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

Figure 3-Source data 1

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Gene neighborhoods and domain architectures of the bacterial TRADD-N domains

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
AKV69521.1	ECF-HTH+TRADD-N+Pentapeptide*→||<-?<-?||ECF-HTH+TRADD-N+Pentapeptide→	ECF-HTH+TRADD-N+Pentapeptide	463	VL20_4620	cyanobacteria	Microcystis panniformis FACHB-1757	Pentapeptide repeat family protein [Microcystis panniformis FACHB-1757]	GCA_001264245.1
AKV69524.1	ECF-HTH+TRADD-N+Pentapeptide→||<-?<-?||ECF-HTH+TRADD-N+Pentapeptide*→	ECF-HTH+TRADD-N+Pentapeptide	430	VL20_4623	cyanobacteria	Microcystis panniformis FACHB-1757	Pentapeptide repeat family protein [Microcystis panniformis FACHB-1757]	GCA_001264245.1
AOW98657.1	TRADD-N+Pentapeptide→ TRADD-N-aHTH1+TRADD-N+Pentapeptide→?→||<-?||TRADD-N-aHTH1+TRADD-N+Pentapeptide*→	TRADD-N-aHTH1+TRADD-N+Pentapeptide	359	BJP34_03640	cyanobacteria	Moorea producens PAL-8-15-08-1	hypothetical protein BJP34_03640 [Moorea producens PAL-8-15-08-1]	GCA_001767235.1
AOX04112.1	TRADD-N+Pentapeptide*→ TRADD-N-aHTH1+TRADD-N+Pentapeptide→?→||<-?||TRADD-N-aHTH1+TRADD-N+Pentapeptide→	TRADD-N+Pentapeptide	345	BJP34_03620	cyanobacteria	Moorea producens PAL-8-15-08-1	hypothetical protein BJP34_03620 [Moorea producens PAL-8-15-08-1]	GCA_001767235.1
AOX04113.1	TRADD-N+Pentapeptide→ TRADD-N-aHTH1+TRADD-N+Pentapeptide*→?→||<-?||TRADD-N-aHTH1+TRADD-N+Pentapeptide→	TRADD-N-aHTH1+TRADD-N+Pentapeptide	462	BJP34_03625	cyanobacteria	Moorea producens PAL-8-15-08-1	hypothetical protein BJP34_03625 [Moorea producens PAL-8-15-08-1]	GCA_001767235.1
AOY81242.1	TRADD-N*→ TRADD-N+Pentapeptide→	TRADD-N	93	BJP36_16370	cyanobacteria	Moorea producens JHB	hypothetical protein BJP36_16370 [Moorea producens JHB]	GCA_001854205.1
AOY84499.1	TRADD-N-aHTH1+TRADD-N+Pentapeptide*→	TRADD-N-aHTH1+TRADD-N+Pentapeptide	351	BJP36_03795	cyanobacteria	Moorea producens JHB	hypothetical protein BJP36_03795 [Moorea producens JHB]	GCA_001854205.1
ASQ04924.1	NTase+helical-region+TRADD-N+X*→	NTase+helical-region+TRADD-N+X	553	CDO23_13830	alphaproteobacteria	Sinorhizobium meliloti	hypothetical protein CDO23_13830 [Sinorhizobium meliloti]	GCA_002197105.1
ASY58478.1	HNH+TRADD-N+STAND+TPRs*→	HNH+TRADD-N+STAND+TPRs	1591	SS05631_c35640	alphaproteobacteria	Sinorhizobium sp. CCBAU 05631	hypothetical protein SS05631_c35640 [Sinorhizobium sp. CCBAU 05631]	GCA_002288505.1
AUB41700.1	TRADD-N-aHTH1+TRADD-N+Pentapeptide*→	TRADD-N-aHTH1+TRADD-N+Pentapeptide	478	COO91_07762	cyanobacteria	Nostoc flagelliforme CCNUN1	putative protein YjbI, containings pentapeptide repeats [Nostoc flagelliforme CCNUN1]	GCA_002813575.1
BAU04807.1	??→ TRADD-N+TPRs*→ EACC2+CASPASE+CHASE2+TM+TM→ TM+beta_rich+TPRs→ TPRs+CASPASE→	TRADD-N+TPRs	201	FIS3754_06960	cyanobacteria	Fischerella sp. NIES-3754	hypothetical protein FIS3754_06960 [Fischerella sp. NIES-3754]	GCA_001548455.1
BAY32115.1	CASPASE+TRADD-N+??*→ Uma2_REase→	CASPASE+TRADD-N+??	303	NIES2107_40010	cyanobacteria	Nostoc carneum NIES-2107	hypothetical protein NIES2107_40010 [Nostoc carneum NIES-2107]	GCA_002368155.1
BAZ00462.1	MetJarc-HTH/ParD_antitoxin→ CASPASE+TRADD-N+PAS+HTH*→	CASPASE+TRADD-N+PAS+HTH	517	NIES37_44540	cyanobacteria	Tolypothrix tenuis PCC 7101	hypothetical protein NIES37_44540 [Tolypothrix tenuis PCC 7101]	GCA_002368295.1
BAZ15419.1	CASPASE+TRADD-N+helical-region+HTH+HTH*→	CASPASE+TRADD-N+helical-region+HTH+HTH	704	NIES4071_72910	cyanobacteria	Calothrix sp. NIES-4071	hypothetical protein NIES4071_72910 [Calothrix sp. NIES-4071]	GCA_002368455.1

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
BBC23917.1	CASPASE+TRADD-N+vWA*→	CASPASE+TRADD-N+vWA	495	ABRG53_1660	cyanobacteria	Pseudanabaena sp. ABRG5-3	von Willebrand factor type A [Pseudanabaena sp. ABRG5-3]	GCA_003967015.1
BBC25632.1	TRADD-N-aHTH1+TRADD-N+Pentapeptide*→	TRADD-N-aHTH1+TRADD-N+Pentapeptide	429	ABRG53_3375	cyanobacteria	Pseudanabaena sp. ABRG5-3	pentapeptide repeat protein [Pseudanabaena sp. ABRG5-3]	GCA_003967015.1
CCI08969.1	TRADD-N+Pentapeptide*→	TRADD-N+Pentapeptide	249	MICAD_3610002	cyanobacteria	Microcystis aeruginosa PCC 7941	Genome sequencing data, contig C319 [Microcystis aeruginosa PCC 7941]	GCA_000312205.1
EDX70590.1	TRADD-N-aHTH1+TRADD-N+Pentapeptide*→ adh_short→	TRADD-N-aHTH1+TRADD-N+Pentapeptide	436	MC7420_162	cyanobacteria	Coleofasciculus chthonoplastes PCC 7420	Pentapeptide repeat protein [Coleofasciculus chthonoplastes PCC 7420]	GCA_000155555.1
EIN00431.1	NTase+helical-region+TRADD-N+X*→	NTase+helical-region+TRADD-N+X	526	WQE_15411	betaproteobacteria	Paraburkholderia hospita	hypothetical protein WQE_15411 [Paraburkholderia hospita]	GCA_000265115.1
ELP52905.1	ECF-HTH+TRADD-N+Pentapeptide*→	ECF-HTH+TRADD-N+Pentapeptide	433	O53_4634	cyanobacteria	Microcystis aeruginosa TAIHU98	pentapeptide repeats family protein [Microcystis aeruginosa TAIHU98]	GCA_000330925.1
ELS45411.1	ECF-HTH+TRADD-N+Pentapeptide*→ SIG→||<-?<-XisI	ECF-HTH+TRADD-N+Pentapeptide	403	C789_4786	cyanobacteria	Microcystis aeruginosa DIANCHI905	pentapeptide repeats family protein [Microcystis aeruginosa DIANCHI905]	GCA_000332585.1
ETD83219.1	NTase+helical-region+TRADD-N+X*→	NTase+helical-region+TRADD-N+X	511	U703_10115	alphaproteobacteria	Rhodobacter capsulatus YW1	hypothetical protein U703_10115 [Rhodobacter capsulatus YW1]	GCA_000506525.2
GAL95421.1	ECF-HTH+TRADD-N+Pentapeptide*→	ECF-HTH+TRADD-N+Pentapeptide	433	N44_04276	cyanobacteria	Microcystis aeruginosa NIES-44	hypothetical protein N44_04276 [Microcystis aeruginosa NIES-44]	GCA_000787675.1
GBE74065.1	ECF-HTH+TRADD-N+Pentapeptide*→	ECF-HTH+TRADD-N+Pentapeptide	390	myaer87_12920	cyanobacteria	Microcystis aeruginosa NIES-87	hypothetical protein myaer87_12920 [Microcystis aeruginosa NIES-87]	GCA_002933835.1
HCB01408.1	TIR+TRADD-N+TM+TM*→	TIR+TRADD-N+TM+TM	516	DEP19_03405	Chloroflexi	Anaerolineae bacterium	TPA: hypothetical protein DEP19_03405 [Anaerolineae bacterium].	GCA_003519565.1
HCK67110.1	TRADD-N*→	TRADD-N	203	DHW49_12675	Chloroflexi	Anaerolineae bacterium	TPA: hypothetical protein DHW49_12675, partial [Anaerolineae bacterium].	GCA_003526495.1
HCR71678.1	TIR+TRADD-N+TM+TM*→	TIR+TRADD-N+TM+TM	508	DIW23_09555	Chloroflexi	Anaerolineae bacterium	TPA: hypothetical protein DIW23_09555 [Anaerolineae bacterium].	GCA_003524705.1
HFK75788.1	TRADD-N+HTH+TM*→	TRADD-N+HTH+TM	519	ENR96_10195	Chloroflexi	Anaerolineae bacterium	TPA: hypothetical protein ENR96_10195, partial [Anaerolineae bacterium].	GCA_011329465.1
HFK76016.1	HTH+TRADD-N+Pentapeptide+Pentapeptide+TM+TM*→	HTH+TRADD-N+Pentapeptide+Pentapeptide+TM+TM	428	ENR96_11345	Chloroflexi	Anaerolineae bacterium	TPA: pentapeptide repeat-containing protein [Anaerolineae bacterium].	GCA_011329465.1
KAA3644872.1	Coiled-coil+TRADD-N+APATPase+TPR+TPR*→?→?→ PCRF+RF-1→	Coiled-coil+TRADD-N+APATPase+TPR+TPR	1021	DWQ07_15840	Chloroflexi	Chloroflexi bacterium	tetratricopeptide repeat protein [Chloroflexi bacterium].	GCA_008501685.1
KDR56649.1	EAD4+TRADD-N+STAND*→	EAD4+TRADD-N+STAND	541	APPUASWS_015575	cyanobacteria	Arthrospira platensis str. Paraca	hypothetical protein APPUASWS_015575 [Arthrospira platensis str. Paraca]	GCA_000175415.3
KEZ00677.1	ZNR+HTH+HTH+TIR→ PNPase+TRADD-N+STAND+wHTH+TPRs*→??+HEPN→??+SIR2+??+STAND→	PNPase+TRADD-N+STAND+wHTH+TPRs	1719	AI27_03035	alphaproteobacteria	Sphingomonas sp. BHC-A	hypothetical protein AI27_03035 [Sphingomonas sp. BHC-A]	GCA_000576455.2

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
KIF37416.1	TRADD-N-aHTH1+TRADD-N+Pentapeptide*→	TRADD-N-aHTH1+TRADD-N+Pentapeptide	436	PI95_05020	cyanobacteria	Hassallia byssoidea VB512170	hypothetical protein PI95_05020 [Hassallia byssoidea VB512170]	-
KPK03089.1	EAD7→?→||||<-?||?→ EAD7+TRADD-N+TM*→	EAD7+TRADD-N+TM	234	AMJ56_20055	Chloroflexi	Anaerolineae bacterium SG8_19	hypothetical protein AMJ56_20055, partial [Anaerolineae bacterium SG8_19].	GCA_001303105.1
KST65300.1	EAD1+TRADD-N+Pentapeptide*→	EAD1+TRADD-N+Pentapeptide	705	BC008_21105	cyanobacteria	Mastigocoleus testarum BC008	hypothetical protein BC008_21105 [Mastigocoleus testarum BC008]	GCA_001456025.1
KST65646.1	EAD1+TRADD-N+Pentapeptide*→	EAD1+TRADD-N+Pentapeptide	744	BC008_21980	cyanobacteria	Mastigocoleus testarum BC008	hypothetical protein BC008_21980 [Mastigocoleus testarum BC008]	GCA_001456025.1
KVE14567.1	PNPase+TRADD-N+STAND+wHTH+TPRs*→	PNPase+TRADD-N+STAND+wHTH+TPRs	1631	WS66_12190	betaproteobacteria	Burkholderia sp. LA-2-3-30-S1-D2	hypothetical protein WS66_12190 [Burkholderia sp. LA-2-3-30-S1-D2]	GCA_001523915.1
MBC8162005.1	<-Cluster22_2clades||TIR+TRADD-N+TPR*→ TPR-repeats+CASPASE+TM→?→ TPR-repeats→	TIR+TRADD-N+TPR	643	H7Z42_12380	Chloroflexi	Roseiflexaceae bacterium	toll/interleukin-1 receptor domain-containing protein [Roseiflexaceae bacterium].	GCA_014381165.1
MBC8265192.1	TM+APATPase+TPR+TPR→ REase+TRADD-N+Zf-TRC1+GNAT*→	REase+TRADD-N+Zf-TRC1+GNAT	524	H8E47_13840	Chloroflexi	Anaerolineales bacterium	zinc-ribbon domain containing protein [Anaerolineales bacterium].	GCA_014382145.1
MBD2211899.1	HTH+TRADD-N+Pentapeptide*→ SIG+NACHT→||||<-?||?→||||<-?||?→||||<-TRADDN+Pentapeptide+TM+TM+TM+TM+TM+Pentapeptide-repeats	HTH+TRADD-N+Pentapeptide	542	H6G27_18785	Cyanobacteria	Nostoc linckia FACHB-104	pentapeptide repeat-containing protein [Nostoc linckia FACHB-104].	GCA_014696615.1
MBE0669634.1	TIR+TRADD-N+TM+TM*→	TIR+TRADD-N+TM+TM	524	IH588_03520	Chloroflexi	Anaerolineales bacterium	TIR domain-containing protein [Anaerolineales bacterium].	GCA_014860805.1
MBE7472266.1	APATPase→ TPR-repeats→||||<-?||HTH+TRADD-N+TM+IG+GBD-PPC*→	HTH+TRADD-N+TM+IG+GBD-PPC	1056	HS114_24290	Chloroflexi	Anaerolineales bacterium	Ig-like domain-containing protein [Anaerolineales bacterium].	GCA_015075405.1
MBE7530003.1	<-TPR-repeats<-?||?→?→ STAND+TRADD-N+EAD7*→	STAND+TRADD-N+EAD7	514	HS099_09760	Chloroflexi	Ardenticatenaceae bacterium	hypothetical protein HS099_09760 [Ardenticatenaceae bacterium].	GCA_015075765.1
MBE7552287.1	TPR-repeats→||||<-?||?→ EAD7+TRADD-N+TPR+TM*→	EAD7+TRADD-N+TPR+TM	649	HS126_14560	Chloroflexi	Anaerolineales bacterium	hypothetical protein HS126_14560 [Anaerolineales bacterium].	GCA_015075185.1
MBI1926498.1	HNH+TRADD-N+Dehydrogenase-Rossmann*→	HNH+TRADD-N+Dehydrogenase-Rossmann	411	HYR99_19920	Bacteria	Candidatus Poribacteria bacterium	nucleotide sugar dehydrogenase, partial [Candidatus Poribacteria bacterium].	GCA_016178185.1
MBI5950754.1	TIR+TRADD-N+NACHT*→	TIR+TRADD-N+NACHT	624	HY865_03780	Chloroflexi	Chloroflexi bacterium	toll/interleukin-1 receptor domain-containing protein, partial [Chloroflexi bacterium].	GCA_016234555.1
NEO19477.1	<-Pkinase+GUN4+TM<-?||?→ Pentapeptide-repeats→?→||||<-?<-?||HTH+TRADD-N+Pentapeptide*→	HTH+TRADD-N+Pentapeptide	409	F6K57_08850	Cyanobacteria	Moorea sp. SIO4A5	pentapeptide repeat-containing protein [Moorea sp. SIO4A5].	GCA_010672005.1
NEO36452.1	HTH+TRADDN+Pentapeptide-repeats→?→||||<-?||?→||||<-?||HTH+TRADD-N+Pentapeptide*→	HTH+TRADD-N+Pentapeptide	493	F6J90_09010	Cyanobacteria	Moorea sp. SIOASIH	pentapeptide repeat-containing protein [Moorea sp. SIOASIH].	GCA_010671925.1
NEO62923.1	HTH+TRADD-N+Pentapeptide*→	HTH+TRADD-N+Pentapeptide	424	F6J98_21785	Cyanobacteria	Moorea sp. SIO4G2	pentapeptide repeat-containing protein [Moorea sp. SIO4G2].	GCA_010692345.1
NEO66288.1	HTH+TRADD-N+Pentapeptide*→	HTH+TRADD-N+Pentapeptide	375	F6J98_40265	Cyanobacteria	Moorea sp. SIO4G2	pentapeptide repeat-containing protein [Moorea sp. SIO4G2].	GCA_010692345.1

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NEO94808.1	Trypsin+TRADD-N+EAD7+TM+TM+TM*→	Trypsin+TRADD-N+EAD7+TM+TM+TM	672	F6K56_33295	Cyanobacteria	Moorea sp. SIO3G5	trypsin-like peptidase domain-containing protein [Moorea sp. SIO3G5].	GCA_010692495.1
NEP53221.1	HTH+TRADD-N+Pentapeptide*→	HTH+TRADD-N+Pentapeptide	622	F6K65_32240	Cyanobacteria	Moorea sp. SIO3C2	pentapeptide repeat-containing protein [Moorea sp. SIO3C2].	GCA_010692465.1
NEQ53750.1	CASPASE+TRADD-N*→	CASPASE+TRADD-N	293	F6K11_27065	Cyanobacteria	Leptolyngbya sp. SIO3F4	CHAT domain-containing protein, partial [Leptolyngbya sp. SIO3F4].	GCA_010672145.1
NEQ58411.1	<-Pkinase+GUN4+TM<-?||?→?→||||<-?||HTH+TRADD-N+Pentapeptide*→	HTH+TRADD-N+Pentapeptide	385	F6K53_13800	Cyanobacteria	Moorea sp. SIO4A1	pentapeptide repeat-containing protein [Moorea sp. SIO4A1].	GCA_010672065.1
NEQ87655.1	HTH+TRADD-N+Pentapeptide*→	HTH+TRADD-N+Pentapeptide	376	F6K26_49000	Cyanobacteria	Moorea sp. SIO2I5	pentapeptide repeat-containing protein [Moorea sp. SIO2I5].	GCA_010672285.1
NEQ87826.1	HTH+TRADD-N*→	HTH+TRADD-N	243	F6K26_49970	Cyanobacteria	Moorea sp. SIO2I5	pentapeptide repeat-containing protein, partial [Moorea sp. SIO2I5].	GCA_010672285.1
NES20938.1	HTH+TRADD-N+Pentapeptide*→	HTH+TRADD-N+Pentapeptide	574	F6K41_18895	Cyanobacteria	Caldora sp. SIO3E6	pentapeptide repeat-containing protein [Caldora sp. SIO3E6].	GCA_010672185.1
NJM06280.1	<-Cluster22_2clades||TIR+TRADD-N+TM+TPR*→ TPR-repeats→ APATPase→	TIR+TRADD-N+TM+TPR	679	HC891_08905	Bacteria	Candidatus Gracilibacteria bacterium	toll/interleukin-1 receptor domain-containing protein [Candidatus Gracilibacteria bacterium].	GCA_012031775.1
NJO84451.1	TRADD-N+TPR*→ TPR-repeats→	TRADD-N+TPR	271	HC828_17885	Alphaproteobacteria	Blastochloris sp.	tetratricopeptide repeat protein [Blastochloris sp.].	GCA_012033475.1
NJP07803.1	TRADD-N*→||||<-TCAD4+CASPASE+TM+TM+TM+TM+TM+TM	TRADD-N	500	HC837_20375	Chloroflexi	Chloroflexaceae bacterium	hypothetical protein HC837_20375 [Chloroflexaceae bacterium].	GCA_012034075.1
NQS90905.1	TRADD-N*→ HEPN→	TRADD-N	490	HQ574_00730	Chloroflexi	Chloroflexi bacterium	hypothetical protein HQ574_00730 [Chloroflexi bacterium].	GCA_013202705.1
OAE61635.1	NTase+helical-region+TRADD-N+X*→	NTase+helical-region+TRADD-N+X	526	A7J71_09945	betaproteobacteria	Achromobacter insolitus	hypothetical protein A7J71_09945 [Achromobacter insolitus]	GCA_001641515.1
OBQ35868.1	TRADD-N-aHTH1+TRADD-N+Pentapeptide*→	TRADD-N-aHTH1+TRADD-N+Pentapeptide	505	AN487_14515	cyanobacteria	Anabaena sp. CRKS33	hypothetical protein AN487_14515 [Anabaena sp. CRKS33]	GCA_001672075.1
OCQ96999.1	TRADD-N-aHTH1+TRADD-N+Pentapeptide*→	TRADD-N-aHTH1+TRADD-N+Pentapeptide	342	BCD64_15540	cyanobacteria	Nostoc sp. MBR 210	hypothetical protein BCD64_15540 [Nostoc sp. MBR 210]	GCA_001698435.1
OCY15932.1	ECF-HTH+TRADD-N+Pentapeptide*→	ECF-HTH+TRADD-N+Pentapeptide	350	BEV12_00535	cyanobacteria	Microcystis aeruginosa CACIAM 03	hypothetical protein BEV12_00535 [Microcystis aeruginosa CACIAM 03]	GCA_001706385.1
ODV36416.1	ECF-HTH+TRADD-N+Pentapeptide*→	ECF-HTH+TRADD-N+Pentapeptide	403	BFG60_4120	cyanobacteria	Microcystis aeruginosa NIES-98	Pentapeptide repeat family protein [Microcystis aeruginosa NIES-98]	GCA_001725075.1
OEU65679.1	TRADD-N+NACHT+helical-region+TPRs*→ Pentapeptide→	TRADD-N+NACHT+helical-region+TPRs	1359	BBJ57_01575	deltaproteobacteria	Desulfobacterales bacterium PC51MH44	hypothetical protein BBJ57_01575, partial [Desulfobacterales bacterium PC51MH44]	GCA_001751165.1
OGA89041.1	NTase+helical-region+TRADD-N+X*→	NTase+helical-region+TRADD-N+X	510	A2Z90_14570	betaproteobacteria	Burkholderiales bacterium GWA2_64_37	hypothetical protein A2Z90_14570 [Burkholderiales bacterium GWA2_64_37]	GCA_001770675.1

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OJJ27191.1	HTH+TRADD-N+TPRs*→ EACC2+CASPASE+STAND+TPRs→	HTH+TRADD-N+TPRs	327	BI308_01500	cyanobacteria	Roseofilum reptotaenium AO1-A	hypothetical protein BI308_01500 [Roseofilum reptotaenium AO1-A]	GCA_001890975.1
OKH33849.1	TRADD-N-aHTH1+TRADD-N+Pentapeptide*→	TRADD-N-aHTH1+TRADD-N+Pentapeptide	578	NIES2119_22150	cyanobacteria	Phormidium ambiguum IAM M-71	hypothetical protein NIES2119_22150 [Phormidium ambiguum IAM M-71]	GCA_001904725.1
OLT63091.1	TRADD-N-aHTH1+TRADD-N+Pentapeptide*→	TRADD-N-aHTH1+TRADD-N+Pentapeptide	377	BJP37_03960	cyanobacteria	Moorea bouillonii PNG	hypothetical protein BJP37_03960 [Moorea bouillonii PNG]	GCA_001942495.1
OMQ34815.1	NTase+helical-region+TRADD-N+X*→	NTase+helical-region+TRADD-N+X	520	BKP54_32310	alphaproteobacteria	Ensifer sp. 1H6	hypothetical protein BKP54_32310 [Ensifer sp. 1H6]	GCA_001976035.1
OQW92716.1	helical-region+TRADD-N+TPRs*→ EACC2+CASPASE+NACHT+68TM-wHTH+NACHT+68TM-wHTH→	helical-region+TRADD-N+TPRs	469	BWK78_00820	gammaproteobacteria	Thiotrichaceae bacterium IS1	hypothetical protein BWK78_00820 [Thiotrichaceae bacterium IS1]	GCA_002083855.1
OQX07180.1	TRADD-N+helical-region*→	TRADD-N+helical-region	473	BWK80_49815	deltaproteobacteria	Desulfobacteraceae bacterium IS3	hypothetical protein BWK80_49815 [Desulfobacteraceae bacterium IS3]	GCA_002083955.1
OUC12593.1	TRADD-N-aHTH1+TRADD-N+Pentapeptide*→	TRADD-N-aHTH1+TRADD-N+Pentapeptide	447	B0A82_21820	cyanobacteria	Alkalinema sp. CACIAM 70d	hypothetical protein B0A82_21820 [Alkalinema sp. CACIAM 70d]	GCA_002148405.1
OUL32398.1	TRADD-N-aHTH1+TRADD-N+Pentapeptide*→	TRADD-N-aHTH1+TRADD-N+Pentapeptide	387	BV375_10070	cyanobacteria	Nostoc sp. 106C	hypothetical protein BV375_10070 [Nostoc sp. 106C]	GCA_002154725.1
PBB89920.1	wHTH+TIR→ STAND→ PNPase→ TRADD-N+STAND+wHTH+TPRs*→	TRADD-N+STAND+wHTH+TPRs	1433	CK215_24450	alphaproteobacteria	Mesorhizobium sp. WSM3864	hypothetical protein CK215_24450 [Mesorhizobium sp. WSM3864]	GCA_002294955.1
PHJ69131.1	TRADD-N-aHTH1+TRADD-N+Pentapeptide*→||<-?||TM→ TRADD-N-aHTH1+TRADD-N+Pentapeptide→	TRADD-N-aHTH1+TRADD-N+Pentapeptide	417	VF02_00530	cyanobacteria	Nostoc linckia z1	hypothetical protein VF02_00530 [Nostoc linckia z1]	GCA_002607965.1
PHJ69278.1	TRADD-N-aHTH1+TRADD-N+Pentapeptide→||<-?||TM→ TRADD-N-aHTH1+TRADD-N+Pentapeptide*→	TRADD-N-aHTH1+TRADD-N+Pentapeptide	425	VF02_00510	cyanobacteria	Nostoc linckia z1	hypothetical protein VF02_00510 [Nostoc linckia z1]	GCA_002607965.1
PHJ73282.1	TRADD-N-aHTH1+TRADD-N+Pentapeptide*→	TRADD-N-aHTH1+TRADD-N+Pentapeptide	417	VF05_01545	cyanobacteria	Nostoc linckia z3	hypothetical protein VF05_01545 [Nostoc linckia z3]	GCA_002608015.1
PKP02884.1	Calcineurin+TRADD-N+STAND+wHTH+helical-region*→	Calcineurin+TRADD-N+STAND+wHTH+helical-region	1155	CVU11_10430	bacteroidetes	Bacteroidetes bacterium HGW-Bacteroidetes-6	hypothetical protein CVU11_10430 [Bacteroidetes bacterium HGW-Bacteroidetes-6]	GCA_002842495.1
PSB60411.1	TRADD-N-aHTH1+TRADD-N+Pentapeptide*→	TRADD-N-aHTH1+TRADD-N+Pentapeptide	530	C7B79_25840	cyanobacteria	Chroococcidiopsis cubana CCALA 043	hypothetical protein C7B79_25840, partial [Chroococcidiopsis cubana CCALA 043]	GCA_003003835.1
RAQ43000.1	EAD4+TRADD-N*→	EAD4+TRADD-N	223	B9S53_11830	cyanobacteria	Arthrospira sp. O9.13F	hypothetical protein B9S53_11830, partial [Arthrospira sp. O9.13F]	GCA_003268325.1
RKS67322.1	NTase+helical-region+TRADD-N+X*→	NTase+helical-region+TRADD-N+X	437	DFS04_2001	betaproteobacteria	Herbaspirillum sp. XFZ15 10_5	hypothetical protein DFS04_2001 [Herbaspirillum sp. XFZ15 10_5]	GCA_003634405.1
RLC20956.1	CASPASE+TRADD-N+TM+TM+TM+IG+FGS*→	CASPASE+TRADD-N+TM+TM+TM+IG+FGS	879	DRI57_03535	Deltaproteobacteria	Deltaproteobacteria bacterium	hypothetical protein DRI57_03535 [Deltaproteobacteria bacterium].	GCA_003647425.1

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RMF77178.1	DrHyd+TRADD-N+TIR+TPR*→	DrHyd+TRADD-N+TIR+TPR	580	D6737_18470	Chloroflexi	Chloroflexi bacterium	DUF4062 domain-containing protein [Chloroflexi bacterium].	GCA_003695675.1
RUS94453.1	HTH+TRADD-N+Pentapeptide+TM+TM*→	HTH+TRADD-N+Pentapeptide+TM+TM	484	DSM106972_093480	Cyanobacteria	Calothrix desertica PCC 7102	hypothetical protein DSM106972_093480 [Calothrix desertica PCC 7102].	GCA_003991905.1
RWI99965.1	Methylase_S→?→ HNH+TRADD-N+SF2-helicase*→	HNH+TRADD-N+SF2-helicase	1207	EOR23_31910	Alphaproteobacteria	Mesorhizobium sp.	HsdR family type I site-specific deoxyribonuclease [Mesorhizobium sp.].	GCA_004018865.1
SCY06844.1	NTase+helical-region+TRADD-N+NACHT+alpha-rich-tail*→	NTase+helical-region+TRADD-N+NACHT+alpha-rich-tail	987	SAMN05192588_0977	Bacteroidetes	Nonlabens sp. Hel1_33_55	hypothetical protein SAMN05192588_0977 [Nonlabens sp. Hel1_33_55]	GCA_900101765.1
SHF09466.1	NTase+helical-region+TRADD-N+X*→	NTase+helical-region+TRADD-N+X	504	SAMN02745157_1624	Alphaproteobacteria	Kaistia soli DSM 19436	hypothetical protein SAMN02745157_1624 [Kaistia soli DSM 19436]	GCA_900129325.1
SNS54311.1	TRADD-N+Calcineurin*→	TRADD-N+Calcineurin	465	SAMN04488107_2944	Actinobacteria	Geodermatophilus saharensis	3',5'-cyclic AMP phosphodiesterase CpdA [Geodermatophilus saharensis].	GCA_900188205.1
TEU17517.1	TIR+TRADD-N+TM+CBM9*→	TIR+TRADD-N+TM+CBM9	464	E3J21_08170	Chloroflexi	Anaerolineales bacterium	TIR domain-containing protein [Anaerolineales bacterium].	GCA_004377365.1
TXI20304.1	SIG+TIR+TRADD-N+NACHT+68TM-wHTH*→||||<-PCRF+RF-1	SIG+TIR+TRADD-N+NACHT+68TM-wHTH	892	E6Q62_02005	Betaproteobacteria	Nitrosomonas sp.	TIR domain-containing protein [Nitrosomonas sp.].	GCA_008015565.1
WP_002751650.1	ECF-HTH+TRADD-N+Pentapeptide*→	ECF-HTH+TRADD-N+Pentapeptide	470	-	cyanobacteria	Microcystis aeruginosa	pentapeptide repeat-containing protein [Microcystis aeruginosa]	GCF_000307995.1
WP_002759140.1	ECF-HTH+TRADD-N+Pentapeptide*→	ECF-HTH+TRADD-N+Pentapeptide	450	-	cyanobacteria	Microcystis aeruginosa	pentapeptide repeat-containing protein [Microcystis aeruginosa]	GCF_000312165.1
WP_002766355.1	ECF-HTH+TRADD-N+Pentapeptide*→	ECF-HTH+TRADD-N+Pentapeptide	432	-	cyanobacteria	Microcystis aeruginosa	hypothetical protein [Microcystis aeruginosa]	GCF_000312185.1
WP_002781357.1	ECF-HTH+TRADD-N+Pentapeptide*→	ECF-HTH+TRADD-N+Pentapeptide	405	-	cyanobacteria	Microcystis aeruginosa	pentapeptide repeat-containing protein [Microcystis aeruginosa]	GCF_000312725.1
WP_002790455.1	ECF-HTH+TRADD-N+Pentapeptide*→	ECF-HTH+TRADD-N+Pentapeptide	432	-	cyanobacteria	Microcystis aeruginosa	pentapeptide repeat-containing protein [Microcystis aeruginosa]	GCF_000312225.1
WP_002790923.1	ECF-HTH+TRADD-N+Pentapeptide*→	ECF-HTH+TRADD-N+Pentapeptide	425	-	cyanobacteria	Microcystis aeruginosa	pentapeptide repeat-containing protein [Microcystis aeruginosa]	GCF_000312245.1
WP_002798711.1	ECF-HTH+TRADD-N+Pentapeptide*→	ECF-HTH+TRADD-N+Pentapeptide	442	-	cyanobacteria	Microcystis aeruginosa	pentapeptide repeat-containing protein [Microcystis aeruginosa]	GCF_000312265.1
WP_006508060.1	TRADD-N+Pentapeptide*→	TRADD-N+Pentapeptide	393	-	cyanobacteria	Xenococcus sp. PCC 7305	pentapeptide repeat-containing protein [Xenococcus sp. PCC 7305]	GCF_000332055.1
WP_006624703.1	EAD4+TRADD-N+STAND+wHTH+HEAT_repeats*→	EAD4+TRADD-N+STAND+wHTH+HEAT_repeats	1746	-	cyanobacteria	Arthrospira platensis	NACHT domain-containing protein [Arthrospira platensis]	GCF_000307915.1
WP_006669967.1	EAD4+TRADD-N+STAND+wHTH+HEAT_repeats*→	EAD4+TRADD-N+STAND+wHTH+HEAT_repeats	1822	-	cyanobacteria	Arthrospira maxima	NACHT domain-containing protein [Arthrospira maxima]	-
WP_006669976.1	HTH+TRADD-N+STAND+wHTH+HEAT_repeats*→	HTH+TRADD-N+STAND+wHTH+HEAT_repeats	1177	-	cyanobacteria	Arthrospira maxima	NACHT domain-containing protein [Arthrospira maxima]	-
WP_007303210.1	TRADD-N*→	TRADD-N	131	-	cyanobacteria	Crocosphaera watsonii	hypothetical protein [Crocosphaera watsonii]	GCF_000167195.1
WP_007311526.1	TRADD-N+Pentapeptide*→	TRADD-N+Pentapeptide	323	-	cyanobacteria	Crocosphaera watsonii	pentapeptide repeat-containing protein [Crocosphaera watsonii]	GCF_000235665.1
WP_007686738.1	ZNR+HTH+HTH+TIR→ PNPase+TRADD-N+STAND+wHTH+TPRs*→??+HEPN→??+SIR2+??+STAND→	PNPase+TRADD-N+STAND+wHTH+TPRs	1737	-	alphaproteobacteria	Sphingomonadaceae	MULTISPECIES: hypothetical protein [Sphingomonadaceae]	GCF_000264945.2

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WP_008050000.1	EAD4+TRADD-N+STAND+wHTH+HEAT_repeats*→	EAD4+TRADD-N+STAND+wHTH+HEAT_repeats	1378	-	cyanobacteria	Arthrospira sp. PCC 8005	NACHT domain-containing protein [Arthrospira sp. PCC 8005]	GCF_000176895.2
WP_008177582.1	TRADD-N-aHTH1+TRADD-N+Pentapeptide*→	TRADD-N-aHTH1+TRADD-N+Pentapeptide	544	-	cyanobacteria	Moorea producens	hypothetical protein [Moorea producens]	GCF_000211815.1
WP_008190049.1	TRADD-N-aHTH1+TRADD-N+Pentapeptide*→	TRADD-N-aHTH1+TRADD-N+Pentapeptide	383	-	cyanobacteria	Moorea producens	low-complexity protein [Moorea producens]	GCF_000211815.1
WP_008203869.1	ECF-HTH+TRADD-N+Pentapeptide*→	ECF-HTH+TRADD-N+Pentapeptide	436	-	cyanobacteria	Microcystis sp. T1-4	pentapeptide repeat-containing protein [Microcystis sp. T1-4]	GCF_000297435.1
WP_009545863.1	preATP-grasp+BtrJ-ATPgrasp+alpha/beta-Hammerhead/Barrel-sandwich_hybrid→ TRADD-N+Pentapeptide*→ TM_region→ Aldose_epim→ tRNA→	TRADD-N+Pentapeptide	325	-	cyanobacteria	Cyanothece	MULTISPECIES: pentapeptide repeat-containing protein [Cyanothece]	GCF_000017845.1
WP_012167159.1	TPR-repeats+CASPASE→||||<-?<-SIG+Pkinase+TM+TPR<-?<-?||?→?→ PNPase+TRADD-N+HTH*→	PNPase+TRADD-N+HTH	576	-	Cyanobacteria	Acaryochloris marina	hypothetical protein [Acaryochloris marina].	GCF_000018105.1
WP_012362559.1	HTH→ TRADD-N+TPRs*→||<-Pentapeptide+TM_region+Pentapeptide+EACC2+CASPASE	TRADD-N+TPRs	348	-	cyanobacteria	Cyanothece	MULTISPECIES: DUF1822 family protein [Cyanothece]	-
WP_012599489.1	TRADD-N-aHTH1+TRADD-N+TPRs*→ EACC2+CASPASE+APATPase+GUN4→??→	TRADD-N-aHTH1+TRADD-N+TPRs	326	-	cyanobacteria	Cyanothece sp. PCC 7424	hypothetical protein [Cyanothece sp. PCC 7424]	GCF_000021825.1
WP_014276969.1	EAD4+TRADD-N+STAND→ *PSE→||<-EAD4+TRADD-N+STAND*	EAD4+TRADD-N+STAND	525	-	cyanobacteria	Arthrospira platensis	NACHT domain-containing protein [Arthrospira platensis]	-
WP_015117156.1	EAD1+TRADD-N+GUN4*→ AAA+HEAT_repeats→ STAND+HEAT_repeats+TM→	EAD1+TRADD-N+GUN4	351	-	cyanobacteria	Rivularia sp. PCC 7116	GUN4 protein [Rivularia sp. PCC 7116]	GCF_000316665.1
WP_015117657.1	TRADD-N+Pentapeptide*→	TRADD-N+Pentapeptide	312	-	cyanobacteria	Rivularia sp. PCC 7116	pentapeptide repeat-containing protein [Rivularia sp. PCC 7116]	GCF_000316665.1
WP_015121169.1	TRADD-N-aHTH1+TRADD-N+Pentapeptide*→	TRADD-N-aHTH1+TRADD-N+Pentapeptide	487	-	cyanobacteria	Rivularia sp. PCC 7116	pentapeptide repeat-containing protein [Rivularia sp. PCC 7116]	GCF_000316665.1
WP_015121187.1	ADH_N+ADH_zinc_N→ TRADD-N+Pentapeptide*→	TRADD-N+Pentapeptide	436	-	cyanobacteria	Rivularia sp. PCC 7116	putative low-complexity protein [Rivularia sp. PCC 7116]	GCF_000316665.1
WP_015128708.1	helical-region+TRADD-N+TPRs*→ EACC2+CASPASE+DZR+DZR+Pkinase→	helical-region+TRADD-N+TPRs	453	-	cyanobacteria	Calothrix sp. PCC 7507	DUF1822 family protein [Calothrix sp. PCC 7507]	GCF_000316575.1
WP_015139478.1	TRADD-N-aHTH1+TRADD-N+TPRs*→	TRADD-N-aHTH1+TRADD-N+TPRs	360	-	cyanobacteria	Nostoc sp. PCC 7524	hypothetical protein [Nostoc sp. PCC 7524]	GCF_000316645.1
WP_015148075.1	EAD4+TRADD-N+TPRs*→ EACC2+CASPASE+TM_region→ Acetyltransf→	EAD4+TRADD-N+TPRs	415	-	cyanobacteria	Oscillatoria acuminata	DUF1822 family protein [Oscillatoria acuminata]	-
WP_015150426.1	HTH+TRADD-N+TPRs*→	HTH+TRADD-N+TPRs	362	-	cyanobacteria	Oscillatoria acuminata	DUF1822 family protein [Oscillatoria acuminata]	GCF_000317105.1
WP_015195683.1	HTH+TRADD-N+TPRs*→	HTH+TRADD-N+TPRs	433	-	cyanobacteria	Stanieria cyanosphaera	DUF1822 family protein [Stanieria cyanosphaera]	GCF_000317575.1
WP_015217750.1	TRADD-N-aHTH1+TRADD-N+Pentapeptide*→	TRADD-N-aHTH1+TRADD-N+Pentapeptide	475	-	cyanobacteria	Anabaena cylindrica	transcriptional regulator, XRE family [Anabaena cylindrica]	GCF_000317695.1
WP_016516706.1	ECF-HTH+TRADD-N+Pentapeptide*→	ECF-HTH+TRADD-N+Pentapeptide	425	-	cyanobacteria	Microcystis aeruginosa	pentapeptide repeat-containing protein [Microcystis aeruginosa]	GCF_000412595.1
WP_016562538.1	TRADD-N-aHTH1+TRADD-N+Pentapeptide*→	TRADD-N-aHTH1+TRADD-N+Pentapeptide	459	-	cyanobacteria	Trichormus variabilis	pentapeptide repeat-containing protein [Trichormus variabilis]	-
WP_016867683.1	??→ TRADD-N+TPRs*→ EACC2+CASPASE+CHASE2+TM+TM→ TM+beta_rich+TPRs→ TPRs+CASPASE→	TRADD-N+TPRs	204	-	cyanobacteria	Fischerella	MULTISPECIES: DUF1822 family protein [Fischerella]	-
WP_017298126.1	HTH+HTH+TRADD-N+VMAP-M0*→	HTH+HTH+TRADD-N+VMAP-M0	427	-	cyanobacteria	Nodosilinea nodulosa	sigma-70 family RNA polymerase sigma factor [Nodosilinea nodulosa]	GCF_000309385.1

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WP_017307182.1	TRADD-N+helical-region*→	TRADD-N+helical-region	543	-	cyanobacteria	Spirulina subsalsa	hypothetical protein [Spirulina subsalsa]	GCF_000314005.1
WP_017719549.1	??→ HTH+TRADD-N+TPRs*→ EACC2+CASPASE+BetaPropeller→	HTH+TRADD-N+TPRs	401	-	cyanobacteria	Oscillatoria sp. PCC 10802	DUF1822 family protein [Oscillatoria sp. PCC 10802]	GCF_000332335.1
WP_019486969.1	TRADD-N-aHTH1+TRADD-N+Pentapeptide*→	TRADD-N-aHTH1+TRADD-N+Pentapeptide	490	-	cyanobacteria	Kamptonema formosum	pentapeptide repeat-containing protein [Kamptonema formosum]	GCF_000332155.1
WP_019496109.1	TRADD-N-aHTH1+TRADD-N+Pentapeptide*→	TRADD-N-aHTH1+TRADD-N+Pentapeptide	768	-	cyanobacteria	Calothrix sp. PCC 7103	hypothetical protein [Calothrix sp. PCC 7103]	GCF_000331305.1
WP_019496191.1	TRADD-N-aHTH1+TRADD-N+Pentapeptide+TPRs→||<-?||TRADD-N-aHTH1+TRADD-N+Pentapeptide→ TRADD-N-aHTH1+TRADD-N+Pentapeptide+TPRs*→||<-TM+TM+TM	TRADD-N-aHTH1+TRADD-N+Pentapeptide+TPRs	702	-	cyanobacteria	Calothrix sp. PCC 7103	hypothetical protein [Calothrix sp. PCC 7103]	-
WP_019496192.1	TRADD-N-aHTH1+TRADD-N+Pentapeptide+TPRs→||<-?||TRADD-N-aHTH1+TRADD-N+Pentapeptide*→ TRADD-N-aHTH1+TRADD-N+Pentapeptide+TPRs→||<-TM+TM+TM	TRADD-N-aHTH1+TRADD-N+Pentapeptide	324	-	cyanobacteria	Calothrix sp. PCC 7103	pentapeptide repeat-containing protein [Calothrix sp. PCC 7103]	GCF_000331305.1
WP_019496194.1	TRADD-N-aHTH1+TRADD-N+Pentapeptide+TPRs*→||<-?||TRADD-N-aHTH1+TRADD-N+Pentapeptide→ TRADD-N-aHTH1+TRADD-N+Pentapeptide+TPRs→||<-TM+TM+TM	TRADD-N-aHTH1+TRADD-N+Pentapeptide+TPRs	583	-	cyanobacteria	Calothrix sp. PCC 7103	hypothetical protein [Calothrix sp. PCC 7103]	GCF_000331305.1
WP_019496514.1	TRADD-N-aHTH1+TRADD-N+Pentapeptide*→	TRADD-N-aHTH1+TRADD-N+Pentapeptide	950	-	cyanobacteria	Calothrix sp. PCC 7103	hypothetical protein [Calothrix sp. PCC 7103]	-
WP_019606632.1	TM+helical-region→ TIR+TRADD-N*→	TIR+TRADD-N	342	-	gammaproteobacteria	Teredinibacter turnerae	toll/interleukin-1 receptor domain-containing protein [Teredinibacter turnerae]	GCF_000381665.1
WP_020471543.1	HTH+TRADD-N+TM+TM*→??→	HTH+TRADD-N+TM+TM	461	-	planctomycetes	Zavarzinella formosa	hypothetical protein [Zavarzinella formosa]	-
WP_021831880.1	TRADD-N*→	TRADD-N	113	-	cyanobacteria	Crocosphaera watsonii	hypothetical protein [Crocosphaera watsonii]	GCF_001039555.1
WP_023669251.1	HNH+TRADD-N+STAND+TPRs*→	HNH+TRADD-N+STAND+TPRs	1617	-	alphaproteobacteria	Mesorhizobium	MULTISPECIES: AAA family ATPase [Mesorhizobium]	-
WP_023692716.1	HNH+TRADD-N+STAND+TPRs*→	HNH+TRADD-N+STAND+TPRs	1617	-	alphaproteobacteria	Mesorhizobium	MULTISPECIES: AAA family ATPase [Mesorhizobium]	-
WP_026099162.1	HTH+TRADD-N+TPRs*→ Pentapeptide+TM_region+Pentapeptide+EACC2+CASPASE→	HTH+TRADD-N+TPRs	305	-	cyanobacteria	Oscillatoria sp. PCC 10802	DUF1822 family protein [Oscillatoria sp. PCC 10802]	-
WP_026724013.1	TRADD-N-aHTH1+TRADD-N+Pentapeptide*→	TRADD-N-aHTH1+TRADD-N+Pentapeptide	426	-	cyanobacteria	Fischerella sp. PCC 9431	hypothetical protein [Fischerella sp. PCC 9431]	GCF_000447295.1
WP_027029362.1	PNPase+TRADD-N+STAND+wHTH+TPRs*→ SIR2+??→	PNPase+TRADD-N+STAND+wHTH+TPRs	1737	-	alphaproteobacteria	Mesorhizobium loti	hypothetical protein [Mesorhizobium loti]	GCF_013170845.1
WP_029630437.1	HTH+TRADD-N+TM+TM*→??→	HTH+TRADD-N+TM+TM	435	-	planctomycetes	Zavarzinella formosa	XRE family transcriptional regulator [Zavarzinella formosa]	GCF_000255705.1
WP_032992391.1	NTase+helical-region+TRADD-N+X*→	NTase+helical-region+TRADD-N+X	511	-	alphaproteobacteria	Rhizobium leguminosarum	hypothetical protein [Rhizobium leguminosarum]	GCF_000427765.1
WP_035737013.1	EAD4+TRADD-N+STAND→*//<-PSE<-EAD4+TRADD-N+STAND*	EAD4+TRADD-N+STAND	525	-	cyanobacteria	Arthrospira platensis	NACHT domain-containing protein [Arthrospira platensis]	GCF_000175415.3
WP_036402801.1	ECF-HTH+TRADD-N+Pentapeptide*→	ECF-HTH+TRADD-N+Pentapeptide	405	-	cyanobacteria	Microcystis aeruginosa	pentapeptide repeat-containing protein [Microcystis aeruginosa]	GCF_000332585.1
WP_041005222.1	PNPase+TRADD-N+STAND+wHTH+TPRs*→	PNPase+TRADD-N+STAND+wHTH+TPRs	1731	-	alphaproteobacteria	Mesorhizobium plurifarium	AAA family ATPase [Mesorhizobium plurifarium]	-
WP_042790997.1	ECF-HTH+TRADD-N+Pentapeptide*→	ECF-HTH+TRADD-N+Pentapeptide	435	-	cyanobacteria	Microcystis aeruginosa	pentapeptide repeat-containing protein [Microcystis aeruginosa]	GCF_000330925.1
WP_045056756.1	helical-region+TRADD-N+TM*→	helical-region+TRADD-N+TM	333	-	cyanobacteria	Aliterella atlantica	hypothetical protein [Aliterella atlantica]	-
WP_045361906.1	ECF-HTH+TRADD-N+Pentapeptide*→	ECF-HTH+TRADD-N+Pentapeptide	440	-	cyanobacteria	Microcystis aeruginosa	pentapeptide repeat-containing protein [Microcystis aeruginosa]	GCF_000787675.1

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WP_046320853.1	HTH+TRADD-N+STAND+wHTH+HEAT_repeats*→	HTH+TRADD-N+STAND+wHTH+HEAT_repeats	1162	-	cyanobacteria	Arthrospira	MULTISPECIES: NACHT domain-containing protein [Arthrospira]	-
WP_051502925.1	helical-region+TRADD-N+TPRs*→ EACC2+CASPASE+DZR+Pkinase→	helical-region+TRADD-N+TPRs	511	-	cyanobacteria	[Scytonema hofmanni] UTEX B 1581	DUF1822 family protein [[Scytonema hofmanni] UTEX B 1581]	GCF_014698435.1
WP_051503073.1	TRADD-N-aHTH1+TRADD-N+Pentapeptide*→	TRADD-N-aHTH1+TRADD-N+Pentapeptide	383	-	cyanobacteria	[Scytonema hofmanni] UTEX B 1581	hypothetical protein [[Scytonema hofmanni] UTEX B 1581]	GCF_000582685.1
WP_052277454.1	ECF-HTH+TRADD-N+Pentapeptide*→	ECF-HTH+TRADD-N+Pentapeptide	432	-	cyanobacteria	Microcystis aeruginosa	pentapeptide repeat-containing protein [Microcystis aeruginosa]	GCF_014218745.1
WP_052490229.1	helical-region+TRADD-N+TPRs*→	helical-region+TRADD-N+TPRs	469	-	cyanobacteria	Tolypothrix campylonemoides	DUF1822 family protein [Tolypothrix campylonemoides]	-
WP_053458907.1	HTH→ TRADD-N+Pentapeptide*→	TRADD-N+Pentapeptide	252	-	cyanobacteria	Hapalosiphon sp. MRB220	pentapeptide repeat-containing protein [Hapalosiphon sp. MRB220]	-
WP_054359398.1	PNPase+TRADD-N+STAND+wHTH+TPRs*→	PNPase+TRADD-N+STAND+wHTH+TPRs	1763	-	alphaproteobacteria	Prosthecomicrobium hirschii	AAA family ATPase [Prosthecomicrobium hirschii]	GCF_001305515.1
WP_054465896.1	TM→??→ TRADD-N-aHTH1+TRADD-N+TPRs*→	TRADD-N-aHTH1+TRADD-N+TPRs	325	-	cyanobacteria	Planktothricoides sp. SR001	DUF1822 family protein [Planktothricoides sp. SR001]	GCF_001276715.1
WP_054466474.1	EAD4→ TRADD-N+TPRs*→ EACC2+CASPASE+TM_region→ TM+TM+TM→	TRADD-N+TPRs	287	-	cyanobacteria	Planktothricoides sp. SR001	DUF1822 family protein [Planktothricoides sp. SR001]	GCF_001276715.1
WP_058183652.1	TRADD-N-aHTH1+TRADD-N+Pentapeptide*→	TRADD-N-aHTH1+TRADD-N+Pentapeptide	404	-	cyanobacteria	Mastigocoleus testarum	pentapeptide repeat-containing protein [Mastigocoleus testarum]	GCF_001456025.1
WP_061431382.1	ECF-HTH+TRADD-N+Pentapeptide*→	ECF-HTH+TRADD-N+Pentapeptide	427	-	cyanobacteria	Microcystis aeruginosa	pentapeptide repeat-containing protein [Microcystis aeruginosa]	GCF_001578075.1
WP_062291418.1	TRADD-N-aHTH1+TRADD-N+Pentapeptide*→	TRADD-N-aHTH1+TRADD-N+Pentapeptide	350	-	cyanobacteria	Nostoc piscinale	pentapeptide repeat-containing protein [Nostoc piscinale]	GCF_001298445.1
WP_062587307.1	PNPase+TRADD-N+STAND+wHTH+TPRs*→ SLATT→	PNPase+TRADD-N+STAND+wHTH+TPRs	1417	-	alphaproteobacteria	Rhizobium sp. Leaf311	ATP-binding protein [Rhizobium sp. Leaf311]	GCF_001423445.1
WP_063712050.1	TRADD-N-aHTH1+TRADD-N+Pentapeptide*→	TRADD-N-aHTH1+TRADD-N+Pentapeptide	463	-	cyanobacteria	Coleofasciculus chthonoplastes	pentapeptide repeat-containing protein [Coleofasciculus chthonoplastes]	GCF_000155555.1
WP_064835079.1	NTase+helical-region+TRADD-N+X*→	NTase+helical-region+TRADD-N+X	517	-	alphaproteobacteria	Rhizobium phaseoli	hypothetical protein [Rhizobium phaseoli]	-
WP_068789484.1	EAD4+TRADD-N+STAND+wHTH+HEAT_repeats*→	EAD4+TRADD-N+STAND+wHTH+HEAT_repeats	1398	-	cyanobacteria	Phormidium willei	NACHT domain-containing protein [Phormidium willei]	GCF_001637315.1
WP_069475331.1	ECF-HTH+TRADD-N+Pentapeptide*→	ECF-HTH+TRADD-N+Pentapeptide	410	-	cyanobacteria	Microcystis aeruginosa	pentapeptide repeat-containing protein [Microcystis aeruginosa]	GCF_001725075.1
WP_070393194.1	TRADD-N-aHTH1+TRADD-N+Pentapeptide*→	TRADD-N-aHTH1+TRADD-N+Pentapeptide	514	-	cyanobacteria	Moorea producens	hypothetical protein [Moorea producens]	GCF_001767235.1
WP_071102675.1	TRADD-N-aHTH1+TRADD-N+Pentapeptide→ TRADD-N-aHTH1+TRADD-N+Pentapeptide*→||<-?<-?||TRADD-N-aHTH1+TRADD-N+Pentapeptide→	TRADD-N-aHTH1+TRADD-N+Pentapeptide	499	-	cyanobacteria	Moorea producens	hypothetical protein [Moorea producens]	GCF_001854205.1
WP_071104586.1	TRADD-N+Pentapeptide*→	TRADD-N+Pentapeptide	201	-	cyanobacteria	Moorea producens	pentapeptide repeat-containing protein [Moorea producens]	GCF_001854205.1
WP_071107626.1	TRADD-N-aHTH1+TRADD-N+Pentapeptide*→ TRADD-N-aHTH1+TRADD-N+Pentapeptide→||<-?<-?||TRADD-N-aHTH1+TRADD-N+Pentapeptide→	TRADD-N-aHTH1+TRADD-N+Pentapeptide	568	-	cyanobacteria	Moorea producens	pentapeptide repeat-containing protein [Moorea producens]	GCF_001854205.1
WP_072619436.1	TRADD-N+helical-region*→	TRADD-N+helical-region	533	-	cyanobacteria	Spirulina major	hypothetical protein [Spirulina major]	GCF_001890765.1
WP_072722590.1	HTH+TRADD-N+helical-region*→ TPR_region+CASPASE→	HTH+TRADD-N+helical-region	316	-	cyanobacteria	Planktothrix tepida	XRE family transcriptional regulator [Planktothrix tepida]	GCF_900009145.1

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WP_072926218.1	ECF-HTH+TRADD-N+Pentapeptide*→	ECF-HTH+TRADD-N+Pentapeptide	352	-	cyanobacteria	Microcystis aeruginosa	pentapeptide repeat-containing protein, partial [Microcystis aeruginosa]	GCF_001895325.1
WP_073555229.1	??→ TRADD-N+TPRs*→ EACC2+CASPASE+CHASE2+TM+TM→ TM+beta_rich+TPRs→ TPRs+CASPASE→	TRADD-N+TPRs	204	-	cyanobacteria	Fischerella major	DUF1822 family protein [Fischerella major]	-
WP_073619092.1	TRADD-N-aHTH1+TRADD-N+Pentapeptide+TPRs+Pentapeptide*→	TRADD-N-aHTH1+TRADD-N+Pentapeptide+TPRs+Pentapeptide	782	-	cyanobacteria	Calothrix sp. HK-06	hypothetical protein [Calothrix sp. HK-06]	GCF_001904745.1
WP_075224986.1	PNPase+TRADD-N+STAND+wHTH+TPRs*→	PNPase+TRADD-N+STAND+wHTH+TPRs	1748	-	alphaproteobacteria	Rhizobium leguminosarum	hypothetical protein [Rhizobium leguminosarum]	GCF_001927265.1
WP_077514517.1	HNH+TRADD-N+SNF2-helicase+LPD33*→	HNH+TRADD-N+SNF2-helicase+LPD33	1204	-	Gammaproteobacteria	Rhodanobacter sp. B05	DEAD/DEAH box helicase family protein [Rhodanobacter sp. B05].	GCF_002001085.1
WP_079209656.1	ECF-HTH+TRADD-N+Pentapeptide+TRADD-N+Pentapeptide*→ DDE+DDE_Tnp_1→ Heme_oxygenase→	ECF-HTH+TRADD-N+Pentapeptide+TRADD-N+Pentapeptide	620	-	cyanobacteria	Microcystis aeruginosa	pentapeptide repeat-containing protein [Microcystis aeruginosa]	-
WP_080880220.1	TIR+TRADD-N+NACHT+68TM+wHTH*→	TIR+TRADD-N+NACHT+68TM+wHTH	917	-	nitrospirae	Nitrospira sp. ND1	TIR domain-containing protein [Nitrospira sp. ND1]	GCF_900170025.1
WP_081431064.1	TRADD-N-aHTH1+TRADD-N+Pentapeptide*→	TRADD-N-aHTH1+TRADD-N+Pentapeptide	389	-	cyanobacteria	Moorea bouillonii	pentapeptide repeat-containing protein [Moorea bouillonii]	GCF_001942495.1
WP_081618935.1	alpha-helical-protein→ TRADD-N+Pentapeptide*→ ISOCOT_Eif2b→	TRADD-N+Pentapeptide	383	-	cyanobacteria	filamentous cyanobacterium ESFC-1	hypothetical protein [filamentous cyanobacterium ESFC-1]	-
WP_082241536.1	TRADD-N+AB_hydrolase*→	TRADD-N+AB_hydrolase	362	-	alphaproteobacteria	Rhodovulum sulfidophilum	hypothetical protein [Rhodovulum sulfidophilum]	GCF_001548075.1
WP_082348721.1	??→ TRADD-N+TPRs*→ BrnT_toxin→ CopG_antitoxin→	TRADD-N+TPRs	188	-	cyanobacteria	Planktothricoides sp. SR001	DUF1822 family protein [Planktothricoides sp. SR001]	-
WP_082728980.1	PNPase+TRADD-N+STAND+wHTH+TPRs*→	PNPase+TRADD-N+STAND+wHTH+TPRs	1725	-	betaproteobacteria	Burkholderia sp. LA-2-3-30-S1-D2	hypothetical protein [Burkholderia sp. LA-2-3-30-S1-D2]	GCF_001523915.2
WP_083304982.1	TRADD-N-aHTH1+TRADD-N+Pentapeptide*→ TRADD-N-aHTH1+TRADD-N+Pentapeptide→?→||<-?||TRADD-N-aHTH1+TRADD-N+Pentapeptide→	TRADD-N-aHTH1+TRADD-N+Pentapeptide	591	-	cyanobacteria	Moorea producens	pentapeptide repeat-containing protein [Moorea producens]	-
WP_083304983.1	TRADD-N-aHTH1+TRADD-N+Pentapeptide→ TRADD-N-aHTH1+TRADD-N+Pentapeptide*→?→||<-?||TRADD-N-aHTH1+TRADD-N+Pentapeptide→	TRADD-N-aHTH1+TRADD-N+Pentapeptide	487	-	cyanobacteria	Moorea producens	pentapeptide repeat-containing protein [Moorea producens]	GCF_001767235.1
WP_083304984.1	TRADD-N-aHTH1+TRADD-N+Pentapeptide→ TRADD-N-aHTH1+TRADD-N+Pentapeptide→?→||<-?||TRADD-N-aHTH1+TRADD-N+Pentapeptide*→	TRADD-N-aHTH1+TRADD-N+Pentapeptide	352	-	cyanobacteria	Moorea producens	pentapeptide repeat-containing protein [Moorea producens]	GCF_001767235.1
WP_083374064.1	TRADD-N-aHTH1+TRADD-N+Pentapeptide→ TRADD-N-aHTH1+TRADD-N+Pentapeptide→||<-?<-?||TRADD-N-aHTH1+TRADD-N+Pentapeptide*→	TRADD-N-aHTH1+TRADD-N+Pentapeptide	372	-	cyanobacteria	Moorea producens	pentapeptide repeat-containing protein [Moorea producens]	GCF_001854205.1
WP_083604910.1	TRADD-N+REC+HISKIN+REC*→	TRADD-N+REC+HISKIN+REC	599	-	cyanobacteria	Calothrix sp. HK-06	response regulator [Calothrix sp. HK-06]	-
WP_083825169.1	TM+TM+TM→ TIR→ TIR+TRADD-N+DsrC_HTH*→	TIR+TRADD-N+DsrC_HTH	276	-	gammaproteobacteria	endosymbiont of Tevnia jerichonana	TusE/DsrC/DsvC family sulfur relay protein [endosymbiont of Tevnia jerichonana]	GCF_000224925.1
WP_083853982.1	HNH+TRADD-N+STAND+TPRs*→	HNH+TRADD-N+STAND+TPRs	1629	-	alphaproteobacteria	Sinorhizobium sp. CCBAU 05631	AAA family ATPase [Sinorhizobium sp. CCBAU 05631]	-
WP_084555219.1	CASPASE+HTH+TRADD-N+Pentapeptide*→	CASPASE+HTH+TRADD-N+Pentapeptide	749	-	cyanobacteria	Phormidium ambiguum	CHAT domain-containing protein [Phormidium ambiguum]	-
WP_084613256.1	HTH+TRADD-N+STAND+HEAT_repeats*→	HTH+TRADD-N+STAND+HEAT_repeats	1228	-	cyanobacteria	Planktothrix rubescens	NACHT domain-containing protein [Planktothrix rubescens]	GCF_000464785.1
WP_086759910.1	TRADD-N-aHTH1+TRADD-N+Pentapeptide*→	TRADD-N-aHTH1+TRADD-N+Pentapeptide	415	-	cyanobacteria	Nostoc sp. 106C	hypothetical protein [Nostoc sp. 106C]	GCF_002154725.1

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WP_086834672.1	TRADD-N+Pentapeptide*→	TRADD-N+Pentapeptide	120	-	cyanobacteria	Nostoc sp. RF31Y	hypothetical protein [Nostoc sp. RF31Y]	GCF_002155185.1
WP_086834681.1	TM→ TRADD-N-aHTH1+TRADD-N+Pentapeptide*→	TRADD-N-aHTH1+TRADD-N+Pentapeptide	373	-	cyanobacteria	Nostoc sp. RF31Y	pentapeptide repeat-containing protein [Nostoc sp. RF31Y]	GCF_002155185.1
WP_088240080.1	TRADD-N+TPRs*→	TRADD-N+TPRs	191	-	cyanobacteria	Calothrix rhizosoleniae	DUF1822 family protein [Calothrix rhizosoleniae]	GCF_900185595.1
WP_088430566.1	TIR+TRADD-N+??*→ APATPase→ TPRs→	TIR+TRADD-N+??	347	-	cyanobacteria	Halomicronema hongdechloris	toll/interleukin-1 receptor domain-containing protein [Halomicronema hongdechloris]	GCF_002075285.3
WP_089126482.1	TRADD-N-aHTH1+TRADD-N+Pentapeptide*→	TRADD-N-aHTH1+TRADD-N+Pentapeptide	426	-	cyanobacteria	Tolypothrix sp. NIES-4075	hypothetical protein [Tolypothrix sp. NIES-4075]	GCF_002218085.1
WP_091585698.1	HNH+TRADD-N+STAND+TPRs*→	HNH+TRADD-N+STAND+TPRs	1614	-	alphaproteobacteria	Mesorhizobium qingshengii	AAA family ATPase [Mesorhizobium qingshengii]	GCF_900103325.1
WP_094530172.1	HTH+TRADD-N+TPRs*→ EACC2+CASPASE+STAND+BetaPropeller+PDZ+BetaPropeller→	HTH+TRADD-N+TPRs	358	-	cyanobacteria	Pseudanabaena sp. SR411	DUF1822 family protein [Pseudanabaena sp. SR411]	GCF_002251945.1
WP_094672516.1	TRADD-N+Pentapeptide*→	TRADD-N+Pentapeptide	457	-	cyanobacteria	Hydrocoleum sp. CS-953	hypothetical protein [Hydrocoleum sp. CS-953]	GCF_002260545.1
WP_094672636.1	helical-region+TRADD-N+TPRs*→ XisI→	helical-region+TRADD-N+TPRs	356	-	cyanobacteria	Hydrocoleum sp. CS-953	DUF1822 family protein [Hydrocoleum sp. CS-953]	GCF_002260545.1
WP_094676040.1	TRADD-N+Pentapeptide*→	TRADD-N+Pentapeptide	439	-	cyanobacteria	Hydrocoleum sp. CS-953	hypothetical protein [Hydrocoleum sp. CS-953]	-
WP_095496078.1	PNPase+TRADD-N+STAND+wHTH+TPRs*→	PNPase+TRADD-N+STAND+wHTH+TPRs	1728	-	alphaproteobacteria	Mesorhizobium temperatum	AAA family ATPase [Mesorhizobium temperatum]	GCF_002284575.1
WP_095825962.1	wHTH+TIR→ STAND→ PNPase+TRADD-N+STAND+wHTH+TPRs*→	PNPase+TRADD-N+STAND+wHTH+TPRs	1770	-	alphaproteobacteria	Mesorhizobium sp. WSM3882	hypothetical protein [Mesorhizobium sp. WSM3882]	GCF_002294765.1
WP_096606018.1	HTH→ TRADD-N+TPRs*→ CASPASE+TM_region→ SIG+TM+Abi→	TRADD-N+TPRs	196	-	cyanobacteria	Calothrix sp. NIES-2100	DUF1822 family protein [Calothrix sp. NIES-2100]	GCF_002368195.1
WP_096648825.1	TRADD-N-aHTH1+TRADD-N+Pentapeptide*→	TRADD-N-aHTH1+TRADD-N+Pentapeptide	478	-	cyanobacteria	Calothrix brevissima	pentapeptide repeat-containing protein [Calothrix brevissima]	GCF_002367995.1
WP_096655265.1	TRADD-N+Pentapeptide*→	TRADD-N+Pentapeptide	445	-	cyanobacteria	Calothrix parasitica	hypothetical protein [Calothrix parasitica]	GCF_002368095.1
WP_096660958.1	HTH→ TRADD-N+TPRs*→	TRADD-N+TPRs	201	-	cyanobacteria	Calothrix parasitica	DUF1822 family protein [Calothrix parasitica]	GCF_002368095.1
WP_096691930.1	??→ CASPASE+TRADD-N+helical-region*→	CASPASE+TRADD-N+helical-region	424	-	cyanobacteria	Calothrix	MULTISPECIES: CHAT domain-containing protein [Calothrix]	GCF_002368455.1
WP_096695037.1	EAD1+TRADD-N+helical-region+HTH+HTH*→	EAD1+TRADD-N+helical-region+HTH+HTH	514	-	cyanobacteria	Calothrix	MULTISPECIES: sigma-70 family RNA polymerase sigma factor [Calothrix]	GCF_002368455.1
WP_096829425.1	HTH+TRADD-N+TPRs*→	HTH+TRADD-N+TPRs	365	-	cyanobacteria	Tychonema bourrellyi	DUF1822 family protein [Tychonema bourrellyi]	-
WP_099065822.1	TM→ TRADD-N-aHTH1+TRADD-N+Pentapeptide*→	TRADD-N-aHTH1+TRADD-N+Pentapeptide	436	-	cyanobacteria	Nostoc linckia	hypothetical protein [Nostoc linckia]	GCF_002607965.1
WP_099065844.1	TRADD-N+Pentapeptide→?→||<-?||TM→ TRADD-N-aHTH1+TRADD-N+Pentapeptide*→	TRADD-N-aHTH1+TRADD-N+Pentapeptide	453	-	cyanobacteria	Nostoc linckia	transcriptional regulator, XRE family protein [Nostoc linckia]	GCF_002607965.1
WP_099066009.1	TRADD-N+Pentapeptide*→?→||<-?||TM→ TRADD-N-aHTH1+TRADD-N+Pentapeptide→	TRADD-N+Pentapeptide	367	-	cyanobacteria	Nostoc linckia	hypothetical protein [Nostoc linckia]	GCF_002607965.1
WP_099076546.1	TRADD-N+Pentapeptide*→?→||<-?||TM→ TRADD-N-aHTH1+TRADD-N+Pentapeptide→	TRADD-N+Pentapeptide	367	-	cyanobacteria	Nostoc linckia	hypothetical protein [Nostoc linckia]	GCF_002608015.1
WP_099148846.1	HsdM_N+METHYLASE→ TRD+TRD→ REase+SF2+Helicase_C+EcoR124_C+TRADD-N*→	REase+SF2+Helicase_C+EcoR124_C+TRADD-N	1190	-	bacteroidetes	Lewinella nigricans	type I restriction endonuclease subunit R [Lewinella nigricans]	GCF_002646595.1

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WP_099153795.1	TRADD-N+Pentapeptide*→	TRADD-N+Pentapeptide	340	-	bacteroidetes	Lewinella nigricans	pentapeptide repeat-containing protein [Lewinella nigricans]	GCF_002646595.1
WP_100903218.1	TRADD-N-aHTH1+TRADD-N+Pentapeptide*→	TRADD-N-aHTH1+TRADD-N+Pentapeptide	450	-	cyanobacteria	Nostoc flagelliforme	pentapeptide repeat-containing protein [Nostoc flagelliforme]	GCF_002813575.1
WP_102179539.1	wHTH?→ TRADD-N+TPRs*→ PSE→ TPRs+CASPASE→	TRADD-N+TPRs	204	-	cyanobacteria	Fischerella thermalis	DUF1822 family protein [Fischerella thermalis]	-
WP_103112689.1	ECF-HTH+TRADD-N+Pentapeptide*→	ECF-HTH+TRADD-N+Pentapeptide	420	-	cyanobacteria	Microcystis aeruginosa	pentapeptide repeat-containing protein [Microcystis aeruginosa]	GCF_002897315.1
WP_103127034.1	TRADD-N-aHTH1+TRADD-N+Pentapeptide*→	TRADD-N-aHTH1+TRADD-N+Pentapeptide	409	-	cyanobacteria	Nostoc cycadae	pentapeptide repeat-containing protein [Nostoc cycadae]	-
WP_103127406.1	ECF-HTH+TRADD-N+Pentapeptide*→	ECF-HTH+TRADD-N+Pentapeptide	420	-	cyanobacteria	Microcystis aeruginosa	pentapeptide repeat-containing protein [Microcystis aeruginosa]	GCF_002897275.1
WP_105530726.1	TRADD-N*→??→	TRADD-N	168	-	betaproteobacteria	Solimicrobium silvestre	hypothetical protein [Solimicrobium silvestre]	GCF_002976435.1
WP_106168212.1	TM+TRADD-N+TM+TM*→	TM+TRADD-N+TM+TM	354	-	cyanobacteria	Chroococcidiopsis cubana	hypothetical protein [Chroococcidiopsis cubana]	GCF_003003835.1
WP_106216281.1	TRADD-N+TM+TM*→ Haemagg_act→ Haemagg_act→ SIG+TPRs+CASPASE→	TRADD-N+TM+TM	556	-	cyanobacteria	Cyanosarcina burmensis	pentapeptide repeat-containing protein [Cyanosarcina burmensis]	GCF_003004015.1
WP_106303880.1	all-helical-protein→ TRADD-N+helical-region*→	TRADD-N+helical-region	295	-	cyanobacteria	Chamaesiphon polymorphus	hypothetical protein [Chamaesiphon polymorphus]	GCF_003003845.1
WP_106868049.1	SIG+TM+TM→ TM+TRADD-N*→ TM+all-helical-region→	TM+TRADD-N	190	-	cyanobacteria	filamentous cyanobacterium CCP4	hypothetical protein [filamentous cyanobacterium CCP4]	-
WP_106903024.1	SIG+TM+TM→ TM+TRADD-N*→ TM+all-helical-region→	TM+TRADD-N	177	-	cyanobacteria	filamentous cyanobacterium CCT1	hypothetical protein [filamentous cyanobacterium CCT1]	-
WP_106922102.1	HTH→ TIR+TRADD-N+??*→ APATPase+TPRs→	TIR+TRADD-N+??	349	-	cyanobacteria	filamentous cyanobacterium CCP3	toll/interleukin-1 receptor domain-containing protein [filamentous cyanobacterium CCP3]	-
WP_110578064.1	ECF-HTH+TRADD-N+Pentapeptide*→	ECF-HTH+TRADD-N+Pentapeptide	539	-	cyanobacteria	Microcystis aeruginosa	pentapeptide repeat-containing protein [Microcystis aeruginosa]	GCF_003206555.1
WP_124033433.1	Coiled-coil+TRADD-N+TM*→	Coiled-coil+TRADD-N+TM	415	-	Chloroflexi	Herpetosiphon llansteffanensis	hypothetical protein [Herpetosiphon llansteffanensis].	GCF_003205875.1
WP_153009599.1	TRADD-N+Pentapeptide*→	TRADD-N+Pentapeptide	370	-	Cyanobacteria	Mastigocoleus testarum	pentapeptide repeat-containing protein [Mastigocoleus testarum].	-
WP_153228487.1	HTH+TRADD-N+Pentapeptide*→	HTH+TRADD-N+Pentapeptide	487	-	Cyanobacteria	Nostocaceae	MULTISPECIES: pentapeptide repeat-containing protein [Nostocaceae].	GCF_009498015.1
WP_162271610.1	bDLD3→?→ McrA-NTD+HNH→?→||<-?||?→?→ PNPase+TRADD-N+CASPASE+bDLD3*→ APATPase+TPR+TPR→||<-?<-?||SIG+NPCBM→	PNPase+TRADD-N+CASPASE+bDLD3	816	VT84_RS06140	Planctomycetes	Gemmata sp. SH-PL17	caspase family protein [Gemmata sp. SH-PL17].	GCF_001610855.1
WP_162666668.1	SIG+TPR→||<-?||?→?→?→||<-?||?→ ACYC+FGS+TRADD-N+CASPASE*→?→ MoxR-AAA→ PSE→ FGS→ FGS→ FGS→ FGS→	ACYC+FGS+TRADD-N+CASPASE	622	SOIL9_RS04980	Planctomycetes	Gemmata massiliana	hypothetical protein [Gemmata massiliana].	-
WP_163926701.1	HTH+TRADD-N+Pentapeptide*→	HTH+TRADD-N+Pentapeptide	511	-	Cyanobacteria	Nostoc sp. UIC 10630	pentapeptide repeat-containing protein [Nostoc sp. UIC 10630].	GCF_010747425.1
WP_172109858.1	Methylase_S→ HNH+TRADD-N+SF2-helicase*→ PSE→?→?→||||<-?<-TPR-repeats	HNH+TRADD-N+SF2-helicase	1180	-	Alphaproteobacteria	Bradyrhizobium sp. 83012	HsdR family type I site-specific deoxyribonuclease [Bradyrhizobium sp. 83012].	GCF_013178925.1

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WP_190623519.1	HTH+TRADD-N+Pentapeptide*→	HTH+TRADD-N+Pentapeptide	386	-	Cyanobacteria	Calothrix membranacea	pentapeptide repeat-containing protein, partial [Calothrix membranacea].	GCF_014696315.1
WP_190677679.1	HTH+TRADD-N+Pentapeptide*→	HTH+TRADD-N+Pentapeptide	362	-	Cyanobacteria	Nostoc sp. FACHB-190	pentapeptide repeat-containing protein [Nostoc sp. FACHB-190].	GCF_014696905.1
WP_190734619.1	TRADD-N+TM+TM+TM+TM+TM+TM+TM+Pentapeptide*→ Pentapeptide-repeats→?→||||<-?||?→ Pentapeptide+TM+TM+TM+Pentapeptide→	TRADD-N+TM+TM+TM+TM+TM+TM+TM+Pentapeptide	884	-	Cyanobacteria	Nostoc sp. FACHB-888	pentapeptide repeat-containing protein [Nostoc sp. FACHB-888].	GCF_014696655.1
WP_190756292.1	<-Methylase_S<-?<-?<-?||HTH+TRADD-N+Pentapeptide*→||||<-?<-PSE<-?<-?<-?<-TPR-repeats+CASPASE	HTH+TRADD-N+Pentapeptide	478	-	Cyanobacteria	Nostoc sp. FACHB-145	pentapeptide repeat-containing protein [Nostoc sp. FACHB-145].	GCF_014697455.1
WP_193968417.1	TIR→ TRADD-N*→	TRADD-N	311	-	Cyanobacteria	Nodosilinea sp. LEGE 07088	hypothetical protein [Nodosilinea sp. LEGE 07088].	GCF_015207395.1
WP_198126279.1	HTH+TRADD-N+Pentapeptide*→	HTH+TRADD-N+Pentapeptide	558	-	Cyanobacteria	Nostoc sp. CENA67	pentapeptide repeat-containing protein [Nostoc sp. CENA67].	GCF_016056305.1
WP_199349019.1	HTH+TRADD-N+Pentapeptide*→	HTH+TRADD-N+Pentapeptide	1121	-	Cyanobacteria	Calothrix sp. FACHB-156	pentapeptide repeat-containing protein [Calothrix sp. FACHB-156].	GCF_014697055.1
YP_009217716.1	??→ TRADD-N+Pentapeptide*→ Pentapeptide→ SIG→??→	TRADD-N+Pentapeptide	300	AVV41_gp032	caudovirales	Microcystis phage MaMV-DC	hypothetical protein MaMVDC_32 [Microcystis phage MaMV-DC]	GCF_001505175.1