobacterium sp.].	GCA_004210875.1
RZL63110.1	PIN*→	PIN	307	EOO93_08085	Bacteroidetes	Pedobacter sp.	MAG: hypothetical protein EOO93_08085 [Pedobacter sp.].	GCA_004295955.1
RZL84003.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1323	EOP66_03300	Alphaproteobacteria	Sphingomonas sp.	MAG: tetratricopeptide repeat protein [Sphingomonas sp.].	GCA_004296035.1
SCB54124.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1171	GA0061098_102379	Alphaproteobacteria	Bradyrhizobium shewense	Transcription elongation factor, GreA/GreB family [Bradyrhizobium shewense].	GCA_900094605.1
SCE01180.1	TPR+PIN*→||||<-NUDIX	TPR+PIN	1134	GA0115241_108994	Actinobacteria	Streptomyces sp. DpondAA-D4	hypothetical protein GA0115241_108994 [Streptomyces sp. DpondAA-D4].	GCA_900091745.1
SCF05211.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1358	GA0070215_1072	Actinobacteria	Micromonospora marina	hypothetical protein GA0070215_1072 [Micromonospora marina].	GCA_900091565.1
SCF05420.1	SAD+HNH→ X+PIN*→	X+PIN	1233	GA0070562_5649	Actinobacteria	Micromonospora tulbaghiae	hypothetical protein GA0070562_5649 [Micromonospora tulbaghiae].	GCA_900091605.1
SCL17674.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1264	GA0074694_2093	Actinobacteria	Micromonospora inyonensis	Tfp pilus assembly protein PilF [Micromonospora inyonensis].	GCA_900091415.1
SCQ18794.1	CHC2+Toprim-DNAG→?→?→?→ HTH→ SIG+TM→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1126	TFUB4_00594	Bacteroidetes	Tannerella forsythia	hypothetical protein TFUB4_00594 [Tannerella forsythia].	GCA_900096725.1
SCQ19220.1	CHC2+Toprim-DNAG→?→?→?→ HTH→ SIG+TM→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1126	TFUB20_00631	Bacteroidetes	Tannerella forsythia	hypothetical protein TFUB20_00631 [Tannerella forsythia].	GCA_900096735.1
SEP47521.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	975	SAMN02787149_1275	Gammaproteobacteria	Pseudomonas sp. Snoq117.2	hypothetical protein SAMN02787149_1275 [Pseudomonas sp. Snoq117.2].	GCA_900110545.1
SFD04359.1	<-KAP_NTPase||TPR+PIN*→	TPR+PIN	1216	SAMN04487968_1267	Actinobacteria	Nocardioides terrae	hypothetical protein SAMN04487968_1267 [Nocardioides terrae].	GCA_900112345.1
SFF03357.1	<-Cas_Cas1<-?||?→?→?→?→ REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1349	SAMN05428977_10446	Betaproteobacteria	Nitrosomonas sp. Nm166	hypothetical protein SAMN05428977_10446 [Nitrosomonas sp. Nm166].	GCA_900112825.1
SHH05937.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1445	SAMN05428948_2561	Betaproteobacteria	Massilia sp. CF038	hypothetical protein SAMN05428948_2561 [Massilia sp. CF038].	GCA_900129765.1
SHN30683.1	PAIREDC-HTH→ REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1588	SAMN02787076_04976	Betaproteobacteria	Rhizobacter sp. OV335	hypothetical protein SAMN02787076_04976 [Rhizobacter sp. OV335].	GCA_900142965.1
SIO63359.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1291	SAMN05444166_7323	Planctomycetes	Singulisphaera sp. GP187	Transcription elongation factor, GreA/GreB family [Singulisphaera sp. GP187].	GCA_900129635.1
SOZ22209.1	REase+TPR+GreAB-C+PIN→?→?→ PIN*→	PIN	271	CBM2604_U10003	Betaproteobacteria	Cupriavidus taiwanensis	hypothetical protein CBM2604_U10003 [Cupriavidus taiwanensis].	GCA_900249855.1
SPT59210.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1218	NCTC11373_05764	Actinobacteria	Actinomadura madurae	Flp pilus assembly protein TadD, contains TPR repeats [Actinomadura madurae].	GCA_900445005.1
SPY99988.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1146	NCTC11842_00133	Gammaproteobacteria	Pseudomonas luteola	Uncharacterised protein [Pseudomonas luteola].	GCA_900455515.1

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SQK85244.1	DOC+HTH→ REase+TOPC→ HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1088	NCTC9433_00599	Gammaproteobacteria	Pseudomonas aeruginosa	Uncharacterised protein [Pseudomonas aeruginosa].	GCA_900478745.1
SSC09307.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1137	BTURTLESOX_2492	unclassified Bacteria	bacterium endosymbiont of Bathymodiolus sp. 5 South	hypothetical protein BTURTLESOX_2492 [bacterium endosymbiont of Bathymodiolus sp. 5 South].	GCA_900127295.1
STJ38438.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1093	NCTC9110_01467	Gammaproteobacteria	Escherichia coli	Uncharacterised protein [Escherichia coli].	GCA_900449425.1
STR27356.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1303	NCTC8661_05000	Betaproteobacteria	Janthinobacterium lividum	Putative Zn-dependent protease, contains TPR repeats [Janthinobacterium lividum].	GCA_900451225.1
SUJ03282.1	PIN*→	PIN	223	NCTC4822_01389	Firmicutes	Sporosarcina pasteurii	Uncharacterised protein [Sporosarcina pasteurii].	GCA_900457495.1
TAA79883.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1069	PMCND_08490	Gammaproteobacteria	Pasteurella multocida	hypothetical protein PMCND_08490 [Pasteurella multocida].	GCA_004286935.1
TAJ47852.1	TPR+PIN*→	TPR+PIN	1186	EPO52_06520	Actinobacteria	Herbiconiux sp.	MAG: hypothetical protein EPO52_06520 [Herbiconiux sp.].	GCA_004297105.1
TAM51231.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1301	EPN57_18445	Betaproteobacteria	Paraburkholderia sp.	MAG: hypothetical protein EPN57_18445 [Paraburkholderia sp.].	GCA_004322045.1
TAM55201.1	REase+TPR+GreAB-C+PIN*→||||<-?||AbiJ-NTD3+REase→	REase+TPR+GreAB-C+PIN	1335	EPN57_04160	Betaproteobacteria	Paraburkholderia sp.	MAG: hypothetical protein EPN57_04160 [Paraburkholderia sp.].	GCA_004322045.1
TCU73661.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1313	EDE10_104327	Alphaproteobacteria	Bradyrhizobium sp. Y-H1	tetratricopeptide repeat protein [Bradyrhizobium sp. Y-H1].	GCA_004346395.1
TDM08142.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1202	C4K60_01155	Betaproteobacteria	Ideonella sp. MAG2	MAG: hypothetical protein C4K60_01155 [Ideonella sp. MAG2].	GCA_004359425.1
TDZ78257.1	TPR+PIN*→	TPR+PIN	1185	DE4585_04094	Actinobacteria	Mycobacteroides salmoniphilum	hypothetical protein DE4585_04094 [Mycobacteroides salmoniphilum].	GCA_004366855.1
TIN45883.1	TPR+GreAB-C+PIN*→ TPR→	TPR+GreAB-C+PIN	539	E5Y32_12205	Alphaproteobacteria	Mesorhizobium sp.	MAG: GreA/GreB family elongation factor [Mesorhizobium sp.].	GCA_004961865.1
TIT34473.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	502	E5W78_10605	Alphaproteobacteria	Mesorhizobium sp.	MAG: hypothetical protein E5W78_10605, partial [Mesorhizobium sp.].	GCA_004965505.1
TIX43905.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	708	E5V40_01360	Alphaproteobacteria	Mesorhizobium sp.	MAG: GreA/GreB family elongation factor [Mesorhizobium sp.].	GCA_004964855.1
TLM83646.1	TPR+PIN*→	TPR+PIN	1179	FDW83_09305	Actinobacteria	Pseudarthrobacter sp. NamE2	tetratricopeptide repeat protein [Pseudarthrobacter sp. NamE2].	GCA_005796205.1
TMA89552.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1299	E6J74_25025	Deltaproteobacteria	Deltaproteobacteria bacterium	MAG: hypothetical protein E6J74_25025 [Deltaproteobacteria bacterium].	GCA_005879255.1
TMJ19619.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1331	E6G92_07565	Alphaproteobacteria	Alphaproteobacteria bacterium	MAG: hypothetical protein E6G92_07565 [Alphaproteobacteria bacterium].	GCA_005883305.1
TOF36973.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	785	CGJ28_20670	Gammaproteobacteria	Vibrio parahaemolyticus	hypothetical protein CGJ28_20670 [Vibrio parahaemolyticus].	GCA_006371865.1
TOH27190.1	GreAB-C*→	GreAB-C	599	CGI84_22675	Gammaproteobacteria	Vibrio parahaemolyticus	hypothetical protein CGI84_22675, partial [Vibrio parahaemolyticus].	GCA_006372765.1
TQE99579.1	REase+SNF2→ REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1230	FKY71_07895	Gammaproteobacteria	Spiribacter salinus	MAG: hypothetical protein FKY71_07895 [Spiribacter salinus].	GCA_006569195.1
TQS42859.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1252	FL583_22685	Actinobacteria	Cryptosporangium phraense	DUF4365 domain-containing protein [Cryptosporangium phraense].	GCA_006912135.1
TSP11291.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1314	FGG12_18885	Betaproteobacteria	Cupriavidus campinensis	DUF4365 domain-containing protein [Cupriavidus campinensis].	GCA_007572485.1
TVP63446.1	EAD10+SWACOS→?→ EAD10+TPR+GreAB-C+PIN*→	EAD10+TPR+GreAB-C+PIN	1213	EA343_08005	Cyanobacteria	Nodularia sp. (in: Bacteria)	MAG: hypothetical protein EA343_08005 [Nodularia sp. (in: Bacteria)].	GCA_007692755.1
TWD39045.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1117	FBY13_107200	Gammaproteobacteria	Pantoea sp. SJZ147	hypothetical protein FBY13_107200 [Pantoea sp. SJZ147].	GCA_007828605.1
TWI95027.1	TPR+GreAB-C+PIN→ PIN*→	PIN	240	JN11_04456	Bacteroidetes	Mucilaginibacter frigoritolerans	hypothetical protein JN11_04456 [Mucilaginibacter frigoritolerans].	GCA_007830615.1

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TXH46669.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1345	E6Q92_01630	Betaproteobacteria	Burkholderiaceae bacterium	MAG: tetratricopeptide repeat protein [Burkholderiaceae bacterium].	GCA_008012415.1
TXJ01161.1	X+PIN*→	X+PIN	1259	E6Q32_04910	Betaproteobacteria	Neisseriales bacterium	MAG: hypothetical protein E6Q32_04910 [Neisseriales bacterium].	GCA_008017145.1
VBE91451.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1327	SAMEA2066717_00371	Betaproteobacteria	Burkholderia pseudomallei	Uncharacterised protein [Burkholderia pseudomallei].	GCA_900591745.1
VBP17170.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1327	SAMEA2065229_01356	Betaproteobacteria	Burkholderia pseudomallei	Uncharacterised protein [Burkholderia pseudomallei].	GCA_900593515.1
VBP73370.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1327	SAMEA2068240_03247	Betaproteobacteria	Burkholderia pseudomallei	Uncharacterised protein [Burkholderia pseudomallei].	GCA_900593615.1
VEA49048.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1107	NCTC7306_04489	Gammaproteobacteria	Salmonella enterica subsp. arizonae	Uncharacterised protein [Salmonella enterica subsp. arizonae].	GCA_900635595.1
VTU02511.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	2231	GCJUQL4_63830	Planctomycetes	Gemmataceae bacterium	atpase aaa : Uncharacterized protein OS=delta proteobacterium MLMS-1 GN=MldDRAFT_0410 PE=4 SV=1: TPR_9 [Gemmataceae bacterium].	GCA_901538445.1
VUO82246.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1284	MFJNGALL_01363	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein MFJNGALL_01363 [Stenotrophomonas maltophilia].	GCA_902157665.1
VUP91206.1	REase+TPR→ TPR+PIN*→	TPR+PIN	777	MKCCKLKB_00143	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein MKCCKLKB_00143 [Stenotrophomonas maltophilia].	GCA_902158105.1
VVH66851.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1163	BSPLISOX_572	environmental samples	uncultured Gammaproteobacteria bacterium	hypothetical protein BSPLISOX_572 [uncultured Gammaproteobacteria bacterium].	GCA_902497535.1
VVM25671.1	TPR→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	622	BSPWISOXPB_7707	environmental samples	uncultured Gammaproteobacteria bacterium	hypothetical protein BSPWISOXPB_7707 [uncultured Gammaproteobacteria bacterium].	GCA_902497575.1
WP_000012642.1	TPR+PIN*→	TPR+PIN	1218	-	Firmicutes	Bacillus cereus	hypothetical protein [Bacillus cereus].	GCF_000291235.1
WP_000989353.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1094	-	Gammaproteobacteria	Escherichia	MULTISPECIES: hypothetical protein [Escherichia].	GCF_000503375.1
WP_002163366.1	TPR+PIN*→	TPR+PIN	1214	-	Firmicutes	Bacillus paranthracis	hypothetical protein [Bacillus paranthracis].	GCF_900176925.1
WP_002203277.1	TPR+PIN*→	TPR+PIN	1158	-	Firmicutes	Bacillus cereus	hypothetical protein [Bacillus cereus].	GCF_000293545.1
WP_002981151.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1137	-	Bacteroidetes	Chryseobacterium	MULTISPECIES: hypothetical protein [Chryseobacterium].	GCF_003815675.1
WP_003193440.1	TPR+PIN*→	TPR+PIN	1179	-	Firmicutes	Bacillus mycoides	hypothetical protein [Bacillus mycoides].	GCF_000003925.1
WP_003320554.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1148	-	Firmicutes	Alkalihalobacillus alcalophilus	hypothetical protein [Alkalihalobacillus alcalophilus].	GCF_000292245.2
WP_003365555.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1052	-	Firmicutes	Clostridium botulinum	hypothetical protein [Clostridium botulinum].	GCF_000171095.1
WP_004107781.1	REase+TPR+TPR+GreAB-C+PIN*→	REase+TPR+TPR+GreAB-C+PIN	1363	-	Alphaproteobacteria	Rhizobium freirei	restriction endonuclease [Rhizobium freirei].	GCF_000359745.1
WP_004552328.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1345	-	Betaproteobacteria	Burkholderia pseudomallei	hypothetical protein [Burkholderia pseudomallei].	GCF_000259815.1
WP_005336021.1	X+PIN*→ HTH→?→?→ HTH→	X+PIN	1180	-	Firmicutes	Dorea formicigenerans	hypothetical protein [Dorea formicigenerans].	GCF_000169235.1
WP_005619555.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1313	-	Alphaproteobacteria	Epibacterium mobile	tetratricopeptide repeat protein [Epibacterium mobile].	GCF_000376545.2
WP_005875010.1	HTH→ SIG+TM→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1125	-	Bacteroidetes	Porphyromonas gingivalis	hypothetical protein [Porphyromonas gingivalis].	GCF_000007585.1
WP_007114289.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1116	-	Gammaproteobacteria	Halomonas boliviensis	hypothetical protein [Halomonas boliviensis].	GCF_000236035.1
WP_007575774.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1298	-	Actinobacteria	Patulibacter medicamentivorans	hypothetical protein [Patulibacter medicamentivorans].	GCF_000240225.1
WP_008074062.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1116	-	Gammaproteobacteria	Vibrio sinaloensis	hypothetical protein [Vibrio sinaloensis].	GCF_000189275.1
WP_008371053.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	916	-	Gammaproteobacteria	Pseudomonas sp. M47T1	hypothetical protein [Pseudomonas sp. M47T1].	GCF_000263855.1
WP_008676251.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1224	-	Planctomycetes	Rhodopirellula sallentina	phosphorylase family 1 protein [Rhodopirellula sallentina].	GCF_000346505.1
WP_008891423.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1287	-	Alphaproteobacteria	Thalassospira profundimaris	tetratricopeptide repeat protein [Thalassospira profundimaris].	GCF_000300275.1
WP_009135826.1	X+PIN*→	X+PIN	1248	-	Bacteroidetes	Odoribacter laneus	hypothetical protein [Odoribacter laneus].	GCF_902374615.1
WP_009204273.1	X+PIN*→	X+PIN	1224	-	Firmicutes	Anaerostipes hadrus	hypothetical protein [Anaerostipes hadrus].	GCF_000332875.2

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WP_009805247.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1334	-	Alphaproteobacteria	Pseudooceanicola batsensis	restriction endonuclease [Pseudooceanicola batsensis].	GCF_000152725.1
WP_009857784.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1374	-	Betaproteobacteria	Rubrivivax benzoatilyticus	restriction endonuclease [Rubrivivax benzoatilyticus].	GCF_000190375.1
WP_009899558.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1069	-	Firmicutes	Clostridioides difficile	hypothetical protein [Clostridioides difficile].	GCF_000211235.1
WP_010516915.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1323	-	Alphaproteobacteria	Komagataeibacter oboediens	tetratricopeptide repeat protein [Komagataeibacter oboediens].	GCF_000227565.1
WP_010555470.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1100	-	Gammaproteobacteria	Pseudoalteromonas arctica	hypothetical protein [Pseudoalteromonas arctica].	GCF_000238395.3
WP_011204815.1	REase+TPR+GreAB-C+PIN*→||||<-HTH+HTH	REase+TPR+GreAB-C+PIN	1344	-	Betaproteobacteria	Burkholderia pseudomallei	hypothetical protein [Burkholderia pseudomallei].	GCF_000350505.1
WP_011691689.1	TPR+PIN*→	TPR+PIN	1180	-	Actinobacteria	Arthrobacter sp. FB24	tetratricopeptide repeat protein [Arthrobacter sp. FB24].	GCF_000196235.1
WP_012187551.1	TPR+PIN*→	TPR+PIN	1280	-	Gammaproteobacteria	Fluoribacter dumoffii	hypothetical protein [Fluoribacter dumoffii].	-
WP_012304478.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1090	-	Gammaproteobacteria	Yersinia pseudotuberculosis	hypothetical protein [Yersinia pseudotuberculosis].	GCF_000019465.1
WP_012365289.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1351	-	Betaproteobacteria	Burkholderia ambifaria	hypothetical protein [Burkholderia ambifaria].	GCF_000019925.1
WP_012655030.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1290	-	Alphaproteobacteria	Agrobacterium vitis	tetratricopeptide repeat protein [Agrobacterium vitis].	GCF_000016285.1
WP_013320645.1	<-TIR+CASPASE<-?<-?||PNPase+TPR+GreAB-C+PIN*→	PNPase+TPR+GreAB-C+PIN	1389	-	Cyanobacteria	Gloeothece verrucosa	purine or other phosphorylase family 1 [Gloeothece verrucosa].	GCF_000147335.1
WP_013724217.1	HetE-N1→ MNS-Npun2340+TPR+GreAB-C+PIN*→	MNS-Npun2340+TPR+GreAB-C+PIN	1094	-	Gammaproteobacteria	Aeromonas veronii	hypothetical protein [Aeromonas veronii].	GCF_000204115.1
WP_013846680.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1311	-	Alphaproteobacteria	Sphingobium chlorophenolicum	hypothetical protein [Sphingobium chlorophenolicum].	GCF_000147835.2
WP_013921742.1	Mbetalac→ Trypsin+TPR+GreAB-C+PIN*→	Trypsin+TPR+GreAB-C+PIN	1363	-	Bacteroidetes	Runella slithyformis	trypsin-like peptidase domain-containing protein [Runella slithyformis].	GCF_000218895.1
WP_014399772.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1160	-	Deltaproteobacteria	Corallococcus coralloides	GreA/GreB family elongation factor [Corallococcus coralloides].	GCF_000255295.1
WP_015949235.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1112	-	Deltaproteobacteria	Desulfatibacillum aliphaticivorans	hypothetical protein [Desulfatibacillum aliphaticivorans].	GCF_000021905.1
WP_016083038.1	TPR+PIN*→	TPR+PIN	1154	-	Firmicutes	Bacillus cereus	hypothetical protein [Bacillus cereus].	GCF_000399005.1
WP_016796932.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1236	-	Gammaproteobacteria	Vibrio cyclitrophicus	hypothetical protein [Vibrio cyclitrophicus].	GCF_000256385.2
WP_016981456.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1113	-	Gammaproteobacteria	Pseudomonas amygdali	hypothetical protein [Pseudomonas amygdali].	GCF_000275945.1
WP_017010147.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1114	-	Gammaproteobacteria	Enterovibrio norvegicus	hypothetical protein [Enterovibrio norvegicus].	GCF_000286875.2
WP_017056082.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1088	-	Gammaproteobacteria	Vibrio kanaloae	hypothetical protein [Vibrio kanaloae].	GCF_000272165.2
WP_017278805.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1158	-	Gammaproteobacteria	Pseudomonas syringae	hypothetical protein [Pseudomonas syringae].	GCF_001913215.1
WP_017307658.1	EAD10→?→?→ EAD10+TPR+GreAB-C+PIN*→	EAD10+TPR+GreAB-C+PIN	1214	-	Cyanobacteria	Fischerella sp. PCC 9339	hypothetical protein [Fischerella sp. PCC 9339].	GCF_000315585.1
WP_017684618.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1438	-	Gammaproteobacteria	Pseudomonas syringae	hypothetical protein [Pseudomonas syringae].	GCF_000233815.1
WP_017867504.1	X+PIN*→	X+PIN	1207	-	Firmicutes	Ligilactobacillus pobuzihii	DUF4365 domain-containing protein [Ligilactobacillus pobuzihii].	GCF_001433815.1
WP_018464656.1	TPR+PIN*→	TPR+PIN	1200	-	Bacteroidetes	Prevotella paludivivens	hypothetical protein [Prevotella paludivivens].	GCF_000613605.1
WP_019086277.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1323	-	Alphaproteobacteria	Komagataeibacter europaeus	tetratricopeptide repeat protein [Komagataeibacter europaeus].	GCF_000285295.1
WP_019092358.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1323	-	Alphaproteobacteria	Acetobacteraceae	MULTISPECIES: tetratricopeptide repeat protein [Acetobacteraceae].	GCF_003850965.1
WP_019865944.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1111	-	Gammaproteobacteria	Methylovulum miyakonense	hypothetical protein [Methylovulum miyakonense].	GCF_000384075.1
WP_019949723.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	909	-	Bacteroidetes	Hymenobacter aerophilus	hypothetical protein [Hymenobacter aerophilus].	GCF_000382225.1
WP_020099407.1	TPR+PIN*→	TPR+PIN	1185	-	Actinobacteria	Mycobacterium sp. 360MFTsu5.1	hypothetical protein [Mycobacterium sp. 360MFTsu5.1].	GCF_000383495.1
WP_020795266.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1112	-	Gammaproteobacteria	Pseudomonas sp. G5(2012)	hypothetical protein [Pseudomonas sp. G5(2012)].	GCF_000408945.1
WP_021554497.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1093	-	Gammaproteobacteria	Enterobacteriaceae	MULTISPECIES: hypothetical protein [Enterobacteriaceae].	GCF_002110225.1
WP_021876213.1	PIN*→	PIN	1097	-	Firmicutes	Clostridium chauvoei	tetratricopeptide repeat protein [Clostridium chauvoei].	GCF_002327205.1

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WP_022388983.1	X+PIN*→	X+PIN	1200	-	Firmicutes	Blautia obeum	hypothetical protein [Blautia obeum].	GCF_013299585.1
WP_022619607.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1069	-	Firmicutes	Clostridioides difficile	hypothetical protein [Clostridioides difficile].	GCF_000530295.1
WP_022674357.1	REase→?→ REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1290	-	Alphaproteobacteria	Novosphingopyxis baekryungensis	hypothetical protein [Novosphingopyxis baekryungensis].	GCF_000420305.1
WP_024552132.1	HNH→?→?→ HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1092	-	Gammaproteobacteria	Franconibacter helveticus	hypothetical protein [Franconibacter helveticus].	GCF_000485945.1
WP_024678816.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1317	-	Gammaproteobacteria	Pseudomonas syringae	DUF4365 domain-containing protein [Pseudomonas syringae].	GCF_000452685.1
WP_024698051.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1438	-	Gammaproteobacteria	Pseudomonas avellanae	hypothetical protein [Pseudomonas avellanae].	GCF_000452845.1
WP_024925158.1	REase+TPR+TPR+GreAB-C+PIN*→	REase+TPR+TPR+GreAB-C+PIN	1315	-	Alphaproteobacteria	Mesorhizobium	MULTISPECIES: GreA/GreB family elongation factor [Mesorhizobium].	GCF_000568635.1
WP_025240246.1	REase+TOPC→ HetE-N1→ HetE-N1+TPR+GreAB-C+PIN*→	HetE-N1+TPR+GreAB-C+PIN	952	-	Gammaproteobacteria	Pseudomonas stutzeri	hypothetical protein [Pseudomonas stutzeri].	GCF_000590475.1
WP_026105277.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	611	-	Alphaproteobacteria	Methylobacterium sp. MB200	hypothetical protein [Methylobacterium sp. MB200].	GCF_000333655.1
WP_026508802.1	HEPN+SNF→?→?→?→ X+PIN*→?→ CITB-HTH+LexA-protease→	X+PIN	1212	-	Firmicutes	Butyrivibrio sp. MC2013	hypothetical protein [Butyrivibrio sp. MC2013].	GCF_000424585.1
WP_026811785.1	TPR+PIN*→	TPR+PIN	1261	-	Bacteroidetes	Arenibacter certesii	hypothetical protein [Arenibacter certesii].	GCF_000429545.1
WP_027471277.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1073	-	Bacteroidetes	Saccharicrinis fermentans	hypothetical protein [Saccharicrinis fermentans].	GCF_000517085.1
WP_028048816.1	HTH+PNPase+TPR+GreAB-C+PIN*→	HTH+PNPase+TPR+GreAB-C+PIN	1518	-	Actinobacteria	Cellulomonas sp. URHD0024	helix-turn-helix domain-containing protein [Cellulomonas sp. URHD0024].	GCF_000426185.1
WP_029071033.1	X+PIN*→	X+PIN	1212	-	Firmicutes	Kandleria vitulina	hypothetical protein [Kandleria vitulina].	GCF_000622125.1
WP_029379391.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1438	-	Gammaproteobacteria	Pseudomonas fuscovaginae	hypothetical protein [Pseudomonas fuscovaginae].	GCF_000251185.1
WP_031437352.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1323	-	Gammaproteobacteria	Methylobacter tundripaludum	DUF4365 domain-containing protein [Methylobacter tundripaludum].	GCF_000733835.1
WP_031445473.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1244	-	Bacteroidetes	Arenibacter algicola	hypothetical protein [Arenibacter algicola].	GCF_000733925.1
WP_031548868.1	REase→ X+PIN*→?→?→?→?→?→?→ MACRODOMAIN→	X+PIN	1209	-	Firmicutes	Oribacterium sp. FC2011	hypothetical protein [Oribacterium sp. FC2011].	GCF_000701645.1
WP_032661435.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1139	-	Gammaproteobacteria	Pseudomonas syringae	hypothetical protein [Pseudomonas syringae].	GCF_000800685.1
WP_032902625.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1438	-	Gammaproteobacteria	Pseudomonas	MULTISPECIES: hypothetical protein [Pseudomonas].	GCF_000511155.2
WP_033132679.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1074	-	Gammaproteobacteria	Acinetobacter sp. MN12	hypothetical protein [Acinetobacter sp. MN12].	GCF_000764915.1
WP_033469897.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1282	-	Betaproteobacteria	Bordetella bronchiseptica	hypothetical protein [Bordetella bronchiseptica].	GCF_000690175.1
WP_033736921.1	HetE-N1→?→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	760	-	Gammaproteobacteria	Pantoea sp. Sc1	hypothetical protein [Pantoea sp. Sc1].	GCF_000255315.1
WP_034127539.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1158	-	Gammaproteobacteria	Pseudomonas fluorescens	hypothetical protein [Pseudomonas fluorescens].	GCF_000801795.1
WP_034129364.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1244	-	Gammaproteobacteria	Acinetobacter baumannii	hypothetical protein [Acinetobacter baumannii].	GCF_000802915.1
WP_034392332.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1413	-	Betaproteobacteria	Delftia acidovorans	hypothetical protein [Delftia acidovorans].	GCF_001598795.1
WP_034708052.1	HetE-N1→?→?→ GreAB-C+PIN*→	GreAB-C+PIN	575	-	Gammaproteobacteria	Acinetobacter bereziniae	hypothetical protein [Acinetobacter bereziniae].	GCF_000368505.1
WP_035460854.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1104	-	Gammaproteobacteria	unclassified Alcanivorax	MULTISPECIES: hypothetical protein [unclassified Alcanivorax].	GCF_000524665.1
WP_035530189.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1332	-	Alphaproteobacteria	Hoeflea sp. BAL378	hypothetical protein [Hoeflea sp. BAL378].	GCF_000759435.1
WP_035646445.1	REase+TPR+TPR+GreAB-C+PIN*→	REase+TPR+TPR+GreAB-C+PIN	1316	-	Alphaproteobacteria	Bradyrhizobium sp. ORS 285	hypothetical protein [Bradyrhizobium sp. ORS 285].	GCF_000239755.1
WP_036748977.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1130	-	Gammaproteobacteria	Photobacterium galatheae	hypothetical protein [Photobacterium galatheae].	GCF_000695255.1
WP_036783497.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1104	-	Gammaproteobacteria	Photorhabdus aegyptia	hypothetical protein [Photorhabdus aegyptia].	GCF_000612035.1
WP_038397119.1	<-HTH<-?<-?||HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1107	-	Gammaproteobacteria	Salmonella enterica	hypothetical protein [Salmonella enterica].	GCF_000756465.1
WP_039292971.1	TPR+PIN*→	TPR+PIN	1180	-	Firmicutes	Paenibacillus sp. IHB B 3415	hypothetical protein [Paenibacillus sp. IHB B 3415].	GCF_000802655.2
WP_039419134.1	CHC2+Toprim-DNAG→?→?→?→ HTH→ SIG+TM→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1140	-	Bacteroidetes	Porphyromonas gulae	hypothetical protein [Porphyromonas gulae].	GCF_000765945.1
WP_039490314.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1093	-	Gammaproteobacteria	Pectobacterium odoriferum	hypothetical protein [Pectobacterium odoriferum].	GCF_000754765.1
WP_039768974.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1438	-	Gammaproteobacteria	Pseudomonas fluorescens	hypothetical protein [Pseudomonas fluorescens].	GCF_000817905.1
WP_040182639.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1319	-	Alphaproteobacteria	Phaeobacter sp. S60	hypothetical protein [Phaeobacter sp. S60].	GCF_000826845.1
WP_040439475.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1318	-	Alphaproteobacteria	Labrenzia aggregata	hypothetical protein [Labrenzia aggregata].	GCF_000168975.1
WP_041272554.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1294	-	Firmicutes	Desulfitobacterium hafniense	tetratricopeptide repeat protein [Desulfitobacterium hafniense].	GCF_000010045.1

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WP_041475188.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1321	-	Gammaproteobacteria	Pseudomonas	MULTISPECIES: DUF4365 domain-containing protein [Pseudomonas].	GCF_000012445.1
WP_041609504.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1086	-	Gammaproteobacteria	Tolumonas auensis	hypothetical protein [Tolumonas auensis].	GCF_000023065.1
WP_042089608.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1245	-	Gammaproteobacteria	Acinetobacter bereziniae	hypothetical protein [Acinetobacter bereziniae].	GCF_000825165.1
WP_042562078.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1438	-	Gammaproteobacteria	Pseudomonas fluorescens	hypothetical protein [Pseudomonas fluorescens].	GCF_000827755.1
WP_043355224.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1332	-	Betaproteobacteria	Cupriavidus	MULTISPECIES: hypothetical protein [Cupriavidus].	GCF_001652915.1
WP_043626766.1	REase+TPR+TPR+GreAB-C+PIN*→	REase+TPR+TPR+GreAB-C+PIN	1357	-	Alphaproteobacteria	Ensifer sp. ZNC0028	hypothetical protein [Ensifer sp. ZNC0028].	GCF_000799055.1
WP_043752287.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1318	-	Alphaproteobacteria	Pseudooceanicola atlanticus	restriction endonuclease [Pseudooceanicola atlanticus].	GCF_000768315.1
WP_044036524.1	TPR→ TPR→?→?→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	473	-	Alphaproteobacteria	Octadecabacter arcticus	hypothetical protein [Octadecabacter arcticus].	GCF_000155735.2
WP_044439030.1	X+PIN*→	X+PIN	1051	-	Actinobacteria	Agreia bicolorata	hypothetical protein [Agreia bicolorata].	GCF_000938265.1
WP_045324066.1	TPR+PIN*→	TPR+PIN	1167	-	Actinobacteria	Streptomyces sp. NRRL F-4428	hypothetical protein [Streptomyces sp. NRRL F-4428].	GCF_000956015.1
WP_045495160.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1086	-	Gammaproteobacteria	Vibrio hyugaensis	hypothetical protein [Vibrio hyugaensis].	GCF_000818475.1
WP_046103485.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1314	-	Alphaproteobacteria	Devosia chinhatensis	hypothetical protein [Devosia chinhatensis].	GCF_000969445.1
WP_047008502.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1236	-	-	Vibrio diabolicus	hypothetical protein [Vibrio diabolicus].	GCF_001010935.1
WP_047057492.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1106	-	Gammaproteobacteria	Enterobacter hormaechei	hypothetical protein [Enterobacter hormaechei].	GCF_001011695.1
WP_047274590.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1321	-	Gammaproteobacteria	Pseudomonas	MULTISPECIES: DUF4365 domain-containing protein [Pseudomonas].	GCF_012986325.1
WP_047583000.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1105	-	Gammaproteobacteria	unclassified Pseudomonas	MULTISPECIES: hypothetical protein [unclassified Pseudomonas].	GCF_000763225.1
WP_047736827.1	HetE-N1→ HetE-N1+TPR+GreAB-C+PIN*→	HetE-N1+TPR+GreAB-C+PIN	1122	-	Gammaproteobacteria	Pseudomonas chlororaphis	hypothetical protein [Pseudomonas chlororaphis].	GCF_001023535.1
WP_047738516.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1111	-	Gammaproteobacteria	Pseudomonas chlororaphis	hypothetical protein [Pseudomonas chlororaphis].	GCF_001023535.1
WP_047741525.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1106	-	Gammaproteobacteria	Enterobacter cloacae complex	MULTISPECIES: hypothetical protein [Enterobacter cloacae complex].	GCF_014982105.1
WP_047744683.1	HetE-N1→ HetE-N1+TPR+GreAB-C+PIN*→	HetE-N1+TPR+GreAB-C+PIN	1092	-	Gammaproteobacteria	Enterobacter ludwigii	hypothetical protein [Enterobacter ludwigii].	GCF_001022445.2
WP_048126291.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1292	-	Euryarchaeota	Methanosarcina lacustris	hypothetical protein [Methanosarcina lacustris].	GCF_000970265.1
WP_048377212.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1321	-	Gammaproteobacteria	Pseudomonas	MULTISPECIES: DUF4365 domain-containing protein [Pseudomonas].	GCF_012986365.1
WP_048411963.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1163	-	Betaproteobacteria	Chromobacterium sp. LK1	hypothetical protein [Chromobacterium sp. LK1].	GCF_001043555.1
WP_049042149.1	HetE-N1→ HetE-N1+TPR+GreAB-C+PIN*→	HetE-N1+TPR+GreAB-C+PIN	1094	-	Gammaproteobacteria	Citrobacter braakii	hypothetical protein [Citrobacter braakii].	GCF_001059745.1
WP_049582258.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1098	-	Gammaproteobacteria	Photorhabdus luminescens	hypothetical protein [Photorhabdus luminescens].	GCF_900102985.1
WP_050091697.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1096	-	Gammaproteobacteria	Yersinia pseudotuberculosis	hypothetical protein [Yersinia pseudotuberculosis].	GCF_001123345.1
WP_050298251.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1095	-	Gammaproteobacteria	Yersinia enterocolitica	hypothetical protein [Yersinia enterocolitica].	GCF_001160345.1
WP_050323220.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1121	-	Gammaproteobacteria	Yersinia enterocolitica	hypothetical protein [Yersinia enterocolitica].	GCF_001182365.1
WP_050376143.1	TPR+GreAB-C+PIN*→||||<-HTH+HTH	TPR+GreAB-C+PIN	872	-	Betaproteobacteria	Burkholderia pseudomallei	hypothetical protein [Burkholderia pseudomallei].	GCF_006538545.1
WP_050590144.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1423	-	Gammaproteobacteria	Pseudomonas sp. URMO17WK12:I12	hypothetical protein [Pseudomonas sp. URMO17WK12:I12].	GCF_000514395.1
WP_051097719.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1140	-	Gammaproteobacteria	Pseudomonas sp. 10-1B	hypothetical protein [Pseudomonas sp. 10-1B].	GCF_000935045.1
WP_051560695.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1098	-	Gammaproteobacteria	Photorhabdus aegyptia	hypothetical protein [Photorhabdus aegyptia].	GCF_000612035.1
WP_051570263.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1248	-	Actinobacteria	Cryptosporangium arvum	DUF4365 domain-containing protein [Cryptosporangium arvum].	GCF_000585375.1
WP_052241169.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1236	-	Actinobacteria	Microbacterium hominis	DUF4365 domain-containing protein [Microbacterium hominis].	GCF_000813805.1
WP_052515067.1	PNPase+TPR+GreAB-C+PIN*→	PNPase+TPR+GreAB-C+PIN	1617	-	Deltaproteobacteria	Dethiosulfatarculus sandiegensis	hypothetical protein [Dethiosulfatarculus sandiegensis].	GCF_000931935.2
WP_052917795.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1094	-	Gammaproteobacteria	Escherichia coli	hypothetical protein [Escherichia coli].	GCF_001265885.1
WP_053052653.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1129	-	Gammaproteobacteria	Vibrio harveyi	hypothetical protein [Vibrio harveyi].	GCF_001262735.1
WP_053269091.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1438	-	Gammaproteobacteria	Pseudomonas chlororaphis	hypothetical protein [Pseudomonas chlororaphis].	GCF_001269595.1
WP_053316591.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	982	-	Gammaproteobacteria	Vibrio parahaemolyticus	hypothetical protein [Vibrio parahaemolyticus].	GCF_001268015.1
WP_053446146.1	TPR+PIN*→	TPR+PIN	1160	-	Firmicutes	Bacillus toyonensis	hypothetical protein [Bacillus toyonensis].	GCF_001275045.2

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WP_053882512.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1094	-	Gammaproteobacteria	Escherichia coli	hypothetical protein [Escherichia coli].	GCF_001284445.1
WP_054070021.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1140	-	Gammaproteobacteria	Pseudomonas syringae group genomosp. 3	hypothetical protein [Pseudomonas syringae group genomosp. 3].	GCF_016803175.1
WP_054211402.1	BirA-HTH→ HEPN→ REase+TPR+TPR+GreAB-C+PIN*→	REase+TPR+TPR+GreAB-C+PIN	1333	-	Alphaproteobacteria	Bosea vaviloviae	hypothetical protein [Bosea vaviloviae].	GCF_001298265.1
WP_054464024.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1094	-	Gammaproteobacteria	Escherichia coli	hypothetical protein [Escherichia coli].	GCF_001277455.1
WP_055843189.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1293	-	Alphaproteobacteria	Sphingomonas sp. Leaf343	tetratricopeptide repeat protein [Sphingomonas sp. Leaf343].	GCF_001423765.1
WP_056497005.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1110	-	Alphaproteobacteria	Methylobacterium sp. Leaf111	hypothetical protein [Methylobacterium sp. Leaf111].	GCF_001423285.1
WP_056734772.1	TPR+PIN*→	TPR+PIN	1204	-	Actinobacteria	Agromyces sp. Soil535	hypothetical protein [Agromyces sp. Soil535].	GCF_001428255.1
WP_056836493.1	TPR+PIN*→	TPR+PIN	1174	-	Firmicutes	Paenibacillus sp. Soil787	hypothetical protein [Paenibacillus sp. Soil787].	GCF_001429545.1
WP_057430028.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1438	-	Gammaproteobacteria	Pseudomonas syringae group genomosp. 3	hypothetical protein [Pseudomonas syringae group genomosp. 3].	GCF_001401385.1
WP_057580842.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1233	-	Firmicutes	Paeniclostridium sordellii	hypothetical protein [Paeniclostridium sordellii].	GCF_001373055.1
WP_057657430.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1287	-	Gammaproteobacteria	Pseudoxanthomonas dokdonensis	tetratricopeptide repeat protein [Pseudoxanthomonas dokdonensis].	GCF_001431405.1
WP_057831910.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1091	-	Gammaproteobacteria	Colwellia sp. TT2012	hypothetical protein [Colwellia sp. TT2012].	GCF_001440345.1
WP_057932289.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1276	-	Bacteroidetes	Pedobacter ginsenosidimutans	tetratricopeptide repeat protein [Pedobacter ginsenosidimutans].	GCF_001442625.1
WP_058039540.1	TPR+GreAB-C+PIN*→||||<-HTH+HTH	TPR+GreAB-C+PIN	872	-	Betaproteobacteria	Burkholderia pseudomallei	hypothetical protein [Burkholderia pseudomallei].	GCF_001445875.1
WP_058297418.1	TPR+PIN*→	TPR+PIN	1225	-	Firmicutes	Bacillus enclensis	hypothetical protein [Bacillus enclensis].	GCF_900094975.1
WP_058461037.1	TPR+PIN*→	TPR+PIN	1277	-	Gammaproteobacteria	Fluoribacter bozemanae	hypothetical protein [Fluoribacter bozemanae].	GCF_900640135.1
WP_058587024.1	<-MarR-HTH||?→?→?→||||<-?||?→ HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1117	-	Gammaproteobacteria	Citrobacter amalonaticus	hypothetical protein [Citrobacter amalonaticus].	GCF_001471655.2
WP_058721158.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1509	-	Betaproteobacteria	Paucibacter sp. KCTC 42545	hypothetical protein [Paucibacter sp. KCTC 42545].	GCF_001477625.1
WP_058751880.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1317	-	Alphaproteobacteria	Sphingomonas sanguinis	tetratricopeptide repeat protein [Sphingomonas sanguinis].	GCF_001476905.1
WP_058820070.1	<-HTH<-?<-?||HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1107	-	Gammaproteobacteria	Salmonella enterica	hypothetical protein [Salmonella enterica].	GCF_001952125.1
WP_059294982.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1106	-	Gammaproteobacteria	Enterobacter hormaechei	hypothetical protein [Enterobacter hormaechei].	GCF_001518595.1
WP_059458986.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1335	-	Betaproteobacteria	Burkholderia vietnamiensis	hypothetical protein [Burkholderia vietnamiensis].	GCF_001523785.1
WP_059543415.1	TPR+GreAB-C+PIN*→||||<-HTH+HTH	TPR+GreAB-C+PIN	872	-	Betaproteobacteria	Burkholderia	MULTISPECIES: hypothetical protein [Burkholderia].	GCF_001523065.1
WP_059687512.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1355	-	Betaproteobacteria	Burkholderia cepacia	hypothetical protein [Burkholderia cepacia].	GCF_001524765.1
WP_059702921.1	REase+TPR→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	954	-	Betaproteobacteria	Burkholderia sp. RF2-non_BP3	hypothetical protein [Burkholderia sp. RF2-non_BP3].	GCF_001522185.1
WP_059764594.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1321	-	Gammaproteobacteria	unclassified Pseudomonas	MULTISPECIES: DUF4365 domain-containing protein [unclassified Pseudomonas].	GCF_001529305.1
WP_059837999.1	TPR+GreAB-C+PIN*→||||<-HTH+HTH	TPR+GreAB-C+PIN	872	-	Betaproteobacteria	Burkholderia ubonensis	hypothetical protein [Burkholderia ubonensis].	GCF_001528175.1
WP_059992407.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1345	-	Betaproteobacteria	Burkholderia ubonensis	hypothetical protein [Burkholderia ubonensis].	GCF_001527095.1
WP_060002797.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	872	-	Betaproteobacteria	Burkholderia gladioli	hypothetical protein [Burkholderia gladioli].	GCF_902831175.1
WP_060217774.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1355	-	Betaproteobacteria	Burkholderia cepacia	hypothetical protein [Burkholderia cepacia].	GCF_001530905.1
WP_060322122.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1351	-	Betaproteobacteria	Burkholderia ubonensis	hypothetical protein [Burkholderia ubonensis].	GCF_001718975.1
WP_060322181.1	REase+TPR+GreAB-C+PIN*→||||<-HEPN	REase+TPR+GreAB-C+PIN	1345	-	Betaproteobacteria	Burkholderia diffusa	hypothetical protein [Burkholderia diffusa].	GCF_001533185.1
WP_060360485.1	REase+TPR+GreAB-C+PIN*→||||<-HEPN	REase+TPR+GreAB-C+PIN	1351	-	Betaproteobacteria	Burkholderia territorii	hypothetical protein [Burkholderia territorii].	GCF_001533385.1
WP_061510730.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1304	-	Alphaproteobacteria	Gluconobacter thailandicus	hypothetical protein [Gluconobacter thailandicus].	GCF_001580835.1
WP_061928567.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1323	-	Alphaproteobacteria	Gluconobacter japonicus	hypothetical protein [Gluconobacter japonicus].	GCF_001580865.1
WP_062265952.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1319	-	Euryarchaeota	Methanoculleus bourgensis	tetratricopeptide repeat protein [Methanoculleus bourgensis].	GCF_900036045.1
WP_062316067.1	TPR+PIN*→	TPR+PIN	1207	-	Actinobacteria	Demequina maris	hypothetical protein [Demequina maris].	GCF_000971375.1
WP_062477592.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1109	-	Gammaproteobacteria	Lacimicrobium alkaliphilum	hypothetical protein [Lacimicrobium alkaliphilum].	GCF_001466725.1
WP_062692005.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	941	-	Gammaproteobacteria	Photobacterium sanguinicancri	hypothetical protein [Photobacterium sanguinicancri].	GCF_001563765.1

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WP_062794399.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1127	-	Betaproteobacteria	Cupriavidus metallidurans	hypothetical protein, partial [Cupriavidus metallidurans].	GCF_001598775.1
WP_063146823.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1106	-	Gammaproteobacteria	Enterobacter cloacae complex	MULTISPECIES: hypothetical protein [Enterobacter cloacae complex].	GCF_013635495.1
WP_063496996.1	TIR+DnaB→ REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1364	-	Betaproteobacteria	Paraburkholderia phytofirmans	hypothetical protein [Paraburkholderia phytofirmans].	GCF_001634365.1
WP_063800929.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1351	-	Betaproteobacteria	Burkholderia ubonensis	hypothetical protein [Burkholderia ubonensis].	GCF_001526225.1
WP_063809712.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1117	-	Gammaproteobacteria	Salmonella enterica	hypothetical protein [Salmonella enterica].	GCF_008727555.1
WP_063897359.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1351	-	Betaproteobacteria	Burkholderia ubonensis	hypothetical protein [Burkholderia ubonensis].	GCF_001529725.1
WP_063906337.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1354	-	Betaproteobacteria	Burkholderia ubonensis	hypothetical protein [Burkholderia ubonensis].	GCF_001534425.1
WP_063932878.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1034	-	Gammaproteobacteria	Enterobacter hormaechei	hypothetical protein [Enterobacter hormaechei].	GCF_900076145.1
WP_064273010.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1328	-	Alphaproteobacteria	Gluconobacter cerinus	tetratricopeptide repeat protein [Gluconobacter cerinus].	GCF_001645165.1
WP_064374215.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1116	-	Gammaproteobacteria	Pantoea ananatis	hypothetical protein [Pantoea ananatis].	GCF_001543055.1
WP_064477497.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	879	-	Betaproteobacteria	Ralstonia	MULTISPECIES: hypothetical protein [Ralstonia].	GCF_014884725.1
WP_065176860.1	HetE-N1→ GreAB-C*→	GreAB-C	1123	-	Gammaproteobacteria	Photobacterium aquimaris	hypothetical protein [Photobacterium aquimaris].	GCF_001676065.1
WP_065192964.1	HetE-N1→ GreAB-C*→	GreAB-C	1128	-	Gammaproteobacteria	Photobacterium phosphoreum	hypothetical protein [Photobacterium phosphoreum].	GCF_001676135.1
WP_065645553.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1085	-	Gammaproteobacteria	Vibrio diabolicus	hypothetical protein [Vibrio diabolicus].	GCF_001691185.1
WP_065663920.1	BirA-HTH→ HEPN→ REase+TPR+TPR+GreAB-C+PIN*→	REase+TPR+TPR+GreAB-C+PIN	1333	-	Alphaproteobacteria	Agrobacterium sp. B131/95	GreA/GreB family elongation factor [Agrobacterium sp. B131/95].	GCF_001692155.1
WP_065996373.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1244	-	Gammaproteobacteria	Acinetobacter baumannii	hypothetical protein [Acinetobacter baumannii].	GCF_001704675.1
WP_066036869.1	TPR+PIN*→	TPR+PIN	1175	-	Firmicutes	Lysinibacillus sp. AR18-8	hypothetical protein [Lysinibacillus sp. AR18-8].	GCF_001705465.1
WP_066542710.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1122	-	Alphaproteobacteria	Sphingomonas sp. CCH18-B1	tetratricopeptide repeat protein [Sphingomonas sp. CCH18-B1].	GCF_001555895.1
WP_066945120.1	HTH+PNPase+PIN*→	HTH+PNPase+PIN	1527	-	Actinobacteria	Streptomyces lushanensis	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase [Streptomyces lushanensis].	GCF_001700515.1
WP_067386574.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1361	-	Gammaproteobacteria	Marinobacterium aestuarii	hypothetical protein [Marinobacterium aestuarii].	GCF_001651805.1
WP_067584887.1	GreAB-C*→	GreAB-C	1154	-	Gammaproteobacteria	Endozoicomonas ascidiicola	hypothetical protein [Endozoicomonas ascidiicola].	GCF_001646955.1
WP_067776912.1	PNPase+TPR+GreAB-C+PIN*→	PNPase+TPR+GreAB-C+PIN	1386	-	Cyanobacteria	Nostoc sp. NIES-3756	hypothetical protein [Nostoc sp. NIES-3756].	GCF_001548375.1
WP_067990948.1	TPR+PIN*→||||<-KAP_NTPase	TPR+PIN	1216	-	Actinobacteria	Mycobacterium sp. YC-RL4	hypothetical protein [Mycobacterium sp. YC-RL4].	GCF_001644575.1
WP_068215362.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1166	-	Bacteroidetes	Roseivirga spongicola	hypothetical protein [Roseivirga spongicola].	GCF_001592965.1
WP_069047857.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1383	-	Betaproteobacteria	Hydrogenophaga sp. RAC07	hypothetical protein [Hydrogenophaga sp. RAC07].	GCF_001713375.1
WP_069206296.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1323	-	Alphaproteobacteria	Sphingomonas panacis	hypothetical protein [Sphingomonas panacis].	GCF_001717955.1
WP_069604736.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1147	-	Firmicutes	Bacillus cereus group	MULTISPECIES: tetratricopeptide repeat protein [Bacillus cereus group].	GCF_001729295.1
WP_069859257.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1244	-	Bacteroidetes	Arenibacter sp. NBRC 103722	hypothetical protein [Arenibacter sp. NBRC 103722].	GCF_001748465.2
WP_069931472.1	REase+PIN*→	REase+PIN	1282	-	Actinobacteria	Streptomyces agglomeratus	DUF4365 domain-containing protein [Streptomyces agglomeratus].	GCF_001746465.1
WP_070715046.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1094	-	Gammaproteobacteria	Hafnia sp. HMSC23F03	hypothetical protein [Hafnia sp. HMSC23F03].	GCF_001816025.1
WP_070991866.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1106	-	Gammaproteobacteria	Pseudoalteromonas byunsanensis	hypothetical protein [Pseudoalteromonas byunsanensis].	GCF_001854475.1
WP_071234936.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1111	-	Gammaproteobacteria	Vibrio rotiferianus	hypothetical protein [Vibrio rotiferianus].	GCF_001858245.1
WP_071684330.1	HetE-N1→ HetE-N1+TPR+GreAB-C+PIN*→	HetE-N1+TPR+GreAB-C+PIN	1094	-	Gammaproteobacteria	Citrobacter freundii	hypothetical protein [Citrobacter freundii].	GCF_014901875.1
WP_071741873.1	TPR+PIN*→	TPR+PIN	1160	-	Firmicutes	Bacillus paranthracis	hypothetical protein [Bacillus paranthracis].	GCF_001883995.1
WP_071769547.1	PIN*→	PIN	341	-	Betaproteobacteria	Burkholderia ubonensis	hypothetical protein [Burkholderia ubonensis].	GCF_001882755.1
WP_071890709.1	TPR+GreAB-C+PIN*→||||<-HTH	TPR+GreAB-C+PIN	1157	-	Gammaproteobacteria	Pseudomonas putida	tetratricopeptide repeat protein [Pseudomonas putida].	GCF_001886975.1
WP_072702162.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1125	-	Alphaproteobacteria	Donghicola eburneus	hypothetical protein [Donghicola eburneus].	GCF_900095785.1

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WP_073552134.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1131	-	Bacteroidetes	Elizabethkingia meningoseptica	hypothetical protein [Elizabethkingia meningoseptica].	GCF_900143665.1
WP_073772512.1	REase+PIN*→	REase+PIN	1292	-	Actinobacteria	Streptomyces sp. MJM1172	DUF4365 domain-containing protein [Streptomyces sp. MJM1172].	GCF_001905425.1
WP_074449514.1	CHC2+Toprim-DNAG→?→?→?→ HTH→ SIG+TM→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1141	-	Bacteroidetes	Tannerella forsythia	hypothetical protein [Tannerella forsythia].	GCF_900096735.1
WP_074452850.1	CHC2+Toprim-DNAG→?→ PSE→?→ HTH→ SIG+TM→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1141	-	Bacteroidetes	Bacteroidales	MULTISPECIES: hypothetical protein [Bacteroidales].	GCF_900096725.1
WP_074647048.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1184	-	Alphaproteobacteria	Celeribacter baekdonensis	hypothetical protein [Celeribacter baekdonensis].	GCF_900102315.1
WP_074661038.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1127	-	Bacteroidetes	Flavobacterium frigidimaris	hypothetical protein [Flavobacterium frigidimaris].	GCF_002217275.1
WP_074804411.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1335	-	Betaproteobacteria	Burkholderia cenocepacia	hypothetical protein [Burkholderia cenocepacia].	GCF_900100915.1
WP_074854446.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1161	-	Gammaproteobacteria	Pseudomonas salomonii	hypothetical protein [Pseudomonas salomonii].	GCF_900107155.1
WP_075042282.1	REase+TPR+TPR+GreAB-C+PIN*→	REase+TPR+TPR+GreAB-C+PIN	1332	-	Alphaproteobacteria	Brucella intermedia	GreA/GreB family elongation factor [Brucella intermedia].	GCF_001917355.1
WP_075481088.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1236	-	Gammaproteobacteria	Moritella viscosa	hypothetical protein [Moritella viscosa].	GCF_900120145.1
WP_075594884.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1086	-	Alphaproteobacteria	Komagataeibacter hansenii	hypothetical protein [Komagataeibacter hansenii].	GCF_001938745.1
WP_076004144.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1301	-	Chloroflexi	Dehalogenimonas formicexedens	hypothetical protein [Dehalogenimonas formicexedens].	GCF_001953175.1
WP_076215124.1	TPR+PIN*→	TPR+PIN	1179	-	Firmicutes	Paenibacillus odorifer	tetratricopeptide repeat protein [Paenibacillus odorifer].	GCF_001954655.1
WP_076272073.1	TPR+PIN*→	TPR+PIN	1180	-	Firmicutes	Paenibacillus odorifer	hypothetical protein [Paenibacillus odorifer].	GCF_001954285.1
WP_076387298.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1130	-	Bacteroidetes	Kaistella chaponensis	hypothetical protein [Kaistella chaponensis].	GCF_900156725.1
WP_076506278.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1137	-	Bacteroidetes	Chryseobacterium shigense	hypothetical protein [Chryseobacterium shigense].	GCF_900156575.1
WP_076822916.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1162	-	Actinobacteria	Frankia asymbiotica	hypothetical protein [Frankia asymbiotica].	GCF_001983105.1
WP_076832171.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1129	-	Alphaproteobacteria	Bradyrhizobium sp. UFLA 03-321	hypothetical protein [Bradyrhizobium sp. UFLA 03-321].	GCF_001969825.1
WP_076835387.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1345	-	Betaproteobacteria	Burkholderia pseudomallei	hypothetical protein [Burkholderia pseudomallei].	GCF_001980695.1
WP_078005484.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1131	-	Bacteroidetes	Flavobacterium sp. KBS0721	hypothetical protein [Flavobacterium sp. KBS0721].	GCF_002007065.3
WP_078350655.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1286	-	Bacteroidetes	Mucilaginibacter pedocola	hypothetical protein [Mucilaginibacter pedocola].	GCF_002013915.1
WP_078403924.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1140	-	Bacteroidetes	Elizabethkingia ursingii	hypothetical protein [Elizabethkingia ursingii].	GCF_002022125.1
WP_078946818.1	REase+PIN*→	REase+PIN	1277	-	Actinobacteria	Streptomyces sp. NRRL B-3648	DUF4365 domain-containing protein [Streptomyces sp. NRRL B-3648].	GCF_001279545.1
WP_079454673.1	REase+TPR+GreAB-C+PIN*→||||<-?||HTH→	REase+TPR+GreAB-C+PIN	1250	-	Gammaproteobacteria	Acinetobacter baumannii	GreA/GreB family elongation factor [Acinetobacter baumannii].	GCF_902728005.1
WP_079469502.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1234	-	Bacteroidetes	Chitinophaga ginsengisegetis	hypothetical protein [Chitinophaga ginsengisegetis].	GCF_900168065.1
WP_079579807.1	X+PIN*→	X+PIN	1007	-	Epsilonproteobacteria	Malaciobacter marinus	hypothetical protein [Malaciobacter marinus].	GCF_900168035.1
WP_079820569.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1117	-	Gammaproteobacteria	Salmonella enterica	hypothetical protein [Salmonella enterica].	GCF_016071195.1
WP_079943789.1	<-HTH<-?<-?||HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	998	-	Gammaproteobacteria	Salmonella enterica	hypothetical protein [Salmonella enterica].	GCF_002045995.1
WP_079951728.1	<-HTH<-?<-?||HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	993	-	Gammaproteobacteria	Salmonella enterica	hypothetical protein [Salmonella enterica].	GCF_002052255.1
WP_079954008.1	<-HTH<-?<-?||HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	998	-	Gammaproteobacteria	Salmonella enterica	hypothetical protein [Salmonella enterica].	GCF_002045095.1
WP_079959318.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1119	-	Gammaproteobacteria	Salmonella enterica	hypothetical protein [Salmonella enterica].	GCF_002046115.1
WP_079973127.1	<-HTH<-?<-?||HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1106	-	Gammaproteobacteria	Salmonella enterica	hypothetical protein [Salmonella enterica].	GCF_002046215.1
WP_080170163.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1106	-	Gammaproteobacteria	Salmonella enterica	hypothetical protein [Salmonella enterica].	GCF_016863875.1
WP_080323117.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1334	-	Betaproteobacteria	Burkholderia cenocepacia	hypothetical protein [Burkholderia cenocepacia].	GCF_002071875.1
WP_080865316.1	PIN+GNAT→?→?→ REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1290	-	Alphaproteobacteria	Agrobacterium tumefaciens	hypothetical protein [Agrobacterium tumefaciens].	GCF_900012605.1
WP_081143626.1	TPR+PIN*→	TPR+PIN	1157	-	Firmicutes	Bacillus cereus	hypothetical protein [Bacillus cereus].	GCF_002078195.1
WP_082055264.1	NACHT→ REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1329	-	Betaproteobacteria	Cupriavidus basilensis	DUF4365 domain-containing protein [Cupriavidus basilensis].	GCF_000832305.1
WP_082573822.1	HTH+PNPase+TPR+GreAB-C+PIN*→	HTH+PNPase+TPR+GreAB-C+PIN	1517	-	Actinobacteria	Cellulomonas sp. Root137	hypothetical protein [Cellulomonas sp. Root137].	GCF_001426725.1

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WP_082991752.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1320	-	Betaproteobacteria	Paraburkholderia tropica	DUF4365 domain-containing protein [Paraburkholderia tropica].	GCF_001673675.1
WP_083024260.1	TPR+GreAB-C*→	TPR+GreAB-C	833	-	Gammaproteobacteria	Halomonas lionensis	hypothetical protein [Halomonas lionensis].	GCF_002087295.1
WP_083366146.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1112	-	Gammaproteobacteria	Pseudomonas koreensis	hypothetical protein [Pseudomonas koreensis].	GCF_014646955.1
WP_083417785.1	REase+TPR+GreAB-C+PIN*→||||<-TIR	REase+TPR+GreAB-C+PIN	1329	-	Betaproteobacteria	Burkholderia contaminans	DUF4365 domain-containing protein [Burkholderia contaminans].	GCF_001865715.1
WP_083925131.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1307	-	Gammaproteobacteria	Thioalkalivibrio sp. ALJ15	GreA/GreB family elongation factor [Thioalkalivibrio sp. ALJ15].	GCF_000383695.1
WP_084371210.1	X+PIN*→	X+PIN	1158	-	Bacteroidetes	Reichenbachiella faecimaris	hypothetical protein [Reichenbachiella faecimaris].	GCF_900176375.1
WP_084886264.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	999	-	Gammaproteobacteria	Pantoea septica	hypothetical protein [Pantoea septica].	GCF_002095575.1
WP_085383443.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1301	-	Alphaproteobacteria	Bradyrhizobium canariense	hypothetical protein [Bradyrhizobium canariense].	GCF_002108905.1
WP_085905967.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1176	-	Alphaproteobacteria	Kiloniella majae	hypothetical protein [Kiloniella majae].	GCF_002118275.1
WP_086630532.1	HetE-N1→ TPR+GreAB-C+PIN+TM+TM*→	TPR+GreAB-C+PIN+TM+TM	1106	-	Gammaproteobacteria	Klebsiella aerogenes	hypothetical protein [Klebsiella aerogenes].	GCF_002152925.1
WP_086759874.1	APATPase+BetaPropeller→ PNPase+TPR+GreAB-C+PIN*→	PNPase+TPR+GreAB-C+PIN	1399	-	Cyanobacteria	Nostoc sp. 106C	tetratricopeptide repeat protein [Nostoc sp. 106C].	GCF_002154725.1
WP_086979350.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	940	-	Gammaproteobacteria	Pseudomonas putida	hypothetical protein [Pseudomonas putida].	GCF_002157515.1
WP_087258361.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1189	-	Firmicutes	[Clostridium] spiroforme	hypothetical protein [[Clostridium] spiroforme].	GCF_002160695.1
WP_087391814.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1189	-	Firmicutes	[Clostridium] spiroforme	hypothetical protein [[Clostridium] spiroforme].	GCF_002160645.1
WP_088070184.1	TPR+PIN*→	TPR+PIN	1157	-	Firmicutes	Bacillus thuringiensis	hypothetical protein [Bacillus thuringiensis].	GCF_002148155.1
WP_088082523.1	TPR+PIN*→	TPR+PIN	1179	-	Firmicutes	Bacillus thuringiensis	hypothetical protein [Bacillus thuringiensis].	GCF_002147935.1
WP_088087080.1	TPR+PIN*→	TPR+PIN	1176	-	Firmicutes	Bacillus sp. OV166	hypothetical protein [Bacillus sp. OV166].	GCF_900177675.1
WP_088476259.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1284	-	Gammaproteobacteria	Stenotrophomonas pavanii	GreA/GreB family elongation factor [Stenotrophomonas pavanii].	GCF_002205885.1
WP_089172847.1	BirA-HTH→ HEPN→ REase+TPR+TPR+GreAB-C+PIN*→	REase+TPR+TPR+GreAB-C+PIN	1332	-	Alphaproteobacteria	unclassified Bosea	MULTISPECIES: hypothetical protein [unclassified Bosea].	GCF_002220095.1
WP_090371407.1	REase→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1155	-	Betaproteobacteria	Nitrosospira sp. Nl5	hypothetical protein [Nitrosospira sp. Nl5].	GCF_900102495.1
WP_090455730.1	HetE-N1→ TPR+GreAB-C+PIN*→||||<-TIR	TPR+GreAB-C+PIN	1112	-	Gammaproteobacteria	Pseudomonas jessenii	hypothetical protein [Pseudomonas jessenii].	GCF_900104905.1
WP_090543864.1	TIR+TPR+GreAB-C+PIN*→	TIR+TPR+GreAB-C+PIN	1348	-	Betaproteobacteria	Nitrosomonas sp. Nm132	toll/interleukin-1 receptor domain-containing protein [Nitrosomonas sp. Nm132].	GCF_900100485.1
WP_090721286.1	<-Cas_Cas1<-?||?→?→?→?→ REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1380	-	Betaproteobacteria	Nitrosomonas sp. Nm166	hypothetical protein [Nitrosomonas sp. Nm166].	GCF_900112825.1
WP_091343709.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1098	-	Gammaproteobacteria	Alkalimonas amylolytica	hypothetical protein [Alkalimonas amylolytica].	GCF_900107845.1
WP_091456057.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1259	-	Actinobacteria	Micromonospora inyonensis	hypothetical protein [Micromonospora inyonensis].	GCF_900091415.1
WP_091965577.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1229	-	Alphaproteobacteria	Bradyrhizobium shewense	hypothetical protein [Bradyrhizobium shewense].	GCF_900094605.1
WP_092226352.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1306	-	Alphaproteobacteria	Bradyrhizobium sp. Gha	tetratricopeptide repeat protein [Bradyrhizobium sp. Gha].	GCF_900113735.1
WP_092234200.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1321	-	Gammaproteobacteria	Pseudomonas proteolytica	DUF4365 domain-containing protein [Pseudomonas proteolytica].	GCF_900105955.1
WP_092689872.1	HTH→ HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1077	-	Gammaproteobacteria	Acinetobacter kyonggiensis	hypothetical protein [Acinetobacter kyonggiensis].	GCF_900107285.1
WP_093257662.1	HetE-N1→ HetE-N1+TPR+GreAB-C+PIN*→	HetE-N1+TPR+GreAB-C+PIN	1120	-	Gammaproteobacteria	Pseudomonas	MULTISPECIES: hypothetical protein [Pseudomonas].	GCF_900110545.1
WP_093289087.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1291	-	Gammaproteobacteria	Pseudoxanthomonas sp. CF125	hypothetical protein [Pseudoxanthomonas sp. CF125].	GCF_900104085.1
WP_095032727.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1104	-	Gammaproteobacteria	Klebsiella quasivariicola	hypothetical protein [Klebsiella quasivariicola].	GCF_002269255.1
WP_095064594.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1105	-	Gammaproteobacteria	Pseudomonas sp. Irchel s3f19	hypothetical protein [Pseudomonas sp. Irchel s3f19].	GCF_900187555.1
WP_095490577.1	HetE-N1→ HetE-N1+TPR+GreAB-C+PIN*→	HetE-N1+TPR+GreAB-C+PIN	1088	-	Gammaproteobacteria	Vibrio cholerae	hypothetical protein [Vibrio cholerae].	GCF_002284425.1
WP_095570744.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1086	-	Gammaproteobacteria	Vibrio coralliilyticus	hypothetical protein [Vibrio coralliilyticus].	GCF_002286405.1
WP_095743432.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1300	-	Betaproteobacteria	Variovorax boronicumulans	hypothetical protein [Variovorax boronicumulans].	GCF_002291405.1
WP_096138380.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1321	-	Gammaproteobacteria	Pseudomonas syringae	DUF4365 domain-containing protein [Pseudomonas syringae].	GCF_002318715.1
WP_096145332.1	PIN*→	PIN	1088	-	Firmicutes	Clostridium chauvoei	tetratricopeptide repeat protein [Clostridium chauvoei].	GCF_002327185.1
WP_096360261.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	2100	-	Gammaproteobacteria	Sulfuricaulis limicola	hypothetical protein [Sulfuricaulis limicola].	GCF_002355735.1

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WP_096444074.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1088	-	Gammaproteobacteria	Vibrio mediterranei	hypothetical protein [Vibrio mediterranei].	GCF_002995655.1
WP_096819326.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1424	-	Gammaproteobacteria	Pseudomonas fluorescens	tetratricopeptide repeat protein [Pseudomonas fluorescens].	GCF_002417665.1
WP_096985931.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1094	-	Gammaproteobacteria	Escherichia coli	hypothetical protein [Escherichia coli].	GCF_013372365.1
WP_097373330.1	PIN*→	PIN	245	-	Alphaproteobacteria	Celeribacter manganoxidans	hypothetical protein [Celeribacter manganoxidans].	GCF_002504165.1
WP_097730210.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1094	-	Gammaproteobacteria	Escherichia coli	hypothetical protein [Escherichia coli].	GCF_002535535.1
WP_097759664.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1094	-	Gammaproteobacteria	Escherichia coli	hypothetical protein [Escherichia coli].	GCF_002538945.1
WP_097979402.1	TPR+PIN*→	TPR+PIN	1217	-	Firmicutes	Bacillus toyonensis	hypothetical protein [Bacillus toyonensis].	GCF_002552775.1
WP_098090392.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1101	-	Gammaproteobacteria	Pseudomonas putida	hypothetical protein [Pseudomonas putida].	GCF_002554535.1
WP_098280847.1	TPR+PIN*→	TPR+PIN	1183	-	Firmicutes	Bacillus cereus	hypothetical protein [Bacillus cereus].	GCF_002560075.1
WP_098365372.1	TPR+PIN*→	TPR+PIN	1217	-	Firmicutes	Bacillus cereus	hypothetical protein [Bacillus cereus].	GCF_002561575.1
WP_098420086.1	TPR+PIN*→	TPR+PIN	1183	-	Firmicutes	Bacillus cereus	hypothetical protein [Bacillus cereus].	GCF_002562505.1
WP_098433845.1	TPR+PIN*→	TPR+PIN	1184	-	Firmicutes	Priestia megaterium	hypothetical protein [Priestia megaterium].	GCF_002564705.1
WP_098573825.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1147	-	Firmicutes	Bacillus wiedmannii	tetratricopeptide repeat protein [Bacillus wiedmannii].	GCF_002568785.1
WP_098687609.1	TPR+PIN*→	TPR+PIN	1157	-	Firmicutes	Bacillus toyonensis	hypothetical protein [Bacillus toyonensis].	GCF_002571615.1
WP_099262235.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1243	-	Planctomycetes	Rhodopirellula bahusiensis	GreA/GreB family elongation factor [Rhodopirellula bahusiensis].	GCF_002727185.1
WP_099438436.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1252	-	Bacteroidetes	Pedobacter ginsengisoli	hypothetical protein [Pedobacter ginsengisoli].	GCF_002736205.1
WP_100140263.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1066	-	Betaproteobacteria	Snodgrassella alvi	hypothetical protein [Snodgrassella alvi].	GCF_002777775.1
WP_100151648.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1066	-	Betaproteobacteria	Snodgrassella alvi	hypothetical protein [Snodgrassella alvi].	GCF_002777655.1
WP_100344325.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1215	-	Actinobacteria	Compostimonas suwonensis	DUF4365 domain-containing protein [Compostimonas suwonensis].	GCF_002797855.1
WP_100632757.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1321	-	Gammaproteobacteria	Pseudomonas qingdaonensis	DUF4365 domain-containing protein [Pseudomonas qingdaonensis].	GCF_002806685.1
WP_101291505.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1094	-	Gammaproteobacteria	Escherichia coli	hypothetical protein [Escherichia coli].	GCF_002843705.1
WP_102155042.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1270	-	Alphaproteobacteria	Tsuneonella flava	GreA/GreB family elongation factor [Tsuneonella flava].	GCF_002870965.1
WP_102488850.1	HetE-N1→ HetE-N1+TPR+GreAB-C+PIN*→	HetE-N1+TPR+GreAB-C+PIN	1088	-	Gammaproteobacteria	Vibrio splendidus	hypothetical protein [Vibrio splendidus].	GCF_002875305.1
WP_102520861.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1088	-	Gammaproteobacteria	Shewanella sp. 10N.286.48.A6	hypothetical protein [Shewanella sp. 10N.286.48.A6].	GCF_002873135.1
WP_102570991.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1088	-	Gammaproteobacteria	Vibrio splendidus	hypothetical protein [Vibrio splendidus].	GCF_002875585.1
WP_102574526.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1116	-	Gammaproteobacteria	Vibrio splendidus	hypothetical protein [Vibrio splendidus].	GCF_002877195.1
WP_102576920.1	HetE-N1→ HetE-N1+TPR+GreAB-C+PIN*→	HetE-N1+TPR+GreAB-C+PIN	1091	-	Gammaproteobacteria	Vibrio splendidus	hypothetical protein [Vibrio splendidus].	GCF_002877345.1
WP_103206664.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1213	-	Actinobacteria	Microbacterium testaceum	hypothetical protein [Microbacterium testaceum].	GCF_002899925.1
WP_103448257.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1421	-	Gammaproteobacteria	Pseudomonas	MULTISPECIES: hypothetical protein [Pseudomonas].	GCF_015680835.1
WP_103712798.1	REase+TPR+GreAB-C+PIN*→||||<-KAP_NTPase	REase+TPR+GreAB-C+PIN	1321	-	Gammaproteobacteria	Pseudomonas syringae	DUF4365 domain-containing protein [Pseudomonas syringae].	GCF_002916275.1
WP_103713374.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1107	-	Gammaproteobacteria	Pseudomonas syringae	hypothetical protein [Pseudomonas syringae].	GCF_002917155.1
WP_103715293.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1131	-	Bacteroidetes	Flavobacterium columnare	hypothetical protein [Flavobacterium columnare].	GCF_002916795.1
WP_103949560.1	HetE-N1→ HetE-N1+TPR+GreAB-C+PIN*→	HetE-N1+TPR+GreAB-C+PIN	1094	-	Gammaproteobacteria	Lelliottia	MULTISPECIES: hypothetical protein [Lelliottia].	GCF_002922995.1
WP_104189366.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1110	-	Gammaproteobacteria	unclassified Pantoea	MULTISPECIES: hypothetical protein [unclassified Pantoea].	GCF_002928355.1
WP_104723186.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1321	-	Gammaproteobacteria	Pseudomonas syringae	DUF4365 domain-containing protein [Pseudomonas syringae].	GCF_900235865.1
WP_104925436.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1118	-	Gammaproteobacteria	Rahnella sp. ERMR1:05	hypothetical protein [Rahnella sp. ERMR1:05].	GCF_002951615.1
WP_105080712.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1111	-	Gammaproteobacteria	Pantoea	MULTISPECIES: hypothetical protein [Pantoea].	GCF_017920435.1
WP_105696567.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1321	-	Gammaproteobacteria	Pseudomonas poae	DUF4365 domain-containing protein [Pseudomonas poae].	GCF_002980135.1
WP_105730942.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1344	-	Betaproteobacteria	Malikia spinosa	hypothetical protein [Malikia spinosa].	GCF_002980625.1
WP_105731559.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1278	-	Alphaproteobacteria	Ochrobactrum sp. MYb29	hypothetical protein [Ochrobactrum sp. MYb29].	GCF_002979345.1

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WP_105794455.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1351	-	Betaproteobacteria	Burkholderia multivorans	hypothetical protein [Burkholderia multivorans].	GCF_002981485.1
WP_106098487.1	SIG+TM→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1129	-	Bacteroidetes	Capnocytophaga sp. oral taxon 878	hypothetical protein [Capnocytophaga sp. oral taxon 878].	GCF_002999135.1
WP_106374900.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1145	-	Gammaproteobacteria	Halomonas songnenensis	hypothetical protein [Halomonas songnenensis].	GCF_003002925.1
WP_106946809.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1155	-	Alphaproteobacteria	Bradyrhizobium sp. MOS002	hypothetical protein [Bradyrhizobium sp. MOS002].	GCF_003020115.1
WP_107027340.1	REase+TPR+TPR+GreAB-C+PIN*→	REase+TPR+TPR+GreAB-C+PIN	1357	-	Alphaproteobacteria	Ensifer sp. NM-2	hypothetical protein [Ensifer sp. NM-2].	GCF_003024455.1
WP_107248740.1	HetE-N1→ GreAB-C*→	GreAB-C	1128	-	Gammaproteobacteria	Photobacterium kishitanii	hypothetical protein [Photobacterium kishitanii].	GCF_003025535.1
WP_107289369.1	HetE-N1→ GreAB-C*→	GreAB-C	1164	-	Gammaproteobacteria	Photobacterium kishitanii	hypothetical protein [Photobacterium kishitanii].	GCF_003025915.1
WP_107901223.1	TPR+PIN*→	TPR+PIN	1216	-	Firmicutes	Bacillus sp. OV186	hypothetical protein [Bacillus sp. OV186].	GCF_003053645.1
WP_108393929.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1106	-	Gammaproteobacteria	Enterobacter hormaechei	hypothetical protein [Enterobacter hormaechei].	GCF_003056805.1
WP_108462916.1	REase+TPR+TPR+GreAB-C+PIN*→	REase+TPR+TPR+GreAB-C+PIN	1323	-	Alphaproteobacteria	Devosia naphthalenivorans	GreA/GreB family elongation factor [Devosia naphthalenivorans].	GCF_003056355.1
WP_108677990.1	HetE-N1→ HetE-N1+TPR+GreAB-C+PIN*→	HetE-N1+TPR+GreAB-C+PIN	1088	-	Gammaproteobacteria	Vibrio vulnificus	hypothetical protein [Vibrio vulnificus].	GCF_011754395.1
WP_108816955.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1311	-	Alphaproteobacteria	Loktanella sp. Alg231-35	hypothetical protein [Loktanella sp. Alg231-35].	GCF_900143545.1
WP_109158749.1	X+PIN*→	X+PIN	1041	-	Epsilonproteobacteria	Aliarcobacter skirrowii	hypothetical protein [Aliarcobacter skirrowii].	GCF_003122145.1
WP_109211325.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1211	-	Actinobacteria	Microbacterium	MULTISPECIES: DUF4365 domain-containing protein [Microbacterium].	GCF_015278315.1
WP_109426752.1	TPR→ TPR+GreAB-C+PIN*→||||<-?||HTH→	TPR+GreAB-C+PIN	494	-	Gammaproteobacteria	Acinetobacter baumannii	GreA/GreB family elongation factor [Acinetobacter baumannii].	GCF_013416255.1
WP_109802449.1	TPR+PIN*→	TPR+PIN	1203	-	Actinobacteria	Micromonospora sp. 4G51	hypothetical protein [Micromonospora sp. 4G51].	GCF_003172935.1
WP_109937286.1	HetE-N1→ HetE-N1+TPR+GreAB-C+PIN*→	HetE-N1+TPR+GreAB-C+PIN	1123	-	Gammaproteobacteria	Pseudomonas sp. RW407	hypothetical protein [Pseudomonas sp. RW407].	GCF_003176655.1
WP_109950172.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1332	-	-	Methylobacterium sp. 17Sr1-43	hypothetical protein [Methylobacterium sp. 17Sr1-43].	GCF_003173735.1
WP_109967732.1	PNPase+TPR+GreAB-C+PIN*→	PNPase+TPR+GreAB-C+PIN	1415	-	Euryarchaeota	Methanospirillum lacunae	hypothetical protein [Methanospirillum lacunae].	GCF_003173355.1
WP_110317339.1	HTH+PNPase+TPR+GreAB-C+PIN*→	HTH+PNPase+TPR+GreAB-C+PIN	1518	-	Actinobacteria	Mycolicibacterium moriokaense	hypothetical protein [Mycolicibacterium moriokaense].	GCF_003201655.1
WP_110434863.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	950	-	Gammaproteobacteria	Gilliamella apicola	hypothetical protein [Gilliamella apicola].	GCF_003202655.1
WP_110455267.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1126	-	Gammaproteobacteria	Gilliamella apicola	hypothetical protein [Gilliamella apicola].	GCF_003202815.1
WP_110459582.1	HetE-N1→ HetE-N1+TPR+GreAB-C+PIN*→	HetE-N1+TPR+GreAB-C+PIN	1107	-	Gammaproteobacteria	Pseudomonas syringae	hypothetical protein [Pseudomonas syringae].	GCF_003202975.1
WP_110575159.1	HetE-N1→ HetE-N1+TPR+GreAB-C+PIN*→?→ MACRODOMAIN→	HetE-N1+TPR+GreAB-C+PIN	1099	-	Gammaproteobacteria	Marinomonas alcarazii	hypothetical protein [Marinomonas alcarazii].	GCF_003208215.1
WP_110766563.1	REase+TPR+GreAB-C+PIN*→||||<-KAP_NTPase	REase+TPR+GreAB-C+PIN	1321	-	Gammaproteobacteria	Pseudomonas syringae	DUF4365 domain-containing protein [Pseudomonas syringae].	GCF_003205895.1
WP_110818130.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1140	-	Gammaproteobacteria	Pseudomonas syringae	hypothetical protein [Pseudomonas syringae].	GCF_003205965.1
WP_111087282.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1208	-	Actinobacteria	Curtobacterium sp. MCLR17_055	DUF4365 domain-containing protein [Curtobacterium sp. MCLR17_055].	GCF_003234305.1
WP_112353670.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1235	-	Gammaproteobacteria	Shewanella benthica	hypothetical protein [Shewanella benthica].	GCF_900476435.1
WP_112921055.1	HNH→?→?→ PSE→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1092	-	Gammaproteobacteria	Escherichia coli	hypothetical protein [Escherichia coli].	GCF_003292515.1
WP_114150230.1	TPR+GreAB-C+PIN*→?→||||<-?||?→ PAIREDC-HTH→	TPR+GreAB-C+PIN	900	-	Gammaproteobacteria	Acinetobacter baumannii	GreA/GreB family elongation factor [Acinetobacter baumannii].	GCF_017726575.1
WP_114915524.1	TPR+PIN*→	TPR+PIN	1187	-	Firmicutes	Oceanobacillus zhaokaii	hypothetical protein [Oceanobacillus zhaokaii].	GCF_003352005.1
WP_115015610.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1087	-	Gammaproteobacteria	Shewanella putrefaciens	hypothetical protein [Shewanella putrefaciens].	GCF_900457065.1
WP_115596495.1	TPR+GreAB-C+PIN*→?→||||<-?||?→ PAIREDC-HTH→	TPR+GreAB-C+PIN	756	-	Gammaproteobacteria	Acinetobacter baumannii	GreA/GreB family elongation factor [Acinetobacter baumannii].	GCF_900444745.1
WP_116227219.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1121	-	Gammaproteobacteria	Pectobacterium aquaticum	hypothetical protein [Pectobacterium aquaticum].	GCF_003382595.2
WP_116600438.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1438	-	Gammaproteobacteria	Pseudomonas sp. HMWF011	hypothetical protein [Pseudomonas sp. HMWF011].	GCF_003094675.1
WP_116893902.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1158	-	Gammaproteobacteria	Pseudomonas syringae	hypothetical protein [Pseudomonas syringae].	GCF_003412595.1
WP_116994473.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1327	-	Betaproteobacteria	Duganella sp. BJB476	hypothetical protein [Duganella sp. BJB476].	GCF_003416895.1
WP_117157406.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1117	-	Gammaproteobacteria	Enterobacteriaceae	MULTISPECIES: hypothetical protein [Enterobacteriaceae].	GCF_017814635.1
WP_117181470.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1438	-	Gammaproteobacteria	Pseudomonas cichorii	hypothetical protein [Pseudomonas cichorii].	GCF_003416755.1

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WP_117831329.1	HEPN+SNF→?→?→?→ X+PIN*→	X+PIN	1212	-	Firmicutes	Roseburia sp. TF10-5	hypothetical protein [Roseburia sp. TF10-5].	GCF_003462365.1
WP_118235377.1	X+PIN*→	X+PIN	1200	-	Firmicutes	Blautia obeum	hypothetical protein [Blautia obeum].	GCF_003470555.1
WP_118282562.1	X+PIN*→?→ CITB-HTH+LexA-protease→	X+PIN	1212	-	Firmicutes	Roseburia sp. AM16-25	hypothetical protein [Roseburia sp. AM16-25].	GCF_003473825.1
WP_118371145.1	X+PIN*→	X+PIN	1200	-	Firmicutes	Lachnospira eligens	hypothetical protein [Lachnospira eligens].	GCF_003474735.1
WP_118468213.1	Mbetalac→ Trypsin+TPR+PIN*→	Trypsin+TPR+PIN	1933	-	Firmicutes	unclassified Clostridium	MULTISPECIES: trypsin-like peptidase domain-containing protein [unclassified Clostridium].	GCF_003477925.1
WP_118891177.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1327	-	Betaproteobacteria	Ralstonia solanacearum	DUF4365 domain-containing protein [Ralstonia solanacearum].	GCF_003515285.1
WP_118897359.1	X+PIN*→	X+PIN	1033	-	Epsilonproteobacteria	Malaciobacter marinus	hypothetical protein [Malaciobacter marinus].	GCF_003544855.1
WP_118994196.1	HetE-N1→ HetE-N1+TPR+GreAB-C+PIN*→	HetE-N1+TPR+GreAB-C+PIN	1104	-	Betaproteobacteria	Pusillimonas	MULTISPECIES: hypothetical protein [Pusillimonas].	GCF_004022565.1
WP_119088708.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1271	-	Bacteria	Candidatus Cryosericum terrychapinii	hypothetical protein [Candidatus Cryosericum terrychapinii].	GCF_003570925.1
WP_119196537.1	X+PIN*→ HTH→?→?→ HTH→	X+PIN	1109	-	Firmicutes	Dorea formicigenerans	hypothetical protein [Dorea formicigenerans].	GCF_003465045.1
WP_119369914.1	REase+TPR+GreAB-C+PIN*→||||<-?<-TPR	REase+TPR+GreAB-C+PIN	1436	-	Gammaproteobacteria	Pseudomonas monteilii	GreA/GreB family elongation factor [Pseudomonas monteilii].	GCF_003576045.1
WP_119587627.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1290	-	Alphaproteobacteria	Aurantiacibacter zhengii	hypothetical protein [Aurantiacibacter zhengii].	GCF_003584125.1
WP_119956833.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1511	-	Gammaproteobacteria	Pseudomonas sp. K1S02-6	tetratricopeptide repeat protein [Pseudomonas sp. K1S02-6].	GCF_003596405.1
WP_119992948.1	TM+TM+TPR+PIN*→	TM+TM+TPR+PIN	1208	-	Bacteroidetes	Bacteroides sp. AM41-16	hypothetical protein [Bacteroides sp. AM41-16].	GCF_003603495.1
WP_120172805.1	TM+TM+TPR+PIN*→	TM+TM+TPR+PIN	1208	-	Bacteroidetes	Bacteroides sp. AF20-13LB	hypothetical protein [Bacteroides sp. AF20-13LB].	GCF_003603065.1
WP_120777109.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1192	-	Actinobacteria	Microbacterium sp. CGR2	hypothetical protein [Microbacterium sp. CGR2].	GCF_003626735.1
WP_121482750.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1233	-	Alphaproteobacteria	Brevundimonas naejangsanensis	hypothetical protein [Brevundimonas naejangsanensis].	GCF_003627995.1
WP_122071999.1	PAIREDC-HTH→?→?→?→ GreAB-C+PIN*→	GreAB-C+PIN	683	-	Gammaproteobacteria	Acinetobacter wuhouensis	hypothetical protein [Acinetobacter wuhouensis].	GCF_002165345.2
WP_122252741.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1158	-	Gammaproteobacteria	Pseudomonas savastanoi	hypothetical protein [Pseudomonas savastanoi].	GCF_003703035.1
WP_122265719.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1140	-	Gammaproteobacteria	Pseudomonas syringae	hypothetical protein [Pseudomonas syringae].	GCF_003700575.1
WP_122311960.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1143	-	Gammaproteobacteria	Pseudomonas coronafaciens	hypothetical protein [Pseudomonas coronafaciens].	GCF_003699785.1
WP_122314252.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1436	-	Gammaproteobacteria	Pseudomonas cichorii	hypothetical protein [Pseudomonas cichorii].	GCF_003700275.1
WP_122364448.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1438	-	Gammaproteobacteria	Pseudomonas	MULTISPECIES: hypothetical protein [Pseudomonas].	GCF_014842015.1
WP_122365799.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1140	-	Gammaproteobacteria	Pseudomonas syringae group genomosp. 3	hypothetical protein [Pseudomonas syringae group genomosp. 3].	GCF_003702755.1
WP_122471279.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1100	-	Gammaproteobacteria	Pseudomonas viridiflava	hypothetical protein [Pseudomonas viridiflava].	GCF_900582365.1
WP_122509345.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1140	-	Gammaproteobacteria	Pseudomonas viridiflava	hypothetical protein [Pseudomonas viridiflava].	GCF_900581635.1
WP_122559800.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1438	-	Gammaproteobacteria	Pseudomonas viridiflava	hypothetical protein [Pseudomonas viridiflava].	GCF_900580935.1
WP_122732542.1	HetE-N1→ HetE-N1+TPR+GreAB-C+PIN*→	HetE-N1+TPR+GreAB-C+PIN	1106	-	Gammaproteobacteria	Pseudomonas viridiflava	hypothetical protein [Pseudomonas viridiflava].	GCF_900591195.1
WP_122848883.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1321	-	Gammaproteobacteria	Pseudomonas viridiflava	DUF4365 domain-containing protein [Pseudomonas viridiflava].	GCF_900585905.1
WP_122887609.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1345	-	Betaproteobacteria	Burkholderia pseudomallei	hypothetical protein [Burkholderia pseudomallei].	GCF_900593895.1
WP_123094036.1	HetE-N1→ TPR+GreAB-C+PIN*→?→ MACRODOMAIN→	TPR+GreAB-C+PIN	1099	-	Gammaproteobacteria	Marinomonas hwangdonensis	hypothetical protein [Marinomonas hwangdonensis].	GCF_003721245.1
WP_123338621.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1210	-	Actinobacteria	Curtobacterium sp. PhB171	DUF4365 domain-containing protein [Curtobacterium sp. PhB171].	GCF_003752665.1
WP_123718714.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1112	-	Gammaproteobacteria	Pseudomonas poae	hypothetical protein [Pseudomonas poae].	GCF_003731985.1
WP_123788903.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1351	-	Betaproteobacteria	Burkholderia multivorans	hypothetical protein [Burkholderia multivorans].	GCF_003812365.1
WP_123901658.1	TPR+GreAB-C+PIN→ GreAB-C+PIN*→	GreAB-C+PIN	535	-	Bacteroidetes	Chryseobacterium bernardetii	hypothetical protein [Chryseobacterium bernardetii].	GCF_003815955.1
WP_124017047.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	838	-	Gammaproteobacteria	Shewanella vesiculosa	hypothetical protein [Shewanella vesiculosa].	GCF_003797885.1
WP_124131211.1	DOC+HTH→ REase+TOPC→?→ HetE-N1→ HetE-N1+TPR+GreAB-C+PIN*→	HetE-N1+TPR+GreAB-C+PIN	1124	-	Gammaproteobacteria	Pseudomonas aeruginosa	hypothetical protein [Pseudomonas aeruginosa].	GCF_003836815.1
WP_124132190.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1140	-	Gammaproteobacteria	Pseudomonas aeruginosa	hypothetical protein [Pseudomonas aeruginosa].	GCF_003836445.1

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WP_124135313.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1158	-	Gammaproteobacteria	Pseudomonas aeruginosa	hypothetical protein [Pseudomonas aeruginosa].	GCF_003836905.1
WP_124172921.1	DOC+HTH→ REase+TOPC→?→ HetE-N1→ HetE-N1+TPR+GreAB-C+PIN*→	HetE-N1+TPR+GreAB-C+PIN	1124	-	Gammaproteobacteria	Pseudomonas aeruginosa	hypothetical protein [Pseudomonas aeruginosa].	GCF_003839465.1
WP_124325287.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1139	-	Gammaproteobacteria	Pseudomonas chlororaphis	hypothetical protein [Pseudomonas chlororaphis].	GCF_003850385.1
WP_124410055.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1110	-	Gammaproteobacteria	Pseudomonas sp. R4-34-07	hypothetical protein [Pseudomonas sp. R4-34-07].	GCF_003852375.1
WP_124421918.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1157	-	Gammaproteobacteria	Pseudomonas orientalis	hypothetical protein [Pseudomonas orientalis].	GCF_003851585.1
WP_124432744.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1321	-	Gammaproteobacteria	Pseudomonas orientalis	DUF4365 domain-containing protein [Pseudomonas orientalis].	GCF_003852045.1
WP_124433851.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1321	-	Gammaproteobacteria	Pseudomonas orientalis	DUF4365 domain-containing protein [Pseudomonas orientalis].	GCF_003852045.1
WP_124551445.1	HEPN→?→?→ REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1498	-	Betaproteobacteria	Burkholderia sp. Bp9015	tetratricopeptide repeat protein [Burkholderia sp. Bp9015].	GCF_003853505.1
WP_124582885.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1248	-	Bacteroidetes	Pedobacter sp. KBW06	hypothetical protein [Pedobacter sp. KBW06].	GCF_003852525.1
WP_124686982.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1344	-	Betaproteobacteria	Cupriavidus pauculus	tetratricopeptide repeat protein [Cupriavidus pauculus].	GCF_003854935.1
WP_124885098.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1351	-	Betaproteobacteria	Burkholderia stagnalis	hypothetical protein [Burkholderia stagnalis].	GCF_003857545.1
WP_124919377.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1500	-	Betaproteobacteria	Burkholderia	MULTISPECIES: tetratricopeptide repeat protein [Burkholderia].	GCF_001528845.1
WP_124920354.1	HEPN→?→?→ REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1289	-	Betaproteobacteria	Burkholderia stagnalis	tetratricopeptide repeat protein [Burkholderia stagnalis].	GCF_003857615.1
WP_125127612.1	X+PIN*→?→?→?→?→ MACRODOMAIN→	X+PIN	1232	-	Firmicutes	Schaedlerella arabinosiphila	hypothetical protein [Schaedlerella arabinosiphila].	GCF_003885045.1
WP_125255381.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1327	-	Alphaproteobacteria	Brevundimonas fluminis	DUF4365 domain-containing protein [Brevundimonas fluminis].	GCF_003934285.1
WP_125429200.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1284	-	Gammaproteobacteria	Stenotrophomonas maltophilia	GreA/GreB family elongation factor [Stenotrophomonas maltophilia].	GCF_003935615.1
WP_125440526.1	<-REase+nSTAND3||TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1282	-	Bacteroidetes	Hymenobacter perfusus	hypothetical protein [Hymenobacter perfusus].	GCF_003944765.1
WP_125601225.1	HetE-N1→ MNS-Npun2340+TPR+GreAB-C+PIN*→	MNS-Npun2340+TPR+GreAB-C+PIN	1094	-	Gammaproteobacteria	Aeromonas salmonicida	hypothetical protein [Aeromonas salmonicida].	GCF_003947375.1
WP_125730033.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1094	-	Gammaproteobacteria	Aeromonas salmonicida	hypothetical protein [Aeromonas salmonicida].	GCF_003947355.1
WP_126243019.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1333	-	Betaproteobacteria	Burkholderia gladioli	hypothetical protein [Burkholderia gladioli].	GCF_902829535.1
WP_126550729.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1140	-	Gammaproteobacteria	Pseudomonas aeruginosa	hypothetical protein [Pseudomonas aeruginosa].	GCF_001516225.2
WP_126566690.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1043	-	Gammaproteobacteria	Pseudomonas aeruginosa	hypothetical protein [Pseudomonas aeruginosa].	GCF_003968275.1
WP_126570139.1	DOC+HTH→ REase+TOPC→?→ HetE-N1→ HetE-N1→ GreAB-C+PIN*→	GreAB-C+PIN	523	-	Gammaproteobacteria	Pseudomonas aeruginosa	hypothetical protein [Pseudomonas aeruginosa].	GCF_003969065.1
WP_127030837.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1093	-	Gammaproteobacteria	Pectobacterium versatile	hypothetical protein [Pectobacterium versatile].	GCF_003990505.1
WP_127257681.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1287	-	Alphaproteobacteria	Mesorhizobium sp. M7A.F.Ca.US.008.03.1.1	hypothetical protein [Mesorhizobium sp. M7A.F.Ca.US.008.03.1.1].	GCF_003997495.1
WP_127294273.1	REase+TPR+TPR+GreAB-C+PIN*→	REase+TPR+TPR+GreAB-C+PIN	1333	-	Alphaproteobacteria	Mesorhizobium sp. M6A.T.Ce.TU.016.01.1.1	GreA/GreB family elongation factor [Mesorhizobium sp. M6A.T.Ce.TU.016.01.1.1].	GCF_003997065.1
WP_127581798.1	BirA-HTH→?→ REase+TPR+TPR+GreAB-C+PIN*→	REase+TPR+TPR+GreAB-C+PIN	1322	-	Alphaproteobacteria	Sinorhizobium medicae	hypothetical protein [Sinorhizobium medicae].	GCF_004002295.1
WP_128106456.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1323	-	Alphaproteobacteria	Acetobacter oryzoeni	tetratricopeptide repeat protein [Acetobacter oryzoeni].	GCF_004014775.2
WP_128141476.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1616	-	Betaproteobacteria	Janthinobacterium lividum	hypothetical protein [Janthinobacterium lividum].	GCF_900451225.1
WP_128142627.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1269	-	Betaproteobacteria	Janthinobacterium lividum	hypothetical protein [Janthinobacterium lividum].	GCF_900451225.1
WP_128181279.1	REase+TPR+TPR+GreAB-C+PIN*→	REase+TPR+TPR+GreAB-C+PIN	1330	-	Alphaproteobacteria	Sinirhodobacter populi	hypothetical protein [Sinirhodobacter populi].	GCF_004022225.1
WP_128291227.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1320	-	Alphaproteobacteria	Afifella aestuarii	hypothetical protein [Afifella aestuarii].	GCF_004023665.1
WP_128326676.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1493	-	Gammaproteobacteria	Pseudomonas alkylphenolica	hypothetical protein [Pseudomonas alkylphenolica].	GCF_004025535.1
WP_128384334.1	X+PIN*→	X+PIN	1055	-	Gammaproteobacteria	Hydrogenovibrio thermophilus	hypothetical protein [Hydrogenovibrio thermophilus].	GCF_004028275.1
WP_128449906.1	REase+TPR+TPR+GreAB-C+PIN*→	REase+TPR+TPR+GreAB-C+PIN	1385	-	Alphaproteobacteria	Rhizobium leguminosarum	hypothetical protein [Rhizobium leguminosarum].	GCF_004054135.1
WP_128549293.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1187	-	Alphaproteobacteria	Salipiger	MULTISPECIES: tetratricopeptide repeat protein [Salipiger].	GCF_014637265.1
WP_128552168.1	DOC+HTH→ REase+TOPC→ HetE-N1→ HetE-N1+TPR+GreAB-C+PIN*→	HetE-N1+TPR+GreAB-C+PIN	1123	-	Gammaproteobacteria	Pseudomonas aeruginosa	hypothetical protein [Pseudomonas aeruginosa].	GCF_003698765.1

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WP_128664039.1	DOC+HTH→ REase+TOPC→?→ HetE-N1→ HetE-N1+TPR+GreAB-C+PIN*→	HetE-N1+TPR+GreAB-C+PIN	1124	-	Gammaproteobacteria	Pseudomonas	MULTISPECIES: hypothetical protein [Pseudomonas].	GCF_016624455.1
WP_128715623.1	SIG+HIN-HTH→?→ GreAB-C+PIN*→	GreAB-C+PIN	540	-	Alphaproteobacteria	Rhizobium acidisoli	hypothetical protein [Rhizobium acidisoli].	GCF_002531755.2
WP_128816805.1	REase→ TPR+PIN*→	TPR+PIN	875	-	Actinobacteria	Streptomyces sp. S063	tetratricopeptide repeat protein [Streptomyces sp. S063].	GCF_002832675.1
WP_128912272.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1277	-	Acidobacteria	Granulicella sibirica	hypothetical protein [Granulicella sibirica].	GCF_004115155.1
WP_129013963.1	TPR+GreAB-C+PIN*→?→?→?→?→?→?→ TIR+TPR+TPR→	TPR+GreAB-C+PIN	1046	-	Epsilonproteobacteria	Arcobacter cloacae	hypothetical protein [Arcobacter cloacae].	GCF_013201935.1
WP_129107976.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1200	-	Epsilonproteobacteria	Halarcobacter bivalviorum	hypothetical protein [Halarcobacter bivalviorum].	GCF_004116705.1
WP_129330071.1	HetE-N1→?→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	739	-	Gammaproteobacteria	Salmonella enterica	hypothetical protein [Salmonella enterica].	GCF_004120835.1
WP_129368690.1	HetE-N1→?→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	855	-	Gammaproteobacteria	Salmonella enterica	hypothetical protein [Salmonella enterica].	GCF_004120585.1
WP_129411798.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1323	-	Alphaproteobacteria	Mesorhizobium sp. Pch-S	hypothetical protein [Mesorhizobium sp. Pch-S].	GCF_004136315.1
WP_129485462.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1468	-	Gammaproteobacteria	Pseudomonas syringae	hypothetical protein [Pseudomonas syringae].	GCF_004124725.1
WP_129893847.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1309	-	Chloroflexi	Ktedonosporobacter rubrisoli	tetratricopeptide repeat protein [Ktedonosporobacter rubrisoli].	GCF_004208415.1
WP_130007120.1	HetE-N1→ HetE-N1+TPR+GreAB-C+PIN*→	HetE-N1+TPR+GreAB-C+PIN	1104	-	Betaproteobacteria	Pusillimonas ginsengisoli	hypothetical protein [Pusillimonas ginsengisoli].	GCF_004153455.1
WP_130044922.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1116	-	Gammaproteobacteria	Aliivibrio finisterrensis	hypothetical protein [Aliivibrio finisterrensis].	GCF_004167675.1
WP_130132480.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1245	-	Gammaproteobacteria	Acinetobacter wuhouensis	hypothetical protein [Acinetobacter wuhouensis].	GCF_004209325.1
WP_130204115.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1113	-	Gammaproteobacteria	Pseudomonas moorei	hypothetical protein [Pseudomonas moorei].	GCF_004212425.1
WP_130252287.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1114	-	Gammaproteobacteria	Vibrio vulnificus	hypothetical protein [Vibrio vulnificus].	GCF_004214575.1
WP_130472343.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1348	-	Alphaproteobacteria	Candidatus Magnetaquicoccus inordinatus	hypothetical protein [Candidatus Magnetaquicoccus inordinatus].	GCF_004217665.1
WP_130525307.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1086	-	Gammaproteobacteria	Pasteurella multocida	hypothetical protein [Pasteurella multocida].	GCF_003428945.1
WP_130555679.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1086	-	Gammaproteobacteria	Pasteurella multocida	hypothetical protein [Pasteurella multocida].	GCF_001578435.2
WP_130710767.1	REase+TPR+TPR+GreAB-C+PIN*→	REase+TPR+TPR+GreAB-C+PIN	1343	-	Alphaproteobacteria	Rhizobium leguminosarum	hypothetical protein [Rhizobium leguminosarum].	GCF_004304355.1
WP_130725527.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1255	-	Alphaproteobacteria	Rhizobium leguminosarum	hypothetical protein [Rhizobium leguminosarum].	GCF_004303985.1
WP_130928792.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1438	-	Gammaproteobacteria	Pseudomonas sp. Sample_20	hypothetical protein [Pseudomonas sp. Sample_20].	GCF_004307585.1
WP_131049955.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1092	-	Gammaproteobacteria	Raoultella ornithinolytica	hypothetical protein [Raoultella ornithinolytica].	GCF_004312065.1
WP_131189445.1	HetE-N1→ HetE-N1+TPR+GreAB-C+PIN*→	HetE-N1+TPR+GreAB-C+PIN	1125	-	Gammaproteobacteria	Pseudomonas kirkiae	hypothetical protein [Pseudomonas kirkiae].	GCF_004327175.1
WP_131590605.1	TPR+PIN*→	TPR+PIN	1153	-	Actinobacteria	Mycolicibacterium setense	hypothetical protein [Mycolicibacterium setense].	GCF_000805375.1
WP_131623255.1	REase+TPR+TPR+GreAB-C+PIN*→	REase+TPR+TPR+GreAB-C+PIN	1361	-	Alphaproteobacteria	Rhizobium leguminosarum	hypothetical protein [Rhizobium leguminosarum].	GCF_004330075.1
WP_131714066.1	REase+TPR+TPR+GreAB-C+PIN*→	REase+TPR+TPR+GreAB-C+PIN	1337	-	Alphaproteobacteria	Rhizobium leguminosarum	hypothetical protein [Rhizobium leguminosarum].	GCF_004330185.1
WP_131718233.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	556	-	Alphaproteobacteria	Rhizobium leguminosarum	hypothetical protein [Rhizobium leguminosarum].	GCF_004330625.1
WP_131814603.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	595	-	Alphaproteobacteria	Cognatishimia maritima	hypothetical protein [Cognatishimia maritima].	GCF_900129685.1
WP_131869160.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1306	-	Alphaproteobacteria	unclassified Bradyrhizobium	MULTISPECIES: tetratricopeptide repeat protein [unclassified Bradyrhizobium].	GCF_004346395.1
WP_132139369.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1368	-	Betaproteobacteria	Massilia sp. GV090	hypothetical protein [Massilia sp. GV090].	GCF_004341465.1
WP_132251347.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1114	-	Alphaproteobacteria	Methylobacterium segetis	tetratricopeptide repeat protein [Methylobacterium segetis].	GCF_004348265.1
WP_132403375.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1266	-	Bacteroidetes	Pedobacter sp. CF074	hypothetical protein [Pedobacter sp. CF074].	GCF_004342125.1
WP_132537157.1	BirA-HTH→ HEPN→ REase+TPR+TPR+GreAB-C+PIN*→	REase+TPR+TPR+GreAB-C+PIN	1332	-	Alphaproteobacteria	Rhizobium sp. PP-F2F-G48	GreA/GreB family elongation factor [Rhizobium sp. PP-F2F-G48].	GCF_004342335.1
WP_132665856.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1297	-	Alphaproteobacteria	Rhizobium sp. PP-CC-3G-465	tetratricopeptide repeat protein [Rhizobium sp. PP-CC-3G-465].	GCF_004343445.1
WP_132831667.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1188	-	Alphaproteobacteria	Antarcticimicrobium sediminis	hypothetical protein [Antarcticimicrobium sediminis].	GCF_004348975.1
WP_132850706.1	TPR+PIN*→	TPR+PIN	1135	-	Actinobacteria	Streptomyces sp. BK308	tetratricopeptide repeat protein [Streptomyces sp. BK308].	GCF_004346005.1
WP_133023868.1	TPR+PIN*→	TPR+PIN	1216	-	Actinobacteria	Streptomyces sp. BK329	hypothetical protein [Streptomyces sp. BK329].	GCF_004341055.1
WP_133030467.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1317	-	Alphaproteobacteria	Sphingomonas sp. PP-CE-1G-424	tetratricopeptide repeat protein [Sphingomonas sp. PP-CE-1G-424].	GCF_004341085.1

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WP_133031998.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1323	-	Alphaproteobacteria	Sphingomonas sp. PP-CE-1G-424	hypothetical protein [Sphingomonas sp. PP-CE-1G-424].	GCF_004341085.1
WP_133117283.1	REase+TPR+TPR+GreAB-C+PIN*→	REase+TPR+TPR+GreAB-C+PIN	1332	-	Alphaproteobacteria	Mesorhizobium sanjuanii	hypothetical protein [Mesorhizobium sanjuanii].	GCF_002529485.1
WP_133245819.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1322	-	Alphaproteobacteria	Candidatus Phycosocius bacilliformis	hypothetical protein [Candidatus Phycosocius bacilliformis].	GCF_003112735.1
WP_133303262.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1082	-	Alphaproteobacteria	Rhodopseudomonas palustris	hypothetical protein [Rhodopseudomonas palustris].	GCF_013415845.1
WP_133404970.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1260	-	Actinobacteria	Arthrobacter crusticola	DUF4365 domain-containing protein [Arthrobacter crusticola].	GCF_004357995.1
WP_133633736.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1321	-	Gammaproteobacteria	Pseudomonas sp. OV184	DUF4365 domain-containing protein [Pseudomonas sp. OV184].	GCF_004363115.1
WP_133936590.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1489	-	Betaproteobacteria	Comamonas kerstersii	tetratricopeptide repeat protein [Comamonas kerstersii].	GCF_002002425.1
WP_134016909.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1313	-	Alphaproteobacteria	Litoreibacter halocynthiae	hypothetical protein [Litoreibacter halocynthiae].	GCF_004365635.1
WP_134268494.1	PIN*→	PIN	186	-	Firmicutes	Sporosarcina pasteurii	hypothetical protein [Sporosarcina pasteurii].	GCF_004379295.1
WP_134281591.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1159	-	Gammaproteobacteria	Pseudomonas	MULTISPECIES: hypothetical protein [Pseudomonas].	GCF_013522725.1
WP_135194680.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1327	-	Alphaproteobacteria	Brevundimonas intermedia	DUF4365 domain-containing protein [Brevundimonas intermedia].	GCF_004614235.1
WP_135269295.1	TPR+PIN*→	TPR+PIN	1211	-	Actinobacteria	Nocardioides seonyuensis	hypothetical protein [Nocardioides seonyuensis].	GCF_004683965.1
WP_135300409.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1130	-	Gammaproteobacteria	Photobacterium damselae	hypothetical protein [Photobacterium damselae].	GCF_004683985.2
WP_135312567.1	REase+TPR+GreAB-C+PIN→ PIN*→	PIN	479	-	Alphaproteobacteria	Paracoccus liaowanqingii	hypothetical protein [Paracoccus liaowanqingii].	GCF_004683865.2
WP_135953001.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	987	-	Gammaproteobacteria	Pasteurella multocida	hypothetical protein [Pasteurella multocida].	GCF_004792575.1
WP_135961458.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1086	-	Gammaproteobacteria	Pasteurella multocida	hypothetical protein [Pasteurella multocida].	GCF_004792555.1
WP_136247578.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1103	-	Gammaproteobacteria	Halomonas borealis	hypothetical protein [Halomonas borealis].	GCF_004798905.1
WP_136878408.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1248	-	Bacteroidetes	Pedobacter sp. AR-2-6	hypothetical protein [Pedobacter sp. AR-2-6].	GCF_005116475.1
WP_137004448.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1290	-	Alphaproteobacteria	Agrobacterium tumefaciens	hypothetical protein [Agrobacterium tumefaciens].	GCF_005221405.1
WP_137059419.1	TPR+PIN*→	TPR+PIN	1157	-	Firmicutes	Bacillus mycoides	hypothetical protein [Bacillus mycoides].	GCF_005217805.1
WP_137213367.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1139	-	Gammaproteobacteria	Pseudomonas sp. CFBP13508	hypothetical protein [Pseudomonas sp. CFBP13508].	GCF_005233515.1
WP_137383131.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1091	-	Gammaproteobacteria	Citrobacter sp. wls619	hypothetical protein [Citrobacter sp. wls619].	GCF_005281345.1
WP_137387523.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1101	-	Gammaproteobacteria	Pantoea sp. SO10	hypothetical protein [Pantoea sp. SO10].	GCF_005281435.1
WP_137434419.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1288	-	Gammaproteobacteria	Marinobacter sp. PJ-16	hypothetical protein [Marinobacter sp. PJ-16].	GCF_005298175.1
WP_137735239.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1437	-	Betaproteobacteria	Aquabacterium pictum	hypothetical protein [Aquabacterium pictum].	GCF_005403045.1
WP_137905827.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1130	-	Bacteroidetes	Chryseobacterium sp. 2VB	hypothetical protein [Chryseobacterium sp. 2VB].	GCF_005503635.1
WP_138242320.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1130	-	Gammaproteobacteria	Photobacterium damselae	hypothetical protein [Photobacterium damselae].	GCF_005819845.1
WP_138262872.1	X+PIN*→	X+PIN	1204	-	Firmicutes	Enterocloster clostridioformis	hypothetical protein [Enterocloster clostridioformis].	GCF_015548065.1
WP_138402485.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1137	-	Bacteroidetes	Chryseobacterium indologenes	hypothetical protein [Chryseobacterium indologenes].	GCF_005862425.1
WP_138437829.1	HetE-N1→ GreAB-C*→	GreAB-C	802	-	Gammaproteobacteria	Marinobacter	MULTISPECIES: hypothetical protein [Marinobacter].	GCF_005871095.1
WP_138616099.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1106	-	Gammaproteobacteria	Pseudoalteromonas sp. S2721	hypothetical protein [Pseudoalteromonas sp. S2721].	GCF_005887425.1
WP_139051161.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1158	-	Gammaproteobacteria	unclassified Pseudomonas	MULTISPECIES: hypothetical protein [unclassified Pseudomonas].	GCF_901007645.1
WP_139100594.1	TPR+PIN*→	TPR+PIN	1197	-	Actinobacteria	Amycolatopsis alkalitolerans	hypothetical protein [Amycolatopsis alkalitolerans].	GCF_006152065.1
WP_139135497.1	X+PIN*→	X+PIN	1093	-	Actinobacteria	Micromonospora tulbaghiae	hypothetical protein [Micromonospora tulbaghiae].	GCF_900091605.1
WP_139156465.1	HetE-N1→?→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	523	-	Gammaproteobacteria	Salmonella enterica	hypothetical protein [Salmonella enterica].	GCF_003071545.1
WP_139230170.1	TPR+PIN*→	TPR+PIN	1206	-	Actinobacteria	Nocardioides terrae	hypothetical protein [Nocardioides terrae].	GCF_900112345.1
WP_139231027.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1155	-	Gammaproteobacteria	Pseudomonas sagittaria	hypothetical protein [Pseudomonas sagittaria].	GCF_900115715.1

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WP_139231685.1	REase+TPR+GreAB-C+PIN*→?→?→ Calcineurin→ Calcineurin→?→ Calcineurin→	REase+TPR+GreAB-C+PIN	1314	-	Alphaproteobacteria	Methylobacterium phyllosphaerae	hypothetical protein [Methylobacterium phyllosphaerae].	GCF_001936175.1
WP_139585558.1	TPR+PIN*→	TPR+PIN	1173	-	Actinobacteria	Micromonospora orduensis	hypothetical protein [Micromonospora orduensis].	GCF_006228125.1
WP_139699848.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1163	-	unclassified Bacteria	bacterium endosymbiont of Bathymodiolus sp. 5 South	tetratricopeptide repeat protein [bacterium endosymbiont of Bathymodiolus sp. 5 South].	GCF_900127295.1
WP_139711990.1	TPR+PIN*→	TPR+PIN	816	-	Actinobacteria	Streptomyces sp. NP160	hypothetical protein [Streptomyces sp. NP160].	GCF_006335115.1
WP_139741421.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1086	-	Gammaproteobacteria	Aeromonas veronii	hypothetical protein [Aeromonas veronii].	GCF_006243415.1
WP_139832542.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1427	-	Gammaproteobacteria	Pseudomonas sp. B26(2017)	hypothetical protein [Pseudomonas sp. B26(2017)].	GCF_002113045.1
WP_139834254.1	HetE-N1→?→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	686	-	Gammaproteobacteria	Pseudomonas sp. B11(2017)	hypothetical protein [Pseudomonas sp. B11(2017)].	GCF_002113285.1
WP_140034365.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1111	-	Gammaproteobacteria	Pantoea vagans	hypothetical protein [Pantoea vagans].	GCF_006385385.1
WP_140089969.1	GreAB-C*→	GreAB-C	561	-	Gammaproteobacteria	Vibrio parahaemolyticus	hypothetical protein [Vibrio parahaemolyticus].	GCF_006372765.1
WP_140136560.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	381	-	Gammaproteobacteria	Vibrio parahaemolyticus	hypothetical protein, partial [Vibrio parahaemolyticus].	GCF_006369095.1
WP_140150658.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1100	-	Gammaproteobacteria	Vibrio parahaemolyticus	hypothetical protein [Vibrio parahaemolyticus].	GCF_006375025.1
WP_140184851.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1133	-	Gammaproteobacteria	Vibrio parahaemolyticus	hypothetical protein [Vibrio parahaemolyticus].	GCF_006375315.1
WP_140247351.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1114	-	Gammaproteobacteria	Vibrio parahaemolyticus	hypothetical protein [Vibrio parahaemolyticus].	GCF_006371495.1
WP_140523105.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1330	-	Alphaproteobacteria	unclassified Mesorhizobium	MULTISPECIES: tetratricopeptide repeat protein [unclassified Mesorhizobium].	GCF_006439485.1
WP_140649671.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1330	-	Alphaproteobacteria	Mesorhizobium sp. B2-4-10	tetratricopeptide repeat protein [Mesorhizobium sp. B2-4-10].	GCF_006442675.1
WP_140682745.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1113	-	Gammaproteobacteria	Pseudomonas mandelii	hypothetical protein [Pseudomonas mandelii].	GCF_006438925.1
WP_140739373.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	994	-	Alphaproteobacteria	unclassified Mesorhizobium	MULTISPECIES: hypothetical protein [unclassified Mesorhizobium].	GCF_006440845.1
WP_141097119.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1209	-	Actinobacteria	Microbacterium sp. AISO3	hypothetical protein [Microbacterium sp. AISO3].	GCF_002204305.1
WP_141144329.1	X+PIN*→	X+PIN	1189	-	Actinobacteria	Schumannella sp. 10F1B-5-1	hypothetical protein [Schumannella sp. 10F1B-5-1].	GCF_006517535.1
WP_141202816.1	TPR+PIN*→	TPR+PIN	1217	-	Actinobacteria	Streptomyces griseorubiginosus	hypothetical protein [Streptomyces griseorubiginosus].	GCF_006516935.1
WP_141414632.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1106	-	Gammaproteobacteria	Enterobacter hormaechei	hypothetical protein [Enterobacter hormaechei].	GCF_006546545.1
WP_141566570.1	TPR+PIN*→	TPR+PIN	1237	-	-	Pseudonocardia sp. N23	hypothetical protein [Pseudonocardia sp. N23].	GCF_002583555.1
WP_141708179.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1338	-	Actinobacteria	Micromonospora marina	hypothetical protein [Micromonospora marina].	GCF_900091565.1
WP_141709791.1	TPR+PIN*→||||<-NUDIX	TPR+PIN	1088	-	Actinobacteria	Streptomyces	MULTISPECIES: hypothetical protein [Streptomyces].	GCF_000514055.1
WP_142342557.1	TPR+PIN*→	TPR+PIN	1016	-	Firmicutes	Bacillus cereus	hypothetical protein [Bacillus cereus].	GCF_002577165.1
WP_142621974.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	456	-	Gammaproteobacteria	Vibrio cholerae	hypothetical protein [Vibrio cholerae].	GCF_006802685.1
WP_142996755.1	<-REase||TPR+PIN*→	TPR+PIN	993	-	Firmicutes	Bacillus sp. KQ-3	hypothetical protein [Bacillus sp. KQ-3].	GCF_003710255.1
WP_143042354.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1329	-	Alphaproteobacteria	Citreimonas salinaria	restriction endonuclease [Citreimonas salinaria].	GCF_900107235.1
WP_143064837.1	TPR+PIN*→	TPR+PIN	1134	-	Actinobacteria	Streptomyces sp. PAN_FS17	hypothetical protein [Streptomyces sp. PAN_FS17].	GCF_900105465.1
WP_143167506.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1482	-	Betaproteobacteria	Massilia sp. CF038	hypothetical protein [Massilia sp. CF038].	GCF_900129765.1
WP_143171741.1	PAIREDC-HTH→ REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1539	-	Betaproteobacteria	Rhizobacter sp. OV335	hypothetical protein [Rhizobacter sp. OV335].	GCF_900142965.1
WP_143206624.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1273	-	Planctomycetes	Singulisphaera sp. GP187	hypothetical protein [Singulisphaera sp. GP187].	GCF_900129635.1
WP_143268820.1	REase+TPR+GreAB-C+PIN→ PIN*→	PIN	279	-	Actinobacteria	Amycolatopsis vastitatis	hypothetical protein [Amycolatopsis vastitatis].	GCF_002234595.1
WP_143494315.1	DOC+HTH→ REase+TOPC→ HetE-N1→ HetE-N1+TPR+GreAB-C+PIN*→	HetE-N1+TPR+GreAB-C+PIN	1124	-	Gammaproteobacteria	Pseudomonas putida	hypothetical protein [Pseudomonas putida].	GCF_007049805.1
WP_143685467.1	TPR+PIN*→	TPR+PIN	1135	-	Actinobacteria	Streptomyces sp. 1222.2	hypothetical protein [Streptomyces sp. 1222.2].	GCF_900215595.1
WP_143686526.1	TPR+PIN*→	TPR+PIN	1189	-	Actinobacteria	Streptomyces sp. 61	hypothetical protein [Streptomyces sp. 61].	GCF_002754535.1
WP_143775988.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1312	-	Alphaproteobacteria	Sphingorhabdus contaminans	hypothetical protein [Sphingorhabdus contaminans].	GCF_007280415.1
WP_144044861.1	HetE-N1→ GreAB-C*→ TPR+GreAB-C+PIN→	GreAB-C	779	-	Gammaproteobacteria	Shewanella sp. YLB-06	GreA/GreB family elongation factor [Shewanella sp. YLB-06].	GCF_007197555.1

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WP_144084411.1	HetE-N1→ TPR+TPR+GreAB-C+PIN*→	TPR+TPR+GreAB-C+PIN	1108	-	Gammaproteobacteria	Pseudomonas monteilii	hypothetical protein [Pseudomonas monteilii].	GCF_000510285.1
WP_144190111.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1126	-	Gammaproteobacteria	Gilliamella apicola	hypothetical protein [Gilliamella apicola].	GCF_007559165.1
WP_144217154.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1236	-	Gammaproteobacteria	Vibrio cholerae	hypothetical protein [Vibrio cholerae].	GCF_007623805.1
WP_144226215.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1101	-	Gammaproteobacteria	Shewanella algae	hypothetical protein [Shewanella algae].	GCF_007595165.1
WP_144269797.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1288	-	Gammaproteobacteria	Pseudomonas fluorescens	DUF4365 domain-containing protein [Pseudomonas fluorescens].	GCF_000262325.2
WP_144298906.1	X+PIN*→	X+PIN	676	-	Actinobacteria	Streptomyces sp. TLI_235	hypothetical protein [Streptomyces sp. TLI_235].	GCF_002300355.1
WP_144431187.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1441	-	Gammaproteobacteria	Pseudomonas syringae pv. coryli	hypothetical protein [Pseudomonas syringae pv. coryli].	GCF_000972175.1
WP_144762711.1	X+PIN*→	X+PIN	1177	-	Actinobacteria	Curtobacterium sp. 9128	hypothetical protein [Curtobacterium sp. 9128].	GCF_007673775.1
WP_144916164.1	TPR+GreAB-C+PIN→ PIN*→	PIN	238	-	Bacteroidetes	Mucilaginibacter frigoritolerans	hypothetical protein [Mucilaginibacter frigoritolerans].	GCF_007830615.1
WP_145052948.1	TPR+PIN*→	TPR+PIN	1410	-	Planctomycetes	Lignipirellula cremea	hypothetical protein [Lignipirellula cremea].	GCF_007751035.1
WP_145376920.1	TPR+PIN*→	TPR+PIN	2081	-	Planctomycetes	Symmachiella dynata	hypothetical protein [Symmachiella dynata].	GCF_007747995.1
WP_145427683.1	REase+TPR+GreAB-C+PIN→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	514	-	Planctomycetes	Symmachiella dynata	hypothetical protein [Symmachiella dynata].	GCF_007744975.1
WP_145441613.1	TPR+PIN*→	TPR+PIN	2077	-	Planctomycetes	Gimesia chilikensis	hypothetical protein [Gimesia chilikensis].	GCF_007746535.1
WP_145577942.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1084	-	Gammaproteobacteria	Vibrio crassostreae	hypothetical protein [Vibrio crassostreae].	GCF_017916675.1
WP_145860820.1	TPR+GreAB-C+PIN→ PIN*→	PIN	347	-	Bacteroidetes	Pedobacter suwonensis	hypothetical protein [Pedobacter suwonensis].	GCF_007833675.1
WP_145895823.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1508	-	Betaproteobacteria	Caenimonas sp. HX-9-20	hypothetical protein [Caenimonas sp. HX-9-20].	GCF_007833165.1
WP_145923949.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1170	-	Gammaproteobacteria	Pseudomonas citronellolis	hypothetical protein [Pseudomonas citronellolis].	GCF_001586155.1
WP_145975538.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1365	-	Deinococci	Deinococcus gobiensis	hypothetical protein [Deinococcus gobiensis].	GCF_000252445.1
WP_145980369.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1113	-	Gammaproteobacteria	Pseudomonas lurida	hypothetical protein [Pseudomonas lurida].	GCF_001708485.1
WP_145994348.1	REase+TPR+TPR+GreAB-C+PIN*→	REase+TPR+TPR+GreAB-C+PIN	1339	-	Alphaproteobacteria	Mesorhizobium loti	hypothetical protein [Mesorhizobium loti].	GCF_002858745.1
WP_146048182.1	PIN*→	PIN	371	-	Gammaproteobacteria	Acinetobacter sp. ACNIH3	hypothetical protein [Acinetobacter sp. ACNIH3].	GCF_002918965.1
WP_146113387.1	TPR+PIN*→	TPR+PIN	1210	-	Actinobacteria	unclassified Arthrobacter	MULTISPECIES: hypothetical protein [unclassified Arthrobacter].	GCF_002975405.1
WP_146162727.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1197	-	Gammaproteobacteria	Vibrio splendidus	hypothetical protein [Vibrio splendidus].	GCF_003050425.1
WP_146163497.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1094	-	Gammaproteobacteria	Aeromonas veronii	hypothetical protein [Aeromonas veronii].	GCF_003036425.1
WP_146169670.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1355	-	Actinobacteria	Actinoplanes italicus	hypothetical protein [Actinoplanes italicus].	GCF_016862235.1
WP_146174202.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1185	-	Alphaproteobacteria	Litoreibacter ponti	hypothetical protein [Litoreibacter ponti].	GCF_003054285.1
WP_146175347.1	X+PIN*→	X+PIN	1323	-	Actinobacteria	Conexibacter sp. Seoho-28	hypothetical protein [Conexibacter sp. Seoho-28].	GCF_003044185.1
WP_146181743.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1094	-	Gammaproteobacteria	Aeromonas sp. HMWF014	hypothetical protein [Aeromonas sp. HMWF014].	GCF_003061085.1
WP_146562359.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1275	-	Planctomycetes	Posidoniimonas corsicana	hypothetical protein [Posidoniimonas corsicana].	GCF_007859765.1
WP_146571406.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1140	-	Planctomycetes	Botrimarina hoheduenensis	hypothetical protein [Botrimarina hoheduenensis].	GCF_007859815.1
WP_146752056.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1230	-	Actinobacteria	Microbacterium sp. SMR1	hypothetical protein [Microbacterium sp. SMR1].	GCF_003289625.1
WP_146766012.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1147	-	Gammaproteobacteria	Pseudomonas	MULTISPECIES: hypothetical protein [Pseudomonas].	GCF_013522795.1
WP_146779203.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1133	-	Bacteroidetes	Flavobacterium psychrolimnae	hypothetical protein [Flavobacterium psychrolimnae].	GCF_003312425.1
WP_146877508.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1076	-	Actinobacteria	Actinomadura madurae	hypothetical protein [Actinomadura madurae].	GCF_900445005.1
WP_146915636.1	TIR→ TPR+GreAB-C+PIN*→||||<-HTH	TPR+GreAB-C+PIN	1255	-	Bacteroidetes	Algoriphagus aquimarinus	hypothetical protein [Algoriphagus aquimarinus].	GCF_007997215.1
WP_146943293.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1126	-	Bacteroidetes	Chryseobacterium hagamense	hypothetical protein [Chryseobacterium hagamense].	GCF_007991455.1
WP_146990354.1	REase+TPR+TPR+GreAB-C+PIN*→	REase+TPR+TPR+GreAB-C+PIN	1315	-	Alphaproteobacteria	Bradyrhizobium macuxiense	hypothetical protein [Bradyrhizobium macuxiense].	GCF_007993935.1
WP_147282746.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1118	-	Betaproteobacteria	Comamonas sp. AG1104	hypothetical protein [Comamonas sp. AG1104].	GCF_003350425.1
WP_147289649.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1110	-	Gammaproteobacteria	Pantoea agglomerans	hypothetical protein [Pantoea agglomerans].	GCF_900454505.1
WP_147309007.1	REase+TPR+GreAB-C+PIN→?→ PIN*→	PIN	256	-	Betaproteobacteria	Cupriavidus taiwanensis	hypothetical protein [Cupriavidus taiwanensis].	GCF_900249855.1
WP_147316401.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1139	-	Gammaproteobacteria	Pseudomonas aeruginosa	hypothetical protein [Pseudomonas aeruginosa].	GCF_003412045.2
WP_147329285.1	X+PIN*→ HTH→?→?→ HTH→	X+PIN	1180	-	Firmicutes	Dorea formicigenerans	hypothetical protein [Dorea formicigenerans].	GCF_003437395.1
WP_147334977.1	TM+TM+TPR+PIN*→	TM+TM+TPR+PIN	1154	-	Bacteroidetes	Phocaeicola coprocola	hypothetical protein [Phocaeicola coprocola].	GCF_003458565.1

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WP_147344604.1	Mbetalac→ Trypsin→?→ TPR+PIN*→	TPR+PIN	1394	-	Firmicutes	Eubacterium sp. AM49-13BH	hypothetical protein, partial [Eubacterium sp. AM49-13BH].	GCF_003464165.1
WP_147352805.1	Mbetalac→ Trypsin→ TPR+PIN*→	TPR+PIN	1645	-	Firmicutes	Clostridium sp. AM48-13	hypothetical protein [Clostridium sp. AM48-13].	GCF_003478455.1
WP_147353595.1	Mbetalac→ Trypsin+TPR+PIN*→	Trypsin+TPR+PIN	1710	-	Firmicutes	Clostridium sp. AF37-7	trypsin-like peptidase domain-containing protein, partial [Clostridium sp. AF37-7].	GCF_003477595.1
WP_147364185.1	X+PIN*→ HTH→?→?→ HTH→	X+PIN	1179	-	Firmicutes	Dorea formicigenerans	hypothetical protein [Dorea formicigenerans].	GCF_003475555.1
WP_147402393.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1139	-	Gammaproteobacteria	Pseudomonas aeruginosa	hypothetical protein [Pseudomonas aeruginosa].	GCF_003585235.1
WP_147402585.1	DOC+HTH→ REase+TOPC→ HetE-N1→ HetE-N1+TPR+GreAB-C+PIN*→	HetE-N1+TPR+GreAB-C+PIN	1123	-	Gammaproteobacteria	Pseudomonas aeruginosa	hypothetical protein [Pseudomonas aeruginosa].	GCF_003585225.1
WP_147432801.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1375	-	Actinobacteria	Catellatospora citrea	hypothetical protein [Catellatospora citrea].	GCF_016862615.1
WP_147432945.1	<-TIR<-?||REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1245	-	Actinobacteria	Catellatospora citrea	DUF4365 domain-containing protein [Catellatospora citrea].	GCF_016862615.1
WP_147450330.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1306	-	Deltaproteobacteria	Corallococcus carmarthensis	hypothetical protein [Corallococcus carmarthensis].	GCF_003611695.1
WP_147453837.1	TPR+PIN*→ PAIREDC-HTH→	TPR+PIN	1206	-	Actinobacteria	Nocardiopsis sp. Huas11	hypothetical protein [Nocardiopsis sp. Huas11].	GCF_003634495.1
WP_147481098.1	TPR+PIN*→	TPR+PIN	1134	-	Actinobacteria	Streptomyces shenzhenensis	tetratricopeptide repeat protein [Streptomyces shenzhenensis].	GCF_003688995.1
WP_147627327.1	REase+TPR+GreAB-C+PIN→ SIG+HIN-HTH→?→ PIN*→	PIN	507	-	Gammaproteobacteria	Rhodanobacter glycinis	hypothetical protein [Rhodanobacter glycinis].	GCF_008000795.1
WP_147831354.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1107	-	Alphaproteobacteria	Methylobacterium sp. WL19	hypothetical protein [Methylobacterium sp. WL19].	GCF_008040005.1
WP_147893054.1	X+PIN*→	X+PIN	1120	-	Actinobacteria	Microbacterium hatanonis	hypothetical protein [Microbacterium hatanonis].	GCF_008017415.1
WP_148210527.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1107	-	Alphaproteobacteria	Beijerinckia indica	hypothetical protein [Beijerinckia indica].	GCF_000019845.1
WP_148306266.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1259	-	Gemmatimonadetes	Gemmatirosa kalamazoonesis	hypothetical protein [Gemmatirosa kalamazoonesis].	GCF_000522985.1
WP_148421250.1	<-MarR-HTH||?→?→?→||||<-?||?→ HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1117	-	Gammaproteobacteria	Enterobacter cloacae	hypothetical protein [Enterobacter cloacae].	GCF_013376835.1
WP_148564915.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1243	-	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_001274595.1
WP_149326491.1	HetE-N1→ TPR+GreAB-C+PIN*→ PhospholipaseD→	TPR+GreAB-C+PIN	1103	-	Gammaproteobacteria	Halomonas sp. L5	hypothetical protein [Halomonas sp. L5].	GCF_008297955.1
WP_149369557.1	TPR+PIN*→	TPR+PIN	1189	-	Actinobacteria	Mycolicibacterium sp. P9-64	hypothetical protein [Mycolicibacterium sp. P9-64].	GCF_008329605.1
WP_150024336.1	TPR+GreAB-C+PIN*→||||<-?||HTH→	TPR+GreAB-C+PIN	804	-	Gammaproteobacteria	Acinetobacter baumannii	GreA/GreB family elongation factor [Acinetobacter baumannii].	GCF_008630895.1
WP_150359822.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1240	-	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_008693985.1
WP_150409130.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1284	-	Gammaproteobacteria	Xanthomonas sacchari	GreA/GreB family elongation factor [Xanthomonas sacchari].	GCF_008705275.1
WP_150412179.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1314	-	Alphaproteobacteria	Sphingobium limneticum	hypothetical protein [Sphingobium limneticum].	GCF_008710155.1
WP_150784121.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1318	-	Gammaproteobacteria	Pseudomonas fluorescens	DUF4365 domain-containing protein [Pseudomonas fluorescens].	GCF_902497995.1
WP_150981548.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1329	-	Betaproteobacteria	Cupriavidus pauculus	GreA/GreB family elongation factor [Cupriavidus pauculus].	GCF_008801835.1
WP_151013632.1	TPR+PIN*→	TPR+PIN	1145	-	Actinobacteria	Micromonospora aurantiaca	hypothetical protein [Micromonospora aurantiaca].	GCF_008806405.1
WP_151024479.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1499	-	Betaproteobacteria	Castellaniella defragrans	hypothetical protein [Castellaniella defragrans].	GCF_014203015.1
WP_151868021.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	463	-	Gammaproteobacteria	Acinetobacter soli	hypothetical protein, partial [Acinetobacter soli].	GCF_009013695.1
WP_152091999.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1107	-	Gammaproteobacteria	Pseudomonas sp. KUIN-1	hypothetical protein [Pseudomonas sp. KUIN-1].	GCF_009176725.1
WP_152099374.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1188	-	Planctomycetes	Lacipirellula parvula	tetratricopeptide repeat protein [Lacipirellula parvula].	GCF_009177095.1
WP_152217660.1	REase+TPR+TPR+GreAB-C+PIN*→	REase+TPR+TPR+GreAB-C+PIN	1333	-	Alphaproteobacteria	Parvibaculum sedimenti	hypothetical protein [Parvibaculum sedimenti].	GCF_009184905.1
WP_152508433.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1208	-	Alphaproteobacteria	unclassified Labrenzia	MULTISPECIES: hypothetical protein [unclassified Labrenzia].	GCF_009363315.1
WP_152533063.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1484	-	Gammaproteobacteria	Pseudomonas syringae	hypothetical protein [Pseudomonas syringae].	GCF_000452465.1
WP_152541917.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	529	-	Bacteroidetes	Saccharicrinis fermentans	hypothetical protein [Saccharicrinis fermentans].	GCF_000583675.1
WP_152640028.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	395	-	Firmicutes	Blautia obeum	hypothetical protein [Blautia obeum].	GCF_003463085.1

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WP_152648143.1	REase+TPR+TPR+GreAB-C+PIN*→	REase+TPR+TPR+GreAB-C+PIN	1321	-	Alphaproteobacteria	Bradyrhizobium elkanii	hypothetical protein [Bradyrhizobium elkanii].	GCF_000878305.1
WP_152803033.1	REase+TPR+GreAB-C+PIN*→||||<-HTH	REase+TPR+GreAB-C+PIN	1328	-	Betaproteobacteria	Rugamonas sp. FT103W	hypothetical protein [Rugamonas sp. FT103W].	GCF_009380165.1
WP_152993715.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	677	-	Gammaproteobacteria	Pseudomonas aeruginosa	hypothetical protein [Pseudomonas aeruginosa].	GCF_001451965.1
WP_153001774.1	PIN*→	PIN	483	-	Actinobacteria	Curtobacterium oceanosedimentum	hypothetical protein [Curtobacterium oceanosedimentum].	GCF_001476135.1
WP_153041348.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1322	-	Alphaproteobacteria	Pseudovibrio sp. Ad5	hypothetical protein [Pseudovibrio sp. Ad5].	GCF_001623095.1
WP_153065368.1	REase→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1111	-	Gammaproteobacteria	Xanthomonas arboricola	hypothetical protein [Xanthomonas arboricola].	GCF_003352905.1
WP_153226839.1	TPR+PIN*→	TPR+PIN	1140	-	Actinobacteria	Mycobacteroides salmoniphilum	hypothetical protein [Mycobacteroides salmoniphilum].	GCF_004366855.1
WP_153278476.1	TM+TPR+PIN*→	TM+TPR+PIN	1138	-	Actinobacteria	Saccharothrix syringae	hypothetical protein [Saccharothrix syringae].	GCF_009498035.1
WP_153574636.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1139	-	Gammaproteobacteria	Pseudomonas aeruginosa	hypothetical protein [Pseudomonas aeruginosa].	GCF_000791765.1
WP_153576067.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1170	-	Gammaproteobacteria	Pseudomonas aeruginosa	hypothetical protein [Pseudomonas aeruginosa].	GCF_000795585.1
WP_153576415.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1158	-	Gammaproteobacteria	Pseudomonas aeruginosa	hypothetical protein [Pseudomonas aeruginosa].	GCF_000796465.1
WP_153786096.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1139	-	Gammaproteobacteria	Pseudomonas sp. EMN2	hypothetical protein [Pseudomonas sp. EMN2].	GCF_009650555.1
WP_154691510.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1325	-	Alphaproteobacteria	Novosphingobium sp. Gsoil 351	hypothetical protein [Novosphingobium sp. Gsoil 351].	GCF_009707465.1
WP_154808640.1	TPR+GreAB-C+PIN*→||||<-?<-?<-?<-?||?→?→ Cas_Cas1→	TPR+GreAB-C+PIN	1207	-	Euryarchaeota	Methanolobus vulcani	GreA/GreB family elongation factor [Methanolobus vulcani].	GCF_006546655.1
WP_154898518.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	970	-	Planctomycetes	Gimesia maris	GreA/GreB family elongation factor [Gimesia maris].	GCF_007747015.1
WP_155001003.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1157	-	Gammaproteobacteria	Pseudomonas fluorescens	hypothetical protein [Pseudomonas fluorescens].	GCF_902497965.1
WP_155247385.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1356	-	Actinobacteria	Salinispora arenicola	hypothetical protein [Salinispora arenicola].	GCF_000375205.1
WP_155347963.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1228	-	Actinobacteria	Acrocarpospora pleiomorpha	DUF4365 domain-containing protein [Acrocarpospora pleiomorpha].	GCF_009687885.1
WP_155468027.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1410	-	Betaproteobacteria	Duganella radicis	DUF4365 domain-containing protein [Duganella radicis].	GCF_009720825.1
WP_155543363.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1179	-	Actinobacteria	Amycolatopsis sp. A23	DUF4365 domain-containing protein [Amycolatopsis sp. A23].	GCF_902497555.1
WP_155546438.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1244	-	Actinobacteria	Amycolatopsis sp. A23	DUF4365 domain-containing protein [Amycolatopsis sp. A23].	GCF_902497555.1
WP_155620995.1	TPR+PIN*→	TPR+PIN	1179	-	Firmicutes	Paenibacillus macerans	hypothetical protein [Paenibacillus macerans].	GCF_009725145.1
WP_155672395.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1088	-	Gammaproteobacteria	Aliivibrio fischeri	hypothetical protein [Aliivibrio fischeri].	GCF_009727805.1
WP_155681246.1	DOC+HTH→ REase+TOPC→ HetE-N1→ HetE-N1+TPR+GreAB-C+PIN*→	HetE-N1+TPR+GreAB-C+PIN	1123	-	Gammaproteobacteria	Pseudomonas aeruginosa	hypothetical protein [Pseudomonas aeruginosa].	GCF_009727245.1
WP_155728442.1	HetE-N1→ MNS-Npun2340+TPR+GreAB-C+PIN*→	MNS-Npun2340+TPR+GreAB-C+PIN	1094	-	Gammaproteobacteria	Aeromonas veronii	hypothetical protein [Aeromonas veronii].	GCF_001593245.1
WP_155754272.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1265	-	Betaproteobacteria	Burkholderia vietnamiensis	hypothetical protein [Burkholderia vietnamiensis].	GCF_001528565.1
WP_155849001.1	TPR+PIN*→	TPR+PIN	1211	-	Actinobacteria	Amycolatopsis vancoresmycina	hypothetical protein [Amycolatopsis vancoresmycina].	GCF_000388135.1
WP_155854387.1	TPR+PIN*→	TPR+PIN	1219	-	Actinobacteria	Arthrobacter sp. MA-N2	hypothetical protein [Arthrobacter sp. MA-N2].	GCF_000517125.1
WP_155858633.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1245	-	Gammaproteobacteria	Acinetobacter soli	hypothetical protein [Acinetobacter soli].	GCF_001953195.1
WP_155950759.1	HetE-N1→ TPR+TPR+GreAB-C+PIN*→	TPR+TPR+GreAB-C+PIN	1108	-	Gammaproteobacteria	Pseudomonas taiwanensis	hypothetical protein [Pseudomonas taiwanensis].	GCF_000425785.1
WP_155952204.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1443	-	Gammaproteobacteria	Pseudomonas sp. CHM02	hypothetical protein [Pseudomonas sp. CHM02].	GCF_000612585.1
WP_155956985.1	HTH+PNPase+TPR+GreAB-C+PIN*→	HTH+PNPase+TPR+GreAB-C+PIN	1520	-	Actinobacteria	Rhodococcus sp. UNC23MFCrub1.1	helix-turn-helix domain-containing protein [Rhodococcus sp. UNC23MFCrub1.1].	GCF_000686025.1
WP_156093738.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1179	-	Actinobacteria	Lentzea aerocolonigenes	DUF4365 domain-containing protein [Lentzea aerocolonigenes].	GCF_000974445.1
WP_156124401.1	HetE-N1→ HetE-N1+TPR+GreAB-C+PIN*→	HetE-N1+TPR+GreAB-C+PIN	1122	-	Betaproteobacteria	Achromobacter sp. RTa	hypothetical protein [Achromobacter sp. RTa].	GCF_000757485.1
WP_156177573.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1471	-	Gammaproteobacteria	Pseudomonas sp. CCOS 191	hypothetical protein [Pseudomonas sp. CCOS 191].	GCF_001007005.1
WP_156289500.1	TPR+PIN*→	TPR+PIN	1076	-	Firmicutes	Oceanobacillus salinisoli	hypothetical protein [Oceanobacillus salinisoli].	GCF_009733865.1
WP_156340841.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1470	-	Gammaproteobacteria	Pseudomonas sp. NBRC 111124	hypothetical protein [Pseudomonas sp. NBRC 111124].	GCF_001320245.1

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WP_156343172.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1368	-	Gammaproteobacteria	Pseudomonas sp. NBRC 111134	hypothetical protein [Pseudomonas sp. NBRC 111134].	GCF_001320655.1
WP_156369768.1	TPR+PIN*→	TPR+PIN	1065	-	Actinobacteria	Arthrobacter sp. Leaf145	hypothetical protein [Arthrobacter sp. Leaf145].	GCF_001423565.1
WP_156457128.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1119	-	Alphaproteobacteria	Bradyrhizobium sp. CCH5-F6	hypothetical protein [Bradyrhizobium sp. CCH5-F6].	GCF_001556045.1
WP_156523151.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1289	-	Betaproteobacteria	Bordetella ansorpii	hypothetical protein [Bordetella ansorpii].	GCF_900078315.1
WP_156681909.1	-	-	1775	-	Actinobacteria	Rhodococcus sp. SC4	helix-turn-helix domain-containing protein [Rhodococcus sp. SC4].	-
WP_156749419.1	TPR+PIN*→	TPR+PIN	1166	-	Actinobacteria	Mycobacterium sp. E1747	hypothetical protein [Mycobacterium sp. E1747].	GCF_001667775.1
WP_156792330.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1110	-	Deltaproteobacteria	Desulfotalea psychrophila	hypothetical protein [Desulfotalea psychrophila].	GCF_000025945.1
WP_156831299.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1304	-	Gammaproteobacteria	Arhodomonas aquaeolei	hypothetical protein [Arhodomonas aquaeolei].	GCF_000374645.1
WP_156924526.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1326	-	Betaproteobacteria	Derxia gummosa	hypothetical protein [Derxia gummosa].	GCF_000482785.1
WP_156945361.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1305	-	Alphaproteobacteria	Hyphomonas johnsonii	hypothetical protein [Hyphomonas johnsonii].	GCF_000685275.1
WP_156971043.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1141	-	Alphaproteobacteria	Beijerinckia mobilis	tetratricopeptide repeat protein [Beijerinckia mobilis].	GCF_000745425.1
WP_157119081.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1521	-	Betaproteobacteria	Azohydromonas lata	hypothetical protein [Azohydromonas lata].	GCF_001571085.1
WP_157228354.1	TPR+PIN*→	TPR+PIN	1070	-	Actinobacteria	Gordonia amicalis	hypothetical protein [Gordonia amicalis].	GCF_000332995.1
WP_157237724.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	801	-	Deltaproteobacteria	Desulfobacter curvatus	hypothetical protein [Desulfobacter curvatus].	GCF_000373985.1
WP_157376943.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1354	-	Betaproteobacteria	Burkholderia ubonensis	hypothetical protein [Burkholderia ubonensis].	GCF_001523425.1
WP_157516442.1	TPR+PIN*→	TPR+PIN	1239	-	Actinobacteria	Oerskovia enterophila	hypothetical protein [Oerskovia enterophila].	GCF_001624335.1
WP_157553798.1	X+PIN*→?→ Calcineurin→	X+PIN	1140	-	Actinobacteria	Microbacterium hominis	hypothetical protein [Microbacterium hominis].	GCF_001592125.1
WP_157561005.1	TPR+PIN*→	TPR+PIN	758	-	Actinobacteria	Humibacter albus	hypothetical protein [Humibacter albus].	GCF_000421825.1
WP_157621026.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1092	-	Gammaproteobacteria	Vibrio sp. HENC-03	hypothetical protein [Vibrio sp. HENC-03].	GCF_000305755.2
WP_157678465.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1297	-	Alphaproteobacteria	Mesorhizobium sp. WSM1497	hypothetical protein [Mesorhizobium sp. WSM1497].	GCF_001672455.2
WP_157721532.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1240	-	Gammaproteobacteria	Stenotrophomonas sp. WZN-1	hypothetical protein [Stenotrophomonas sp. WZN-1].	GCF_002192255.1
WP_157768703.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1380	-	Betaproteobacteria	Acidovorax avenae	hypothetical protein [Acidovorax avenae].	GCF_000176855.2
WP_157788679.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1382	-	Gammaproteobacteria	Pseudomonas fluorescens	GreA/GreB family elongation factor [Pseudomonas fluorescens].	GCF_000308175.1
WP_157822505.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	769	-	Gammaproteobacteria	Psychromonas sp. Urea-02u-13	hypothetical protein, partial [Psychromonas sp. Urea-02u-13].	GCF_002835995.1
WP_157852789.1	TPR+PIN*→	TPR+PIN	1134	-	Actinobacteria	Streptomyces iakyrus	hypothetical protein [Streptomyces iakyrus].	GCF_000717055.1
WP_157874592.1	REase+TPR+TPR+GreAB-C+PIN*→	REase+TPR+TPR+GreAB-C+PIN	1330	-	Actinobacteria	Streptomyces sp. AcH 505	hypothetical protein [Streptomyces sp. AcH 505].	GCF_000818175.1
WP_157937504.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	964	-	Gammaproteobacteria	Vibrio splendidus	hypothetical protein, partial [Vibrio splendidus].	GCF_002874795.1
WP_157972098.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1234	-	Bacteroidetes	Negadavirga sp. SW125	hypothetical protein [Negadavirga sp. SW125].	GCF_003347495.1
WP_158764527.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	761	-	Alphaproteobacteria	Terricaulis silvestris	hypothetical protein [Terricaulis silvestris].	GCF_009792355.1
WP_158793614.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1358	-	Acidobacteria	Granulicella sp. L60	hypothetical protein [Granulicella sp. L60].	GCF_009765825.1
WP_158941358.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1279	-	Acidobacteria	Granulicella sp. S190	hypothetical protein [Granulicella sp. S190].	GCF_009766095.1
WP_159057317.1	TPR+PIN*→	TPR+PIN	1196	-	Actinobacteria	Streptomyces scabiei	hypothetical protein [Streptomyces scabiei].	GCF_001550225.1
WP_159073521.1	TPR+PIN*→	TPR+PIN	1075	-	Actinobacteria	Streptomyces sp. RTd22	hypothetical protein [Streptomyces sp. RTd22].	GCF_001650215.1
WP_159104186.1	TPR+PIN*→	TPR+PIN	1211	-	Actinobacteria	Streptomyces sp. CdTB01	hypothetical protein [Streptomyces sp. CdTB01].	GCF_001484565.1
WP_159389385.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1423	-	Gammaproteobacteria	Pseudomonas sp. R32	hypothetical protein [Pseudomonas sp. R32].	GCF_009866705.1
WP_159401920.1	TPR+PIN*→	TPR+PIN	1075	-	Actinobacteria	Streptomyces hygroscopicus	hypothetical protein [Streptomyces hygroscopicus].	GCF_001705785.1
WP_159477578.1	Mbetalac→ Trypsin+TPR+GreAB-C+PIN*→	Trypsin+TPR+GreAB-C+PIN	1359	-	Bacteroidetes	Dyadobacter sp. 3J3	hypothetical protein [Dyadobacter sp. 3J3].	GCF_009801115.1
WP_159617138.1	PIN*→	PIN	499	-	Actinobacteria	Arthrobacter zhaoguopingii	hypothetical protein [Arthrobacter zhaoguopingii].	GCF_009828605.1
WP_159719775.1	TPR+PIN*→	TPR+PIN	1170	-	Firmicutes	Anoxybacillus sp. PDR2	hypothetical protein [Anoxybacillus sp. PDR2].	GCF_009834045.1
WP_159964006.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1113	-	Alphaproteobacteria	Profundibacterium mesophilum	hypothetical protein [Profundibacterium mesophilum].	GCF_009835145.1
WP_160086901.1	BTLCP+SFI-helicase+REase→?→ REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1492	-	Gammaproteobacteria	Pseudomonas sp. 9AZ	GreA/GreB family elongation factor [Pseudomonas sp. 9AZ].	GCF_902506525.1

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WP_160308988.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1249	-	Deltaproteobacteria	Anaeromyxobacter sp. PSR-1	GreA/GreB family elongation factor [Anaeromyxobacter sp. PSR-1].	GCF_000964525.1
WP_160382728.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1329	-	Alphaproteobacteria	Pseudooceanicola pacificus	hypothetical protein [Pseudooceanicola pacificus].	GCF_009789075.1
WP_160512238.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1094	-	Gammaproteobacteria	Escherichia coli	hypothetical protein [Escherichia coli].	GCF_009820085.1
WP_160657313.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1114	-	Gammaproteobacteria	Photobacterium alginatilyticum	hypothetical protein [Photobacterium alginatilyticum].	GCF_009910675.1
WP_160663512.1	TPR+PIN*→	TPR+PIN	1180	-	Actinobacteria	Pseudarthrobacter sp. ATCC 49987	hypothetical protein [Pseudarthrobacter sp. ATCC 49987].	GCF_009928425.1
WP_160778164.1	REase→ PSE→ REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1252	-	Alphaproteobacteria	Parerythrobacter jejuensis	hypothetical protein [Parerythrobacter jejuensis].	GCF_009827995.1
WP_160856107.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1263	-	Betaproteobacteria	Delftia sp. CH05	hypothetical protein [Delftia sp. CH05].	GCF_009827015.1
WP_160933674.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1351	-	Betaproteobacteria	unclassified Burkholderia	MULTISPECIES: hypothetical protein [unclassified Burkholderia].	GCF_009826925.1
WP_161036960.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1075	-	Betaproteobacteria	Duganella fentianensis	hypothetical protein [Duganella fentianensis].	GCF_009857835.1
WP_161077003.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1292	-	Betaproteobacteria	Duganella sp. CY15W	restriction endonuclease [Duganella sp. CY15W].	GCF_009857555.1
WP_161352699.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1351	-	Alphaproteobacteria	Maritimibacter sp. DP07	hypothetical protein [Maritimibacter sp. DP07].	GCF_009882975.1
WP_161505253.1	TPR+PIN*→?→?→||||<-TIR	TPR+PIN	1268	-	Gammaproteobacteria	Legionella pneumophila	hypothetical protein [Legionella pneumophila].	GCF_009933055.1
WP_161571911.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1117	-	Gammaproteobacteria	Cronobacter malonaticus	hypothetical protein [Cronobacter malonaticus].	GCF_009938405.1
WP_161629377.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	488	-	Gammaproteobacteria	Marinobacter sp. EVN1	hypothetical protein, partial [Marinobacter sp. EVN1].	GCF_000475375.1
WP_161722347.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1135	-	Alphaproteobacteria	unclassified Microvirga	MULTISPECIES: tetratricopeptide repeat protein [unclassified Microvirga].	GCF_009910725.1
WP_161796830.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1210	-	Alphaproteobacteria	Devosia soli	GreA/GreB family elongation factor [Devosia soli].	GCF_000970455.1
WP_161897930.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1110	-	Gammaproteobacteria	Pseudomonas sp. MY50	hypothetical protein [Pseudomonas sp. MY50].	GCF_009932725.1
WP_161916726.1	X+PIN*→	X+PIN	1235	-	Actinobacteria	Cellulomonas sp. APG4	hypothetical protein [Cellulomonas sp. APG4].	GCF_009996735.1
WP_161984907.1	HTH→ HetE-N1→ HetE-N1+GreAB-C+PIN*→	HetE-N1+GreAB-C+PIN	1077	-	Gammaproteobacteria	Acinetobacter haemolyticus	hypothetical protein [Acinetobacter haemolyticus].	GCF_010014695.1
WP_162386033.1	Mbetalac→ Trypsin+TPR+GreAB-C+PIN*→	Trypsin+TPR+GreAB-C+PIN	1366	-	Bacteroidetes	Spirosoma endbachense	hypothetical protein [Spirosoma endbachense].	GCF_010233585.1
WP_162486659.1	REase+TPR+GreAB-C+PIN*→||||<-HTH+HTH	REase+TPR+GreAB-C+PIN	1334	-	Betaproteobacteria	Burkholderia pseudomallei	hypothetical protein [Burkholderia pseudomallei].	GCF_000011545.1
WP_162599154.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1027	-	Gammaproteobacteria	Shewanella algidipiscicola	hypothetical protein [Shewanella algidipiscicola].	GCF_900380485.1
WP_162599389.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1158	-	Gammaproteobacteria	Pseudomonas aeruginosa	hypothetical protein [Pseudomonas aeruginosa].	GCF_900406905.1
WP_162672520.1	HTH→ GT4+HEPN+TPR+GreAB-C+PIN*→	GT4+HEPN+TPR+GreAB-C+PIN	1685	-	Planctomycetes	Gemmata massiliana	glycosyltransferase [Gemmata massiliana].	GCF_901538265.1
WP_162916214.1	PIN*→	PIN	348	-	Betaproteobacteria	Burkholderia sp. PAMC 26561	hypothetical protein [Burkholderia sp. PAMC 26561].	GCF_001557535.2
WP_162940198.1	X+PIN*→	X+PIN	1169	-	Actinobacteria	Gryllotalpicola protaetiae	hypothetical protein [Gryllotalpicola protaetiae].	GCF_003627055.1
WP_162960625.1	DOC+HTH→ REase+TOPC→?→ HetE-N1→ HetE-N1+TPR+GreAB-C+PIN*→	HetE-N1+TPR+GreAB-C+PIN	770	-	Gammaproteobacteria	Pseudomonas aeruginosa	hypothetical protein, partial [Pseudomonas aeruginosa].	GCF_003630455.1
WP_163210080.1	TM+TM+TPR+PIN*→	TM+TM+TPR+PIN	1195	-	Bacteroidetes	Bacteroides sp. 519	hypothetical protein [Bacteroides sp. 519].	GCF_010500955.1
WP_163325035.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1227	-	Bacteroidetes	Draconibacterium sp. GM2-18	hypothetical protein [Draconibacterium sp. GM2-18].	GCF_010586825.1
WP_163385713.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	509	-	Gammaproteobacteria	Enterobacter hormaechei	hypothetical protein, partial [Enterobacter hormaechei].	GCF_011006815.1
WP_163511264.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1231	-	Actinobacteria	Fodinicola acaciae	DUF4365 domain-containing protein [Fodinicola acaciae].	GCF_010993745.1
WP_163806192.1	TPR+PIN*→	TPR+PIN	1223	-	Actinobacteria	Mycolicibacterium anyangense	hypothetical protein [Mycolicibacterium anyangense].	GCF_010731855.1
WP_163887020.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1290	-	Alphaproteobacteria	Pseudoruegeria sp. M32A2M	tetratricopeptide repeat protein [Pseudoruegeria sp. M32A2M].	GCF_010374725.1
WP_164141894.1	TPR+PIN*→	TPR+PIN	1215	-	Actinobacteria	Streptomyces coelicoflavus	hypothetical protein [Streptomyces coelicoflavus].	GCF_010548435.1
WP_164363703.1	TPR+PIN*→	TPR+PIN	1135	-	Actinobacteria	Streptomyces griseus	hypothetical protein [Streptomyces griseus].	GCF_010548565.1
WP_164366948.1	TPR+PIN*→	TPR+PIN	1215	-	Actinobacteria	Streptomyces diastaticus	hypothetical protein [Streptomyces diastaticus].	GCF_010548605.1
WP_164922417.1	TRD+TRD→?→?→ REase+SNF2→?→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1273	-	Planctomycetes	Rhodopirellula baltica	hypothetical protein [Rhodopirellula baltica].	GCF_000196115.1
WP_165069081.1	TPR+PIN*→	TPR+PIN	1123	-	Actinobacteria	Marisediminicola senii	hypothetical protein [Marisediminicola senii].	GCF_011057645.1
WP_165087560.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1326	-	Betaproteobacteria	Caballeronia sp. SBC2	hypothetical protein [Caballeronia sp. SBC2].	GCF_011039955.1

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WP_165198604.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1240	-	Alphaproteobacteria	Pseudohalocynthiibacter aestuariivivens	hypothetical protein [Pseudohalocynthiibacter aestuariivivens].	GCF_011040495.1
WP_165399219.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1316	-	Alphaproteobacteria	Komagataeibacter xylinus	GreA/GreB family elongation factor [Komagataeibacter xylinus].	GCF_004302915.1
WP_165684855.1	TPR+PIN*→	TPR+PIN	1088	-	Actinobacteria	Streptomyces sp. KO7888	hypothetical protein [Streptomyces sp. KO7888].	GCF_011317205.1
WP_165714007.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	924	-	Betaproteobacteria	Rubrivivax benzoatilyticus	hypothetical protein, partial [Rubrivivax benzoatilyticus].	GCF_011365705.1
WP_165715394.1	HetE-N1→?→?→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	776	-	Gammaproteobacteria	Salmonella enterica	hypothetical protein [Salmonella enterica].	GCF_011368495.1
WP_165722314.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1113	-	Gammaproteobacteria	unclassified Pseudoalteromonas	MULTISPECIES: hypothetical protein [unclassified Pseudoalteromonas].	GCF_011378665.1
WP_165919434.1	REase+TPR+GreAB-C+PIN*→ TPR→	REase+TPR+GreAB-C+PIN	1252	-	Actinobacteria	Promicromonospora sp. CF082	DUF4365 domain-containing protein [Promicromonospora sp. CF082].	GCF_004341335.1
WP_166221458.1	HTH→ HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1076	-	Gammaproteobacteria	Acinetobacter shaoyimingii	hypothetical protein [Acinetobacter shaoyimingii].	GCF_011578045.1
WP_166315930.1	X+PIN*→	X+PIN	1081	-	Actinobacteria	Microbacterium excoecariae	hypothetical protein [Microbacterium excoecariae].	GCF_011326725.1
WP_166694175.1	Mbetalac→ Trypsin+TPR+GreAB-C+PIN*→	Trypsin+TPR+GreAB-C+PIN	1365	-	Bacteroidetes	Fibrella aestuarina	trypsin-like serine protease [Fibrella aestuarina].	GCF_011742925.1
WP_166748348.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1323	-	Alphaproteobacteria	Sphingomonas aerolata	hypothetical protein [Sphingomonas aerolata].	GCF_011759485.1
WP_166760128.1	X+PIN*→	X+PIN	1124	-	Actinobacteria	Frigoribacterium faeni	hypothetical protein [Frigoribacterium faeni].	GCF_011761235.1
WP_166908249.1	TPR+PIN*→	TPR+PIN	1129	-	Actinobacteria	Mycobacterium sp. DL440	hypothetical protein [Mycobacterium sp. DL440].	GCF_011745145.1
WP_167081447.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1510	-	Betaproteobacteria	‘Massilia aquatica’ Holochova et al. 2020	hypothetical protein [‘Massilia aquatica’ Holochova et al. 2020].	GCF_011682045.1
WP_167302996.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1316	-	Alphaproteobacteria	Sphingobium vermicomposti	hypothetical protein [Sphingobium vermicomposti].	GCF_011762025.1
WP_167344464.1	TPR+PIN*→||||<-NUDIX	TPR+PIN	1134	-	Actinobacteria	Streptomyces griseolus	hypothetical protein [Streptomyces griseolus].	GCF_000721185.1
WP_167432534.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1111	-	Gammaproteobacteria	Pantoea	MULTISPECIES: hypothetical protein [Pantoea].	GCF_011800365.1
WP_168003144.1	TM+TPR+PIN*→	TM+TPR+PIN	1126	-	Actinobacteria	Micromonospora sp. HSS6-12	hypothetical protein, partial [Micromonospora sp. HSS6-12].	GCF_012034245.1
WP_168341898.1	REase+TPR+TPR+GreAB-C+PIN*→	REase+TPR+TPR+GreAB-C+PIN	1233	-	Alphaproteobacteria	Rhizobium leguminosarum	hypothetical protein [Rhizobium leguminosarum].	GCF_012276075.1
WP_168426515.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	461	-	Gammaproteobacteria	Pseudomonas sp. SST3	hypothetical protein, partial [Pseudomonas sp. SST3].	GCF_003325755.1
WP_168560628.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1337	-	Betaproteobacteria	Rhizobacter sp. SG703	hypothetical protein [Rhizobacter sp. SG703].	GCF_012275445.1
WP_168617642.1	TPR+PIN*→	TPR+PIN	1210	-	Actinobacteria	Nocardioides sp. JQ2195	hypothetical protein [Nocardioides sp. JQ2195].	GCF_012272695.1
WP_168725201.1	TPR+PIN*→	TPR+PIN	1218	-	Actinobacteria	Streptomyces galbus	hypothetical protein [Streptomyces galbus].	GCF_014650535.1
WP_168927382.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	546	-	Gammaproteobacteria	Enterobacter hormaechei	hypothetical protein, partial [Enterobacter hormaechei].	GCF_902166805.1
WP_169321903.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1137	-	Bacteroidetes	Chryseobacterium	MULTISPECIES: hypothetical protein [Chryseobacterium].	GCF_012952015.1
WP_169448013.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1243	-	Gammaproteobacteria	Stenotrophomonas maltophilia	hypothetical protein [Stenotrophomonas maltophilia].	GCF_012971765.1
WP_169574578.1	REase+TPR+GreAB-C+PIN→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	628	-	Alphaproteobacteria	Sphingobium psychrophilum	hypothetical protein [Sphingobium psychrophilum].	GCF_012927105.1
WP_169902587.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1321	-	Gammaproteobacteria	Pseudomonas rhodesiae	DUF4365 domain-containing protein [Pseudomonas rhodesiae].	GCF_012985855.1
WP_169912953.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1140	-	Gammaproteobacteria	Pseudomonas chlororaphis	hypothetical protein [Pseudomonas chlororaphis].	GCF_012986925.1
WP_169922112.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1148	-	Gammaproteobacteria	Pseudomonas sp. WS 5503	hypothetical protein [Pseudomonas sp. WS 5503].	GCF_012985385.1
WP_170029824.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1470	-	Gammaproteobacteria	Pseudomonas sp. SK	hypothetical protein [Pseudomonas sp. SK].	GCF_012975065.1
WP_170117623.1	HNH+TPR+GreAB-C+PIN*→	HNH+TPR+GreAB-C+PIN	1207	-	Bacteroidetes	Chitinophaga ginsengisoli	hypothetical protein [Chitinophaga ginsengisoli].	GCF_003014595.1
WP_170323822.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1251	-	Actinobacteria	Cryptosporangium phraense	DUF4365 domain-containing protein [Cryptosporangium phraense].	GCF_006912135.1
WP_170431548.1	REase+TPR+GreAB-C+PIN*→?→||||<-?<-?<-BTLCP+SFI-helicase+REase	REase+TPR+GreAB-C+PIN	1310	-	Alphaproteobacteria	Ruegeria arenilitoris	tetratricopeptide repeat protein [Ruegeria arenilitoris].	GCF_013032225.1
WP_171027511.1	TPR+PIN*→	TPR+PIN	973	-	Actinobacteria	Pseudarthrobacter sp. NamE2	tetratricopeptide repeat protein [Pseudarthrobacter sp. NamE2].	GCF_005796205.1

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WP_171071268.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1155	-	Gammaproteobacteria	Acinetobacter baumannii	GreA/GreB family elongation factor, partial [Acinetobacter baumannii].	GCF_000580875.1
WP_171275163.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1094	-	Gammaproteobacteria	Aeromonas media	hypothetical protein [Aeromonas media].	GCF_013085485.1
WP_171434497.1	DOC+HTH→ REase+TOPC→?→ HetE-N1→ HetE-N1+TPR+GreAB-C+PIN*→	HetE-N1+TPR+GreAB-C+PIN	1124	-	Gammaproteobacteria	Pseudomonas aeruginosa	hypothetical protein [Pseudomonas aeruginosa].	GCF_013115755.1
WP_171451709.1	DOC+HTH→ REase+TOPC→?→ HetE-N1→ HetE-N1→ GreAB-C+PIN*→	GreAB-C+PIN	523	-	Gammaproteobacteria	Pseudomonas aeruginosa	hypothetical protein [Pseudomonas aeruginosa].	GCF_013115805.1
WP_171477953.1	TPR+GreAB-C+PIN*→||||<-?||HTH→	TPR+GreAB-C+PIN	652	-	Gammaproteobacteria	Acinetobacter baumannii	GreA/GreB family elongation factor, partial [Acinetobacter baumannii].	GCF_006491975.1
WP_171493638.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	816	-	Gammaproteobacteria	Acinetobacter soli	hypothetical protein, partial [Acinetobacter soli].	GCF_008987205.1
WP_171564538.1	TPR+PIN*→	TPR+PIN	1172	-	Firmicutes	Brevibacillus sp. MCWH	hypothetical protein [Brevibacillus sp. MCWH].	GCF_018195675.1
WP_171662370.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1496	-	Betaproteobacteria	Achromobacter deleyi	hypothetical protein [Achromobacter deleyi].	GCF_013116765.1
WP_171694982.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1120	-	Gammaproteobacteria	Methylomonas sp. ZR1	hypothetical protein [Methylomonas sp. ZR1].	GCF_013141865.1
WP_171798091.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1323	-	Alphaproteobacteria	unclassified Novosphingobium	MULTISPECIES: hypothetical protein [unclassified Novosphingobium].	GCF_013149315.1
WP_172598885.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	709	-	Alphaproteobacteria	Sphingobium sp. YG1	hypothetical protein [Sphingobium sp. YG1].	GCF_003609795.1
WP_172685391.1	REase+TPR+GreAB-C+PIN*→?→?→ Calcineurin→ Calcineurin→?→ Calcineurin→	REase+TPR+GreAB-C+PIN	1311	-	Alphaproteobacteria	Methylobacterium oryzae	hypothetical protein [Methylobacterium oryzae].	-
WP_172806748.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	766	-	Gammaproteobacteria	Endozoicomonas arenosclerae	hypothetical protein [Endozoicomonas arenosclerae].	GCF_001562015.1
WP_172870236.1	TPR+GreAB-C*→	TPR+GreAB-C	233	-	Firmicutes	Bacillus velezensis	hypothetical protein, partial [Bacillus velezensis].	GCF_013267055.1
WP_172883554.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1159	-	Gammaproteobacteria	Pseudomonas stutzeri	hypothetical protein [Pseudomonas stutzeri].	GCF_013267085.1
WP_173054693.1	TM+TPR+PIN*→ REase→	TM+TPR+PIN	1322	-	Actinobacteria	Phytohabitans houttuyneae	hypothetical protein [Phytohabitans houttuyneae].	GCF_011764425.1
WP_173520689.1	REase+TPR+TPR+GreAB-C+PIN*→	REase+TPR+TPR+GreAB-C+PIN	1357	-	Alphaproteobacteria	Ensifer sesbaniae	hypothetical protein [Ensifer sesbaniae].	GCF_013283665.1
WP_173522752.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1313	-	Actinobacteria	Nonomuraea sp. NN258	hypothetical protein [Nonomuraea sp. NN258].	GCF_013283785.1
WP_173794050.1	NACHT→ X+PIN*→ HTH→?→?→ HTH→	X+PIN	1179	-	Firmicutes	Dorea formicigenerans	hypothetical protein [Dorea formicigenerans].	GCF_013301385.1
WP_173821757.1	X+PIN*→ HTH→?→?→ HTH→	X+PIN	1178	-	Firmicutes	Dorea formicigenerans	hypothetical protein [Dorea formicigenerans].	GCF_013301365.1
WP_173853982.1	TPR+GreAB-C+PIN→ PIN*→	PIN	248	-	Bacteroidetes	Flavobacterium sp. 28A	hypothetical protein [Flavobacterium sp. 28A].	GCF_013294005.1
WP_173968533.1	GreAB-C+PIN*→	GreAB-C+PIN	552	-	Bacteroidetes	Flavobacterium collinsii	hypothetical protein, partial [Flavobacterium collinsii].	GCF_902804485.1
WP_173994169.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1181	-	Alphaproteobacteria	Agrobacterium fabrum	hypothetical protein [Agrobacterium fabrum].	GCF_013318355.1
WP_174011044.1	HEPN→ REase+TPR+TPR+GreAB-C+PIN*→	REase+TPR+TPR+GreAB-C+PIN	1333	-	Alphaproteobacteria	Agrobacterium rhizogenes	GreA/GreB family elongation factor [Agrobacterium rhizogenes].	GCF_013321105.1
WP_174166670.1	BirA-HTH→ HEPN→ REase+TPR+TPR+GreAB-C+PIN*→	REase+TPR+TPR+GreAB-C+PIN	1341	-	Alphaproteobacteria	Agrobacterium rhizogenes	hypothetical protein [Agrobacterium rhizogenes].	GCF_013322015.1
WP_174168420.1	BirA-HTH→ HEPN→ REase+TPR+TPR+GreAB-C+PIN*→	REase+TPR+TPR+GreAB-C+PIN	1333	-	Alphaproteobacteria	Agrobacterium rhizogenes	GreA/GreB family elongation factor [Agrobacterium rhizogenes].	GCF_013321875.1
WP_174361404.1	HetE-N1→?→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	512	-	Gammaproteobacteria	Citrobacter gillenii	hypothetical protein [Citrobacter gillenii].	GCF_013337685.1
WP_175386063.1	PIN*→	PIN	434	-	Gammaproteobacteria	Pseudomonas corrugata	hypothetical protein [Pseudomonas corrugata].	GCF_013359545.1
WP_175666066.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1351	-	Betaproteobacteria	Burkholderia ambifaria	hypothetical protein [Burkholderia ambifaria].	GCF_902829825.1
WP_175722904.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1351	-	Betaproteobacteria	Burkholderia ambifaria	hypothetical protein [Burkholderia ambifaria].	GCF_902829925.1
WP_175818825.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1335	-	Betaproteobacteria	Burkholderia sp. BCC0419	hypothetical protein [Burkholderia sp. BCC0419].	GCF_902830285.1
WP_175896466.1	TPR+GreAB-C+PIN*→||||<-HTH+HTH	TPR+GreAB-C+PIN	872	-	Betaproteobacteria	Burkholderia cepacia	hypothetical protein [Burkholderia cepacia].	GCF_902830675.1
WP_176170943.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1244	-	Actinobacteria	Amycolatopsis sp. Hca4	DUF4365 domain-containing protein [Amycolatopsis sp. Hca4].	GCF_013364075.1
WP_176203105.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	681	-	Gammaproteobacteria	Salmonella enterica	hypothetical protein, partial [Salmonella enterica].	GCF_002044735.1
WP_176308009.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1351	-	Betaproteobacteria	Burkholderia ambifaria	hypothetical protein [Burkholderia ambifaria].	GCF_902830205.1
WP_176329154.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1335	-	Betaproteobacteria	Burkholderia vietnamiensis	hypothetical protein [Burkholderia vietnamiensis].	GCF_902833435.1
WP_176389972.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1374	-	Betaproteobacteria	Janthinobacterium sp. BJB401	hypothetical protein [Janthinobacterium sp. BJB401].	GCF_013372745.1
WP_176422167.1	REase+TPR+TPR+GreAB-C+PIN*→	REase+TPR+TPR+GreAB-C+PIN	1325	-	Alphaproteobacteria	Bradyrhizobium sp. 2S1	hypothetical protein [Bradyrhizobium sp. 2S1].	GCF_011516625.2
WP_176457673.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1516	-	Gammaproteobacteria	Pseudomonas mandelii	hypothetical protein [Pseudomonas mandelii].	GCF_000257545.3
WP_176459502.1	REase+TPR+GreAB-C+PIN*→?→ Trypsin→	REase+TPR+GreAB-C+PIN	1228	-	Actinobacteria	Rhodococcus sp. OK302	DUF4365 domain-containing protein [Rhodococcus sp. OK302].	GCF_002245895.1
WP_176508867.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1548	-	Gammaproteobacteria	Pseudomonas sp. BML-PP042	hypothetical protein [Pseudomonas sp. BML-PP042].	GCF_013373915.1

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WP_177062188.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1424	-	Gammaproteobacteria	Pseudomonas reactans	hypothetical protein [Pseudomonas reactans].	GCF_013386305.1
WP_177327801.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1404	-	Gammaproteobacteria	Pseudomonas sp. 5	GreA/GreB family elongation factor [Pseudomonas sp. 5].	GCF_000955815.1
WP_179038946.1	REase+TPR+TPR+GreAB-C+PIN*→	REase+TPR+TPR+GreAB-C+PIN	1350	-	Alphaproteobacteria	Rhizobium leguminosarum	hypothetical protein [Rhizobium leguminosarum].	GCF_013391705.1
WP_179093684.1	TPR+GreAB-C+PIN*→||||<-HTH+HTH	TPR+GreAB-C+PIN	872	-	Betaproteobacteria	Burkholderia pseudomallei	hypothetical protein [Burkholderia pseudomallei].	GCF_002880985.1
WP_179103158.1	TPR+GreAB-C+PIN*→||||<-HTH+HTH	TPR+GreAB-C+PIN	872	-	Betaproteobacteria	Burkholderia pseudomallei	hypothetical protein [Burkholderia pseudomallei].	GCF_001981185.1
WP_179448733.1	-	-	914	-	Gammaproteobacteria	Pseudomonas yamanorum	hypothetical protein [Pseudomonas yamanorum].	GCF_013403585.1
WP_179622762.1	DOC+HTH→ REase+TOPC→?→ HetE-N1→ HetE-N1+TPR+GreAB-C+PIN*→	HetE-N1+TPR+GreAB-C+PIN	1124	-	Gammaproteobacteria	Pseudomonas mendocina	hypothetical protein [Pseudomonas mendocina].	GCF_013410555.1
WP_179654574.1	REase+TPR+TPR+GreAB-C+PIN*→ REase→	REase+TPR+TPR+GreAB-C+PIN	1329	-	Alphaproteobacteria	Mesorhizobium sp. YL-MPnR-2016	hypothetical protein [Mesorhizobium sp. YL-MPnR-2016].	GCF_013408905.1
WP_179833445.1	REase+TPR+PIN*→	REase+TPR+PIN	1241	-	Actinobacteria	Actinomadura citrea	DUF4365 domain-containing protein [Actinomadura citrea].	GCF_014648455.1
WP_179902819.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1094	-	Gammaproteobacteria	Aeromonas veronii	hypothetical protein [Aeromonas veronii].	GCF_013415825.1
WP_180191279.1	HTH→ HetE-N1→ HetE-N1+GreAB-C+PIN*→	HetE-N1+GreAB-C+PIN	1077	-	Gammaproteobacteria	Acinetobacter sp. YH01006	hypothetical protein [Acinetobacter sp. YH01006].	GCF_013420445.1
WP_180269129.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1231	-	Bacteroidetes	Sphingobacterium sp. 1.A.5	tetratricopeptide repeat protein [Sphingobacterium sp. 1.A.5].	GCF_002734235.1
WP_180491971.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1106	-	Gammaproteobacteria	Escherichia fergusonii	hypothetical protein [Escherichia fergusonii].	GCF_903932165.1
WP_180778225.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1117	-	Gammaproteobacteria	Pectobacterium aroidearum	hypothetical protein [Pectobacterium aroidearum].	GCF_013449715.1
WP_180799798.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	796	-	Gammaproteobacteria	Vibrio parahaemolyticus	hypothetical protein, partial [Vibrio parahaemolyticus].	GCF_006371865.1
WP_180830729.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	764	-	Gammaproteobacteria	Vibrio parahaemolyticus	hypothetical protein, partial [Vibrio parahaemolyticus].	GCF_006375165.1
WP_180977515.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1154	-	Betaproteobacteria	Janthinobacterium sp. ROICE36	hypothetical protein, partial [Janthinobacterium sp. ROICE36].	GCF_002869965.1
WP_181464939.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	762	-	Betaproteobacteria	Herbaspirillum rubrisubalbicans	tetratricopeptide repeat protein [Herbaspirillum rubrisubalbicans].	GCF_003263475.1
WP_181641518.1	TPR+PIN*→	TPR+PIN	1210	-	Actinobacteria	Nocardioides massiliensis	hypothetical protein [Nocardioides massiliensis].	GCF_900067705.2
WP_181834083.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	678	-	Alphaproteobacteria	Brucella anthropi	hypothetical protein, partial [Brucella anthropi].	GCF_003325675.1
WP_182064218.1	TPR+PIN*→	TPR+PIN	1177	-	Actinobacteria	Curtobacterium sp. ME12	hypothetical protein [Curtobacterium sp. ME12].	GCF_903970855.1
WP_182166026.1	REase+TPR+GreAB-C+PIN*→||||<-HTH	REase+TPR+GreAB-C+PIN	1304	-	Betaproteobacteria	Duganella sp. LX20W	hypothetical protein [Duganella sp. LX20W].	GCF_014042345.1
WP_182270399.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1092	-	Gammaproteobacteria	Citrobacter freundii	hypothetical protein [Citrobacter freundii].	GCF_014101305.1
WP_182650750.1	GreAB-C+PIN*→	GreAB-C+PIN	566	-	Bacteroidetes	Flavobacterium sp. SOK18b	hypothetical protein, partial [Flavobacterium sp. SOK18b].	GCF_014156605.1
WP_182869571.1	PIN*→	PIN	188	-	Alphaproteobacteria	Bradyrhizobium diazoefficiens	hypothetical protein [Bradyrhizobium diazoefficiens].	GCF_014163475.1
WP_182925384.1	REase+TPR+GreAB-C+PIN*→||||<-?||HTH→	REase+TPR+GreAB-C+PIN	1250	-	Gammaproteobacteria	Acinetobacter baumannii	GreA/GreB family elongation factor [Acinetobacter baumannii].	GCF_014169655.1
WP_183061688.1	CARF+PIN*→	CARF+PIN	1208	-	Actinobacteria	Motilibacter peucedani	hypothetical protein [Motilibacter peucedani].	GCF_003634695.1
WP_183296812.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1234	-	Actinobacteria	Cellulomonas cellasea	DUF4365 domain-containing protein [Cellulomonas cellasea].	GCF_014190965.1
WP_183420610.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1219	-	Actinobacteria	Microbacterium proteolyticum	DUF4365 domain-containing protein [Microbacterium proteolyticum].	GCF_014192415.1
WP_183438886.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1161	-	Alphaproteobacteria	Methylobacterium sp. R2-1	hypothetical protein [Methylobacterium sp. R2-1].	GCF_014191355.1
WP_183694785.1	REase+TPR+TPR+GreAB-C+PIN*→	REase+TPR+TPR+GreAB-C+PIN	1363	-	Alphaproteobacteria	Rhizobium lusitanum	restriction endonuclease [Rhizobium lusitanum].	GCF_014189535.1
WP_183714092.1	TIR→?→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1131	-	Alphaproteobacteria	Bradyrhizobium sp. ERR14	hypothetical protein [Bradyrhizobium sp. ERR14].	GCF_014198235.1
WP_183806882.1	REase+TPR+TPR+GreAB-C+PIN*→	REase+TPR+TPR+GreAB-C+PIN	1345	-	Alphaproteobacteria	Rhizobium azooxidifex	tetratricopeptide repeat protein [Rhizobium azooxidifex].	GCF_014196765.1
WP_183919890.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1290	-	Alphaproteobacteria	Rhizobium lentis	hypothetical protein [Rhizobium lentis].	GCF_014200135.1
WP_183998882.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1313	-	Alphaproteobacteria	Sphingomonas kyeonggiensis	hypothetical protein [Sphingomonas kyeonggiensis].	GCF_014196745.1
WP_184249301.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1318	-	Betaproteobacteria	Paraburkholderia atlantica	DUF4365 domain-containing protein [Paraburkholderia atlantica].	GCF_014200895.1

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WP_184301652.1	REase+TPR+GreAB-C+PIN*→?→?→ URI+RAMA→	REase+TPR+GreAB-C+PIN	1255	-	Planctomycetes	Rhodopirellula rubra	hypothetical protein [Rhodopirellula rubra].	GCF_014192335.1
WP_184659486.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1265	-	Bacteroidetes	Pedobacter cryoconitis	hypothetical protein [Pedobacter cryoconitis].	GCF_014207145.1
WP_184790984.1	TM+TPR+PIN*→	TM+TPR+PIN	1158	-	Actinobacteria	Phytomonospora endophytica	hypothetical protein [Phytomonospora endophytica].	GCF_016862855.1
WP_184920984.1	REase+PIN*→	REase+PIN	1270	-	Actinobacteria	Saccharothrix ecbatanensis	DUF4365 domain-containing protein [Saccharothrix ecbatanensis].	GCF_014205015.1
WP_185002860.1	-	-	1209	-	Actinobacteria	unclassified Curtobacterium	MULTISPECIES: DUF4365 domain-containing protein [unclassified Curtobacterium].	GCF_003752345.1
WP_186065300.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1351	-	Betaproteobacteria	Burkholderia gladioli	hypothetical protein [Burkholderia gladioli].	GCF_902831285.1
WP_186083524.1	REase+TPR+GreAB-C+PIN*→||||<-?<-?<-HEPN	REase+TPR+GreAB-C+PIN	1333	-	Betaproteobacteria	Burkholderia gladioli	hypothetical protein [Burkholderia gladioli].	GCF_902831185.1
WP_186117779.1	HEPN→?→?→ REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1498	-	Betaproteobacteria	Burkholderia gladioli	tetratricopeptide repeat protein [Burkholderia gladioli].	GCF_902831505.1
WP_186135768.1	REase+TPR+GreAB-C+PIN*→||||<-HEPN	REase+TPR+GreAB-C+PIN	1351	-	Betaproteobacteria	Burkholderia gladioli	hypothetical protein [Burkholderia gladioli].	GCF_902831685.1
WP_186296902.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1297	-	Betaproteobacteria	Cupriavidus campinensis	DUF4365 domain-containing protein [Cupriavidus campinensis].	GCF_007572485.1
WP_186384760.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1117	-	Gammaproteobacteria	Klebsiella sp. Kpp	hypothetical protein [Klebsiella sp. Kpp].	GCF_014267405.1
WP_186426553.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1039	-	Betaproteobacteria	Cupriavidus metallidurans	hypothetical protein [Cupriavidus metallidurans].	GCF_900185755.1
WP_187028576.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1238	-	Bacteroidetes	Pontibacter sp. KCTC 32443	hypothetical protein [Pontibacter sp. KCTC 32443].	GCF_014297265.1
WP_187110408.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1301	-	Betaproteobacteria	Variovorax sp. PAMC26660	hypothetical protein [Variovorax sp. PAMC26660].	GCF_014302995.1
WP_187305744.1	X+PIN*→ HTH→?→?→ HTH→	X+PIN	762	-	Firmicutes	Dorea formicigenerans	hypothetical protein [Dorea formicigenerans].	GCF_003458845.1
WP_187328643.1	HTH+PNPase+TPR+GreAB-C+PIN*→	HTH+PNPase+TPR+GreAB-C+PIN	1523	-	Actinobacteria	Rhodococcus sp. WS3	hypothetical protein [Rhodococcus sp. WS3].	GCF_003797085.1
WP_187494340.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1094	-	Gammaproteobacteria	Pantoea agglomerans	hypothetical protein [Pantoea agglomerans].	GCF_014353705.1
WP_187598162.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1341	-	Betaproteobacteria	Diaphorobacter ruginosibacter	hypothetical protein [Diaphorobacter ruginosibacter].	GCF_014395975.1
WP_187723864.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	545	-	Betaproteobacteria	Diaphorobacter aerolatus	hypothetical protein [Diaphorobacter aerolatus].	GCF_014489535.1
WP_187993242.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	557	-	Gammaproteobacteria	Vibrio harveyi	hypothetical protein [Vibrio harveyi].	GCF_014525195.1
WP_188104481.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1312	-	Alphaproteobacteria	Bradyrhizobium campsiandrae	tetratricopeptide repeat protein [Bradyrhizobium campsiandrae].	GCF_014529705.1
WP_188533557.1	TPR+PIN*→	TPR+PIN	1228	-	Firmicutes	Paenibacillus abyssi	hypothetical protein [Paenibacillus abyssi].	GCF_014640295.1
WP_189032568.1	TPR+PIN*→	TPR+PIN	531	-	Firmicutes	Paenibacillus albidus	hypothetical protein [Paenibacillus albidus].	GCF_014644435.1
WP_189091600.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1377	-	Deinococci	Deinococcus ruber	tetratricopeptide repeat protein [Deinococcus ruber].	GCF_014648095.1
WP_189152287.1	TPR+PIN*→	TPR+PIN	1218	-	Actinobacteria	Streptomyces lacrimifluminis	hypothetical protein [Streptomyces lacrimifluminis].	GCF_014646095.1
WP_189484308.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1026	-	Gammaproteobacteria	Shewanella indica	hypothetical protein [Shewanella indica].	GCF_014652115.1
WP_189568857.1	Mbetalac→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1342	-	Bacteroidetes	Persicitalea jodogahamensis	hypothetical protein [Persicitalea jodogahamensis].	GCF_014651615.1
WP_189617689.1	HetE-N1→?→ GreAB-C*→	GreAB-C	498	-	Gammaproteobacteria	Shewanella fodinae	hypothetical protein [Shewanella fodinae].	GCF_014651955.1
WP_189635482.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1307	-	Alphaproteobacteria	Gemmobacter lanyuensis	restriction endonuclease [Gemmobacter lanyuensis].	GCF_014652355.1
WP_189677864.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1323	-	Alphaproteobacteria	Sphingomonas glacialis	tetratricopeptide repeat protein [Sphingomonas glacialis].	GCF_014653575.1
WP_189835257.1	TPR+PIN*→	TPR+PIN	1215	-	Actinobacteria	Streptomyces zaomyceticus	hypothetical protein [Streptomyces zaomyceticus].	GCF_014656215.1
WP_190462433.1	PNPase+TPR+GreAB-C+PIN*→ TPR+TPR→ TPR+TPR→	PNPase+TPR+GreAB-C+PIN	1385	-	Cyanobacteria	unclassified Planktothrix	MULTISPECIES: hypothetical protein [unclassified Planktothrix].	GCF_014696265.1
WP_190659344.1	BTLCP+NACHT→ APATPase+BetaPropeller→ APATPase+BetaPropeller→ PNPase+TPR+GreAB-C+PIN*→	PNPase+TPR+GreAB-C+PIN	1399	-	Cyanobacteria	Nostoc linckia	tetratricopeptide repeat protein [Nostoc linckia].	GCF_014696615.1
WP_190786133.1	<-REase+nSTAND3||TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1282	-	Bacteroidetes	Hymenobacter sp. BT646	hypothetical protein [Hymenobacter sp. BT646].	GCF_014698995.1
WP_191117766.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1091	-	Gammaproteobacteria	Vibrio campbellii	hypothetical protein [Vibrio campbellii].	GCF_014769105.1
WP_191340685.1	REase+SNF2→ URI+RAMA→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1182	-	Firmicutes	Massilimicrobiota sp. An134	hypothetical protein [Massilimicrobiota sp. An134].	GCF_904393125.1
WP_191375963.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	879	-	Firmicutes	[Clostridium] spiroforme	hypothetical protein [[Clostridium] spiroforme].	GCF_904395875.1

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WP_191791215.1	TPR+PIN*→	TPR+PIN	1225	-	Actinobacteria	Oerskovia sp. Sa2CUA8	hypothetical protein [Oerskovia sp. Sa2CUA8].	GCF_014836745.1
WP_191917190.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1094	-	Gammaproteobacteria	Pantoea agglomerans	hypothetical protein [Pantoea agglomerans].	GCF_014839545.1
WP_191940182.1	X+PIN*→	X+PIN	1078	-	Actinobacteria	Plantibacter sp. CFBP 8775	hypothetical protein [Plantibacter sp. CFBP 8775].	GCF_014839505.1
WP_191950701.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1485	-	Gammaproteobacteria	Pseudomonas fluorescens	hypothetical protein [Pseudomonas fluorescens].	GCF_014839025.1
WP_191971068.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	525	-	Alphaproteobacteria	Methylobacterium soli	hypothetical protein [Methylobacterium soli].	GCF_008806385.1
WP_191999584.1	REase+TPR+GreAB-C+PIN*→||||<-?<-EAD2	REase+TPR+GreAB-C+PIN	1036	-	Gammaproteobacteria	Pseudomonas coleopterorum	hypothetical protein [Pseudomonas coleopterorum].	GCF_014841305.1
WP_192069209.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1105	-	Gammaproteobacteria	Pseudomonas coleopterorum	hypothetical protein [Pseudomonas coleopterorum].	GCF_014842375.1
WP_192163653.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1250	-	Gammaproteobacteria	Rhodanobacter sp. DHG33	hypothetical protein [Rhodanobacter sp. DHG33].	GCF_014843005.1
WP_192260260.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1441	-	Gammaproteobacteria	Pseudomonas sp. Pdm06	hypothetical protein [Pseudomonas sp. Pdm06].	GCF_014851795.1
WP_192264655.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1316	-	Alphaproteobacteria	Komagataeibacter hansenii	hypothetical protein [Komagataeibacter hansenii].	GCF_014843995.1
WP_192393207.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1117	-	Gammaproteobacteria	Methylomonas sp. EbB	hypothetical protein [Methylomonas sp. EbB].	GCF_903064685.1
WP_192433772.1	HEPN→ REase+TPR+TPR+GreAB-C+PIN*→	REase+TPR+TPR+GreAB-C+PIN	1339	-	Alphaproteobacteria	Ensifer sp. ENS11	hypothetical protein [Ensifer sp. ENS11].	GCF_014851895.1
WP_192504527.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1119	-	Gammaproteobacteria	Rouxiella badensis	hypothetical protein [Rouxiella badensis].	GCF_014859005.1
WP_192836185.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1092	-	Gammaproteobacteria	Acinetobacter oleivorans	hypothetical protein [Acinetobacter oleivorans].	GCF_014876825.1
WP_193132365.1	HetE-N1→ TPR+GreAB-C+PIN+TM+TM*→	TPR+GreAB-C+PIN+TM+TM	1086	-	Gammaproteobacteria	Enterobacter hormaechei	hypothetical protein, partial [Enterobacter hormaechei].	GCF_014901495.1
WP_193343548.1	HetE-N1→ TPR+GreAB-C+PIN*→?→ PhospholipaseD→	TPR+GreAB-C+PIN	1103	-	Gammaproteobacteria	Halomonas elongata	hypothetical protein [Halomonas elongata].	GCF_014926355.1
WP_193426153.1	TPR+PIN*→	TPR+PIN	1217	-	Firmicutes	Priestia aryabhattai	hypothetical protein [Priestia aryabhattai].	GCF_014932885.1
WP_193843312.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1090	-	Gammaproteobacteria	Serratia marcescens	hypothetical protein [Serratia marcescens].	GCF_015160915.1
WP_194030396.1	PNPase+TPR+GreAB-C+PIN*→	PNPase+TPR+GreAB-C+PIN	1392	-	Cyanobacteria	Lusitaniella coriacea	hypothetical protein [Lusitaniella coriacea].	GCF_015207425.1
WP_194552914.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1236	-	Gammaproteobacteria	Vibrio anguillarum	hypothetical protein [Vibrio anguillarum].	GCF_015343355.1
WP_194640651.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1123	-	Bacteroidetes	Flavobacterium sp. HJJ	hypothetical protein [Flavobacterium sp. HJJ].	GCF_015351475.1
WP_194689942.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1323	-	Alphaproteobacteria	unclassified Gluconobacter	MULTISPECIES: hypothetical protein [unclassified Gluconobacter].	GCF_015353155.1
WP_194782158.1	TPR+PIN*→	TPR+PIN	1183	-	Actinobacteria	Arthrobacter gandavensis	hypothetical protein [Arthrobacter gandavensis].	GCF_015355785.1
WP_194849029.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1094	-	Gammaproteobacteria	Escherichia coli	hypothetical protein [Escherichia coli].	GCF_015356625.1
WP_194908878.1	TPR+PIN*→	TPR+PIN	1322	-	Actinobacteria	Catenulispora rubra	hypothetical protein [Catenulispora rubra].	GCF_015356825.1
WP_195550768.1	TM+TM+TPR+PIN*→	TM+TM+TPR+PIN	1183	-	Bacteroidetes	Bacteroides uniformis	hypothetical protein [Bacteroides uniformis].	GCF_015557045.1
WP_195789843.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1310	-	Alphaproteobacteria	Bradyrhizobium genosp. L	hypothetical protein [Bradyrhizobium genosp. L].	GCF_015624485.1
WP_196103949.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	468	-	Alphaproteobacteria	Pontivivens sp. MT2928	hypothetical protein [Pontivivens sp. MT2928].	GCF_015679265.1
WP_196165874.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1139	-	Gammaproteobacteria	Pseudomonas monteilii	hypothetical protein [Pseudomonas monteilii].	GCF_015680735.1
WP_196184162.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1545	-	Gammaproteobacteria	Pseudomonas asiatica	hypothetical protein [Pseudomonas asiatica].	GCF_015680805.1
WP_196343881.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1106	-	Gammaproteobacteria	Enterobacter hormaechei	hypothetical protein [Enterobacter hormaechei].	GCF_015704145.1
WP_196402364.1	REase+TPR+TPR+GreAB-C+PIN*→	REase+TPR+TPR+GreAB-C+PIN	1304	-	Alphaproteobacteria	Methylocystis sp. H62	hypothetical protein [Methylocystis sp. H62].	GCF_015709515.1
WP_197022618.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1388	-	Betaproteobacteria	Comamonas aquatica	hypothetical protein [Comamonas aquatica].	GCF_000590985.1
WP_197265512.1	TPR+PIN*→	TPR+PIN	1231	-	Firmicutes	Fictibacillus sp. 23RED33	hypothetical protein [Fictibacillus sp. 23RED33].	GCF_015903925.1
WP_197283942.1	GreAB-C+PIN*→	GreAB-C+PIN	553	-	Alphaproteobacteria	Rhizobium acidisoli	hypothetical protein, partial [Rhizobium acidisoli].	GCF_001297245.1
WP_197310646.1	REase+TPR+TPR+GreAB-C+PIN*→	REase+TPR+TPR+GreAB-C+PIN	1326	-	Alphaproteobacteria	Methylobrevis sp. L22	hypothetical protein [Methylobrevis sp. L22].	GCF_015904235.1
WP_197451745.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1195	-	Planctomycetes	Rosistilla oblonga	GreA/GreB family elongation factor [Rosistilla oblonga].	GCF_007751715.1
WP_197873110.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1139	-	Gammaproteobacteria	Pseudomonas lutea	hypothetical protein [Pseudomonas lutea].	GCF_016009245.1
WP_198113276.1	TPR+GreAB-C+PIN*→||||<-HTH+HTH	TPR+GreAB-C+PIN	872	-	Betaproteobacteria	Burkholderia contaminans	hypothetical protein [Burkholderia contaminans].	GCF_016092105.1
WP_198215548.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1126	-	Gammaproteobacteria	Gilliamella sp. M0320	hypothetical protein [Gilliamella sp. M0320].	GCF_016101635.1
WP_198575560.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1332	-	Alphaproteobacteria	Caulobacter hibisci	DUF4365 domain-containing protein [Caulobacter hibisci].	GCF_016135805.1
WP_198597141.1	HetE-N1→?→ GreAB-C*→	GreAB-C	475	-	Gammaproteobacteria	Vibrio splendidus	hypothetical protein [Vibrio splendidus].	GCF_002877525.1
WP_198628691.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1231	-	Bacteroidetes	Salegentibacter sp. F63223	hypothetical protein [Salegentibacter sp. F63223].	GCF_016236915.1
WP_198694995.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1436	-	Gammaproteobacteria	Pseudomonas viridiflava	hypothetical protein [Pseudomonas viridiflava].	GCF_016308365.1

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WP_198710862.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1321	-	Gammaproteobacteria	Pseudomonas syringae	DUF4365 domain-containing protein [Pseudomonas syringae].	GCF_016308175.1
WP_198739586.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1106	-	Gammaproteobacteria	Enterobacter hormaechei	hypothetical protein [Enterobacter hormaechei].	GCF_016342225.1
WP_198742183.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1106	-	Gammaproteobacteria	Enterobacter hormaechei	hypothetical protein [Enterobacter hormaechei].	GCF_016342135.1
WP_198830693.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1441	-	Gammaproteobacteria	Pseudomonas sp. MF5691	hypothetical protein [Pseudomonas sp. MF5691].	GCF_016405645.1
WP_198862330.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1324	-	Gammaproteobacteria	Pseudomonas carnis	DUF4365 domain-containing protein [Pseudomonas carnis].	GCF_016405215.1
WP_199041247.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1250	-	Gammaproteobacteria	Dyella sp. ASV24	hypothetical protein [Dyella sp. ASV24].	GCF_016428905.1
WP_199059400.1	REase+TPR+TPR+GreAB-C+PIN*→	REase+TPR+TPR+GreAB-C+PIN	1334	-	Alphaproteobacteria	Brevundimonas sp. ASV9	hypothetical protein [Brevundimonas sp. ASV9].	GCF_016429195.1
WP_199059891.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1302	-	Alphaproteobacteria	Brevundimonas sp. ASV9	hypothetical protein [Brevundimonas sp. ASV9].	GCF_016429195.1
WP_199133123.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1258	-	Bacteroidetes	Pedobacter sp. ASV17	hypothetical protein [Pedobacter sp. ASV17].	GCF_016429065.1
WP_199161798.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1140	-	Bacteroidetes	Elizabethkingia sp. ASV34	hypothetical protein [Elizabethkingia sp. ASV34].	GCF_016428745.1
WP_199216499.1	TPR+PIN*→	TPR+PIN	1215	-	Actinobacteria	Streptomyces sp. I5	hypothetical protein [Streptomyces sp. I5].	GCF_016432735.1
WP_199272510.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1359	-	Betaproteobacteria	Paraburkholderia acidisoli	hypothetical protein [Paraburkholderia acidisoli].	GCF_009789675.1
WP_199515964.1	TM+TPR+PIN*→	TM+TPR+PIN	1145	-	Actinobacteria	Pseudosporangium sp. NEAU-24	tetratricopeptide repeat protein [Pseudosporangium sp. NEAU-24].	GCF_016464385.1
WP_199591321.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1505	-	Betaproteobacteria	Pelomonas sp. OAE585	hypothetical protein [Pelomonas sp. OAE585].	GCF_016467315.1
WP_199660563.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1035	-	Gammaproteobacteria	Klebsiella quasipneumoniae	hypothetical protein, partial [Klebsiella quasipneumoniae].	GCF_016491635.1
WP_199707330.1	REase→ PIN*→	PIN	932	-	Actinobacteria	Antrihabitans sp. YC3-6	hypothetical protein [Antrihabitans sp. YC3-6].	GCF_016482825.1
WP_199727385.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1488	-	Gammaproteobacteria	Pseudomonas syringae group genomosp. 7	hypothetical protein [Pseudomonas syringae group genomosp. 7].	GCF_003703295.1
WP_199743158.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1009	-	Alphaproteobacteria	Sphingomonas ginsenosidivorax	tetratricopeptide repeat protein [Sphingomonas ginsenosidivorax].	GCF_007995065.1
WP_199871858.1	HetE-N1→ HetE-N1+TPR+GreAB-C+PIN*→	HetE-N1+TPR+GreAB-C+PIN	1088	-	Gammaproteobacteria	Vibrio anguillarum	hypothetical protein [Vibrio anguillarum].	GCF_015350415.1
WP_200204777.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1116	-	Gammaproteobacteria	Marinobacter sp. 1-3A	hypothetical protein [Marinobacter sp. 1-3A].	GCF_016597775.1
WP_200282902.1	TPR+PIN*→	TPR+PIN	1263	-	Verrucomicrobia	Haloferula rosea	hypothetical protein [Haloferula rosea].	GCF_016595525.1
WP_200597934.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1112	-	Gammaproteobacteria	Pseudomonas stutzeri	hypothetical protein [Pseudomonas stutzeri].	GCF_016622345.1
WP_200602419.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1441	-	Gammaproteobacteria	Pseudomonas sp. S44	hypothetical protein [Pseudomonas sp. S44].	GCF_016624805.1
WP_201009307.1	REase+PIN*→	REase+PIN	1247	-	Actinobacteria	Rhodococcus sp. NKCM2511	DUF4365 domain-containing protein [Rhodococcus sp. NKCM2511].	GCF_014905595.1
WP_201090676.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1083	-	Gammaproteobacteria	Entomomonas sp. F2A	hypothetical protein [Entomomonas sp. F2A].	GCF_016653615.1
WP_201420192.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1442	-	Gammaproteobacteria	Pseudomonas syringae	hypothetical protein [Pseudomonas syringae].	GCF_016694755.2
WP_201621921.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1244	-	Gammaproteobacteria	Psychrobacter urativorans	hypothetical protein [Psychrobacter urativorans].	GCF_904846695.1
WP_201915404.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1321	-	Gammaproteobacteria	Pseudomonas fluorescens	DUF4365 domain-containing protein [Pseudomonas fluorescens].	GCF_016728065.1
WP_201921162.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1094	-	Gammaproteobacteria	Aeromonas caviae	hypothetical protein [Aeromonas caviae].	GCF_016729435.1
WP_201996904.1	HetE-N1→ MNS-Npun2340+TPR+GreAB-C+PIN*→	MNS-Npun2340+TPR+GreAB-C+PIN	1094	-	Gammaproteobacteria	Aeromonas caviae	hypothetical protein [Aeromonas caviae].	GCF_016728955.1
WP_202685167.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1019	-	Alphaproteobacteria	Skermanella mucosa	hypothetical protein, partial [Skermanella mucosa].	GCF_016765655.1
WP_202722978.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1141	-	Gammaproteobacteria	Shewanella schlegeliana	hypothetical protein [Shewanella schlegeliana].	GCF_016765635.1
WP_202727723.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1094	-	Gammaproteobacteria	Serratia fonticola	hypothetical protein [Serratia fonticola].	GCF_016770915.1
WP_203042134.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1106	-	Gammaproteobacteria	Enterobacter hormaechei	hypothetical protein [Enterobacter hormaechei].	GCF_016791625.1
WP_203341318.1	TPR+PIN*→	TPR+PIN	1141	-	Firmicutes	Planomicrobium sp. REN14	hypothetical protein [Planomicrobium sp. REN14].	GCF_016820615.1
WP_203380482.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1231	-	Actinobacteria	Actinoplanes sp. LDG1-06	DUF4365 domain-containing protein [Actinoplanes sp. LDG1-06].	GCF_016834655.1
WP_203735920.1	TPR+PIN*→	TPR+PIN	1176	-	Actinobacteria	Actinoplanes durhamensis	hypothetical protein [Actinoplanes durhamensis].	GCF_016862175.1
WP_203841861.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1259	-	Actinobacteria	Actinoplanes humidus	DUF4365 domain-containing protein [Actinoplanes humidus].	GCF_016862215.1
WP_204008964.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1356	-	Actinobacteria	Micromonospora andamanensis	hypothetical protein [Micromonospora andamanensis].	GCF_016863495.1
WP_204028926.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1338	-	Actinobacteria	Sinosporangium siamense	hypothetical protein [Sinosporangium siamense].	GCF_016863435.1

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WP_204127404.1	HetE-N1→ TPR+GreAB-C+PIN*→||||<-HNH	TPR+GreAB-C+PIN	1110	-	Gammaproteobacteria	Pseudomonas sp. RDP1	hypothetical protein [Pseudomonas sp. RDP1].	GCF_016887885.1
WP_204370319.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	860	-	Betaproteobacteria	Burkholderia cepacia	tetratricopeptide repeat protein, partial [Burkholderia cepacia].	GCF_001052915.1
WP_204511064.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1349	-	Alphaproteobacteria	Bradyrhizobium canariense	tetratricopeptide repeat protein [Bradyrhizobium canariense].	GCF_016907215.1
WP_204648469.1	TPR+PIN*→	TPR+PIN	1235	-	Firmicutes	Gemmiger formicilis	hypothetical protein [Gemmiger formicilis].	GCF_016900095.1
WP_204732305.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1447	-	Betaproteobacteria	Hydrogenophaga laconesensis	hypothetical protein [Hydrogenophaga laconesensis].	GCF_016909585.1
WP_204856598.1	REase+PIN*→	REase+PIN	1247	-	Actinobacteria	Rhodococcus fascians	DUF4365 domain-containing protein [Rhodococcus fascians].	GCF_016909505.1
WP_204934318.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1321	-	Gammaproteobacteria	Pseudomonas stutzeri	DUF4365 domain-containing protein [Pseudomonas stutzeri].	GCF_016909445.1
WP_204944661.1	TPR+PIN*→	TPR+PIN	1203	-	Actinobacteria	Micromonospora luteifusca	hypothetical protein [Micromonospora luteifusca].	GCF_016907275.1
WP_205045164.1	TPR+PIN*→	TPR+PIN	1168	-	Actinobacteria	Streptomyces bryophytorum	hypothetical protein [Streptomyces bryophytorum].	GCF_017164735.1
WP_205483425.1	REase+TPR+GreAB-C+PIN→ TPR→||||<-?||PIN*→	PIN	365	-	Gammaproteobacteria	Pseudomonas sp. 15A4	hypothetical protein [Pseudomonas sp. 15A4].	GCF_016925575.1
WP_206013307.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1090	-	Gammaproteobacteria	Pseudoalteromonas sp. Z9A6	hypothetical protein [Pseudoalteromonas sp. Z9A6].	GCF_011378805.1
WP_206497574.1	REase+PIN*→	REase+PIN	1021	-	Actinobacteria	Rhodococcus sp. KRD175	hypothetical protein [Rhodococcus sp. KRD175].	GCF_017168275.1
WP_206556849.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1116	-	Gammaproteobacteria	Marinobacter daepoensis	hypothetical protein [Marinobacter daepoensis].	GCF_017255165.1
WP_206628468.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1116	-	Gammaproteobacteria	Vibrio vulnificus	hypothetical protein [Vibrio vulnificus].	GCF_017291135.1
WP_206676035.1	HTH→ SIG+TM→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1125	-	Bacteroidetes	Capnocytophaga canis	hypothetical protein [Capnocytophaga canis].	GCF_013276255.1
WP_206820216.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1215	-	Actinobacteria	Microbacterium esteraromaticum	DUF4365 domain-containing protein [Microbacterium esteraromaticum].	GCF_017303135.1
WP_206852091.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1289	-	Gammaproteobacteria	Marinobacter hydrocarbonoclasticus	hypothetical protein [Marinobacter hydrocarbonoclasticus].	GCF_017303195.1
WP_207418840.1	TPR+GreAB-C+PIN*→||||<-HTH+HTH	TPR+GreAB-C+PIN	872	-	Betaproteobacteria	Burkholderia pseudomallei	hypothetical protein [Burkholderia pseudomallei].	GCF_017356705.1
WP_207505725.1	Mbetalac→ Trypsin+TPR+GreAB-C+PIN*→	Trypsin+TPR+GreAB-C+PIN	1362	-	Bacteroidetes	Telluribacter humicola	serine protease [Telluribacter humicola].	GCF_017355935.1
WP_207509935.1	Mbetalac→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1342	-	Bacteroidetes	Telluribacter humicola	hypothetical protein [Telluribacter humicola].	GCF_017355935.1
WP_207967591.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1090	-	Gammaproteobacteria	Yersinia pseudotuberculosis	hypothetical protein [Yersinia pseudotuberculosis].	GCF_017498805.1
WP_207993663.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1122	-	Gammaproteobacteria	Yersinia pseudotuberculosis	hypothetical protein [Yersinia pseudotuberculosis].	GCF_017498865.1
WP_208133228.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1306	-	Bacteroidetes	Siccationidurans ginsengisoli	hypothetical protein [Siccationidurans ginsengisoli].	GCF_017571525.1
WP_208209475.1	REase+TPR+GreAB-C+PIN*→	REase+TPR+GreAB-C+PIN	1543	-	Gammaproteobacteria	Pseudomonas asiatica	hypothetical protein [Pseudomonas asiatica].	GCF_017582485.1
WP_208467197.1	TPR+PIN*→	TPR+PIN	1140	-	Actinobacteria	Actinoplanes sp. NEAU-H7	hypothetical protein [Actinoplanes sp. NEAU-H7].	GCF_017592555.1
WP_208622113.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1022	-	Gammaproteobacteria	Shewanella indica	hypothetical protein, partial [Shewanella indica].	GCF_002836975.1
WP_208660584.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1087	-	Gammaproteobacteria	Shewanella decolorationis	hypothetical protein [Shewanella decolorationis].	GCF_007923045.1
WP_208757658.1	TPR+PIN*→	TPR+PIN	1184	-	Firmicutes	Priestia megaterium	hypothetical protein [Priestia megaterium].	GCF_002872495.1
WP_209187630.1	REase+TPR+GreAB-C+PIN→ *PIN*→	REase+TPR+GreAB-C+PIN	359	-	Alphaproteobacteria	Rhizobium sp. L245/93	hypothetical protein [Rhizobium sp. L245/93].	GCF_017741845.1
WP_209187631.1	-	-	978	-	Alphaproteobacteria	Rhizobium sp. L245/93	hypothetical protein [Rhizobium sp. L245/93].	GCF_017741845.1
WP_209302601.1	X+PIN*→	X+PIN	1221	-	Firmicutes	Anaerostipes hadrus	hypothetical protein [Anaerostipes hadrus].	GCF_017776445.1
WP_209570872.1	TPR+GreAB-C+PIN*→?→||||<-TPR	TPR+GreAB-C+PIN	1131	-	Bacteroidetes	Flavobacterium sp. 1750	hypothetical protein [Flavobacterium sp. 1750].	GCF_017833855.1
WP_209629149.1	<-Calcineurin<-?||?→?→?→ TPR+PIN*→	TPR+PIN	1016	-	Euryarchaeota	Methanofollis sp. W23	hypothetical protein [Methanofollis sp. W23].	GCF_017875325.1
WP_209829315.1	TPR+PIN*→	TPR+PIN	1242	-	Actinobacteria	Cellulosimicrobium sp. BE325	hypothetical protein [Cellulosimicrobium sp. BE325].	GCF_017834095.1
WP_210277108.1	REase+TPR+TPR+GreAB-C+PIN*→	REase+TPR+TPR+GreAB-C+PIN	1346	-	Alphaproteobacteria	Rhizobium leguminosarum	hypothetical protein [Rhizobium leguminosarum].	GCF_014138515.1
WP_210311799.1	TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	812	-	Alphaproteobacteria	Rhizobium soli	hypothetical protein, partial [Rhizobium soli].	GCF_014207075.1
WP_210441888.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1089	-	Gammaproteobacteria	Vibrio crassostreae	hypothetical protein [Vibrio crassostreae].	GCF_017917835.1
WP_210504843.1	HetE-N1→ TPR+GreAB-C+PIN*→	TPR+GreAB-C+PIN	1123	-	Gammaproteobacteria	Pantoea ananatis	hypothetical protein [Pantoea ananatis].	GCF_017920595.1

Gene neighborhoods and domain architectures of the novel STAND1 (nSTAND1) domain

acc	**operon**	**architecture**	**len**	**gen.name**	**taxend**	**species**	**defline**	**gca**
ABW16115.1	<-ABhydrolase<-?<-TIR+CASPASE+APATPase+TPR+TPR||?→||<-?||nSTAND1+BetaPropeller*→ TIR+EACC1+EAD1→	nSTAND1+BetaPropeller	1230	Franean1_6781	actinobacteria	Frankia sp. EAN1pec	WD-40 repeat protein [Frankia sp. EAN1pec].	GCA_000018005.1
AMY09307.1	<-ABhydrolase<-?<-?||?→?→ SIG+TPR→ TIR+DrHyd→ nSTAND1+TM*→||<-?<-?<-?||?→?→||<-?<-ABhydrolase	nSTAND1+TM	884	LuPra_02522	acidobacteria	Luteitalea pratensis	putative family GH19 chitinase [Luteitalea pratensis].	GCA_001618865.1
AQZ62998.1	nSTAND1+BetaPropeller*→?→?→ ParB→	nSTAND1+BetaPropeller	1212	BKM31_17390	actinobacteria	Nonomuraea sp. ATCC 55076	hypothetical protein BKM31_17390 [Nonomuraea sp. ATCC 55076].	GCA_002057455.1
AUG75452.1	<-ABhydrolase||?→||<-?||?→?→||<-?||EACC1→ CASPASE+nSTAND1+TM+BetaPropeller*→	CASPASE+nSTAND1+TM+BetaPropeller	1485	CFP65_0489	actinobacteria	Kitasatospora sp. MMS16-BH015	hypothetical protein CFP65_0489 [Kitasatospora sp. MMS16-BH015].	GCA_002943525.1
BAY12967.1	EAD8+Trypsin→?→?→ MoxR→?→ VWA+nSTAND1*→	VWA+nSTAND1	1139	NIES2098_61590	cyanobacteria	Calothrix sp. NIES-2098	WD-40 repeat-containing protein [Calothrix sp. NIES-2098].	GCA_002368175.1
BAY22501.1	<-ACT||CASPASE+nSTAND1+BetaPropeller*→||<-?<-VWA+SidE||?→ MNS→	CASPASE+nSTAND1+BetaPropeller	1839	NIES2100_22640	cyanobacteria	Calothrix sp. NIES-2100	WD-40 repeat protein [Calothrix sp. NIES-2100].	GCA_002368195.1
BBD52759.1	CASPASE+nSTAND1+TM+BetaPropeller*→	CASPASE+nSTAND1+TM+BetaPropeller	1514	NIES204_00160	cyanobacteria	Planktothrix agardhii NIES-204	WD-40 repeat-containing protein [Planktothrix agardhii NIES-204].	GCA_003609755.1
BBD65423.1	nSTAND1+BetaPropeller*→ BetaPropeller→||<-?<-?<-?||ENOYCOADEHYD→	nSTAND1+BetaPropeller	770	NIES4070_17810	cyanobacteria	Nostoc commune HK-02	WD-40 repeat-containing protein [Nostoc commune HK-02].	GCA_003990685.1
BBD65510.1	Mbetalac→?→ Mbetalac→ CASPASE→ nSTAND1+BetaPropeller*→?→||<-?||ABC-ATPase→	nSTAND1+BetaPropeller	1279	NIES4070_18680	cyanobacteria	Nostoc commune HK-02	WD-40 repeat-containing protein [Nostoc commune HK-02].	GCA_003990685.1
CEJ42488.1	DinB_2+FGS→?→?→||<-?||nSTAND1+BetaPropeller*→	nSTAND1+BetaPropeller	490	apha_00274	cyanobacteria	Chrysosporum ovalisporum	WD-40 repeat protein [Chrysosporum ovalisporum].	GCA_001458455.1
EDM78150.1	Pkinase+TPR→||<-?||Pkinase+TIR+nSTAND1+BetaPropeller+FGS*→	Pkinase+TIR+nSTAND1+BetaPropeller+FGS	1781	PPSIR1_00415	deltaproteobacteria	Plesiocystis pacifica SIR-1	peptidase C14, caspase catalytic subunit p20, partial [Plesiocystis pacifica SIR-1].	GCA_000170895.1
EDN71045.1	nSTAND1+BetaPropeller*→	nSTAND1+BetaPropeller	1207	BGP_1542	gammaproteobacteria	Beggiatoa sp. PS	WD-40 repeat protein [Beggiatoa sp. PS].	GCA_000170715.1
ETX01284.1	TIR+DrHyd→ nSTAND1+TM*→	nSTAND1+TM	561	ETSY1_07910	nitrospinae/tectomicrobia group	Candidatus Entotheonella factor	hypothetical protein ETSY1_07910, partial [Candidatus Entotheonella factor].	GCA_000522425.1

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ETX06250.1	nSTAND1+TM+BetaPropeller*→	nSTAND1+TM+BetaPropeller	810	ETSY2_18270	nitrospinae/tectomicrobia group	Candidatus Entotheonella gemina	hypothetical protein ETSY2_18270, partial [Candidatus Entotheonella gemina].	GCA_000522445.1
ETX08407.1	TIR+DrHyd→ nSTAND1+TM+BetaPropeller+PDZ+BetaPropeller*→	nSTAND1+TM+BetaPropeller+PDZ+BetaPropeller	1401	ETSY2_05600	nitrospinae/tectomicrobia group	Candidatus Entotheonella gemina	hypothetical protein ETSY2_05600 [Candidatus Entotheonella gemina].	GCA_000522445.1
GAK58629.1	SIG+TIR→ nSTAND1*→ nSTAND1+TM→	nSTAND1	191	U27_05603	bacteria	Candidatus Vecturithrix granuli	peptidase C14, caspase catalytic subunit p20 [Candidatus Vecturithrix granuli].	GCA_000739535.1
GCL34384.1	nSTAND1+BetaPropeller+TPR*→ REC→	nSTAND1+BetaPropeller+TPR	1185	PA905_35650	cyanobacteria	Planktothrix agardhii CCAP 1459/11A	WD-40 repeat-containing protein [Planktothrix agardhii CCAP 1459/11A].	GCA_005402765.2
GES04627.1	<-wHTH-4stranded+TPRs+APATPase+TPR+TPR+TPR||?→?→||<-APATPase+TPR||EACC1→ CASPASE+nSTAND1+BetaPropeller*→?→||<-?||REC→?→||<-?<-ABhydrolase	CASPASE+nSTAND1+BetaPropeller	1472	Acor_66950	actinobacteria	Acrocarpospora corrugata	hypothetical protein Acor_66950 [Acrocarpospora corrugata].	GCA_009687845.1
GFJ81020.1	<-REC||?→?→?→?→||<-?||EACC1→ CASPASE+nSTAND1+TM+BetaPropeller*→?→||<-?<-?<-?<-?<-?||REC→	CASPASE+nSTAND1+TM+BetaPropeller	1373	Phou_052000	actinobacteria	Phytohabitans houttuyneae	hypothetical protein Phou_052000 [Phytohabitans houttuyneae].	GCA_011764425.1
HAA13664.1	FAD-NAD-dep-oxidoreductase→?→ TIR+nSTAND1+TM+BetaPropeller*→	TIR+nSTAND1+TM+BetaPropeller	1414	DCE41_19005	bacteroidetes	Cytophagales bacterium	TPA: hypothetical protein DCE41_19005, partial [Cytophagales bacterium].	GCA_003444355.1
HAA18104.1	<-ABhydrolase<-?<-?<-PSE<-?||TIR+DrHyd→ nSTAND1+TM+BetaPropeller*→	nSTAND1+TM+BetaPropeller	1014	DCP28_04755	bacteroidetes	Cytophagales bacterium	TPA: hypothetical protein DCP28_04755 [Cytophagales bacterium].	GCA_003444325.1
HAA22846.1	TIR→ nSTAND1+TM+BetaPropeller*→	nSTAND1+TM+BetaPropeller	1115	DCP28_30300	bacteroidetes	Cytophagales bacterium	TPA: hypothetical protein DCP28_30300 [Cytophagales bacterium].	GCA_003444325.1
HAA23288.1	<-SIG+Trypsin||BetaPropeller+ABhydrolase→||<-?<-?||NUDIX→ PSE→?→ TIR+DrHyd→ nSTAND1+TM+PspA+BetaPropeller*→	nSTAND1+TM+PspA+BetaPropeller	1043	DCP28_32665	bacteroidetes	Cytophagales bacterium	TPA: hypothetical protein DCP28_32665 [Cytophagales bacterium].	GCA_003444325.1
HAA50805.1	Pkinase+TIR+DrHyd→ TIR+DrHyd→ nSTAND1+BetaPropeller*→	nSTAND1+BetaPropeller	2457	DCE43_13910	planctomycetes	Planctomycetaceae bacterium	TPA: hypothetical protein DCE43_13910 [Planctomycetaceae bacterium].	GCA_003444155.1
HAA60996.1	Pkinase+TIR+DrHyd+TIR→ nSTAND1+BetaPropeller*→	nSTAND1+BetaPropeller	1113	DCE39_08695	planctomycetes	Planctomycetaceae bacterium	TPA: hypothetical protein DCE39_08695 [Planctomycetaceae bacterium].	GCA_003444135.1
HAB16129.1	TIR+DrHyd→ nSTAND1+TM+BetaPropeller*→	nSTAND1+TM+BetaPropeller	1225	DCE44_06740	verrucomicrobia	Verrucomicrobiales bacterium	TPA: hypothetical protein DCE44_06740, partial [Verrucomicrobiales bacterium].	GCA_003445095.1
HAB19453.1	TIR+DrHyd→ nSTAND1*→?→||<-p450<-SIG+IES1	nSTAND1	1272	DCE44_23860	verrucomicrobia	Verrucomicrobiales bacterium	TPA: hypothetical protein DCE44_23860 [Verrucomicrobiales bacterium].	GCA_003445095.1

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HAB19519.1	TIR+DrHyd→ nSTAND1+TM+BetaPropeller*→?→ Cluster515_2clades→	nSTAND1+TM+BetaPropeller	1398	DCE44_24195	verrucomicrobia	Verrucomicrobiales bacterium	TPA: hypothetical protein DCE44_24195 [Verrucomicrobiales bacterium].	GCA_003445095.1
HAC65097.1	SIG+IES1+CBS→||<-?<-?<-?||?→?→ nSTAND1+TM*→||<-?<-?<-?<-?<-?<-?||Redoxin→	nSTAND1+TM	781	DCF68_16600	cyanobacteria	Cyanothece sp. UBA12306	TPA: hypothetical protein DCF68_16600 [Cyanothece sp. UBA12306].	GCA_003448685.1
HAE30915.1	TIR+DrHyd→ nSTAND1+BetaPropeller*→	nSTAND1+BetaPropeller	1040	DCF89_07360	bacteroidetes	Flavobacteriales bacterium	TPA: hypothetical protein DCF89_07360 [Flavobacteriales bacterium].	GCA_003448535.1
HAI83309.1	TIR+DrHyd→ TIR+DrHyd→ nSTAND1+BetaPropeller*→	nSTAND1+BetaPropeller	856	DCL43_06560	bacteroidetes	Chitinophagaceae bacterium	TPA: hypothetical protein DCL43_06560, partial [Chitinophagaceae bacterium].	GCA_003450935.1
HAN37555.1	TIR→ nSTAND1+TM*→?→?→?→?→ Cluster106_3clades→	nSTAND1+TM	559	DCQ29_01515	bacteroidetes	Chitinophagaceae bacterium	TPA: hypothetical protein DCQ29_01515, partial [Chitinophagaceae bacterium].	GCA_003456175.1
HAP59714.1	SIG+IES1→||<-?<-?||PSE→?→ SIG+HISKIN+REC+AraC-HTH→ SIG+nSTAND1+TM+BetaPropeller*→	SIG+nSTAND1+TM+BetaPropeller	1024	DCR93_09475	bacteroidetes	Cytophagales bacterium	TPA: hypothetical protein DCR93_09475 [Cytophagales bacterium].	GCA_003454975.1
HAW02034.1	TIR→ nSTAND1+TM*→	nSTAND1+TM	563	DCX10_09905	verrucomicrobia	Verrucomicrobiales bacterium	TPA: hypothetical protein DCX10_09905, partial [Verrucomicrobiales bacterium].	GCA_003543825.1
HAW53197.1	TIR+DrHyd→ nSTAND1+TM*→	nSTAND1+TM	442	DCX54_12865	bacteroidetes	Flavobacteriales bacterium	TPA: High-affnity carbon uptake protein Hat/HatR, partial [Flavobacteriales bacterium].	GCA_003487525.1
HAX76296.1	<-Trypco1||CASPASE+nSTAND1+TM*→ SIG+Pentapeptide→	CASPASE+nSTAND1+TM	797	DCY88_10755	cyanobacteria	Cyanobacteria bacterium UBA11372	TPA: hypothetical protein DCY88_10755, partial [Cyanobacteria bacterium UBA11372].	GCA_003486675.1
HAX87398.1	CASPASE+nSTAND1+BetaPropeller*→	CASPASE+nSTAND1+BetaPropeller	1185	DCY91_14325	cyanobacteria	Cyanobacteria bacterium UBA11370	TPA: hypothetical protein DCY91_14325 [Cyanobacteria bacterium UBA11370].	GCA_003486645.1
HAZ02032.1	TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+cNMP→?→ TIR+DrHyd→ nSTAND1+BetaPropeller*→	nSTAND1+BetaPropeller	1055	DCY97_07630	bacteroidetes	Marinilabiliales bacterium	TPA: hypothetical protein DCY97_07630 [Marinilabiliales bacterium].	GCA_003485835.1
HAZ49897.1	EACC2+CASPASE+nSTAND1+BetaPropeller*→||<-?<-?||SIG+TPR→ SIG+TPR→||<-?||Uma2→	EACC2+CASPASE+nSTAND1+BetaPropeller	1758	DCZ55_36965	cyanobacteria	Cyanobacteria bacterium UBA11371	TPA: hypothetical protein DCZ55_36965 [Cyanobacteria bacterium UBA11371].	GCA_003486305.1
HBB96021.1	nSTAND1+TM+BetaPropeller*→||<-?<-?<-?<-?<-Cluster533_2clades	nSTAND1+TM+BetaPropeller	1196	DC054_11585	acidobacteria	Blastocatellia bacterium	TPA: hypothetical protein DC054_11585 [Blastocatellia bacterium].	GCA_003487805.1
HBE43600.1	MORC→?→ AAA→ TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+cNMP→ nSTAND1+TM+BetaPropeller*→	nSTAND1+TM+BetaPropeller	953	DDW27_20875	bacteroidetes	Bacteroidales bacterium	TPA: hypothetical protein DDW27_20875, partial [Bacteroidales bacterium].	GCA_003501665.1

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HBH24377.1	TIR+DrHyd→ nSTAND1+BetaPropeller*→	nSTAND1+BetaPropeller	1031	DDY13_13250	bacteroidetes	Cytophagales bacterium	TPA: hypothetical protein DDY13_13250 [Cytophagales bacterium].	GCA_003500135.1
HBK97025.1	SIG+Trypsin+PDZ→?→ EACC2+CASPASE+nSTAND1+BetaPropeller*→?→?→?→||<-XisI	EACC2+CASPASE+nSTAND1+BetaPropeller	1576	DD001_06660	cyanobacteria	Microcoleaceae bacterium UBA10368	TPA: hypothetical protein DD001_06660 [Microcoleaceae bacterium UBA10368].	GCA_003506815.1
HBL28746.1	TIR+TIR→ nSTAND1+TIR+TM*→	nSTAND1+TIR+TM	926	DD490_18070	acidobacteria	Acidobacteria bacterium	TPA: hypothetical protein DD490_18070 [Acidobacteria bacterium].	GCA_003504885.1
HBL30162.1	TIR+DrHyd→ nSTAND1+TM+BetaPropeller*→?→?→ tRNA→?→?→ PSE→?→ AbiEii→	nSTAND1+TM+BetaPropeller	1255	DD490_25280	acidobacteria	Acidobacteria bacterium	TPA: hypothetical protein DD490_25280 [Acidobacteria bacterium].	GCA_003504885.1
HBR00557.1	nSTAND1*→?→||<-?<-?||GUN4→	nSTAND1	454	DD761_18925	cyanobacteria	Cyanobacteria bacterium UBA11691	TPA: hypothetical protein DD761_18925 [Cyanobacteria bacterium UBA11691].	GCA_003535175.1
HBY06929.1	wHTH-4stranded+TPRs+Pkinase+nSTAND1+TM+BetaPropeller*→	wHTH-4stranded+TPRs+Pkinase+nSTAND1+TM+BetaPropeller	1319	DEH22_03775	chloroflexi	Chloroflexi bacterium	TPA: hypothetical protein DEH22_03775, partial [Chloroflexi bacterium].	GCA_003512075.1
HBY08818.1	Pkinase+nSTAND1*→	Pkinase+nSTAND1	633	DEH22_13955	chloroflexi	Chloroflexi bacterium	TPA: hypothetical protein DEH22_13955, partial [Chloroflexi bacterium].	GCA_003512075.1
HCA49859.1	TIR+DrHyd→ nSTAND1+BetaPropeller+7TMR-DISMED1*→	nSTAND1+BetaPropeller+7TMR-DISMED1	1946	DEP12_05575	planctomycetes	Planctomycetaceae bacterium	TPA: hypothetical protein DEP12_05575, partial [Planctomycetaceae bacterium].	GCA_003519945.1
HCD01670.1	Pkinase+TIR+DrHyd→ nSTAND1+BetaPropeller+TPR+TPR*→	nSTAND1+BetaPropeller+TPR+TPR	2680	DER64_14220	planctomycetes	Planctomycetaceae bacterium	TPA: hypothetical protein DER64_14220 [Planctomycetaceae bacterium].	GCA_003517085.1
HCM75174.1	TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+cNMP→ TIR+DrHyd→ nSTAND1+TM+BetaPropeller*→	nSTAND1+TM+BetaPropeller	1054	DIS90_02245	bacteroidetes	Cytophagales bacterium	TPA: High-affnity carbon uptake protein Hat/HatR [Cytophagales bacterium].	GCA_003535515.1
HDN27296.1	TIR+DrHyd→ nSTAND1+TM+BetaPropeller*→	nSTAND1+TM+BetaPropeller	784	ENG03_09425	gammaproteobacteria	Thioploca sp.	TPA: hypothetical protein ENG03_09425, partial [Thioploca sp.].	-
HDV39880.1	Pkinase+nSTAND1+TM*→||<-?<-?||?→?→?→?→ REC→	Pkinase+nSTAND1+TM	922	ENQ62_18990	chloroflexi	Chloroflexi bacterium	TPA: serine/threonine protein kinase [Chloroflexi bacterium].	-
HDX76165.1	nSTAND1+TM+BetaPropeller*→	nSTAND1+TM+BetaPropeller	810	ENQ42_15745	chloroflexi	Chloroflexi bacterium	TPA: hypothetical protein ENQ42_15745 [Chloroflexi bacterium].	-
HEB93882.1	TIR+nSTAND1+BetaPropeller*→	TIR+nSTAND1+BetaPropeller	1688	ENI94_10555	gammaproteobacteria	Gammaproteobacteria bacterium	TPA: TIR domain-containing protein, partial [Gammaproteobacteria bacterium].	-
HEC44295.1	MORC→?→ AAA→||<-?||TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+cNMP→?→ TIR+DrHyd→ SIG+nSTAND1+TM+BetaPropeller*→?→?→?→||<-Mbetalac	SIG+nSTAND1+TM+BetaPropeller	1041	ENI20_15845	bacteroidetes	Bacteroides sp.	TPA: hypothetical protein ENI20_15845 [Bacteroides sp.].	-

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HEC84902.1	Pkinase+nSTAND1*→	Pkinase+nSTAND1	801	ENI48_06635	gammaproteobacteria	Thioploca sp.	TPA: hypothetical protein ENI48_06635, partial [Thioploca sp.].	-
HEP84957.1	nSTAND1+TM+TPR*→?→ CASPASE→||<-SWACOS+TPR+TPR	nSTAND1+TM+TPR	1040	ENQ97_01465	chloroflexi	Chloroflexi bacterium	TPA: ATP-binding protein [Chloroflexi bacterium].	-
HET82137.1	SIG+nSTAND1+BetaPropeller*→	SIG+nSTAND1+BetaPropeller	1664	ENQ84_03870	chloroflexi	Chloroflexi bacterium	TPA: hypothetical protein ENQ84_03870 [Chloroflexi bacterium].	-
HEY47862.1	SIG+LexA-HTH+LexA-protease→||<-?||tRNA→?→ tRNA→ tRNA→ wHTH-4stranded+TPRs+STYKIN+nSTAND1+BetaPropeller→ wHTH-4stranded+TPRs+STYKIN+nSTAND1+BetaPropeller*→ SWACOS+TPR+TPR→	wHTH-4stranded+TPRs+STYKIN+nSTAND1+BetaPropeller	1765	G4O14_13900	chloroflexi	Anaerolineae bacterium	TPA: protein kinase [Anaerolineae bacterium].	GCA_011174825.1
HFG28088.1	TIR+DrHyd→ nSTAND1+BetaPropeller*→||<-?<-?<-?||TM→?→?→ Cluster157_3clades→	nSTAND1+BetaPropeller	1281	ENS73_14620	verrucomicrobia	Verrucomicrobia subdivision 3 bacterium	TPA: hypothetical protein ENS73_14620 [Verrucomicrobia subdivision 3 bacterium].	-
HFK76611.1	TCAD9+Pkinase+nSTAND1+TM+BetaPropeller*→	TCAD9+Pkinase+nSTAND1+TM+BetaPropeller	1386	ENR96_14405	chloroflexi	Anaerolineae bacterium	TPA: hypothetical protein ENR96_14405, partial [Anaerolineae bacterium].	-
HFN01514.1	CASPASE+nSTAND1+BetaPropeller*→	CASPASE+nSTAND1+BetaPropeller	1643	ENR64_27960	cyanobacteria	Oscillatoriales cyanobacterium SpSt-418	TPA: hypothetical protein ENR64_27960 [Oscillatoriales cyanobacterium SpSt-418].	-
HGT17894.1	SIG+Pentapeptide→||<-?||PSE→?→?→ MED15→?→ CASPASE+nSTAND1+TM+BetaPropeller*→	CASPASE+nSTAND1+TM+BetaPropeller	1526	ENT48_13530	chloroflexi	Chloroflexi bacterium	TPA: CHAT domain-containing protein [Chloroflexi bacterium].	-
HGV41566.1	HxxxH→?→?→ Cluster515_2clades→?→||<-?||SIG+Trypsin→ SIG+TM+nSTAND1+TM+BetaPropeller*→?→?→ nSTAND1+TM+Tox-ODYAM1+BetaPropeller→	SIG+TM+nSTAND1+TM+BetaPropeller	1587	ENT18_00225	chloroflexi	Chloroflexi bacterium	TPA: hypothetical protein ENT18_00225 [Chloroflexi bacterium].	-
HGX16402.1	HTH+Pkinase+nSTAND1+TM+BetaPropeller*→	HTH+Pkinase+nSTAND1+TM+BetaPropeller	1240	ENR56_13340	chloroflexi	Anaerolineae bacterium	TPA: helix-turn-helix domain-containing protein, partial [Anaerolineae bacterium].	-
HIG27385.1	nSTAND1+BetaPropeller+SUN+TPR*→	nSTAND1+BetaPropeller+SUN+TPR	1629	EYQ50_06160	verrucomicrobia	Verrucomicrobiales bacterium	TPA: hypothetical protein EYQ50_06160 [Verrucomicrobiales bacterium].	-
HIG31009.1	nSTAND1+TM*→	nSTAND1+TM	482	EYQ50_25695	verrucomicrobia	Verrucomicrobiales bacterium	TPA: ATP-binding protein, partial [Verrucomicrobiales bacterium].	-
HIG83463.1	TIR+DrHyd→ nSTAND1+TM+BetaPropeller*→	nSTAND1+TM+BetaPropeller	938	EYQ23_05285	verrucomicrobia	Verrucomicrobiales bacterium	TPA: hypothetical protein EYQ23_05285, partial [Verrucomicrobiales bacterium].	-
KAA0256025.1	<-REC+NtrC-AAA+FIS-HTH<-?<-?<-ABC-ATPase||TIR+DrHyd→ nSTAND1+BetaPropeller*→?→ TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+cNMP→ TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+cNMP→?→?→||<-SIG+IES1	nSTAND1+BetaPropeller	1035	EDX89_02880	acidobacteria	Acidobacteria bacterium	hypothetical protein EDX89_02880 [Acidobacteria bacterium].	-
KAA3662250.1	<-HAD||?→ EAD7+nSTAND1+TM+FGS*→	EAD7+nSTAND1+TM+FGS	781	DWQ04_13990	chloroflexi	Chloroflexi bacterium	hypothetical protein DWQ04_13990, partial [Chloroflexi bacterium].	-
KAB2902286.1	Pkinase+nSTAND1+TM+EP1*→	Pkinase+nSTAND1+TM+EP1	937	F9K40_07755	deltaproteobacteria	Kofleriaceae bacterium	protein kinase [Kofleriaceae bacterium].	-

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KEI67755.1	CASPASE→ nSTAND1+BetaPropeller*→ REC→	nSTAND1+BetaPropeller	1315	A19Y_2900	cyanobacteria	Planktothrix agardhii NIVA-CYA 126/8	putative WD40 repeat-containing protein [Planktothrix agardhii NIVA-CYA 126/8].	GCA_000710505.1
KKD36164.1	nSTAND1+BetaPropeller*→	nSTAND1+BetaPropeller	1221	WN50_21290	cyanobacteria	Limnoraphis robusta CS-951	peptidase C14 [Limnoraphis robusta CS-951].	GCA_000972705.2
KKO17953.1	TIR→ SIG+nSTAND1+TM+BetaPropeller*→ BetaPropeller→	SIG+nSTAND1+TM+BetaPropeller	1179	BROFUL_03361	planctomycetes	Candidatus Brocadia fulgida	hypothetical protein BROFUL_03361 [Candidatus Brocadia fulgida].	GCA_000987375.1
KOX34481.1	nSTAND1+TM+BetaPropeller*→	nSTAND1+TM+BetaPropeller	1229	ADK67_03315	actinobacteria	Saccharothrix sp. NRRL B-16348	hypothetical protein ADK67_03315 [Saccharothrix sp. NRRL B-16348].	GCA_001280085.1
KPA09462.1	TIR→ nSTAND1+CarboxypepD-reg-IG+FGS*→	nSTAND1+CarboxypepD-reg-IG+FGS	1095	MHK_010294	deltaproteobacteria	Candidatus Magnetomorum sp. HK-1	Sulphatase-modifying factor domain protein [Candidatus Magnetomorum sp. HK-1].	GCA_001292585.1
KPA09563.1	TIR+DrHyd→ nSTAND1+BetaPropeller*→	nSTAND1+BetaPropeller	1143	MHK_010235	deltaproteobacteria	Candidatus Magnetomorum sp. HK-1	repeat-containing protein [Candidatus Magnetomorum sp. HK-1].	GCA_001292585.1
KPK06025.1	Pkinase+LuxR-HTH+nSTAND1+BetaPropeller*→	Pkinase+LuxR-HTH+nSTAND1+BetaPropeller	1617	AMJ56_15120	chloroflexi	Anaerolineae bacterium SG8_19	hypothetical protein AMJ56_15120 [Anaerolineae bacterium SG8_19].	GCA_001303105.1
KPK11168.1	wHTH-4stranded+TPRs+nSTAND1+TM+BetaPropeller*→	wHTH-4stranded+TPRs+nSTAND1+TM+BetaPropeller	1833	AMJ56_06610	chloroflexi	Anaerolineae bacterium SG8_19	hypothetical protein AMJ56_06610 [Anaerolineae bacterium SG8_19].	GCA_001303105.1
KPK13148.1	wHTH-4stranded+TPRs+nSTAND1+TM+BetaPropeller*→	wHTH-4stranded+TPRs+nSTAND1+TM+BetaPropeller	1822	AMJ56_03150	chloroflexi	Anaerolineae bacterium SG8_19	hypothetical protein AMJ56_03150 [Anaerolineae bacterium SG8_19].	GCA_001303105.1
KPK92042.1	nSTAND1+BetaPropeller→ wHTH-4stranded+TPRs+STYKIN+nSTAND1+BetaPropeller*→ SWACOS+TPR+TPR→	wHTH-4stranded+TPRs+STYKIN+nSTAND1+BetaPropeller	1764	AMJ88_11890	chloroflexi	Anaerolineae bacterium SM23_ 63	hypothetical protein AMJ88_11890 [Anaerolineae bacterium SM23_ 63].	GCA_001303965.1
KPL74836.1	TIR+nSTAND1+BetaPropeller*→?→?→ SIG+ApbE→	TIR+nSTAND1+BetaPropeller	1565	ADN00_13440	chloroflexi	Ornatilinea apprima	hypothetical protein ADN00_13440 [Ornatilinea apprima].	GCA_001306115.1
KPQ33209.1	CASPASE+CASPASE+nSTAND1+BetaPropeller*→||<-?<-?<-?<-?<-?||PKinase+SWACOS→	CASPASE+CASPASE+nSTAND1+BetaPropeller	1796	HLUCCA11_19215	cyanobacteria	Phormidesmis priestleyi Ana	WD-40 repeat-containing protein [Phormidesmis priestleyi Ana].	GCA_001314865.1
KWW98255.1	Cluster157_3clades→?→||<-?||CASPASE+nSTAND1+TM+BetaPropeller*→	CASPASE+nSTAND1+TM+BetaPropeller	1514	TH66_19845	actinobacteria	Streptomyces thermoautotrophicus	hypothetical protein TH66_19845 [Streptomyces thermoautotrophicus].	GCA_001543895.1
KXK14067.1	<-SIG+TPR<-?||Pkinase+LuxR-HTH+nSTAND1+BetaPropeller*→	Pkinase+LuxR-HTH+nSTAND1+BetaPropeller	1564	UZ15_CFX003003150	chloroflexi	Chloroflexi bacterium OLB15	NB-ARC domain-containing protein [Chloroflexi bacterium OLB15].	GCA_001567085.1

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<tr><td>MAM90836.1</td><td>TIR+DrHyd→ nSTAND1+TM+BetaPropeller*→</td><td>nSTAND1+TM+BetaPropeller</td><td>1106</td><td>CMI15_05100</td><td>verrucomicrobia</td><td>Opitutaceae bacterium</td><td>hypothetical protein CMI15_05100, partial [Opitutaceae bacterium].</td><td>GCA_002694885.1</td></tr>
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MBL59695.1	<-ABhydrolase<-?<-?||TIR+DrHyd→ nSTAND1+BetaPropeller*→	nSTAND1+BetaPropeller	1446	CMO75_08500	verrucomicrobia	Verrucomicrobiales bacterium	hypothetical protein CMO75_08500 [Verrucomicrobiales bacterium].	GCA_002721375.1
MBO11083.1	Pkinase+DrHyd→ SIG+nSTAND1+BetaPropeller+TPR*→	SIG+nSTAND1+BetaPropeller+TPR	2094	CMJ68_09995	planctomycetes	Planctomycetaceae bacterium	hypothetical protein CMJ68_09995 [Planctomycetaceae bacterium].	GCA_002724415.1
MBO89933.1	TIR+DrHyd→ nSTAND1+TM+BetaPropeller*→	nSTAND1+TM+BetaPropeller	1371	CMP14_10460	alphaproteobacteria	Rickettsiales bacterium	hypothetical protein CMP14_10460, partial [Rickettsiales bacterium].	GCA_002724555.1
MBT32320.1	TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+cNMP→ TIR→ nSTAND1+BetaPropeller*→	nSTAND1+BetaPropeller	783	CMO01_21870	alphaproteobacteria	Thalassobius sp.	hypothetical protein CMO01_21870, partial [Thalassobius sp.].	GCA_002729595.1
MBV59171.1	TIR+DrHyd→ nSTAND1+BetaPropeller*→	nSTAND1+BetaPropeller	966	CMO58_06170	verrucomicrobia	Verrucomicrobiales bacterium	hypothetical protein CMO58_06170, partial [Verrucomicrobiales bacterium].	GCA_002731855.1
MRR18651.1	AAA+TPR→?→ SIG+TM→ MORC→?→ AAA→?→ nSTAND1+TM+BetaPropeller*→?→?→?→||<-SIG+IES1+CBS<-?<-?<-SIG+TPR	nSTAND1+TM+BetaPropeller	1007	EG827_00520	bacteria	bacterium	hypothetical protein EG827_00520 [bacterium].	GCA_009668865.1
MSR57801.1	Pkinase→ TIR→ TIR+DrHyd→ nSTAND1+BetaPropeller+PDZ*→	nSTAND1+BetaPropeller+PDZ	1868	EXS05_09020	planctomycetes	Planctomycetaceae bacterium	PDZ domain-containing protein [Planctomycetaceae bacterium].	GCA_009691905.1
MSV29424.1	<-SIG+Metallopeptidase||TPR→?→ nSTAND1+TM+BetaPropeller*→ SIG+BetaPropeller→	nSTAND1+TM+BetaPropeller	957	EXQ52_11895	acidobacteria	Bryobacterales bacterium	hypothetical protein EXQ52_11895 [Bryobacterales bacterium].	GCA_009697455.1
MSV29798.1	TIR→ nSTAND1+FGS*→	nSTAND1+FGS	844	EXQ52_13790	acidobacteria	Bryobacterales bacterium	hypothetical protein EXQ52_13790 [Bryobacterales bacterium].	GCA_009697455.1
MZQ49612.1	nSTAND1+TM+BetaPropeller*→	nSTAND1+TM+BetaPropeller	1023	GT598_11475	bacteroidetes	Bacteroidales bacterium	hypothetical protein GT598_11475 [Bacteroidales bacterium].	-
NBC83322.1	MORC→?→ AAA→||<-?||TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+cNMP→ TIR+DrHyd→ nSTAND1+BetaPropeller*→	nSTAND1+BetaPropeller	1023	GVY19_08055	bacteroidetes	Bacteroidetes bacterium	hypothetical protein GVY19_08055 [Bacteroidetes bacterium].	-
NBQ24983.1	TIR→ TIR+DrHyd→ nSTAND1+BetaPropeller+BetaPropeller*→	nSTAND1+BetaPropeller+BetaPropeller	1109	EBU26_12125	verrucomicrobia	Verrucomicrobia bacterium	hypothetical protein EBU26_12125, partial [Verrucomicrobia bacterium].	GCA_009920095.1
NBW34856.1	SIG+HISKIN+REC+AraC-HTH→?→?→ SIG+ASH-IG→?→?→ TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+cNMP→ nSTAND1+TM+BetaPropeller*→	nSTAND1+TM+BetaPropeller	1061	EBR30_07525	bacteroidetes	Cytophagia bacterium	hypothetical protein EBR30_07525 [Cytophagia bacterium].	-
NCF64926.1	Pkinase+LuxR-HTH+nSTAND1+BetaPropeller*→ BetaPropeller→?→||<-?<-?<-?<-ABhydrolase	Pkinase+LuxR-HTH+nSTAND1+BetaPropeller	1614	GWP61_03065	chloroflexi	Chloroflexi bacterium	protein kinase [Chloroflexi bacterium].	-
NCF85778.1	TIR+DrHyd→ nSTAND1+TM+BetaPropeller*→?→?→||<-?||ABhydrolase→	nSTAND1+TM+BetaPropeller	1368	GWQ08_09620	verrucomicrobia	Verrucomicrobiaceae bacterium	hypothetical protein GWQ08_09620 [Verrucomicrobiaceae bacterium].	-
NCR43132.1	CASPASE+nSTAND1+TM+BetaPropeller*→	CASPASE+nSTAND1+TM+BetaPropeller	1425	GPJ09_01855	cyanobacteria	Microcystis aeruginosa SX13-01	hypothetical protein GPJ09_01855 [Microcystis aeruginosa SX13-01].	-

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NCS30183.1	<-Trypco1||CASPASE+nSTAND1+FGS*→	CASPASE+nSTAND1+FGS	1065	GPJ18_17185	cyanobacteria	Microcystis aeruginosa F13-15	SUMF1/EgtB/PvdO family nonheme iron enzyme [Microcystis aeruginosa F13-15].	-
NDE10486.1	TIR+TIR→ nSTAND1+BetaPropeller*→	nSTAND1+BetaPropeller	1021	EBZ95_07970	bacteroidetes	Chitinophagia bacterium	hypothetical protein EBZ95_07970 [Chitinophagia bacterium].	-
NDJ26297.1	nSTAND1+TM*→	nSTAND1+TM	850	GS682_33040	cyanobacteria	Nostoc sp. B(2019)	hypothetical protein GS682_33040, partial [Nostoc sp. B(2019)].	-
NDJ53782.1	wHTH-4stranded+TPRs+nSTAND1+TM+BetaPropeller*→	wHTH-4stranded+TPRs+nSTAND1+TM+BetaPropeller	1239	GYB68_11940	chloroflexi	Chloroflexi bacterium	hypothetical protein GYB68_11940 [Chloroflexi bacterium].	-
NDJ62327.1	Pkinase+nSTAND1+TM+BetaPropeller*→	Pkinase+nSTAND1+TM+BetaPropeller	1217	GYB67_14465	chloroflexi	Chloroflexi bacterium	protein kinase, partial [Chloroflexi bacterium].	-
NDJ75022.1	<-SIG+ABhydrolase<-?||Pkinase+LuxR-HTH+nSTAND1+BetaPropeller*→	Pkinase+LuxR-HTH+nSTAND1+BetaPropeller	1613	GYB65_02080	chloroflexi	Chloroflexi bacterium	protein kinase [Chloroflexi bacterium].	-
NDJ75955.1	<-REC||?→?→||<-?<-SIG+ABhydrolase||Pkinase+LuxR-HTH+nSTAND1+BetaPropeller*→ ROK-HTH→ SIG+TM+TM+TM+TM+TM→ SIG+TM+TM+TM+TM+TM→	Pkinase+LuxR-HTH+nSTAND1+BetaPropeller	1599	GYB65_06825	chloroflexi	Chloroflexi bacterium	protein kinase [Chloroflexi bacterium].	-
NDJ77885.1	Pkinase+nSTAND1+BetaPropeller*→	Pkinase+nSTAND1+BetaPropeller	1485	GYB65_16675	chloroflexi	Chloroflexi bacterium	protein kinase [Chloroflexi bacterium].	-
NDJ85618.1	REC→?→ Pkinase+nSTAND1+BetaPropeller*→||<-VWA+FHA||?→?→||<-ABC-ATPase	Pkinase+nSTAND1+BetaPropeller	1487	GYB66_07010	chloroflexi	Chloroflexi bacterium	protein kinase [Chloroflexi bacterium].	-
NDQ57070.1	ROK-HTH→?→ ABhydrolase→ TIR+DrHyd→ nSTAND1+TPR*→?→||<-?<-?<-?<-?||SIG+VIT+VWA+TM→	nSTAND1+TPR	939	GZ088_08360	acidobacteria	Acidipila sp.	tetratricopeptide repeat protein [Acidipila sp.].	-
NEO05953.1	<-Cluster59_2clades||APATPase+BetaPropeller→?→||<-?<-?||PSE→ nSTAND1+BetaPropeller+TPR*→	nSTAND1+BetaPropeller+TPR	1521	F6K51_10425	cyanobacteria	Moorea sp. SIO3I8	hypothetical protein F6K51_10425 [Moorea sp. SIO3I8].	-
NEO22392.1	APATPase+BetaPropeller→?→||<-?<-?||PSE→ nSTAND1+TM+BetaPropeller+TPR*→ Cluster59_2clades→	nSTAND1+TM+BetaPropeller+TPR	1415	F6K57_24570	cyanobacteria	Moorea sp. SIO4A5	hypothetical protein F6K57_24570 [Moorea sp. SIO4A5].	-
NEO24022.1	Trypsin+nSTAND1+BetaPropeller*→	Trypsin+nSTAND1+BetaPropeller	1347	F6K57_33355	cyanobacteria	Moorea sp. SIO4A5	hypothetical protein F6K57_33355 [Moorea sp. SIO4A5].	-
NEO40588.1	RVT→ RVT→ RVT→ PSE→ PSE→?→||<-?||?→?→ nSTAND1*→ BetaPropeller→	nSTAND1	417	F6J90_31350	cyanobacteria	Moorea sp. SIOASIH	hypothetical protein F6J90_31350 [Moorea sp. SIOASIH].	-
NEO55095.1	<-SUA||?→ nSTAND1+BetaPropeller+TPR*→	nSTAND1+BetaPropeller+TPR	1462	F6K54_19650	cyanobacteria	Okeania sp. SIO3B5	WD40 repeat domain-containing protein [Okeania sp. SIO3B5].	-
NEO77038.1	EACC2+CASPASE+nSTAND1+BetaPropeller*→	EACC2+CASPASE+nSTAND1+BetaPropeller	1208	F6J99_12650	cyanobacteria	Moorea sp. SIO4G3	CHAT domain-containing protein, partial [Moorea sp. SIO4G3].	-
NEO88965.1	Pentapeptide→ CASPASE→ nSTAND1+BetaPropeller*→	nSTAND1+BetaPropeller	1295	F6K56_01245	cyanobacteria	Moorea sp. SIO3G5	hypothetical protein F6K56_01245 [Moorea sp. SIO3G5].	-
NEO95082.1	Trypsin+nSTAND1+ThuA-GATase*→	Trypsin+nSTAND1+ThuA-GATase	909	F6K56_34765	cyanobacteria	Moorea sp. SIO3G5	trypsin-like serine protease [Moorea sp. SIO3G5].	-
NEP00479.1	<-PKinase+SWACOS+GAF+SHELIX+HISKIN+REC<-?<-?<-TPR+TPR<-?<-MNS||?→ nSTAND1+*→	nSTAND1+	776	F6K58_17710	cyanobacteria	Symploca sp. SIO2E9	hypothetical protein F6K58_17710 [Symploca sp. SIO2E9].	-

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NEP10746.1	<-Cluster108_2clades||?→ PKinase+SWACOS+GAF+SHELIX+HISKIN+REC→?→?→?→||<-Trypco1||CASPASE+nSTAND1+TM+GUN4*→	CASPASE+nSTAND1+TM+GUN4	1012	F6K14_11125	cyanobacteria	Symploca sp. SIO2C1	hypothetical protein F6K14_11125 [Symploca sp. SIO2C1].	-
NEP16657.1	ABhydrolase→?→?→||<-?||CASPASE+nSTAND1*→	CASPASE+nSTAND1	919	F6J97_07085	cyanobacteria	Leptolyngbya sp. SIO4C1	hypothetical protein F6J97_07085 [Leptolyngbya sp. SIO4C1].	-
NEP23856.1	CASPASE+nSTAND1+TM+BetaPropeller*→?→||<-?<-?<-SIG+TM+TM+TM+TM+TM+TM+TM+TM	CASPASE+nSTAND1+TM+BetaPropeller	1358	F6K49_18200	cyanobacteria	Moorea sp. SIO3I6	CHAT domain-containing protein [Moorea sp. SIO3I6].	-
NEQ36510.1	GUN4→ CASPASE+EAD10→?→ EAD10+nSTAND1+TM+BetaPropeller*→	EAD10+nSTAND1+TM+BetaPropeller	1351	F6K40_09560	cyanobacteria	Okeania sp. SIO3I5	WD40 repeat domain-containing protein [Okeania sp. SIO3I5].	-
NEQ36637.1	RRM→||<-?||?→ Trypsin+nSTAND1+BetaPropeller*→	Trypsin+nSTAND1+BetaPropeller	1463	F6K40_10255	cyanobacteria	Okeania sp. SIO3I5	trypsin-like serine protease [Okeania sp. SIO3I5].	-
NEQ38190.1	<-SIG+TPR||?→ Trypsin+nSTAND1+TM+TPR+TPR+TPR*→	Trypsin+nSTAND1+TM+TPR+TPR+TPR	1116	F6K40_18755	cyanobacteria	Okeania sp. SIO3I5	tetratricopeptide repeat protein, partial [Okeania sp. SIO3I5].	-
NEQ49185.1	<-NUDIX<-?||?→?→||<-ParA-Soj-PloopNTPase||TIR+nSTAND1*→	TIR+nSTAND1	848	F6K11_03505	cyanobacteria	Leptolyngbya sp. SIO3F4	TIR domain-containing protein [Leptolyngbya sp. SIO3F4].	-
NEQ50781.1	<-Pentapeptide||TIR+nSTAND1*→ TIR+TM+BetaPropeller→	TIR+nSTAND1	927	F6K11_11700	cyanobacteria	Leptolyngbya sp. SIO3F4	TIR domain-containing protein [Leptolyngbya sp. SIO3F4].	-
NEQ65990.1	CASPASE+nSTAND1+TM+BetaPropeller*→ PSE→?→||<-?<-TM	CASPASE+nSTAND1+TM+BetaPropeller	1386	F6K21_10900	cyanobacteria	Symploca sp. SIO2D2	hypothetical protein F6K21_10900 [Symploca sp. SIO2D2].	-
NEQ66888.1	<-SIG+Pentapeptide<-Trypco1||CASPASE+nSTAND1+TM+BetaPropeller*→ BetaPropeller→	CASPASE+nSTAND1+TM+BetaPropeller	1422	F6K21_15565	cyanobacteria	Symploca sp. SIO2D2	peptidase C14, partial [Symploca sp. SIO2D2].	-
NEQ68332.1	nSTAND1+TM+BetaPropeller*→	nSTAND1+TM+BetaPropeller	1227	F6K21_23100	cyanobacteria	Symploca sp. SIO2D2	hypothetical protein F6K21_23100 [Symploca sp. SIO2D2].	-
NER26420.1	<-ABhydrolase<-Trypco1||CASPASE+nSTAND1+GUN4*→||<-?||?→ ParA-Soj-PloopNTPase→	CASPASE+nSTAND1+GUN4	980	F6J89_02035	cyanobacteria	Symploca sp. SIO1C4	hypothetical protein F6J89_02035 [Symploca sp. SIO1C4].	-
NER33117.1	CASPASE+nSTAND1+BetaPropeller*→	CASPASE+nSTAND1+BetaPropeller	1563	F6J93_03400	cyanobacteria	Oscillatoria sp. SIO1A7	hypothetical protein F6J93_03400 [Oscillatoria sp. SIO1A7].	-
NER37564.1	EAD8+Trypsin→||<-?||HTH+nSTAND1+TM+BetaPropeller*→	HTH+nSTAND1+TM+BetaPropeller	1342	F6J93_26975	cyanobacteria	Oscillatoria sp. SIO1A7	hypothetical protein F6J93_26975 [Oscillatoria sp. SIO1A7].	-
NER38168.1	<-TM<-?||CASPASE+nSTAND1+BetaPropeller*→||<-Uma2<-?<-?<-?<-SIG+TM+TM||?→ Uma2→	CASPASE+nSTAND1+BetaPropeller	1954	F6J93_30125	cyanobacteria	Oscillatoria sp. SIO1A7	hypothetical protein F6J93_30125 [Oscillatoria sp. SIO1A7].	-
NER71216.1	<-ABhydrolase<-?<-?||?→||<-Trypco1||CASPASE+nSTAND1*→	CASPASE+nSTAND1	926	F6J95_03475	cyanobacteria	Leptolyngbya sp. SIO1E4	peptidase C14 [Leptolyngbya sp. SIO1E4].	-
NER94406.1	<-EAD4+APATPase+BetaPropeller||?→?→||<-?<-?<-Trypco1||PASE+nSTAND1+TM+Pentapeptide*→	PASE+nSTAND1+TM+Pentapeptide	1064	F6J86_11280	cyanobacteria	Symploca sp. SIO1B1	hypothetical protein F6J86_11280 [Symploca sp. SIO1B1].	-
NES05250.1	CASPASE+EAD10→?→ EAD10+nSTAND1+TM+BetaPropeller*→	EAD10+nSTAND1+TM+BetaPropeller	1461	F6K22_21960	cyanobacteria	Okeania sp. SIO2F4	hypothetical protein F6K22_21960 [Okeania sp. SIO2F4].	-

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NES64500.1	Cluster59_2clades→ GUN4→ nSTAND1*→	nSTAND1	623	F6K24_04135	cyanobacteria	Okeania sp. SIO2D1	S-layer homology domain-containing protein [Okeania sp. SIO2D1].	-
NES65413.1	nSTAND1+TM+BetaPropeller*→	nSTAND1+TM+BetaPropeller	1165	F6K24_09195	cyanobacteria	Okeania sp. SIO2D1	WD40 repeat domain-containing protein, partial [Okeania sp. SIO2D1].	-
NES97446.1	nSTAND1+BetaPropeller*→	nSTAND1+BetaPropeller	1191	F6K32_19940	cyanobacteria	Desertifilum sp. SIO1I2	WD40 repeat domain-containing protein, partial [Desertifilum sp. SIO1I2].	-
NET34881.1	CASPASE+nSTAND1+TM*→	CASPASE+nSTAND1+TM	975	F6K19_23135	cyanobacteria	Cyanothece sp. SIO1E1	hypothetical protein F6K19_23135 [Cyanothece sp. SIO1E1].	-
NET36631.1	<-MNS<-?||?→||<-?||CASPASE+nSTAND1*→	CASPASE+nSTAND1	704	F6K19_32150	cyanobacteria	Cyanothece sp. SIO1E1	hypothetical protein F6K19_32150 [Cyanothece sp. SIO1E1].	-
NET37730.1	CASPASE+nSTAND1*→	CASPASE+nSTAND1	567	F6K19_37925	cyanobacteria	Cyanothece sp. SIO1E1	hypothetical protein F6K19_37925, partial [Cyanothece sp. SIO1E1].	-
NET40110.1	nSTAND1*→	nSTAND1	497	F6K19_50595	cyanobacteria	Cyanothece sp. SIO1E1	ATP-binding protein, partial [Cyanothece sp. SIO1E1].	-
NET86531.1	<-FAD-NAD-dep-oxidoreductase<-?<-TM<-?||?→?→ EACC2+CASPASE+nSTAND1+BetaPropeller*→	EACC2+CASPASE+nSTAND1+BetaPropeller	1577	F6K45_00165	cyanobacteria	Kamptonema sp. SIO1D9	CHAT domain-containing protein [Kamptonema sp. SIO1D9].	-
NET91215.1	CASPASE+nSTAND1+TM+BetaPropeller*→	CASPASE+nSTAND1+TM+BetaPropeller	1474	F6K45_24510	cyanobacteria	Kamptonema sp. SIO1D9	hypothetical protein F6K45_24510 [Kamptonema sp. SIO1D9].	-
NIM11146.1	TIR+DrHyd→ nSTAND1+BetaPropeller*→?→?→?→?→ TIR→	nSTAND1+BetaPropeller	1081	GTO81_04125	bacteria	Candidatus Aminicenantes bacterium	AAA family ATPase [Candidatus Aminicenantes bacterium].	-
NIM60309.1	TIR+DrHyd→ nSTAND1+BetaPropeller*→ BetaPropeller→	nSTAND1+BetaPropeller	1137	GTO30_01255	acidobacteria	Acidobacteria bacterium	hypothetical protein GTO30_01255 [Acidobacteria bacterium].	-
NIN64528.1	wHTH-4stranded+TPRs+nSTAND1+BetaPropeller*→ PSE→?→?→ ICLR-HTH→	wHTH-4stranded+TPRs+nSTAND1+BetaPropeller	1481	GTO63_07465	chloroflexi	Anaerolineae bacterium	hypothetical protein GTO63_07465 [Anaerolineae bacterium].	-
NIO87402.1	nSTAND1*→	nSTAND1	271	GTN68_43335	bacteria	Candidatus Aminicenantes bacterium	hypothetical protein GTN68_43335, partial [Candidatus Aminicenantes bacterium].	-
NIP95306.1	TIR+DrHyd→ nSTAND1*→ nSTAND1→	nSTAND1	157	GWO24_18410	verrucomicrobia	Akkermansiaceae bacterium	ATP-binding protein, partial [Akkermansiaceae bacterium].	-
NIQ11829.1	Pkinase+LuxR-HTH+nSTAND1*→ nSTAND1→	Pkinase+LuxR-HTH+nSTAND1	550	GWO23_20275	gammaproteobacteria	Gammaproteobacteria bacterium	protein kinase [Gammaproteobacteria bacterium].	-
NIR47522.1	nSTAND1*→	nSTAND1	215	GWO09_03595	bacteria	candidate division KSB1 bacterium	hypothetical protein GWO09_03595, partial [candidate division KSB1 bacterium].	-

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NJD08806.1	TIR→ nSTAND1+TM+TM+TM+TM*→	nSTAND1+TM+TM+TM+TM	793	FIA97_20290	gammaproteobacteria	Methylococcaceae bacterium	hypothetical protein FIA97_20290 [Methylococcaceae bacterium].	-
NJK52968.1	SIG+nSTAND1*→	SIG+nSTAND1	216	HC936_09320	cyanobacteria	Leptolyngbyaceae cyanobacterium SU_3_3	ATP-binding protein, partial [Leptolyngbyaceae cyanobacterium SU_3_3].	-
NJK55885.1	CASPASE+CASPASE+nSTAND1+BetaPropeller*→||<-?||?→?→ ABhydrolase→ HOP2→	CASPASE+CASPASE+nSTAND1+BetaPropeller	1614	HC939_07740	cyanobacteria	Pleurocapsa sp. SU_5_0	NACHT domain-containing protein [Pleurocapsa sp. SU_5_0].	-
NJL22036.1	<-SIG+TPR||CASPASE+nSTAND1*→ nSTAND1→	CASPASE+nSTAND1	461	HC895_16420	cyanobacteria	Leptolyngbyaceae cyanobacterium SM1_3_5	hypothetical protein HC895_16420 [Leptolyngbyaceae cyanobacterium SM1_3_5].	-
NJL38884.1	nSTAND1+BetaPropeller*→ SIG+TPR→	nSTAND1+BetaPropeller	1232	HC899_20695	cyanobacteria	Leptolyngbyaceae cyanobacterium SM1_4_3	hypothetical protein HC899_20695 [Leptolyngbyaceae cyanobacterium SM1_4_3].	-
NJL61102.1	<-ENOYCOADEHYD<-ENOYCOADEHYD||VWA+FHA→?→||<-Trypco1||CASPASE+nSTAND1*→ Pentapeptide→	CASPASE+nSTAND1	666	HC903_03770	verrucomicrobia	Methylacidiphilales bacterium	hypothetical protein HC903_03770 [Methylacidiphilales bacterium].	-
NJL84534.1	<-Trypco1||CASPASE+nSTAND1+TM*→	CASPASE+nSTAND1+TM	783	HC890_19295	chloroflexi	Chloroflexaceae bacterium	AAA family ATPase [Chloroflexaceae bacterium].	-
NJM08748.1	HTH+CR-Kinase+nSTAND1*→ nSTAND1→	HTH+CR-Kinase+nSTAND1	746	HC891_25000	bacteria	Candidatus Gracilibacteria bacterium	protein kinase [Candidatus Gracilibacteria bacterium].	-
NJM70522.1	<-Trypco1||CASPASE+nSTAND1*→	CASPASE+nSTAND1	957	HC862_09975	cyanobacteria	Scytonema sp. RU_4_4	hypothetical protein HC862_09975 [Scytonema sp. RU_4_4].	-
NJM71751.1	nSTAND1*→ nSTAND1→	nSTAND1	293	HC862_16985	cyanobacteria	Scytonema sp. RU_4_4	hypothetical protein HC862_16985 [Scytonema sp. RU_4_4].	-
NJM72049.1	TIR+DrHyd→ nSTAND1+TM+BetaPropeller*→?→?→||<-?<-AAA	nSTAND1+TM+BetaPropeller	1212	HC862_18715	cyanobacteria	Scytonema sp. RU_4_4	hypothetical protein HC862_18715 [Scytonema sp. RU_4_4].	-
NJM73217.1	Pkinase→?→||<-?||?→ EACC2+CASPASE+nSTAND1+BetaPropeller*→	EACC2+CASPASE+nSTAND1+BetaPropeller	1020	HC862_25525	cyanobacteria	Scytonema sp. RU_4_4	CHAT domain-containing protein, partial [Scytonema sp. RU_4_4].	-
NJM73324.1	nSTAND1+BetaPropeller*→||<-PSE<-?<-TPR	nSTAND1+BetaPropeller	1058	HC862_26150	cyanobacteria	Scytonema sp. RU_4_4	hypothetical protein HC862_26150 [Scytonema sp. RU_4_4].	-
NJM74119.1	EACC2+CASPASE+nSTAND1*→ nSTAND1→	EACC2+CASPASE+nSTAND1	595	HC862_30810	cyanobacteria	Scytonema sp. RU_4_4	CHAT domain-containing protein [Scytonema sp. RU_4_4].	-
NJN08585.1	Pentapeptide→ CASPASE+nSTAND1+TM*→	CASPASE+nSTAND1+TM	758	HC815_11555	cyanobacteria	Richelia sp. RM1_1_1	hypothetical protein HC815_11555 [Richelia sp. RM1_1_1].	-

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NJN41702.1	TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+cNMP→?→ nSTAND1+BetaPropeller*→ BetaPropeller→	nSTAND1+BetaPropeller	821	HC811_05160	bacteroidetes	Flammeovirgaceae bacterium	High-affinity carbon uptake protein Hat/HatR [Flammeovirgaceae bacterium].	-
NJN44056.1	Pkinase→?→ nSTAND1+TM+BetaPropeller*→	nSTAND1+TM+BetaPropeller	724	HC806_04550	chloroflexi	Anaerolineae bacterium	hypothetical protein HC806_04550 [Anaerolineae bacterium].	-
NJN57460.1	nSTAND1+BetaPropeller*→?→||<-?<-?||?→ REC→?→ TM+HAMP+GAF+GAF+GAF+GAF+MCPsignal→	nSTAND1+BetaPropeller	1198	HC879_08140	cyanobacteria	Leptolyngbyaceae cyanobacterium SL_5_9	hypothetical protein HC879_08140, partial [Leptolyngbyaceae cyanobacterium SL_5_9].	-
NJN73136.1	Uma2→ PSE→||<-?<-PSE||?→||<-Trypco1||CASPASE+nSTAND1*→?→?→||<-?<-PSE<-?||SIG+TM+TM+TM+TM+TM→	CASPASE+nSTAND1	902	HC799_10205	cyanobacteria	Limnothrix sp. RL_2_0	peptidase C14 [Limnothrix sp. RL_2_0].	-
NJN87470.1	SIG+nSTAND1*→ nSTAND1+BetaPropeller→||<-GGDEF+EAL	SIG+nSTAND1	393	HC881_15635	cyanobacteria	Leptolyngbyaceae cyanobacterium SL_7_1	hypothetical protein HC881_15635 [Leptolyngbyaceae cyanobacterium SL_7_1].	-
NJO16618.1	REC→ GGDEF+EAL→?→?→?→ TIR+DrHyd+TIR→ nSTAND1+BetaPropeller*→	nSTAND1+BetaPropeller	1205	HC877_13005	gammaproteobacteria	Thioploca sp.	hypothetical protein HC877_13005 [Thioploca sp.].	-
NJP11832.1	<-Trypco1||CASPASE+nSTAND1*→	CASPASE+nSTAND1	1033	HC866_22115	cyanobacteria	Leptolyngbyaceae cyanobacterium RU_5_1	AAA family ATPase [Leptolyngbyaceae cyanobacterium RU_5_1].	-
NJR38187.1	SIG+TPR→?→?→ nSTAND1*→ nSTAND1→ BetaPropeller→	nSTAND1	274	HC781_04220	cyanobacteria	Leptolyngbyaceae cyanobacterium CSU_1_4	ATP-binding protein [Leptolyngbyaceae cyanobacterium CSU_1_4].	-
NJR62416.1	HTH+APATPase+BetaPropeller→||<-?||?→||<-TPR||CASPASE+nSTAND1+BetaPropeller*→	CASPASE+nSTAND1+BetaPropeller	1723	HC769_28590	cyanobacteria	Cyanobacteria bacterium CRU_2_1	hypothetical protein HC769_28590 [Cyanobacteria bacterium CRU_2_1].	-
NJR67118.1	CASPASE+nSTAND1+BetaPropeller*→	CASPASE+nSTAND1+BetaPropeller	1120	HC772_20280	cyanobacteria	Leptolyngbyaceae cyanobacterium CRU_2_3	hypothetical protein HC772_20280, partial [Leptolyngbyaceae cyanobacterium CRU_2_3].	-
NJR75219.1	TIR+DrHyd→ nSTAND1→ nSTAND1+TM+BetaPropeller*→ BetaPropeller→	nSTAND1+TM+BetaPropeller	760	HC773_19440	cyanobacteria	Scytonema sp. CRU_2_7	WD40 repeat domain-containing protein [Scytonema sp. CRU_2_7].	-
NKQ34063.1	Pkinase+nSTAND1+BetaPropeller*→	Pkinase+nSTAND1+BetaPropeller	1595	HF973_00435	chloroflexi	Chloroflexi bacterium	protein kinase [Chloroflexi bacterium].	-
NLF66968.1	<-REC<-?<-?<-HTH+MED15||?→?→ bDLD1+nSTAND1*→	bDLD1+nSTAND1	1094	GX579_20460	chloroflexi	Chloroflexi bacterium	ATP-binding protein [Chloroflexi bacterium].	-
NLF75477.1	TIR+TM+NACHT+TM+TM+TM+TM+TM+TM+TM+FGS→?→||<-SIG+ABhydrolase<-SIG+ABhydrolase<-?<-SIG+ABhydrolase<-?||wHTH-4stranded+TPRs+nSTAND1+TM+BetaPropeller*→	wHTH-4stranded+TPRs+nSTAND1+TM+BetaPropeller	1465	GX573_07245	chloroflexi	Chloroflexi bacterium	hypothetical protein GX573_07245 [Chloroflexi bacterium].	-
NLF76559.1	Pkinase+nSTAND1+TM+BetaPropeller*→	Pkinase+nSTAND1+TM+BetaPropeller	1037	GX573_12755	chloroflexi	Chloroflexi bacterium	protein kinase, partial [Chloroflexi bacterium].	-

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NLF76682.1	wHTH-4stranded+TPRs+nSTAND1+TM+BetaPropeller*→	wHTH-4stranded+TPRs+nSTAND1+TM+BetaPropeller	1439	GX573_13375	chloroflexi	Chloroflexi bacterium	PQQ-binding-like beta-propeller repeat protein, partial [Chloroflexi bacterium].	-
NNE66468.1	<-Pkinase+TPR||?→ TIR+TIR→ nSTAND1*→	nSTAND1	181	HKN33_07865	acidobacteria	Pyrinomonadaceae bacterium	hypothetical protein HKN33_07865, partial [Pyrinomonadaceae bacterium].	-
NNF77676.1	nSTAND1+TM+BetaPropeller*→	nSTAND1+TM+BetaPropeller	821	HKN05_06570	alphaproteobacteria	Rhizobiales bacterium	WD40 repeat domain-containing protein, partial [Rhizobiales bacterium].	-
NNL69935.1	TPRs+nSTAND1+PBPB*→	TPRs+nSTAND1+PBPB	1201	HKO70_08255	actinobacteria	Acidimicrobiia bacterium	transporter substrate-binding domain-containing protein, partial [Acidimicrobiia bacterium].	-
NNM23296.1	<-Patatin||TIR→ nSTAND1+BetaPropeller*→||<-?<-?<-?||?→?→||<-TPR	nSTAND1+BetaPropeller	1191	HKO54_07065	bacteroidetes	Flavobacteriaceae bacterium	hypothetical protein HKO54_07065 [Flavobacteriaceae bacterium].	-
NOG19904.1	<-SUA<-?<-?<-?||?→ CASPASE+nSTAND1+BetaPropeller*→||<-?||?→?→ HOP2→	CASPASE+nSTAND1+BetaPropeller	1739	HAV12_42195	bacteroidetes	Flavobacterium sp. CLA17	AAA family ATPase [Flavobacterium sp. CLA17].	-
OFV91558.1	TIR+DrHyd→ nSTAND1+TPR*→?→||<-?<-?||?→?→||<-S1COLD	nSTAND1+TPR	928	A3H95_01005	acidobacteria	Acidobacteria bacterium RIFC-SPLOWO2_02_FULL_64_15	hypothetical protein A3H95_01005 [Acidobacteria bacterium RIFC-SPLOWO2_02_FULL_64_15].	GCA_001767165.1
OFW18721.1	AbiEii→ TIR+DrHyd→ nSTAND1+TM+TPR*→?→ tRNA→||<-?<-?<-ACET	nSTAND1+TM+TPR	935	A3H97_17825	acidobacteria	Acidobacteria bacterium RIFC-SPLOWO2_02_FULL_65_29	hypothetical protein A3H97_17825 [Acidobacteria bacterium RIFC-SPLOWO2_02_FULL_65_29].	GCA_001767435.1
OFX23090.1	<-ABhydrolase||?→ TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+cNMP→?→ TIR+DrHyd→ nSTAND1+BetaPropeller*→	nSTAND1+BetaPropeller	1019	A2041_06150	bacteroidetes	Bacteroidetes bacterium GWA2_31_9b	hypothetical protein A2041_06150 [Bacteroidetes bacterium GWA2_31_9b].	GCA_001769005.1
OFX91075.1	SIG+TM→?→ MORC→?→ AAA→ TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+cNMP→?→ nSTAND1+TM+BetaPropeller*→	nSTAND1+TM+BetaPropeller	1030	A2X06_13615	bacteroidetes	Bacteroidetes bacterium GWC2_40_22	hypothetical protein A2X06_13615 [Bacteroidetes bacterium GWC2_40_22].	GCA_001768305.1
OFX95806.1	SIG+TM→?→ MORC→?→ AAA→ TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+cNMP→?→ nSTAND1+TM+BetaPropeller*→	nSTAND1+TM+BetaPropeller	1030	A2X05_06820	bacteroidetes	Bacteroidetes bacterium GWE2_41_25	hypothetical protein A2X05_06820 [Bacteroidetes bacterium GWE2_41_25].	GCA_001768485.1
OFY35811.1	TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+cNMP→?→ TIR+DrHyd→ SIG+nSTAND1+TM+BetaPropeller*→?→?→?→?→||<-?<-?||SIG+TPR→	SIG+nSTAND1+TM+BetaPropeller	1024	A2W91_17400	bacteroidetes	Bacteroidetes bacterium GWF2_38_335	hypothetical protein A2W91_17400 [Bacteroidetes bacterium GWF2_38_335].	GCA_001769535.1

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OGA98753.1	nSTAND1+prokYEATS*→||<-?<-?||ABC-ATPase→	nSTAND1+prokYEATS	746	A3E25_24070	betaproteobacteria	Burkholderiales bacterium RIFCSPHIGHO2_12_FULL_69_20	hypothetical protein A3E25_24070 [Burkholderiales bacterium RIFCSPHIGHO2_12_FULL_69_20].	GCA_001770815.1
OGB06577.1	TIR+TIR→ nSTAND1+TM+TM+TM*→||<-?||?→||<-Cluster510_2clades	nSTAND1+TM+TM+TM	787	A3E25_20360	betaproteobacteria	Burkholderiales bacterium RIFCSPHIGHO2_12_FULL_69_20	hypothetical protein A3E25_20360 [Burkholderiales bacterium RIFCSPHIGHO2_12_FULL_69_20].	GCA_001770815.1
OGO35294.1	FGS→ PSE→?→?→?→?→||<-?||TIR+nSTAND1+BetaPropeller*→ PSE→ TIR+CASPASE→	TIR+nSTAND1+BetaPropeller	1217	A2W35_01450	chloroflexi	Chloroflexi bacterium RBG_16_57_11	hypothetical protein A2W35_01450, partial [Chloroflexi bacterium RBG_16_57_11].	GCA_001795165.1
OGO45061.1	nSTAND1→||<-?<-PSE||HTH+nSTAND1+BetaPropeller*→ PSE→ PSE→ PSE→?→ PSE→ PSE→||<-?||?→?→ NUDIX→	HTH+nSTAND1+BetaPropeller	1317	A2W37_00850	chloroflexi	Chloroflexi bacterium RBG_16_63_12	hypothetical protein A2W37_00850 [Chloroflexi bacterium RBG_16_63_12].	GCA_001796945.1
OGO66215.1	SIG+ABhydrolase→||<-PSE<-PSE<-?||?→ SIG+nSTAND1+BetaPropeller*→	SIG+nSTAND1+BetaPropeller	1671	A2Z45_02015	chloroflexi	Chloroflexi bacterium RBG_19FT_COMBO_55_16	hypothetical protein A2Z45_02015 [Chloroflexi bacterium RBG_19FT_COMBO_55_16].	GCA_001795335.1
OJJ20442.1	TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+cNMP→ TIR+DrHyd→ nSTAND1+BetaPropeller*→?→?→?→ TPR+TPR→?→ SIG+TPR→	nSTAND1+BetaPropeller	1084	BKI52_18460	bacteroidetes	marine bacterium AO1-C	hypothetical protein BKI52_18460 [marine bacterium AO1-C].	GCA_001890965.1
OLF10306.1	<-ABhydrolase||?→?→ APATPase+TPR→||<-?||nSTAND1+TM+BetaPropeller*→?→?→?→||<-?<-?<-STYKIN	nSTAND1+TM+BetaPropeller	1150	BLA60_17405	actinobacteria	Actinophytocola xinjiangensis	hypothetical protein BLA60_17405 [Actinophytocola xinjiangensis].	GCA_001921215.1
OOO02143.1	TIR→ nSTAND1*→ nSTAND1+TM+TPR→	nSTAND1	241	USCGTAYLOR_01645	gammaproteobacteria	Chromatiales bacterium USCg_Taylor	hypothetical protein USCGTAYLOR_01645 [Chromatiales bacterium USCg_Taylor].	GCA_002007425.1
OQW92136.1	<-Trypco1||CASPASE+nSTAND1+TM+BetaPropeller*→	CASPASE+nSTAND1+TM+BetaPropeller	1686	BWK78_02590	gammaproteobacteria	Thiotrichaceae bacterium IS1	hypothetical protein BWK78_02590, partial [Thiotrichaceae bacterium IS1].	GCA_002083855.1
OQY53884.1	Uma2→ TIR+DrHyd+TIR→ nSTAND1+BetaPropeller*→||<-?<-ABhydrolase<-?<-?<-ParA-Soj-PloopNTPase	nSTAND1+BetaPropeller	1231	B6247_13565	gammaproteobacteria	Beggiatoa sp. 4572_84	hypothetical protein B6247_13565 [Beggiatoa sp. 4572_84].	GCA_002085445.1
OUC13656.1	CASPASE+nSTAND1*→?→?→?→ TPR→	CASPASE+nSTAND1	967	B0A82_16145	cyanobacteria	Alkalinema sp. CACIAM 70d	hypothetical protein B0A82_16145 [Alkalinema sp. CACIAM 70d].	GCA_002148405.1
OUC14859.1	<-ABhydrolase||?→?→?→?→ CASPASE+CASPASE+nSTAND1+BetaPropeller*→||<-?<-?||?→?→?→ TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM→	CASPASE+CASPASE+nSTAND1+BetaPropeller	1735	B0A82_11125	cyanobacteria	Alkalinema sp. CACIAM 70d	hypothetical protein B0A82_11125 [Alkalinema sp. CACIAM 70d].	GCA_002148405.1
OUV42838.1	TIR+DrHyd→ nSTAND1+MA+BetaPropeller*→	nSTAND1+MA+BetaPropeller	1144	CBC62_02045	verrucomicrobia	Opitutae bacterium TMED102	hypothetical protein CBC62_02045, partial [Opitutae bacterium TMED102].	GCA_002171405.1

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OYD95156.1	Pentapeptide→ Pentapeptide→ NACHT+TM+TM+TM→?→?→ PSE→ PSE→ Pentapeptide→ NACHT+TM+TM+TM→ nSTAND1+*→?→ TIR→?→?→ MoxR→ VWA+FGS→ FGS→	nSTAND1+	814	CDG77_10550	cyanobacteria	Nostoc sp. ‘Peltigera membranacea cyanobiont’ 213	hypothetical protein CDG77_10550 [Nostoc sp. ‘Peltigera membranacea cyanobiont’ 213].	GCA_002245975.1
PCH95772.1	TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+cNMP→?→ TIR+DrHyd→ nSTAND1+BetaPropeller*→	nSTAND1+BetaPropeller	1001	COB85_04230	bacteroidetes	Bacteroidetes bacterium	hypothetical protein COB85_04230, partial [Bacteroidetes bacterium].	GCA_002401055.1
PJF20968.1	Pkinase+nSTAND1*→	Pkinase+nSTAND1	712	CUN56_13480	chloroflexi	Candidatus Thermofonsia Clade 2 bacterium	hypothetical protein CUN56_13480, partial [Candidatus Thermofonsia Clade 2 bacterium].	GCA_002794505.1
PJF22587.1	TIR+nSTAND1+TM+BetaPropeller+SH3*→	TIR+nSTAND1+TM+BetaPropeller+SH3	1467	CUN56_05240	chloroflexi	Candidatus Thermofonsia Clade 2 bacterium	hypothetical protein CUN56_05240 [Candidatus Thermofonsia Clade 2 bacterium].	GCA_002794505.1
PJF29877.1	TIR+nSTAND1+TM+BetaPropeller+SH3*→||<-?<-?<-REC<-REC	TIR+nSTAND1+TM+BetaPropeller+SH3	1475	CUN52_06100	chloroflexi	Candidatus Thermofonsia Clade 2 bacterium	hypothetical protein CUN52_06100 [Candidatus Thermofonsia Clade 2 bacterium].	GCA_002794515.1
PJF40565.1	<-ABC-ATPase||?→ Pkinase+nSTAND1+fvmX2+BetaPropeller*→	Pkinase+nSTAND1+fvmX2+BetaPropeller	1488	CUN54_04825	chloroflexi	Candidatus Thermofonsia Clade 2 bacterium	hypothetical protein CUN54_04825 [Candidatus Thermofonsia Clade 2 bacterium].	GCA_002794595.1
PJF43571.1	<-FAD-NAD-dep-oxidoreductase<-?||?→ Pkinase+nSTAND1+TM+BetaPropeller*→	Pkinase+nSTAND1+TM+BetaPropeller	1074	CUN55_08445	chloroflexi	Candidatus Thermofonsia Clade 2 bacterium	hypothetical protein CUN55_08445, partial [Candidatus Thermofonsia Clade 2 bacterium].	GCA_002794585.1
PKP08385.1	TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+cNMP→?→ TIR+DrHyd→ nSTAND1+BetaPropeller*→	nSTAND1+BetaPropeller	1044	CVU09_16155	bacteroidetes	Bacteroidetes bacterium HGW-Bacteroidetes-4	hypothetical protein CVU09_16155 [Bacteroidetes bacterium HGW-Bacteroidetes-4].	GCA_002840905.1
PLX14833.1	TIR+DrHyd→ nSTAND1+BetaPropeller*→	nSTAND1+BetaPropeller	1026	C0597_09500	bacteroidetes	Marinilabiliales bacterium	hypothetical protein C0597_09500 [Marinilabiliales bacterium].	GCA_002869305.1
PSO51577.1	<-REC||?→?→?→?→ CASPASE+CASPASE+nSTAND1+BetaPropeller*→||<-?<-?<-Cluster59_2clades	CASPASE+CASPASE+nSTAND1+BetaPropeller	1683	BRC33_00055	cyanobacteria	Cyanobacteria bacterium SW_9_44_58	hypothetical protein BRC33_00055 [Cyanobacteria bacterium SW_9_44_58].	GCA_003021905.1
PTQ78533.1	<-SIG+Trypsin+PDZ||?→?→||<-?<-?||tRNA→ TIR→ TIR+DrHyd→ nSTAND1+BetaPropeller*→?→||<-SLATT	nSTAND1+BetaPropeller	1071	C8R26_102101	betaproteobacteria	Nitrosomonas oligotropha	WD40 repeat protein [Nitrosomonas oligotropha].	GCA_003050805.1
PWH17201.1	nSTAND1+TM+BetaPropeller+TM+TM+TM+TM+TM*→||<-?<-?||?→||<-?<-?<-?<-FAD-NAD-dep-oxidoreductase	nSTAND1+TM+BetaPropeller+TM+TM+TM+TM+TM	1488	DDG60_02865	chloroflexi	Anaerolineae bacterium	hypothetical protein DDG60_02865 [Anaerolineae bacterium].	GCA_003130845.1
PWT98015.1	<-REC<-?||TIR+DrHyd→ nSTAND1+TM+TM+TM*→	nSTAND1+TM+TM+TM	748	C5B51_30205	acidobacteria	Acidobacteriia bacterium	hypothetical protein C5B51_30205 [Acidobacteriia bacterium].	GCA_003175985.1
PWU20186.1	TPRs+ACYC+nSTAND1+BetaPropeller*→||<-?<-?<-?<-SWACOS+TPR+TPR	TPRs+ACYC+nSTAND1+BetaPropeller	1499	C5B48_12805	bacteria	Candidatus Rokubacteria bacterium	hypothetical protein C5B48_12805, partial [Candidatus Rokubacteria bacterium].	GCA_003176155.1

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PYP60217.1	TIR→ SLATT→ TIR+TIR→ nSTAND1+BetaPropeller+BetaPropeller+TPRs*→	nSTAND1+BetaPropeller+BetaPropeller+TPRs	2017	DMD40_01135	gemmatimonadetes	Gemmatimonadetes bacterium	hypothetical protein DMD40_01135 [Gemmatimonadetes bacterium].	GCA_003223395.1
PYQ05559.1	SIGMA-HTH→ PSE→||<-PSE||?→?→ TIR+DrHyd→ nSTAND1+TM*→	nSTAND1+TM	791	DMF82_08210	acidobacteria	Acidobacteria bacterium	hypothetical protein DMF82_08210 [Acidobacteria bacterium].	GCA_003223575.1
PYS22176.1	TIR+DrHyd→ nSTAND1+TM+TPR*→	nSTAND1+TM+TPR	1292	DMF72_14520	acidobacteria	Acidobacteria bacterium	hypothetical protein DMF72_14520 [Acidobacteria bacterium].	GCA_003222895.1
PYS83976.1	TIR+DrHyd+TIR→ nSTAND1+TPR+TPR*→	nSTAND1+TPR+TPR	1090	DMF67_06825	acidobacteria	Acidobacteria bacterium	hypothetical protein DMF67_06825 [Acidobacteria bacterium].	GCA_003222975.1
PYS96660.1	nSTAND1+TM+TPR*→	nSTAND1+TM+TPR	940	DMF65_12750	acidobacteria	Acidobacteria bacterium	hypothetical protein DMF65_12750, partial [Acidobacteria bacterium].	GCA_003223015.1
PYS98866.1	TIR+TIR→ nSTAND1*→ nSTAND1+TIR→	nSTAND1	360	DMF65_09895	acidobacteria	Acidobacteria bacterium	hypothetical protein DMF65_09895 [Acidobacteria bacterium].	GCA_003223015.1
PZN54462.1	<-REC<-REC||?→||<-?<-?<-?||Pkinase+nSTAND1+BetaPropeller*→	Pkinase+nSTAND1+BetaPropeller	962	DIU68_10520	chloroflexi	Chloroflexi bacterium	hypothetical protein DIU68_10520, partial [Chloroflexi bacterium].	GCA_003242205.1
PZO11654.1	CASPASE+nSTAND1*→?→ GGDEF+EAL→	CASPASE+nSTAND1	915	DCF25_18990	cyanobacteria	Leptolyngbya foveolarum	hypothetical protein DCF25_18990 [Leptolyngbya foveolarum].	GCA_003242035.1
PZV25433.1	CASPASE+nSTAND1+TM*→	CASPASE+nSTAND1+TM	1002	DCF12_14930	cyanobacteria	Snowella sp.	hypothetical protein DCF12_14930 [Snowella sp.].	GCA_003249095.1
QDL09256.1	EACC2+CASPASE+nSTAND1+BetaPropeller*→	EACC2+CASPASE+nSTAND1+BetaPropeller	1599	DP114_16315	cyanobacteria	Brasilonema sennae CENA114	hypothetical protein DP114_16315 [Brasilonema sennae CENA114].	GCA_006968745.1
QDL10821.1	EACC2+CASPASE+nSTAND1*→	EACC2+CASPASE+nSTAND1	600	DP114_25545	cyanobacteria	Brasilonema sennae CENA114	hypothetical protein DP114_25545 [Brasilonema sennae CENA114].	GCA_006968745.1
RCJ19564.1	TPR+CASPASE→?→?→ nSTAND1+BetaPropeller*→?→?→?→||<-REC<-REC	nSTAND1+BetaPropeller	1246	A6770_05315	cyanobacteria	Nostoc minutum NIES-26	hypothetical protein A6770_05315 [Nostoc minutum NIES-26].	GCA_003326215.1
RCJ22548.1	REC→ Pentapeptide→ nSTAND1+TM*→	nSTAND1+TM	901	A6770_29780	cyanobacteria	Nostoc minutum NIES-26	hypothetical protein A6770_29780 [Nostoc minutum NIES-26].	GCA_003326215.1
REK19006.1	wHTH-4stranded+TPRs+Pkinase+nSTAND1+BetaPropeller*→	wHTH-4stranded+TPRs+Pkinase+nSTAND1+BetaPropeller	1641	DWQ40_07995	actinobacteria	Actinobacteria bacterium	hypothetical protein DWQ40_07995, partial [Actinobacteria bacterium].	GCA_003388545.1
RIK38666.1	TIR+nSTAND1+BetaPropeller*→ TIR+nSTAND1→	TIR+nSTAND1+BetaPropeller	1082	DCC58_16370	chloroflexi	Chloroflexi bacterium	hypothetical protein DCC58_16370 [Chloroflexi bacterium].	GCA_003577355.1
RIK57209.1	TIR+nSTAND1+BetaPropeller*→ TIR+CASPASE→	TIR+nSTAND1+BetaPropeller	1528	DCC57_02180	chloroflexi	Chloroflexi bacterium	hypothetical protein DCC57_02180 [Chloroflexi bacterium].	GCA_003577365.1

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RIL11133.1	SIG+ACYC+nSTAND1+BetaPropeller*→	SIG+ACYC+nSTAND1+BetaPropeller	1397	DCC79_05805	bacteria	bacterium	hypothetical protein DCC79_05805 [bacterium].	GCA_003576755.1
RKZ38698.1	TIR+TIR→ nSTAND1+BetaPropeller*→||<-?<-?||?→ ICP8OBfold→	nSTAND1+BetaPropeller	1240	DRQ49_13590	gammaproteobacteria	Gammaproteobacteria bacterium	hypothetical protein DRQ49_13590 [Gammaproteobacteria bacterium].	GCA_003646115.1
RKZ43202.1	nSTAND1+TM+BetaPropeller*→	nSTAND1+TM+BetaPropeller	1128	DRQ41_05855	gammaproteobacteria	Gammaproteobacteria bacterium	hypothetical protein DRQ41_05855, partial [Gammaproteobacteria bacterium].	GCA_003645175.1
RKZ45073.1	nSTAND1+TM+BetaPropeller*→||<-?<-ABC-ATPase	nSTAND1+TM+BetaPropeller	1431	DRQ41_01220	gammaproteobacteria	Gammaproteobacteria bacterium	hypothetical protein DRQ41_01220, partial [Gammaproteobacteria bacterium].	GCA_003645175.1
RKZ52679.1	<-TM<-?||?→?→ CASPASE+nSTAND1+TPR*→?→?→ XisI→	CASPASE+nSTAND1+TPR	990	DRR00_07525	gammaproteobacteria	Gammaproteobacteria bacterium	hypothetical protein DRR00_07525 [Gammaproteobacteria bacterium].	GCA_003645185.1
RKZ62359.1	TIR+DrHyd+TIR→?→?→ nSTAND1+BetaPropeller*→	nSTAND1+BetaPropeller	935	DRR08_06350	gammaproteobacteria	Gammaproteobacteria bacterium	hypothetical protein DRR08_06350, partial [Gammaproteobacteria bacterium].	GCA_003646135.1
RKZ80031.1	PKinase+SWACOS+GAF+SHELIX+HISKIN+REC→ nSTAND1*→	nSTAND1	253	DRR19_24185	gammaproteobacteria	Gammaproteobacteria bacterium	hypothetical protein DRR19_24185, partial [Gammaproteobacteria bacterium].	GCA_003646175.1
RLD63389.1	<-SIG+TPR||?→||<-?||TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+cNMP→?→ TIR+DrHyd→ nSTAND1+TM+BetaPropeller*→	nSTAND1+TM+BetaPropeller	1040	DRJ01_03910	bacteroidetes	Bacteroidetes bacterium	hypothetical protein DRJ01_03910 [Bacteroidetes bacterium].	GCA_003648455.1
RLE12060.1	wHTH-4stranded+TPRs+ACYC+CR-Kinase+nSTAND1+TM*→	wHTH-4stranded+TPRs+ACYC+CR-Kinase+nSTAND1+TM	1147	DRJ28_09685	actinobacteria	Actinobacteria bacterium	hypothetical protein DRJ28_09685, partial [Actinobacteria bacterium].	GCA_003648875.1
RLU96809.1	HTH+nSTAND1+TM+BetaPropeller*→ SIG+TM+TM+TM+TM+TM→?→ ABC-ATPase→	HTH+nSTAND1+TM+BetaPropeller	1311	CTZ27_17585	actinobacteria	Streptomyces griseocarneus	DNA-binding protein [Streptomyces griseocarneus].	GCA_003674045.1
RMD57402.1	nSTAND1+TM+BetaPropeller*→	nSTAND1+TM+BetaPropeller	733	D6828_03745	nitrospirae	Nitrospirae bacterium	hypothetical protein D6828_03745, partial [Nitrospirae bacterium].	GCA_003693935.1
RMF02938.1	nSTAND1+TM+FGS*→	nSTAND1+TM+FGS	996	D6768_07070	chloroflexi	Chloroflexi bacterium	hypothetical protein D6768_07070, partial [Chloroflexi bacterium].	GCA_003695455.1
RMF02990.1	nSTAND1+BetaPropeller*→	nSTAND1+BetaPropeller	1236	D6768_06945	chloroflexi	Chloroflexi bacterium	hypothetical protein D6768_06945, partial [Chloroflexi bacterium].	GCA_003695455.1
RMF76640.1	Pkinase+nSTAND1+TM+BetaPropeller*→	Pkinase+nSTAND1+TM+BetaPropeller	1222	D6737_19790	chloroflexi	Chloroflexi bacterium	hypothetical protein D6737_19790, partial [Chloroflexi bacterium].	GCA_003695675.1
RMH78629.1	SIG+Trypsin+BetaPropeller→||<-TM<-?||CASPASE+nSTAND1+TM*→	CASPASE+nSTAND1+TM	828	D6680_01360	cyanobacteria	Cyanobacteria bacterium J007	caspase family protein, partial [Cyanobacteria bacterium J007].	GCA_003695985.1

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RPH30586.1	TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+cNMP→?→ TIR+DrHyd→ nSTAND1+TM+PspA+BetaPropeller*→	nSTAND1+TM+PspA+BetaPropeller	1019	EHM93_15545	bacteroidetes	Bacteroidales bacterium	High-affinity carbon uptake protein Hat/HatR [Bacteroidales bacterium].	GCA_003818205.1
RPH58066.1	nSTAND1*→	nSTAND1	216	EHM81_10640	chloroflexi	Chloroflexi bacterium	ATP-binding protein, partial [Chloroflexi bacterium].	GCA_003818555.1
RPI91735.1	RRM→?→?→?→||<-?||?→ SIG+nSTAND1+TM*→	SIG+nSTAND1+TM	777	EHM40_14820	chloroflexi	Chloroflexi bacterium	ATP-binding protein, partial [Chloroflexi bacterium].	GCA_003820075.1
RPI98474.1	Pkinase+nSTAND1*→	Pkinase+nSTAND1	646	EHM39_07925	chloroflexi	Chloroflexi bacterium	serine/threonine protein kinase, partial [Chloroflexi bacterium].	GCA_003818635.1
RPJ24401.1	wHTH-4stranded+TPRs+ACYC+nSTAND1+BetaPropeller*→	wHTH-4stranded+TPRs+ACYC+nSTAND1+BetaPropeller	1323	EHM33_17965	chloroflexi	Chloroflexi bacterium	hypothetical protein EHM33_17965, partial [Chloroflexi bacterium].	GCA_003820175.1
RQW03303.1	TIR+DrHyd→ nSTAND1+TM+CHASE2+TM+TM+TM*→	nSTAND1+TM+CHASE2+TM+TM+TM	828	EH223_10290	bacteria	candidate division KSB1 bacterium	CHASE2 domain-containing protein [candidate division KSB1 bacterium].	GCA_003854975.1
RYD57998.1	TIR→ nSTAND1+BetaPropeller*→?→ Cluster106_3clades→	nSTAND1+BetaPropeller	1019	EOP56_06920	bacteroidetes	Sphingobacteriales bacterium	hypothetical protein EOP56_06920 [Sphingobacteriales bacterium].	GCA_004144175.1
RZO55510.1	TIR+DrHyd+TIR→ nSTAND1+BetaPropeller*→	nSTAND1+BetaPropeller	1385	EVA72_06320	verrucomicrobia	Verrucomicrobia subdivision 3 bacterium	hypothetical protein EVA72_06320 [Verrucomicrobia subdivision 3 bacterium].	GCA_004213515.1
SBO96141.1	ABC-ATPase→ ABC-ATPase→?→||<-?||?→ nSTAND1+BetaPropeller*→?→ SIG+HOP2→?→ AAA+TPR→	nSTAND1+BetaPropeller	1263	BN4615_P5657	actinobacteria	Nonomuraea gerenzanensis	High-affinity carbon uptake protein Hat/HatR [Nonomuraea gerenzanensis].	-
SBO97731.1	ABhydrolase→?→ SIG+nSTAND1+TM+BetaPropeller*→||<-?||?→||<-?<-?<-SIG+TM+TM+TM+TM+TM<-SIG+TM+TM+TM+TM+TM	SIG+nSTAND1+TM+BetaPropeller	1766	BN4615_P7247	actinobacteria	Nonomuraea gerenzanensis	High-affinity carbon uptake protein Hat/HatR [Nonomuraea gerenzanensis].	-
SBV24853.1	HTH+nSTAND1+TM+BetaPropeller*→||<-?<-?<-?||?→ tRNA→||<-?<-TM+TM+TM+TM+TM+TM<-ABC-ATPase	HTH+nSTAND1+TM+BetaPropeller	1258	GA0070620_0295	actinobacteria	Micromonospora krabiensis	WD40 repeat [Micromonospora krabiensis].	GCA_900091425.1
SCG38369.1	SIG+nSTAND1+TM+BetaPropeller*→	SIG+nSTAND1+TM+BetaPropeller	1396	GA0070614_0509	actinobacteria	Micromonospora coxensis	WD40 repeat [Micromonospora coxensis].	GCA_900090295.1
SEF93234.1	<-SIG+HOP2<-?<-?||?→ nSTAND1+BetaPropeller*→||<-?<-?<-p450	nSTAND1+BetaPropeller	1224	SAMN05444920_1011053	actinobacteria	Nonomuraea solani	WD40 repeat [Nonomuraea solani].	GCA_900108335.1
SMD22401.1	nSTAND1+BetaPropeller*→	nSTAND1+BetaPropeller	1243	SAMN05661093_07396	actinobacteria	Kibdelosporangium aridum	WD40 repeat [Kibdelosporangium aridum].	GCA_900176515.1
SPL89441.1	nSTAND1+BetaPropeller*→	nSTAND1+BetaPropeller	1231	KIS93_02102	actinobacteria	Actinomadura parvosata subsp. kistnae	High-affinity carbon uptake protein Hat/HatR [Actinomadura parvosata subsp. kistnae].	GCA_900323885.1
TAH51625.1	wHTH-4stranded+TPRs+nSTAND1+BetaPropeller*→	wHTH-4stranded+TPRs+nSTAND1+BetaPropeller	1534	EYC68_09685	chloroflexi	Chloroflexi bacterium	hypothetical protein EYC68_09685 [Chloroflexi bacterium].	GCA_004295045.1

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TCS45832.1	nSTAND1+BetaPropeller*→	nSTAND1+BetaPropeller	1284	EV585_125129	actinobacteria	Streptomyces sp. BK335	WD-40 repeat-containing protein [Streptomyces sp. BK335].	GCA_004343515.1
TDI65915.1	TIR+DrHyd→ nSTAND1+TM+BetaPropeller*→	nSTAND1+TM+BetaPropeller	1178	E2O88_09730	bacteroidetes	Bacteroidetes bacterium	hypothetical protein E2O88_09730 [Bacteroidetes bacterium].	GCA_004356345.1
TDX54622.1	nSTAND1+TM+BetaPropeller*→	nSTAND1+TM+BetaPropeller	1232	CLW03_1390	actinobacteria	Streptomyces sp. 25	WD40 repeat protein [Streptomyces sp. 25].	GCA_004365455.1
TFG73542.1	TIR→ nSTAND1*→	nSTAND1	184	E4H26_09660	bacteroidetes	Flavobacteriales bacterium	hypothetical protein E4H26_09660, partial [Flavobacteriales bacterium].	GCA_004525075.1
TLU54259.1	TIR+DrHyd→ nSTAND1+TPR*→	nSTAND1+TPR	934	FDX18_11420	chlorobi	Chlorobium sp.	hypothetical protein FDX18_11420 [Chlorobium sp.].	GCA_005843805.1
TMA13290.1	SLATT→||<-?||TIR→ nSTAND1+TM+TM+TM*→	nSTAND1+TM+TM+TM	677	E6J89_01820	deltaproteobacteria	Deltaproteobacteria bacterium	ATP-binding protein, partial [Deltaproteobacteria bacterium].	GCA_005878685.1
TMC17178.1	TIR+nSTAND1+TM+Beta-helix*→	TIR+nSTAND1+TM+Beta-helix	948	E6J34_19025	chloroflexi	Chloroflexi bacterium	TIR domain-containing protein, partial [Chloroflexi bacterium].	GCA_005879655.1
TMC23062.1	nSTAND1+TM+Beta-helix→ Pkinase+TIR+nSTAND1+TM+Beta-helix*→?→||<-?<-?<-?<-?<-ABhydrolase	Pkinase+TIR+nSTAND1+TM+Beta-helix	1380	E6J34_04260	chloroflexi	Chloroflexi bacterium	TIR domain-containing protein [Chloroflexi bacterium].	GCA_005879655.1
TMD76903.1	TIR+nSTAND1+TM*→	TIR+nSTAND1+TM	914	E6I97_10225	chloroflexi	Chloroflexi bacterium	TIR domain-containing protein [Chloroflexi bacterium].	GCA_005880275.1
TMD99845.1	TIR+nSTAND1+TM*→	TIR+nSTAND1+TM	908	E6I80_27410	chloroflexi	Chloroflexi bacterium	hypothetical protein E6I80_27410 [Chloroflexi bacterium].	GCA_005881495.1
TME05606.1	TIR+nSTAND1+TM*→	TIR+nSTAND1+TM	884	E6I80_16835	chloroflexi	Chloroflexi bacterium	TIR domain-containing protein, partial [Chloroflexi bacterium].	GCA_005881495.1
TMH35459.1	TIR→ TIR+DrHyd→ nSTAND1+TM+TPR*→?→||<-?<-ABC-ATPase||?→?→ Cluster106_3clades→	nSTAND1+TM+TPR	759	E6H66_07570	betaproteobacteria	Betaproteobacteria bacterium	ATP-binding protein [Betaproteobacteria bacterium].	GCA_005882995.1
TNF40174.1	TIR→ nSTAND1+TM+prokYEATS*→	nSTAND1+TM+prokYEATS	681	EP310_09390	bacteroidetes	Bacteroidetes bacterium	hypothetical protein EP310_09390 [Bacteroidetes bacterium].	GCA_006226805.1
TQM00650.1	nSTAND1+BetaPropeller*→	nSTAND1+BetaPropeller	1393	FB559_6366	actinobacteria	Actinoallomurus bryophytorum	WD40 repeat protein [Actinoallomurus bryophytorum].	GCA_006716425.1
VFJ52061.1	nSTAND1+BetaPropeller*→?→?→ ABC-ATPase→	nSTAND1+BetaPropeller	1305	BECKFM1743C_GA0114222_101051	gammaproteobacteria	Candidatus Kentron sp. FM	WD40 repeat [Candidatus Kentron sp. FM].	-
VFJ73513.1	TIR→ MoxR→?→ TIR→ nSTAND1+BetaPropeller*→?→ ABC-ATPase→	nSTAND1+BetaPropeller	1354	BECKFW1821C_GA0114237_105215	gammaproteobacteria	Candidatus Kentron sp. FW	WD40 repeat [Candidatus Kentron sp. FW].	-
WP_006105558.1	CASPASE+nSTAND1+BetaPropeller*→	CASPASE+nSTAND1+BetaPropeller	1249	MC7420_RS35880	cyanobacteria	Coleofasciculus chthonoplastes	caspase family protein [Coleofasciculus chthonoplastes].	GCF_000155555.1
WP_006458142.1	CASPASE+CASPASE+nSTAND1+BetaPropeller*→	CASPASE+CASPASE+nSTAND1+BetaPropeller	1660	S7335_RS22355	cyanobacteria	Synechococcus sp. PCC 7335	caspase family protein [Synechococcus sp. PCC 7335].	GCF_000155595.1

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WP_007305744.1	<-Trypco1||?→ CASPASE+nSTAND1*→	CASPASE+nSTAND1	961	CWATDRAFT_RS14705	cyanobacteria	Crocosphaera watsonii	pentapeptide repeat-containing protein [Crocosphaera watsonii].	GCF_000167195.1
WP_008178364.1	FAD-NAD-dep-oxidoreductase→||<-Trypco1||CASPASE+nSTAND1*→	CASPASE+nSTAND1	1005	BI334_RS09780	cyanobacteria	Moorea producens	caspase family protein [Moorea producens].	GCF_000211815.1
WP_011141629.1	<-SIG+Metallopeptidase||?→||<-?<-?||CASPASE+CASPASE+nSTAND1+BetaPropeller*→||<-?<-?||?→?→||<-?<-?||DinB_2+FGS→	CASPASE+CASPASE+nSTAND1+BetaPropeller	1730	GLL_RS08460	cyanobacteria	Gloeobacter violaceus	caspase family protein [Gloeobacter violaceus].	GCF_000011385.1
WP_011142241.1	ABhydrolase→||<-?<-?||CASPASE+CASPASE+nSTAND1+BetaPropeller*→?→?→?→?→ ABC-ATPase→	CASPASE+CASPASE+nSTAND1+BetaPropeller	1721	GLL_RS11610	cyanobacteria	Gloeobacter violaceus	caspase family protein [Gloeobacter violaceus].	GCF_000011385.1
WP_011316937.1	CASPASE+CASPASE+nSTAND1+BetaPropeller*→	CASPASE+CASPASE+nSTAND1+BetaPropeller	1686	AVA_RS00195	cyanobacteria	Nostocaceae	MULTISPECIES: caspase family protein [Nostocaceae].	GCF_000204075.1
WP_011318971.1	CASPASE+NACHT+BetaPropeller→ CASPASE+nSTAND1+BetaPropeller*→?→ RVe+MutnpC→	CASPASE+nSTAND1+BetaPropeller	1240	AVA_RS29445	cyanobacteria	Trichormus variabilis	caspase family protein [Trichormus variabilis].	GCF_000204075.1
WP_011319818.1	<-REC<-SIG+Trypsin+PDZ<-HAD||?→||<-HSP20||?→ CASPASE+nSTAND1+BetaPropeller→ CASPASE+CASPASE+nSTAND1+BetaPropeller*→ PSE→||<-?<-?<-?||?→||<-?||?→ Na+ORC-AAA→	CASPASE+CASPASE+nSTAND1+BetaPropeller	1760	AVA_RS15560	cyanobacteria	Nostocaceae	MULTISPECIES: caspase family protein [Nostocaceae].	GCF_000204075.1
WP_012163883.1	CASPASE+CASPASE+nSTAND1+BetaPropeller*→	CASPASE+CASPASE+nSTAND1+BetaPropeller	1703	AM1_RS15835	cyanobacteria	Acaryochloris marina	caspase family protein [Acaryochloris marina].	GCF_000018105.1
WP_012165630.1	Redoxin→ CASPASE+nSTAND1+TM*→	CASPASE+nSTAND1+TM	1013	AM1_RS24605	cyanobacteria	Acaryochloris marina	caspase family protein [Acaryochloris marina].	GCF_000018105.1
WP_015103078.1	HTH+nSTAND1+TM+BetaPropeller*→||<-?<-PSE||NACHT→?→ NACHT→	HTH+nSTAND1+TM+BetaPropeller	1307	BN6_RS27490	actinobacteria	Saccharothrix espanaensis	helix-turn-helix domain-containing protein [Saccharothrix espanaensis].	GCF_000328705.1
WP_015104506.1	nSTAND1+TM+BetaPropeller*→	nSTAND1+TM+BetaPropeller	969	BN6_RS34550	actinobacteria	Saccharothrix espanaensis	hypothetical protein [Saccharothrix espanaensis].	GCF_000328705.1
WP_015118666.1	EACC2+CASPASE+nSTAND1+BetaPropeller*→||<-PSE<-?<-?||?→?→?→ Uma2→	EACC2+CASPASE+nSTAND1+BetaPropeller	1548	RIV7116_RS12515	cyanobacteria	Rivularia sp. PCC 7116	WD40 repeat domain-containing protein [Rivularia sp. PCC 7116].	GCF_000316665.1
WP_015158653.1	nSTAND1+BetaPropeller*→	nSTAND1+BetaPropeller	1104	CHA6605_RS06215	cyanobacteria	Chamaesiphon minutus	WD40 repeat domain-containing protein [Chamaesiphon minutus].	GCF_000317145.1
WP_015205337.1	CASPASE+CASPASE+nSTAND1+BetaPropeller*→	CASPASE+CASPASE+nSTAND1+BetaPropeller	1759	CRI9333_RS21890	cyanobacteria	Crinalium epipsammum	caspase family protein [Crinalium epipsammum].	GCF_000317495.1
WP_015210065.1	<-Trypco1||CASPASE+nSTAND1+TM*→||<-?||?→?→||<-?||Cluster108_2clades→	CASPASE+nSTAND1+TM	895	CYLST_RS22615	cyanobacteria	Cylindrospermum stagnale	pentapeptide repeat-containing protein [Cylindrospermum stagnale].	GCF_000317535.1
WP_015691683.1	nSTAND1+TM+BetaPropeller*→	nSTAND1+TM+BetaPropeller	1119	SGRA_RS05810	bacteroidetes	Saprospira grandis	hypothetical protein [Saprospira grandis].	GCF_000250635.1
WP_015724204.1	TIR+DrHyd+TIR→ nSTAND1+TM+Ntox24+PDZ*→	nSTAND1+TM+Ntox24+PDZ	1380	DESPR_RS17200	deltaproteobacteria	Desulfobulbus propionicus	YD repeat-containing protein [Desulfobulbus propionicus].	GCF_000186885.1
WP_015795480.1	<-ABhydrolase<-?||HTH+nSTAND1+TM+BetaPropeller*→||<-nSTAND1	HTH+nSTAND1+TM+BetaPropeller	1334	CACI_RS46450	actinobacteria	Catenulispora acidiphila	helix-turn-helix domain-containing protein [Catenulispora acidiphila].	GCF_000024025.1
WP_016952361.1	ABC-ATPase→ Cluster158_2clades→ SIG+TM+TM+TM+TM+TM→||<-Trypco1||CASPASE+nSTAND1+TM+BetaPropeller*→||<-?<-TM+HAMP+GAF+GAF+GAF+GAF+MCPsignal<-?<-REC	CASPASE+nSTAND1+TM+BetaPropeller	1622	ANA7108_RS0118800	cyanobacteria	Anabaena sp. PCC 7108	caspase family protein [Anabaena sp. PCC 7108].	GCF_000332135.1

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WP_016953798.1	EACC2+CASPASE+nSTAND1+BetaPropeller*→?→?→?→?→?→ ParA-Soj-PloopNTPase→ ParB→	EACC2+CASPASE+nSTAND1+BetaPropeller	1578	ANA7108_RS0126175	cyanobacteria	Anabaena sp. PCC 7108	CHAT domain-containing protein [Anabaena sp. PCC 7108].	GCF_000332135.1
WP_017315667.1	CASPASE→ nSTAND1+BetaPropeller→ nSTAND1*→	nSTAND1	312	MAS10914_RS0109350	cyanobacteria	Mastigocladopsis repens	ATP-binding protein [Mastigocladopsis repens].	GCF_000315565.1
WP_017324258.1	ABhydrolase→||<-Uma2<-Uma2||TIR+TIR→ SIG+nSTAND1+TM+BetaPropeller*→||<-?||?→?→ ABC-ATPase→	SIG+nSTAND1+TM+BetaPropeller	1203	SYN7336_RS02075	cyanobacteria	Synechococcus sp. PCC 7336	hypothetical protein [Synechococcus sp. PCC 7336].	GCF_000332275.1
WP_017652542.1	SIG+TM+TM+TM+TM+TM→?→||<-?<-?||?→||<-PSE||CASPASE+CASPASE+nSTAND1+BetaPropeller*→	CASPASE+CASPASE+nSTAND1+BetaPropeller	1714	MIC7126_RS0107600	cyanobacteria	Fortiea contorta	caspase family protein [Fortiea contorta].	GCF_000332295.1
WP_017712679.1	Pkinase+TIR+DrHyd→||<-?<-?<-?||?→?→ CASPASE+nSTAND1+BetaPropeller*→	CASPASE+nSTAND1+BetaPropeller	1866	PRO9006_RS0111975	cyanobacteria	Prochlorothrix hollandica	hypothetical protein [Prochlorothrix hollandica].	GCF_000332315.1
WP_017715273.1	<-TM<-?||CASPASE+nSTAND1+TM+BetaPropeller*→?→ PSE→||<-?<-?<-ABhydrolase<-?<-ENOYCOADEHYD	CASPASE+nSTAND1+TM+BetaPropeller	1430	OSC10802_RS38460	cyanobacteria	Oscillatoria sp. PCC 10802	caspase family protein [Oscillatoria sp. PCC 10802].	GCF_000332335.1
WP_017717001.1	<-ACET<-?||?→||<-?||?→?→ EACC2+CASPASE+nSTAND1*→||<-?||?→ PSE→||<-?||?→?→||<-Pkinase+TPR	EACC2+CASPASE+nSTAND1	829	OSC10802_RS39855	cyanobacteria	Oscillatoria sp. PCC 10802	CHAT domain-containing protein [Oscillatoria sp. PCC 10802].	GCF_000332335.1
WP_017717209.1	CASPASE+CASPASE+nSTAND1+BetaPropeller*→	CASPASE+CASPASE+nSTAND1+BetaPropeller	1766	OSC10802_RS0113050	cyanobacteria	Oscillatoria sp. PCC 10802	caspase family protein [Oscillatoria sp. PCC 10802].	GCF_000332335.1
WP_017720241.1	<-S4+PSYN<-TM<-?<-TPR+TPR+TPR+CASPASE<-?<-TPR+TPR+TPR+TPR||?→ EACC2+CASPASE+nSTAND1+IES1*→?→||<-?<-SIG+Trypsin<-?<-?||?→||<-SIG+Pentapeptide	EACC2+CASPASE+nSTAND1+IES1	1048	OSC10802_RS42290	cyanobacteria	Oscillatoria sp. PCC 10802	DUF1822 family protein [Oscillatoria sp. PCC 10802].	GCF_000332335.1
WP_018342883.1	MED15→ TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+cNMP→ TIR→ nSTAND1+BetaPropeller*→	nSTAND1+BetaPropeller	1044	A3EE_RS0107780	bacteroidetes	Cytophaga aurantiaca	hypothetical protein [Cytophaga aurantiaca].	GCF_000379725.1
WP_018504462.1	nSTAND1+BetaPropeller*→	nSTAND1+BetaPropeller	1541	B056_RS0124325	actinobacteria	Frankia discariae	hypothetical protein [Frankia discariae].	GCF_000373365.1
WP_019487727.1	<-AAA+TPR<-?<-?<-?<-PSE||?→?→?→ nSTAND1+Pentapeptide*→	nSTAND1+Pentapeptide	725	OSCIL6407_RS0123130	cyanobacteria	Kamptonema formosum	pentapeptide repeat-containing protein [Kamptonema formosum].	GCF_000332155.1
WP_019492639.1	CASPASE+CASPASE+nSTAND1+BetaPropeller*→	CASPASE+CASPASE+nSTAND1+BetaPropeller	1697	CAL7103_RS0122950	cyanobacteria	Calothrix sp. PCC 7103	caspase family protein [Calothrix sp. PCC 7103].	GCF_000331305.1
WP_019493356.1	<-REC<-PKinase+SWACOS+GAF+SHELIX+HISKIN+REC||Pentapeptide→ CASPASE+nSTAND1+TM+BetaPropeller*→||<-?<-?<-?<-PSE||MNS→	CASPASE+nSTAND1+TM+BetaPropeller	1446	CAL7103_RS0126645	cyanobacteria	Calothrix sp. PCC 7103	caspase family protein [Calothrix sp. PCC 7103].	GCF_000331305.1
WP_023071899.1	<-Trypco1||CASPASE+nSTAND1+Pentapeptide*→	CASPASE+nSTAND1+Pentapeptide	969	N836_RS48210	cyanobacteria	Leptolyngbya sp. Heron Island J	pentapeptide repeat-containing protein [Leptolyngbya sp. Heron Island J].	GCF_000482245.1
WP_023173850.1	CASPASE+CASPASE+nSTAND1+BetaPropeller*→	CASPASE+CASPASE+nSTAND1+BetaPropeller	1707	GKIL_RS11810	cyanobacteria	Gloeobacter kilaueensis	caspase family protein [Gloeobacter kilaueensis].	GCF_000484535.1
WP_026073174.1	CASPASE+nSTAND1+BetaPropeller→||<-?<-?||SIG+HTH+ACYC+APATPase+BetaPropeller→?→ nSTAND1+BetaPropeller*→||<-?<-?||?→||<-Cluster510_2clades	nSTAND1+BetaPropeller	1233	LEPTO7104_RS0128640	cyanobacteria	Nodosilinea nodulosa	WD40 repeat domain-containing protein [Nodosilinea nodulosa].	GCF_000309385.1
WP_026316665.1	nSTAND1+BetaPropeller*→||<-?<-?||?→?→||<-?<-AraC-HTH+AraC-HTH	nSTAND1+BetaPropeller	1263	C503_RS0124640	actinobacteria	Actinokineospora enzanensis	hypothetical protein [Actinokineospora enzanensis].	GCF_000374445.1
WP_026735835.1	<-Trypco1||PASE+nSTAND1+TM+Pentapeptide*→	PASE+nSTAND1+TM+Pentapeptide	969	FIS9605_RS0129725	cyanobacteria	Fischerella sp. PCC 9605	pentapeptide repeat-containing protein [Fischerella sp. PCC 9605].	GCF_000517105.1
WP_027844322.1	CASPASE+CASPASE+nSTAND1+BetaPropeller*→?→?→?→?→ XisI→	CASPASE+CASPASE+nSTAND1+BetaPropeller	1804	BC008_RS42445	cyanobacteria	Mastigocoleus testarum	caspase family protein [Mastigocoleus testarum].	GCF_001456025.1

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WP_027930056.1	ACT→||<-ICLR-HTH<-ABhydrolase||Pkinase+TPR→ EACC1→ CASPASE+nSTAND1+TM+BetaPropeller*→	CASPASE+nSTAND1+TM+BetaPropeller	1457	AMYTH_RS0109125	actinobacteria	Amycolatopsis thermoflava	caspase family protein [Amycolatopsis thermoflava].	GCF_000473265.1
WP_028922565.1	ABhydrolase→ ABhydrolase→?→ nSTAND1+BetaPropeller+BetaPropeller*→ nSTAND1+TM+TPR→	nSTAND1+BetaPropeller+BetaPropeller	1251	N912_RS60190	actinobacteria	Pseudonocardia acaciae	hypothetical protein [Pseudonocardia acaciae].	GCF_000620785.1
WP_035149788.1	<-Trypco1||CASPASE+nSTAND1+TM*→	CASPASE+nSTAND1+TM	1012	IJ00_RS02610	cyanobacteria	Calothrix sp. 336/3	pentapeptide repeat-containing protein [Calothrix sp. 336/3].	GCF_000734895.2
WP_035956063.1	SWC3+CASPASE+nSTAND1+TM+BetaPropeller*→ TIR+nSTAND1+BetaPropeller→	SWC3+CASPASE+nSTAND1+TM+BetaPropeller	1650	FREUN1FDRAFT_RS33550	actinobacteria	Frankia sp. EUN1f	hypothetical protein [Frankia sp. EUN1f].	GCF_000177675.1
WP_038089860.1	EACC2+CASPASE+nSTAND1+BetaPropeller*→	EACC2+CASPASE+nSTAND1+BetaPropeller	1523	HC643_RS24730	cyanobacteria	Tolypothrix bouteillei	CHAT domain-containing protein [Tolypothrix bouteillei].	GCF_000760695.4
WP_038091175.1	EACC2+CASPASE+nSTAND1+BetaPropeller*→	EACC2+CASPASE+nSTAND1+BetaPropeller	1527	bacteria>cyanobacteria	Tolypothrix bouteillei	-	740250270	-
WP_042222922.1	nSTAND1+BetaPropeller*→?→?→ REC→ REC→||<-?<-?<-REC	nSTAND1+BetaPropeller	1227	KALB_RS34215	actinobacteria	Kutzneria albida	hypothetical protein [Kutzneria albida].	GCF_000525635.1
WP_044290980.1	Pentapeptide→ CASPASE+nSTAND1+TM*→?→ BetaPropeller→	CASPASE+nSTAND1+TM	817	RIV7116_RS15845	cyanobacteria	Rivularia sp. PCC 7116	caspase family protein [Rivularia sp. PCC 7116].	GCF_000316665.1
WP_045225177.1	TIR+DrHyd→ nSTAND1+FGS*→	nSTAND1+FGS	817	EK23_RS09735	gammaproteobacteria	Methyloterricola oryzae	SUMF1/EgtB/PvdO family nonheme iron enzyme [Methyloterricola oryzae].	GCF_000934725.1
WP_045872156.1	nSTAND1+BetaPropeller*→||<-?<-?||CASPASE→||<-?||CASPASE→||<-?<-MNS	nSTAND1+BetaPropeller	1200	FDUTEX481_RS24680	cyanobacteria	Nostocales	MULTISPECIES: WD40 repeat domain-containing protein [Nostocales].	GCF_002368275.1
WP_046725303.1	<-ABhydrolase<-?||?→ nSTAND1+BetaPropeller*→||<-?<-SIG+TM+TM+TM+TM+TM<-SIG+TM+TM+TM+TM+TM||TRPR-HTH+PBPI→||<-TRPR-HTH+PBPI||?→ SIG+TM+TM+TM+TM+TM→	nSTAND1+BetaPropeller	1285	SXIM_RS26680	actinobacteria	Streptomyces xiamenensis	PD40 domain-containing protein [Streptomyces xiamenensis].	GCF_000993785.3
WP_048709317.1	SIG+TIR→ TIR+nSTAND1+RHS+RHS*→ PSE→?→?→?→||<-?||?→ TIR→	TIR+nSTAND1+RHS+RHS	1623	HMMV_RS27495	alphaproteobacteria	Microvirga massiliensis	TIR domain-containing protein [Microvirga massiliensis].	GCF_902385745.1
WP_049564506.1	nSTAND1+BetaPropeller*→	nSTAND1+BetaPropeller	1250	ADY01_RS01750	actinobacteria	Streptomyces sp. SBT349	hypothetical protein [Streptomyces sp. SBT349].	GCF_001083795.1
WP_049565443.1	REC→?→?→?→||<-?||?→?→ SIG+nSTAND1+BetaPropeller*→?→?→||<-?<-?<-?<-ABC-ATPase	SIG+nSTAND1+BetaPropeller	1425	ADY59_RS23235	actinobacteria	Nonomuraea sp. SBT364	hypothetical protein [Nonomuraea sp. SBT364].	GCF_001083785.1
WP_049641845.1	Patatin→?→?→ nSTAND1+TM+TPR*→||<-?||?→||<-?<-Cluster157_3clades<-FAD-NAD-dep-oxidoreductase<-?<-Cluster428_2clades	nSTAND1+TM+TPR	945	AIOL_RS04910	alphaproteobacteria	Candidatus Rhodobacter lobularis	hypothetical protein [Candidatus Rhodobacter lobularis].	GCF_001078595.1
WP_050045050.1	CASPASE+nSTAND1+Pentapeptide+Pentapeptide*→	CASPASE+nSTAND1+Pentapeptide+Pentapeptide	1134	bacteria>cyanobacteria	Tolypothrix bouteillei	-	910240059	-
WP_050366129.1	nSTAND1+TM+BetaPropeller*→	nSTAND1+TM+BetaPropeller	1266	HS99_RS15320	actinobacteria	Kitasatospora aureofaciens	WD40 repeat domain-containing protein [Kitasatospora aureofaciens].	GCF_002082605.1
WP_051169531.1	SIG+TPR→ EACC1→ CASPASE+nSTAND1+TM+BetaPropeller*→	CASPASE+nSTAND1+TM+BetaPropeller	1539	ON19_RS32425	actinobacteria	Nocardia abscessus	caspase family protein [Nocardia abscessus].	GCF_000308455.1
WP_051292932.1	TRPR-HTH+PBPI→?→ TIR+DrHyd→ nSTAND1+BetaPropeller*→	nSTAND1+BetaPropeller	1067	A37S_RS24150	bacteroidetes	Olivibacter sitiensis	hypothetical protein [Olivibacter sitiensis].	GCF_000427965.1
WP_051675149.1	TRPR-HTH+PBPI→||<-?<-?<-?||nSTAND1+BetaPropeller*→||<-?<-?<-?||ABhydrolase→	nSTAND1+BetaPropeller	1279	N545_RS24235	actinobacteria	Streptomyces sp. URHA0041	PD40 domain-containing protein [Streptomyces sp. URHA0041].	GCF_000701325.1

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WP_051737318.1	EACC1→ CASPASE+nSTAND1+TM+BetaPropeller*→||<-TM	CASPASE+nSTAND1+TM+BetaPropeller	1475	OQ00_RS16195	actinobacteria	Pseudonocardia autotrophica	WD40 repeat domain-containing protein [Pseudonocardia autotrophica].	GCF_000717175.1
WP_051766655.1	CHTH+nSTAND1+BetaPropeller*→	CHTH+nSTAND1+BetaPropeller	1272	OQ01_RS52670	actinobacteria	Saccharothrix syringae	helix-turn-helix domain-containing protein [Saccharothrix syringae].	GCF_009498035.1
WP_051945655.1	TIR+TM+BetaPropeller→||<-SIG+TIR<-?<-nSTAND1+TM<-TIR||TIR+DrHyd→ nSTAND1*→||<-?<-?||TIR→||<-TIR+nSTAND1	nSTAND1	1322	BV106_RS35440	verrucomicrobia	Verrucomicrobium sp. BvORR106	ATP-binding protein [Verrucomicrobium sp. BvORR106].	GCF_000739655.1
WP_052288432.1	ABhydrolase→?→?→||<-?||?→ nSTAND1+BetaPropeller*→||<-?||ABC-ATPase→ TM+TM+TM+TM+TM+TM→?→?→ TM+TM+TM→	nSTAND1+BetaPropeller	1340	DYY88_RS24230	bacteria	Cyanobacteria	MULTISPECIES: hypothetical protein [Cyanobacteria].	GCF_000817775.2
WP_052335365.1	<-TM<-?||CASPASE+nSTAND1+TM+BetaPropeller*→ BetaPropeller→ PSE→?→?→||<-?<-RRM||ParA-Soj-PloopNTPase→ ParB→	CASPASE+nSTAND1+TM+BetaPropeller	1092	FDU-TEX481_RS45850	cyanobacteria	Tolypothrix sp. PCC 7601	caspase family protein [Tolypothrix sp. PCC 7601].	GCF_000300115.1
WP_052335392.1	<-TM<-?||CASPASE+nSTAND1+Trypsin→*?*→ *CASPASE+nSTAND1+BetaPropeller+BetaPropeller*→ BetaPropeller→	CASPASE+nSTAND1+Trypsin	1348	FDU-TEX481_RS40400	cyanobacteria	Nostocales	MULTISPECIES: caspase family protein [Nostocales].	GCF_001548455.1
WP_052335393.1	CASPASE+nSTAND1+Trypsin*→	CASPASE+nSTAND1+Trypsin	986	FDU-TEX481_RS33325	cyanobacteria	Nostocales	MULTISPECIES: trypsin-like peptidase domain-containing protein [Nostocales].	GCF_001548455.1
WP_052490005.1	EAD4+nSTAND1+BetaPropeller*→||<-pPIWI+MID+RNaseH<-pPIWI+DnaA-AAA+AAA<-pPIWI	EAD4+nSTAND1+BetaPropeller	1298	SD81_RS16770	cyanobacteria	Tolypothrix campylonemoides	AAA family ATPase [Tolypothrix campylonemoides].	GCF_000828075.3
WP_052490177.1	ParA-Soj-PloopNTPase→||<-?<-?<-?||PSE→||<-?||nSTAND1*→ PSE→ BetaPropeller→	nSTAND1	394	SD81_RS06920	cyanobacteria	Tolypothrix campylonemoides	hypothetical protein [Tolypothrix campylonemoides].	GCF_000828075.3
WP_052490698.1	<-TM<-?||CASPASE+nSTAND1+BetaPropeller*→?→?→||<-?<-?<-PSE<-PSE||?→?→ TPR+CASPASE→	CASPASE+nSTAND1+BetaPropeller	889	SD81_RS38450	cyanobacteria	Tolypothrix campylonemoides	caspase family protein [Tolypothrix campylonemoides].	GCF_000828075.3
WP_052508296.1	CASPASE→ nSTAND1+TM*→	nSTAND1+TM	800	SP67_RS33610	cyanobacteria	Mastigocladus laminosus	pentapeptide repeat-containing protein [Mastigocladus laminosus].	GCF_000934435.1
WP_052596711.1	<-ABhydrolase||?→ nSTAND1+TM+BetaPropeller*→	nSTAND1+TM+BetaPropeller	1134	CG11_RS12640	bacteroidetes	Aureispira sp. CCB-QB1	hypothetical protein [Aureispira sp. CCB-QB1].	GCF_000724545.1
WP_052668847.1	wHTH-4stranded+TPRs+nSTAND1+BetaPropeller*→||<-?||?→?→?→?→||<-ABhydrolase<-TPR	wHTH-4stranded+TPRs+nSTAND1+BetaPropeller	1431	NITAL_RS24320	actinobacteria	Nitriliruptor alkaliphilus	hypothetical protein [Nitriliruptor alkaliphilus].	GCF_000969705.1
WP_052691807.1	TIR→ nSTAND1+TM+TM+TM+TM+TM*→	nSTAND1+TM+TM+TM+TM+TM	926	K380_RS22645	gammaproteobacteria	Cellvibrionaceae bacterium Bs12	RDD family protein [Cellvibrionaceae bacterium Bs12].	GCF_000966245.1
WP_053662778.1	<-Pkinase+PASTA||?→ PSE→?→ nSTAND1+BetaPropeller*→	nSTAND1+BetaPropeller	1284	ADK64_RS26775	actinobacteria	Streptomyces sp. MMG1121	hypothetical protein [Streptomyces sp. MMG1121].	GCF_001280015.1
WP_054153119.1	TIR→ nSTAND1+TM+TM+TM+TM+TM*→?→?→||<-?||?→||<-Na+ORC-AAA<-?||ParA-Soj-PloopNTPase→	nSTAND1+TM+TM+TM+TM+TM	1122	D621_RS07050	betaproteobacteria	beta proteobacterium AAP51	RDD family protein [beta proteobacterium AAP51].	GCF_001295905.1
WP_054290262.1	<-p450<-?<-ABC-ATPase||?→||<-AraC-HTH+AraC-HTH||PSE→||<-?||nSTAND1+TM+BetaPropeller*→ REC→||<-?<-?||?→||<-?<-REC	nSTAND1+TM+BetaPropeller	960	AOZ06_RS16850	actinobacteria	Kibdelosporangium phytohabitans	PD40 domain-containing protein [Kibdelosporangium phytohabitans].	GCF_001302585.1
WP_055568262.1	nSTAND1+BetaPropeller*→	nSTAND1+BetaPropeller	1173	AOK03_RS28690	actinobacteria	Streptomyces atriruber	hypothetical protein [Streptomyces atriruber].	GCF_001418325.1

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WP_057232519.1	nSTAND1+BetaPropeller*→?→||<-ABhydrolase	nSTAND1+BetaPropeller	1319	ASC99_RS15845	actinobacteria	unclassified Kitasatospora	MULTISPECIES: hypothetical protein [unclassified Kitasatospora].	GCF_001424875.1
WP_058184087.1	EAD10+nSTAND1+TM+BetaPropeller*→ CASPASE→	EAD10+nSTAND1+TM+BetaPropeller	1369	BC008_RS28055	cyanobacteria	Mastigocoleus testarum	WD40 repeat domain-containing protein [Mastigocoleus testarum].	GCF_001456025.1
WP_058883925.1	<-REC<-?<-?||CASPASE+nSTAND1+BetaPropeller*→	CASPASE+nSTAND1+BetaPropeller	1732	AVR62_RS18820	cyanobacteria	Oscillatoriales cyanobacterium MTP1	PD40 domain-containing protein [Oscillatoriales cyanobacterium MTP1].	GCF_001482745.2
WP_058941697.1	ABhydrolase→?→ nSTAND1+BetaPropeller*→||<-?||?→ ABhydrolase→	nSTAND1+BetaPropeller	1281	ATE80_RS09355	actinobacteria	Streptomyces kanasensis	WD40 repeat domain-containing protein [Streptomyces kanasensis].	GCF_001484625.1
WP_062291516.1	RVe+MutnpC→?→?→||<-TM<-?||CASPASE+nSTAND1+TM*→?→||<-?||?→?→?→?→ REC→	CASPASE+nSTAND1+TM	853	ACX27_RS09860	cyanobacteria	Nostoc piscinale	caspase family protein [Nostoc piscinale].	GCF_001298445.1
WP_062716636.1	nSTAND1+BetaPropeller*→||<-?<-PSE<-?<-?<-?<-?<-ROK-HTH	nSTAND1+BetaPropeller	1299	AQJ67_RS04560	actinobacteria	Streptomyces caeruleatus	WD40 repeat domain-containing protein [Streptomyces caeruleatus].	GCF_001514235.1
WP_066377691.1	XisI→||<-?<-HAD||?→||<-HSP20<-PSE||?→ PSE→?→ CASPASE+CASPASE+nSTAND1+BetaPropeller*→||<-?||?→||<-SIG+TPR	CASPASE+CASPASE+nSTAND1+BetaPropeller	1750	A3776_RS06945	cyanobacteria	Anabaena sp. CA = ATCC 33047	caspase family protein [Anabaena sp. CA = ATCC 33047].	GCF_001597855.1
WP_067768577.1	<-SIG+TPR||ABC-ATPase→?→||<-?<-?<-?<-Trypco1||CASPASE+nSTAND1+TM+BetaPropeller*→||<-?||?→||<-?<-?<-ABC-ATPase	CASPASE+nSTAND1+TM+BetaPropeller	1611	NOS3756_RS11575	cyanobacteria	Nostoc sp. NIES-3756	caspase family protein [Nostoc sp. NIES-3756].	GCF_001548375.1
WP_068382524.1	CASPASE+CASPASE+nSTAND1+BetaPropeller*→ Uma2→||<-?||?→?→ SIG+TM+TM+TM+TM+TM→	CASPASE+CASPASE+nSTAND1+BetaPropeller	1612	LEP3755_RS08100	cyanobacteria	Leptolyngbya sp. NIES-3755	caspase family protein [Leptolyngbya sp. NIES-3755].	GCF_001548435.1
WP_068789388.1	nSTAND1+TM+BetaPropeller*→||<-REC	nSTAND1+TM+BetaPropeller	1292	AY600_RS10555	cyanobacteria	Phormidium willei	WD40 repeat domain-containing protein [Phormidium willei].	GCF_001637315.1
WP_069068225.1	RRM→?→ Pkinase+TPR→?→?→ nSTAND1+BetaPropeller*→?→ PSE→ SIG+Pentapeptide→?→||<-?<-?<-zinc_ribbon_2+Pkinase+TM+TM+TM+TM	nSTAND1+BetaPropeller	1225	A4S05_RS02400	cyanobacteria	Nostoc sp. KVJ20	WD40 repeat domain-containing protein [Nostoc sp. KVJ20].	GCF_001712795.1
WP_069471539.1	ACT→?→?→?→ tRNA→ tRNA→?→||<-SIG+ApbE||?→ nSTAND1+TM+BetaPropeller→ *?→?→ nSTAND1+BetaPropeller→*	nSTAND1+TM+BetaPropeller	1371	BHU68_RS00110	gammaproteobacteria	Candidatus Marithrix sp. Canyon 246	WD40 repeat domain-containing protein [Candidatus Marithrix sp. Canyon 246].	GCF_001723675.1
WP_069471542.1	nSTAND1+BetaPropeller*→	nSTAND1+BetaPropeller	1154	BHU68_RS00095	gammaproteobacteria	Candidatus Marithrix sp. Canyon 246	hypothetical protein [Candidatus Marithrix sp. Canyon 246].	GCF_001723675.1
WP_069472735.1	S4+PSYN→?→?→ nSTAND1+BetaPropeller*→	nSTAND1+BetaPropeller	1471	BHU65_RS01520	gammaproteobacteria	Candidatus Marithrix sp. Canyon 246	ABC transporter substrate-binding protein, partial [Candidatus Marithrix sp. Canyon 246].	GCF_001723755.1
WP_069775370.1	<-AraC-HTH+AraC-HTH||?→ HTH+nSTAND1+TM+BetaPropeller*→ SIG+NLPC→	HTH+nSTAND1+TM+BetaPropeller	1301	BGM19_RS05250	actinobacteria	Streptomyces agglomeratus	helix-turn-helix domain-containing protein [Streptomyces agglomeratus].	GCF_001746475.1
WP_071926783.1	EACC1→ CASPASE+nSTAND1+BetaPropeller*→?→||<-?<-?||PSE→||<-?<-TM+TM+TM+TM+TM+TM<-ABC-ATPase	CASPASE+nSTAND1+BetaPropeller	1400	BOX37_RS06100	actinobacteria	Nocardia mangyaensis	hypothetical protein [Nocardia mangyaensis].	GCF_001886715.1

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WP_073484145.1	HTH+nSTAND1+TM+BetaPropeller*→	HTH+nSTAND1+TM+BetaPropeller	1258	BUE43_RS16570	actinobacteria	Streptoalloteichus hindustanus	helix-turn-helix domain-containing protein [Streptoalloteichus hindustanus].	GCF_900129375.1
WP_073549910.1	CASPASE+CASPASE+nSTAND1+BetaPropeller*→ SIG+TPR→	CASPASE+CASPASE+nSTAND1+BetaPropeller	1691	NIES1031_RS13280	cyanobacteria	Chroogloeocystis siderophila	caspase family protein [Chroogloeocystis siderophila].	GCF_001904655.1
WP_073619116.1	Pentapeptide→?→?→?→||<-Trypco1||CASPASE+nSTAND1+Pentapeptide+Pentapeptide+Pentapeptide*→	CASPASE+nSTAND1+Pentapeptide+Pentapeptide+Pentapeptide	1155	NIES2101_RS45020	cyanobacteria	Calothrix sp. HK-06	pentapeptide repeat-containing protein [Calothrix sp. HK-06].	GCF_001904745.1
WP_075128359.1	HTH+nSTAND1+TM+BetaPropeller*→	HTH+nSTAND1+TM+BetaPropeller	1232	BU204_RS25880	actinobacteria	Actinophytocola xanthii	helix-turn-helix domain-containing protein [Actinophytocola xanthii].	GCF_001921205.1
WP_075900997.1	<-ABhydrolase||?→?→?→||<-Trypco1||CASPASE+nSTAND1+TM+BetaPropeller*→	CASPASE+nSTAND1+TM+BetaPropeller	1830	BJP37_RS36840	cyanobacteria	Moorea bouillonii	caspase family protein [Moorea bouillonii].	GCF_001942495.1
WP_075905263.1	CASPASE+nSTAND1+BetaPropeller*→||<-?||MED15→||<-?<-Uma2	CASPASE+nSTAND1+BetaPropeller	1452	BJP37_RS32685	cyanobacteria	Moorea bouillonii	caspase family protein [Moorea bouillonii].	GCF_001942495.1
WP_076082468.1	nSTAND1*→||<-?||PSE→||<-ACET||?→||<-?<-VWA<-MoxR-AAA	nSTAND1	584	AV521_RS01825	actinobacteria	Streptomyces sp. IMTB 2501	ATP-binding protein [Streptomyces sp. IMTB 2501].	GCF_001953885.1
WP_076440611.1	nSTAND1+BetaPropeller*→||<-?<-ParA-Soj-PloopNTPase	nSTAND1+BetaPropeller	1266	BXA11_RS32200	actinobacteria	Microbispora rosea	hypothetical protein [Microbispora rosea].	GCF_900156315.1
WP_076985819.1	Pkinase→||<-?||?→?→?→||<-?||PSE→||<-?||HTH+nSTAND1+BetaPropeller*→	HTH+nSTAND1+BetaPropeller	1262	ALI144C_RS05040	actinobacteria	Actinosynnema sp. ALI-1.44	PD40 domain-containing protein [Actinosynnema sp. ALI-1.44].	GCF_001984155.1
WP_078616701.1	HTH+nSTAND1+TM+BetaPropeller*→	HTH+nSTAND1+TM+BetaPropeller	1390	H295_RS0120055	actinobacteria	Streptomyces sp. 351MFTsu5.1	helix-turn-helix domain-containing protein [Streptomyces sp. 351MFTsu5.1].	GCF_000383655.1
WP_078831679.1	TIR+DrHyd→ nSTAND1+BetaPropeller*→	nSTAND1+BetaPropeller	1025	B5D42_RS11600	bacteroidetes	Sediminibacterium ginsengisoli	hypothetical protein [Sediminibacterium ginsengisoli].	GCF_900167075.1
WP_079315441.1	<-ABC-ATPase<-ABC-ATPase<-?<-PSE<-?<-PSE<-?||?→ nSTAND1+BetaPropeller*→||<-PSE<-?<-tRNA<-tRNA<-?<-SIG+PDZ+LonC<-?<-?||?→ NUDIX→	nSTAND1+BetaPropeller	1250	B1L11_RS17305	actinobacteria	Microbispora sp. GKU 823	hypothetical protein [Microbispora sp. GKU 823].	GCF_002027145.1
WP_079432573.1	<-ICP8OBfold||?→?→?→?→ TIR+DrHyd→ nSTAND1+BetaPropeller*→	nSTAND1+BetaPropeller	1076	B4920_RS00090	betaproteobacteria	Zoogloea sp. LCSB751	WD40 repeat domain-containing protein [Zoogloea sp. LCSB751].	GCF_002028455.1
WP_080045844.1	ENOYCOADEHYD→||<-?<-?<-?<-?<-?<-?||nSTAND1+BetaPropeller*→||<-?<-?<-?<-?||?→ Pkinase→	nSTAND1+BetaPropeller	1207	BKM31_RS55895	actinobacteria	Nonomuraea sp. ATCC 55076	hypothetical protein [Nonomuraea sp. ATCC 55076].	GCF_002057455.1
WP_080808279.1	<-NACHT||?→||<-PSE<-?<-?||PSE→ PSE→||<-?||?→ nSTAND1*→ nSTAND1+TM+TPR→?→?→?→?→||<-PSE||Uma2→	nSTAND1	353	XM38_RS18855	cyanobacteria	Halomicronema hongdechloris	ATP-binding protein [Halomicronema hongdechloris].	GCF_002075285.3
WP_081771813.1	TIR+TIR→ nSTAND1+BetaPropeller*→ SLATT+SLATT→	nSTAND1+BetaPropeller	1486	A3CW_RS50325	betaproteobacteria	Paraburkholderia nodosa	AAA family ATPase [Paraburkholderia nodosa].	GCF_000519185.1
WP_083582706.1	<-REC<-PSE||?→||<-?<-Trypco1||CASPASE+nSTAND1*→	CASPASE+nSTAND1	995	BRW63_RS04300	cyanobacteria	Phormidesmis priestleyi	caspase family protein [Phormidesmis priestleyi].	GCF_001895925.1
WP_084556682.1	HTH+nSTAND1+BetaPropeller*→	HTH+nSTAND1+BetaPropeller	1331	bacteria>actinobacteria	Couchioplanes caeruleus	-	1181239683	-
WP_086168347.1	<-S1COLD||?→ nSTAND1+BetaPropeller*→?→||<-?<-?<-CASPASE+nSTAND1+BetaPropeller<-?<-EACC1	nSTAND1+BetaPropeller	1276	OQI_RS06360	actinobacteria	Streptomyces pharetrae	hypothetical protein [Streptomyces pharetrae].	GCF_002128465.1

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WP_086476322.1	TIR→ nSTAND1+TM*→	nSTAND1+TM	707	BV214_RS04690	bacteroidetes	Arenibacter sp. AK53	hypothetical protein [Arenibacter sp. AK53].	GCF_002150785.1
WP_086667199.1	<-HAD<-?||?→?→||<-?<-ABC-ATPase||?→ nSTAND1+TM+BetaPropeller*→	nSTAND1+TM+BetaPropeller	945	B0F77_RS34380	actinobacteria	Lentzea kentuckyensis	hypothetical protein [Lentzea kentuckyensis].	GCF_002150765.1
WP_086687140.1	SIG+HOP2→||<-ABhydrolase<-?<-?||?→?→ nSTAND1+BetaPropeller*→||<-?<-?<-?<-ABhydrolase	nSTAND1+BetaPropeller	1159	BV372_RS14140	cyanobacteria	Nostoc sp. T09	AAA family ATPase [Nostoc sp. T09].	GCF_002154695.1
WP_086756226.1	<-Trypco1||CASPASE+nSTAND1+BetaPropeller*→	CASPASE+nSTAND1+BetaPropeller	906	BV375_RS00710	cyanobacteria	Nostoc sp. 106C	caspase family protein [Nostoc sp. 106C].	GCF_002154725.1
WP_087545319.1	<-Cluster158_2clades<-?||?→ SLATT→ TIR+DrHyd→ nSTAND1+BetaPropeller*→||<-PSE||?→||<-?<-?<-HxxxH	nSTAND1+BetaPropeller	1320	BZZ01_RS31645	cyanobacteria	Nostocales cyanobacterium HT-58-2	hypothetical protein [Nostocales cyanobacterium HT-58-2].	GCF_002163975.1
WP_090879784.1	<-ParA-Soj-PloopNTPase<-?||?→||<-PSE<-?||?→||<-?||TIR+DrHyd+TIR→ nSTAND1+EP1*→	nSTAND1+EP1	2283	BLT60_RS20960	alphaproteobacteria	Bauldia litoralis	hypothetical protein [Bauldia litoralis].	GCF_900104485.1
WP_090933370.1	<-wHTH-4stranded+TPRs+APATPase||HTH+nSTAND1+TM+BetaPropeller*→	HTH+nSTAND1+TM+BetaPropeller	1266	BLS95_RS20045	actinobacteria	Nonomuraea jiangxiensis	hypothetical protein [Nonomuraea jiangxiensis].	GCF_900099965.1
WP_090944045.1	SIG+Trypsin+PDZ→||<-?<-?||?→?→||<-ABhydrolase<-?||nSTAND1+TM+BetaPropeller*→||<-?<-?<-?<-?||?→||<-HTH+MED15<-ACT	nSTAND1+TM+BetaPropeller	1222	BLS95_RS39570	actinobacteria	Nonomuraea jiangxiensis	hypothetical protein [Nonomuraea jiangxiensis].	GCF_900099965.1
WP_091280677.1	CASPASE+nSTAND1+TM+BetaPropeller*→	CASPASE+nSTAND1+TM+BetaPropeller	1556	AWX74_RS22975	actinobacteria	Frankia irregularis	WD40 repeat domain-containing protein [Frankia irregularis].	GCF_001536285.1
WP_091294574.1	nSTAND1+TM+BetaPropeller*→	nSTAND1+TM+BetaPropeller	1264	BLV57_RS30410	actinobacteria	Amycolatopsis xylanica	hypothetical protein [Amycolatopsis xylanica].	GCF_900107045.1
WP_092636218.1	ABC-ATPase→ ABC-ATPase→ TIR→ nSTAND1+TM+TPR+TPR+TPR+TPR+TPR*→?→||<-?<-AraC-HTH+AraC-HTH	nSTAND1+TM+TPR+TPR+TPR+TPR+TPR	1612	BLV06_RS20590	alphaproteobacteria	Rhizobiales bacterium GAS113	ATP-binding protein [Rhizobiales bacterium GAS113].	GCF_900103895.1
WP_092980844.1	SLATT→ TIR→ nSTAND1+TM*→||<-?<-?<-TPR	nSTAND1+TM	809	BM318_RS03935	bacteroidetes	Robiginitalea myxolifaciens	hypothetical protein [Robiginitalea myxolifaciens].	GCF_900115205.1
WP_093158527.1	nSTAND1+BetaPropeller*→	nSTAND1+BetaPropeller	1257	ATL45_RS01025	actinobacteria	Saccharopolyspora antimicrobica	AAA family ATPase [Saccharopolyspora antimicrobica].	GCF_900114905.1
WP_093269708.1	ACET→||<-?<-?||?→ CASPASE+nSTAND1+TM+BetaPropeller*→	CASPASE+nSTAND1+TM+BetaPropeller	1659	BLW84_RS25305	actinobacteria	Saccharopolyspora shandongensis	caspase family protein [Saccharopolyspora shandongensis].	-
WP_094341574.1	Trypsin+nSTAND1+BetaPropeller*→	Trypsin+nSTAND1+BetaPropeller	1438	CDG79_RS07440	cyanobacteria	Nostoc sp. ‘Peltigera membranacea cyanobiont’ 232	trypsin-like peptidase domain-containing protein [Nostoc sp. ‘Peltigera membranacea cyanobiont’ 232].	GCF_002245985.1
WP_094349283.1	nSTAND1+BetaPropeller→?→||<-Trypco1||CASPASE+nSTAND1+TM+BetaPropeller*→	CASPASE+nSTAND1+TM+BetaPropeller	1387	CDG76_RS12330	cyanobacteria	Nostoc sp. ‘Peltigera membranacea cyanobiont’ 210A	caspase family protein [Nostoc sp. ‘Peltigera membranacea cyanobiont’ 210A].	GCF_002246015.1
WP_094555851.1	TIR+DrHyd→ nSTAND1+BetaPropeller+BetaPropeller*→	nSTAND1+BetaPropeller+BetaPropeller	1242	CJZ82_RS11170	cyanobacteria	Synechococcus sp. 1G10	hypothetical protein [Synechococcus sp. 1G10].	GCF_002252625.1
WP_095722688.1	CASPASE+CASPASE+nSTAND1+BetaPropeller*→	CASPASE+CASPASE+nSTAND1+BetaPropeller	1706	CK510_RS16200	cyanobacteria	Calothrix elsteri	caspase family protein [Calothrix elsteri].	GCF_002289455.1
WP_096542102.1	<-Trypco1||CASPASE+nSTAND1+Pentapeptide*→?→?→ XisI→	CASPASE+nSTAND1+Pentapeptide	996	CA726_RS33005	cyanobacteria	Nostoc linckia	pentapeptide repeat-containing protein [Nostoc linckia].	GCF_002368035.1
WP_096556689.1	<-HAD||?→||<-HSP20||?→||<-REC<-?||CASPASE+CASPASE+nSTAND1+BetaPropeller*→	CASPASE+CASPASE+nSTAND1+BetaPropeller	1739	CDC32_RS19410	cyanobacteria	Nostoc sp. NIES-4103	caspase family protein [Nostoc sp. NIES-4103].	GCF_002368335.1

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WP_096563584.1	HSP20→||<-ABhydrolase||?→||<-PSE||?→?→ nSTAND1+BetaPropeller+TPR*→ CASPASE→?→||<-?<-?||ABhydrolase→	nSTAND1+BetaPropeller+TPR	1393	CDC39_RS16830	cyanobacteria	Scytonema sp. NIES-4073	hypothetical protein [Scytonema sp. NIES-4073].	GCF_002368435.1
WP_096586192.1	Pentapeptide→ nSTAND1+BetaPropeller*→||<-?||?→||<-TM+TM+NACHT+FGS+GUN4<-CASPASE||?→||<-PSE<-?<-ParA-Soj-PloopNTPase	nSTAND1+BetaPropeller	1298	CA723_RS30235	cyanobacteria	Anabaenopsis circularis	PD40 domain-containing protein [Anabaenopsis circularis].	GCF_002367975.1
WP_096624791.1	Redoxin→||<-?<-?<-?||?→?→?→ CASPASE+CASPASE+nSTAND1+BetaPropeller*→||<-?<-?||?→ SIG+Pentapeptide→?→ ncRNA→||<-REC	CASPASE+CASPASE+nSTAND1+BetaPropeller	1715	CDC37_RS20940	cyanobacteria	Calothrix sp. NIES-3974	caspase family protein [Calothrix sp. NIES-3974].	GCF_002368395.1
WP_096641665.1	<-Cluster108_2clades||TPR+CASPASE→ CASPASE+nSTAND1+FGS*→	CASPASE+nSTAND1+FGS	1012	CA724_RS00570	cyanobacteria	Calothrix brevissima	SUMF1/EgtB/PvdO family nonheme iron enzyme [Calothrix brevissima].	GCF_002367995.1
WP_096655823.1	Pentapeptide→ CASPASE+nSTAND1+TM*→	CASPASE+nSTAND1+TM	767	CA729_RS11090	cyanobacteria	Calothrix parasitica	caspase family protein [Calothrix parasitica].	GCF_002368095.1
WP_096661654.1	RVT→?→?→?→||<-?<-Trypco1||CASPASE+nSTAND1+Pentapeptide*→||<-NACHT+BetaPropeller	CASPASE+nSTAND1+Pentapeptide	991	CA729_RS36575	cyanobacteria	Calothrix parasitica	pentapeptide repeat-containing protein [Calothrix parasitica].	GCF_002368095.1
WP_096677027.1	<-TM<-?||CASPASE+nSTAND1+BetaPropeller*→||<-?<-?<-?||?→||<-?<-?||HxxxH→	CASPASE+nSTAND1+BetaPropeller	1263	CDC30_RS18535	cyanobacteria	Fischerella sp. NIES-4106	caspase family protein [Fischerella sp. NIES-4106].	GCF_002368315.1
WP_096682926.1	APATPase+BetaPropeller→||<-Pentapeptide<-?||PSE→ PSE→||<-?||NACHT+TM+TM+TM→ FGS→ nSTAND1+TM+BetaPropeller*→ ABhydrolase→ Pentapeptide→ NACHT→?→ NACHT+HEAT→||<-?||Pentapeptide→	nSTAND1+TM+BetaPropeller	1278	CA737_RS29000	cyanobacteria	Nostoc sp. NIES-2111	peptidase C14 [Nostoc sp. NIES-2111].	GCF_002368215.1
WP_096684184.1	nSTAND1+BetaPropeller*→ CASPASE→	nSTAND1+BetaPropeller	1280	CDC41_RS02675	cyanobacteria	unclassified Calothrix	MULTISPECIES: WD40 repeat domain-containing protein [unclassified Calothrix].	GCF_002368455.1
WP_096722951.1	<-ATPcone<-?<-?<-?<-?||?→||<-REC||CASPASE+CASPASE+nSTAND1+BetaPropeller*→	CASPASE+CASPASE+nSTAND1+BetaPropeller	1589	CDC35_RS17615	cyanobacteria	Chondrocystis sp. NIES-4102	caspase family protein [Chondrocystis sp. NIES-4102].	GCF_002368355.1
WP_099198599.1	<-SIG+ASH-IG<-?||?→ nSTAND1+BetaPropeller*→||<-?<-?<-?||Cluster106_3clades→	nSTAND1+BetaPropeller	1284	CYQ11_RS04175	actinobacteria	Streptomyces cinnamoneus	hypothetical protein [Streptomyces cinnamoneus].	GCF_002727115.1
WP_101833019.1	nSTAND1+BetaPropeller*→	nSTAND1+BetaPropeller	1222	bacteria>actinobacteria	Frankia canadensis	-	1325963764	-
WP_102179560.1	EACC2+CASPASE+nSTAND1+BetaPropeller*→||<-ABhydrolase<-NUDIX	EACC2+CASPASE+nSTAND1+BetaPropeller	1565	CEN45_RS19405	cyanobacteria	Fischerella thermalis	CHAT domain-containing protein [Fischerella thermalis].	GCF_002870635.1
WP_102939115.1	SIG+TM+TM+TM+TM+TM→ SIG+TM+TM+TM+TM+TM→ ABC-ATPase→||<-?||?→?→ EACC2+CASPASE+nSTAND1+BetaPropeller*→	EACC2+CASPASE+nSTAND1+BetaPropeller	1603	CEP15_RS15365	cyanobacteria	Cylindrospermopsis raciborskii	PQQ-binding-like beta-propeller repeat protein [Cylindrospermopsis raciborskii].	GCF_002893125.1
WP_103138901.1	TM+TM+TM→?→?→||<-?<-?<-?||?→ nSTAND1+BetaPropeller*→?→?→?→||<-Uma2	nSTAND1+BetaPropeller	1225	CLI64_RS20305	cyanobacteria	Nostoc sp. CENA543	hypothetical protein [Nostoc sp. CENA543].	GCF_002896875.1
WP_103964494.1	SIG+nSTAND1+BetaPropeller*→?→||<-?||PSE→||<-?||?→ PSE→||<-pPIWI+MID+RNaseH<-pPIWI+viral-AAA<-pPIWI	SIG+nSTAND1+BetaPropeller	1377	C4V41_RS57390	actinobacteria	Nonomuraea solani	AAA family ATPase [Nonomuraea solani].	GCF_900108335.1
WP_104899206.1	EACC2+CASPASE+nSTAND1+BetaPropeller*→||<-XisI<-?||?→?→ EACC2+CASPASE+nSTAND1+BetaPropeller→	EACC2+CASPASE+nSTAND1+BetaPropeller	1559	NPM_RS08915	cyanobacteria	Nostoc sp. ‘Peltigera membranacea cyanobiont’ N6	CHAT domain-containing protein [Nostoc sp. ‘Peltigera membranacea cyanobiont’ N6].	GCF_002949735.1
WP_106172461.1	<-TPR||CASPASE+nSTAND1+BetaPropeller*→ Redoxin→	CASPASE+nSTAND1+BetaPropeller	1796	C7B76_RS10855	cyanobacteria	filamentous cyanobacterium CCP2	caspase family protein [filamentous cyanobacterium CCP2].	GCF_003003615.1

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WP_106238916.1	Cluster59_2clades→ TPR→?→?→||<-?||nSTAND1+BetaPropeller*→?→?→||<-?||PSE→?→ ACT→?→ Cluster108_2clades→	nSTAND1+BetaPropeller	1232	B0I32_RS14395	actinobacteria	Nonomuraea fuscirosea	WD40 repeat domain-containing protein [Nonomuraea fuscirosea].	GCF_003001935.1
WP_106256509.1	CASPASE+nSTAND1+BetaPropeller*→	CASPASE+nSTAND1+BetaPropeller	1771	C7B82_RS11920	cyanobacteria	Leptolyngbya frigida	PD40 domain-containing protein [Leptolyngbya frigida].	GCF_003003795.1
WP_106259571.1	CASPASE+nSTAND1+TM*→?→||<-?||PSE→?→?→?→ Pentapeptide→	CASPASE+nSTAND1+TM	985	C7B82_RS25475	cyanobacteria	Leptolyngbya frigida	caspase family protein [Leptolyngbya frigida].	GCF_003003795.1
WP_106259865.1	TIR+DrHyd→ nSTAND1+TM+BetaPropeller+TPR*→	nSTAND1+TM+BetaPropeller+TPR	1061	C7B82_RS26795	cyanobacteria	Leptolyngbya frigida	hypothetical protein [Leptolyngbya frigida].	GCF_003003795.1
WP_106288913.1	<-FHA+Pkinase<-?<-?<-?||?→?→||<-?||CASPASE+CASPASE+nSTAND1+BetaPropeller*→?→?→?→?→?→ Uma2→	CASPASE+CASPASE+nSTAND1+BetaPropeller	1761	C7B64_RS12100	cyanobacteria	Merismopedia glauca	caspase family protein [Merismopedia glauca].	GCF_003003775.1
WP_106409482.1	HTH+nSTAND1+TM+BetaPropeller*→?→||<-?||ABhydrolase→	HTH+nSTAND1+TM+BetaPropeller	1356	WH07_RS00620	actinobacteria	Streptomyces odonnellii	helix-turn-helix domain-containing protein [Streptomyces odonnellii].	GCF_000981895.1
WP_106859678.1	<-AAA+TPR||?→ nSTAND1+TM+BetaPropeller*→	nSTAND1+TM+BetaPropeller	1282	DAA54_RS06965	acidobacteria	Candidatus Sulfopaludibacter sp. SbA4	WD40 repeat domain-containing protein [Candidatus Sulfopaludibacter sp. SbA4].	GCF_900290305.1
WP_106870381.1	TIR+DrHyd→ nSTAND1+BetaPropeller*→||<-?||ABC-ATPase→	nSTAND1+BetaPropeller	1551	C7293_RS12420	cyanobacteria	unclassified Cyanobacteria (miscellaneous)	MULTISPECIES: pre-peptidase C-terminal domain-containing protein [unclassified Cyanobacteria (miscellaneous)].	GCF_003017855.1
WP_109279715.1	<-nSTAND1+BetaPropeller||?→?→?→ EACC1→ CASPASE+nSTAND1+TM+BetaPropeller*→	CASPASE+nSTAND1+TM+BetaPropeller	1552	CV755_RS09465	actinobacteria	Streptomyces orinoci	caspase family protein [Streptomyces orinoci].	GCF_003121295.1
WP_109364478.1	SWACOS+TPR+TPR→?→?→ nSTAND1+BetaPropeller*→||<-?<-?||APATPase+TPR→	nSTAND1+BetaPropeller	1274	DF268_RS38315	actinobacteria	Streptomyces sp. V2	hypothetical protein [Streptomyces sp. V2].	GCF_003129505.1
WP_111843756.1	TIR→ nSTAND1+TM*→?→?→||<-?<-?<-SIGMA-HTH	nSTAND1+TM	949	ESU54_RS03485	bacteroidetes	Aequorivita antarctica	hypothetical protein [Aequorivita antarctica].	GCF_900489835.1
WP_111882267.1	TIR→ nSTAND1+TM*→	nSTAND1+TM	744	DSY54_RS14580	bacteroidetes	Aequorivita sp. CIP111184	hypothetical protein [Aequorivita sp. CIP111184].	GCF_900489465.1
WP_112443263.1	nSTAND1+BetaPropeller*→	nSTAND1+BetaPropeller	1291	DN051_RS43725	actinobacteria	Streptomyces sp. ZFG47	hypothetical protein [Streptomyces sp. ZFG47].	GCF_003261055.1
WP_114006120.1	REC→?→?→?→?→ TIR+DrHyd→ nSTAND1+BetaPropeller*→?→?→||<-?<-?<-SIG+HISKIN+REC+AraC-HTH	nSTAND1+BetaPropeller	1022	DJ568_RS15045	bacteroidetes	Mucilaginibacter hurinus	hypothetical protein [Mucilaginibacter hurinus].	GCF_003324525.1
WP_114324839.1	TIR+DrHyd→ nSTAND1*→	nSTAND1	259	DWA31_RS01095	gammaproteobacteria	Candidatus Colwellia aromaticivorans	hypothetical protein [Candidatus Colwellia aromaticivorans].	GCF_003333305.1
WP_116215210.1	HTH+nSTAND1+TM+BetaPropeller*→||<-?<-?<-?||?→?→||<-?||ABhydrolase→	HTH+nSTAND1+TM+BetaPropeller	1291	DXZ73_RS36490	actinobacteria	Streptomyces olivoreticuli	helix-turn-helix domain-containing protein [Streptomyces olivoreticuli].	GCF_003391135.1
WP_117303390.1	Redoxin→?→?→||<-?||?→ TIR+DrHyd→ nSTAND1+TM+TPR*→||<-SIG+TPR	nSTAND1+TM+TPR	1216	D0Y96_RS19515	acidobacteria	Acidipila sp. 4G-K13	hypothetical protein [Acidipila sp. 4G-K13].	GCF_003428625.1
WP_120036984.1	p450→ NUDIX→||<-?<-PSE||?→||<-?||EACC1→ CASPASE+nSTAND1+TM+BetaPropeller*→||<-tRNA||?→||<-?||?→||<-SIG+PDZ+LonC	CASPASE+nSTAND1+TM+BetaPropeller	1417	D5S18_RS01040	actinobacteria	Nocardia panacis	caspase family protein [Nocardia panacis].	GCF_003598715.1
WP_121179107.1	EACC1→ CASPASE+nSTAND1+TM+BetaPropeller*→	CASPASE+nSTAND1+TM+BetaPropeller	1551	BX285_RS31390	actinobacteria	Streptomyces sp. 1114.5	hypothetical protein [Streptomyces sp. 1114.5].	GCF_003635085.1

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
WP_121407767.1	ABhydrolase→||<-?||HTH+nSTAND1+TM+BetaPropeller*→ SIG+NLPC→||<-TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM	HTH+nSTAND1+TM+BetaPropeller	1288	CLZ79_RS27460	actinobacteria	Streptomyces sp. 57	helix-turn-helix domain-containing protein [Streptomyces sp. 57].	GCF_003664315.1
WP_121432864.1	ABhydrolase→||<-?||EACC1→ CASPASE+nSTAND1+TM+BetaPropeller*→	CASPASE+nSTAND1+TM+BetaPropeller	1529	BZB76_RS03830	actinobacteria	Actinomadura pelletieri	caspase family protein [Actinomadura pelletieri].	GCF_003634705.1
WP_121894653.1	CASPASE+nSTAND1+TM+BetaPropeller*→?→ PSE→||<-PSE<-PSE<-PSE||?→||<-?||REC→	CASPASE+nSTAND1+TM+BetaPropeller	1525	CTZ28_RS39810	actinobacteria	Streptomyces shenzhenensis	caspase family protein [Streptomyces shenzhenensis].	GCF_003688995.1
WP_121906839.1	TIR→ nSTAND1+TM*→?→||<-?<-REC+NtrC-AAA+FIS-HTH||?→ ABC-ATPase→	nSTAND1+TM	934	BXY75_RS06160	bacteroidetes	Ulvibacter antarcticus	hypothetical protein [Ulvibacter antarcticus].	GCF_003688405.1
WP_121971445.1	CASPASE+nSTAND1*→	CASPASE+nSTAND1	921	CKL79_RS20690	cyanobacteria	Leptolyngbya sp. BC1307	caspase family protein [Leptolyngbya sp. BC1307].	GCF_002286735.1
WP_124450359.1	TIR→ nSTAND1+BetaPropeller+BetaPropeller*→||<-?<-?<-SIG+TM+TM+TM+TM+TM<-SIG+TM+TM+TM+TM+TM<-ABC-ATPase<-Cluster158_2clades	nSTAND1+BetaPropeller+BetaPropeller	1395	DBR47_RS12145	betaproteobacteria	Paucibacter sp. KBW04	AAA family ATPase [Paucibacter sp. KBW04].	GCF_003852425.1
WP_125486544.1	<-TPR<-SIG+BetaPropeller<-TRPR-HTH+PBPI<-?<-?||SIG+BetaPropeller→ TIR+DrHyd+TIR→ nSTAND1+NACHT+TPR*→?→ SLATT→||<-SIG+ASH-IG<-?<-?<-?||REC→	nSTAND1+NACHT+TPR	940	EDE15_RS18050	acidobacteria	Edaphobacter aggregans	ATP-binding protein [Edaphobacter aggregans].	GCF_003945235.1
WP_125646125.1	nSTAND1+BetaPropeller*→	nSTAND1+BetaPropeller	1367	DMB42_RS45370	actinobacteria	Nonomuraea sp. WAC 01424	hypothetical protein [Nonomuraea sp. WAC 01424].	GCF_003947315.1
WP_125647756.1	EACC1→ CASPASE+nSTAND1+BetaPropeller*→	CASPASE+nSTAND1+BetaPropeller	1501	DMB42_RS48695	actinobacteria	Nonomuraea sp. WAC 01424	caspase family protein [Nonomuraea sp. WAC 01424].	GCF_003947315.1
WP_126614131.1	<-SIG+TM+TM+TM+TM+TM+TM+TM+TM||HxxxH→?→ tRNA→ tRNA→ tRNA→ tRNA→ tRNA→ tRNA→ tRNA→ tRNA→?→?→?→ TIR+DrHyd→ nSTAND1+TM+BetaPropeller*→	nSTAND1+TM+BetaPropeller	1051	EI427_RS09850	bacteroidetes	Flammeovirga pectinis	hypothetical protein [Flammeovirga pectinis].	GCF_003970675.1
WP_127056740.1	CASPASE+CASPASE+nSTAND1+BetaPropeller*→||<-?<-PSE<-?<-?||SIG+VIT+VWA+TM→||<-?<-?<-ABhydrolase	CASPASE+CASPASE+nSTAND1+BetaPropeller	1675	DSM107003_RS25415	cyanobacteria	Trichormus variabilis	caspase family protein [Trichormus variabilis].	GCF_003991935.1
WP_127150006.1	<-ABC-ATPase<-?||?→ nSTAND1+BetaPropeller*→?→||<-NUDIX	nSTAND1+BetaPropeller	1287	D9V26_RS29450	actinobacteria	Streptomyces lydicus	hypothetical protein [Streptomyces lydicus].	GCF_003994375.1
WP_128433449.1	SIG+nSTAND1+TM+BetaPropeller*→?→?→?→||<-?||SIG+TM+TM→	SIG+nSTAND1+TM+BetaPropeller	1296	EHO50_RS25360	actinobacteria	Streptomyces cyaneus	AAA family ATPase [Streptomyces cyaneus].	GCF_004028635.1
WP_129567753.1	TIR→ SIG+nSTAND1+TM+BetaPropeller+TPR*→ SLATT→ PSE→||<-?<-ABhydrolase	SIG+nSTAND1+TM+BetaPropeller+TPR	1355	DIU36_RS01770	bacteroidetes	Mucilaginibacter rubeus	hypothetical protein [Mucilaginibacter rubeus].	GCF_003286445.1
WP_129958652.1	<-TIR<-?<-?<-?<-?<-?||PSE→ TIR+TIR→ nSTAND1+TM+RHS+RHS+PDZ*→||<-?<-TRPR-HTH+PBPI	nSTAND1+TM+RHS+RHS+PDZ	1555	EVC45_RS14430	betaproteobacteria	Paraburkholderia sp. UYCP14C	hypothetical protein [Paraburkholderia sp. UYCP14C].	GCF_004197395.1
WP_131334817.1	HTH+nSTAND1+TM+BetaPropeller*→||<-?||?→||<-?<-?<-SIG+TM+TM+TM+TM+TM<-SIG+TM+TM+TM+TM+TM	HTH+nSTAND1+TM+BetaPropeller	1311	E0H45_RS03495	actinobacteria	Kribbella soli	helix-turn-helix domain-containing protein [Kribbella soli].	GCF_004331345.1
WP_132126505.1	ABhydrolase→||<-?||nSTAND1+TM+BetaPropeller*→	nSTAND1+TM+BetaPropeller	947	EV192_RS53305	actinobacteria	Actinocrispum wychmicini	hypothetical protein [Actinocrispum wychmicini].	GCF_004345645.1
WP_132170809.1	nSTAND1+BetaPropeller*→ SWACOS+TPR+TPR→	nSTAND1+BetaPropeller	1283	E1264_RS07080	actinobacteria	Actinomadura sp. KC216	PD40 domain-containing protein [Actinomadura sp. KC216].	GCF_004348535.1
WP_132171295.1	<-APATPase||nSTAND1+BetaPropeller*→?→ NACHT+TM+TM+TM+TM+TM+TM+TM+TM→ SWACOS+TPR+TPR→	nSTAND1+BetaPropeller	1155	E1264_RS08360	actinobacteria	Actinomadura sp. KC216	WD40 repeat domain-containing protein [Actinomadura sp. KC216].	GCF_004348535.1
WP_133475184.1	TIR→ nSTAND1+TM+BetaPropeller*→	nSTAND1+TM+BetaPropeller	1045	BC659_RS12750	bacteroidetes	Sediminibacterium goheungense	hypothetical protein [Sediminibacterium goheungense].	GCF_004361915.1
WP_135106243.1	FGS→?→ PSE→?→||<-PSE||?→ nSTAND1+BetaPropeller*→||<-?<-?<-?<-PSE<-RVe+MutnpC||PSE→ RVT→	nSTAND1+BetaPropeller	1364	BLD44_RS07925	cyanobacteria	Mastigocladus laminosus	hypothetical protein [Mastigocladus laminosus].	GCF_001990805.2

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<tr><td>WP_141634977.1</td><td>nSTAND1+TM+BetaPropeller*→ BetaPropeller→</td><td>nSTAND1+TM+BetaPropeller</td><td>991</td><td>E6W39_RS21975</td><td>actinobacteria</td><td>Kitasatospora sp. MMS16-CNU292</td><td>hypothetical protein [Kitasatospora sp. MMS16-CNU292].</td><td>GCF_006636205.1</td></tr>
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acc	**operon**	**architecture**	**len**	**gen.name**	**taxend**	**species**	**defline**	**gca**
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WP_149853426.1	nSTAND1+BetaPropeller*→ nSTAND1+BetaPropeller→||<-MED15<-?<-?||?→ BetaPropeller+ABhydrolase→	nSTAND1+BetaPropeller	1270	F0L68_RS31105	actinobacteria	Goodfellowiella sp. AN110305	hypothetical protein [Goodfellowiella sp. AN110305].	GCF_008386585.1
WP_149854623.1	nSTAND1*→	nSTAND1	264	F0L68_RS37265	actinobacteria	Goodfellowiella sp. AN110305	ATP-binding protein, partial [Goodfellowiella sp. AN110305].	GCF_008386585.1
WP_150477790.1	nSTAND1+TM+BetaPropeller*→	nSTAND1+TM+BetaPropeller	1249	CP975_RS04485	actinobacteria	Streptomyces alboniger	hypothetical protein [Streptomyces alboniger].	GCF_008704395.1
WP_151694506.1	SIG+Pentapeptide→ REC→?→?→ nSTAND1+TM+BetaPropeller*→	nSTAND1+TM+BetaPropeller	1253	MiAbW_RS00775	cyanobacteria	Microcystis aeruginosa	WD40 repeat domain-containing protein [Microcystis aeruginosa].	GCF_008974145.1
WP_151729819.1	wHTH-4stranded+TPRs+SWACOS+TPR+TPR→?→?→?→ HOP2→?→||<-?||Pkinase+TIR+nSTAND1+FilH*→?→?→||<-?<-ABC-ATPase<-ABC-ATPase	Pkinase+TIR+nSTAND1+FilH	1507	KTAU_RS18765	chloroflexi	Thermogemmatispora aurantia	protein kinase [Thermogemmatispora aurantia].	GCF_008974285.1
WP_151998675.1	TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+cNMP→ TIR+DrHyd→ nSTAND1+TM+LPD8+BetaPropeller*→	nSTAND1+TM+LPD8+BetaPropeller	1056	GC130_RS12600	bacteroidetes	Imperialibacter sp. EC-SDR9	High-affnity carbon uptake protein Hat/HatR [Imperialibacter sp. EC-SDR9].	GCF_902498805.1
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WP_152780064.1	HTH+nSTAND1+TM+BetaPropeller*→	HTH+nSTAND1+TM+BetaPropeller	1251	FNH04_RS03190	actinobacteria	Streptomyces phyllanthi	hypothetical protein [Streptomyces phyllanthi].	GCF_009377205.1
WP_153167482.1	<-Cluster428_2clades<-?<-?||TIR→ SIG+nSTAND1+BetaPropeller*→	SIG+nSTAND1+BetaPropeller	1296	GH664_RS07725	betaproteobacteria	Thauera sp. 2A1	hypothetical protein [Thauera sp. 2A1].	GCF_009469595.1
WP_153167675.1	<-REC<-?||?→||<-PSE||?→ TIR+DrHyd→ nSTAND1+BetaPropeller*→?→?→ HOP2→	nSTAND1+BetaPropeller	1225	GH664_RS08515	betaproteobacteria	Thauera sp. 2A1	AAA family ATPase [Thauera sp. 2A1].	GCF_009469595.1
WP_155176087.1	TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+cNMP→ TIR+DrHyd→ nSTAND1+TM+BetaPropeller*→	nSTAND1+TM+BetaPropeller	1054	E1163_RS26420	bacteroidetes	Fulvivirga kasyanovii	High-affnity carbon uptake protein Hat/HatR [Fulvivirga kasyanovii].	GCF_009711405.1
WP_155342137.1	nSTAND1+BetaPropeller*→	nSTAND1+BetaPropeller	1430	Acor_RS40905	actinobacteria	Acrocarpospora corrugata	AAA family ATPase [Acrocarpospora corrugata].	GCF_009687845.1
WP_155349768.1	HTH+nSTAND1+TM+BetaPropeller*→	HTH+nSTAND1+TM+BetaPropeller	1306	Aple_RS38900	actinobacteria	Acrocarpospora pleiomorpha	helix-turn-helix domain-containing protein [Acrocarpospora pleiomorpha].	GCF_009687885.1
WP_155356770.1	<-SIG+TM+TM+TM+TM+TM<-?||ABhydrolase→?→?→?→?→ nSTAND1+BetaPropeller*→	nSTAND1+BetaPropeller	1404	Amac_RS24660	actinobacteria	Acrocarpospora macrocephala	hypothetical protein [Acrocarpospora macrocephala].	GCF_009687865.1
WP_155743298.1	CASPASE+ABhydrolase→ CASPASE+nSTAND1+BetaPropeller→ CASPASE+nSTAND1+TM+BetaPropeller*→	CASPASE+nSTAND1+TM+BetaPropeller	1444	F7734_RS02865	cyanobacteria	Scytonema sp. UIC 10036	caspase family protein [Scytonema sp. UIC 10036].	GCF_009725235.1
WP_155744071.1	CASPASE+nSTAND1+TM+BetaPropeller*→	CASPASE+nSTAND1+TM+BetaPropeller	1426	F7734_RS07420	cyanobacteria	Scytonema sp. UIC 10036	CHAT domain-containing protein [Scytonema sp. UIC 10036].	GCF_009725235.1
WP_157357215.1	nSTAND1+BetaPropeller*→	nSTAND1+BetaPropeller	1257	bacteria>actinobacteria	Amycolatopsis nigrescens	-	1786243365	-

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
WP_158887400.1	<-ABhydrolase<-?||?→||<-?||?→||<-?||HTH+nSTAND1+TM+BetaPropeller*→	HTH+nSTAND1+TM+BetaPropeller	1240	FXO23_RS22610	actinobacteria	Amycolatopsis sp. EGI 650086	PD40 domain-containing protein [Amycolatopsis sp. EGI 650086].	GCF_009765355.1
WP_158891295.1	<-ABC-ATPase<-ABC-ATPase<-?<-?<-?||nSTAND1+TM+BetaPropeller*→||<-?<-?<-?<-?<-?<-ABhydrolase	nSTAND1+TM+BetaPropeller	1241	FXO23_RS37595	actinobacteria	Amycolatopsis sp. EGI 650086	hypothetical protein [Amycolatopsis sp. EGI 650086].	GCF_009765355.1
WP_159585268.1	TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+cNMP→ TIR+DrHyd→ nSTAND1+TM+BetaPropeller*→	nSTAND1+TM+BetaPropeller	1086	GV030_RS20605	bacteroidetes	Marinoscillum sp. 108	hypothetical protein [Marinoscillum sp. 108].	GCF_902506655.1
WP_159788932.1	<-TM<-?||CASPASE+nSTAND1+TM+BetaPropeller*→ SIG+TPR→	CASPASE+nSTAND1+TM+BetaPropeller	1524	L855_RS13815	cyanobacteria	Microcoleus sp. IPPAS B-353	caspase family protein [Microcoleus sp. IPPAS B-353].	GCF_009846485.1
WP_160147137.1	ABC-ATPase→ TM+TM+TM+TM+TM+TM→ HTH+nSTAND1+TM+BetaPropeller*→||<-?||?→||<-?<-?<-?<-SIG+TM+TM+TM+TM+TM<-SIG+TM+TM+TM+TM+TM	HTH+nSTAND1+TM+BetaPropeller	1267	C4U03_RS30005	actinobacteria	Actinomadura echinospora	helix-turn-helix domain-containing protein [Actinomadura echinospora].	GCF_900108175.1
WP_160846342.1	TIR→ SIG+nSTAND1+TM+BetaPropeller+TPR*→ SLATT→?→||<-?<-ABhydrolase	SIG+nSTAND1+TM+BetaPropeller+TPR	1335	GS399_RS19525	bacteroidetes	Pedobacter sp. HMF7647	hypothetical protein [Pedobacter sp. HMF7647].	GCF_009834875.1
WP_161602925.1	<-ABC-ATPase<-?<-?<-?<-?<-?||?→ CASPASE+nSTAND1+TPR*→?→||<-ABhydrolase	CASPASE+nSTAND1+TPR	902	SD80_RS22720	cyanobacteria	Scytonema tolypothrichoides	tetratricopeptide repeat protein [Scytonema tolypothrichoides].	GCF_000828085.3
WP_162442111.1	TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+cNMP→ TIR+DrHyd→ nSTAND1+TM+fvmX2+BetaPropeller*→	nSTAND1+TM+fvmX2+BetaPropeller	1036	GXP67_RS04800	bacteroidetes	Rhodocytophaga sp. 172606-1	High-affnity carbon uptake protein Hat/HatR [Rhodocytophaga sp. 172606-1].	GCF_010119975.1
WP_162444893.1	TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+cNMP→ TIR+DrHyd→ nSTAND1+BetaPropeller*→	nSTAND1+BetaPropeller	1040	GXP67_RS20705	bacteroidetes	Rhodocytophaga sp. 172606-1	High-affnity carbon uptake protein Hat/HatR [Rhodocytophaga sp. 172606-1].	GCF_010119975.1
WP_162795474.1	SIG+nSTAND1*→	SIG+nSTAND1	336	DQW85_RS29495	actinobacteria	Nonomuraea sp. NEAU-YG30	AAA family ATPase, partial [Nonomuraea sp. NEAU-YG30].	GCF_003313395.1
WP_163697206.1	CASPASE+ABhydrolase→?→ CASPASE+nSTAND1+TM+BetaPropeller→ *CASPASE+nSTAND1+TM+BetaPropeller*→||<-?<-EAD4+APATPase+BetaPropeller	CASPASE+nSTAND1+TM+BetaPropeller	1573	DXZ20_RS06775	cyanobacteria	Leptolyngbyaceae cyanobacterium CCMR0081	PD40 domain-containing protein [Leptolyngbyaceae cyanobacterium CCMR0081].	GCF_011009555.1
WP_163697208.1	CASPASE+nSTAND1+BetaPropeller*→	CASPASE+nSTAND1+BetaPropeller	1477	DXZ20_RS06780	cyanobacteria	Leptolyngbyaceae cyanobacterium CCMR0081	caspase family protein [Leptolyngbyaceae cyanobacterium CCMR0081].	GCF_011009555.1
WP_163938808.1	<-TM<-?||CASPASE+nSTAND1+TM+BetaPropeller*→	CASPASE+nSTAND1+TM+BetaPropeller	1216	G1O98_RS35625	cyanobacteria	Nostoc sp. UIC 10630	caspase family protein, partial [Nostoc sp. UIC 10630].	GCF_010747425.1
WP_164607717.1	HTH+nSTAND1+TM+BetaPropeller*→ SIG+NLPC→	HTH+nSTAND1+TM+BetaPropeller	1254	G3I60_RS24410	actinobacteria	Streptomyces sp. SID13666	helix-turn-helix domain-containing protein [Streptomyces sp. SID13666].	GCF_010548325.1
WP_164737886.1	HTH+nSTAND1+TM+BetaPropeller*→||<-?||?→?→?→ ABC-ATPase→ ABC-ATPase→	HTH+nSTAND1+TM+BetaPropeller	1245	EKH77_RS28040	actinobacteria	Streptomyces luteoverticillatus	DNA-binding protein [Streptomyces luteoverticillatus].	GCF_003970715.1
WP_165253283.1	TIR+TIR→ nSTAND1+BetaPropeller*→||<-?||TIR+nSTAND1+BetaPropeller→	nSTAND1+BetaPropeller	1322	G6O68_RS30360	planctomycetes	Paludisphaera sp. JC670	hypothetical protein [Paludisphaera sp. JC670].	GCF_011064595.1

acc	**operon**	**architecture**	**len**	**gen.name**	**taxend**	**species**	**defline**	**gca**
WP_165741954.1	TIR+nSTAND1+BetaPropeller*→	TIR+nSTAND1+BetaPropeller	1776	HBF22_RS11055	gammaproteobacteria	Candidatus Thiosymbion oneisti	hypothetical protein, partial [Candidatus Thiosymbion oneisti].	GCF_011392785.1
WP_165977045.1	<-APATPase||nSTAND1+BetaPropeller*→?→ NACHT+TM+TM+TM+TM+TM+TM+TM+TM→||<-?<-?<-?||REC→	nSTAND1+BetaPropeller	1163	E1294_RS02715	actinobacteria	Nonomuraea sp. KC712	AAA family ATPase [Nonomuraea sp. KC712].	GCF_004349015.1
WP_166362185.1	TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+cNMP→?→ TIR+DrHyd→ nSTAND1+TM+RapA-C+BetaPropeller*→	nSTAND1+TM+RapA-C+BetaPropeller	1020	G8O23_RS04390	bacteroidetes	Bacteroidales bacterium M08MB	High-affnity carbon uptake protein Hat/HatR [Bacteroidales bacterium M08MB].	GCF_011174675.1
WP_167485984.1	nSTAND1+BetaPropeller*→||<-?||?→||<-?<-PSE||?→ PSE→?→||<-?<-ICLR-HTH	nSTAND1+BetaPropeller	1286	F6W96_RS10530	actinobacteria	Nocardia terpenica	hypothetical protein [Nocardia terpenica].	GCF_011801165.1
WP_168094374.1	HTH+nSTAND1+TM+BetaPropeller*→	HTH+nSTAND1+TM+BetaPropeller	1232	HCK01_RS21035	actinobacteria	Streptomyces sp. AA8	helix-turn-helix domain-containing protein [Streptomyces sp. AA8].	GCF_012034305.1
WP_169156509.1	CASPASE+nSTAND1+TM+BetaPropeller*→	CASPASE+nSTAND1+TM+BetaPropeller	1399	DP116_RS18170	cyanobacteria	Brasilonema bromeliae	CHAT domain-containing protein [Brasilonema bromeliae].	GCF_012912135.1
WP_169616265.1	<-TPR+nSTAND1+BetaPropeller<-?||?→ nSTAND1+BetaPropeller→*//<-?//nSTAND1+BetaPropeller*→	nSTAND1+BetaPropeller	1227	E1H13_RS20825	cyanobacteria	Nodosilinea sp. P-1105	AAA family ATPase [Nodosilinea sp. P-1105].	GCF_012911975.1
WP_169616268.1	nSTAND1+BetaPropeller*→	nSTAND1+BetaPropeller	1430	E1H13_RS20835	cyanobacteria	Nodosilinea sp. P-1105	AAA family ATPase [Nodosilinea sp. P-1105].	GCF_012911975.1
WP_169682334.1	TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+cNMP→ TIR+DrHyd→ nSTAND1+BetaPropeller*→	nSTAND1+BetaPropeller	1042	HH304_RS13030	bacteroidetes	Flammeovirgaceae bacterium KN852	hypothetical protein [Flammeovirgaceae bacterium KN852].	GCF_012926615.1