Supplementary Material

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

Gurmeet Kaur†, Lakshminarayan M. Iyer†, A. Maxwell Burroughs, L. Aravind*

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Abstract

Several homologous domains are shared by eukaryotic immunity and programmed cell-death systems and poorly understood bacterial proteins. Recent studies show these to be components of a network of highly regulated systems connecting apoptotic processes to counter-invader immunity, in prokaryotes with a multicellular habit. However, the provenance of key adaptor domains, namely those of the Death-like and TRADD-N superfamilies, a quintessential feature of metazoan apoptotic systems, remained murky. Here, we use sensitive sequence analysis and comparative genomics methods to identify unambiguous bacterial homologs of the Death-like and TRADD-N superfamilies. We show the former to have arisen as part of a radiation of effector-associated α-helical adaptor domains that likely mediate homotypic interactions bringing together diverse effector and signaling domains in predicted bacterial apoptosis- and counter-invader systems. Similarly, we show that the TRADD-N domain defines a key, widespread signaling bridge that links effector deployment to invader-sensing in multicellular bacterial and metazoan counter-invader systems. TRADD-N domains are expanded in aggregating marine invertebrates and point to distinctive diversifying immune strategies probably directed both at RNA and retro- viruses and cellular pathogens that might infect such communities. These TRADD-N and Death-like domains helped identify several new bacterial and metazoan counter-invader systems featuring under-appreciated, common functional principles: the use of intracellular invader-sensing lectin-like (NPCBM and FGS), transcription elongation GreA/B-C, glycosyltransferase-4 family, inactive NTPase (serving as nucleic-acid-receptors) and invader-sensing GTPase switch domains. Finally, these findings point to the possibility of multicellular bacteria-stem metazoan symbiosis in the emergence of the immune/apoptotic systems of the latter.

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Figure 6-Source data 1

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Source data. Gene neighborhoods and domain architectures of the bacterial GT4-like glycosyltransferases described in this study

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<tr><td>ADU34882.1</td><td>GT4+B12-binding+RADICAL-SAM*→</td><td>GT4+B12-binding+RADICAL-SAM</td><td>1405</td><td>Varpa_0662</td><td>Betaproteobacteria</td><td>Variovorax paradoxus EPS</td><td>Radical SAM domain protein [Variovorax paradoxus EPS]</td><td>GCA_000184745.1</td></tr>
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<tr><td>AMB84622.1</td><td>APATPase+GT4*→</td><td>APATPase+GT4</td><td>1299</td><td>AWM79_04595</td><td>Gammaproteobacteria</td><td>Pseudomonas agarici</td><td>hypothetical protein AWM79_04595 [Pseudomonas agarici]</td><td>GCA_001543125.1</td></tr>
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EKX63918.1	ZetaToxin+GT4+NUDIX+ART+NTase*→?→?→||||<-Caspase<-?||?→?→||||<-NLPC	ZetaToxin+GT4+NUDIX+ART+NTase	2156	STRIP9103_04937	Actinobacteria	Streptomyces ipomoeae 91-03	hydrolase, NUDIX family [Streptomyces ipomoeae 91-03]	GCA_000317595.1
EWM12074.1	<-CATASP||CATRA-N+CATRA-C+GT4*→||||<-HTH+APATPase+TPR	CATRA-N+CATRA-C+GT4	750	KUTG_02378	Actinobacteria	Kutzneria sp. 744	LigA protein [Kutzneria sp. 744]	GCA_000568255.1
GBE24927.1	Asparaginase_II→ Acetyltransf_6→ GT4*→?→?→?→||||<-?<-SIG+TM+TM+TM<-THUMP+ThiI	GT4	407	mshA	unclassified Bacteria	bacterium BMS3Bbin02	D-inositol 3-phosphate glycosyltransferase [bacterium BMS3Bbin02]	GCA_002898115.1
HBN24878.1	GT4*→	GT4	721	DD447_07855	Firmicutes	Lachnospiraceae bacterium	TPA: hypothetical protein DD447_07855 [Lachnospiraceae bacterium]	GCA_003503295.1
HCI14011.1	GT4+APATPase+TPR*→	GT4+APATPase+TPR	1340	DFK12_08625	Betaproteobacteria	Gallionellaceae bacterium	TPA: hypothetical protein DFK12_08625 [Gallionellaceae bacterium]	GCA_003521785.1
HCS09332.1	<-MODE-HTH+PBPII||?→||||<-?<-PSE<-PrpF||?→ PSE→ STAND+TPR+GT4*→	STAND+TPR+GT4	1081	DIW67_19725	Gammaproteobacteria	Pseudomonas sp.	TPA: glycosyltransferase [Pseudomonas sp.]	GCA_003531165.1
HDL41796.1	GT4*→	GT4	345	ENG98_02120	Actinobacteria	Actinobacteria bacterium	TPA: glycosyltransferase, partial [Actinobacteria bacterium]	GCA_011041235.1
KDN80799.1	MNS+GT4*→||||<-?||?→ ABC_tran→	MNS+GT4	1137	KCH_74340	Actinobacteria	Kitasatospora cheerisanensis KCTC 2395	hypothetical protein KCH_74340 [Kitasatospora cheerisanensis KCTC 2395]	GCA_000696185.1
KNY05162.1	GT4*→	GT4	533	AKH00_12305	Actinobacteria	Microbacterium sp. GCS4	hypothetical protein AKH00_12305 [Microbacterium sp. GCS4]	GCA_001262495.1
KOX13006.1	<-ABC_tran||?→?→||||<-?<-TIR+NACHT||HTH+APATPase+TPR+GT4*→	HTH+APATPase+TPR+GT4	1158	ADK67_45665	Actinobacteria	Saccharothrix sp. NRRL B-16348	NTPase [Saccharothrix sp. NRRL B-16348]	GCA_001280085.1
KQM59620.1	GT4*→||||<-TRPR-HTH+PBPI<-?<-?<-?<-?||PSE→?→ PfkB→	GT4	155	ASE64_09860	Actinobacteria	Agreia sp. Leaf210	hypothetical protein ASE64_09860 [Agreia sp. Leaf210]	GCA_001421485.1

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
KQW27056.1	STAND+GT4*→	STAND+GT4	1005	ASC85_27055	Gammaproteobacteria	Pseudomonas sp. Root401	hypothetical protein ASC85_27055 [Pseudomonas sp. Root401]	GCA_001425105.1
KVF32402.1	<-SIG+RCDG1+YidC_periplas+60KD_IMP<-?<-?<-?||?→?→?→ GT4+B12-binding+RADICAL-SAM*→||||<-rve_3	GT4+B12-binding+RADICAL-SAM	1400	WJ08_12515	Betaproteobacteria	Burkholderia vietnamiensis	radical SAM protein [Burkholderia vietnamiensis]	GCA_001524025.1
KVM90153.1	GT4+B12-binding+RADICAL-SAM*→	GT4+B12-binding+RADICAL-SAM	1404	WT05_03580	Betaproteobacteria	Burkholderia stagnalis	radical SAM protein [Burkholderia stagnalis]	GCA_001527545.1
KVM94412.1	TniB→?→ NLPC→||||<-?||?→ GT4+B12-binding+RADICAL-SAM*→	GT4+B12-binding+RADICAL-SAM	1404	WT07_28140	Betaproteobacteria	Burkholderia stagnalis	radical SAM protein [Burkholderia stagnalis]	GCA_001527585.1
KVX13946.1	GT4*→||||<-?||ABhydrolase→||||<-TRANSGLUTAMINASE	GT4	282	WL03_19390	Betaproteobacteria	Burkholderia ubonensis	hypothetical protein WL03_19390 [Burkholderia ubonensis]	GCA_001539165.1
KVZ11040.1	GT4+APATPase+TPR+TPR*→	GT4+APATPase+TPR+TPR	1278	WL11_04565	Betaproteobacteria	Burkholderia ubonensis	hypothetical protein WL11_04565 [Burkholderia ubonensis]	GCA_001530465.1
KWI84975.1	GT4*→||||<-?||ABhydrolase→||||<-TRANSGLUTAMINASE	GT4	325	WM08_23745	Betaproteobacteria	Burkholderia ubonensis	hypothetical protein WM08_23745 [Burkholderia ubonensis]	GCA_001534135.1
KWK82218.1	NACHT+TPR+GT4*→	NACHT+TPR+GT4	1024	WM17_17155	Betaproteobacteria	Burkholderia ubonensis	hypothetical protein WM17_17155 [Burkholderia ubonensis]	GCA_001533745.1
MBA3007143.1	APATPase+GT4+TPR+TPR+TPR+TPR+TPR*→	APATPase+GT4+TPR+TPR+TPR+TPR+TPR	1488	FP810_11305	Deltaproteobacteria	Desulfocapsa sp.	tetratricopeptide repeat protein [Desulfocapsa sp.]	GCA_013792135.1
MBA3548505.1	GT4*→	GT4	125	H0T76_18640	Deltaproteobacteria	Nannocystis sp.	glycosyltransferase [Nannocystis sp.]	GCA_013812955.1
MBS82255.1	NACHT+GT4*→?→?→?→||||<-?<-?<-SIG+rve	NACHT+GT4	1659	CMO32_42310	Betaproteobacteria	Variovorax sp.	hypothetical protein CMO32_42310 [Variovorax sp.]	GCA_002729445.1

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
MQY06528.1	REase+SFI-ATPase→?→?→||||<-?||?→||||<-?||GT4+APATPase+TPR+TPR*→	GT4+APATPase+TPR+TPR	1104	mshA_10	Actinobacteria	Actinomadura sp. RB68	D-inositol-3-phosphate glycosyltransferase [Actinomadura sp. RB68]	GCA_009604375.1
MQY24997.1	ESX-1_EspG→||||<-?<-?||?→?→?→ WXG+TOXIN-PL+ART+Caspase+ZetaToxin+GT4*→	WXG+TOXIN-PL+ART+Caspase+ZetaToxin+GT4	3249	mshA_3	Actinobacteria	Nocardia sp. RB56	D-inositol-3-phosphate glycosyltransferase [Nocardia sp. RB56]	GCA_009604425.1
MSV29911.1	GT4+APATPase+BetaPropeller*→	GT4+APATPase+BetaPropeller	1058	EXQ52_14375	Acidobacteria	Bryobacterales bacterium	glycosyltransferase [Bryobacterales bacterium]	GCA_009697455.1
MWJ13606.1	ABC_tran→?→||||<-?||GT4*→||||<-?||?→?→?→||||<-?||tRNA→?→ Pribosyltran_N+Pribosyl_synth→	GT4	267	DOT98_12255	Actinobacteria	Clavibacter michiganensis subsp. michiganensis	hypothetical protein DOT98_12255 [Clavibacter michiganensis subsp. michiganensis]	GCA_009793225.1
NED51435.1	GT4*→	GT4	88	G3I24_11000	Actinobacteria	Micromonospora aurantiaca	glycosyl transferase family 1, partial [Micromonospora aurantiaca]	GCA_010550585.1
NNJ62389.1	DUF4913→?→ GT4*→	GT4	464	HKP61_15900	Actinobacteria	Dactylosporangium sp.	glycosyltransferase family 4 protein [Dactylosporangium sp.]	GCA_013041765.1
NOX21677.1	Asparaginase_II→ Acetyltransf_6→ GT4*→?→?→||||<-?<-SIG+TM+TM+TM<-THUMP+ThiI	GT4	407	GXP36_01090	Actinobacteria	Actinobacteria bacterium	glycosyltransferase [Actinobacteria bacterium]	GCA_013151445.1
NQZ33933.1	GT4+APATPase*→	GT4+APATPase	841	HRU06_21905	Gammaproteobacteria	Oceanospirillaceae bacterium	glycosyltransferase, partial [Oceanospirillaceae bacterium]	GCA_013215375.1
NTC82454.1	<-TniB<-?<-?<-?||?→?→?→ NACHT+GT4*→	NACHT+GT4	1640	G6M81_07325	Alphaproteobacteria	Agrobacterium tumefaciens	glycosyltransferase [Agrobacterium tumefaciens]	GCA_013319045.1
NUQ74496.1	SIR2+TPR+SAVED+GT4*→	SIR2+TPR+SAVED+GT4	1362	HUU21_13150	Deltaproteobacteria	Polyangiaceae bacterium	glycosyltransferase [Polyangiaceae bacterium]	GCA_013360665.1

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NUS43770.1	GT4*→	GT4	631	HOQ24_08805	Actinobacteria	Mycobacteriaceae bacterium	glycosyltransferase family 4 protein, partial [Mycobacteriaceae bacterium]	GCA_013362555.1
NUS72884.1	SIG+GT4+ZetaToxin*→	SIG+GT4+ZetaToxin	750	HOQ05_05695	Actinobacteria	Corynebacteriales bacterium	glycosyltransferase [Corynebacteriales bacterium]	GCA_013362805.1
NUT53093.1	SWACOS+GT4*→	SWACOS+GT4	1162	HOV94_38270	Actinobacteria	Saccharothrix sp.	glycosyltransferase [Saccharothrix sp.]	GCA_013362745.1
OAI03591.1	GT4+APATPase+TPR*→	GT4+APATPase+TPR	1115	A1332_15425	Gammaproteobacteria	Methylomonas methanica	hypothetical protein A1332_15425, partial [Methylomonas methanica]	GCA_001644035.1
ODT28534.1	GT4*→||||<-?<-?||?→||||<-?<-?||?→ NUDIX→	GT4	325	ABS63_03615	Actinobacteria	Microbacterium sp. SCN 70-27	hypothetical protein ABS63_03615 [Microbacterium sp. SCN 70-27]	GCA_001724425.1
OGS75014.1	GT4+APATPase+TPR*→	GT4+APATPase+TPR	1314	A2063_09475	Betaproteobacteria	Gallionellales bacterium GWA2_60_142	hypothetical protein A2063_09475 [Gallionellales bacterium GWA2_60_142]	GCA_001801085.1
OKJ80919.1	<-TPR+Caspase<-CATASP||CATRA-N+CATRA-C+GT4*→ HTH+APATPase+TPR→?→?→||||<-?<-CATASP	CATRA-N+CATRA-C+GT4	694	AMK32_24710	Actinobacteria	Streptomyces sp. CB01883	hypothetical protein AMK32_24710 [Streptomyces sp. CB01883]	GCA_001905855.1
OLT27035.1	ZetaToxin+GT4+NUDIX+ART*→	ZetaToxin+GT4+NUDIX+ART	1451	BJF83_19460	Actinobacteria	Nocardiopsis sp. CNR-923	hypothetical protein BJF83_19460 [Nocardiopsis sp. CNR-923]	GCA_001942255.1
ONI48735.1	<-TPR+Caspase<-CATASP||CATRA-N+CATRA-C+GT4*→ HTH+APATPase+TPR→||||<-HTH||?→?→?→||||<-?<-CATASP	CATRA-N+CATRA-C+GT4	727	mshA_4	Actinobacteria	Streptomyces sp. IB2014 011-1	D-inositol 3-phosphate glycosyltransferase [Streptomyces sp. IB2014 011-1]	GCA_001983595.1
OPK01862.1	GT4+B12-binding+RADICAL-SAM*→	GT4+B12-binding+RADICAL-SAM	1407	BZ164_25460	Gammaproteobacteria	Pseudomonas veronii	hypothetical protein BZ164_25460 [Pseudomonas veronii]	GCA_002029325.1

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OWQ88588.1	GT4+HD*→	GT4+HD	1415	CDN99_17225	Betaproteobacteria	Roseateles aquatilis	hypothetical protein CDN99_17225 [Roseateles aquatilis]	GCA_002205645.1
OXM47905.1	<-TIR+APATPase||HTH+APATPase+TPR+GT4*→	HTH+APATPase+TPR+GT4	1166	CFP75_23295	Actinobacteria	Amycolatopsis alba DSM 44262	NTPase [Amycolatopsis alba DSM 44262]	GCA_002234385.1
OZV80564.1	<-TPR+Caspase||GT4*→?→?→||||<-?<-?<-ABC_tran	GT4	587	CA850_14545	Actinobacteria	Micromonospora echinospora	hypothetical protein CA850_14545 [Micromonospora echinospora]	GCA_002266845.1
PBV03828.1	STAND+GT4*→	STAND+GT4	1006	CJU35_32055	Gammaproteobacteria	Pseudomonas aeruginosa	hypothetical protein CJU35_32055 [Pseudomonas aeruginosa]	GCA_002326115.1
PJI96546.1	GT4+B12-binding+RADICAL-SAM*→?→?→||||<-?<-LexA	GT4+B12-binding+RADICAL-SAM	1404	CLU85_1299	Betaproteobacteria	Acidovorax sp. 69	radical SAM superfamily enzyme YgiQ (UPF0313 family) [Acidovorax sp. 69]	GCA_002797445.1
PJO54021.1	GT4*→	GT4	721	CR156_18515	Gammaproteobacteria	Stenotrophomonas lactitubi	hypothetical protein CR156_18515 [Stenotrophomonas lactitubi]	GCA_002803515.1
PKN17915.1	NACHT+GT4*→	NACHT+GT4	1644	CVU71_10310	Deltaproteobacteria	Deltaproteobacteria bacterium HGW-Deltaproteobacteria-6	hypothetical protein CVU71_10310 [Deltaproteobacteria bacterium HGW-Deltaproteobacteria-6]	GCA_002840435.1
PKV83308.1	HTH→?→?→||||<-?<-?||Caspase+NACHT+GT4*→	Caspase+NACHT+GT4	1229	BX283_0808	Actinobacteria	Streptomyces sp. TLI_146	glycosyltransferase involved in cell wall biosynthesis [Streptomyces sp. TLI_146]	GCA_002846415.1
PNA01938.1	GT4+APATPase+TPR+TPR*→	GT4+APATPase+TPR+TPR	1383	C1X79_03750	Gammaproteobacteria	Pseudomonas sp. FW305-42	hypothetical protein C1X79_03750 [Pseudomonas sp. FW305-42]	GCA_002883975.1

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<tr><td>ROV69600.1</td><td><-ABC_tran<-?||PSE→ Caspase+NACHT+GT4*→</td><td>Caspase+NACHT+GT4</td><td>1187</td><td>D3105_04960</td><td>Actinobacteria</td><td>Streptomyces globisporus</td><td>glycosyltransferase [Streptomyces globisporus]</td><td>GCA_003501885.1</td></tr>
<tr><td>RSM57832.1</td><td>cNMP_binding+HTH_Crp_2→?→ GT4*→||||<-ACYC+APATPase+TPR</td><td>GT4</td><td>411</td><td>DMH03_26130</td><td>Actinobacteria</td><td>Amycolatopsis sp. WAC 01376</td><td>hypothetical protein DMH03_26130 [Amycolatopsis sp. WAC 01376]</td><td>GCA_003947415.1</td></tr>
<tr><td>RWH25252.1</td><td><-Vsr||?→?→?→||||<-?||GT4+Trypsin+PNPase*→</td><td>GT4+Trypsin+PNPase</td><td>961</td><td>EOQ76_19695</td><td>Alphaproteobacteria</td><td>Mesorhizobium sp.</td><td>glycosyltransferase [Mesorhizobium sp.]</td><td>GCA_004019165.1</td></tr>
</table>

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
RYG90150.1	GT4*→	GT4	425	EON59_00395	Alphaproteobacteria	Alphaproteobacteria bacterium	glycosyltransferase, partial [Alphaproteobacteria bacterium]	GCA_004145145.1
RYZ67144.1	GT4*→	GT4	290	EOP09_11535	Proteobacteria	Proteobacteria bacterium	glycosyltransferase family 1 protein, partial [Proteobacteria bacterium]	GCA_004174565.1
SCF29539.1	<-TPR+Caspase||GT4*→?→?→||||<-?<-?<-ABC_tran	GT4	549	GA0070618_4943	Actinobacteria	Micromonospora echinospora	Glycosyltransferase involved in cell wall bisynthesis [Micromonospora echinospora]	GCA_900091495.1
SCF46304.1	<-WXG<-?<-?<-?<-?<-TPR+Caspase||GT4*→	GT4	549	GA0070563_114162	Actinobacteria	Micromonospora carbonacea	Glycosyltransferase involved in cell wall bisynthesis [Micromonospora carbonacea]	GCA_900091535.1
SCH34126.1	GT4*→ TIR→	GT4	721	SAMEA3545339_00864	Firmicutes	uncultured Clostridium sp.	glycosyltransferase%2C MSMEG_0565 family [uncultured Clostridium sp.]	GCA_900066565.1
SCL28302.1	<-TPR+Caspase||GT4*→	GT4	545	GA0074694_5072	Actinobacteria	Micromonospora inyonensis	Glycosyltransferase involved in cell wall bisynthesis [Micromonospora inyonensis]	GCA_900091415.1
SCZ75034.1	SWACOS+GT4*→?→||||<-?<-?||MFS→	SWACOS+GT4	1147	SAMN03159460_05304	Gammaproteobacteria	Pseudomonas sp. NFPP17	Glycosyltransferase involved in cell wall bisynthesis [Pseudomonas sp. NFPP17]	GCA_900102935.1
SDU29240.1	rve_3→ GT4*→	GT4	362	SAMN04488548_134376	Actinobacteria	Gordonia westfalica	Glycosyltransferase involved in cell wall bisynthesis [Gordonia westfalica]	GCA_900105725.1
SDX14297.1	LRR+AP-GTPase+COR→ GT4*→	GT4	472	SAMN05216300_1202	Betaproteobacteria	Nitrosomonas oligotropha	Glycosyltransferase involved in cell wall bisynthesis [Nitrosomonas oligotropha]	GCA_900106555.1

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
SEK03344.1	<-Sigma||?→||||<-?<-?<-?||GT4+B12-binding*→	GT4+B12-binding	1051	SAMN05518849_113037	Alphaproteobacteria	Sphingobium sp. AP50	Glycosyltransferase involved in cell wall bisynthesis [Sphingobium sp. AP50]	GCA_900109095.1
SIO56974.1	STAND+TPR+GT4*→	STAND+TPR+GT4	1125	SAMN05444165_3787	Betaproteobacteria	Paraburkholderia phenazinium	Glycosyltransferase involved in cell wall bisynthesis [Paraburkholderia phenazinium]	GCA_900142845.1
SNR45646.1	HTH_Tnp_1→ TnpB_IS66→?→ NACHT+GT4*→	NACHT+GT4	1639	SAMN06265370_105216	Alphaproteobacteria	Puniceibacterium sediminis	Glycosyltransferase involved in cell wall bisynthesis [Puniceibacterium sediminis]	GCA_900188035.1
TAK32775.1	GT4*→	GT4	646	EPO40_01735	Deltaproteobacteria	Myxococcaceae bacterium	glycosyltransferase [Myxococcaceae bacterium]	GCA_004297725.1
TCO61886.1	GT4*→||||<-TPR	GT4	392	EV192_10223	Actinobacteria	Actinocrispum wychmicini	glycosyltransferase involved in cell wall biosynthesis [Actinocrispum wychmicini]	GCA_004345645.1
TDP89614.1	GT4*→ TIR+APATPase+TPR→ TPR+Caspase→||||<-TPR+Caspase<-CATASP||CATRA-N+CATRA-C+GT4→	GT4	328	EV186_11214	Actinobacteria	Labedaea rhizosphaerae	glycosyltransferase involved in cell wall biosynthesis [Labedaea rhizosphaerae]	GCA_004362825.1
TGX49078.1	GT4+NACHT*→	GT4+NACHT	1219	E5A73_19725	Alphaproteobacteria	Sphingomonas gei	glycosyltransferase [Sphingomonas gei]	GCA_004792685.1
TPG40509.1	GT4*→	GT4	136	EAH79_11405	Alphaproteobacteria	Sphingomonas koreensis	glycosyltransferase [Sphingomonas koreensis]	GCA_006438735.1
TQL90659.1	<-DUF4242<-?<-?<-PSE||?→||||<-HTH+APATPase+TPR<-TPR+Caspase<-CATASP||CATRA-N+CATRA-C+GT4*→||||<-?<-?<-?<-?<-?<-REase+SFI-ATPase	CATRA-N+CATRA-C+GT4	735	FB559_7970	Actinobacteria	Actinoallomurus bryophytorum	glycosyltransferase involved in cell wall biosynthesis [Actinoallomurus bryophytorum]	GCA_006716425.1

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
TWH06591.1	<-TPR+Caspase||GT4*→?→?→||||<-?<-?<-ABC_tran	GT4	587	JD80_04174	Actinobacteria	Micromonospora echinospora	glycosyltransferase involved in cell wall biosynthesis [Micromonospora echinospora]	GCA_007829475.1
TWJ29688.1	<-TPR+Caspase||GT4*→?→||||<-?<-?<-ABC_tran	GT4	549	JD81_03199	Actinobacteria	Micromonospora sagamiensis	glycosyltransferase involved in cell wall biosynthesis [Micromonospora sagamiensis]	GCA_007829995.1
TXH45940.1	GT4+nSTAND1+ANK+ANK*→	GT4+nSTAND1+ANK+ANK	1838	E6Q92_02710	Betaproteobacteria	Burkholderiaceae bacterium	hypothetical protein E6Q92_02710 [Burkholderiaceae bacterium]	GCA_008012415.1
VBB15457.1	GT4+B12-binding+RADICAL-SAM*→	GT4+B12-binding+RADICAL-SAM	1404	BSTAB16_5653	Betaproteobacteria	Burkholderia stabilis	radical SAM protein [Burkholderia stabilis]	GCA_900240005.1
VBK75063.1	GT4+B12-binding+RADICAL-SAM*→	GT4+B12-binding+RADICAL-SAM	1404	SAMEA2064914_03874	Betaproteobacteria	Burkholderia pseudomallei	Glycogen synthase [Burkholderia pseudomallei]	GCA_900592755.1
WP_005483680.1	TRANSGLUTAMINASE→||||<-?<-Zeta_toxin<-?<-?||?→ GT4*→||||<-?<-?<-?<-?<-DUF4913	GT4	590	SBD_RS28370	Actinobacteria	Streptomyces	MULTISPECIES: glycosyltransferase [Streptomyces]	GCF_000340335.1
WP_007453552.1	Multi-TM→?→ STAND→?→ DUF4913→||||<-?||?→ GT4*→?→?→?→ NUDIX→||||<-?||?→ PSE→ ABC_tran→	GT4	437	MILUP08_RS00205	Actinobacteria	Micromonospora lupini	glycosyltransferase family 4 protein [Micromonospora lupini]	GCF_000297395.2
WP_007734957.1	STAND+TPR+GT4*→	STAND+TPR+GT4	1062	B5Z53_RS05165	Betaproteobacteria	Paraburkholderia hospita	glycosyltransferase [Paraburkholderia hospita]	GCF_900167965.1
WP_007954182.1	SQHop_cyclase_C+Prenyltrans+GT4*→?→||||<-?||?→||||<-?||?→ XylR_N+V4R+Sigma54_activat+HTH_8→	SQHop_cyclase_C+Prenyltrans+GT4	779	JBW_RS18725	Firmicutes	Pelosinus fermentans	glycosyltransferase [Pelosinus fermentans]	GCF_000271665.2
WP_010223837.1	GT4+STAND*→ TPR→||||<-MODE-HTH+PBPII	GT4+STAND	546	UW3_RS0116985	Gammaproteobacteria	Pseudomonas donghuensis	glycosyltransferase [Pseudomonas donghuensis]	GCF_000259195.1
WP_013226178.1	<-TIR+APATPase||HTH+APATPase+TPR+GT4*→	HTH+APATPase+TPR+GT4	1178	IW14_RS45345	Actinobacteria	Amycolatopsis mediterranei	glycosyltransferase [Amycolatopsis mediterranei]	GCF_000196835.1
WP_017131143.1	APATPase+GT4*→	APATPase+GT4	1299	BMX68_RS11845	Gammaproteobacteria	Pseudomonas agarici	glycosyltransferase [Pseudomonas agarici]	GCF_900109755.1

<table>
<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>WP_017594508.1</td><td>GT4*→</td><td>GT4</td><td>503</td><td>D459_RS0118565</td><td>Actinobacteria</td><td>Nocardiopsis potens</td><td>glycosyltransferase family 4 protein [Nocardiopsis potens]</td><td>GCF_000341105.1</td></tr>
<tr><td>WP_018327601.1</td><td><-TniB<-?||?→||||<-?<-?||GT4+B12-binding+RADICAL-SAM*→||||<-?<-?||SIG+rve→</td><td>GT4+B12-binding+RADICAL-SAM</td><td>1381</td><td>GGD55_RS15170</td><td>Alphaproteobacteria</td><td>Rhizobium giardinii</td><td>B12-binding domain-containing radical SAM protein [Rhizobium giardinii]</td><td>GCF_014200295.1</td></tr>
<tr><td>WP_018612920.1</td><td>STAND+TPR+GT4*→</td><td>STAND+TPR+GT4</td><td>1063</td><td>CFII68_RS03385</td><td>Gammaproteobacteria</td><td>Pseudomonas sp. CFII68</td><td>glycosyltransferase [Pseudomonas sp. CFII68]</td><td>GCF_000416195.1</td></tr>
<tr><td>WP_019063569.1</td><td>MFS→||||<-?<-TPR+Caspase<-CATASP||CATRA-N+CATRA-C+GT4*→
HTH+APATPase+TPR→||||<-PSE||?→?→||||<-?<-CATASP<-TPR+Caspase</td><td>CATRA-N+CATRA-C+GT4</td><td>720</td><td>SPR02S_RS44725</td><td>Actinobacteria</td><td>Streptomyces prunicolor</td><td>glycosyltransferase family 4 protein [Streptomyces prunicolor]</td><td>GCF_000367365.1</td></tr>
<tr><td>WP_019093712.1</td><td>SWACOS+GT4*→</td><td>SWACOS+GT4</td><td>1138</td><td>BK646_RS17250</td><td>Gammaproteobacteria</td><td>Pseudomonas protegens</td><td>glycosyltransferase [Pseudomonas protegens]</td><td>GCF_003732085.1</td></tr>
<tr><td>WP_019609270.1</td><td><-AbiEii<-AbiEi_4||?→ GT4*→</td><td>GT4</td><td>497</td><td>G011_RS0115485</td><td>Actinobacteria</td><td>Nocardiopsis sp. CNS-639</td><td>glycosyltransferase family 4 protein [Nocardiopsis sp. CNS-639]</td><td>GCF_000381685.1</td></tr>
<tr><td>WP_020647322.1</td><td><-TIR+APATPase||HTH+APATPase+TPR+GT4*→</td><td>HTH+APATPase+TPR+GT4</td><td>1192</td><td>A3CE_RS0148230</td><td>Actinobacteria</td><td>Amycolatopsis balhimycina</td><td>tetratricopeptide repeat protein [Amycolatopsis balhimycina]</td><td>GCF_000384295.1</td></tr>
<tr><td>WP_023267980.1</td><td>GT4+APATPase+TPR+TPR*→</td><td>GT4+APATPase+TPR+TPR</td><td>1323</td><td>SHD_RS15540</td><td>Gammaproteobacteria</td><td>Shewanella decolorationis</td><td>tetratricopeptide repeat protein [Shewanella decolorationis]</td><td>GCF_000485795.1</td></tr>
<tr><td>WP_024631061.1</td><td><-AAA_21||GT4*→</td><td>GT4</td><td>1140</td><td>P364_RS0115745</td><td>Firmicutes</td><td>Paenibacillus sp. MAEPY2</td><td>glycosyltransferase [Paenibacillus sp. MAEPY2]</td><td>GCF_000499205.1</td></tr>
<tr><td>WP_027196515.1</td><td>Cluster214_2clades→ GT4*→</td><td>GT4</td><td>760</td><td>BJG93_RS27460</td><td>Betaproteobacteria</td><td>Paraburkholderia sprentiae</td><td>glycosyltransferase family 4 protein [Paraburkholderia sprentiae]</td><td>GCF_001865575.1</td></tr>
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acc	operon	architecture	len	gen.name	taxend	species	defline	gca
WP_031021212.1	ABC_tran→||||<-?<-CATASP||CATRA-N+CATRA-C+GT4*→ HTH+APATPase+TPR→||||<-HTH||?→?→?→||||<-?<-CATASP	CATRA-N+CATRA-C+GT4	705	IF98_RS0120305	Actinobacteria	Streptomyces sp. NRRL S-1314	glycosyltransferase family 4 protein [Streptomyces sp. NRRL S-1314]	GCF_000719785.1
WP_031063336.1	ABC_tran→||||<-?<-CATASP||CATRA-N+CATRA-C+GT4*→ HTH+APATPase+TPR→||||<-HTH||?→?→?→||||<-?<-CATASP	CATRA-N+CATRA-C+GT4	705	IH17_RS0118610	Actinobacteria	Streptomyces sp. NRRL F-5527	glycosyltransferase family 4 protein [Streptomyces sp. NRRL F-5527]	GCF_014649055.1
WP_033524509.1	TRANSGLUTAMINASE→||||<-?||?→||||<-?||GT4+NUDIX+ART+PolB-NTase→*////<-?<-?<-?//?→ GT4*→||||<-?<-?<-?<-?<-DUF4913	GT4+NUDIX+ART+PolB-NTase	589	KS09_RS00195	Actinobacteria	Streptomyces galbus	glycosyltransferase [Streptomyces galbus]	GCF_000772895.1
WP_035284396.1	APATPase+TPR→ GT4*→	GT4	502	UO65_RS36825	Actinobacteria	Actinokineospora spheciospongiae	glycosyltransferase [Actinokineospora spheciospongiae]	GCF_000564855.1
WP_036515011.1	WXG+MPTase→ WXG+SecA+HTH+HTH+HTH+HTH+HTH+ST-Hiskin+PP2C+MPTase+GT4+TetR-HTH+TetR-HTH+TM+TM+TM+TM+TM+TM+LuxR-HTH+LuxR-HTH+LuxR-HTH+LuxR-HTH+LuxR-HTH+LuxR-HTH+LuxR-HTH+GNTR-HTH+GNTR-HTH+GNTR-HTH+GNTR-HTH+GNTR-HTH+GNTR-HTH*→	WXG+SecA+HTH+HTH+HTH+HTH+HTH+ST-Hiskin+PP2C+MPTase+GT4+TetR-HTH+TetR-HTH+TM+TM+TM+TM+TM+TM+LuxR-HTH+LuxR-HTH+LuxR-HTH+LuxR-HTH+LuxR-HTH+LuxR-HTH+LuxR-HTH+GNTR-HTH+GNTR-HTH+GNTR-HTH+GNTR-HTH+GNTR-HTH+GNTR-HTH	12585	NRH01S_RS188[illegible]0	Actinobacteria	Nocardia rhamnosiphila	GntR family transcriptional regulator [Nocardia rhamnosiphila]	GCF_001613485.1
WP_036994826.1	MFS→||||<-?||GT4+APATPase+TPR*→||||<-MODE-HTH+PBPII	GT4+APATPase+TPR	1318	BV82_RS07620	Gammaproteobacteria	Pseudomonas donghuensis	glycosyltransferase [Pseudomonas donghuensis]	GCF_000696345.1
WP_037254756.1	cNMP_binding+HTH_Crp_2→?→ GT4*→||||<-ACYC+APATPase+TPR	GT4	404	DMH04_42005	Actinobacteria	Kibdelosporangium aridum	glycosyltransferase [Kibdelosporangium aridum]	-
WP_039793765.1	<-TIR+APATPase||HTH+APATPase+TPR+GT4*→	HTH+APATPase+TPR+GT4	1175	CFP75_RS23290	Actinobacteria	Amycolatopsis alba	glycosyltransferase [Amycolatopsis alba]	GCF_000384215.1
WP_040866957.1	WXG+MPTase→ WXG+SecA+GT4+TetR-HTH+MPTase+HTH+HTH+HTH+HTH+HTH+HTH+HTH+HTH*→	WXG+SecA+GT4+TetR-HTH+MPTase+HTH+HTH+HTH+HTH+HTH+HTH+HTH+HTH	5345	ON29_RS15345	Actinobacteria	Nocardia exalbida	helix-turn-helix domain-containing protein [Nocardia exalbida]	GCF_000308575.1
WP_041117337.1	SWACOS+GT4*→?→||||<-?<-?||MFS→	SWACOS+GT4	1138	PPC_RS11795	Gammaproteobacteria	Pseudomonas protegens	glycosyltransferase [Pseudomonas protegens]	GCF_000828695.1
WP_042132624.1	GT4+B12-binding+RADICAL-SAM*→	GT4+B12-binding+RADICAL-SAM	1393	BJQ15_RS27760	Gammaproteobacteria	Pseudomonas	MULTISPECIES: B12-binding domain-containing radical SAM protein [Pseudomonas]	GCF_000730605.1

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WP_043243023.1	Ribosomal_L20→?→?→?→?→ tRNA→?→ GT4+B12-binding+RADICAL-SAM*→	GT4+B12-binding+RADICAL-SAM	1402	TX97_RS10150	Gammaproteobacteria	Pseudomonas alcaligenes	B12-binding domain-containing radical SAM protein [Pseudomonas alcaligenes]	GCF_000474255.1
WP_043510995.1	WXG+GT4+GT4+REase*→	WXG+GT4+GT4+REase	4153	ACSP50_RS07520	Actinobacteria	unclassified Actinoplanes	MULTISPECIES: glycosyltransferase [unclassified Actinoplanes]	GCF_000237145.1
WP_043738635.1	WXG+MPTase→ WXG+SecA+GT4+TetR-HTH+TetR-HTH+MPTase+HTH+HTH+HTH+HTH+HTH+HTH*→	WXG+SecA+GT4+TetR-HTH+TetR-HTH+MPTase+HTH+HTH+HTH+HTH+HTH+HTH	8037	ON27_RS37615	Actinobacteria	Nocardia asiatica	helix-turn-helix domain-containing protein [Nocardia asiatica]	GCF_000308415.1
WP_045583922.1	<-SIG+HTH_23+HTH_32||GT4+TPR*→	GT4+TPR	1241	VY88_RS20945	Alphaproteobacteria	Azospirillum thiophilum	tetratricopeptide repeat protein [Azospirillum thiophilum]	GCF_001305595.1
WP_050363680.1	Multi-TM→?→ STAND→?→ DUF4913→?→ GT4*→?→ Zeta_toxin→||||<-ABC_tran	GT4	555	DC095_RS07800	Actinobacteria	Streptomyces	MULTISPECIES: glycosyltransferase family 4 protein [Streptomyces]	GCF_000700005.2
WP_050791877.1	GT4+B12-binding+RADICAL-SAM*→?→||||<-PSE<-?||?→||||<-?<-?||Sigma→	GT4+B12-binding+RADICAL-SAM	1403	BUBO0001_RS30235	Betaproteobacteria	Burkholderia ubonensis	B12-binding domain-containing radical SAM protein [Burkholderia ubonensis]	GCF_000170335.1
WP_051466857.1	TPR+Caspase→ CATRA-N+CATRA-C+GT4*→ HTH+APATPase+TPR→||||<-TPR+Caspase||CATASP→	CATRA-N+CATRA-C+GT4	812	BCD49_RS04570	Actinobacteria	Frankia	MULTISPECIES: glycosyltransferase family 4 protein [Frankia]	GCF_000235425.2
WP_051653780.1	MNS+GT4*→||||<-?||PSE→ ABC_tran→	MNS+GT4	1132	KCH_RS38295	Actinobacteria	Kitasatospora cheerisanensis	glycosyltransferase [Kitasatospora cheerisanensis]	GCF_000696185.1
WP_051722648.1	Multi-TM→?→ STAND→?→ DUF4913→?→ GT4*→?→ Zeta_toxin→	GT4	561	IF83_RS0111160	Actinobacteria	Streptomyces albus	glycosyltransferase family 4 protein [Streptomyces albus]	GCF_000719865.1
WP_051765847.1	<-CASPASE+FGS<-?<-?<-?||GT4*→	GT4	406	OQ01_RS21365	Actinobacteria	Saccharothrix syringae	glycosyltransferase [Saccharothrix syringae]	GCF_000716755.1
WP_051865326.1	GT4*→	GT4	621	IG99_RS44170	Actinobacteria	Streptomyces griseus	glycosyltransferase [Streptomyces griseus]	GCF_000720255.1

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WP_052457075.1	<-TPR+Caspase<-CATASP||CATRA-N+CATRA-C+GT4*→ PSE→ PSE→ APATPase+TPR→||||<-HTH||?→||||<-?<-CATASP<-TPR+Caspase	CATRA-N+CATRA-C+GT4	747	HY68_RS39570	Actinobacteria	Streptomyces sp. AcH 505	glycosyltransferase [Streptomyces sp. AcH 505]	GCF_000818175.1
WP_052479793.1	TIR+APATPase+GT4*→	TIR+APATPase+GT4	810	APS67_RS01150	Actinobacteria	unclassified Streptomyces	MULTISPECIES: TIR domain-containing protein [unclassified Streptomyces]	GCF_000829695.1
WP_053258773.1	GT4+B12-binding+RADICAL-SAM*→	GT4+B12-binding+RADICAL-SAM	1401	ALQ35_RS05775	Gammaproteobacteria	Pseudomonas fluorescens	cobalamin B12-binding domain-containing protein [Pseudomonas fluorescens]	GCF_002091595.1
WP_053682326.1	MFS→?→||||<-?<-?||?→||||<-?||MPTase+GT4*→?→?→||||<-?<-?<-?<-ABC_tran	MPTase+GT4	764	ADK55_RS26505	Actinobacteria	Streptomyces sp. WM4235	DUF4157 domain-containing protein [Streptomyces sp. WM4235]	GCF_001279725.1
WP_054048489.1	TPR+Caspase→ TIR+APATPase+TPR→||||<-APATPase+TPR||GT4*→||||<-HTH+APATPase+TPR	GT4	456	BN1701_RS12505	Actinobacteria	Alloactinosynnema sp. L-07	glycosyltransferase family 4 protein [Alloactinosynnema sp. L-07]	GCF_900070365.1
WP_055337289.1	STAND+TPR+GT4*→?→ SIG+HTH_23+HTH_32→||||<-?<-?||DJ-1_PfpI→	STAND+TPR+GT4	1061	HXP36_RS10750	Betaproteobacteria	Ralstonia solanacearum	glycosyltransferase [Ralstonia solanacearum]	GCF_001373335.1
WP_055417577.1	MNS+GT4*→	MNS+GT4	1164	B1H29_RS20255	Actinobacteria	Streptomyces pactum	glycosyltransferase [Streptomyces pactum]	GCF_002005225.1
WP_055618904.1	NACHT+MNS→ MNS+GT4*→	MNS+GT4	754	JHAN_RS00420	Actinobacteria	Streptomyces sp. JHA19	glycosyltransferase [Streptomyces sp. JHA19]	GCF_001417695.1
WP_055624376.1	MNS+GT4*→	MNS+GT4	1149	JHAN_RS28925	Actinobacteria	Streptomyces sp. JHA19	AAA family ATPase [Streptomyces sp. JHA19]	GCF_001417695.1
WP_057006131.1	GT4*→	GT4	773	TU80_RS30870	Gammaproteobacteria	Pseudomonas	MULTISPECIES: glycosyltransferase [Pseudomonas]	GCF_900104875.1
WP_058422527.1	GT4+B12-binding+RADICAL-SAM*→	GT4+B12-binding+RADICAL-SAM	1407	AO063_RS26420	Gammaproteobacteria	Pseudomonas fluorescens	radical SAM protein [Pseudomonas fluorescens]	GCF_001466835.1

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
WP_058721560.1	STAND+TPR+GT4*→||||<-?<-?<-?<-ABC_tran	STAND+TPR+GT4	1063	AT984_RS19735	Betaproteobacteria	Paucibacter sp. KCTC 42545	glycosyltransferase [Paucibacter sp. KCTC 42545]	GCF_001477625.1
WP_060944940.1	MNS+GT4*→	MNS+GT4	1149	AXW62_RS14785	Actinobacteria	Streptomyces hygroscopicus	glycosyltransferase [Streptomyces hygroscopicus]	GCF_001553455.1
WP_062579281.1	GT4*→||||<-?||?→?→?→?→ SIG+SnoaL→	GT4	372	ASG42_RS32705	Alphaproteobacteria	Rhizobium sp. Leaf391	glycosyltransferase family 1 protein [Rhizobium sp. Leaf391]	GCF_001424505.1
WP_062720264.1	<-TPR+Caspase||GT4*→	GT4	610	AQJ67_RS19460	Actinobacteria	Streptomyces caeruleatus	glycosyltransferase [Streptomyces caeruleatus]	GCF_001514235.1
WP_062723774.1	MNS+GT4*→	MNS+GT4	1219	AQJ67_RS36455	Actinobacteria	Streptomyces caeruleatus	glycosyltransferase [Streptomyces caeruleatus]	GCF_001514235.1
WP_062964870.1	WXG+MPTase→ WXG+SecA+ST-Hiskin+LuxR-HTH+LuxR-HTH+LuxR-HTH+LuxR-HTH+ST-Hiskin+GT4+TetR-HTH+TetR-HTH+Tox-ART-RSE+LuxR-HTH+PP2C+MPTase+MPTase*→?→ ABhydrolase→	WXG+SecA+ST-Hiskin+LuxR-HTH+LuxR-HTH+LuxR-HTH+LuxR-HTH+ST-Hiskin+GT4+TetR-HTH+TetR-HTH+Tox-ART-RSE+LuxR-HTH+PP2C+MPTase+MPTase	9117	NA3_RS18555	Actinobacteria	Nocardia africana	glycosyltransferase [Nocardia africana]	GCF_001612635.1
WP_063038911.1	WXG+TM+TM+TM→?→?→?→?→?→ WXG+ZetaToxin+GT4*→	WXG+ZetaToxin+GT4	1614	NP3_RS06870	Actinobacteria	Nocardia pseudovaccinii	zeta toxin family protein [Nocardia pseudovaccinii]	GCF_001613225.1
WP_063127006.1	Zeta_toxin→||||<-?||MPTase→?→ WXG+TM+TM+TM+TM+GT4*→	WXG+TM+TM+TM+TM+GT4	1018	NF4_RS09930	Actinobacteria	Nocardia fusca	glycosyltransferase [Nocardia fusca]	-
WP_063882776.1	GT4+APATPase+TPR+TPR*→	GT4+APATPase+TPR+TPR	1322	A1L58_RS04155	Gammaproteobacteria	Shewanella baltica	tetratricopeptide repeat protein [Shewanella baltica]	GCF_001620325.1
WP_063889953.1	GT4+B12-binding+RADICAL-SAM*→||||<-?||?→||||<-?||?→||||<-?||?→||||<-TRPR-HTH+PBPI	GT4+B12-binding+RADICAL-SAM	1415	WI77_RS33765	Betaproteobacteria	Burkholderia ubonensis	radical SAM protein [Burkholderia ubonensis]	GCF_001525885.1
WP_064054195.1	<-HTH_3||?→?→||||<-?<-Cluster466_2clades||STAND+GT4*→||||<-?<-Sigma	STAND+GT4	1084	ALQ29_RS11960	Gammaproteobacteria	Pseudomonas marginalis	glycosyltransferase [Pseudomonas marginalis]	GCF_001645105.1
WP_064273456.1	GT4*→	GT4	135	A7B19_RS17315	Actinobacteria	Streptomyces sp. RTd22	hypothetical protein [Streptomyces sp. RTd22]	GCF_001650215.1

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
WP_065910241.1	GT4+B12-binding+RADICAL-SAM*→	GT4+B12-binding+RADICAL-SAM	1393	C9382_RS17200	Gammaproteobacteria	unclassified Pseudomonas	MULTISPECIES: cobalamin B12-binding domain-containing protein [unclassified Pseudomonas]	GCF_001702265.1
WP_067257069.1	GT4*→	GT4	398	AQJ58_RS33820	Actinobacteria	Streptomyces sp. DSM 15324	glycosyltransferase family 4 protein [Streptomyces sp. DSM 15324]	GCF_001514285.1
WP_067481412.1	HTH→?→||||<-?||NACHT+MNS→ MNS+GT4*→	MNS+GT4	764	AH6_RS18370	Actinobacteria	Actinomadura hibisca	glycosyltransferase [Actinomadura hibisca]	GCF_001552635.1
WP_067904030.1	SWACOS+GT4*→	SWACOS+GT4	1149	ACH01S_RS37935	Actinobacteria	Actinomadura chibensis	glycosyltransferase [Actinomadura chibensis]	GCF_001552135.1
WP_068874779.1	HTH_3→?→||||<-?<-?||?→ MPTase→?→ NACHT+GT4*→||||<-?||?→||||<-?<-?<-PSE<-?||?→ SIG+Lipase_GDSL_2→	NACHT+GT4	1671	AX747_RS22605	Alphaproteobacteria	unclassified Phenylobacterium	MULTISPECIES: glycosyltransferase [unclassified Phenylobacterium]	GCF_001557235.1
WP_069042340.1	NACHT+GT4*→	NACHT+GT4	1642	BSY240_RS11090	Alphaproteobacteria	Agrobacterium sp. RAC06	glycosyltransferase [Agrobacterium sp. RAC06]	GCF_001713475.1
WP_070086299.1	GT4+B12-binding+RADICAL-SAM*→	GT4+B12-binding+RADICAL-SAM	1393	BJQ21_RS10430	Gammaproteobacteria	unclassified Pseudomonas	MULTISPECIES: radical SAM protein [unclassified Pseudomonas]	GCF_001753875.1
WP_071611953.1	GT4*→?→?→?→ PadR→?→||||<-?<-ABC_tran	GT4	724	F7R00_RS19755	Firmicutes	Clostridium estertheticum	glycosyltransferase family 4 protein [Clostridium estertheticum]	GCF_001877035.1
WP_071621050.1	<-AbiEii<-AbiEi_4||?→ GT4*→	GT4	497	CGQ36_RS01685	Actinobacteria	Nocardiopsis dassonvillei	glycosyltransferase family 4 protein [Nocardiopsis dassonvillei]	GCF_001877055.1
WP_072444656.1	SWACOS+GT4*→?→||||<-?<-?||MFS→	SWACOS+GT4	1138	BM382_RS27510	Gammaproteobacteria	unclassified Pseudomonas	MULTISPECIES: glycosyltransferase [unclassified Pseudomonas]	GCF_900102935.1
WP_073746098.1	CASPASE→ tRNA→||||<-?||MNS+GT4*→	MNS+GT4	1169	AMK28_RS33605	Actinobacteria	Streptomyces sp. CB02115	glycosyltransferase [Streptomyces sp. CB02115]	GCF_001905645.1

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WP_074374750.1	DctM→?→?→?→?→||||<-?||GT4*→	GT4	488	VSP9026_RS20020	Gammaproteobacteria	Vibrio spartinae	glycosyltransferase family 4 protein [Vibrio spartinae]	GCF_900149295.1
WP_074848880.1	GT4*→	GT4	397	BLU62_RS07095	Actinobacteria	Gordonia westfalica	glycosyltransferase [Gordonia westfalica]	GCF_900105725.1
WP_076845054.1	WXG+TM+GT4+GT4*→	WXG+TM+GT4+GT4	1675	BL254_RS27435	Actinobacteria	Frankia sp. BMG5.30	hypothetical protein [Frankia sp. BMG5.30]	GCF_001983005.1
WP_077298179.1	PrpF→?→||||<-?<-?||?→||||<-?||GT4+nSTAND3+TPR*→||||<-rve+rve_3||?→ tRNA-synt_1b+S4→	GT4+nSTAND3+TPR	972	BXU06_RS07175	Betaproteobacteria	Aquaspirillum sp. LM1	hypothetical protein [Aquaspirillum sp. LM1]	GCF_002002905.1
WP_078753771.1	GT4+APATPase+TPR+TPR*→	GT4+APATPase+TPR+TPR	1333	B5D35_RS17215	Gammaproteobacteria	Enterovibrio nigricans	tetratricopeptide repeat protein [Enterovibrio nigricans]	GCF_900167155.1
WP_078789290.1	XylR_N+V4R+Sigma54_activat+HTH_8→?→ GT4+APATPase+TPR*→	GT4+APATPase+TPR	1307	B5D39_RS04945	Deltaproteobacteria	Geobacter thiogenes	tetratricopeptide repeat protein [Geobacter thiogenes]	GCF_900167465.1
WP_078936874.1	-	-	1884	KS09_RS00220	Actinobacteria	Streptomyces galbus	glycosyltransferase family 4 protein [Streptomyces galbus]	GCF_000772895.1
WP_078960520.1	TIR+APATPase+GT4*→	TIR+APATPase+GT4	839	ADL01_RS15000	Actinobacteria	Streptomyces sp. NRRL WC-3618	TIR domain-containing protein [Streptomyces sp. NRRL WC-3618]	GCF_001280005.1
WP_079101522.1	GT4*→	GT4	542	AOK16_RS25865	Actinobacteria	Streptomyces pathocidini	glycosyltransferase [Streptomyces pathocidini]	GCF_001418495.1
WP_080416707.1	AA_permease→?→ GT4+APATPase+TPR+TPR*→	GT4+APATPase+TPR+TPR	1339	WL41_RS32965	Betaproteobacteria	Burkholderia ubonensis	tetratricopeptide repeat protein [Burkholderia ubonensis]	GCF_001529565.1
WP_080417742.1	GT4+APATPase+TPR+TPR*→	GT4+APATPase+TPR+TPR	1293	WJ64_RS17075	Betaproteobacteria	Burkholderia ubonensis	tetratricopeptide repeat protein [Burkholderia ubonensis]	GCF_001527745.1
WP_080419087.1	STAND+TPR+GT4*→||||<-?||ABhydrolase→||||<-TRANSGLUTAMINASE	STAND+TPR+GT4	1126	WL82_RS32325	Betaproteobacteria	Burkholderia ubonensis	glycosyltransferase [Burkholderia ubonensis]	-
WP_080421888.1	AA_permease→?→ GT4+APATPase+TPR+TPR*→	GT4+APATPase+TPR+TPR	1339	WK71_RS32030	Betaproteobacteria	Burkholderia ubonensis	tetratricopeptide repeat protein [Burkholderia ubonensis]	GCF_001529155.1

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WP_080422913.1	GT4+APATPase+TPR+TPR*→	GT4+APATPase+TPR+TPR	1339	WL11_RS09715	Betaproteobacteria	Burkholderia ubonensis	tetratricopeptide repeat protein [Burkholderia ubonensis]	GCF_001530465.1
WP_080436327.1	NACHT+TPR+GT4*→	NACHT+TPR+GT4	1226	WM18_RS12015	Betaproteobacteria	Burkholderia ubonensis	glycosyltransferase [Burkholderia ubonensis]	GCF_001533745.1
WP_080492181.1	AA_permease→?→ GT4+APATPase+TPR+TPR*→	GT4+APATPase+TPR+TPR	1293	BGV55_RS22015	Betaproteobacteria	Burkholderia ubonensis	tetratricopeptide repeat protein [Burkholderia ubonensis]	GCF_001882545.1
WP_082136219.1	GT4+APATPase+TPR+TPR*→	GT4+APATPase+TPR+TPR	1282	TR67_RS23240	Gammaproteobacteria	Pseudomonas deceptionensis	glycosyltransferase [Pseudomonas deceptionensis]	GCF_900106095.1
WP_082297595.1	GT4*→	GT4	599	AKH00_RS12250	Actinobacteria	Microbacterium sp. GCS4	glycosyltransferase family 4 protein [Microbacterium sp. GCS4]	GCF_001262495.1
WP_082404817.1	<-ABC_tran||?→?→||||<-?<-TIR+NACHT||HTH+APATPase+TPR+GT4*→	HTH+APATPase+TPR+GT4	1223	ADK67_RS45535	Actinobacteria	Saccharothrix sp. NRRL B-16348	glycosyltransferase [Saccharothrix sp. NRRL B-16348]	GCF_001280085.1
WP_082466077.1	GT4*→||||<-TRPR-HTH+PBPI<-?<-?<-?<-?||ABC_tran→	GT4	618	ASE64_RS17155	Actinobacteria	Agreia sp. Leaf210	glycosyltransferase [Agreia sp. Leaf210]	GCF_001421485.1
WP_083469142.1	GT4+NUDIX*→	GT4+NUDIX	750	VQ02_RS35520	Alphaproteobacteria	Methylobacterium variabile	glycosyltransferase family 4 protein [Methylobacterium variabile]	GCF_001043975.1
WP_083731258.1	Multi-TM→?→ STAND→?→ DUF4913→?→||||<-?||GT4+NUDIX+ART+PolB-NTase*→	GT4+NUDIX+ART+PolB-NTase	1854	BL254_RS25375	Actinobacteria	Frankia sp. BMG5.30	glycosyltransferase [Frankia sp. BMG5.30]	GCF_001983005.1
WP_083895344.1	WXG→?→?→ WXG→?→?→?→ WXG+Caspase+VWA+Papain+ZetaToxin+GT4*→	WXG+Caspase+VWA+Papain+ZetaToxin+GT4	3035	ON40_RS01890	Actinobacteria	Nocardia jiangxiensis	zeta toxin family protein [Nocardia jiangxiensis]	GCF_000308615.1
WP_085710134.1	<-LexA||GT4+APATPase+TPR+TPR*→||||<-?<-?<-ABC_tran	GT4+APATPase+TPR+TPR	1389	CAG24_RS08895	Gammaproteobacteria	unclassified Pseudomonas	MULTISPECIES: glycosyltransferase [unclassified Pseudomonas]	GCF_002112315.1
WP_086055635.1	DUF4913→?→||||<-?||GT4+NUDIX+ART+PolB-NTase*→	GT4+NUDIX+ART+PolB-NTase	1854	FrCorBMG51_RS27570	Actinobacteria	Frankia coriariae	glycosyltransferase [Frankia coriariae]	-
WP_086802688.1	GT4+NUDIX+ART+PolB-NTase*→	GT4+NUDIX+ART+PolB-NTase	1883	CCN48_RS29200	Actinobacteria	Streptomyces scabiei	glycosyltransferase family 4 protein [Streptomyces scabiei]	GCF_002155725.1

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<tr><td>WP_087651531.1</td><td>GT4+Trypsin+PNPase*→</td><td>GT4+Trypsin+PNPase</td><td>929</td><td>S1001342_RS03745</td><td>Alphaproteobacteria</td><td>Acetobacter pasteurianus</td><td>glycosyltransferase [Acetobacter pasteurianus]</td><td>GCF_002173735.1</td></tr>
<tr><td>WP_088088251.1</td><td>GT4*→</td><td>GT4</td><td>624</td><td>CCK98_RS20350</td><td>Firmicutes</td><td>Bacillus sp. OV166</td><td>glycosyltransferase family 4 protein [Bacillus sp. OV166]</td><td>GCF_900177675.1</td></tr>
<tr><td>WP_088287445.1</td><td>GT4+APATPase+TPR+TPR*→</td><td>GT4+APATPase+TPR+TPR</td><td>1066</td><td>EOINJALH_RS30615</td><td>Betaproteobacteria</td><td>Ideonella sp. A 288</td><td>tetratricopeptide repeat protein [Ideonella sp. A 288]</td><td>GCF_002198735.1</td></tr>
<tr><td>WP_090142138.1</td><td>GT4*→</td><td>GT4</td><td>516</td><td>AMM33_RS15110</td><td>Betaproteobacteria</td><td>Limnohabitans sp. DM1</td><td>glycosyltransferase family 4 protein [Limnohabitans sp. DM1]</td><td>GCF_001269385.1</td></tr>
<tr><td>WP_091283948.1</td><td>TPR+Caspase→ TPR+Caspase→||||<-CATASP||CATRA-N+CATRA-C+GT4*→||||<-?||HTH+APATPase+TPR→</td><td>CATRA-N+CATRA-C+GT4</td><td>839</td><td>AWX74_RS30820</td><td>Actinobacteria</td><td>Frankia irregularis</td><td>glycosyltransferase family 4 protein [Frankia irregularis]</td><td>GCF_001536285.1</td></tr>
<tr><td>WP_091296338.1</td><td>cNMP_binding+HTH_Crp_2→?→ GT4*→||||<-ACYC+APATPase+TPR</td><td>GT4</td><td>406</td><td>BLV57_RS34110</td><td>Actinobacteria</td><td>Amycolatopsis xylanica</td><td>glycosyltransferase family 4 protein [Amycolatopsis xylanica]</td><td>GCF_900107045.1</td></tr>
<tr><td>WP_091582937.1</td><td>STAND→?→ DUF4913→||||<-?<-?||?→ GT4*→?→?→?→ NUDIX→||||<-?<-ABC_tran</td><td>GT4</td><td>438</td><td>GA0070622_RS30350</td><td>Actinobacteria</td><td>Micromonospora sediminicola</td><td>glycosyltransferase family 4 protein [Micromonospora sediminicola]</td><td>GCF_900089585.1</td></tr>
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<tr><td>WP_092992899.1</td><td>GT4+TPR+TPR*→</td><td>GT4+TPR+TPR</td><td>1441</td><td>BLP65_RS04115</td><td>Gammaproteobacteria</td><td>Thiohalomonas denitrificans</td><td>tetratricopeptide repeat protein [Thiohalomonas denitrificans]</td><td>GCF_900102855.1</td></tr>
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acc	operon	architecture	len	gen.name	taxend	species	defline	gca
WP_096876300.1	GT4+APATPase*→	GT4+APATPase	888	MKLM6_RS16005	Gammaproteobacteria	Methylomonas koyamae	glycosyltransferase [Methylomonas koyamae]	GCF_002441955.1
WP_097325277.1	WXG→?→ GT4*→	GT4	626	CRP55_RS32890	Actinobacteria	Actinoplanes atraurantiacus	glycosyltransferase family 4 protein [Actinoplanes atraurantiacus]	GCF_900215205.1
WP_097329102.1	wHTH+TPR+APATPase→?→?→||||<-?||GT4*→||||<-?||?→?→?→?→||||<-?<-WXG+Caspase	GT4	510	CRP55_RS49635	Actinobacteria	Actinoplanes atraurantiacus	glycosyltransferase family 4 protein [Actinoplanes atraurantiacus]	GCF_900215205.1
WP_097811834.1	GT4*→	GT4	600	CN930_RS12860	Firmicutes	Bacillus cereus	glycosyltransferase [Bacillus cereus]	GCF_002574885.1
WP_097931751.1	<-DNA_methylase||?→?→?→?→?→||||<-?||MNS+GT4*→	MNS+GT4	1170	CR483_RS02605	Actinobacteria	unclassified Streptomyces	MULTISPECIES: glycosyltransferase [unclassified Streptomyces]	GCF_002551215.1
WP_098141735.1	GT4*→?→?→?→?→?→ NLPC→	GT4	541	CN671_RS19510	Firmicutes	Bacillus toyonensis	glycosyltransferase [Bacillus toyonensis]	GCF_012395365.1
WP_098743858.1	STAND→?→ DUF4913→||||<-?<-?||?→ GT4*→?→?→?→ NUDIX→||||<-?<-ABC_tran	GT4	438	COO58_RS03965	Actinobacteria	Micromonospora sp. WMMA1996	glycosyltransferase family 4 protein [Micromonospora sp. WMMA1996]	GCF_002573675.1
WP_099013704.1	MNS+GT4*→	MNS+GT4	1149	SMALA_RS12770	Actinobacteria	Streptomyces malaysiensis	AAA family ATPase [Streptomyces malaysiensis]	GCF_002591335.1
WP_100783315.1	MFS→||||<-?||GT4+APATPase+TPR*→||||<-MODE-HTH+PBPII	GT4+APATPase+TPR	1318	COO64_RS24545	Gammaproteobacteria	Pseudomonas donghuensis	glycosyltransferase [Pseudomonas donghuensis]	GCF_002811135.1
WP_101210325.1	GT4*→ TPR→	GT4	541	AT251_RS15815	Gammaproteobacteria	Enterovibrio nigricans	hypothetical protein [Enterovibrio nigricans]	-
WP_101386266.1	-	-	1324	-	Actinobacteria	Streptomyces sp. TLI_146	caspase family protein [Streptomyces sp. TLI_146]	-
WP_101718466.1	<-ABC_tran<-?<-?<-?<-PSE<-?||?→?→ GT4*→	GT4	612	SGCZBJ_RS13280	Alphaproteobacteria	Caulobacter zeae	glycosyltransferase [Caulobacter zeae]	GCF_002858925.1

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
WP_102909088.1	NUDIX→?→ GT4*→	GT4	433	C1J00_RS12325	Actinobacteria	Streptomyces sp. 13K301	glycosyltransferase family 4 protein [Streptomyces sp. 13K301]	GCF_002891435.1
WP_103291295.1	SWACOS+GT4*→?→||||<-?<-?||MFS→	SWACOS+GT4	1138	C1633_RS27595	Gammaproteobacteria	Pseudomonas protegens	glycosyltransferase [Pseudomonas protegens]	GCF_002899905.1
WP_103660162.1	NACHT+GT4*→	NACHT+GT4	1646	CPJ18_RS23160	Alphaproteobacteria	Agrobacterium rosae	glycosyltransferase [Agrobacterium rosae]	GCF_002915175.1
WP_104365810.1	GT4*→	GT4	428	C5E51_RS10910	Actinobacteria	Nocardia nova	glycosyltransferase family 4 protein [Nocardia nova]	GCF_002933545.1
WP_105007055.1	GT4*→?→||||<-PSE||?→?→ Calcineurin→	GT4	606	CUJ84_RS16890	Alphaproteobacteria	Rhizobium leguminosarum	glycosyltransferase family 4 protein [Rhizobium leguminosarum]	GCF_002953715.1
WP_106119969.1	Cluster214_2clades→ GT4*→	GT4	736	C7A11_RS23785	Gammaproteobacteria	Pseudomonas simiae	glycosyltransferase family 4 protein [Pseudomonas simiae]	GCF_003001535.1
WP_107027343.1	NACHT+GT4*→||||<-?<-?||PSE→ TIR→	NACHT+GT4	1646	C6558_RS13435	Alphaproteobacteria	Ensifer sp. NM-2	glycosyltransferase [Ensifer sp. NM-2]	GCF_003024455.1
WP_107161461.1	GT4+NACHT+BetaPropeller*→	GT4+NACHT+BetaPropeller	1536	C8054_RS26470	Actinobacteria	Micromonospora sp. RP3T	glycosyltransferase [Micromonospora sp. RP3T]	GCF_003027925.1
WP_107259933.1	nSTAND3→?→?→ GT4*→||||<-?<-?||?→||||<-?||?→ PSE→||||<-NUDIX	GT4	596	C6W10_RS21380	Actinobacteria	Plantactinospora sp. BB1	glycosyltransferase family 4 protein [Plantactinospora sp. BB1]	GCF_003030385.1
WP_107266333.1	nSTAND3→?→?→ GT4*→	GT4	596	C6361_RS00275	Actinobacteria	Plantactinospora sp. BC1	glycosyltransferase [Plantactinospora sp. BC1]	GCF_003030345.1
WP_107402046.1	Multi-TM→?→ STAND→?→ DUF4913→?→ GT4*→ Zeta_toxin→	GT4	374	AN216_RS27375	Actinobacteria	Streptomyces oceani	glycosyltransferase [Streptomyces oceani]	GCF_001751245.1
WP_107867044.1	LRR+LRR+LRR+AP-GTPase+COR+GT4*→	LRR+LRR+LRR+AP-GTPase+COR+GT4	1510	C8N29_RS15840	Firmicutes	Agitococcus lubricus	leucine-rich repeat protein [Agitococcus lubricus]	GCF_003051055.1

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
WP_108006164.1	<-HTH+APATPase+TPR||GT4*→?→||||<-?<-?<-?||TPR→	GT4	421	C7821_RS00535	Actinobacteria	Streptomyces sp. VMFN-G11Ma	glycosyltransferase family 4 protein [Streptomyces sp. VMFN-G11Ma]	GCF_003046555.1
WP_108666907.1	NLPC→?→?→||||<-?||GT4*→	GT4	564	CUC05_RS14855	Actinobacteria	Euzebya rosea	glycosyltransferase family 4 protein [Euzebya rosea]	GCF_003073135.1
WP_109448176.1	MPTase+GT4*→	MPTase+GT4	753	CK485_RS28700	Actinobacteria	Streptomyces sp. ICBB 8177	DUF4157 domain-containing protein [Streptomyces sp. ICBB 8177]	GCF_003144095.1
WP_112357576.1	GT4*→	GT4	628	DTY03_RS10805	Alphaproteobacteria	Rhizobiales bacterium	glycosyltransferase family 4 protein [Rhizobiales bacterium]	-
WP_112733881.1	GT4+APATPase+TPR*→	GT4+APATPase+TPR	1361	ONO86_RS28915	Actinobacteria	Micromonospora noduli	glycosyltransferase [Micromonospora noduli]	GCF_003264435.1
WP_113016426.1	HTH+MPTase→||||<-?<-?<-?||GT4+B12-binding+RADICAL-SAM*→	GT4+B12-binding+RADICAL-SAM	1381	DUD68_RS27095	Alphaproteobacteria	Rhizobiales bacterium	radical SAM protein [Rhizobiales bacterium]	-
WP_113272579.1	HTH+MPTase→?→ Helicase_C→ SIG+DUF1998→||||<-?<-?||?→ NACHT+GT4*→	NACHT+GT4	1640	DUJ98_RS17735	Alphaproteobacteria	Rhizobiales bacterium	glycosyltransferase [Rhizobiales bacterium]	-
WP_114055463.1	TIR+APATPase+GT4*→	TIR+APATPase+GT4	775	C0216_RS13195	Actinobacteria	Streptomyces globosus	TIR domain-containing protein [Streptomyces globosus]	GCF_003325375.1
WP_114396907.1	GT4*→	GT4	529	DEF24_RS15180	Actinobacteria	Marinitenerispora sediminis	glycosyltransferase family 4 protein [Marinitenerispora sediminis]	GCF_003336445.1
WP_116211561.1	NACHT→ GT4*→	GT4	406	DXZ73_RS15355	Actinobacteria	Streptomyces olivoreticuli	glycosyltransferase family 4 protein [Streptomyces olivoreticuli]	GCF_003391135.1
WP_116568912.1	GT4*→?→||||<-?<-?||?→||||<-?<-MODE-HTH+PBPII	GT4	612	DDF65_RS17385	Alphaproteobacteria	Caulobacter radicis	glycosyltransferase [Caulobacter radicis]	GCF_003094595.1

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
WP_120733613.1	GT4+B12-binding+RADICAL-SAM*→	GT4+B12-binding+RADICAL-SAM	1400	D7M10_RS18130	Gammaproteobacteria	Pseudomonas fluorescens	radical SAM protein [Pseudomonas fluorescens]	GCF_003626995.1
WP_120967974.1	GT4+APATPase+TPR+TPR*→	GT4+APATPase+TPR+TPR	1425	EAO39_RS12970	Betaproteobacteria	Comamonas sp. lk	tetratricopeptide repeat protein [Comamonas sp. lk]	GCF_900564145.1
WP_121165351.1	Sigma→?→?→?→?→?→ LRR+LRR+LRR+AP-GTPase+COR+GT4*→	LRR+LRR+LRR+AP-GTPase+COR+GT4	1488	B0H84_RS06470	Betaproteobacteria	Nitrosomonas sp. Nm120	leucine-rich repeat domain-containing protein [Nitrosomonas sp. Nm120]	GCF_003664085.1
WP_121799508.1	Multi-TM→?→ STAND→?→ DUF4913→?→ GT4*→	GT4	488	CTZ27_RS14745	Actinobacteria	Streptomyces griseocarneus	glycosyltransferase family 4 protein [Streptomyces griseocarneus]	GCF_003674045.1
WP_122257475.1	GT4+B12-binding+RADICAL-SAM*→	GT4+B12-binding+RADICAL-SAM	1421	ALP97_05253	Gammaproteobacteria	Pseudomonas salomonii	radical SAM protein [Pseudomonas salomonii]	-
WP_122528181.1	STAND+TPR+GT4*→	STAND+TPR+GT4	1067	EE945_RS06325	Gammaproteobacteria	Pseudomonas viridiflava	glycosyltransferase [Pseudomonas viridiflava]	GCF_900580695.1
WP_123299261.1	GT4+B12-binding+RADICAL-SAM*→||||<-?||?→?→||||<-?<-?<-?||MODE-HTH+PBPII→	GT4+B12-binding+RADICAL-SAM	1405	EC845_RS16630	Betaproteobacteria	Comamonas sp. BIGb0124	cobalamin B12-binding domain-containing protein [Comamonas sp. BIGb0124]	GCF_003752175.1
WP_123439297.1	<-TPR+Caspase<-CATASP||CATRA-N+CATRA-C+GT4*→ HTH+APATPase+TPR→||||<-HTH||?→?→?→||||<-?<-CATASP	CATRA-N+CATRA-C+GT4	694	EDD94_RS26400	Actinobacteria	Streptomyces sp. PanSC9	glycosyltransferase family 4 protein [Streptomyces sp. PanSC9]	GCF_003751985.1
WP_124130642.1	STAND+GT4*→	STAND+GT4	1082	CJU35_RS32065	Gammaproteobacteria	Pseudomonas aeruginosa	glycosyltransferase [Pseudomonas aeruginosa]	GCF_901482505.1
WP_124284015.1	NUDIX→?→||||<-?||?→ MNS+GT4*→	MNS+GT4	1151	EES39_RS04745	Actinobacteria	Streptomyces sp. ADI92-24	glycosyltransferase [Streptomyces sp. ADI92-24]	GCF_003846195.1
WP_124458549.1	STAND+TPR+GT4*→||||<-?<-?<-?||Calcineurin→	STAND+TPR+GT4	1054	DBV14_RS07405	Betaproteobacteria	Variovorax sp. KBW07	glycosyltransferase [Variovorax sp. KBW07]	GCF_003852515.1

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WP_125624986.1	Multi-TM→?→ STAND→?→ DUF4913→?→ GT4*→?→ Zeta_toxin→||||<-ABC_tran	GT4	547	DMH02_RS17910	Actinobacteria	Streptomyces sp. WAC 00631	glycosyltransferase family 4 protein [Streptomyces sp. WAC 00631]	GCF_003947265.1
WP_125642507.1	MNS+GT4*→	MNS+GT4	1274	EF918_07135	Actinobacteria	Streptomyces sp. WAC06614	glycosyltransferase [Streptomyces sp. WAC06614]	-
WP_125650904.1	Caspase+NACHT+GT4*→	Caspase+NACHT+GT4	1208	EF918_25550	Actinobacteria	Streptomyces sp. WAC06614	glycosyltransferase [Streptomyces sp. WAC06614]	-
WP_125870434.1	GT4+B12-binding+RADICAL-SAM*→	GT4+B12-binding+RADICAL-SAM	1426	EGJ08_07220	Gammaproteobacteria	Pseudomonas stutzeri	radical SAM protein [Pseudomonas stutzeri]	-
WP_125995743.1	NACHT+GT4*→	NACHT+GT4	1650	BRX43_RS14145	Alphaproteobacteria	Sphingomonas sp. S-NIH.Pt15_0812	glycosyltransferase [Sphingomonas sp. S-NIH.Pt15_0812]	GCF_003951315.1
WP_127872272.1	NACHT+GT4*→||||<-Vsr	NACHT+GT4	1637	EN845_RS20190	Alphaproteobacteria	unclassified Mesorhizobium	MULTISPECIES: glycosyltransferase family 4 protein [unclassified Mesorhizobium]	-
WP_128145588.1	MPTase→ WXG+SecA→?→?→ GT4+TetR-HTH+TetR-HTH+Tox-ART-RSE+LuxR-HTH*→?→?→ ABhydrolase→	GT4+TetR-HTH+TetR-HTH+Tox-ART-RSE+LuxR-HTH	2725	NCTC13184_06625	Actinobacteria	Nocardia africana	glycosyltransferase [Nocardia africana]	-
WP_129557405.1	<-TnpB_IS66<-HTH_Tnp_1||?→ SIG+GT4→ *GT4*→ tRNA→||||<-?<-PSE||?→||||<-?<-PSE<-?<-?||Calcineurin→||||<-cNMP_binding+HTH_Crp_2	SIG+GT4	316	NK6_RS51120	Alphaproteobacteria	Bradyrhizobium diazoefficiens	glycosyltransferase [Bradyrhizobium diazoefficiens]	GCF_001549695.1
WP_130174915.1	GT4+B12-binding+RADICAL-SAM*→	GT4+B12-binding+RADICAL-SAM	1409	EUX58_RS06685	Gammaproteobacteria	Pseudomonas	MULTISPECIES: radical SAM protein [Pseudomonas]	GCF_005930695.1
WP_130264935.1	GT4+APATPase+TPR+TPR*→||||<-MODE-HTH+PBPII	GT4+APATPase+TPR+TPR	1330	EXN22_RS15725	Gammaproteobacteria	Pseudomonas sp. SNU WT1	glycosyltransferase family 4 protein [Pseudomonas sp. SNU WT1]	GCF_004214895.1
WP_130343732.1	WXG+TM+EDA39C+Papain+Caspase+GT4*→?→ GT4→	WXG+TM+EDA39C+Papain+Caspase+GT4	2616	EV193_RS09710	Actinobacteria	Herbihabitans rhizosphaerae	glycosyltransferase [Herbihabitans rhizosphaerae]	GCF_004216555.1
WP_130721989.1	CASPASE→?→?→?→ GT4*→	GT4	606	ELI52_RS15625	Alphaproteobacteria	Rhizobium leguminosarum	glycosyltransferase [Rhizobium leguminosarum]	GCF_004303135.1

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acc	operon	architecture	len	gen.name	taxend	species	defline	gca
WP_133739590.1	STAND→?→?→ DUF4913→||||<-AbiEii<-AbiEi_4||?→ GT4*→	GT4	493	EV190_RS01575	Actinobacteria	Actinorugispora endophytica	glycosyltransferase family 4 protein [Actinorugispora endophytica]	GCF_004363075.1
WP_133854316.1	Helicase_C→ SIG+DUF1998→||||<-?||?→?→||||<-?||?→ GT4→ *TIR+APATPase+TPR→ TPR+Caspase→||||<-TPR+Caspase<-CATASP||CATRA-N+CATRA-C+GT4→*	GT4	423	EV186_RS37520	Actinobacteria	Labedaea rhizosphaerae	glycosyltransferase family 4 protein [Labedaea rhizosphaerae]	GCF_004362825.1
WP_133925636.1	GT4*→	GT4	622	EV573_RS04015	Actinobacteria	Streptomyces sp. BK161	glycosyltransferase [Streptomyces sp. BK161]	GCF_004364215.1
WP_133927416.1	SWACOS+GT4*→||||<-?<-?||?→||||<-?<-?<-ABC_tran	SWACOS+GT4	1159	EV573_RS13335	Actinobacteria	Streptomyces sp. BK161	glycosyltransferase [Streptomyces sp. BK161]	GCF_004364215.1
WP_133932223.1	<-Sigma<-?<-TPR||GT4*→	GT4	410	EV573_RS39315	Actinobacteria	Streptomyces sp. BK161	glycosyltransferase family 4 protein [Streptomyces sp. BK161]	GCF_004364215.1
WP_134939719.1	GT4+B12-binding+RADICAL-SAM*→	GT4+B12-binding+RADICAL-SAM	1421	BZ164_RS25605	Gammaproteobacteria	Pseudomonas veronii	radical SAM protein [Pseudomonas veronii]	-
WP_135904996.1	<-Vsr||?→?→?→||||<-?<-?||GT4+Trypsin+PNPase*→	GT4+Trypsin+PNPase	836	EN818_RS17550	Alphaproteobacteria	unclassified Mesorhizobium	MULTISPECIES: glycosyltransferase [unclassified Mesorhizobium]	-
WP_136526013.1	SWACOS+GT4*→	SWACOS+GT4	1144	E8L22_RS15545	Deltaproteobacteria	Geomonas ferrireducens	glycosyltransferase [Geomonas ferrireducens]	-
WP_136738577.1	GT4*→	GT4	394	FCH28_RS05590	Actinobacteria	Streptomyces sp. jys28	glycosyltransferase family 4 protein [Streptomyces sp. jys28]	GCF_005048155.1
WP_136743126.1	MNS+GT4*→	MNS+GT4	1188	FCH28_RS29075	Actinobacteria	Streptomyces sp. jys28	glycosyltransferase [Streptomyces sp. jys28]	GCF_005048155.1
WP_138637396.1	NUDIX→?→ GT4*→	GT4	432	ETD96_RS16755	Actinobacteria	Actinomadura geliboluensis	glycosyltransferase family 4 protein [Actinomadura geliboluensis]	GCF_005889745.1
WP_141100843.1	GT4+HD*→	GT4+HD	1421	CDN99_RS17245	Betaproteobacteria	Roseateles aquatilis	HD domain-containing protein [Roseateles aquatilis]	GCF_002205645.1

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WP_141569577.1	ZetaToxin+GT4+NUDIX+ART+NTase*→?→?→?→||||<-Caspase	ZetaToxin+GT4+NUDIX+ART+NTase	2159	SipoB123_RS12910	Actinobacteria	Streptomyces ipomoeae	zeta toxin family protein [Streptomyces ipomoeae]	GCF_006547165.1
WP_141585352.1	ZetaToxin+GT4+NUDIX+ART+NTase*→?→?→?→||||<-Caspase<-?||?→ PSE→||||<-NLPC	ZetaToxin+GT4+NUDIX+ART+NTase	2156	Sipo7851_RS16610	Actinobacteria	Streptomyces ipomoeae	zeta toxin family protein [Streptomyces ipomoeae]	GCF_006547175.1
WP_141714270.1	<-TPR+Caspase||GT4*→	GT4	542	GA0074694_RS24775	Actinobacteria	Micromonospora inyonensis	glycosyltransferase [Micromonospora inyonensis]	GCF_900091415.1
WP_141749885.1	GT4+NACHT*→||||<-MFS	GT4+NACHT	1197	JAB9_RS27490	Betaproteobacteria	Janthinobacterium sp. HH107	glycosyltransferase family 4 protein [Janthinobacterium sp. HH107]	GCF_001758765.1
WP_141888935.1	MFS→||||<-ABC_tran<-?<-?<-?<-?||GT4*→	GT4	608	FB468_RS16790	Actinobacteria	Leucobacter komagatae	glycosyltransferase [Leucobacter komagatae]	GCF_006716085.1
WP_141962659.1	<-HTH+APATPase+TPR<-TPR+Caspase<-CATASP||CATRA-N+CATRA-C+GT4*→||||<-?<-?<-?<-?<-?<-REase+SFI-ATPase	CATRA-N+CATRA-C+GT4	732	FB559_RS39205	Actinobacteria	Actinoallomurus bryophytorum	glycosyltransferase [Actinoallomurus bryophytorum]	GCF_006716425.1
WP_142260239.1	MNS+GT4*→?→||||<-?<-Sigma<-?||ABC_tran→	MNS+GT4	1152	FHX40_RS15230	Actinobacteria	Thermopolyspora flexuosa	glycosyltransferase [Thermopolyspora flexuosa]	GCF_014647775.1
WP_142588942.1	NACHT+GT4*→	NACHT+GT4	1640	HNP80_RS07130	Alphaproteobacteria	Rhizobium halotolerans	glycosyltransferase [Rhizobium halotolerans]	GCF_902153235.2
WP_143026968.1	LRR+AP-GTPase+COR→ GT4*→	GT4	484	BMY41_RS11080	Betaproteobacteria	Nitrosomonas oligotropha	glycosyltransferase [Nitrosomonas oligotropha]	GCF_900106555.1
WP_143176277.1	AA_permease→?→ GT4+APATPase+TPR+TPR*→	GT4+APATPase+TPR+TPR	1172	BGV47_RS35370	Betaproteobacteria	Burkholderia ubonensis	tetratricopeptide repeat protein, partial [Burkholderia ubonensis]	GCF_001901485.1
WP_143660221.1	<-TPR+Caspase<-CATASP||CATRA-N+CATRA-C+GT4*→ HTH+APATPase+TPR→||||<-HTH||?→?→?→||||<-?<-CATASP	CATRA-N+CATRA-C+GT4	703	DDV98_RS32255	Actinobacteria	unclassified Streptomyces	MULTISPECIES: glycosyltransferase [unclassified Streptomyces]	GCF_001983595.1
WP_143740316.1	<-TPR+Caspase||GT4*→?→?→||||<-?<-?<-ABC_tran	GT4	546	GA0070618_RS24540	Actinobacteria	Micromonospora echinospora	glycosyltransferase [Micromonospora echinospora]	GCF_900091495.1

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
WP_143788398.1	STAND+TPR+GT4*→	STAND+TPR+GT4	1136	BUS12_RS18575	Betaproteobacteria	Paraburkholderia phenazinium	glycosyltransferase [Paraburkholderia phenazinium]	GCF_900142845.1
WP_143860247.1	WXG+MPTase→ WXG+SecA+LuxR-HTH+LuxR-HTH+LuxR-HTH+LuxR-HTH+ST-Hiskin+MPTase+GT4+TetR-HTH+TetR-HTH+Tox-ART-RSE+LuxR-HTH+LuxR-HTH+LuxR-HTH+GNTR-HTH+LuxR-HTH+LuxR-HTH+ST-Hiskin+ST-Hiskin+XPC-C+TM+TM+TM+TM+LuxR-HTH*→	WXG+SecA+LuxR-HTH+LuxR-HTH+LuxR-HTH+LuxR-HTH+ST-Hiskin+MPTase+GT4+TetR-HTH+TetR-HTH+Tox-ART-RSE+LuxR-HTH+LuxR-HTH+LuxR-HTH+GNTR-HTH+LuxR-HTH+LuxR-HTH+ST-Hiskin+ST-Hiskin+XPC-C+TM+TM+TM+TM+LuxR-HTH	11649	B7C42_RS30150	Actinobacteria	Nocardia cerradoensis	MFS transporter, partial [Nocardia cerradoensis]	GCF_002236815.1
WP_144299077.1	GT4+B12-binding+RADICAL-SAM*→	GT4+B12-binding+RADICAL-SAM	1385	VARPA_RS03315	Betaproteobacteria	Variovorax paradoxus	radical SAM protein [Variovorax paradoxus]	GCF_000184745.1
WP_144384941.1	Multi-TM→?→ STAND→?→ DUF4913→?→ GT4*→	GT4	497	CD790_RS21520	Actinobacteria	Streptomyces sp. SAJ15	glycosyltransferase [Streptomyces sp. SAJ15]	GCF_007595705.1
WP_145763552.1	NUDIX→?→ MNS+GT4*→	MNS+GT4	1151	FHX80_RS07940	Actinobacteria	Streptomyces brevispora	glycosyltransferase [Streptomyces brevispora]	GCF_007829885.1
WP_145809941.1	MNS+GT4*→?→?→||||<-?||?→ CSD→	MNS+GT4	1180	FHW51_RS26100	Actinobacteria	Streptomyces argenteolus	glycosyltransferase [Streptomyces argenteolus]	GCF_007829855.1
WP_145818563.1	<-TPR+Caspase||GT4*→?→||||<-?<-?<-ABC_tran	GT4	546	JD81_RS15875	Actinobacteria	Micromonospora sagamiensis	glycosyltransferase [Micromonospora sagamiensis]	GCF_014680085.1
WP_145835614.1	<-TPR+Caspase||GT4*→	GT4	546	JD80_RS20680	Actinobacteria	Micromonospora echinospora	glycosyltransferase [Micromonospora echinospora]	GCF_007829475.1
WP_145885265.1	ABhydrolase→||||<-?<-?||?→||||<-?||?→?→ MNS+GT4*→	MNS+GT4	1144	FB157_RS37885	Actinobacteria	Streptomyces sp. BK340	glycosyltransferase [Streptomyces sp. BK340]	GCF_007827595.1
WP_145921569.1	WXG+TM+GT4+GT4*→	WXG+TM+GT4+GT4	3484	FJK98_RS27630	Actinobacteria	Micromonospora sp. HM134	glycosyltransferase [Micromonospora sp. HM134]	GCF_007833915.1
WP_146161226.1	WXG+MPTase→ WXG+LuxR-HTH+LuxR-HTH+LuxR-HTH+LuxR-HTH+TetR-HTH+TetR-HTH+LuxR-HTH+LuxR-HTH+LexA-HTH+LuxR-HTH+LuxR-HTH+LuxR-HTH+LuxR-HTH+LuxR-HTH+PP2C*→?→ ABhydrolase→	WXG+LuxR-HTH+LuxR-HTH+LuxR-HTH+LuxR-HTH+TetR-HTH+TetR-HTH+LuxR-HTH+LuxR-HTH+LexA-HTH+LuxR-HTH+LuxR-HTH+LuxR-HTH+LuxR-HTH+LuxR-HTH+PP2C	14195	C8258_RS13420	Actinobacteria	Nocardia sp. MDA0666	MFS transporter [Nocardia sp. MDA0666]	GCF_003023875.1
WP_146241295.1	APATPase+TPR→||||<-?||GT4*→?→?→ GT4→	GT4	502	DFQ13_RS33200	Actinobacteria	Actinokineospora mzabensis	glycosyltransferase [Actinokineospora mzabensis]	-
WP_146349043.1	<-APATPase<-APATPase||?→ NLPC→ cNMP_binding+HTH_Crp_2→?→ GT4*→||||<-ACYC+APATPase+TPR	GT4	408	FKR81_RS01510	Actinobacteria	Lentzea sp. FXJ1.1311	glycosyltransferase [Lentzea sp. FXJ1.1311]	GCF_007845675.1

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
WP_147321781.1	SWACOS+GT4*→||||<-?<-MFS	SWACOS+GT4	1096	BX279_RS09075	Actinobacteria	Streptomyces sp. Ag82_O1-9	glycosyltransferase [Streptomyces sp. Ag82_O1-9]	GCF_003386845.1
WP_147416956.1	STAND→?→?→ DUF4913→||||<-AbiEii<-AbiEi_4||?→ GT4*→ AbiEi_4→	GT4	495	NI17_RS16590	Actinobacteria	Thermobifida halotolerans	glycosyltransferase [Thermobifida halotolerans]	GCF_003574835.1
WP_147994072.1	TRPR-HTH+PBPI→?→?→||||<-TPR+Caspase||GT4*→	GT4	597	EAO75_RS06975	Actinobacteria	Streptomyces sp. uw30	glycosyltransferase [Streptomyces sp. uw30]	GCF_008042075.1
WP_148348287.1	SWACOS+GT4*→	SWACOS+GT4	1238	FXF65_RS04105	Actinobacteria	Actinomadura syzygii	glycosyltransferase [Actinomadura syzygii]	-
WP_148640710.1	MNS+GT4*→	MNS+GT4	1142	EH183_RS01595	Actinobacteria	Streptomyces sp. CB01881	glycosyltransferase [Streptomyces sp. CB01881]	GCF_002953255.1
WP_148757712.1	STAND→ VWA+vWA-L+STAND+TPR+GT4*→ Sigma→?→ ABC_tran→	VWA+vWA-L+STAND+TPR+GT4	1697	FXF68_RS05215	Actinobacteria	Actinomadura sp. CYP1-5	glycosyltransferase [Actinomadura sp. CYP1-5]	GCF_008121305.1
WP_148758378.1	SWACOS+GT4*→	SWACOS+GT4	1147	FXF68_RS08315	Actinobacteria	Actinomadura sp. CYP1-5	glycosyltransferase [Actinomadura sp. CYP1-5]	GCF_008121305.1
WP_148759187.1	GT4*→	GT4	581	FXF68_RS13230	Actinobacteria	Actinomadura sp. CYP1-5	glycosyltransferase [Actinomadura sp. CYP1-5]	GCF_008121305.1
WP_149263194.1	LexA→||||<-?||?→||||<-?<-?<-?<-cNMP_binding+HTH_Crp_2||GT4*→||||<-HTH+APATPase+TPR	GT4	459	K4S16_RS34110	Actinobacteria	Actinomadura sp. K4S16	glycosyltransferase [Actinomadura sp. K4S16]	GCF_008327685.1
WP_149830792.1	<-HTH+APATPase+TPR||GT4*→?→||||<-?<-?<-?<-?||TPR→	GT4	419	F3T56_RS42265	Actinobacteria	Streptomyces sp. TRM68348	glycosyltransferase [Streptomyces sp. TRM68348]	GCF_008386495.1
WP_149896003.1	NACHT+GT4*→	NACHT+GT4	1646	DXU01_RS22280	Alphaproteobacteria	Agrobacterium rosae	glycosyltransferase [Agrobacterium rosae]	GCF_008501885.1
WP_151009920.1	<-cNMP_binding+HTH_Crp_2||GT4*→||||<-HTH+APATPase+TPR	GT4	457	F7P10_RS15075	Actinobacteria	Actinomadura sp. WMMB 499	glycosyltransferase [Actinomadura sp. WMMB 499]	GCF_008824145.1
WP_153338839.1	ESX-1_EspG→||||<-?<-?||?→?→?→ WXG+TOXIN-PL+ART+Caspase+ZetaToxin+GT4*→	WXG+TOXIN-PL+ART+Caspase+ZetaToxin+GT4	3261	NRB56_RS02760	Actinobacteria	Nocardia sp. RB56	zeta toxin family protein [Nocardia sp. RB56]	GCF_009604425.1

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
WP_153430492.1	GT4*→	GT4	1126	GFJ39_RS06035	Alphaproteobacteria	Gluconobacter sp. AC10	glycosyltransferase [Gluconobacter sp. AC10]	-
WP_153467262.1	GT4*→	GT4	460	F7Q99_RS30660	Actinobacteria	Streptomyces kaniharaensis	glycosyltransferase [Streptomyces kaniharaensis]	-
WP_153535837.1	REase+SFI-ATPase→||||<-?||?→||||<-?||?→ GT4+APATPase+TPR+TPR*→	GT4+APATPase+TPR+TPR	1190	ACRB68_RS23060	Actinobacteria	Actinomadura sp. RB68	tetratricopeptide repeat protein [Actinomadura sp. RB68]	-
WP_154363881.1	TniB→?→ STAND+TPR+GT4*→	STAND+TPR+GT4	1054	GJ697_RS09905	Betaproteobacteria	Duganella	MULTISPECIES: glycosyltransferase [Duganella]	GCF_009674525.1
WP_155055777.1	TIR+APATPase+GT4*→	TIR+APATPase+GT4	772	GFH49_RS11700	Actinobacteria	Streptomyces sp. TRM63209	TIR domain-containing protein [Streptomyces sp. TRM63209]	GCF_009709555.1
WP_155097668.1	GT4*→	GT4	609	GL286_RS21805	Alphaproteobacteria	Paracoccus aestuariivivens	hypothetical protein [Paracoccus aestuariivivens]	GCF_009711225.1
WP_155252689.1	Multi-TM→?→ STAND→?→ DUF4913→||||<-?||?→ GT4*→?→?→?→ NUDIX→	GT4	438	B170_RS0111915	Actinobacteria	Salinispora pacifica	glycosyltransferase [Salinispora pacifica]	GCF_000514515.1
WP_156002545.1	<-AbiEii<-AbiEi_4||AbiEi_4→ AbiEii→||||<-AbiEii<-AbiEi_4||?→ GT4*→||||<-DUF4913<-?<-?<-STAND	GT4	494	FZ103_RS17370	Actinobacteria	Streptomonospora sp. PA3	glycosyltransferase [Streptomonospora sp. PA3]	GCF_009728995.1
WP_156395661.1	STAND+GT4*→	STAND+GT4	1081	ASC85_RS19490	Gammaproteobacteria	Pseudomonas sp. Root401	glycosyltransferase [Pseudomonas sp. Root401]	GCF_001425105.1
WP_156427756.1	APATPase+TPR+GT4*→	APATPase+TPR+GT4	1394	ML01_RS15555	Gammaproteobacteria	Thiohalocapsa sp. ML1	tetratricopeptide repeat protein [Thiohalocapsa sp. ML1]	GCF_001469165.1
WP_156551292.1	NACHT+GT4*→	NACHT+GT4	1640	GOZ95_RS24735	Alphaproteobacteria	Agrobacterium vitis	glycosyltransferase [Agrobacterium vitis]	GCF_009744055.1
WP_156901549.1	GT4*→?→||||<-?<-?<-?||?→||||<-MFS	GT4	643	K328_RS25440	Alphaproteobacteria	Nisaea denitrificans	glycosyltransferase, partial [Nisaea denitrificans]	GCF_000426505.1

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
WP_157059028.1	GT4*→	GT4	261	AN191_RS16995	Alphaproteobacteria	Loktanella sp. 5RATIMAR09	glycosyltransferase family 4 protein, partial [Loktanella sp. 5RATIMAR09]	GCF_001419985.1
WP_157097111.1	GT4*→?→||||<-?<-?<-?||HTH→	GT4	608	FHS67_RS12310	Alphaproteobacteria	Aminobacter aminovorans	glycosyltransferase [Aminobacter aminovorans]	GCF_001605015.1
WP_157104014.1	WXG+MPTase→ WXG+SecA+ST-Hiskin+HTH+HTH+HTH+HTH+HTH+HTH+HTH+HTH+ST-Hiskin+MPTase+GT4+TetR-HTH+TetR-HTH+LuxR-HTH+LuxR-HTH+LuxR-HTH+GNTR-HTH+LuxR-HTH+LuxR-HTH+ST-Hiskin+ST-Hiskin+LuxR-HTH+TM+TM+TM+TM+MPTase+MPTase*→?→ ABhydrolase→	WXG+SecA+ST-Hiskin+HTH+HTH+HTH+HTH+HTH+HTH+HTH+HTH+ST-Hiskin+MPTase+GT4+TetR-HTH+TetR-HTH+LuxR-HTH+LuxR-HTH+LuxR-HTH+GNTR-HTH+LuxR-HTH+LuxR-HTH+ST-Hiskin+ST-Hiskin+LuxR-HTH+TM+TM+TM+TM+MPTase+MPTase	11529	NK1_RS00230	Actinobacteria	Nocardia kruczakiae	MFS transporter [Nocardia kruczakiae]	GCF_001612965.1
WP_157106745.1	MPTase→ WXG+SecA+GT4+TetR-HTH+TetR-HTH+MPTase+HTH+HTH+HTH+HTH+HTH+CHTH+HTH+HTH*→	WXG+SecA+GT4+TetR-HTH+TetR-HTH+MPTase+HTH+HTH+HTH+HTH+HTH+CHTH+HTH+HTH	5359	NA8_RS16815	Actinobacteria	Nocardia arthritidis	helix-turn-helix domain-containing protein [Nocardia arthritidis]	GCF_001612765.1
WP_157114874.1	<-ABC_tran<-?<-?||?→?→ MPTase→ WXG+SecA+GT4+TetR-HTH+TetR-HTH+HTH+HTH+HTH+HTH+HTH+CHTH+MPTase*→	WXG+SecA+GT4+TetR-HTH+TetR-HTH+HTH+HTH+HTH+HTH+HTH+CHTH+MPTase	6963	NNI01S_RS19995	Actinobacteria	Nocardia niwae	helix-turn-helix domain-containing protein [Nocardia niwae]	GCF_001613465.1
WP_157120634.1	TRPR-HTH+HTH+HTH+HTH+CHTH+HTH+HTH+NUDIX+NUDIX+Tox-MCF+GT4*→?→||||<-ESX-1_EspG<-?<-PSE||?→?→||||<-?||WXG+TM+TM+TM+TM+FN3+MPTase+MPTase+MPTase+MPTase+MPTase+MPTase+MPTase+MPTase+MPTase+MPTase+MPTase+MPTase+MPTase+MPTase+MPTase→	TRPR-HTH+HTH+HTH+HTH+CHTH+HTH+HTH+NUDIX+NUDIX+Tox-MCF+GT4	11280	NF4_RS27240	Actinobacteria	Nocardia fusca	helix-turn-helix domain-containing protein [Nocardia fusca]	GCF_001618425.1
WP_157120699.1	<-MPTase<-?||?→?→ MPTase→ WXG+SecA+GT4+MPTase+LuxR-HTH+Abhydrolase*→?→||||<-?<-?||PSE→?→||||<-?||SIG+SnoaL→	WXG+SecA+GT4+MPTase+LuxR-HTH+Abhydrolase	4137	NF4_RS31035	Actinobacteria	Nocardia fusca	glycosyltransferase [Nocardia fusca]	GCF_001618425.1
WP_157121874.1	WXG+MPTase→ WXG+SecA+ST-Hiskin+LuxR-HTH+LuxR-HTH+LuxR-HTH+LuxR-HTH+GT4+TetR-HTH+TetR-HTH+ART+SIGMA-HTH+LuxR-HTH+LuxR-HTH+LuxR-HTH+GNTR-HTH+LuxR-HTH+LuxR-HTH+ST-Hiskin+ST-Hiskin+XPC-C+LuxR-HTH+LuxR-HTH+MFS(6xTM)+PP2C+STYKinase-like*→?→ ABhydrolase→	WXG+SecA+ST-Hiskin+LuxR-HTH+LuxR-HTH+LuxR-HTH+LuxR-HTH+GT4+TetR-HTH+TetR-HTH+ART+SIGMA-HTH+LuxR-HTH+LuxR-HTH+LuxR-HTH+GNTR-HTH+LuxR-HTH+LuxR-HTH+ST-Hiskin+ST-Hiskin+XPC-C+LuxR-HTH+LuxR-HTH+MFS(6xTM)+PP2C+STYKinase-like	12511	NV5_RS14795	Actinobacteria	Nocardia violaceofusca	MFS transporter [Nocardia violaceofusca]	GCF_001613525.1
WP_157126117.1	WXG+MPTase→ WXG+SecA+ST-Hiskin+HTH+HTH+HTH+HTH+HTH+HTH+HTH+HTH+ST-Hiskin+MPTase+GT4+TetR-HTH+TetR-HTH+LuxR-HTH+LuxR-HTH+LuxR-HTH+LuxR-HTH+GNTR-HTH+LuxR-HTH+LuxR-HTH+PP2C+MPTase+MPTase+8TMR-UT+TM+TM+ST-Hiskin*→?→ ABhydrolase→	WXG+SecA+ST-Hiskin+HTH+HTH+HTH+HTH+HTH+HTH+HTH+HTH+ST-Hiskin+MPTase+GT4+TetR-HTH+TetR-HTH+LuxR-HTH+LuxR-HTH+LuxR-HTH+LuxR-HTH+GNTR-HTH+LuxR-HTH+LuxR-HTH+PP2C+MPTase+MPTase+8TMR-UT+TM+TM+ST-Hiskin	15995	NMI01S_RS10045	Actinobacteria	Nocardia mikamii	MFS transporter [Nocardia mikamii]	GCF_001613505.1
WP_157129222.1	HTH+APATPase+TPR→?→ GT4*→||||<-?<-?<-AAA_21	GT4	601	NA4_RS22535	Actinobacteria	Nocardia amamiensis	glycosyltransferase [Nocardia amamiensis]	GCF_001612745.1
WP_157163478.1	WXG+MPTase→ WXG+SecA+ST-Hiskin+LuxR-HTH+LuxR-HTH+LuxR-HTH+LuxR-HTH+GT4+TetR-HTH+TetR-HTH+ART+SIGMA-HTH+LuxR-HTH+LuxR-HTH+LuxR-HTH+GNTR-HTH+LuxR-HTH+LuxR-HTH+ST-Hiskin+ST-Hiskin+XPC-C+LuxR-HTH+LuxR-HTH+MFS(6xTM)+PP2C+STYKinase-like*→?→ ABhydrolase→	WXG+SecA+ST-Hiskin+LuxR-HTH+LuxR-HTH+LuxR-HTH+LuxR-HTH+GT4+TetR-HTH+TetR-HTH+ART+SIGMA-HTH+LuxR-HTH+LuxR-HTH+LuxR-HTH+GNTR-HTH+LuxR-HTH+LuxR-HTH+ST-Hiskin+ST-Hiskin+XPC-C+LuxR-HTH+LuxR-HTH+MFS(6xTM)+PP2C+STYKinase-like	12510	RJ03_RS22280	Actinobacteria	Nocardia aobensis	MFS transporter [Nocardia aobensis]	GCF_000308375.1
WP_157170272.1	WXG+MPTase→ WXG+SecA+LuxR-HTH+LuxR-HTH+LuxR-HTH+LuxR-HTH+ST-Hiskin+MPTase+GT4+TetR-HTH+TetR-HTH+Tox-ART-RSE+LuxR-HTH+LuxR-HTH+LuxR-HTH+GNTR-HTH+LuxR-HTH+LuxR-HTH+ST-Hiskin+ST-Hiskin+XPC-C+TM+TM+TM+TM+LuxR-HTH*→	WXG+SecA+LuxR-HTH+LuxR-HTH+LuxR-HTH+LuxR-HTH+ST-Hiskin+MPTase+GT4+TetR-HTH+TetR-HTH+Tox-ART-RSE+LuxR-HTH+LuxR-HTH+LuxR-HTH+GNTR-HTH+LuxR-HTH+LuxR-HTH+ST-Hiskin+ST-Hiskin+XPC-C+TM+TM+TM+TM+LuxR-HTH	11647	ON23_RS23640	Actinobacteria	Nocardia cerradoensis	MFS transporter, partial [Nocardia cerradoensis]	GCF_000308535.1
WP_157172575.1	ESX-1_EspG→?→?→?→ WXG+GT4+PP2C+GDPD+Amidohydrolase+Abhydrolase+GT4*→	WXG+GT4+PP2C+GDPD+Amidohydrolase+Abhydrolase+GT4	27919	ON34_RS32865	Actinobacteria	Nocardia pneumoniae	glycosyltransferase [Nocardia pneumoniae]	GCF_000308755.1
WP_157180627.1	WXG+TM+GT4+GT4*→	WXG+TM+GT4+GT4	1681	FrCorBMG51_RS28730	Actinobacteria	Frankia coriariae	hypothetical protein [Frankia coriariae]	GCF_001017755.1

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
WP_157204012.1	GT4+APATPase+TPR*→	GT4+APATPase+TPR	1141	A1332_RS13095	Gammaproteobacteria	Methylomonas methanica	tetratricopeptide repeat protein, partial [Methylomonas methanica]	-
WP_157224231.1	WXG+ZetaToxin+GT4*→?→||||<-WXG+MPTase	WXG+ZetaToxin+GT4	1061	ON32_RS18080	Actinobacteria	Nocardia paucivorans	zeta toxin family protein [Nocardia paucivorans]	GCF_000308675.1
WP_157229180.1	MPTase→ WXG+SecA+GT4+TetR-HTH+TetR-HTH+MFS+MFS(12x)+ABhydrolase+ST-Hiskin*→||||<-?||CSD→	WXG+SecA+GT4+TetR-HTH+TetR-HTH+MFS+MFS(12x)+ABhydrolase+ST-Hiskin	4779	ON20_RS32170	Actinobacteria	Nocardia brevicatena	MFS transporter [Nocardia brevicatena]	GCF_000308495.1
WP_157355048.1	GT4*→	GT4	618	ARA48_RS12920	Bacteroidetes	Parabacteroides distasonis	glycosyltransferase [Parabacteroides distasonis]	GCF_001405935.1
WP_157419626.1	<-cNMP_binding+HTH_Crp_2||GT4*→||||<-HTH+APATPase+TPR	GT4	468	AKI01S_RS02785	Actinobacteria	Actinomadura kijaniata	glycosyltransferase [Actinomadura kijaniata]	GCF_001552175.1
WP_157468665.1	CATRA-N+CATRA-C+GT4*→||||<-TPR+Caspase<-?<-?<-?<-?||CHTH+APATPase+TPR+TPR→ CATASP→	CATRA-N+CATRA-C+GT4	825	FRAQA3DRAFT_RS22440	Actinobacteria	Frankia sp. QA3	glycosyltransferase [Frankia sp. QA3]	GCF_000262465.1
WP_157494479.1	<-CATASP||CATRA-N+CATRA-C+GT4*→||||<-HTH+APATPase+TPR	CATRA-N+CATRA-C+GT4	786	KUTG_RS53310	Actinobacteria	Kutzneria sp. 744	glycosyltransferase [Kutzneria sp. 744]	-
WP_157528945.1	ART+Caspase+GT4*→?→ GT4→	ART+Caspase+GT4	1289	BN1199_RS39095	Actinobacteria	Kibdelosporangium sp. MJ126-NF4	glycosyltransferase [Kibdelosporangium sp. MJ126-NF4]	-
WP_157636396.1	STAND+TPR+GT4*→||||<-?||ABhydrolase→||||<-TRANSGLUTAMINASE	STAND+TPR+GT4	1130	WL03_RS32310	Betaproteobacteria	Burkholderia ubonensis	glycosyltransferase [Burkholderia ubonensis]	GCF_001528155.1
WP_157851161.1	<-TPR+Caspase<-CATASP||CATRA-N+CATRA-C+GT4*→ HTH+APATPase+TPR→||||<-HTH||?→?→?→||||<-?<-CATASP	CATRA-N+CATRA-C+GT4	703	IF17_RS1000000138590	Actinobacteria	Streptomyces cyaneofuscatus	glycosyltransferase [Streptomyces cyaneofuscatus]	GCF_000718135.1
WP_157856282.1	ABC_tran→?→?→ NACHT+MNS→?→ GT4*→	GT4	412	BS72_RS20070	Actinobacteria	Streptomyces yeochonensis	glycosyltransferase [Streptomyces yeochonensis]	-
WP_157978213.1	GT4*→	GT4	199	DAT37_RS00050	Actinobacteria	Nocardia sp. SYSU K10002	hypothetical protein [Nocardia sp. SYSU K10002]	-
WP_158075353.1	<-TPR+Caspase<-CATASP||CATRA-N+CATRA-C+GT4*→ HTH+APATPase+TPR→||||<-HTH||?→?→?→||||<-?<-CATASP	CATRA-N+CATRA-C+GT4	718	AMK32_RS25155	Actinobacteria	Streptomyces sp. CB01883	glycosyltransferase [Streptomyces sp. CB01883]	-

<table>
<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>WP_158247498.1</td><td>GT4+APATPase+TPR+TPR*→</td><td>GT4+APATPase+TPR+TPR</td><td>1379</td><td>C1X76_RS08190</td><td>Gammaproteobacteria</td><td>unclassified Pseudomonas</td><td>MULTISPECIES: tetratricopeptide repeat protein [unclassified Pseudomonas]</td><td>GCF_017350895.1</td></tr>
<tr><td>WP_158633123.1</td><td>cNMP_binding+HTH_Crp_2→?→ GT4*→||||<-ACYC+APATPase+TPR</td><td>GT4</td><td>391</td><td>DMH03_RS26200</td><td>Actinobacteria</td><td>Amycolatopsis sp. WAC 01376</td><td>glycosyltransferase [Amycolatopsis sp. WAC 01376]</td><td>GCF_003947415.1</td></tr>
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<tr><td>WP_158893312.1</td><td><-TIR+APATPase||HTH+APATPase+TPR+GT4*→||||<-PSE<-?||?→?→?→ Sigma→</td><td>HTH+APATPase+TPR+GT4</td><td>1166</td><td>FXO23_RS42605</td><td>Actinobacteria</td><td>Amycolatopsis anabasis</td><td>tetratricopeptide repeat protein [Amycolatopsis anabasis]</td><td>GCF_009765355.1</td></tr>
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<tr><td>WP_159058466.1</td><td><-CATASP||CATRA-N+CATRA-C+GT4*→ HTH+APATPase→</td><td>CATRA-N+CATRA-C+GT4</td><td>711</td><td>AWZ10_RS35055</td><td>Actinobacteria</td><td>Streptomyces europaeiscabiei</td><td>glycosyltransferase [Streptomyces europaeiscabiei]</td><td>GCF_001550375.1</td></tr>
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<tr><td>WP_161065972.1</td><td>DUF4913→ GT4*→</td><td>GT4</td><td>463</td><td>GR925_RS14975</td><td>Actinobacteria</td><td>Streptomyces sp. HUCO-GS316</td><td>glycosyltransferase [Streptomyces sp. HUCO-GS316]</td><td>GCF_009827025.1</td></tr>
<tr><td>WP_161268609.1</td><td>CATRA-N+CATRA-C+GT4*→</td><td>CATRA-N+CATRA-C+GT4</td><td>703</td><td>GT040_RS36085</td><td>Actinobacteria</td><td>Streptomyces sp. SID2119</td><td>glycosyltransferase [Streptomyces sp. SID2119]</td><td>GCF_009865505.1</td></tr>
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WP_161606588.1	GT4*→	GT4	962	BHS06_RS25085	Deltaproteobacteria	Myxococcus xanthus	glycosyltransferase [Myxococcus xanthus]	GCF_006401635.1
WP_161684505.1	Sigma→?→?→||||<-?<-?<-TPR+Caspase||GT4*→||||<-PSE<-?||?→||||<-TRPR-HTH+PBPI	GT4	547	GVV04_RS04065	Actinobacteria	Micromonospora sp. NEAU-HG-1	glycosyltransferase [Micromonospora sp. NEAU-HG-1]	GCF_009908295.1
WP_161790163.1	GT4*→||||<-?<-?<-?<-CSD	GT4	353	TR46_RS20005	Actinobacteria	Streptacidiphilus carbonis	glycosyltransferase [Streptacidiphilus carbonis]	GCF_000787775.1
WP_162672520.1	GT4+HEPN+TPR+GreAB-C+PIN*→	GT4+HEPN+TPR+GreAB-C+PIN	1685	SOIL9_RS38685	Planctomycetes	Gemmata massiliana	glycosyltransferase [Gemmata massiliana]	GCF_901538265.1
WP_162688623.1	Caspase+NACHT+GT4*→||||<-?<-?<-?<-?||APATPase→	Caspase+NACHT+GT4	1148	DRB89_RS17705	Actinobacteria	unclassified Streptomyces	MULTISPECIES: caspase family protein [unclassified Streptomyces]	GCF_003287915.1
WP_162948626.1	<-CATASP||CATRA-N+CATRA-C+GT4*→ HTH+APATPase→	CATRA-N+CATRA-C+GT4	711	CQR77_RS44880	Actinobacteria	Streptomyces europaeiscabiei	glycosyltransferase [Streptomyces europaeiscabiei]	GCF_003584825.1
WP_163053769.1	Calcineurin→?→?→ NACHT+MNS→ MNS+GT4*→	MNS+GT4	749	G3I70_RS06860	Actinobacteria	Actinomadura bangladeshensis	glycosyltransferase [Actinomadura bangladeshensis]	GCF_010548065.1
WP_164236650.1	<-TPR+Caspase<-CATASP||CATRA-N+CATRA-C+GT4*→ HTH+APATPase+TPR→||||<-HTH||?→?→?→||||<-?<-CATASP	CATRA-N+CATRA-C+GT4	703	G3I52_RS10700	Actinobacteria	Streptomyces cyaneofuscatus	glycosyltransferase [Streptomyces cyaneofuscatus]	GCF_010548165.1
WP_164336692.1	Calcineurin→?→?→ Caspase+NACHT+GT4*→	Caspase+NACHT+GT4	1126	G3I38_RS20825	Actinobacteria	Streptomyces sp. SID7958	caspase family protein [Streptomyces sp. SID7958]	GCF_010550365.1
WP_164374106.1	NACHT→ GT4→*||||<-?<-PSE<-?<-?<-?||HTH+APATPase→ TPR→||||<-GT4*	GT4	405	G3I62_RS29240	Actinobacteria	Streptomyces sp. SID14446	glycosyltransferase [Streptomyces sp. SID14446]	GCF_010548515.1
WP_164374112.1	-	-	402	G3I62_RS29280	Actinobacteria	Streptomyces sp. SID14446	glycosyltransferase [Streptomyces sp. SID14446]	GCF_010548515.1
WP_164438832.1	Calcineurin→?→?→ Caspase+NACHT+GT4*→	Caspase+NACHT+GT4	1113	G3I53_RS25925	Actinobacteria	Streptomyces sp. SID14436	caspase family protein [Streptomyces sp. SID14436]	GCF_010548465.1
WP_164932131.1	<-HTH+APATPase+TPR||GT4*→?→||||<-?<-?<-?||TPR→	GT4	394	DBB27_RS07160	Actinobacteria	unclassified Streptomyces	MULTISPECIES: glycosyltransferase [unclassified Streptomyces]	GCF_004104505.1

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WP_165781010.1	GT4*→	GT4	631	CR156_RS18515	Gammaproteobacteria	Stenotrophomonas lactitubi	glycosyltransferase [Stenotrophomonas lactitubi]	GCF_014763005.1
WP_166659524.1	-	-	752	EV186_RS37545	Actinobacteria	Labedaea rhizosphaerae	glycosyltransferase family 4 protein [Labedaea rhizosphaerae]	GCF_004362825.1
WP_167375417.1	APATPase+GT4*→	APATPase+GT4	1344	AWM79_RS04595	Gammaproteobacteria	Pseudomonas agarici	glycosyltransferase [Pseudomonas agarici]	GCF_001543125.1
WP_167485160.1	<-ESX-1_EspG<-?<-?<-?||?→?→ WXG+PolB-NTase+GT4+GT4+Caspase*→?→?→ GT4→	WXG+PolB-NTase+GT4+GT4+Caspase	2733	F6W96_RS05200	Actinobacteria	Nocardia terpenica	glycosyltransferase [Nocardia terpenica]	GCF_011801165.1
WP_167531487.1	NACHT+GT4*→||||<-Vsr	NACHT+GT4	1557	EN799_RS48175	Alphaproteobacteria	Mesorhizobium sp. M8A.F.Ca.ET.197.01.1.1	glycosyltransferase [Mesorhizobium sp. M8A.F.Ca.ET.197.01.1.1]	GCF_004791385.1
WP_167631834.1	GT4+APATPase+TPR*→	GT4+APATPase+TPR	1107	HCI87_RS07630	Zetaproteobacteria	Mariprofundus ferrooxydans	tetratricopeptide repeat protein, partial [Mariprofundus ferrooxydans]	GCF_011947535.1
WP_167983001.1	CATRA-N+CATRA-C+GT4*→ HTH+APATPase+TPR→||||<-HTH||?→?→?→||||<-?<-CATASP	CATRA-N+CATRA-C+GT4	845	HCN08_RS12120	Actinobacteria	Streptomyces sp. PRB2-1	glycosyltransferase family 4 protein [Streptomyces sp. PRB2-1]	GCF_012034175.1
WP_167985631.1	GT4*→	GT4	425	HCN08_RS25735	Actinobacteria	Streptomyces sp. PRB2-1	glycosyltransferase [Streptomyces sp. PRB2-1]	GCF_012034175.1
WP_168028895.1	<-ABC_tran<-?<-?<-?<-?||?→ GT4+APATPase*→	GT4+APATPase	988	HC024_RS03995	Gammaproteobacteria	Methylococcaceae bacterium WWC4	glycosyltransferase, partial [Methylococcaceae bacterium WWC4]	-
WP_168031569.1	GT4*→	GT4	644	HC024_RS14290	Gammaproteobacteria	Methylococcaceae bacterium WWC4	glycosyltransferase, partial [Methylococcaceae bacterium WWC4]	-
WP_168435140.1	WXG+MPTase→ WXG+SecA+LuxR-HTH+LuxR-HTH+LuxR-HTH+LuxR-HTH+ST-Hiskin+MPTase+GT4+TetR-HTH+TetR-HTH+Tox-ART-RSE+LuxR-HTH+LuxR-HTH+LuxR-HTH+GNTR-HTH+LuxR-HTH+LuxR-HTH+ST-Hiskin+ST-Hiskin+XPC-C+TM+TM+TM+TM+LuxR-HTH+PP2C+MPTase+MPTase+LuxR-HTH+LuxR-HTH+DOC*→?→ ABhydrolase→	WXG+SecA+LuxR-HTH+LuxR-HTH+LuxR-HTH+LuxR-HTH+ST-Hiskin+MPTase+GT4+TetR-HTH+TetR-HTH+Tox-ART-RSE+LuxR-HTH+LuxR-HTH+LuxR-HTH+GNTR-HTH+LuxR-HTH+LuxR-HTH+ST-Hiskin+ST-Hiskin+XPC-C+TM+TM+TM+TM+LuxR-HTH+PP2C+MPTase+MPTase+LuxR-HTH+LuxR-HTH+DOC	13688	HGB45_RS23560	Actinobacteria	Nocardia cerradoensis	MFS transporter [Nocardia cerradoensis]	GCF_012396065.1
WP_168477813.1	GT4*→?→?→||||<-?||?→||||<-NUDIX	GT4	455	HEP86_RS05755	Actinobacteria	Streptomyces sp. RPA4-5	glycosyltransferase [Streptomyces sp. RPA4-5]	GCF_012273495.1

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WP_168512294.1	<-ABhydrolase||?→?→ GT4*→||||<-?||TRPR-HTH+PBPI→	GT4	650	HEP87_RS39620	Actinobacteria	Streptomyces sp. S1D4-11	glycosyltransferase [Streptomyces sp. S1D4-11]	-
WP_169316088.1	APATPase+GT4*→||||<-?<-?<-?<-?||?→||||<-?<-PSE||GST_N_2+GST_C→	APATPase+GT4	1344	PAGAR_RS28405	Gammaproteobacteria	Pseudomonas agarici	glycosyltransferase [Pseudomonas agarici]	GCF_000280785.1
WP_169804810.1	GT4+APATPase*→	GT4+APATPase	986	HTA01S_RS24340	Betaproteobacteria	Hydrogenophaga taeniospiralis	glycosyltransferase, partial [Hydrogenophaga taeniospiralis]	GCF_001592305.1
WP_169807203.1	GT4*→	GT4	449	AWW66_RS34115	Actinobacteria	Micromonospora rosaria	glycosyltransferase, partial [Micromonospora rosaria]	GCF_001567585.1
WP_169850673.1	GT4+B12-binding+RADICAL-SAM*→	GT4+B12-binding+RADICAL-SAM	1115	HBO43_RS21615	Gammaproteobacteria	Pseudomonas veronii	cobalamin B12-binding domain-containing protein [Pseudomonas veronii]	GCF_012985315.1
WP_170285467.1	SWACOS+GT4*→?→||||<-?||?→ PadR→	SWACOS+GT4	1175	FHX75_RS26815	Actinobacteria	Micromonospora palomenae	glycosyltransferase [Micromonospora palomenae]	GCF_007829925.1
WP_171081495.1	GT4*→	GT4	489	HG542_RS14775	Actinobacteria	Streptomyces morookaense	glycosyltransferase [Streptomyces morookaense]	GCF_014656115.1
WP_171579219.1	<-SIG+RCDG1+YidC_periplas+60KD_IMP<-?<-?||?→ tRNA→?→ NACHT+GT4*→?→?→?→?→?→?→ DUF4242→	NACHT+GT4	1638	HCN58_RS10240	Alphaproteobacteria	Bradyrhizobium sp. WSM 1791	glycosyltransferase [Bradyrhizobium sp. WSM 1791]	GCF_013114825.1
WP_171675029.1	GT4*→	GT4	451	HNR71_RS02445	Actinobacteria	Kribbella sandramycini	glycosyltransferase [Kribbella sandramycini]	GCF_013131805.1
WP_171901162.1	-	-	147	NK6_RS51125	Alphaproteobacteria	Bradyrhizobium diazoefficiens	glycosyltransferase [Bradyrhizobium diazoefficiens]	GCF_001549695.1
WP_172109703.1	SWACOS+GT4*→	SWACOS+GT4	1148	HL667_RS06640	Alphaproteobacteria	Bradyrhizobium sp. 83012	glycosyltransferase [Bradyrhizobium sp. 83012]	GCF_013178925.1
WP_172132695.1	SWACOS+GT4*→	SWACOS+GT4	1148	HL666_RS23775	Alphaproteobacteria	unclassified Bradyrhizobium	MULTISPECIES: glycosyltransferase [unclassified Bradyrhizobium]	GCF_013178945.1

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WP_172175287.1	GT4+B12-binding+RADICAL-SAM*→	GT4+B12-binding+RADICAL-SAM	1278	GNZ13_RS39275	Betaproteobacteria	Paraburkholderia sp. 5N	radical SAM protein [Paraburkholderia sp. 5N]	GCF_013177735.1
WP_173124146.1	<-STAND<-?<-?<-?<-?||cNMP_binding+HTH_Crp_2→?→ GT4*→||||<-ACYC+APATPase+TPR	GT4	409	GC106_RS03330	Actinobacteria	Kibdelosporangium sp. 4NS15	glycosyltransferase [Kibdelosporangium sp. 4NS15]	GCF_013280595.1
WP_173195298.1	GT4+APATPase+TPR+TPR*→	GT4+APATPase+TPR+TPR	1427	HR085_RS00175	Deltaproteobacteria	Geobacter sp. SVR	tetratricopeptide repeat protein [Geobacter sp. SVR]	GCF_016865365.1
WP_173395462.1	DJ-1_PfpI→ LexA→?→||||<-?<-?<-?<-cNMP_binding+HTH_Crp_2||GT4*→||||<-HTH+APATPase+TPR	GT4	438	GWI34_RS19435	Actinobacteria	Actinomadura sp. DSM 109109	glycosyltransferase [Actinomadura sp. DSM 109109]	-
WP_173526832.1	GT4+APATPase+TPR+TPR*→	GT4+APATPase+TPR+TPR	1208	HII36_RS31010	Actinobacteria	Nonomuraea sp. NN258	tetratricopeptide repeat protein [Nonomuraea sp. NN258]	GCF_013283785.1
WP_173991751.1	PfkB→?→?→?→ GT4+B12-binding+RADICAL-SAM*→	GT4+B12-binding+RADICAL-SAM	1387	G6M20_RS23615	Alphaproteobacteria	Agrobacterium salinitolerans	cobalamin B12-binding domain-containing protein [Agrobacterium salinitolerans]	GCF_013317635.1
WP_174156125.1	HTH+MPTase→?→||||<-?||?→?→ NACHT+GT4*→	NACHT+GT4	1640	G6L88_RS21970	Alphaproteobacteria	Rhizobium skierniewicense	glycosyltransferase [Rhizobium skierniewicense]	GCF_013320815.1
WP_174295717.1	GT4*→	GT4	613	G7A66_RS11060	Alphaproteobacteria	Altererythrobacter sp. SALINAS58	glycosyltransferase [Altererythrobacter sp. SALINAS58]	GCF_013336795.1
WP_174397973.1	GT4*→	GT4	602	FEG63_RS11180	Actinobacteria	Mycolicibacterium sphagni	glycosyltransferase [Mycolicibacterium sphagni]	GCF_013337765.1
WP_174527417.1	STAND→?→ DUF4913→||||<-?||?→ GT4*→?→?→?→ NUDIX→||||<-?<-ABC_tran	GT4	438	HUW36_RS07305	Actinobacteria	Micromonospora maritima	glycosyltransferase [Micromonospora maritima]	GCF_902825405.1
WP_175264897.1	NACHT+MNS→ MNS+GT4*→||||<-?<-CASPASE	MNS+GT4	752	HRW23_RS35520	Actinobacteria	Streptomyces lunaelactis	glycosyltransferase [Streptomyces lunaelactis]	GCF_013357925.1
WP_176052200.1	STAND+GT4*→?→||||<-Cluster466_2clades<-?<-?<-?||DNA_methylase→||||<-Vsr	STAND+GT4	1090	HWY02_RS01425	Betaproteobacteria	Paraburkholderia caribensis	glycosyltransferase [Paraburkholderia caribensis]	GCF_902833585.1

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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>
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<tr><td>WP_177204219.1</td><td><-Sigma||?→||||<-?<-?<-?||GT4+B12-binding*→</td><td>GT4+B12-binding</td><td>1122</td><td>BMY84_RS26750</td><td>Alphaproteobacteria</td><td>Sphingobium sp. AP50</td><td>glycosyltransferase [Sphingobium sp. AP50]</td><td>GCF_900109095.1</td></tr>
<tr><td>WP_178066132.1</td><td><-TPR+Caspase||GT4*→</td><td>GT4</td><td>546</td><td>HDA31_RS04955</td><td>Actinobacteria</td><td>Micromonospora carbonacea</td><td>glycosyltransferase [Micromonospora carbonacea]</td><td>GCF_013389765.1</td></tr>
<tr><td>WP_178963184.1</td><td>GT4+B12-binding+RADICAL-SAM*→</td><td>GT4+B12-binding+RADICAL-SAM</td><td>1404</td><td>HX895_RS03680</td><td>Gammaproteobacteria</td><td>Pseudomonas gingeri</td><td>radical SAM protein [Pseudomonas gingeri]</td><td>GCF_013387125.1</td></tr>
<tr><td>WP_178963665.1</td><td><-MFS||?→||||<-?<-?||?→||||<-?||APATPase+GT4*→</td><td>APATPase+GT4</td><td>1336</td><td>HX895_RS14805</td><td>Gammaproteobacteria</td><td>Pseudomonas gingeri</td><td>glycosyltransferase [Pseudomonas gingeri]</td><td>GCF_013387125.1</td></tr>
<tr><td>WP_179766782.1</td><td>TRPR-HTH+PBPI→?→ SIG+Lipase_GDSL_2→?→ Zeta_toxin→?→ GT4*→</td><td>GT4</td><td>461</td><td>HNR12_RS07370</td><td>Actinobacteria</td><td>Streptomonospora nanhaiensis</td><td>glycosyltransferase [Streptomonospora nanhaiensis]</td><td>GCF_013410565.1</td></tr>
<tr><td>WP_179767386.1</td><td>GT4*→?→||||<-?<-?<-tRNA-synt_1b+S4</td><td>GT4</td><td>489</td><td>HNR12_RS10915</td><td>Actinobacteria</td><td>Streptomonospora nanhaiensis</td><td>glycosyltransferase [Streptomonospora nanhaiensis]</td><td>GCF_013410565.1</td></tr>
<tr><td>WP_179826407.1</td><td><-APATPase+TPR||?→ GT4*→</td><td>GT4</td><td>524</td><td>HNR10_RS21750</td><td>Actinobacteria</td><td>Nocardiopsis aegyptia</td><td>hypothetical protein [Nocardiopsis aegyptia]</td><td>GCF_013410755.1</td></tr>
<tr><td>WP_179835700.1</td><td>GT4*→||||<-?<-?<-cNMP_binding+HTH_Crp_2</td><td>GT4</td><td>388</td><td>BJ999_RS25940</td><td>Actinobacteria</td><td>Actinomadura citrea</td><td>glycosyltransferase [Actinomadura citrea]</td><td>GCF_014648455.1</td></tr>
<tr><td>WP_180357038.1</td><td>HTH→?→?→||||<-?<-?||Caspase+NACHT+GT4*→</td><td>Caspase+NACHT+GT4</td><td>1165</td><td>BX283_RS03940</td><td>Actinobacteria</td><td>Streptomyces sp. TLI_146</td><td>caspase family protein [Streptomyces sp. TLI_146]</td><td>GCF_002846415.1</td></tr>
<tr><td>WP_180930380.1</td><td>MNS+GT4*→</td><td>MNS+GT4</td><td>1268</td><td>E0L36_RS19290</td><td>Actinobacteria</td><td>Streptomyces sp. AJS327</td><td>glycosyltransferase [Streptomyces sp. AJS327]</td><td>GCF_013450295.1</td></tr>
<tr><td>WP_181043331.1</td><td>MFS→?→?→ WXG→?→ GT4*→?→ GT4→</td><td>GT4</td><td>391</td><td>CLV40_RS37790</td><td>Actinobacteria</td><td>Actinokineospora auranticolor</td><td>glycosyltransferase family 4 protein [Actinokineospora auranticolor]</td><td>GCF_002934265.1</td></tr>
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acc	**operon**	**architecture**	**len**	**gen.name**	**taxend**	**species**	**defline**	**gca**
WP_181245803.1	GT4*→ APATPase+TPR→||||<-?<-TRPR-HTH+PBPI	GT4	401	B0I28_RS15405	Actinobacteria	Glycomyces artemisiae	glycosyltransferase [Glycomyces artemisiae]	GCF_003002955.1

Source data. Domain architectures of eukaryotic GT4s with a special emphasis on the LSE in Acropora

acc	**architecture**	**len**	**gen.name**	**tax**	**species**	**GCA**
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XP_015747371.1	GT4	492	LOC107327132	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015747395.1	GT4+NACHT	628	LOC107327154	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
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XP_015747753.1	GT4	437	LOC107327516	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
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acc	architecture	len	gen.name	tax	species	GCA
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acc	architecture	len	gen.name	tax	species	GCA
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XP_015764802.1	GT4+DEATH	661	LOC107343730	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015764803.1	GT4+DEATH	661	LOC107343730	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
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XP_015770124.1	GT4+DEATH	668	LOC107348579	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015770346.1	ZU5+ZU5+GT4	847	LOC107348784	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
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XP_015770477.1	GT4	549	LOC107348902	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015771034.1	GT4	411	LOC107349395	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
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XP_015771078.1	GT4	415	LOC107349446	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015771077.1	SIG+GT4	442	LOC107349446	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
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XP_015764733.1	GT4+NACHT	1250	LOC107343665	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
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XP_015779585.1	GT4+NACHT	1318	LOC107357460	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
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EGD71903.1	GT4	378	CSMARM5_0008	Archaea>DPANN group	Candidatus Parvarchaeum acidophilus ARMAN-5_‘5-way FS’	GCA_000192615.1
XP_015768804.1	SIG+GT4+DEATH+sGTP+sGTP	2069	LOC107347416	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015768802.1	SIG+GT4+DEATH+sGTP+sGTP	2089	LOC107347416	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015768801.1	GT4+DEATH+sGTP+sGTP	2091	LOC107347416	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015768800.1	GT4+DEATH+sGTP+sGTP	2092	LOC107347416	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015768799.1	GT4+DEATH+sGTP+sGTP	2092	LOC107347416	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015768797.1	SIG+GT4+DEATH+sGTP+sGTP	2094	LOC107347416	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
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XP_015768794.1	GT4+DEATH+sGTP+sGTP	2094	LOC107347416	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1

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XP_015768836.1	SIG+GT4+DEATH+sGTP+sGTP	2069	LOC107347432	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015768838.1	GT4+DEATH+sGTP+sGTP	2069	LOC107347432	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015768835.1	SIG+GT4+DEATH+sGTP+sGTP	2089	LOC107347432	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015768834.1	GT4+DEATH+sGTP+sGTP	2091	LOC107347432	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015768833.1	GT4+DEATH+sGTP+sGTP	2092	LOC107347432	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
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XP_015768827.1	GT4+DEATH+sGTP+sGTP	2094	LOC107347432	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
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XP_015777366.1	GT4+ANK+ANK	1384	LOC107355329	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
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XP_015777360.1	GT4+ANK+ANK	1404	LOC107355329	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015777359.1	GT4+ANK+ANK	1420	LOC107355329	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015777358.1	GT4+ANK+ANK	1420	LOC107355329	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015777357.1	GT4+ANK+ANK	1436	LOC107355329	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015775968.1	ZU5+ZU5+TM+GT4+APATPase	1462	LOC107354065	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015775965.1	ZU5+ZU5+TM+GT4+APATPase+TPR	1578	LOC107354065	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015775967.1	ZU5+ZU5+TM+GT4+APATPase+TPR	1578	LOC107354065	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015775966.1	ZU5+ZU5+TM+GT4+APATPase+TPR	1578	LOC107354065	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
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XP_015775963.1	ZU5+ZU5+TM+GT4+APATPase+TPR	1626	LOC107354065	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
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XP_015775961.1	ZU5+ZU5+TM+GT4+APATPase+TPR	1674	LOC107354065	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015775960.1	ZU5+ZU5+TM+GT4+APATPase+TPR	1689	LOC107354065	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015775959.1	ZU5+ZU5+TM+GT4+APATPase+TPR	1689	LOC107354065	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015775958.1	ZU5+ZU5+TM+GT4+APATPase+TPR	1689	LOC107354065	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
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XP_015775955.1	ZU5+ZU5+TM+GT4+APATPase+TPR	1693	LOC107354065	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015775954.1	ZU5+ZU5+TM+GT4+APATPase+TPR	1703	LOC107354065	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015775953.1	ZU5+ZU5+TM+GT4+APATPase+TPR	1703	LOC107354065	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015768811.1	GT4+sGTP+sGTP	1904	LOC107347416	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015768810.1	GT4+sGTP+sGTP	1928	LOC107347416	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
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XP_015768808.1	SIG+GT4+sGTP+sGTP	1929	LOC107347416	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
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XP_015768845.1	GT4+sGTP+sGTP	1904	LOC107347432	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015768843.1	GT4+sGTP+sGTP	1928	LOC107347432	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1

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XP_015768844.1	GT4+sGTP+sGTP	1928	LOC107347432	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015768842.1	SIG+GT4+sGTP+sGTP	1929	LOC107347432	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015768841.1	SIG+GT4+sGTP+sGTP	1930	LOC107347432	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015768840.1	SIG+GT4+sGTP+sGTP	1951	LOC107347432	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015768839.1	SIG+GT4+sGTP+sGTP	1953	LOC107347432	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015767989.1	GT4+NACHT	1796	LOC107346689	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015767988.1	SIG+GT4+NACHT	1806	LOC107346689	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015776065.1	GT4+NACHT	1674	LOC107354137	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
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XP_015778874.1	SIG+GT4+VWA+SERAprotease	1218	LOC107356762	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
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XP_015778870.1	SIG+GT4+VWA+SERAprotease	1221	LOC107356762	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
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XP_015778880.1	SIG+GT4+VWA+SERAprotease	1218	LOC107356768	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015778878.1	SIG+GT4+VWA+SERAprotease	1221	LOC107356768	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
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XP_015751628.1	DED+TPR+GT4	2015	LOC107331536	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015751627.1	DED+TPR+GT4	2019	LOC107331536	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015751626.1	DED+TPR+GT4	2020	LOC107331536	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015758975.1	SIG+TPR+GT4	1867	LOC107338255	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
KXJ17955.1	DED+TPR+GT4	1737	AC249_AIPGENE20062	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Exaiptasia diaphana	GCA_001417965.1
KXJ23466.1	DED+GT4	1693	Samd9l	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Exaiptasia diaphana	GCA_001417965.1
XP_001627530.1	DED+GT4	1802	NEMVEDRAFT_v1g214094	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Nematostella vectensis	-
XP_002586741.1	DED+GT4	538	BRAFLDRAFT_105739	Eukaryota>Opisthokonta>Metazoa>Chordata	Branchiostoma floridae	-
XP_002593761.1	sGTP+GT4	511	BRAFLDRAFT_107710	Eukaryota>Opisthokonta>Metazoa>Chordata	Branchiostoma floridae	-
XP_002585662.1	GT4	514	BRAFLDRAFT_111592	Eukaryota>Opisthokonta>Metazoa>Chordata	Branchiostoma floridae	-
XP_002588370.1	SIG+GT4	424	BRAFLDRAFT_63320	Eukaryota>Opisthokonta>Metazoa>Chordata	Branchiostoma floridae	-
XP_002594621.1	GT4	411	BRAFLDRAFT_77600	Eukaryota>Opisthokonta>Metazoa>Chordata	Branchiostoma floridae	-

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XP_002594622.1	DEATH+GT4	506	BRAFLDRAFT_77601	Eukaryota>Opisthokonta>Metazoa>Chordata	Branchiostoma floridae	-
XP_002604494.1	GT4	475	BRAFLDRAFT_79207	Eukaryota>Opisthokonta>Metazoa>Chordata	Branchiostoma floridae	-
XP_002731475.1	GT4	433	LOC100372804	Eukaryota>Opisthokonta>Metazoa>Hemichordata	Saccoglossus kowalevskii	GCF_000003605.2
XP_015772447.1	GT4+TPR	596	LOC107350717	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015772446.1	GT4+TPR	623	LOC107350717	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015772445.1	GT4+TPR	624	LOC107350717	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015772444.1	GT4+TPR	642	LOC107350717	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015772442.1	GT4+TPR	674	LOC107350717	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015772443.1	GT4+TPR	674	LOC107350717	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015775035.1	GT4+TPR	635	LOC107353224	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015770118.1	GT4+sGTP+sGTP+DEATH	1249	LOC107348573	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015770115.1	GT4+sGTP+sGTP+DEATH	1249	LOC107348573	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015770116.1	GT4+sGTP+sGTP+DEATH	1249	LOC107348573	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015770117.1	GT4+sGTP+sGTP+DEATH	1249	LOC107348573	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015770113.1	GT4+sGTP+sGTP+DEATH	1249	LOC107348573	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015776051.1	GT4+sGTP	1386	LOC107354135	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015764075.1	GT4+NACHT	1225	LOC107343052	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015764074.1	GT4+NACHT	1233	LOC107343052	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015764072.1	GT4+NACHT	1238	LOC107343052	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015764073.1	GT4+NACHT	1238	LOC107343052	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015764071.1	GT4+NACHT	1255	LOC107343052	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015764070.1	GT4+NACHT	1259	LOC107343052	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015747310.1	GT4+NACHT	1361	LOC107327069	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015772577.1	GT4+NACHT	1796	LOC107350842	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015772579.1	SAP+GT4+NACHT	2199	LOC107350844	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015776067.1	GT4+NACHT	1600	LOC107354137	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015776066.1	SIG+GT4+NACHT	1671	LOC107354137	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015759030.1	sGTP+GT4+TM	1258	LOC107338309	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015759029.1	sGTP+GT4+TM	1258	LOC107338309	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015759028.1	sGTP+GT4+TM	1271	LOC107338309	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015759026.1	sGTP+GT4+TM	1272	LOC107338309	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015759027.1	sGTP+GT4+TM	1272	LOC107338309	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015749674.1	GT4+PNPase	965	LOC107329499	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015749675.1	GT4+PNPase	965	LOC107329499	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015749860.1	GT4+PNPase+NABD-unk4	933	LOC107329706	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015749859.1	GT4+PNPase+NABD-unk4	961	LOC107329706	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015749858.1	GT4+PNPase+NABD-unk4	982	LOC107329706	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015770482.1	GT4	132	LOC107348905	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015777289.1	GT4	119	LOC107355256	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015777288.1	GT4	135	LOC107355256	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015777287.1	GT4	135	LOC107355256	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015777286.1	GT4	135	LOC107355256	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015754287.1	GT4+ANK	1391	LOC107333936	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015754286.1	GT4+ANK	1391	LOC107333936	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015754284.1	GT4+ANK	1391	LOC107333936	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015779234.1	GT4+ANK+Immank+Immank	1392	LOC107357096	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015780882.1	GT4+DEATH	240	LOC107358816	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015780881.1	GT4+DEATH	243	LOC107358816	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015780880.1	GT4+DEATH	247	LOC107358816	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015780879.1	GT4+DEATH	250	LOC107358816	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015754283.1	GT4+ANK+DED+APATPase+TPR	1546	LOC107333935	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015754282.1	GT4+ANK+DED+APATPase+TPR	1560	LOC107333935	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1

acc	**architecture**	**len**	**gen.name**	**tax**	**species**	**GCA**
XP_015754281.1	GT4+ANK+DED+APATPase+TPR	1597	LOC107333935	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015754288.1	GT4+ANK	1351	LOC107333936	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015778952.1	GT4+ANK+Immank+Immank	1280	LOC107356842	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015779236.1	GT4+Immank+ANK	1086	LOC107357098	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015764079.1	GT4+NACHT	1177	LOC107343052	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015764078.1	GT4+NACHT	1178	LOC107343052	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015764077.1	GT4+NACHT	1188	LOC107343052	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015764083.1	GT4+NACHT	1101	LOC107343052	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015764082.1	GT4+NACHT	1107	LOC107343052	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015764081.1	GT4+NACHT	1161	LOC107343052	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015778876.1	SIG+GT4+VWA+SERAprotease	1080	LOC107356762	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015778875.1	SIG+GT4+VWA+SERAprotease	1145	LOC107356762	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015778882.1	SIG+GT4+VWA+SERAprotease	1145	LOC107356768	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015771521.1	SIG+GT4	729	LOC107349844	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015771522.1	SIG+GT4	729	LOC107349844	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015771520.1	SIG+GT4	756	LOC107349844	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015750317.1	GT4+ZU5	721	LOC107330190	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015770123.1	GT4	704	LOC107348579	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015770122.1	GT4	705	LOC107348579	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015752964.1	SIG+GT4	564	LOC107332737	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015752963.1	SIG+GT4	565	LOC107332737	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015756764.1	SIG+GT4	570	LOC107336220	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
OLD79042.1	GT4	474	AUF62_00760	Archaea	archaeon 13_1_20CM_52_20	GCA_001919675.1
OLC62495.1	GT4	495	AUH73_04505	Archaea	archaeon 13_1_40CM_4_53_4	GCA_001918315.1
OLB46884.1	GT4	495	AUI07_02860	Archaea	archaeon 13_2_20CM_2_53_6	GCA_001915065.1
XP_015765897.1	GT4	245	LOC107344718	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015768791.1	GT4	252	LOC107347414	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015773769.1	GT4	263	LOC107351980	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015754295.1	GT4	202	LOC107333943	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015754297.1	GT4	202	LOC107333943	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015754296.1	GT4	202	LOC107333943	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015764068.1	GT4+NACHT	1309	LOC107343052	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015764067.1	GT4+NACHT	1312	LOC107343052	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015747884.1	RVT+DEATH+ZU5+ZU5+GT4	1232	LOC107327653	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015747883.1	RVT+DEATH+ZU5+ZU5+GT4	1238	LOC107327653	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015765549.1	GT4+ANK	1083	LOC107344415	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015765548.1	GT4+ANK	1084	LOC107344415	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015780922.1	GT4+GT4	738	LOC107358864	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015780923.1	GT4+GT4	738	LOC107358864	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015760897.1	GT4	651	LOC107340068	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015760896.1	GT4	652	LOC107340068	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015748510.1	GT4	305	LOC107328284	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015776097.1	GT4	305	LOC107354170	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_002599631.1	GT4+GTPase-AIG	700	BRAFLDRAFT_102570	Eukaryota>Opisthokonta>Metazoa>Chordata	Branchiostoma floridae	-
XP_002586742.1	GT4	133	BRAFLDRAFT_105740	Eukaryota>Opisthokonta>Metazoa>Chordata	Branchiostoma floridae	-
XP_002606956.1	GT4	718	BRAFLDRAFT_64952	Eukaryota>Opisthokonta>Metazoa>Chordata	Branchiostoma floridae	-
XP_002592892.1	GT4	115	BRAFLDRAFT_65478	Eukaryota>Opisthokonta>Metazoa>Chordata	Branchiostoma floridae	-
XP_002605447.1	GT4	734	BRAFLDRAFT_74262	Eukaryota>Opisthokonta>Metazoa>Chordata	Branchiostoma floridae	-
XP_002598007.1	GT4	253	BRAFLDRAFT_79766	Eukaryota>Opisthokonta>Metazoa>Chordata	Branchiostoma floridae	-
XP_015747221.1	GT4	151	LOC107326989	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015747315.1	GT4	232	LOC107327073	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015748075.1	GT4	636	LOC107327853	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1

acc	architecture	len	gen.name	tax	species	GCA
XP_015759886.1	GT4	685	LOC107339155	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015764084.1	GT4+NACHT	901	LOC107343052	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015767948.1	GT4	201	LOC107346661	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015774918.1	GT4+NACHT	1264	LOC107353111	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015777737.1	GT4	925	LOC107355671	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015748669.1	GT4	245	LOC107328450	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015750057.1	GT4	520	LOC107329915	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015754313.1	GT4	241	LOC107333962	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015761270.1	GT4	712	LOC107340435	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015770112.1	GT4	253	LOC107348572	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015771016.1	GT4	390	LOC107349380	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015771260.1	GT4	491	LOC107349592	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015772349.1	GT4	256	LOC107350627	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015777221.1	GT4	205	LOC107355205	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015778002.1	GT4	437	LOC107355902	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015779016.1	GT4	186	LOC107356899	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015780870.1	GT4	274	LOC107358800	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
AFD00853.1	GT4	431	Mtc_2115	Archaea>Euryarchaeota	Methanocella conradii HZ254	GCA_000251105.1
AGB33684.1	GT4	394	Natpe_3933	Archaea>Euryarchaeota	Natrinema pellirubrum DSM 15624	GCA_000230735.3
XP_015751533.1	GT4+NACHT	797	LOC107331457	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015747435.1	GT4+NACHT	357	LOC107327199	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015759313.1	GT4+NACHT	988	LOC107338581	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015759411.1	GT4+NACHT	1346	LOC107338694	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015769571.1	GT4+NACHT	716	LOC107348075	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015773770.1	GT4+APATPase	1843	LOC107351981	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015779460.1	GT4+NACHT	537	LOC107357334	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015756756.1	GT4+NACHT+NACHT	770	LOC107336211	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015764080.1	GT4+NACHT	1168	LOC107343052	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015764069.1	GT4+NACHT	1295	LOC107343052	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015770110.1	GT4+APATPase+NACHT	1677	LOC107348570	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015749857.1	GT4+PNPase+NABD-unk4	1031	LOC107329706	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015778949.1	GT4+GT4	1007	LOC107356840	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_002610411.1	GT4+DEATH	1032	BRAFLDRAFT_72365	Eukaryota>Opisthokonta>Metazoa>Chordata	Branchiostoma floridae	-
XP_015768823.1	GT4+DEATH	402	LOC107347423	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015761974.1	SIG+GT4	503	LOC107341068	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_002599100.1	GT4	900	BRAFLDRAFT_81765	Eukaryota>Opisthokonta>Metazoa>Chordata	Branchiostoma floridae	-
XP_002601934.1	GT4	652	BRAFLDRAFT_86418	Eukaryota>Opisthokonta>Metazoa>Chordata	Branchiostoma floridae	-
XP_015753083.1	SIG+GT4	678	LOC107332846	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015770111.1	SIG+GT4+NACHT	1452	LOC107348571	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015759562.1	GT4	954	LOC107338825	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015772173.1	GT4	684	LOC107350460	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015767496.1	GT4+PNPase	423	LOC107346243	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_002610420.1	CARD+sGTP+DEATH+GT4	1671	BRAFLDRAFT_72355	Eukaryota>Opisthokonta>Metazoa>Chordata	Branchiostoma floridae	-
XP_002601932.1	CARD+sGTP+DEATH+GT4+CARD	2070	BRAFLDRAFT_86416	Eukaryota>Opisthokonta>Metazoa>Chordata	Branchiostoma floridae	-
XP_002606064.1	GT4+TIR	594	BRAFLDRAFT_92083	Eukaryota>Opisthokonta>Metazoa>Chordata	Branchiostoma floridae	-
XP_015747743.1	GT4+SidE	864	LOC107327511	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015771496.1	GT4+TPR+TPR+TPR+RVT	1988	LOC107349827	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015777375.1	GT4+ANK	878	LOC107355332	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_006812785.1	GT4+PIN+HEPN	648	LOC102807894	Eukaryota>Opisthokonta>Metazoa>Hemichordata	Saccoglossus kowalevskii	GCF_000003605.2
XP_002601187.1	ImmLRR+LRR+sGTP+OTU+GT4	1577	BRAFLDRAFT_75632	Eukaryota>Opisthokonta>Metazoa>Chordata	Branchiostoma floridae	-
XP_015779017.1	GT4+RNA-Helicase+CXC	1910	LOC107356900	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015767918.1	GT4+NACHT	1211	LOC107346622	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1

acc	architecture	len	gen.name	tax	species	GCA
XP_015747744.1	GT4+GT4	1044	LOC107327512	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_006822589.1	TM+TM+BetaPropeller+BetaPropeller+GT4+ANK+Immank+ANK+ANK+Immank+Immank+Immank	3508	LOC102803126	Eukaryota>Opisthokonta>Metazoa>Hemichordata	Saccoglossus kowalevskii	GCF_000003605.2
XP_002608839.1	DED+DED+OTU+GT4+DEATH	1285	BRAFLDRAFT_89707	Eukaryota>Opisthokonta>Metazoa>Chordata	Branchiostoma floridae	-
XP_002602261.1	ANK+DEATH+GT4	983	BRAFLDRAFT_76949	Eukaryota>Opisthokonta>Metazoa>Chordata	Branchiostoma floridae	-
XP_006824651.1	SIG+EGF+EGF+EGF+CLECTIN+GT4	945	LOC102808514	Eukaryota>Opisthokonta>Metazoa>Hemichordata	Saccoglossus kowalevskii	GCF_000003605.2
XP_015754275.1	GT4+GT4+APATPase+TPR	1815	LOC107333926	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015764809.1	GT4+DEATH	660	LOC107343733	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015763304.1	GT4+CR-ATPase4+TPR	1073	LOC107342333	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015765336.1	GT4+UBI+UBI+UBI+UBI	1194	LOC107344209	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015765496.1	GT4+CASPASE	587	LOC107344359	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_002601970.1	DEATH+GT4	1118	BRAFLDRAFT_94541	Eukaryota>Opisthokonta>Metazoa>Chordata	Branchiostoma floridae	-
XP_015756490.1	GT4+NACHT	1270	LOC107335955	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015754270.1	GT4+drhyd+NACHT	1358	LOC107333920	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015780567.1	GT4+ANK	1294	LOC107358478	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015748771.1	GT4+TM+TM	876	LOC107328563	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_002606060.1	GT4+DED+DED+DED+DED	1082	BRAFLDRAFT_92079	Eukaryota>Opisthokonta>Metazoa>Chordata	Branchiostoma floridae	-
XP_015764066.1	GT4+NACHT	1352	LOC107343052	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015754289.1	GT4+ANK	1133	LOC107333936	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_002601931.1	DEATH+GT4	1086	BRAFLDRAFT_86415	Eukaryota>Opisthokonta>Metazoa>Chordata	Branchiostoma floridae	-
XP_015765568.1	SIG+ANK+GT4	607	LOC107344435	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015771899.1	SIG+GT4+NACHT+RVT	942	LOC107350190	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015759049.1	GT4+TPR+TPR+TPR+sGTP+sGTP	2065	LOC107338329	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015765567.1	GT4+ANK	1016	LOC107344434	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_002601929.1	CARD+sGTP+DEATH+GT4+sGTP+DEATH+CARD	3425	BRAFLDRAFT_86413	Eukaryota>Opisthokonta>Metazoa>Chordata	Branchiostoma floridae	-
XP_002607644.1	GT4+DEATH+Phytase-like+DEATH+DEATH+DEATH+ZNF+ZNF+CRN-ZnBind.csq+ZNF+ZNF	3703	BRAFLDRAFT_84667	Eukaryota>Opisthokonta>Metazoa>Chordata	Branchiostoma floridae	-
XP_002608763.1	TPR+TPR+TPR+sGTP+DEATH+GT4	2376	BRAFLDRAFT_73982	Eukaryota>Opisthokonta>Metazoa>Chordata	Branchiostoma floridae	-
XP_002606489.1	SIG+ImmLRR+DEATH+GT4	791	BRAFLDRAFT_91930	Eukaryota>Opisthokonta>Metazoa>Chordata	Branchiostoma floridae	-
XP_015759356.1	APATPase+TPR+ZU5+ZU5+GT4	1494	LOC107338634	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015767926.1	GT4+NACHT	1234	LOC107346634	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_006823290.1	SIG+GT4+TM	1015	LOC102801620	Eukaryota>Opisthokonta>Metazoa>Hemichordata	Saccoglossus kowalevskii	GCF_000003605.2
XP_015777279.1	GT4+sGTP	1178	LOC107355250	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015771245.1	TPR+TPR+TPR+TPR+TPR+sGTP+GT4	1879	LOC107349580	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_002601933.1	sGTP+DEATH+GT4+sGTP+DEATH+GT4+CARD+sGTP+DEATH	4075	BRAFLDRAFT_86417	Eukaryota>Opisthokonta>Metazoa>Chordata	Branchiostoma floridae	-
XP_002601971.1	SIG+CARD+sGTP+DEATH+GT4+CARD+sGTP+DEATH+DEATH	3440	BRAFLDRAFT_94542	Eukaryota>Opisthokonta>Metazoa>Chordata	Branchiostoma floridae	-
KXJ24237.1	DED+GT4+GT4	2343	AC249_AIPGENE4704	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Exaiptasia diaphana	GCA_001417965.1
XP_006814385.1	DED+TM+GT4	488	LOC102807017	Eukaryota>Opisthokonta>Metazoa>Hemichordata	Saccoglossus kowalevskii	GCF_000003605.2
XP_002592882.1	SIG+ZU5+ZU5+GT4	930	BRAFLDRAFT_117744	Eukaryota>Opisthokonta>Metazoa>Chordata	Branchiostoma floridae	-
XP_015778947.1	GT4+ANK+ANK+ANK	1575	LOC107356838	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_002609384.1	SIG+LRR+sGTP+OTU+GT4+Phytase-like	1519	BRAFLDRAFT_86475	Eukaryota>Opisthokonta>Metazoa>Chordata	Branchiostoma floridae	-
XP_002606063.1	GT4+GTPase-AIG	1278	BRAFLDRAFT_92082	Eukaryota>Opisthokonta>Metazoa>Chordata	Branchiostoma floridae	-
XP_002601968.1	ZNF+ZNF+ZNF+CARD+sGTP+DEATH+GT4	1973	BRAFLDRAFT_94539	Eukaryota>Opisthokonta>Metazoa>Chordata	Branchiostoma floridae	-
XP_015778866.1	GT4+VWA	1117	LOC107356760	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_002592893.1	SIG+DEATH+PspA+GT4	873	BRAFLDRAFT_65479	Eukaryota>Opisthokonta>Metazoa>Chordata	Branchiostoma floridae	-
XP_002610413.1	sGTP+DEATH+GT4+CARD+sGTP+sGTP+DEATH+GT4	4179	BRAFLDRAFT_72363	Eukaryota>Opisthokonta>Metazoa>Chordata	Branchiostoma floridae	-
XP_002599992.1	GT4+TPR+TPR+TPR+TPR	1404	BRAFLDRAFT_74113	Eukaryota>Opisthokonta>Metazoa>Chordata	Branchiostoma floridae	-
XP_002598016.1	DEATH+sGTP+ZU5+GT4	2055	BRAFLDRAFT_79758	Eukaryota>Opisthokonta>Metazoa>Chordata	Branchiostoma floridae	-
XP_015765571.1	GT4+GT4	1248	LOC107344438	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_002608841.1	DED+OTU+sGTP+ZU5+DEATH+DEATH+DED+OTU+CASPASE+sGTP+CASPASE+DED+DEATH+OTU+GT4+sGTP+OTU+GT4+DED+DEATH+CASPASE+sGTP+OTU+DED+DEATH	7154	BRAFLDRAFT_89710	Eukaryota>Opisthokonta>Metazoa>Chordata	Branchiostoma floridae	-
XP_015754687.1	SIG+GT4+CR-ATPase4+TPR	1371	LOC107334268	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_014535703.1	GT4	1299	PDIP_38710	Eukaryota>Opisthokonta>Fungi>Ascomycota	Penicillium digitatum Pd1	GCF_000315645.1
XP_015767848.1	GT4+NACHT	1489	LOC107346556	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1

acc	**architecture**	**len**	**gen.name**	**tax**	**species**	**GCA**
XP_002599095.1	DEATH+sGTP+DEATH+GT4	1974	BRAFLDRAFT_81759	Eukaryota>Opisthokonta>Metazoa>Chordata	Branchiostoma floridae	-
XP_015754268.1	GT4+GT4+GT4+IG	2108	LOC107333918	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015747885.1	RVT+DEATH+ZU5+ZU5+GT4	1158	LOC107327653	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015756824.1	GT4+APATPase	727	LOC107336267	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015774399.1	GT4+CASPASE+CASPASE	742	LOC107352599	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015752969.1	GT4	255	LOC107332740	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_006819467.1	GT4+TM+TM+Snf7	1062	LOC102807364	Eukaryota>Opisthokonta>Metazoa>Hemichordata	Saccoglossus kowalevskii	GCF_000003605.2
XP_002602157.1	DEATH+GT4	1248	BRAFLDRAFT_97971	Eukaryota>Opisthokonta>Metazoa>Chordata	Branchiostoma floridae	-
XP_015774318.1	PNPase+TPR+ZU5+ZU5+GT4	1563	LOC107352503	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_006818589.1	TM+GT4	781	LOC100368229	Eukaryota>Opisthokonta>Metazoa>Hemichordata	Saccoglossus kowalevskii	GCF_000003605.2
XP_015749947.1	GT4+CASPASE+CASPASE	619	LOC107329787	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_002610422.1	sGTP+DEATH+GT4	1881	BRAFLDRAFT_72353	Eukaryota>Opisthokonta>Metazoa>Chordata	Branchiostoma floridae	-
XP_009019645.1	GT4	717	HELRODRAFT_161481	Eukaryota>Opisthokonta>Metazoa>Annelida	Helobdella robusta	GCF_000326865.1
XP_015748178.1	GT4	374	LOC107327971	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015750171.1	GT4	397	LOC107330034	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015750733.1	GT4	186	LOC107330680	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_015760591.1	ZU5+GT4	573	LOC107339792	Eukaryota>Opisthokonta>Metazoa>Cnidaria	Acropora digitifera	GCF_000222465.1
XP_002731836.1	GT4	901	LOC100368975	Eukaryota>Opisthokonta>Metazoa>Hemichordata	Saccoglossus kowalevskii	GCF_000003605.2
XP_006814349.1	GT4	1053	LOC102800835	Eukaryota>Opisthokonta>Metazoa>Hemichordata	Saccoglossus kowalevskii	GCF_000003605.2
XP_006811676.1	GT4	814	LOC102807814	Eukaryota>Opisthokonta>Metazoa>Hemichordata	Saccoglossus kowalevskii	GCF_000003605.2

Source data. Gene neighborhoods and domain architectures of the MNS-like STAND domains (nSTAND2) that is present in a 2-gene operon system each containing a STAND NTPase

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
AZF56106.1	??+STAND+wHTH→ nSTAND2+wHTH+TPRs+HEPN*→	nSTAND2+wHTH+TPRs+HEPN	621	C4J84_0196	Gammaproteobacteria	Pseudomonas sp. R11-23-07	hypothetical protein C4J84_0196 [Pseudomonas sp. R11-23-07].	GCA_003852295.1
EEV8712171.1	??+STAND+wHTH→ nSTAND2+wHTH+TPRs+HEPN*→	nSTAND2+wHTH+TPRs+HEPN	596	EHU50_23110	Gammaproteobacteria	Escherichia coli	hypothetical protein EHU50_23110, partial [Escherichia coli].	GCA_012057895.1
EEZ9035304.1	??+STAND+wHTH→ nSTAND2+wHTH*→	nSTAND2+wHTH	308	C2D11_004496	Gammaproteobacteria	Escherichia coli O75	hypothetical protein C2D11_004496, partial [Escherichia coli O75].	GCA_012229525.1
KAA9385705.1	nSTAND2+wHTH+TPRs+HEPN*→	nSTAND2+wHTH+TPRs+HEPN	533	F4V88_04125	Alphaproteobacteria	Neorhizobium galegae	hypothetical protein F4V88_04125 [Neorhizobium galegae].	GCA_008728145.1
KPX30733.1	??+STAND+wHTH→ nSTAND2+wHTH+TPRs+HEPN*→	nSTAND2+wHTH+TPRs+HEPN	621	ALO77_200057	Gammaproteobacteria	Pseudomonas coronafaciens pv. garcae	hypothetical protein ALO77_200057 [Pseudomonas coronafaciens pv. garcae].	GCA_001400345.1
KQY48570.1	nSTAND2+wHTH+TPRs+HEPN*→	nSTAND2+wHTH+TPRs+HEPN	547	ASD32_09250	Alphaproteobacteria	Rhizobium sp. Root483D2	hypothetical protein ASD32_09250 [Rhizobium sp. Root483D2].	GCA_001426685.1
KYF49123.1	??+STAND+wHTH→ nSTAND2+wHTH+TPRs+HEPN*→	nSTAND2+wHTH+TPRs+HEPN	636	BE08_43115	Deltaproteobacteria	Sorangium cellulosum	hypothetical protein BE08_43115 [Sorangium cellulosum].	GCA_001589265.1
MBA3548110.1	??+STAND+wHTH→ nSTAND2+wHTH+TPRs+HEPN*→ Integrin_beta(vWA)→	nSTAND2+wHTH+TPRs+HEPN	632	H0T76_16635	Deltaproteobacteria	Nannocystis sp.	hypothetical protein H0T76_16635 [Nannocystis sp.].	GCA_013812955.1
OJX80461.1	nSTAND2+wHTH+TPRs+HEPN*→||<-??	nSTAND2+wHTH+TPRs+HEPN	533	BGO93_00115	Alphaproteobacteria	Mesorhizobium sp. 65-26	hypothetical protein BGO93_00115 [Mesorhizobium sp. 65-26].	GCA_001899205.1
PMZ92294.1	??+STAND+wHTH→ nSTAND2+wHTH+TPRs+HEPN*→ PSE→??→	nSTAND2+wHTH+TPRs+HEPN	621	C1X61_03125	Gammaproteobacteria	Pseudomonas sp. FW215-T2	hypothetical protein C1X61_03125 [Pseudomonas sp. FW215-T2].	GCA_002883935.1
POD52929.1	??+STAND+wHTH→ nSTAND2+wHTH+TPRs+HEPN*→	nSTAND2+wHTH+TPRs+HEPN	590	BKM15_13675	Gammaproteobacteria	Pseudomonas syringae pv. syringae	hypothetical protein BKM15_13675 [Pseudomonas syringae pv. syringae].	GCA_002905935.1
PWI54427.1	nSTAND2+wHTH+TPRs+HEPN*→	nSTAND2+wHTH+TPRs+HEPN	532	B5K03_09585	Alphaproteobacteria	Rhizobium phaseoli	hypothetical protein B5K03_09585 [Rhizobium phaseoli].	GCA_003150695.1
PZX00307.1	??+STAND+wHTH→ nSTAND2+wHTH+TPRs+HEPN*→	nSTAND2+wHTH+TPRs+HEPN	621	DFS28_10221	Gammaproteobacteria	Pseudomonas sp. 478	hypothetical protein DFS28_10221 [Pseudomonas sp. 478].	GCA_003254125.1
RCM87736.1	??+STAND+wHTH→ nSTAND2+wHTH+TPRs+HEPN*→	nSTAND2+wHTH+TPRs+HEPN	588	PA57_04301	Gammaproteobacteria	Pseudomonas aeruginosa	hypothetical protein PA57_04301 [Pseudomonas aeruginosa].	GCA_003332525.1
RMG61681.1	Membrane-bound-b-barrel→ STAND+wHTH*→ Pkinase+cNMP_cyclase→	STAND+wHTH	408	D6715_13175	Calditrichaeota	Calditrichaeota bacterium	ATP-binding protein [Calditrichaeota bacterium].	GCA_003696445.1
RMS07982.1	??+STAND+wHTH→ nSTAND2+wHTH+TPRs+HEPN*→	nSTAND2+wHTH+TPRs+HEPN	621	ALP73_02675	Gammaproteobacteria	Pseudomonas coronafaciens pv. garcae	hypothetical protein ALP73_02675 [Pseudomonas coronafaciens pv. garcae].	GCA_003701555.1
RWN51709.1	??+STAND+wHTH→ nSTAND2+wHTH+TPRs+HEPN*→	nSTAND2+wHTH+TPRs+HEPN	599	EOR98_25445	Alphaproteobacteria	Mesorhizobium sp.	hypothetical protein EOR98_25445 [Mesorhizobium sp.].	GCA_004020775.1
RYG89382.1	??→??+STAND+wHTH→ nSTAND2+wHTH+TPRs+HEPN*→	nSTAND2+wHTH+TPRs+HEPN	629	EON59_01575	Alphaproteobacteria	Alphaproteobacteria bacterium	hypothetical protein EON59_01575 [Alphaproteobacteria bacterium].	GCA_004145145.1
TIN07909.1	??+STAND+wHTH→ nSTAND2+wHTH+TPRs+HEPN*→	nSTAND2+wHTH+TPRs+HEPN	599	E5Y14_22895	Alphaproteobacteria	Mesorhizobium sp.	hypothetical protein E5Y14_22895 [Mesorhizobium sp.].	GCA_004961475.1
TIT02463.1	??+STAND+wHTH→ nSTAND2+wHTH+TPRs+HEPN*→	nSTAND2+wHTH+TPRs+HEPN	596	E5W87_09945	Alphaproteobacteria	Mesorhizobium sp.	hypothetical protein E5W87_09945 [Mesorhizobium sp.].	GCA_004962925.1

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
TJV17958.1	??+STAND+wHTH→ nSTAND2+wHTH+TPRs+HEPN*→	nSTAND2+wHTH+TPRs+HEPN	626	E5Y07_09865	Alphaproteobacteria	Mesorhizobium sp.	hypothetical protein E5Y07_09865 [Mesorhizobium sp.].	GCA_005046125.1
WP_008322742.1	??+STAND+wHTH→ nSTAND2+wHTH+TPRs+HEPN*→||<-??	nSTAND2+wHTH+TPRs+HEPN	613	-	Gammaproteobacteria	Enterobacteriaceae	MULTISPECIES: hypothetical protein [Enterobacteriaceae].	GCF_000277565.1
WP_026230868.1	??+STAND+wHTH→ nSTAND2+wHTH+TPRs+HEPN*→ SF2-helicase+DEAD_assoc→ Calcineurin→	nSTAND2+wHTH+TPRs+HEPN	637	-	Alphaproteobacteria	Rhizobium	MULTISPECIES: hypothetical protein [Rhizobium].	GCF_014138515.1
WP_027196515.1	??+STAND→ nSTAND2+wHTH+GT4*→	nSTAND2+wHTH+GT4	760	-	Betaproteobacteria	Paraburkholderia sprentiae	glycosyltransferase family 4 protein [Paraburkholderia sprentiae].	GCF_001865575.1
WP_048993481.1	??+STAND+wHTH→ nSTAND2+wHTH+TPRs+HEPN*→||<-??	nSTAND2+wHTH+TPRs+HEPN	613	-	Gammaproteobacteria	Klebsiella pneumoniae	hypothetical protein [Klebsiella pneumoniae].	GCF_001065235.1
WP_072160039.1	nSTAND2+wHTH+TPRs+HEPN*→	nSTAND2+wHTH+TPRs+HEPN	613	-	Gammaproteobacteria	Pluralibacter gergoviae	hypothetical protein [Pluralibacter gergoviae].	GCF_001276415.1
WP_088567149.1	??+STAND+wHTH→ nSTAND2+wHTH+TPRs+HEPN*→||<-??	nSTAND2+wHTH+TPRs+HEPN	613	-	Gammaproteobacteria	Enterobacter hormaechei	hypothetical protein [Enterobacter hormaechei].	GCF_002208275.1
WP_089463191.1	??+STAND→ nSTAND2+wHTH+GT4*→	nSTAND2+wHTH+GT4	768	-	Betaproteobacteria	Burkholderia	MULTISPECIES: glycosyltransferase [Burkholderia].	GCF_002924455.1
WP_094198012.1	??+STAND→ nSTAND2+wHTH+GT4*→	nSTAND2+wHTH+GT4	756	-	Betaproteobacteria	Alcaligenes faecalis	glycosyltransferase family 4 protein [Alcaligenes faecalis].	GCF_002242175.1
WP_097401548.1	nSTAND2+wHTH+TPRs+HEPN*→||<-??	nSTAND2+wHTH+TPRs+HEPN	613	-	Gammaproteobacteria	Enterobacteriaceae	MULTISPECIES: hypothetical protein [Enterobacteriaceae].	GCF_002510255.1
WP_106119969.1	??+STAND→ nSTAND2+wHTH+GT4*→	nSTAND2+wHTH+GT4	736	-	Gammaproteobacteria	Pseudomonas simiae	glycosyltransferase family 4 protein [Pseudomonas simiae].	GCF_003001535.1
WP_107112219.1	??+STAND+wHTH→ nSTAND2+wHTH+TPRs+HEPN*→||<-??	nSTAND2+wHTH+TPRs+HEPN	613	-	Gammaproteobacteria	Klebsiella quasipneumoniae	hypothetical protein [Klebsiella quasipneumoniae].	GCF_002854535.1
WP_116343459.1	??+STAND+wHTH→ nSTAND2+wHTH+TPRs+HEPN*→||<-??	nSTAND2+wHTH+TPRs+HEPN	613	-	Gammaproteobacteria	Enterobacter cloacae	hypothetical protein [Enterobacter cloacae].	GCF_003401145.1
WP_122437975.1	??+STAND+wHTH→ nSTAND2+wHTH+TPRs+HEPN*→	nSTAND2+wHTH+TPRs+HEPN	621	-	Gammaproteobacteria	Pseudomonas viridiflava	hypothetical protein [Pseudomonas viridiflava].	GCF_900580835.1
WP_124434788.1	??+STAND+wHTH→ nSTAND2+wHTH+TPRs+HEPN*→	nSTAND2+wHTH+TPRs+HEPN	598	-	Gammaproteobacteria	Pseudomonas sp. R11-23-07	hypothetical protein [Pseudomonas sp. R11-23-07].	GCF_003852295.1
WP_127426060.1	??+STAND+wHTH→ nSTAND2+wHTH+TPRs+HEPN*→	nSTAND2+wHTH+TPRs+HEPN	606	-	Alphaproteobacteria	unclassified Mesorhizobium	MULTISPECIES: hypothetical protein [unclassified Mesorhizobium].	GCF_004021725.2
WP_132834030.1	??+STAND+wHTH→ nSTAND2+wHTH+TPRs+HEPN*→	nSTAND2+wHTH+TPRs+HEPN	598	-	Gammaproteobacteria	unclassified Pseudomonas	MULTISPECIES: hypothetical protein [unclassified Pseudomonas].	GCF_003254125.1
WP_134049903.1	??+STAND+wHTH→ nSTAND2+wHTH+TPRs+HEPN*→	nSTAND2+wHTH+TPRs+HEPN	621	-	Gammaproteobacteria	Pseudomonas sp. OV144	hypothetical protein [Pseudomonas sp. OV144].	GCF_004368835.1
WP_139645958.1	??+STAND+wHTH→ nSTAND2+wHTH+TPRs+HEPN*→	nSTAND2+wHTH+TPRs+HEPN	623	-	Gammaproteobacteria	Pseudomonas sp. ICMP22404	hypothetical protein [Pseudomonas sp. ICMP22404].	GCF_006227205.1
WP_145962680.1	??+STAND+wHTH→ nSTAND2+wHTH+TPRs+HEPN*→	nSTAND2+wHTH+TPRs+HEPN	592	-	Alphaproteobacteria	Rhizobium phaseoli	hypothetical protein [Rhizobium phaseoli].	GCF_003150695.1
WP_146023689.1	??+STAND+wHTH→ nSTAND2+wHTH+TPRs+HEPN*→ PSE→??→	nSTAND2+wHTH+TPRs+HEPN	598	-	Gammaproteobacteria	unclassified Pseudomonas	MULTISPECIES: hypothetical protein [unclassified Pseudomonas].	GCF_002884305.1
WP_147262087.1	??+STAND+wHTH→ nSTAND2+wHTH+TPRs+HEPN*→	nSTAND2+wHTH+TPRs+HEPN	612	-	Gammaproteobacteria	Pseudomonas aeruginosa	hypothetical protein [Pseudomonas aeruginosa].	GCF_003332525.1
WP_147467220.1	nSTAND2+wHTH+TPRs+HEPN*→	nSTAND2+wHTH+TPRs+HEPN	486	-	Gammaproteobacteria	Pseudomonas coronafaciens	hypothetical protein [Pseudomonas coronafaciens].	GCF_003700475.1
WP_147475620.1	nSTAND2+wHTH+TPRs+HEPN*→	nSTAND2+wHTH+TPRs+HEPN	486	-	Gammaproteobacteria	Pseudomonas coronafaciens	hypothetical protein [Pseudomonas coronafaciens].	GCF_001400345.1
WP_153438665.1	??+STAND+wHTH→ nSTAND2+wHTH+TPRs+HEPN*→	nSTAND2+wHTH+TPRs+HEPN	620	-	Gammaproteobacteria	Pseudomonas helleri	hypothetical protein [Pseudomonas helleri].	GCF_009600265.1
WP_156383024.1	??→ STAND+wHTH→ nSTAND2+wHTH+TPRs+HEPN*→	nSTAND2+wHTH+TPRs+HEPN	602	-	Alphaproteobacteria	Rhizobium sp. Root483D2	hypothetical protein [Rhizobium sp. Root483D2].	GCF_001426685.1

acc	**operon**	**architecture**	**len**	**gen.name**	**taxend**	**species**	**defline**	**gca**
WP_160320279.1	nSTAND2(fragment)*→	nSTAND2(fragment)	113	-	Alphaproteobacteria	Rhizobium ecuadorense	hypothetical protein, partial [Rhizobium ecuadorense].	GCF_001187535.1
WP_160610812.1	??+STAND+wHTH→ nSTAND2+wHTH+TPRs+HEPN*→	nSTAND2+wHTH+TPRs+HEPN	640	-	Alphaproteobacteria	Altererythrobacter aerius	hypothetical protein [Altererythrobacter aerius].	GCF_009827495.1
WP_163011207.1	??+STAND+wHTH→ nSTAND2+wHTH+TPRs+HEPN*→	nSTAND2+wHTH+TPRs+HEPN	621	-	Gammaproteobacteria	Pseudomonas viridiflava	hypothetical protein [Pseudomonas viridiflava].	GCF_900582025.1
WP_163014645.1	nSTAND2+wHTH+TPRs+HEPN*→	nSTAND2+wHTH+TPRs+HEPN	560	-	Gammaproteobacteria	Pseudomonas viridiflava	hypothetical protein [Pseudomonas viridiflava].	GCF_900582435.1
WP_164708313.1	nSTAND2+wHTH+TPRs+HEPN*→	nSTAND2+wHTH+TPRs+HEPN	534	-	Gammaproteobacteria	Pseudomonas viridiflava	hypothetical protein [Pseudomonas viridiflava].	GCF_900602385.1
WP_169852212.1	??+STAND+wHTH→ nSTAND2+wHTH+TPRs+HEPN*→	nSTAND2+wHTH+TPRs+HEPN	623	-	Gammaproteobacteria	Pseudomonas proteolytica	hypothetical protein [Pseudomonas proteolytica].	GCF_012985975.1

Source data. Gene neighborhoods and domain architectures of prokaryotic AP-GTPases described in the text

acc	**operon**	**architecture**	**len**	**gen.name**	**taxend**	**species**	**defline**	**gca**
AAU84033.1	pc1599→ Cluster1746_2clades→ Calcineurin→||<-tRNA||LRR-repeats+AP-GTPase+COR+TM+TM*→?→?→ Aminotran_1_2→||<-?<-?<-?||Cluster1483_2clades→	LRR-repeats+AP-GTPase+COR+TM+TM	737	GZ35D7_19	Archaea	uncultured archaeon GZfos35D7	leucine-rich-repeat protein [uncultured archaeon GZfos35D7].	-
AAX07516.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1016	-	Planctomycetes	Gemmata sp. Wa1-1	GTP-binding protein [Gemmata sp. Wa1-1].	-
ABD75797.1	HISKIN→ LRR-repeats+AP-GTPase+COR+EAD8*→ HISKIN→?→||<-?||Cluster1512_2clades→ TetR-HTH→?→ Ferredoxin-RRM→	LRR-repeats+AP-GTPase+COR+EAD8	847	-	Bacteria	uncultured bacterium	hypothetical protein [uncultured bacterium].	-
ACC84329.1	<-Arginase<-?<-?<-?||LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1109	Npun_F6039	Cyanobacteria	Nostoc punctiforme PCC 73102	Miro domain protein [Nostoc punctiforme PCC 73102].	GCA_000020025.1
ADB42932.1	SIG+TM+TM+TM+HISKIN→?→||<-?||CENPB→?→ Cluster2094_2clades→ LRR-repeats+AP-GTPase+COR*→||<-?<-?<-?<-?<-?<-?||ParA-Soj-PloopNTPase→	LRR-repeats+AP-GTPase+COR	925	Slin_6989	Bacteroidetes	Spirosoma linguale DSM 74	small GTP-binding protein (plasmid) [Spirosoma linguale DSM 74].	GCA_000024525.1
AEE53900.1	35exo→||<-?<-?||?→?→?→ LRR-repeats+AP-GTPase+COR+TIR*→||<-?<-?<-ABC-ATPase+APATPase+ABC-ATPase<-?||SIGMA-HTH→	LRR-repeats+AP-GTPase+COR+TIR	998	Halhy_6078	Bacteroidetes	Haliscomenobacter hydrossis DSM 1100	small GTP-binding protein [Haliscomenobacter hydrossis DSM 1100].	GCA_000212735.1
AEE54359.1	LRR-repeats+AP-GTPase+COR+TIR*→ LRR-repeats+AP-GTPase+COR→ LRR-repeats+AP-GTPase+COR→	LRR-repeats+AP-GTPase+COR+TIR	1058	Halhy_6543	Bacteroidetes	Haliscomenobacter hydrossis DSM 1100	Miro domain protein [Haliscomenobacter hydrossis DSM 1100].	GCA_000212735.1
AEE54482.1	LRR-repeats+AP-GTPase+COR+EAD11*→	LRR-repeats+AP-GTPase+COR+EAD11	1141	Halhy_6666	Bacteroidetes	Haliscomenobacter hydrossis DSM 1100	small GTP-binding protein (plasmid) [Haliscomenobacter hydrossis DSM 1100].	GCA_000212735.1
AEE54508.1	MACRODOMAIN→?→ LRR-repeats+AP-GTPase+COR+EAD11*→	LRR-repeats+AP-GTPase+COR+EAD11	1023	Halhy_6692	Bacteroidetes	Haliscomenobacter hydrossis DSM 1100	Miro domain protein (plasmid) [Haliscomenobacter hydrossis DSM 1100].	GCA_000212735.1
AFY40133.1	<-SIG+Trypsin+PDZ<-?||?→?→ LRR-repeats+AP-GTPase+COR+TCAD2*→	LRR-repeats+AP-GTPase+COR+TCAD2	918	Lepto7376_3994	Cyanobacteria	Leptolyngbya sp. PCC 7376	small GTP-binding protein [Leptolyngbya sp. PCC 7376].	GCA_000316605.1
AFY57475.1	EACC2+CASPASE+LRR-repeats+AP-GTPase*→ AP-GTPase+COR→	EACC2+CASPASE+LRR-repeats+AP-GTPase	982	Riv7116_5077	Cyanobacteria	Rivularia sp. PCC 7116	leucine-rich repeat (LRR) protein [Rivularia sp. PCC 7116].	GCA_000316665.1
AKB24843.1	<-HhH-RADC+JAB||?→ NTP_transf_3→ LRR-repeats+AP-GTPase+COR→?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	599	MSMTP_1374	Euryarchaeota	Methanosarcina sp. MTP4	E3 ubiquitin-protein ligase SspH2 [Methanosarcina sp. MTP4].	GCA_000970045.1
AKB47719.1	LRR-repeats→ LRR-repeats+AP-GTPase+COR+TIR*→?→?→?→?→?→?→||<-TPR-repeats	LRR-repeats+AP-GTPase+COR+TIR	590	MSKOL_1942	Euryarchaeota	Methanosarcina sp. Kolksee	hypothetical protein MSKOL_1942 [Methanosarcina sp. Kolksee].	GCA_000969945.1
AKB51553.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	880	MSBRW_2300	Euryarchaeota	Methanosarcina barkeri str. Wiesmoor	hypothetical protein MSBRW_2300 [Methanosarcina barkeri str. Wiesmoor].	GCA_000969985.1
AKB56819.1	<-SIG+TPR+TPR+TPR+TPR+TPR+TPR||?→||<-?||?→?→?→?→ LRR-repeats+AP-GTPase+COR*→?→?→ PRTase→	LRR-repeats+AP-GTPase+COR	880	MSBR2_0303	Euryarchaeota	Methanosarcina barkeri 227	hypothetical protein MSBR2_0303 [Methanosarcina barkeri 227].	GCA_000970065.1
AKJ07375.1	Cluster971_2clades→?→||<-?<-?||LRR-repeats+AP-GTPase+COR+TIR*→?→||<-?<-?<-?||?→||<-?<-SIG+Lysozyme	LRR-repeats+AP-GTPase+COR+TIR	873	AA314_09001	Deltaproteobacteria	Archangium gephyra	Chaperone protein DnaK [Archangium gephyra].	GCA_001027285.1
AOY82617.1	REC→||<-?<-HNH||REC→||<-TPR-repeats<-?||LRR-repeats→ LRR-repeats+AP-GTPase+COR*→ AP-GTPase+COR+TM+TM→	LRR-repeats+AP-GTPase+COR	252	BJP36_24575	Cyanobacteria	Moorea producens JHB	hypothetical protein BJP36_24575 [Moorea producens JHB].	GCA_001854205.1
AQR64774.1	LRR-repeats+AP-GTPase+COR+TIR*→||<-?<-?<-MarR-HTH||?→||<-MarR-HTH<-?||Thioredoxin→	LRR-repeats+AP-GTPase+COR+TIR	1295	BXU06_06620	Betaproteobacteria	Aquaspirillum sp. LM1	hypothetical protein BXU06_06620 [Aquaspirillum sp. LM1].	GCA_002002905.1

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
AQR65390.1	HSP70→ DNAJ→?→?→ LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	890	BXU06_10225	Betaproteobacteria	Aquaspirillum sp. LM1	hypothetical protein BXU06_10225 [Aquaspirillum sp. LM1].	GCA_002002905.1
AUN33853.1	<-SIG+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM<-?<-?<-?<-?||?→?→ LRR-repeats+AP-GTPase+COR+TIR*→||<-ParB<-ParA-Soj-PloopNTPase	LRR-repeats+AP-GTPase+COR+TIR	965	C0V82_25960	Alphaproteobacteria	Niveispirillum cyanobacteriorum	hypothetical protein C0V82_25960 (plasmid) [Niveispirillum cyanobacteriorum].	GCA_002868735.1
AVH71003.1	LRR-repeats+AP-GTPase+COR+DUF4404*→||<-?||?→||<-?||?→?→ MoxR-AAA→	LRR-repeats+AP-GTPase+COR+DUF4404	1233	NLP_2293	Cyanobacteria	Nostoc sp. ‘Lobaria pulmonaria (5183) cyanobiont’	small GTP-binding protein [Nostoc sp. ‘Lobaria pulmonaria (5183) cyanobiont’].	GCA_002949795.1
AXO38068.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	942	MicB006_5810	Actinobacteria	Micromonospora sp. B006	cytoplasmic membrane protein [Micromonospora sp. B006].	GCA_003408515.1
AYQ35346.1	FGS→ FGS→ FGS→ LRR-repeats+AP-GTPase+COR+CASPASE*→	LRR-repeats+AP-GTPase+COR+CASPASE	998	DTQ70_25690	Bacteroidetes	Runella sp. SP2	CHAT domain-containing protein [Runella sp. SP2].	GCA_003711225.1
BAY10551.1	LRR-repeats→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	793	NIES2098_37230	Cyanobacteria	Calothrix sp. NIES-2098	Miro domain protein [Calothrix sp. NIES-2098].	GCA_002368175.1
BAY18983.1	HISKIN→||<-?||LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	946	NIES21_48420	Cyanobacteria	Anabaenopsis circularis NIES-21	Miro domain-containing protein [Anabaenopsis circularis NIES-21].	GCA_002367975.1
BAY19588.1	LRR-repeats+AP-GTPase+COR+TM+TM*→||<-tRNA<-?||?→?→||<-?<-?<-SNF||RnasePH+RnasePH+KH+S1→	LRR-repeats+AP-GTPase+COR+TM+TM	739	NIES21_54510	Cyanobacteria	Anabaenopsis circularis NIES-21	Miro domain protein [Anabaenopsis circularis NIES-21].	GCA_002367975.1
BAY24777.1	Pro_CA→||<-?<-?||Chromo-N+CHROMO→||<-?||LRR-repeats+AP-GTPase+COR+TIR+TCAD4+CASPASE*→	LRR-repeats+AP-GTPase+COR+TIR+TCAD4+CASPASE	1450	NIES2100_45740	Cyanobacteria	Calothrix sp. NIES-2100	Miro domain-containing protein [Calothrix sp. NIES-2100].	GCA_002368195.1
BAY74940.1	LRR-repeats+AP-GTPase+COR*→||<-ClpABN-AAA+ClpABC-AAA<-?<-?||METHYLASE→	LRR-repeats+AP-GTPase+COR	1016	NIES25_13570	Cyanobacteria	Nostoc linckia NIES-25	Miro domain-containing protein [Nostoc linckia NIES-25].	GCA_002368035.1
BAY88950.1	LRR-repeats→ LRR-repeats+AP-GTPase+COR+CASPASE*→	LRR-repeats+AP-GTPase+COR+CASPASE	963	NIES3275_09520	Cyanobacteria	Fremyella diplosiphon NIES-3275	Miro domain-containing protein [Fremyella diplosiphon NIES-3275].	GCA_002368275.1
BAY98896.1	<-REC<-?||Chromo-N+CHROMO→?→||<-?<-?<-?||LRR-repeats+AP-GTPase+COR+CASPASE*→	LRR-repeats+AP-GTPase+COR+CASPASE	1138	NIES37_28740	Cyanobacteria	Tolypothrix tenuis PCC 7101	Miro domain-containing protein [Tolypothrix tenuis PCC 7101].	GCA_002368295.1
BAZ08233.1	<-ParB<-ParA-Soj-PloopNTPase||?→ LRR-repeats→ LRR-repeats+AP-GTPase+COR+EAD1*→ ParB→||<-NACHT	LRR-repeats+AP-GTPase+COR+EAD1	856	NIES4071_00380	Cyanobacteria	Calothrix sp. NIES-4071	Miro domain-containing protein [Calothrix sp. NIES-4071].	GCA_002368455.1
BAZ30312.1	<-SIG+GT4<-?||?→ LRR-repeats→ LRR-repeats+AP-GTPase+COR+TM+TM*→?→?→||<-?<-Arginase	LRR-repeats+AP-GTPase+COR+TM+TM	638	NIES4074_27680	Cyanobacteria	Cylindrospermum sp. NIES-4074	small GTP-binding protein [Cylindrospermum sp. NIES-4074].	GCA_003994795.1
BBD58750.1	<-DSBH<-?<-?<-?<-ParA-Soj-PloopNTPase<-?||LRR-repeats+AP-GTPase+COR+DUF4404*→	LRR-repeats+AP-GTPase+COR+DUF4404	1041	NIES2109_15280	Cyanobacteria	Nostoc sp. HK-01	small GTP-binding protein domain-containing protein [Nostoc sp. HK-01].	GCA_003990705.1
BBD61760.1	RelE-ParE→?→||<-?<-?||LRR-repeats+AP-GTPase+COR+TM+TM*→||<-tRNA<-?||?→?→||<-?<-?<-SNF	LRR-repeats+AP-GTPase+COR+TM+TM	954	NIES2109_45950	Cyanobacteria	Nostoc sp. HK-01	Miro domain protein [Nostoc sp. HK-01].	GCA_003990705.1
BBD62362.1	HISKIN→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	854	NIES2109_52010	Cyanobacteria	Nostoc sp. HK-01	Miro domain protein [Nostoc sp. HK-01].	GCA_003990705.1
BBH86778.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1152	KTC_15290	Chloroflexi	Thermosporothrix sp. COM3	hypothetical protein KTC_15290 [Thermosporothrix sp. COM3].	-
CAA0113265.1	LRR-repeats+AP-GTPase+COR+DrHyd*→	LRR-repeats+AP-GTPase+COR+DrHyd	947	inlA	Gammaproteobacteria	Halioglobus japonicus	Internalin-A [Halioglobus japonicus].	GCA_902705825.1
CAA6825421.1	TM+TM+TM→ LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	931	HELGO_WM44885	Gammaproteobacteria	uncultured Thiotrichaceae bacterium	GTP-binding protein [uncultured Thiotrichaceae bacterium].	-
CBG70605.1	PAIREDC-HTH→||<-?||LRR-repeats→ LRR-repeats+AP-GTPase+COR*→||<-?||?→||<-?<-SIGMA-HTH<-?<-SIGMA-HTH	LRR-repeats+AP-GTPase+COR	743	SCAB_35141	Actinobacteria	Streptomyces scabiei 87.22	putative GTPase [Streptomyces scabiei 87.22].	GCA_000091305.1
CBS87910.1	LRR-repeats+AP-GTPase+COR+TIR*→||<-?<-?||ABC_membrane+ABC_tran→?→ Cluster968_2clades→	LRR-repeats+AP-GTPase+COR+TIR	1026	AZOLI_2723	Alphaproteobacteria	Azospirillum lipoferum 4B	Conserved protein of unknown function; Leucine-rich repeat domain [Azospirillum lipoferum 4B].	GCA_000283655.1
CCG09157.1	LRR-repeats+AP-GTPase+COR+TIR*→||<-?<-?<-?<-?<-?<-REC	LRR-repeats+AP-GTPase+COR+TIR	756	RSPPHO_02531	Alphaproteobacteria	Pararhodospirillum photometricum DSM 122	Leucine-rich repeat [Pararhodospirillum photometricum DSM 122].	GCA_000284415.2

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
CCH96195.1	LRR-repeats+AP-GTPase+COR+TM+TM*→	LRR-repeats+AP-GTPase+COR+TM+TM	625	MICAB_1690001	Cyanobacteria	Microcystis aeruginosa PCC 9717	Leucine-rich-repeat protein (fragment) [Microcystis aeruginosa PCC 9717].	GCA_000312165.1
CCI18671.1	LRR-repeats+AP-GTPase+COR*→ AP-GTPase+COR+TM+TM→	LRR-repeats+AP-GTPase+COR	302	MICAF_4270008	Cyanobacteria	Microcystis aeruginosa PCC 9807	Leucine-rich-repeat protein (fragment) [Microcystis aeruginosa PCC 9807].	GCA_000312225.1
CCQ52177.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	620	CWATWH8502_1464	Cyanobacteria	Crocosphaera watsonii WH 8502	Leucine-rich repeat [Crocosphaera watsonii WH 8502].	GCA_001039555.1
CCQ56427.1	LRR-repeats+AP-GTPase+COR*→||<-?<-?<-?||RelE→ CHTH→	LRR-repeats+AP-GTPase+COR	761	CWATWH0005_5558	Cyanobacteria	Crocosphaera watsonii WH 0005	Leucine-rich repeat [Crocosphaera watsonii WH 0005].	GCA_001050835.1
CCQ61794.1	LRR-repeats+AP-GTPase+COR*→||<-?<-?||RelE→ CHTH→	LRR-repeats+AP-GTPase+COR	674	CWATWH0401_3405	Cyanobacteria	Crocosphaera watsonii WH 0401	Leucine-rich repeat [Crocosphaera watsonii WH 0401].	GCA_001039615.1
CCQ66314.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	378	CWATWH0402_4408	Cyanobacteria	Crocosphaera watsonii WH 0402	Leucine-rich repeat [Crocosphaera watsonii WH 0402].	GCA_001039635.1
CDA78514.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1064	BN558_01944	Firmicutes	Clostridium sp. CAG:242	miro domain protein [Clostridium sp. CAG:242].	GCA_000435455.1
CDU15633.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1092	VCR17J2_90139	Gammaproteobacteria	Vibrio sp. J2-17	hypothetical protein VCR17J2_90139 [Vibrio sp. J2-17].	GCA_001244075.1
CRH07284.1	LRR-repeats+AP-GTPase+COR*→||<-?||?→?→||<-?<-SIG+Lysozyme	LRR-repeats+AP-GTPase+COR	759	MAGMO_3143	Alphaproteobacteria	Candidatus Magnetococcus massalia	Conserved protein of unknown function. Containing small GTP-binding domain and Leucine-rich repeat (LRR) domain [Candidatus Magnetococcus massalia].	-
EAM49963.1	Cluster1136_2clades→?→||<-?||LRR-repeats→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	715	CwatDRAFT_2830	Cyanobacteria	Crocosphaera watsonii WH 8501	Leucine-rich repeat [Crocosphaera watsonii WH 8501].	GCA_000167195.1
EAY30117.1	LRR-repeats→?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1165	M23134_05450	Bacteroidetes	Microscilla marina ATCC 23134	Rab family protein [Microscilla marina ATCC 23134].	GCA_000169175.1
EDN67620.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	602	BGP_2058	Gammaproteobacteria	Beggiatoa sp. PS	leucine-rich-repeat protein [Beggiatoa sp. PS].	GCA_000170715.1
EDN68964.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	833	BGP_3136	Gammaproteobacteria	Beggiatoa sp. PS	leucine-rich-repeat protein [Beggiatoa sp. PS].	GCA_000170715.1
EDX78020.1	Cluster1415_2clades→?→||<-?||LRR-repeats→ LRR-repeats+AP-GTPase+COR+DUF4404*→	LRR-repeats+AP-GTPase+COR+DUF4404	1115	MC7420_7758	Cyanobacteria	Coleofasciculus chthonoplastes PCC 7420	Ras family, putative [Coleofasciculus chthonoplastes PCC 7420].	GCA_000155555.1
EHJ11819.1	LRR-repeats+AP-GTPase+COR*→||<-?<-?||RelE→ CHTH→	LRR-repeats+AP-GTPase+COR	674	CWATWH0003_3458	Cyanobacteria	Crocosphaera watsonii WH 0003	Leucine-rich repeat [Crocosphaera watsonii WH 0003].	GCA_000235665.2
EIG53576.1	LRR-repeats+AP-GTPase+COR*→?→?→?→ Cluster1496_2clades→	LRR-repeats+AP-GTPase+COR	1279	DesU5LDRAFT_1901	Deltaproteobacteria	Desulfovibrio sp. U5L	small GTP-binding protein domain [Desulfovibrio sp. U5L].	GCA_000245055.1
ESA34932.1	LRR-repeats+AP-GTPase+COR+TM+TM*→	LRR-repeats+AP-GTPase+COR+TM+TM	1002	N836_14320	Cyanobacteria	Leptolyngbya sp. Heron Island J	small gtp-binding protein [Leptolyngbya sp. Heron Island J].	GCA_000482245.1
ESA35951.1	<-NACHT<-?||LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	824	N836_09535	Cyanobacteria	Leptolyngbya sp. Heron Island J	small gtp-binding protein [Leptolyngbya sp. Heron Island J].	GCA_000482245.1
ESA37051.1	LRR-repeats+AP-GTPase+COR*→?→?→?→||<-Pentapeptide-repeats	LRR-repeats+AP-GTPase+COR	818	N836_04700	Cyanobacteria	Leptolyngbya sp. Heron Island J	small gtp-binding protein [Leptolyngbya sp. Heron Island J].	GCA_000482245.1
ESQ09086.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	840	N838_02740	Gammaproteobacteria	Thiohalocapsa sp. PB-PSB1	hypothetical protein N838_02740 [Thiohalocapsa sp. PB-PSB1].	GCA_000495615.1
ETR72570.1	Cluster1438_2clades→?→ LRR-repeats+AP-GTPase+COR+TIR*→ CCTBP→||<-REC	LRR-repeats+AP-GTPase+COR+TIR	808	OMM_01620	Deltaproteobacteria	Candidatus Magnetoglobus multicellularis str. Araruama	leucine-rich repeat-containing protein [Candidatus Magnetoglobus multicellularis str. Araruama].	GCA_000516475.1
ETW97925.1	LRR-repeats+AP-GTPase+COR+DUF4404*→?→||<-RNA-Helicase||?→ SIG+BLBD→	LRR-repeats+AP-GTPase+COR+DUF4404	767	ETSY1_20835	Nitrospinae/Tectomicrobia group	Candidatus Entotheonella factor	hypothetical protein ETSY1_20835, partial [Candidatus Entotheonella factor].	GCA_000522425.1

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ETX07308.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	513	ETSY2_11950	Nitrospinae/Tectomicrobia group	Candidatus Entotheonella gemina	hypothetical protein ETSY2_11950, partial [Candidatus Entotheonella gemina].	GCA_000522445.1
GAK50293.1	<-CR-REase5<-?<-Cluster1448_2clades<-Cluster1281_2clades||?→ LRR-repeats+AP-GTPase*→ COR→	LRR-repeats+AP-GTPase	420	U14_01521	Bacteria	Candidatus Moduliflexus flocculans	leucine-rich-repeat protein [Candidatus Moduliflexus flocculans].	GCA_000739515.1
GBE92899.1	HISKIN→||<-?||?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	946	NCWK1_2658	Cyanobacteria	Nostoc cycadae WK-1	leucine rich repeat (LRR)-containing protein [Nostoc cycadae WK-1].	GCA_002897135.1
GCL40268.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	261	SR1949_54040	Cyanobacteria	Sphaerospermopsis reniformis	small GTP-binding protein [Sphaerospermopsis reniformis].	GCA_005402885.1
GEP41915.1	SIG+TM→?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	809	BGE01nite_12060	Verrucomicrobia	Brevifollis gellanilyticus	hypothetical protein BGE01nite_12060 [Brevifollis gellanilyticus].	GCA_007992435.1
GFZ95281.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	911	CYANOKiyG1_06360	Cyanobacteria	Okeania sp. KiyG1	hypothetical protein CYANOKiyG1_06360 [Okeania sp. KiyG1].	GCA_014132355.1
GFZ95952.1	<-HhH-RADC+JAB<-?||LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	747	CYANOKiyG1_07050	Cyanobacteria	Okeania sp. KiyG1	hypothetical protein CYANOKiyG1_07050 [Okeania sp. KiyG1].	GCA_014132355.1
GGA29094.1	<-RADICAL-SAM||?→ REC→?→ LRR-repeats+AP-GTPase+COR*→||<-?<-NACHT+68TM-wHTH<-?||?→||<-TPR-repeats<-HISKIN	LRR-repeats+AP-GTPase+COR	1395	CYANOKiyG1_45460	Cyanobacteria	Okeania sp. KiyG1	hypothetical protein CYANOKiyG1_45460 [Okeania sp. KiyG1].	GCA_014132355.1
GGA48436.1	LRR-repeats+AP-GTPase+COR*→?→ COR+TM+TM→||<-?<-?<-NUDIX||TPR-repeats→	LRR-repeats+AP-GTPase+COR	405	CYANOKiyG1_67520	Cyanobacteria	Okeania sp. KiyG1	hypothetical protein CYANOKiyG1_67520 [Okeania sp. KiyG1].	GCA_014132355.1
GGD73013.1	LRR-repeats+AP-GTPase+COR+TM+TM*→?→?→||<-?<-Cluster1601_2clades	LRR-repeats+AP-GTPase+COR+TM+TM	937	GCM10011514_41350	Bacteroidetes	Emticicia aquatilis	hypothetical protein GCM10011514_41350 [Emticicia aquatilis].	GCA_014644295.1
GGU83059.1	LRR-repeats+AP-GTPase+COR*→||<-?||?→||<-?<-SIGMA-HTH<-?<-SIGMA-HTH	LRR-repeats+AP-GTPase+COR	996	GCM10010260_14720	Actinobacteria	Streptomyces filipinensis	hypothetical protein GCM10010260_14720 [Streptomyces filipinensis].	GCA_014649495.1
HAA21349.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	805	DCP28_22240	Bacteroidetes	Cytophagales bacterium	TPA: hypothetical protein DCP28_22240, partial [Cytophagales bacterium].	GCA_003444325.1
HAC62039.1	ABC_membrane+ABC_tran→?→ LRR-repeats→ LRR-repeats+AP-GTPase+COR*→||<-Cluster2488_2clades<-Cluster2227_2clades||ISOFLAVOMETHYLASE-HTH→	LRR-repeats+AP-GTPase+COR	852	DCF68_00525	Cyanobacteria	Cyanothece sp. UBA12306	TPA: GTPase, partial [Cyanothece sp. UBA12306].	GCA_003448685.1
HAC64827.1	<-METHYLASE<-?||LRR-repeats+AP-GTPase+COR+TM+TM*→?→||<-?<-?<-SWACOS	LRR-repeats+AP-GTPase+COR+TM+TM	931	DCF68_15170	Cyanobacteria	Cyanothece sp. UBA12306	TPA: GTPase [Cyanothece sp. UBA12306].	GCA_003448685.1
HAG85135.1	Ferredoxin-RRM→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	819	DCL61_29295	Cyanobacteria	Cyanobacteria bacterium UBA12227	TPA: GTPase [Cyanobacteria bacterium UBA12227].	GCA_003450835.1
HAP64559.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	754	DCR93_35450	Bacteroidetes	Cytophagales bacterium	TPA: hypothetical protein DCR93_35450, partial [Cytophagales bacterium].	GCA_003454975.1
HAR63371.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	611	DCS13_07910	Terrabacteria group	Candidatus Margulisbacteria bacterium	TPA: hypothetical protein DCS13_07910, partial [Candidatus Margulisbacteria bacterium].	GCA_003475905.1
HAS39197.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1145	DCS93_01900	Bacteroidetes	Microscillaceae bacterium	TPA: hypothetical protein DCS93_01900 [Microscillaceae bacterium].	GCA_003483885.1
HAS43483.1	LRR-repeats→?→?→||<-?||LRR-repeats+AP-GTPase+COR+EAD11*→||<-PAS+HISKIN	LRR-repeats+AP-GTPase+COR+EAD11	868	DCS93_23590	Bacteroidetes	Microscillaceae bacterium	TPA: hypothetical protein DCS93_23590 [Microscillaceae bacterium].	GCA_003483885.1

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HAS44199.1	LRR-repeats+AP-GTPase+COR→*//<-?<-?<-?//LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	958	DCS93_27220	Bacteroidetes	Microscillaceae bacterium	TPA: hypothetical protein DCS93_27220 [Microscillaceae bacterium].	GCA_003483885.1
HAS44203.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1037	DCS93_27240	Bacteroidetes	Microscillaceae bacterium	TPA: hypothetical protein DCS93_27240 [Microscillaceae bacterium].	GCA_003483885.1
HAS46073.1	<-LRR-repeats<-ABC-ATPase||?→||<-?||?→?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	864	DCS93_36670	Bacteroidetes	Microscillaceae bacterium	TPA: hypothetical protein DCS93_36670 [Microscillaceae bacterium].	GCA_003483885.1
HAV28009.1	Pro_CA→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1019	DCX23_06795	Firmicutes	Lachnospiraceae bacterium	TPA: hypothetical protein DCX23_06795 [Lachnospiraceae bacterium].	GCA_003484485.1
HAW32544.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1236	DCY03_31275	Planctomycetes	Planctomycetaceae bacterium	TPA: hypothetical protein DCY03_31275 [Planctomycetaceae bacterium].	GCA_003487605.1
HAX71152.1	<-Cluster1437_2clades||?→ LRR-repeats→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	869	DCY14_16175	Chloroflexi	Anaerolineae bacterium	TPA: hypothetical protein DCY14_16175, partial [Anaerolineae bacterium].	GCA_003486425.1
HBE20120.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	816	DDW51_21520	Cyanobacteria	Cyanobacteria bacterium UBA11367	TPA: hypothetical protein DDW51_21520 [Cyanobacteria bacterium UBA11367].	GCA_003501765.1
HBE59255.1	LRR-repeats→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	893	DDW56_17600	Cyanobacteria	Cyanobacteria bacterium UBA11366	TPA: hypothetical protein DDW56_17600, partial [Cyanobacteria bacterium UBA11366].	GCA_003501625.1
HBG28935.1	ABC-ATPase+ABC-ATPase→?→?→ S1COLD→ LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1033	DDX75_17760	Planctomycetes	Phycisphaerales bacterium	TPA: serine/threonine protein kinase [Phycisphaerales bacterium].	GCA_003499685.1
HBH73318.1	LRR-repeats→ LRR-repeats+AP-GTPase+COR+DrHyd*→||<-?<-?<-?||?→?→||<-PRTase	LRR-repeats+AP-GTPase+COR+DrHyd	872	DDY43_07685	Cyanobacteria	Synechococcales bacterium UBA10510	TPA: hypothetical protein DDY43_07685, partial [Synechococcales bacterium UBA10510].	GCA_003508015.1
HBH73336.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	698	DDY43_07790	Cyanobacteria	Synechococcales bacterium UBA10510	TPA: hypothetical protein DDY43_07790 [Synechococcales bacterium UBA10510].	GCA_003508015.1
HBK96125.1	LRR-repeats+AP-GTPase+COR+TM+TM*→	LRR-repeats+AP-GTPase+COR+TM+TM	656	DD001_01755	Cyanobacteria	Microcoleaceae bacterium UBA10368	TPA: GTPase, partial [Microcoleaceae bacterium UBA10368].	GCA_003506815.1
HBK98262.1	GTPase-AIG→?→?→||<-?<-?||LRR-repeats+AP-GTPase+COR+DUF4404*→	LRR-repeats+AP-GTPase+COR+DUF4404	1165	DD001_13585	Cyanobacteria	Microcoleaceae bacterium UBA10368	TPA: GTPase [Microcoleaceae bacterium UBA10368].	GCA_003506815.1
HBP89205.1	CHTH→||<-?<-?<-?<-?<-?<-?||LRR-repeats+AP-GTPase+COR+DrHyd*→||<-?<-?<-TM	LRR-repeats+AP-GTPase+COR+DrHyd	948	DD706_16075	Nitrospirae	Nitrospiraceae bacterium	TPA: hypothetical protein DD706_16075 [Nitrospiraceae bacterium].	GCA_003523945.1
HBU22381.1	LRR-repeats+AP-GTPase+COR*→?→?→?→?→?→||<-?||ParA-Soj-PloopNTPase→	LRR-repeats+AP-GTPase+COR	865	DEB17_00005	Chlorobi	Chlorobaculum sp.	TPA: hypothetical protein DEB17_00005, partial [Chlorobaculum sp.].	GCA_003510485.1
HBW31420.1	LRR-repeats+AP-GTPase+COR+DUF4404*→||<-?<-ABC-ATPase<-?||?→||<-REC	LRR-repeats+AP-GTPase+COR+DUF4404	766	DEF48_15370	Cyanobacteria	Nostoc sp. UBA8866	TPA: Ras family protein, partial [Nostoc sp. UBA8866].	GCA_003514525.1
HBY87332.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	930	DEO86_15815	Gammaproteobacteria	Colwellia sp.	TPA: hypothetical protein DEO86_15815 [Colwellia sp.].	GCA_003520945.1

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HCA94361.1	LRR-repeats→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	892	DEP38_06745	Cyanobacteria	Cyanobacteria bacterium UBA9226	TPA: hypothetical protein DEP38_06745, partial [Cyanobacteria bacterium UBA9226].	GCA_003520045.1
HCF17408.1	LRR-repeats+AP-GTPase+COR+TIR*→ TM+TM+TM→	LRR-repeats+AP-GTPase+COR+TIR	737	DEV96_05085	Alphaproteobacteria	Rhodospirillum rubrum	TPA: hypothetical protein DEV96_05085, partial [Rhodospirillum rubrum].	GCA_003530895.1
HCN30450.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1024	DIT64_17260	Verrucomicrobia	Verrucomicrobiales bacterium	TPA: hypothetical protein DIT64_17260 [Verrucomicrobiales bacterium].	GCA_003545395.1
HCO95252.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	809	DIU00_15100	Planctomycetes	Phycisphaerales bacterium	TPA: hypothetical protein DIU00_15100 [Phycisphaerales bacterium].	GCA_003533825.1
HCQ19950.1	LRR-repeats+AP-GTPase+COR*→?→||<-?<-?||TM→	LRR-repeats+AP-GTPase+COR	754	DIU28_00335	Cyanobacteria	Anabaena sp. UBA12330	TPA: hypothetical protein DIU28_00335, partial [Anabaena sp. UBA12330].	GCA_003525565.1
HCQ20817.1	LRR-repeats→ LRR-repeats+AP-GTPase+COR+TM+TM*→||<-?||?→?→?→?→ ABC-ATPase→	LRR-repeats+AP-GTPase+COR+TM+TM	721	DIU28_04955	Cyanobacteria	Anabaena sp. UBA12330	TPA: hypothetical protein DIU28_04955, partial [Anabaena sp. UBA12330].	GCA_003525565.1
HCR54081.1	LRR-repeats→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	797	DIW27_06670	Bacteroidetes	Cytophagales bacterium	TPA: hypothetical protein DIW27_06670 [Cytophagales bacterium].	GCA_003524675.1
HCS91704.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	749	DIW77_17080	Gammaproteobacteria	Chromatiaceae bacterium	TPA: hypothetical protein DIW77_17080 [Chromatiaceae bacterium].	GCA_003525925.1
HCT83732.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	585	DF296_00860	Terrabacteria group	Candidatus Margulisbacteria bacterium	TPA: hypothetical protein DF296_00860 [Candidatus Margulisbacteria bacterium].	GCA_003542625.1
HCU95641.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	896	DHU96_24175	Actinobacteria	Actinobacteria bacterium	TPA: hypothetical protein DHU96_24175 [Actinobacteria bacterium].	GCA_003541285.1
HDN27288.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	598	ENG03_09385	Gammaproteobacteria	Thioploca sp.	TPA: GTP-binding protein, partial [Thioploca sp.].	GCA_011043325.1
HEC83827.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	907	ENI48_01075	Gammaproteobacteria	Thioploca sp.	TPA: GTPase [Thioploca sp.].	GCA_011052595.1
HEG42537.1	<-S1COLD||LRR-repeats+AP-GTPase+COR+TIR*→?→||<-SIG+Alba<-?||?→?→?→ REC→	LRR-repeats+AP-GTPase+COR+TIR	1095	ENH94_00660	Planctomycetes	Phycisphaerales bacterium	TPA: TIR domain-containing protein [Phycisphaerales bacterium].	GCA_011053245.1
HER03270.1	LRR-repeats+AP-GTPase+COR+TIR*→||<-?||?→?→ Cluster1306_2clades→?→ SIG+TM→ RuvB-AAA+RuvB-HTH→	LRR-repeats+AP-GTPase+COR+TIR	910	ENR03_13235	Alphaproteobacteria	Rhizobiales bacterium	TPA: TIR domain-containing protein, partial [Rhizobiales bacterium].	GCA_011046675.1
HEU35175.1	Cluster1718_2clades→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	718	ENQ60_27120	unclassified Bacteria	bacterium	TPA: GTP-binding protein, partial [bacterium].	GCA_011047125.1
HFB99816.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1132	ENJ53_03320	Bacteroidetes	Phaeodactylibacter sp.	TPA: TIR domain-containing protein, partial [Phaeodactylibacter sp.].	GCA_011322485.1
HFS07270.1	Cluster1370_2clades→ LRR-repeats+AP-GTPase+COR+TIR*→||<-?||REase→	LRR-repeats+AP-GTPase+COR+TIR	1009	ENR14_02795	Cyanobacteria	Anabaena sp.	TPA: TIR domain-containing protein [Anabaena sp.].	GCA_011332035.1
HFS07901.1	LRR-repeats+AP-GTPase+COR+TIR*→||<-?<-?<-ParA-Soj-PloopNTPase	LRR-repeats+AP-GTPase+COR+TIR	1021	ENR14_06085	Cyanobacteria	Anabaena sp.	TPA: GTP-binding protein [Anabaena sp.].	GCA_011332035.1
HGZ29232.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	903	ENR17_03505	Bacteroidetes	Bacteroidetes bacterium	TPA: hypothetical protein ENR17_03505 [Bacteroidetes bacterium].	GCA_011331955.1

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HGZ31593.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	868	ENR17_15550	Bacteroidetes	Bacteroidetes bacterium	TPA: TIR domain-containing protein, partial [Bacteroidetes bacterium].	GCA_011331955.1
HHB79310.1	FGS→?→ RVT→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	458	ENK85_08770	Bacteroidetes	Saprospiraceae bacterium	TPA: hypothetical protein ENK85_08770, partial [Saprospiraceae bacterium].	GCA_011371135.1
HHH53255.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	413	ENK91_06320	Bacteroidetes	Bacteroidetes bacterium	TPA: GTP-binding protein, partial [Bacteroidetes bacterium].	GCA_011371025.1
HHV24864.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	716	GXX65_10185	Euryarchaeota	Methanosarcina sp.	TPA: GTP-binding protein [Methanosarcina sp.].	GCA_012839505.1
HIE02480.1	Cluster1917_2clades→?→?→?→?→||<-?||LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	853	EYP59_19720	Gammaproteobacteria	Thiotrichaceae bacterium	TPA: GTPase [Thiotrichaceae bacterium].	GCA_012961805.1
HIE31128.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	636	EYP67_01930	Euryarchaeota	Methanosarcinales archaeon	TPA: GTP-binding protein, partial [Methanosarcinales archaeon].	GCA_012961645.1
HII01375.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	622	HA351_06900	Euryarchaeota	Methanosarcinaceae archaeon	TPA: GTP-binding protein [Methanosarcinaceae archaeon].	GCA_013329415.1
HII91446.1	<-HhH-RADC+JAB||?→?→?→ NTP_transf_3→ LRR-repeats→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	672	HA262_04570	Euryarchaeota	Methanosarcina sp.	TPA: GTP-binding protein, partial [Methanosarcina sp.].	GCA_013331275.1
HII91684.1	NTP_transf_3→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	735	HA262_05815	Euryarchaeota	Methanosarcina sp.	TPA: GTP-binding protein [Methanosarcina sp.].	GCA_013331275.1
KAA3610009.1	MORC→?→ LRR-repeats→ LRR-repeats+AP-GTPase+COR*→?→||<-?<-?<-BetaPropeller+BetaPropeller	LRR-repeats+AP-GTPase+COR	653	DWQ03_18700	Calditrichaeota	Calditrichaeota bacterium	hypothetical protein DWQ03_18700 [Calditrichaeota bacterium].	GCA_008501795.1
KAA3656070.1	LRR-repeats+AP-GTPase+COR+EAD7*→	LRR-repeats+AP-GTPase+COR+EAD7	779	DWQ04_32125	Chloroflexi	Chloroflexi bacterium	GTPase, partial [Chloroflexi bacterium].	GCA_008501785.1
KAA3659887.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	842	DWQ04_20995	Chloroflexi	Chloroflexi bacterium	GTPase [Chloroflexi bacterium].	GCA_008501785.1
KAB8152691.1	<-HISKIN<-?||?→?→ REC→ LRR-repeats+AP-GTPase+COR+TIR*→||<-RADICAL-SAM	LRR-repeats+AP-GTPase+COR+TIR	1007	EZY14_012780	Bacteroidetes	Kordia sp. TARA_039_SRF	TIR domain-containing protein [Kordia sp. TARA_039_SRF].	GCA_006383075.2
KAB8153612.1	LRR-repeats+AP-GTPase+COR+TIR*→||<-?<-?||?→||<-?||TM+RHOMBOID→	LRR-repeats+AP-GTPase+COR+TIR	966	EZY14_010295	Bacteroidetes	Kordia sp. TARA_039_SRF	TIR domain-containing protein [Kordia sp. TARA_039_SRF].	GCA_006383075.2
KAF0107167.1	<-HISKIN<-REC||?→?→?→?→ LRR-repeats+AP-GTPase+COR*→||<-SIG+GT4	LRR-repeats+AP-GTPase+COR	1065	FD146_2008	Chloroflexi	Anaerolineaceae bacterium	hypothetical protein FD146_2008 [Anaerolineaceae bacterium].	GCA_009772985.1
KAF5415978.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	561	C5S48_04205	Euryarchaeota	ANME-2 cluster archaeon	hypothetical protein C5S48_04205 [ANME-2 cluster archaeon].	GCA_013374355.1
KAF5419007.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	865	C5S49_00980	Euryarchaeota	ANME-2 cluster archaeon	hypothetical protein C5S49_00980 [ANME-2 cluster archaeon].	GCA_013374365.1
KAF5420469.1	Cluster1076_2clades→ Cluster1076_2clades→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	878	C5S44_08435	Euryarchaeota	ANME-2 cluster archaeon	hypothetical protein C5S44_08435 [ANME-2 cluster archaeon].	GCA_013374455.1
KAF5421986.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	596	C5S45_02955	Euryarchaeota	ANME-2 cluster archaeon	hypothetical protein C5S45_02955, partial [ANME-2 cluster archaeon].	GCA_013374465.1
KAF5428813.1	<-CBS<-CBS||?→?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	788	C5S39_10445	Euryarchaeota	Methanophagales archaeon	Leucine-rich repeat (LRR) protein [Methanophagales archaeon].	GCA_013374505.1
KAF5432496.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	599	C5S39_03480	Euryarchaeota	Methanophagales archaeon	hypothetical protein C5S39_03480 [Methanophagales archaeon].	GCA_013374505.1
KAF5433375.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	838	C5S35_16480	Euryarchaeota	Methanophagales archaeon	hypothetical protein C5S35_16480 [Methanophagales archaeon].	GCA_013374565.1
KAF5435535.1	SIG+TM+TM+TM+TM+TM+TM→||<-?<-?||?→?→ Aminotran_1_2→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	659	C5S35_10775	Euryarchaeota	Methanophagales archaeon	hypothetical protein C5S35_10775, partial [Methanophagales archaeon].	GCA_013374565.1
KAF5438029.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	787	C5S35_01055	Euryarchaeota	Methanophagales archaeon	internalin A, partial [Methanophagales archaeon].	GCA_013374565.1
KFF11476.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	902	IW20_19515	Bacteroidetes	Flavobacterium hydatis	hypothetical protein IW20_19515 [Flavobacterium hydatis].	GCA_000737695.1

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KJV08837.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	553	VZ95_15215	Alphaproteobacteria	Elstera litoralis	hypothetical protein VZ95_15215, partial [Elstera litoralis].	GCA_000963705.1
KOR30146.1	LRR-repeats+AP-GTPase+COR*→ SIG+RHOD-CDC25→	LRR-repeats+AP-GTPase+COR	653	TI04_06910	Gammaproteobacteria	Achromatium sp. WMS2	hypothetical protein TI04_06910 [Achromatium sp. WMS2].	GCA_001276605.1
KPA09194.1	HNH→?→?→?→?→ LRR-repeats+AP-GTPase+COR*→ McrA-NTD→?→ RlaP→ Cluster2261_2clades→	LRR-repeats+AP-GTPase+COR	923	MHK_010613	Deltaproteobacteria	Candidatus Magnetomorum sp. HK-1	Leucine Rich Repeat (LRR)-containing protein [Candidatus Magnetomorum sp. HK-1].	GCA_001292585.1
KPA10003.1	Cluster2271_2clades→ TPR+TPR→?→?→ LRR-repeats+AP-GTPase+COR+DUF4404*→	LRR-repeats+AP-GTPase+COR+DUF4404	883	MHK_009799	Deltaproteobacteria	Candidatus Magnetomorum sp. HK-1	small GTP-binding protein domain protein [Candidatus Magnetomorum sp. HK-1].	GCA_001292585.1
KPA12970.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	676	MHK_006822	Deltaproteobacteria	Candidatus Magnetomorum sp. HK-1	leucine-rich repeat-containing protein [Candidatus Magnetomorum sp. HK-1].	GCA_001292585.1
KPA13876.1	TIR+LRR-repeats+AP-GTPase+COR+Calcineurin*→	TIR+LRR-repeats+AP-GTPase+COR+Calcineurin	1426	MHK_005915	Deltaproteobacteria	Candidatus Magnetomorum sp. HK-1	small gtp-binding protein [Candidatus Magnetomorum sp. HK-1].	GCA_001292585.1
KPA14771.1	LRR-repeats+AP-GTPase+COR+DrHyd*→	LRR-repeats+AP-GTPase+COR+DrHyd	898	MHK_005023	Deltaproteobacteria	Candidatus Magnetomorum sp. HK-1	leucine-rich repeat-containing protein [Candidatus Magnetomorum sp. HK-1].	GCA_001292585.1
KPA15132.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1146	MHK_004657	Deltaproteobacteria	Candidatus Magnetomorum sp. HK-1	small GTP-binding domain protein [Candidatus Magnetomorum sp. HK-1].	GCA_001292585.1
KPQ33355.1	ARSR-HTH→ Cluster2335_2clades→||<-?||LRR-repeats→ LRR-repeats+AP-GTPase+COR+TIR*→||<-METHYLASE||?→||<-SIG+TM+TM+TM<-ABC_membrane+ABC_tran	LRR-repeats+AP-GTPase+COR+TIR	887	HLUCCA11_18720	Cyanobacteria	Phormidesmis priestleyi Ana	Leucine Rich repeats (2 copies)/TIR domain/Miro-like protein/Leucine rich repeat [Phormidesmis priestleyi Ana].	GCA_001314865.1
KPQ36660.1	<-Cluster54_3clades<-?||LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1200	inlA	Cyanobacteria	Phormidesmis priestleyi Ana	internalin A [Phormidesmis priestleyi Ana].	GCA_001314865.1
KTE25244.1	TetR-HTH→?→||<-?<-?<-?<-?||LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	719	ATE62_22325	Alphaproteobacteria	Sphingopyxis sp. HIX	hypothetical protein ATE62_22325 [Sphingopyxis sp. HIX].	GCA_001468285.1
KTE72816.1	TetR-HTH→?→||<-?<-?<-?<-?||LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	716	ATE72_22070	Alphaproteobacteria	Sphingopyxis sp. HXXIV	hypothetical protein ATE72_22070 [Sphingopyxis sp. HXXIV].	GCA_001468305.1
MAB62252.1	Cluster1163_3clades→?→ Cluster1131_3clades→?→||<-?<-?||?→ LRR-repeats+AP-GTPase+COR+TIR*→?→?→ METHYLASE→ ParA-Soj-PloopNTPase→ ParB→	LRR-repeats+AP-GTPase+COR+TIR	1212	CMK67_03795	Gammaproteobacteria	Pseudoalteromonas sp.	hypothetical protein CMK67_03795 [Pseudoalteromonas sp.].	GCA_002684115.1
MAD04103.1	LRR-repeats+AP-GTPase+COR*→?→||<-?<-?<-?||CNMP+CRP-HTH→	LRR-repeats+AP-GTPase+COR	956	CMK65_10845	Gammaproteobacteria	Pseudoalteromonas sp.	hypothetical protein CMK65_10845 [Pseudoalteromonas sp.].	GCA_002685175.1
MAG37481.1	AP-GTPase+COR+TIR+ACYC→ LRR-repeats+AP-GTPase+COR+DUF4404*→?→||<-?||?→?→?→||<-DOC+CITB-HTH	LRR-repeats+AP-GTPase+COR+DUF4404	884	CL878_14695	Chloroflexi	Dehalococcoidia bacterium	serine/threonine protein kinase [Dehalococcoidia bacterium].	GCA_002688445.1
MAM30487.1	LRR-repeats+AP-GTPase+COR*→||<-?<-tRNA<-?||Nitroreductase-like→||<-FKBP	LRR-repeats+AP-GTPase+COR	839	CMC13_15825	Bacteroidetes	Flavobacteriaceae bacterium	hypothetical protein CMC13_15825 [Flavobacteriaceae bacterium].	GCA_002693005.1
MAS92856.1	<-Cluster1364_2clades||SIG+TM+TM+TM+TM+TM→ TIR+LRR-repeats+AP-GTPase+COR*→||<-?<-?<-?<-SIG+TM+TM+TM	TIR+LRR-repeats+AP-GTPase+COR	1140	CMO55_06625	Verrucomicrobia	Verrucomicrobiales bacterium	hypothetical protein CMO55_06625 [Verrucomicrobiales bacterium].	GCA_002698785.1
MAT45170.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1068	CL609_22815	Chloroflexi	Anaerolineaceae bacterium	hypothetical protein CL609_22815 [Anaerolineaceae bacterium].	GCA_002702705.1
MAT70109.1	<-Cluster1140_2clades<-?||?→||<-?<-?||LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1220	CMJ58_11380	Planctomycetes	Planctomycetaceae bacterium	hypothetical protein CMJ58_11380 [Planctomycetaceae bacterium].	GCA_002702655.1
MAT98393.1	LRR-repeats+AP-GTPase+COR+EAD7*→?→ SIG+PBPB→||<-?||?→||<-SIG+TM+TM+TM+TM+TM+TM+TM+TM+TM<-REC	LRR-repeats+AP-GTPase+COR+EAD7	845	CL608_14715	Chloroflexi	Anaerolineaceae bacterium	hypothetical protein CL608_14715 [Anaerolineaceae bacterium].	GCA_002699125.1
MAY74446.1	ParB→?→||<-?||ClpABN-AAA+ClpABC-AAA→ LRR-repeats+AP-GTPase+COR+TM+TM*→	LRR-repeats+AP-GTPase+COR+TM+TM	1163	CMJ31_06925	Planctomycetes	Phycisphaerae bacterium	hypothetical protein CMJ31_06925 [Phycisphaerae bacterium].	GCA_002706885.1

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MBA2243669.1	LRR-repeats+AP-GTPase+COR+TIR*→?→?→||<-?<-?||Cluster1476_2clades→	LRR-repeats+AP-GTPase+COR+TIR	748	H0W11_01850	Gemmatimonadetes	Gemmatimonadetes bacterium	TIR domain-containing protein [Gemmatimonadetes bacterium].	GCA_013694785.1
MBA2243921.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	693	H0W11_03125	Gemmatimonadetes	Gemmatimonadetes bacterium	TIR domain-containing protein, partial [Gemmatimonadetes bacterium].	GCA_013694785.1
MBA2678589.1	LRR-repeats+AP-GTPase+COR*→?→||<-?<-Cluster2349_2clades	LRR-repeats+AP-GTPase+COR	363	H0U76_09400	Chloroflexi	Ktedonobacteraceae bacterium	leucine-rich repeat domain-containing protein [Ktedonobacteraceae bacterium].	GCA_013697605.1
MBA2681600.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	724	H0U76_24795	Chloroflexi	Ktedonobacteraceae bacterium	leucine-rich repeat domain-containing protein, partial [Ktedonobacteraceae bacterium].	GCA_013697605.1
MBA3240620.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	321	H0T60_05265	Acidobacteria	Acidobacteria bacterium	leucine-rich repeat domain-containing protein, partial [Acidobacteria bacterium].	GCA_013813375.1
MBA3574619.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	706	H0W37_06570	Actinobacteria	Pseudonocardiales bacterium	hypothetical protein H0W37_06570, partial [Pseudonocardiales bacterium].	GCA_013817435.1
MBA3673339.1	Trichomonas-DAM→?→ LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1186	H0W75_00010	Bacteroidetes	Chitinophagaceae bacterium	leucine-rich repeat domain-containing protein [Chitinophagaceae bacterium].	GCA_013816565.1
MBA3805221.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	805	H0X14_05855	Acidobacteria	Acidobacteria bacterium	TIR domain-containing protein [Acidobacteria bacterium].	GCA_013815675.1
MBA3964374.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1028	H0X47_01080	Nitrospirae	Nitrospirales bacterium	leucine-rich repeat domain-containing protein [Nitrospirales bacterium].	GCA_013821375.1
MBA4062951.1	<-NUDIX||?→||<-tRNA||?→?→||<-?||LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	867	C0501_04445	Planctomycetes	Isosphaera sp.	serine/threonine protein kinase [Isosphaera sp.].	GCA_013822345.1
MBB3841051.1	TPR-repeats→?→ TPR-repeats→?→ LRR-repeats+AP-GTPase+COR+TIR*→||<-?||?→||<-?||?→||<-?<-?||TIR+TPR+TPR-S→	LRR-repeats+AP-GTPase+COR+TIR	794	FHS57_005072	Bacteroidetes	Runella defluvii	GTPase SAR1 family protein [Runella defluvii].	GCA_014195535.1
MBB5874185.1	LRR-repeats+AP-GTPase+COR*→||<-?<-?<-?<-BACTERIALFRINGE+TM+TM	LRR-repeats+AP-GTPase+COR	1250	F4553_007619	Actinobacteria	Allocatelliglobosispora scoriae	Leucine-rich repeat (LRR) protein/GTPase SAR1 family protein [Allocatelliglobosispora scoriae].	GCA_014204945.1
MBC6434062.1	LRR-repeats+AP-GTPase+COR*→||<-?<-?||?→||<-?<-PSE<-N-OB	LRR-repeats+AP-GTPase+COR	824	FM036_26905	Cyanobacteria	Nostoc sp. HG1	hypothetical protein FM036_26905, partial [Nostoc sp. HG1].	GCA_014324315.1
MBC7569567.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	863	H7319_07530	Bacteroidetes	Spirosoma sp.	leucine-rich repeat domain-containing protein [Spirosoma sp.].	GCA_014377625.1
MBC7571377.1	Cluster1281_2clades→||<-?||LRR-repeats+AP-GTPase+COR*→||<-?<-?||?→||<-?<-?<-?<-Cluster1413_2clades	LRR-repeats+AP-GTPase+COR	1077	H7319_16850	Bacteroidetes	Spirosoma sp.	leucine-rich repeat domain-containing protein [Spirosoma sp.].	GCA_014377625.1
MBC7773965.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	856	H7246_00900	Planctomycetes	Phycisphaerae bacterium	TIR domain-containing protein [Phycisphaerae bacterium].	GCA_014379065.1
MBC7775420.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	616	H7246_08275	Planctomycetes	Phycisphaerae bacterium	leucine-rich repeat domain-containing protein, partial [Phycisphaerae bacterium].	GCA_014379065.1
MBC7777197.1	LRR-repeats+AP-GTPase+COR+TIR*→?→ HNH→	LRR-repeats+AP-GTPase+COR+TIR	693	H7246_17325	Planctomycetes	Phycisphaerae bacterium	GTP-binding protein, partial [Phycisphaerae bacterium].	GCA_014379065.1
MBC7778407.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	831	H7246_23450	Planctomycetes	Phycisphaerae bacterium	TIR domain-containing protein [Phycisphaerae bacterium].	GCA_014379065.1

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MBC7817185.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	238	IAG10_09885	Planctomycetes	Planctomycetaceae bacterium	hypothetical protein IAG10_09885, partial [Planctomycetaceae bacterium].	GCA_014379175.1
MBC7817749.1	<-RHOD-CDC25||LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	865	IAG10_12720	Planctomycetes	Planctomycetaceae bacterium	leucine-rich repeat domain-containing protein [Planctomycetaceae bacterium].	GCA_014379175.1
MBC7826556.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	752	H7122_02330	Bacteroidetes	Chitinophagaceae bacterium	TIR domain-containing protein, partial [Chitinophagaceae bacterium].	GCA_014379345.1
MBC7848891.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	927	H7Y31_04105	Bacteroidetes	Chitinophagaceae bacterium	leucine-rich repeat domain-containing protein, partial [Chitinophagaceae bacterium].	GCA_014379515.1
MBC7877029.1	RADICAL-SAM→?→?→?→||<-?||?→ LRR-repeats→ LRR-repeats+AP-GTPase+COR*→?→ ABC-ATPase→	LRR-repeats+AP-GTPase+COR	718	H7Y59_07640	Chloroflexi	Anaerolineales bacterium	leucine-rich repeat domain-containing protein [Anaerolineales bacterium].	GCA_014379595.1
MBC7877562.1	<-TM+RHOMBOID<-?<-?<-?||TM→ LRR-repeats+AP-GTPase+COR*→||<-?||SIGMA-HTH→	LRR-repeats+AP-GTPase+COR	1057	H7Y59_10360	Chloroflexi	Anaerolineales bacterium	hypothetical protein H7Y59_10360 [Anaerolineales bacterium].	GCA_014379595.1
MBC8029843.1	<-REC||?→?→ Hsp10→?→ LRR-repeats+AP-GTPase+COR+TIR*→||<-?<-?<-?<-?<-ABC-ATPase	LRR-repeats+AP-GTPase+COR+TIR	871	H7Z16_07010	Acidobacteria	Pyrinomonadaceae bacterium	TIR domain-containing protein [Pyrinomonadaceae bacterium].	GCA_014380365.1
MBC8182613.1	LRR-repeats+AP-GTPase+COR*→?→?→ RelE-ParE→||<-?<-RelE-ParE<-?<-HISKIN	LRR-repeats+AP-GTPase+COR	687	H8E88_16055	Bacteria	candidate division KSB1 bacterium	hypothetical protein H8E88_16055, partial [candidate division KSB1 bacterium].	GCA_014381395.1
MBC8235006.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1069	H8E77_36130	unclassified Bacteria	bacterium	leucine-rich repeat domain-containing protein [bacterium].	GCA_014381605.1
MBC8264797.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	674	H8E47_11810	Chloroflexi	Anaerolineales bacterium	leucine-rich repeat domain-containing protein [Anaerolineales bacterium].	GCA_014382145.1
MBC8291013.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	692	H8E37_11925	Planctomycetes	Planctomycetes bacterium	leucine-rich repeat domain-containing protein, partial [Planctomycetes bacterium].	GCA_014382385.1
MBC8374880.1	Cluster1757_2clades→?→ LRR-repeats+AP-GTPase+COR+DrHyd*→	LRR-repeats+AP-GTPase+COR+DrHyd	931	H8E26_02475	FCB group	FCB group bacterium	50S ribosome-binding GTPase [FCB group bacterium].	GCA_014382565.1
MBC8468948.1	LRR-repeats+AP-GTPase+COR*→||<-?||?→||<-?<-?||?→||<-?<-SIGMA-HTH	LRR-repeats+AP-GTPase+COR	1003	H8D56_05705	Planctomycetes	Planctomycetes bacterium	leucine-rich repeat domain-containing protein [Planctomycetes bacterium].	GCA_014384025.1
MBC9785332.1	Cluster1542_2clades→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	976	H1S01_12510	Firmicutes	Heliobacterium chlorum	leucine-rich repeat domain-containing protein [Heliobacterium chlorum].	-
MBP93715.1	LRR-repeats+AP-GTPase+COR*→||<-?||?→||<-?<-Cluster1995_2clades	LRR-repeats+AP-GTPase+COR	894	CMC55_06315	Bacteroidetes	Flavobacteriaceae bacterium	hypothetical protein CMC55_06315 [Flavobacteriaceae bacterium].	GCA_002726785.1
MBV11156.1	APATPase+BetaPropeller_WD40-repeats→?→||<-?||FGS→ FGS→ FGS→ LRR-repeats+AP-GTPase+COR+TIR*→ Cluster1411_2clades→ FGS→ FGS→ FGS→	LRR-repeats+AP-GTPase+COR+TIR	1075	CMN21_18290	Planctomycetes	Rubinisphaera sp.	hypothetical protein CMN21_18290 [Rubinisphaera sp.].	GCA_002731545.1
MQP68112.1	LRR-repeats+AP-GTPase+COR+TIR*→||<-ParB<-ParA-Soj-PloopNTPase	LRR-repeats+AP-GTPase+COR+TIR	993	GE253_22605	Alphaproteobacteria	Niveispirillum sp. SYP-B3756	TIR domain-containing protein [Niveispirillum sp. SYP-B3756].	GCA_009495745.1
MQY15494.1	<-Cluster2127_2clades<-?||?→ LRR-repeats+AP-GTPase+COR*→?→ REC→ HISKIN→	LRR-repeats+AP-GTPase+COR	980	SRB5_56760	Actinobacteria	Streptomyces sp. RB5	hypothetical protein SRB5_56760 [Streptomyces sp. RB5].	GCA_009604385.1
MSP13971.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	792	EXR62_13575	Chloroflexi	Chloroflexi bacterium	hypothetical protein EXR62_13575, partial [Chloroflexi bacterium].	GCA_009692745.1
MSS71311.1	Cluster1601_2clades→ LRR-repeats+AP-GTPase+COR*→ COR+TIR→||<-Cluster1913_2clades<-?<-RPN10	LRR-repeats+AP-GTPase+COR	556	EXS64_07460	FCB group	Candidatus Latescibacteria bacterium	hypothetical protein EXS64_07460 [Candidatus Latescibacteria bacterium].	GCA_009694805.1

acc	**operon**	**architecture**	**len**	**gen.name**	**taxend**	**species**	**defline**	**gca**
NAS89011.1	POLYSACPOLYMERASE→ LRR-repeats→ LRR-repeats+AP-GTPase+COR*→||<-?<-?||?→?→||<-PIN	LRR-repeats+AP-GTPase+COR	604	C4E24_04665	Euryarchaeota	ANME-1 cluster archaeon AG-394-G21	GTP-binding protein [ANME-1 cluster archaeon AG-394-G21].	GCA_009903435.1
NAT10404.1	Cluster1536_2clades→||<-?<-?<-?||POLYSACPOLYMERASE→?→ LRR-repeats+AP-GTPase+COR→ *LRR-repeats→ LRR-repeats+AP-GTPase+COR*→?→||<-PIN	LRR-repeats+AP-GTPase+COR	688	C4E22_02460	Euryarchaeota	ANME-1 cluster archaeon AG-394-G06	GTP-binding protein [ANME-1 cluster archaeon AG-394-G06].	GCA_009903405.1
NBC32680.1	LRR-repeats+AP-GTPase+COR+TM+TM+TM+TM*→||<-?<-?||?→?→?→||<-TM+RHOMBOID	LRR-repeats+AP-GTPase+COR+TM+TM+TM+TM	806	GVY13_08395	Alphaproteobacteria	Alphaproteobacteria bacterium	GTP-binding protein, partial [Alphaproteobacteria bacterium].	GCA_009909005.1
NCP86657.1	<-XIS-HTH||HTH+HTH→||<-WLM||?→ NACHT+68TM-wHTH→ REase→?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	960	GW829_04700	unclassified Bacteria	bacterium	hypothetical protein GW829_04700, partial [bacterium].	GCA_009994085.1
NCP88511.1	REase→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	336	GW829_14210	unclassified Bacteria	bacterium	hypothetical protein GW829_14210, partial [bacterium].	GCA_009994085.1
NCP88560.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	382	GW829_14460	unclassified Bacteria	bacterium	hypothetical protein GW829_14460, partial [bacterium].	GCA_009994085.1
NCQ69077.1	CHTH→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	382	GPI97_07600	Cyanobacteria	Microcystis aeruginosa W13-16	leucine-rich repeat protein, partial [Microcystis aeruginosa W13-16].	GCA_009995625.1
NCQ78095.1	CHTH→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	359	GPI99_08005	Cyanobacteria	Microcystis aeruginosa W13-15	GTP-binding protein, partial [Microcystis aeruginosa W13-15].	GCA_009995645.1
NCQ94522.1	Ferredoxin-betagrasp→ tRNA→ tRNA→ SAM-methylase→?→||<-?<-SIG+TPM_phosphatase+TM+TM+TM||LRR-repeats+AP-GTPase+COR+TM+TM*→||<-?<-?<-?<-Pro_CA	LRR-repeats+AP-GTPase+COR+TM+TM	805	GPJ33_04160	Cyanobacteria	Microcystis aeruginosa W11-03	leucine-rich repeat protein [Microcystis aeruginosa W11-03].	GCA_009995775.1
NCR15129.1	CHTH→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	413	GPJ24_21065	Cyanobacteria	Microcystis aeruginosa SX13-11	GTP-binding protein, partial [Microcystis aeruginosa SX13-11].	GCA_009995725.1
NCR28927.1	CHTH→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	386	GPJ25_22505	Cyanobacteria	Microcystis aeruginosa LE13-04	leucine-rich repeat protein, partial [Microcystis aeruginosa LE13-04].	GCA_009995995.1
NCR34650.1	LRR-repeats+AP-GTPase+COR+TM+TM*→	LRR-repeats+AP-GTPase+COR+TM+TM	789	GPJ31_03655	Cyanobacteria	Microcystis aeruginosa S11-05	leucine-rich repeat protein [Microcystis aeruginosa S11-05].	GCA_009995785.1
NCR46978.1	CHTH→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	514	GPJ09_24595	Cyanobacteria	Microcystis aeruginosa SX13-01	leucine-rich repeat protein, partial [Microcystis aeruginosa SX13-01].	GCA_009995735.1
NCR55589.1	LRR-repeats+AP-GTPase+COR+TM+TM*→||<-?<-?<-?<-Pro_CA||?→||<-?<-tRNA<-tRNA<-Ferredoxin-betagrasp	LRR-repeats+AP-GTPase+COR+TM+TM	710	GPJ10_20085	Cyanobacteria	Microcystis aeruginosa L211-07	GTP-binding protein, partial [Microcystis aeruginosa L211-07].	GCA_009996085.1
NCR60375.1	CHTH→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	478	GPJ01_22875	Cyanobacteria	Microcystis aeruginosa LL13-06	GTP-binding protein, partial [Microcystis aeruginosa LL13-06].	GCA_009995895.1
NCR68842.1	CHTH→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	545	GPJ34_21175	Cyanobacteria	Microcystis aeruginosa LL11-07	GTP-binding protein, partial [Microcystis aeruginosa LL11-07].	GCA_009995855.1
NCR71934.1	SAM-methylase→?→||<-?<-SIG+TPM_phosphatase+TM+TM+TM||LRR-repeats+AP-GTPase+COR+TM+TM*→||<-?<-?<-?<-Pro_CA	LRR-repeats+AP-GTPase+COR+TM+TM	751	GPI93_12415	Cyanobacteria	Microcystis aeruginosa LG13-12	leucine-rich repeat protein [Microcystis aeruginosa LG13-12].	GCA_009995925.1
NCR77025.1	SIG+TM+TM+TM+TM+TM+TM+TM→||<-?||Mbetalac→ SAM-methylase→?→||<-?<-SIG+TPM_phosphatase+TM+TM+TM||LRR-repeats+AP-GTPase+COR+TM+TM*→	LRR-repeats+AP-GTPase+COR+TM+TM	897	GPI92_16105	Cyanobacteria	Microcystis aeruginosa K13-06	GTP-binding protein [Microcystis aeruginosa K13-06].	GCA_009996165.1
NCR80564.1	SIG+TM+TM+TM+TM+TM+TM+TM→||<-?||Mbetalac→ SAM-methylase→?→||<-?<-SIG+TPM_phosphatase+TM+TM+TM||LRR-repeats+AP-GTPase+COR+TM+TM*→	LRR-repeats+AP-GTPase+COR+TM+TM	805	GPI91_11595	Cyanobacteria	Microcystis aeruginosa K13-10	leucine-rich repeat protein [Microcystis aeruginosa K13-10].	GCA_009996105.1
NCR97058.1	SIG+TM+TM+TM+TM+TM+TM+TM→||<-?||Mbetalac→ SAM-methylase→?→||<-?<-SIG+TPM_phosphatase+TM+TM+TM||LRR-repeats+AP-GTPase+COR+TM+TM*→||<-?<-?<-?<-Pro_CA||?→||<-?<-tRNA<-tRNA<-Ferredoxin-betagrasp	LRR-repeats+AP-GTPase+COR+TM+TM	920	GPJ32_04180	Cyanobacteria	Microcystis aeruginosa L311-01	GTP-binding protein [Microcystis aeruginosa L311-01].	GCA_009996025.1
NCS08858.1	CHTH→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	386	GPJ07_21130	Cyanobacteria	Microcystis aeruginosa G13-07	GTP-binding protein, partial [Microcystis aeruginosa G13-07].	GCA_009996305.1
NCS11263.1	CHTH→ LRR-repeats+AP-GTPase+COR+TM+TM*→	LRR-repeats+AP-GTPase+COR+TM+TM	852	GPJ08_08960	Cyanobacteria	Microcystis aeruginosa G13-09	GTP-binding protein [Microcystis aeruginosa G13-09].	GCA_009996255.1
NCS17812.1	CHTH→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	503	GPJ02_20805	Cyanobacteria	Microcystis aeruginosa G13-12	leucine-rich repeat protein, partial [Microcystis aeruginosa G13-12].	GCA_009996205.1
NCS22942.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	353	GPJ15_26105	Cyanobacteria	Microcystis aeruginosa G11-06	GTP-binding protein, partial [Microcystis aeruginosa G11-06].	GCA_009996385.1
NCS24651.1	LRR-repeats+AP-GTPase+COR+TM+TM*→||<-?<-FGS<-?<-?||?→?→ Aminotran_1_2→	LRR-repeats+AP-GTPase+COR+TM+TM	732	GPI96_09100	Cyanobacteria	Microcystis aeruginosa BS13-02	GTP-binding protein, partial [Microcystis aeruginosa BS13-02].	GCA_009996485.1
NCS52102.1	CHTH→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	397	GPJ23_06895	Cyanobacteria	Microcystis aeruginosa G13-05	leucine-rich repeat protein, partial [Microcystis aeruginosa G13-05].	GCA_009996285.1

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NCS59859.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	339	GPJ16_25035	Cyanobacteria	Microcystis aeruginosa G11-04	GTP-binding protein, partial [Microcystis aeruginosa G11-04].	GCA_009996445.1
NCT21185.1	<-XIS-HTH||HTH+HTH→||<-WLM||?→ NACHT+68TM-wHTH→ REase→?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	956	GW781_08530	unclassified Bacteria	bacterium	hypothetical protein GW781_08530, partial [bacterium].	GCA_009994975.1
NCT65324.1	CHTH→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	434	GPJ03_21265	Cyanobacteria	Microcystis aeruginosa G13-01	leucine-rich repeat protein, partial [Microcystis aeruginosa G13-01].	GCA_009996325.1
NCY16589.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1058	EBX39_07430	Actinobacteria	Actinobacteria bacterium	hypothetical protein EBX39_07430 [Actinobacteria bacterium].	GCA_010021725.1
NEN97779.1	REC→||<-TPR-repeats||LRR-repeats+AP-GTPase+COR+DUF4404*→	LRR-repeats+AP-GTPase+COR+DUF4404	971	F6K50_20310	Cyanobacteria	Moorea sp. SIO3I7	GTPase [Moorea sp. SIO3I7].	GCA_010692375.1
NEO07696.1	SIG+TM+TM+TM+TM+TM+TM+TM→?→ ABC-ATPase→?→ ABC-ATPase→?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1373	F6K51_19885	Cyanobacteria	Moorea sp. SIO3I8	leucine-rich repeat protein [Moorea sp. SIO3I8].	GCA_010692325.1
NEO14597.1	REC→||<-TPR-repeats<-?||LRR-repeats+AP-GTPase+COR+DUF4404*→	LRR-repeats+AP-GTPase+COR+DUF4404	797	F6K46_20370	Cyanobacteria	Moorea sp. SIO3E8	GTPase [Moorea sp. SIO3E8].	GCA_010692445.1
NEO18066.1	ABC-ATPase→||<-?||ABC-ATPase→?→?→||<-?||LRR-repeats+AP-GTPase+COR*→?→||<-?<-HNH<-PSE||?→||<-Cluster5_5clades	LRR-repeats+AP-GTPase+COR	852	F6K57_01150	Cyanobacteria	Moorea sp. SIO4A5	GTPase [Moorea sp. SIO4A5].	GCA_010672005.1
NEO21732.1	REC→||<-?||REC→||<-TPR-repeats||LRR-repeats+AP-GTPase+COR+DUF4404*→	LRR-repeats+AP-GTPase+COR+DUF4404	949	F6K57_21060	Cyanobacteria	Moorea sp. SIO4A5	GTPase [Moorea sp. SIO4A5].	GCA_010672005.1
NEO28667.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	372	F6K03_17765	Cyanobacteria	Kamptonema sp. SIO4C4	GTPase, partial [Kamptonema sp. SIO4C4].	GCA_010692335.1
NEO36773.1	SIG+TM+TM+TM+TM+TM+TM+TM→ ABC-ATPase→?→ ABC-ATPase→||<-?||?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	847	F6J90_10815	Cyanobacteria	Moorea sp. SIOASIH	GTPase [Moorea sp. SIOASIH].	GCA_010671925.1
NEO37599.1	REC→||<-?<-?||REC→||<-TPR-repeats<-?||?→ LRR-repeats+AP-GTPase+COR+DUF4404*→ PSE→||<-?<-PSE||?→?→?→||<-?||TM→	LRR-repeats+AP-GTPase+COR+DUF4404	1099	F6J90_15180	Cyanobacteria	Moorea sp. SIOASIH	leucine-rich repeat protein [Moorea sp. SIOASIH].	GCA_010671925.1
NEO43843.1	SbcC→?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1256	F6K55_06775	Cyanobacteria	Moorea sp. SIO4A3	leucine-rich repeat protein [Moorea sp. SIO4A3].	GCA_010672045.1
NEO48162.1	REC→||<-TPR-repeats||LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	616	F6K55_30210	Cyanobacteria	Moorea sp. SIO4A3	leucine-rich repeat protein, partial [Moorea sp. SIO4A3].	GCA_010672045.1
NEO55671.1	LRR-repeats→?→ AP-GTPase*→||<-?<-SIG+Trypsin+PDZ	AP-GTPase	113	F6K54_22940	Cyanobacteria	Okeania sp. SIO3B5	hypothetical protein F6K54_22940 [Okeania sp. SIO3B5].	GCA_010692555.1
NEO56464.1	LRR-repeats+AP-GTPase+COR*→||<-RelE-ParE	LRR-repeats+AP-GTPase+COR	856	F6K54_27310	Cyanobacteria	Okeania sp. SIO3B5	GTPase [Okeania sp. SIO3B5].	GCA_010692555.1
NEO57234.1	<-RADICAL-SAM||PSE→ REC→?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	472	F6K54_31710	Cyanobacteria	Okeania sp. SIO3B5	GTPase, partial [Okeania sp. SIO3B5].	GCA_010692555.1
NEO68320.1	SIG+PBPI→?→ SIG+TM+TM+TM+TM+TM+TM+TM→?→ ABC-ATPase→ ABC-ATPase→||<-?||LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	884	F6K52_02085	Cyanobacteria	Moorea sp. SIO3H5	leucine-rich repeat protein [Moorea sp. SIO3H5].	GCA_010692395.1
NEO73423.1	REC→||<-TPR-repeats<-?||LRR-repeats+AP-GTPase+COR+DUF4404*→	LRR-repeats+AP-GTPase+COR+DUF4404	933	F6K52_29165	Cyanobacteria	Moorea sp. SIO3H5	GTPase [Moorea sp. SIO3H5].	GCA_010692395.1
NEO79069.1	REC→||<-TPR-repeats||LRR-repeats+AP-GTPase+COR+DUF4404*→	LRR-repeats+AP-GTPase+COR+DUF4404	929	F6J99_23600	Cyanobacteria	Moorea sp. SIO4G3	GTPase [Moorea sp. SIO4G3].	GCA_010692305.1
NEO83336.1	Cluster5_5clades→?→ PSE→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1006	F6J87_03595	Cyanobacteria	Spirulina sp. SIO3F2	leucine-rich repeat protein [Spirulina sp. SIO3F2].	GCA_010672165.1
NEO85545.1	MNS-STAND+CR-REase3→||<-?<-?||?→||<-REC<-REC||HISKIN→ LRR-repeats+AP-GTPase+COR*→||<-HISKIN	LRR-repeats+AP-GTPase+COR	1127	F6J87_15045	Cyanobacteria	Spirulina sp. SIO3F2	GTPase [Spirulina sp. SIO3F2].	GCA_010672165.1
NEO86840.1	TM+TM+TM+TM+TM+TM+TM+TM→?→||<-?<-Pentapeptide-repeats||?→ LRR-repeats+AP-GTPase+COR+DUF4404*→	LRR-repeats+AP-GTPase+COR+DUF4404	1131	F6J87_21660	Cyanobacteria	Spirulina sp. SIO3F2	GTP-binding protein [Spirulina sp. SIO3F2].	GCA_010672165.1
NEO88027.1	LRR-repeats→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	800	F6J87_27790	Cyanobacteria	Spirulina sp. SIO3F2	hypothetical protein F6J87_27790 [Spirulina sp. SIO3F2].	GCA_010672165.1
NEO88064.1	Cluster1048_2clades→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1166	F6J87_27980	Cyanobacteria	Spirulina sp. SIO3F2	GTPase [Spirulina sp. SIO3F2].	GCA_010672165.1
NEO88189.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1134	F6J87_28620	Cyanobacteria	Spirulina sp. SIO3F2	hypothetical protein F6J87_28620 [Spirulina sp. SIO3F2].	GCA_010672165.1
NEP02262.1	LRR-repeats+AP-GTPase+COR*→ ParA-Soj-PloopNTPase→	LRR-repeats+AP-GTPase+COR	814	F6K58_27120	Cyanobacteria	Symploca sp. SIO2E9	leucine-rich repeat protein [Symploca sp. SIO2E9].	GCA_010692645.1
NEP15532.1	LRR-repeats+AP-GTPase+COR+TIR*→?→||<-?||?→||<-?<-?<-?||ABhydrolase→	LRR-repeats+AP-GTPase+COR+TIR	1041	F6J97_01370	Cyanobacteria	Leptolyngbya sp. SIO4C1	TIR domain-containing protein [Leptolyngbya sp. SIO4C1].	GCA_010671975.1

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
NEP17061.1	TM+TM+TM+TM+TM→ LRR-repeats+AP-GTPase+COR+DUF4404*→||<-SIG+TM+TM	LRR-repeats+AP-GTPase+COR+DUF4404	1026	F6J97_09150	Cyanobacteria	Leptolyngbya sp. SIO4C1	GTP-binding protein [Leptolyngbya sp. SIO4C1].	GCA_010671975.1
NEP23180.1	SIG+TM+TM+TM+TM+TM+TM+TM→?→ ABC-ATPase→ ABC-ATPase→||<-?||?→||<-?||LRR-repeats+AP-GTPase+COR*→?→||<-?<-HNH<-PSE||?→||<-Cluster5_5clades	LRR-repeats+AP-GTPase+COR	892	F6K49_14560	Cyanobacteria	Moorea sp. SIO3I6	GTPase [Moorea sp. SIO3I6].	GCA_010672095.1
NEP27050.1	LRR-repeats+AP-GTPase+COR+DUF4404*→	LRR-repeats+AP-GTPase+COR+DUF4404	909	F6K49_35465	Cyanobacteria	Moorea sp. SIO3I6	GTPase [Moorea sp. SIO3I6].	GCA_010672095.1
NEP34707.1	LRR-repeats+AP-GTPase+COR+DUF4404*→	LRR-repeats+AP-GTPase+COR+DUF4404	924	F6K38_25730	Cyanobacteria	Moorea sp. SIO3B2	GTPase, partial [Moorea sp. SIO3B2].	GCA_010692525.1
NEP80618.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	891	F6K39_22060	Cyanobacteria	Okeania sp. SIO3B3	GTPase [Okeania sp. SIO3B3].	GCA_010692535.1
NEP81305.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	790	F6K39_25960	Cyanobacteria	Okeania sp. SIO3B3	GTPase [Okeania sp. SIO3B3].	GCA_010692535.1
NEP82037.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	664	F6K39_30180	Cyanobacteria	Okeania sp. SIO3B3	hypothetical protein F6K39_30180 [Okeania sp. SIO3B3].	GCA_010692535.1
NEP82994.1	LRR-repeats+AP-GTPase*→	LRR-repeats+AP-GTPase	713	F6K39_35565	Cyanobacteria	Okeania sp. SIO3B3	leucine-rich repeat protein [Okeania sp. SIO3B3].	GCA_010692535.1
NEP88726.1	<-HhH-RADC+JAB<-?||LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	800	F6K18_18835	Cyanobacteria	Okeania sp. SIO2C2	GTPase [Okeania sp. SIO2C2].	GCA_010692625.1
NEQ25590.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	329	F6K28_42320	Cyanobacteria	Microcoleus sp. SIO2G3	hypothetical protein F6K28_42320, partial [Microcoleus sp. SIO2G3].	GCA_010672365.1
NEQ30222.1	SF2-DUF3427A→||<-PSE||?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	425	F6K04_04355	Cyanobacteria	Leptolyngbya sp. SIO4C5	GTP-binding protein, partial [Leptolyngbya sp. SIO4C5].	GCA_010671965.1
NEQ30763.1	LRR-repeats+AP-GTPase+COR+DrHyd*→||<-SAM-methylase	LRR-repeats+AP-GTPase+COR+DrHyd	1168	F6K04_07140	Cyanobacteria	Leptolyngbya sp. SIO4C5	hypothetical protein F6K04_07140 [Leptolyngbya sp. SIO4C5].	GCA_010671965.1
NEQ30823.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1087	F6K04_07455	Cyanobacteria	Leptolyngbya sp. SIO4C5	hypothetical protein F6K04_07455 [Leptolyngbya sp. SIO4C5].	GCA_010671965.1
NEQ33180.1	LRR-repeats+AP-GTPase+COR+TIR*→||<-Cluster2398_2clades	LRR-repeats+AP-GTPase+COR+TIR	974	F6K04_19645	Cyanobacteria	Leptolyngbya sp. SIO4C5	TIR domain-containing protein [Leptolyngbya sp. SIO4C5].	GCA_010671965.1
NEQ38623.1	LRR-repeats→||<-?||?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	778	F6K40_21075	Cyanobacteria	Okeania sp. SIO3I5	GTPase [Okeania sp. SIO3I5].	GCA_010672085.1
NEQ39708.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	641	F6K40_27040	Cyanobacteria	Okeania sp. SIO3I5	hypothetical protein F6K40_27040 [Okeania sp. SIO3I5].	GCA_010672085.1
NEQ41322.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	923	F6K40_36055	Cyanobacteria	Okeania sp. SIO3I5	GTPase [Okeania sp. SIO3I5].	GCA_010672085.1
NEQ51480.1	LRR-repeats+AP-GTPase+COR+DrHyd*→||<-?||?→||<-SF2-DUF3427A	LRR-repeats+AP-GTPase+COR+DrHyd	841	F6K11_15280	Cyanobacteria	Leptolyngbya sp. SIO3F4	hypothetical protein F6K11_15280, partial [Leptolyngbya sp. SIO3F4].	GCA_010672145.1
NEQ51880.1	LRR-repeats+AP-GTPase+COR+TM+TM*→	LRR-repeats+AP-GTPase+COR+TM+TM	1022	F6K11_17360	Cyanobacteria	Leptolyngbya sp. SIO3F4	GTP-binding protein [Leptolyngbya sp. SIO3F4].	GCA_010672145.1
NEQ52141.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	825	F6K11_18705	Cyanobacteria	Leptolyngbya sp. SIO3F4	GTP-binding protein, partial [Leptolyngbya sp. SIO3F4].	GCA_010672145.1
NEQ52634.1	LRR-repeats+AP-GTPase+COR+TIR*→ LRR-repeats→	LRR-repeats+AP-GTPase+COR+TIR	827	F6K11_21260	Cyanobacteria	Leptolyngbya sp. SIO3F4	TIR domain-containing protein, partial [Leptolyngbya sp. SIO3F4].	GCA_010672145.1
NEQ54121.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	826	F6K11_28985	Cyanobacteria	Leptolyngbya sp. SIO3F4	TIR domain-containing protein, partial [Leptolyngbya sp. SIO3F4].	GCA_010672145.1
NEQ54707.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	547	F6K11_32030	Cyanobacteria	Leptolyngbya sp. SIO3F4	GTP-binding protein, partial [Leptolyngbya sp. SIO3F4].	GCA_010672145.1
NEQ55863.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	335	F6K11_38165	Cyanobacteria	Leptolyngbya sp. SIO3F4	serine/threonine protein kinase, partial [Leptolyngbya sp. SIO3F4].	GCA_010672145.1
NEQ58292.1	SIG+TM+TM+TM+TM+TM+TM+TM→?→ ABC-ATPase→ ABC-ATPase→?→||<-?||LRR-repeats+AP-GTPase+COR*→?→||<-?<-HNH<-PSE||?→||<-Cluster5_5clades	LRR-repeats+AP-GTPase+COR	849	F6K53_13090	Cyanobacteria	Moorea sp. SIO4A1	GTPase [Moorea sp. SIO4A1].	GCA_010672065.1
NEQ85055.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	554	F6K26_34455	Cyanobacteria	Moorea sp. SIO2I5	GTPase, partial [Moorea sp. SIO2I5].	GCA_010672285.1
NER03418.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	738	F6K17_12770	Cyanobacteria	Okeania sp. SIO3C4	GTPase, partial [Okeania sp. SIO3C4].	GCA_010672215.1
NER25299.1	TM+TM+TM+TM+TM+TM→||<-?||?→ Pkinase→?→ LRR-repeats+AP-GTPase+COR*→ Cluster5_5clades→	LRR-repeats+AP-GTPase+COR	1031	F6J96_32295	Cyanobacteria	Symploca sp. SIO1C2	hypothetical protein F6J96_32295 [Symploca sp. SIO1C2].	GCA_010672925.1

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
NER33110.1	SIG+TM+TM+TM+TM+TM+TM+TM→?→||<-?||PSE→||<-?||?→ LRR-repeats+AP-GTPase+COR*→?→?→?→ ABC_membrane+ABC_tran→||<-NUDIX	LRR-repeats+AP-GTPase+COR	1105	F6J93_03360	Cyanobacteria	Oscillatoria sp. SIO1A7	hypothetical protein F6J93_03360 [Oscillatoria sp. SIO1A7].	GCA_010672965.1
NER35832.1	LRR-repeats+AP-GTPase+COR*→?→ PIN→	LRR-repeats+AP-GTPase+COR	1467	F6J93_17900	Cyanobacteria	Oscillatoria sp. SIO1A7	hypothetical protein F6J93_17900 [Oscillatoria sp. SIO1A7].	GCA_010672965.1
NER38074.1	<-SIG+TM+TM+TM+TM+TM<-ABC-ATPase||?→?→||<-?||?→?→ LRR-repeats+AP-GTPase+COR*→?→?→?→?→ ABC-ATPase→	LRR-repeats+AP-GTPase+COR	1117	F6J93_29640	Cyanobacteria	Oscillatoria sp. SIO1A7	hypothetical protein F6J93_29640 [Oscillatoria sp. SIO1A7].	GCA_010672965.1
NER40156.1	LRR-repeats→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	515	F6J93_40580	Cyanobacteria	Oscillatoria sp. SIO1A7	hypothetical protein F6J93_40580 [Oscillatoria sp. SIO1A7].	GCA_010672965.1
NER70803.1	SIG+DM13→ HISKIN→||<-?<-?<-?||?→ Cluster2343_2clades→ LRR-repeats+AP-GTPase+COR*→||<-Cluster1740_2clades<-?<-?<-?<-?<-Cluster1476_2clades	LRR-repeats+AP-GTPase+COR	1150	F6J95_01375	-	Leptolyngbya sp. SIO1E4	GTPase [Leptolyngbya sp. SIO1E4].	-
NER71871.1	BACTERIALFRINGE+TM+TM→?→?→ SIG+TM+TM+TM+TM+TM+TM+TM→||<-?<-?<-?||LRR-repeats+AP-GTPase+COR+DUF4404*→||<-?<-TM+TM||NACHT→||<-?<-Cluster5_5clades<-Aminotran_1_2	LRR-repeats+AP-GTPase+COR+DUF4404	1283	F6J95_06845	-	Leptolyngbya sp. SIO1E4	GTP-binding protein [Leptolyngbya sp. SIO1E4].	-
NER73482.1	Cluster2482_2clades→?→||<-?||GNTR-HTH→?→ LRR-repeats+AP-GTPase+COR*→ Cluster1404_2clades→?→ Cluster2050_2clades→	LRR-repeats+AP-GTPase+COR	891	F6J95_15105	-	Leptolyngbya sp. SIO1E4	GTPase [Leptolyngbya sp. SIO1E4].	-
NER74435.1	LRR-repeats+AP-GTPase+COR+TIR*→ DSBH→?→?→?→||<-?<-?<-ACT	LRR-repeats+AP-GTPase+COR+TIR	1183	F6J95_19985	-	Leptolyngbya sp. SIO1E4	TIR domain-containing protein [Leptolyngbya sp. SIO1E4].	-
NER74649.1	Cluster2260_2clades→?→ LRR-repeats+AP-GTPase+COR+DrHyd*→ SIG+FAD-NAD-dep-oxidoreductase→||<-Cluster850_2clades||PSE→ SIG+TM+TM+TM+TM→	LRR-repeats+AP-GTPase+COR+DrHyd	1173	F6J95_21075	-	Leptolyngbya sp. SIO1E4	hypothetical protein F6J95_21075 [Leptolyngbya sp. SIO1E4].	-
NER78030.1	Aminotran_1_2→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	904	F6K42_00285	Cyanobacteria	Leptolyngbya sp. SIO1D8	GTP-binding protein [Leptolyngbya sp. SIO1D8].	GCA_010672895.1
NER81647.1	LRR-repeats→ LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	836	F6K42_19200	Cyanobacteria	Leptolyngbya sp. SIO1D8	TIR domain-containing protein [Leptolyngbya sp. SIO1D8].	GCA_010672895.1
NER83464.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	785	F6K42_28715	Cyanobacteria	Leptolyngbya sp. SIO1D8	TIR domain-containing protein [Leptolyngbya sp. SIO1D8].	GCA_010672895.1
NER88741.1	ABC-ATPase→||<-?||ABC-ATPase→?→?→||<-?<-?||LRR-repeats+AP-GTPase+COR*→?→||<-?<-?||?→ PSE→?→||<-Cluster5_5clades	LRR-repeats+AP-GTPase+COR	856	F6K64_17615	Cyanobacteria	Moorea sp. SIO3A2	leucine-rich repeat protein [Moorea sp. SIO3A2].	GCA_010672265.1
NER98009.1	TM+TM+TM+TM+TM+TM→||<-?||?→ Pkinase→?→?→ LRR-repeats+AP-GTPase+COR*→ COR→	LRR-repeats+AP-GTPase+COR	417	F6J86_29885	Cyanobacteria	Symploca sp. SIO1B1	hypothetical protein F6J86_29885 [Symploca sp. SIO1B1].	GCA_010672945.1
NES02436.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	964	F6K22_06035	Cyanobacteria	Okeania sp. SIO2F4	leucine-rich repeat protein [Okeania sp. SIO2F4].	GCA_010672385.1
NES08071.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	502	F6K22_38010	Cyanobacteria	Okeania sp. SIO2F4	leucine-rich repeat protein, partial [Okeania sp. SIO2F4].	GCA_010672385.1
NES23982.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	230	F6K41_34995	Cyanobacteria	Caldora sp. SIO3E6	hypothetical protein F6K41_34995, partial [Caldora sp. SIO3E6].	GCA_010672185.1
NES70611.1	LRR-repeats→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	400	F6K24_38075	Cyanobacteria	Okeania sp. SIO2D1	GTPase, partial [Okeania sp. SIO2D1].	GCA_010672395.1
NES87329.1	LRR-repeats+AP-GTPase+COR+DUF4404*→	LRR-repeats+AP-GTPase+COR+DUF4404	855	F6K10_41780	Cyanobacteria	Moorea sp. SIO2B7	GTPase, partial [Moorea sp. SIO2B7].	GCA_010672555.1
NES99177.1	<-NUDIX||?→?→ LRR-repeats+AP-GTPase+COR+DUF4404*→ PSE→?→?→?→||<-ABC-ATPase	LRR-repeats+AP-GTPase+COR+DUF4404	1012	F6K61_01110	Cyanobacteria	Sphaerospermopsis sp. SIO1G1	GTP-binding protein [Sphaerospermopsis sp. SIO1G1].	GCA_010672785.1
NET13009.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	307	F6K08_09185	Cyanobacteria	Okeania sp. SIO1H6	GTPase, partial [Okeania sp. SIO1H6].	GCA_010672645.1
NET29408.1	LRR-repeats+AP-GTPase+COR*→||<-?<-NACHT+68TM-wHTH||?→||<-?<-PSE<-TPR-repeats<-HISKIN	LRR-repeats+AP-GTPase+COR	1247	F6K01_30010	Cyanobacteria	Okeania sp. SIO1I7	leucine-rich repeat protein [Okeania sp. SIO1I7].	GCA_010672585.1
NET38765.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	802	F6K19_43415	Cyanobacteria	Cyanothece sp. SIO1E1	GTPase [Cyanothece sp. SIO1E1].	GCA_010672835.1
NET39396.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	803	F6K19_46760	Cyanobacteria	Cyanothece sp. SIO1E1	TIR domain-containing protein, partial [Cyanothece sp. SIO1E1].	GCA_010672835.1
NET43146.1	<-RADICAL-SAM||?→ REC→?→||<-PSE||LRR-repeats+AP-GTPase+COR*→||<-?<-NACHT+68TM-wHTH	LRR-repeats+AP-GTPase+COR	927	F6K15_15105	Cyanobacteria	Okeania sp. SIO2B3	GTPase [Okeania sp. SIO2B3].	GCA_010672525.1
NET44979.1	LRR-repeats+AP-GTPase+COR*→||<-?<-PSE<-?<-?||?→?→||<-PSE<-PSE<-PSE<-Cluster5_5clades<-ABC_membrane+ABC_tran	LRR-repeats+AP-GTPase+COR	1085	F6K15_25170	Cyanobacteria	Okeania sp. SIO2B3	GTPase [Okeania sp. SIO2B3].	GCA_010672525.1
NET45691.1	<-HISKIN||?→?→ LRR-repeats+AP-GTPase+COR*→||<-PSE<-?<-?<-NUDIX<-?||?→ TPR-repeats→	LRR-repeats+AP-GTPase+COR	856	F6K15_29075	Cyanobacteria	Okeania sp. SIO2B3	GTPase [Okeania sp. SIO2B3].	GCA_010672525.1
NET64212.1	SIG+TM+TM+TM+TM+TM+TM+TM→ ABC-ATPase→||<-?||ABC-ATPase→?→?→||<-?||LRR-repeats+AP-GTPase+COR*→?→||<-?<-?||?→||<-Cluster5_5clades	LRR-repeats+AP-GTPase+COR	914	F6K63_07330	Cyanobacteria	Moorea sp. SIO1G6	leucine-rich repeat protein [Moorea sp. SIO1G6].	GCA_010672795.1

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NET68629.1	REC→||<-TPR-repeats<-?||LRR-repeats+AP-GTPase+COR+DUF4404*→	LRR-repeats+AP-GTPase+COR+DUF4404	938	F6K63_31235	Cyanobacteria	Moorea sp. SIO1G6	GTPase [Moorea sp. SIO1G6].	GCA_010672795.1
NET73474.1	LRR-repeats+AP-GTPase+COR+DUF4404*→	LRR-repeats+AP-GTPase+COR+DUF4404	821	F6K62_21805	Cyanobacteria	Sphaerospermopsis sp. SIO1G2	GTP-binding protein, partial [Sphaerospermopsis sp. SIO1G2].	GCA_010672725.1
NET83099.1	REC→||<-?||REC→||<-TPR-repeats||LRR-repeats+AP-GTPase+COR+DUF4404*→	LRR-repeats+AP-GTPase+COR+DUF4404	946	F6J94_14560	Cyanobacteria	Moorea sp. SIO1F2	GTPase [Moorea sp. SIO1F2].	GCA_010672755.1
NEZ62303.1	PIN→ LRR-repeats→ LRR-repeats+AP-GTPase+COR*→?→ COR+TIR→ SIG+Trypsin+PDZ→	LRR-repeats+AP-GTPase+COR	318	D0962_05850	Cyanobacteria	Leptolyngbyaceae cyanobacterium CCMR0082	hypothetical protein D0962_05850 [Leptolyngbyaceae cyanobacterium CCMR0082].	GCA_011009535.1
NIM11849.1	S1COLD→||<-?<-?<-?||?→ Cluster54_3clades→ Cluster1093_2clades→ LRR-repeats+AP-GTPase+COR*→||<-?<-Cluster2413_2clades	LRR-repeats+AP-GTPase+COR	882	GTO81_07705	Bacteria	Candidatus Aminicenantes bacterium	GTP-binding protein [Candidatus Aminicenantes bacterium].	GCA_011771225.1
NIM14508.1	Aminotran_1_2→||<-?<-Cluster1540_2clades<-?||?→?→ LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	784	GTO81_21225	Bacteria	Candidatus Aminicenantes bacterium	TIR domain-containing protein [Candidatus Aminicenantes bacterium].	GCA_011771225.1
NIM17826.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	952	GTO81_38090	Bacteria	Candidatus Aminicenantes bacterium	hypothetical protein GTO81_38090 [Candidatus Aminicenantes bacterium].	GCA_011771225.1
NIN06216.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	781	GTO43_07600	Armatimonadetes	Armatimonadetes bacterium	GTPase, partial [Armatimonadetes bacterium].	GCA_011771945.1
NIP25303.1	<-SIG+TIMbarrel||LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	868	GWO38_16175	Planctomycetes	Phycisphaerae bacterium	TIR domain-containing protein [Phycisphaerae bacterium].	GCA_011774285.1
NIP41904.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	457	GWO28_04170	FCB group	candidate division Zixibacteria bacterium	GTPase, partial [candidate division Zixibacteria bacterium].	GCA_011774485.1
NIR09229.1	LRR-repeats+AP-GTPase*→ COR→	LRR-repeats+AP-GTPase	251	GTN82_27750	Bacteria	Candidatus Aminicenantes bacterium	GTP-binding protein, partial [Candidatus Aminicenantes bacterium].	GCA_011773265.1
NIU83786.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	888	GWN64_10000	Asgard group	Candidatus Thorarchaeota archaeon	GTPase [Candidatus Thorarchaeota archaeon].	GCA_011775775.1
NJD78109.1	SAM-methylase→||<-?||?→?→||<-?||?→?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	844	FIB08_13625	Euryarchaeota	Candidatus Methanoperedens sp.	GTP-binding protein [Candidatus Methanoperedens sp.].	GCA_012026835.1
NJK31611.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	784	HC927_03900	Deltaproteobacteria	Deltaproteobacteria bacterium	hypothetical protein HC927_03900 [Deltaproteobacteria bacterium].	GCA_012031025.1
NJK68783.1	LRR-repeats+AP-GTPase+COR*→?→?→?→?→||<-Pentapeptide-repeats	LRR-repeats+AP-GTPase+COR	637	HC941_21705	Cyanobacteria	Microcoleus sp. SU_5_3	GTP-binding protein, partial [Microcoleus sp. SU_5_3].	GCA_012030835.1
NJK99654.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	665	HC910_03475	Cyanobacteria	Spirulinaceae cyanobacterium SM2_1_0	GTP-binding protein [Spirulinaceae cyanobacterium SM2_1_0].	GCA_012031265.1
NJL39962.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	814	HC899_26815	Cyanobacteria	Leptolyngbyaceae cyanobacterium SM1_4_3	GTP-binding protein [Leptolyngbyaceae cyanobacterium SM1_4_3].	GCA_012031415.1
NJL55090.1	LRR-repeats+AP-GTPase+COR+TIR*→||<-REase-4||?→ Cluster5_5clades→?→||<-Cluster2398_2clades	LRR-repeats+AP-GTPase+COR+TIR	879	HC928_07795	unclassified Bacteria	bacterium	TIR domain-containing protein [bacterium].	GCA_012031555.1
NJL55819.1	Cluster1137_2clades→?→ LRR-repeats+AP-GTPase+COR*→ PSE→?→||<-Cluster1102_3clades	LRR-repeats+AP-GTPase+COR	671	HC928_11965	unclassified Bacteria	bacterium	GTP-binding protein [bacterium].	GCA_012031555.1
NJL58018.1	LRR-repeats+AP-GTPase+COR*→ COR→	LRR-repeats+AP-GTPase+COR	365	HC928_25050	unclassified Bacteria	bacterium	hypothetical protein HC928_25050, partial [bacterium].	GCA_012031555.1
NJL60049.1	LRR-repeats+AP-GTPase+COR*→ COR+TIR→	LRR-repeats+AP-GTPase+COR	389	HC887_10835	Deltaproteobacteria	Desulfobacteraceae bacterium	hypothetical protein HC887_10835 [Desulfobacteraceae bacterium].	GCA_012031825.1
NJL77569.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	408	HC892_23555	Bacteroidetes	Saprospiraceae bacterium	hypothetical protein HC892_23555, partial [Saprospiraceae bacterium].	GCA_012031785.1
NJL83760.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	688	HC890_14000	Chloroflexi	Chloroflexaceae bacterium	GTP-binding protein [Chloroflexaceae bacterium].	GCA_012031815.1

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NJL90622.1	<-RelE-ParE<-?||LRR-repeats+AP-GTPase+COR*→?→ PSE→?→ PSE→ RNA-Helicase→	LRR-repeats+AP-GTPase+COR	1140	HC916_13170	Cyanobacteria	Coleofasciculaceae cyanobacterium SM2_1_6	GTP-binding protein [Coleofasciculaceae cyanobacterium SM2_1_6].	GCA_012031635.1
NJL91916.1	LRR-repeats+AP-GTPase+COR*→?→ HNH→	LRR-repeats+AP-GTPase+COR	640	HC916_20640	Cyanobacteria	Coleofasciculaceae cyanobacterium SM2_1_6	GTPase, partial [Coleofasciculaceae cyanobacterium SM2_1_6].	GCA_012031635.1
NJM60379.1	<-SIG+TM+TM+TM<-?||TPR-repeats→||<-?<-Cluster5_5clades||?→?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	729	HC849_09565	Cyanobacteria	Oscillatoriales cyanobacterium RU_3_3	hypothetical protein HC849_09565, partial [Oscillatoriales cyanobacterium RU_3_3].	GCA_012032195.1
NJM78344.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	500	HC852_24405	Cyanobacteria	Acaryochloridaceae cyanobacterium RU_4_10	hypothetical protein HC852_24405 [Acaryochloridaceae cyanobacterium RU_4_10].	GCA_012032135.1
NJM97967.1	LRR-repeats→ LRR-repeats+AP-GTPase+COR*→ AP-GTPase+COR+TM+TM→	LRR-repeats+AP-GTPase+COR	278	HC800_13155	Cyanobacteria	Phormidesmis sp. RL_2_1	hypothetical protein HC800_13155 [Phormidesmis sp. RL_2_1].	GCA_012033015.1
NJN20692.1	LRR-repeats+AP-GTPase+COR*→ TIR→||<-Cluster5_5clades<-Pentapeptide||REC→	LRR-repeats+AP-GTPase+COR	276	HC812_05240	Cyanobacteria	Leptolyngbya sp. RL_3_1	hypothetical protein HC812_05240, partial [Leptolyngbya sp. RL_3_1].	GCA_012032425.1
NJN57594.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1087	HC879_08885	Cyanobacteria	Leptolyngbyaceae cyanobacterium SL_5_9	TIR domain-containing protein [Leptolyngbyaceae cyanobacterium SL_5_9].	GCA_012032565.1
NJN63246.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	747	HC795_18555	Cyanobacteria	Coleofasciculaceae cyanobacterium RL_1_1	hypothetical protein HC795_18555, partial [Coleofasciculaceae cyanobacterium RL_1_1].	GCA_012033105.1
NJN72933.1	LRR-repeats+AP-GTPase+COR+DUF4404*→||<-?||?→ SIG+Classical-AAA→	LRR-repeats+AP-GTPase+COR+DUF4404	832	HC799_09060	Cyanobacteria	Limnothrix sp. RL_2_0	GTP-binding protein [Limnothrix sp. RL_2_0].	GCA_012033055.1
NJN75229.1	LRR-repeats+AP-GTPase→ AP-GTPase*→?→ COR+TM+TM+TM→	AP-GTPase	180	HC796_01955	Cyanobacteria	Synechococcaceae cyanobacterium RL_1_2	hypothetical protein HC796_01955 [Synechococcaceae cyanobacterium RL_1_2].	GCA_012033095.1
NJN88810.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1016	HC881_24165	Cyanobacteria	Leptolyngbyaceae cyanobacterium SL_7_1	GTP-binding protein [Leptolyngbyaceae cyanobacterium SL_7_1].	GCA_012032525.1
NJN89941.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	814	HC878_05910	Cyanobacteria	Leptolyngbyaceae cyanobacterium SL_5_14	GTP-binding protein [Leptolyngbyaceae cyanobacterium SL_5_14].	GCA_012032515.1
NJN96139.1	Cluster1841_2clades→?→ LRR-repeats→ LRR-repeats+AP-GTPase+COR*→ Cluster2316_2clades→ Cluster2224_2clades→?→ Cluster1087_2clades→||<-?<-?<-ABC-ATPase	LRR-repeats+AP-GTPase+COR	573	HC875_19545	Chloroflexi	Anaerolineales bacterium	GTP-binding protein [Anaerolineales bacterium].	GCA_012032575.1
NJO03971.1	LRR-repeats+AP-GTPase+COR+EAD7*→	LRR-repeats+AP-GTPase+COR+EAD7	814	HC880_21890	Bacteroidetes	Bacteroidia bacterium	hypothetical protein HC880_21890 [Bacteroidia bacterium].	GCA_012033155.1
NJO04035.1	LRR-repeats+AP-GTPase+COR+EAD7*→	LRR-repeats+AP-GTPase+COR+EAD7	843	HC880_22270	Bacteroidetes	Bacteroidia bacterium	hypothetical protein HC880_22270 [Bacteroidia bacterium].	GCA_012033155.1
NJO50334.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	510	HC840_13875	Cyanobacteria	Leptolyngbyaceae cyanobacterium RM2_2_4	GTP-binding protein, partial [Leptolyngbyaceae cyanobacterium RM2_2_4].	GCA_012033305.1
NJP08786.1	<-Cluster5_5clades||?→?→?→?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	841	HC866_04300	Cyanobacteria	Leptolyngbyaceae cyanobacterium RU_5_1	GTPase [Leptolyngbyaceae cyanobacterium RU_5_1].	GCA_012034055.1
NJR23767.1	GTPase-AIG→?→?→ LRR-repeats+AP-GTPase+COR+DUF4404*→	LRR-repeats+AP-GTPase+COR+DUF4404	1061	HC786_17240	Cyanobacteria	Richelia sp. CSU_2_1	GTP-binding protein [Richelia sp. CSU_2_1].	GCA_012034575.1
NJR25667.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	856	HC786_27780	Cyanobacteria	Richelia sp. CSU_2_1	hypothetical protein HC786_27780, partial [Richelia sp. CSU_2_1].	GCA_012034575.1
NJR41095.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	677	HC781_22475	Cyanobacteria	Leptolyngbyaceae cyanobacterium CSU_1_4	GTP-binding protein [Leptolyngbyaceae cyanobacterium CSU_1_4].	GCA_012034615.1
NJR68835.1	<-SIGMA-HTH<-?<-?<-?||?→ LRR-repeats+AP-GTPase+COR+TCAD1*→?→||<-?<-?<-?||?→||<-TPR-repeats	LRR-repeats+AP-GTPase+COR+TCAD1	892	HC771_09325	Cyanobacteria	Synechococcales cyanobacterium CRU_2_2	GTPase [Synechococcales cyanobacterium CRU_2_2].	GCA_012034805.1

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NJS09810.1	GTPase-AIG→?→?→||<-?<-?||LRR-repeats+AP-GTPase+COR*→?→?→?→?→||<-Pentapeptide-repeats	LRR-repeats+AP-GTPase+COR	761	HC789_05185	Cyanobacteria	Microcoleus sp. CSU_2_2	GTP-binding protein [Microcoleus sp. CSU_2_2].	GCA_012035135.1
NKC15125.1	LRR-repeats+AP-GTPase+COR+DrHyd*→	LRR-repeats+AP-GTPase+COR+DrHyd	1164	GKR94_23910	Gammaproteobacteria	Gammaproteobacteria bacterium	hypothetical protein GKR94_23910 [Gammaproteobacteria bacterium].	GCA_012103455.1
NKQ34928.1	RelE-ParE→?→?→ PSE→ LRR-repeats+AP-GTPase+COR+EAD7*→	LRR-repeats+AP-GTPase+COR+EAD7	553	HF973_04850	Chloroflexi	Chloroflexi bacterium	hypothetical protein HF973_04850 [Chloroflexi bacterium].	GCA_012329075.1
NLT19133.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	709	GXY10_07015	Firmicutes	Clostridiales bacterium	GTP-binding protein, partial [Clostridiales bacterium].	GCA_012718845.1
NMF86259.1	RelE→ CHTH→?→||<-?<-?<-?<-?||LRR-repeats+AP-GTPase+COR+TIR*→?→||<-?<-?||?→?→||<-?<-RelE-ParE	LRR-repeats+AP-GTPase+COR+TIR	1176	E1H13_23515	Cyanobacteria	Nodosilinea sp. P-1105	TIR domain-containing protein [Nodosilinea sp. P-1105].	GCA_012911975.1
NND77029.1	LRR-repeats+AP-GTPase+COR*→||<-?<-?<-?<-?<-SIG+TM+TM+TM+TM	LRR-repeats+AP-GTPase+COR	842	HKN39_02455	Bacteroidetes	Flavobacteriales bacterium	hypothetical protein HKN39_02455 [Flavobacteriales bacterium].	GCA_013002285.1
NOG45111.1	MORC→?→ LRR-repeats→ LRR-repeats+AP-GTPase+COR*→?→||<-?<-?<-BetaPropeller+BetaPropeller	LRR-repeats+AP-GTPase+COR	652	HND50_07765	Calditrichaeota	Calditrichaeota bacterium	hypothetical protein HND50_07765 [Calditrichaeota bacterium].	GCA_013112635.1
NOH03519.1	DAGKIN→ Cluster1917_2clades→?→||<-?<-?||LRR-repeats→ PSE→ LRR-repeats+AP-GTPase+COR*→?→||<-PSE||?→||<-?<-GTPase-AIG||Thioredoxin→	LRR-repeats+AP-GTPase+COR	345	HND47_16930	Chloroflexi	Chloroflexi bacterium	hypothetical protein HND47_16930 [Chloroflexi bacterium].	GCA_013112685.1
NOH03560.1	REase→ LRR-repeats+AP-GTPase+COR→ *LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	878	HND47_17170	Chloroflexi	Chloroflexi bacterium	hypothetical protein HND47_17170 [Chloroflexi bacterium].	GCA_013112685.1
NOH03561.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	852	HND47_17175	Chloroflexi	Chloroflexi bacterium	GTP-binding protein [Chloroflexi bacterium].	GCA_013112685.1
NOH03734.1	PIN→ PSE→?→?→ LRR-repeats+AP-GTPase+COR*→?→?→?→ PSE→||<-?<-PSE||?→ Cluster2515_2clades→ Cluster2268_2clades→	LRR-repeats+AP-GTPase+COR	973	HND47_18110	Chloroflexi	Chloroflexi bacterium	hypothetical protein HND47_18110 [Chloroflexi bacterium].	GCA_013112685.1
NOQ25006.1	Arginase→ REase→?→?→ LRR-repeats+AP-GTPase+COR+DrHyd*→	LRR-repeats+AP-GTPase+COR+DrHyd	1054	GQ564_06545	Bacteroidetes	Bacteroidales bacterium	GTP-binding protein [Bacteroidales bacterium].	GCA_013138975.1
NOQ25654.1	LRR-repeats+AP-GTPase+COR*→ FGS→ PSE→?→||<-?<-?<-REC	LRR-repeats+AP-GTPase+COR	1082	GQ564_09870	Bacteroidetes	Bacteroidales bacterium	GTP-binding protein [Bacteroidales bacterium].	GCA_013138975.1
NOQ25870.1	LRR-repeats+AP-GTPase+COR*→ Cluster881_3clades→ Polbeta+HEPN→||<-?<-Cluster998_2clades<-?<-RADICAL-SAM	LRR-repeats+AP-GTPase+COR	983	GQ564_10955	Bacteroidetes	Bacteroidales bacterium	GTP-binding protein [Bacteroidales bacterium].	GCA_013138975.1
NOQ35071.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	779	GQ569_04160	Gammaproteobacteria	Methylococcaceae bacterium	hypothetical protein GQ569_04160 [Methylococcaceae bacterium].	GCA_013138855.1
NOQ64054.1	LRR-repeats+AP-GTPase+COR+DrHyd*→	LRR-repeats+AP-GTPase+COR+DrHyd	751	GQ582_06035	Gammaproteobacteria	Methyloprofundus sp.	hypothetical protein GQ582_06035 [Methyloprofundus sp.].	GCA_013138595.1
NOR78337.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	537	GQ523_07950	Euryarchaeota	Methanophagales archaeon	GTP-binding protein, partial [Methanophagales archaeon].	GCA_013139985.1
NOS87464.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	972	HOP34_02800	Gammaproteobacteria	Methylococcaceae bacterium	TIR domain-containing protein [Methylococcaceae bacterium].	GCA_013140465.1
NOT10704.1	Cluster2349_2clades→ PSE→?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	810	HOP23_02545	Gammaproteobacteria	Methylococcaceae bacterium	hypothetical protein HOP23_02545 [Methylococcaceae bacterium].	GCA_013140705.1
NOT87605.1	PNPase→?→ LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1152	HOP03_05430	Gammaproteobacteria	Lysobacter sp.	TIR domain-containing protein [Lysobacter sp.].	GCA_013141175.1
NOU20113.1	SIGMA-HTH→?→ LRR-repeats+AP-GTPase+COR+DrHyd*→ LRR-repeats+AP-GTPase+COR+DrHyd→	LRR-repeats+AP-GTPase+COR+DrHyd	1204	HOO91_21360	Bacteroidetes	Bacteroidales bacterium	hypothetical protein HOO91_21360 [Bacteroidales bacterium].	GCA_013141385.1
NOU47191.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	693	HOO86_09030	Bacteroidetes	Bacteroidales bacterium	GTP-binding protein [Bacteroidales bacterium].	GCA_013141455.1
NOZ36014.1	Cluster1478_2clades→?→?→?→?→ LRR-repeats+AP-GTPase+COR*→||<-?<-?||?→?→ D5ATPase→	LRR-repeats+AP-GTPase+COR	842	GXO80_12040	Chlorobi	Chlorobi bacterium	GTP-binding protein [Chlorobi bacterium].	GCA_013152535.1
NQT12774.1	LRR-repeats+AP-GTPase+COR+DUF4404*→	LRR-repeats+AP-GTPase+COR+DUF4404	936	HQ582_08495	Planctomycetes	Planctomycetes bacterium	leucine-rich repeat domain-containing protein, partial [Planctomycetes bacterium].	GCA_013202485.1
NQT13736.1	LRR-repeats+AP-GTPase+COR*→ TIR→	LRR-repeats+AP-GTPase+COR	583	HQ582_13365	Planctomycetes	Planctomycetes bacterium	hypothetical protein HQ582_13365, partial [Planctomycetes bacterium].	GCA_013202485.1

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NQT64030.1	TM+TM+TM→?→?→?→?→ SIG+LRR-repeats+AP-GTPase+COR+TIR*→	SIG+LRR-repeats+AP-GTPase+COR+TIR	1188	HQ556_13800	FCB group	Candidatus Marinimicrobia bacterium	TIR domain-containing protein [Candidatus Marinimicrobia bacterium].	GCA_013202495.1
NQT91808.1	LRR-repeats+AP-GTPase+COR+DUF4404*→	LRR-repeats+AP-GTPase+COR+DUF4404	843	HQ559_03535	Lentisphaerae	Lentisphaerae bacterium	serine/threonine protein kinase [Lentisphaerae bacterium].	GCA_013202215.1
NQU06371.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	749	HQ568_09785	Calditrichaeota	Calditrichaeota bacterium	GTP-binding protein [Calditrichaeota bacterium].	GCA_013202805.1
NQU20766.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	813	HQ567_05735	Bacteria	Candidatus Nealsonbacteria bacterium	TIR domain-containing protein [Candidatus Nealsonbacteria bacterium].	GCA_013202865.1
NQU25297.1	LRR-repeats+AP-GTPase+COR*→ TIR→	LRR-repeats+AP-GTPase+COR	608	HQ567_28770	Bacteria	Candidatus Nealsonbacteria bacterium	hypothetical protein HQ567_28770 [Candidatus Nealsonbacteria bacterium].	GCA_013202865.1
NQU51997.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	946	HQ522_05615	Bacteroidetes	Bacteroidetes bacterium	leucine-rich repeat domain-containing protein [Bacteroidetes bacterium].	GCA_013203755.1
NQU93487.1	RVT→ LRR-repeats+AP-GTPase+COR+TIR*→?→?→ TM+TM+TM→	LRR-repeats+AP-GTPase+COR+TIR	903	HQ540_23735	Bacteroidetes	Bacteroidetes bacterium	TIR domain-containing protein [Bacteroidetes bacterium].	GCA_013203545.1
NQY23053.1	S4→?→?→?→?→ LRR-repeats+AP-GTPase+COR+DrHyd*→||<-?<-Cluster1695_2clades||TraJ-RHH→ RelE-ParE→?→?→ ACET→	LRR-repeats+AP-GTPase+COR+DrHyd	962	HRT41_03420	Epsilonproteobacteria	Campylobacteraceae bacterium	leucine-rich repeat domain-containing protein [Campylobacteraceae bacterium].	GCA_013215945.1
NQZ07155.1	GDSL→ Cluster2260_2clades→ LRR-repeats+AP-GTPase+COR+E59-ABC*→?→ RelE→ CHTH→	LRR-repeats+AP-GTPase+COR+E59-ABC	1302	HRT35_08335	Gammaproteobacteria	Algicola sp.	leucine-rich repeat domain-containing protein [Algicola sp.].	GCA_013216025.1
NQZ07918.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	815	HRT35_12215	Gammaproteobacteria	Algicola sp.	GTP-binding protein [Algicola sp.].	GCA_013216025.1
NQZ09239.1	<-MNS-STAND+CR-REase3||LRR-repeats+AP-GTPase+COR*→ Cluster5_5clades→	LRR-repeats+AP-GTPase+COR	1075	HRT35_18935	Gammaproteobacteria	Algicola sp.	leucine-rich repeat domain-containing protein [Algicola sp.].	GCA_013216025.1
NQZ10194.1	LRR-repeats+AP-GTPase+COR+TIR*→?→||<-?<-HSP70	LRR-repeats+AP-GTPase+COR+TIR	972	HRT35_23840	Gammaproteobacteria	Algicola sp.	TIR domain-containing protein [Algicola sp.].	GCA_013216025.1
NQZ62063.1	Cluster1136_2clades→?→||<-?||LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	829	HRT59_07970	Cyanobacteria	Crocosphaera sp.	leucine-rich repeat domain-containing protein [Crocosphaera sp.].	GCA_013215395.1
NQZ63007.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	689	HRT59_12970	Cyanobacteria	Crocosphaera sp.	leucine-rich repeat domain-containing protein, partial [Crocosphaera sp.].	GCA_013215395.1
NRA27019.1	FGS→?→ FGS→ RVT→ FGS→ LRR-repeats+AP-GTPase+COR*→||<-?<-nSTAND3+REase-DUF4143<-tRNA<-?||Pro_CA→||<-Cluster1292_2clades	LRR-repeats+AP-GTPase+COR	859	HRU10_07210	Verrucomicrobia	Opitutales bacterium	hypothetical protein HRU10_07210 [Opitutales bacterium].	GCA_013215165.1
NRT54298.1	LRR-repeats+AP-GTPase+COR+TIR*→||<-?<-ABC_membrane+ABC_tran||Cyanophycinsyn-ATPgrasp→ Cyanophycinsyn-ATPgrasp→	LRR-repeats+AP-GTPase+COR+TIR	788	HNQ01_000005	Betaproteobacteria	Leptothrix sp. C29	internalin A [Leptothrix sp. C29].	GCA_013294065.1
NTV46488.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	657	HGB11_08225	Chlorobi	Chlorobiales bacterium	TIR domain-containing protein, partial [Chlorobiales bacterium].	GCA_013334725.1
NTV66504.1	LRR-repeats+AP-GTPase+COR+TIR*→?→?→?→ PurT-ATPgrasp→	LRR-repeats+AP-GTPase+COR+TIR	755	HGB06_02250	Chlorobi	Chlorobaculum sp.	TIR domain-containing protein [Chlorobaculum sp.].	GCA_013334855.1
NTV67443.1	REase→||<-?<-SIG+TM||LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	453	HGB06_07145	Chlorobi	Chlorobaculum sp.	hypothetical protein HGB06_07145 [Chlorobaculum sp.].	GCA_013334855.1
NTW50168.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	839	HGB19_10655	Chlorobi	Chlorobiales bacterium	TIR domain-containing protein [Chlorobiales bacterium].	GCA_013334605.1
NTW54860.1	LRR-repeats+AP-GTPase+COR*→?→?→?→?→?→?→ Cluster2062_2clades→	LRR-repeats+AP-GTPase+COR	1090	HGB15_08930	Chlorobi	Chlorobaculum sp.	hypothetical protein HGB15_08930 [Chlorobaculum sp.].	GCA_013334655.1
NTW70387.1	DAM→ LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	876	HGB23_11195	Chlorobi	Chlorobiaceae bacterium	TIR domain-containing protein [Chlorobiaceae bacterium].	GCA_013334485.1

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NTW83729.1	<-NUDIX||?→?→?→ LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	892	HGB36_10245	Chlorobi	Chlorobiaceae bacterium	TIR domain-containing protein [Chlorobiaceae bacterium].	GCA_013334225.1
NUM66201.1	SHS2→ LRR-repeats+AP-GTPase+COR*→?→?→ Cluster1134_2clades→ SNF→	LRR-repeats+AP-GTPase+COR	1051	HUU39_13110	Bacteria	candidate division KSB1 bacterium	hypothetical protein HUU39_13110 [candidate division KSB1 bacterium].	GCA_013359425.1
NUM68318.1	LRR-repeats+AP-GTPase+COR*→?→?→ FGS→	LRR-repeats+AP-GTPase+COR	955	HUU39_24115	Bacteria	candidate division KSB1 bacterium	leucine-rich repeat domain-containing protein [candidate division KSB1 bacterium].	GCA_013359425.1
NUO01599.1	<-S18-HTH<-Cluster1004_3clades<-?<-?<-?||FGS→ LRR-repeats+_AP-GTPase+COR+EAD11+TIR*→ FGS→	LRR-repeats+_AP-GTPase+COR+EAD11+TIR	1085	HUU01_13415	Bacteroidetes	Saprospiraceae bacterium	TIR domain-containing protein [Saprospiraceae bacterium].	GCA_013361075.1
NUO02098.1	LRR-repeats+AP-GTPase+COR+TM+TM+TM*→?→||<-Cluster2427_2clades	LRR-repeats+AP-GTPase+COR+TM+TM+TM	791	HUU01_15950	Bacteroidetes	Saprospiraceae bacterium	hypothetical protein HUU01_15950, partial [Saprospiraceae bacterium].	GCA_013361075.1
NUO79752.1	SIG+7TMR-DISMED1→||<-?<-?||LRR-repeats+AP-GTPase+COR+TIR*→||<-Cluster2261_2clades<-RlaP||SIG+TIMbarrel→	LRR-repeats+AP-GTPase+COR+TIR	968	HUU05_06725	Bacteria	candidate division KSB1 bacterium	leucine-rich repeat domain-containing protein [candidate division KSB1 bacterium].	GCA_013361015.1
NUO80023.1	ABhydrolase→?→ Cluster1134_2clades→?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	824	HUU05_08095	Bacteria	candidate division KSB1 bacterium	leucine-rich repeat domain-containing protein [candidate division KSB1 bacterium].	GCA_013361015.1
NUO97795.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	986	HOW59_07675	Actinobacteria	Nonomuraea sp.	hypothetical protein HOW59_07675, partial [Nonomuraea sp.].	GCA_013361365.1
NUP68620.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1447	HOW71_41335	Actinobacteria	Nonomuraea sp.	hypothetical protein HOW71_41335 [Nonomuraea sp.].	GCA_013361665.1
NUQ24465.1	FGS→?→||<-?||EAD11+LRR-repeats+S1+S1+AP-GTPase+COR*→	EAD11+LRR-repeats+S1+S1+AP-GTPase+COR	1140	HUU34_10980	Bacteroidetes	Saprospiraceae bacterium	leucine-rich repeat domain-containing protein [Saprospiraceae bacterium].	GCA_013360405.1
NUQ25704.1	PIN→ FGS→?→ RVT→?→ LRR-repeats+AP-GTPase+COR+TIR*→?→?→?→ TM+TM+TM→	LRR-repeats+AP-GTPase+COR+TIR	826	HUU34_17280	Bacteroidetes	Saprospiraceae bacterium	TIR domain-containing protein [Saprospiraceae bacterium].	GCA_013360405.1
NUQ26825.1	LRR-repeats+AP-GTPase+COR+TM*→ FGS→	LRR-repeats+AP-GTPase+COR+TM	924	HUU34_23015	Bacteroidetes	Saprospiraceae bacterium	hypothetical protein HUU34_23015 [Saprospiraceae bacterium].	GCA_013360405.1
NUQ46249.1	LRR-repeats+AP-GTPase+COR*→ ABC_membrane+ABC_tran→	LRR-repeats+AP-GTPase+COR	843	HUU22_09465	Planctomycetes	Phycisphaerae bacterium	leucine-rich repeat domain-containing protein, partial [Phycisphaerae bacterium].	GCA_013360645.1
NUQ73394.1	LRR-repeats+AP-GTPase+COR+TM+TM*→	LRR-repeats+AP-GTPase+COR+TM+TM	869	HUU21_07550	Deltaproteobacteria	Polyangiaceae bacterium	GTP-binding protein [Polyangiaceae bacterium].	GCA_013360665.1
NUQ87064.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	767	HOQ43_01165	Actinobacteria	Glycomyces artemisiae	hypothetical protein HOQ43_01165 [Glycomyces artemisiae].	GCA_013361895.1
NUR27723.1	REC→?→?→?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	958	HOV83_18080	Actinobacteria	Catenulispora sp.	hypothetical protein HOV83_18080 [Catenulispora sp.].	GCA_013362085.1
NUS08684.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1447	HOV97_39690	Actinobacteria	Nonomuraea sp.	hypothetical protein HOV97_39690 [Nonomuraea sp.].	GCA_013362305.1
NVM16177.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1327	HWN80_00570	Asgard group	Candidatus Lokiarchaeota archaeon	leucine-rich repeat protein [Candidatus Lokiarchaeota archaeon].	GCA_013375495.1
NVM57338.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	588	HWN51_04390	Deltaproteobacteria	Desulfobacterales bacterium	leucine-rich repeat domain-containing protein, partial [Desulfobacterales bacterium].	GCA_013375265.1
NVO09292.1	<-SIG+TM+VWA+TM<-SIG+TM+VWA+TM<-?<-VWA<-?<-MoxR-AAA||?→ LRR-repeats+AP-GTPase+COR*→?→?→?→||<-?<-?<-?||DSBH→	LRR-repeats+AP-GTPase+COR	965	HXX16_04945	Bacteroidetes	Bacteroidales bacterium	leucine-rich repeat domain-containing protein [Bacteroidales bacterium].	GCA_013376985.1

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NZD48025.1	LRR-repeats+AP-GTPase+COR+TIR*→||<-?<-ABC_membrane+ABC_tran||Cyanophycinsyn-ATPgrasp→ Cyanophycinsyn-ATPgrasp→	LRR-repeats+AP-GTPase+COR+TIR	885	HZU84_19525	Betaproteobacteria	Sphaerotilus natans subsp. sulfidivorans	leucine-rich repeat domain-containing protein [Sphaerotilus natans subsp. sulfidivorans].	GCA_013426975.1
OAB01099.1	LRR-repeats+AP-GTPase+COR*→||<-?||?→||<-?<-SIGMA-HTH<-SIGMA-HTH	LRR-repeats+AP-GTPase+COR	996	A6P39_08275	Actinobacteria	Streptomyces sp. FXJ1.172	hypothetical protein A6P39_08275 [Streptomyces sp. FXJ1.172].	GCA_001636945.1
OAI12102.1	Cluster5_5clades→?→?→ HTH→ LRR-repeats+AP-GTPase+COR+TIR*→ Cluster1019_2clades→?→||<-?<-?<-?||Cluster833_2clades→	LRR-repeats+AP-GTPase+COR+TIR	1065	A1507_19115	Gammaproteobacteria	Methylomonas koyamae	hypothetical protein A1507_19115 [Methylomonas koyamae].	GCA_001644135.1
OBQ24605.1	S18-HTH→?→||<-tRNA||Ferredoxin-betagrasp→?→?→ LRR-repeats+AP-GTPase+COR*→?→||<-?||TM→	LRR-repeats+AP-GTPase+COR	1095	AN488_00160	Cyanobacteria	Anabaena sp. WA113	GTPase [Anabaena sp. WA113].	GCA_001672155.1
OBQ25153.1	LRR-repeats+AP-GTPase+COR*→?→||<-?||TM→	LRR-repeats+AP-GTPase+COR	780	AN481_11440	Cyanobacteria	Aphanizomenon flos-aquae LD13	hypothetical protein AN481_11440, partial [Aphanizomenon flos-aquae LD13].	GCA_001672165.1
OBQ31054.1	S18-HTH→?→||<-tRNA||Ferredoxin-betagrasp→?→?→ LRR-repeats+AP-GTPase+COR*→?→||<-?||TM→	LRR-repeats+AP-GTPase+COR	942	AN483_02530	Cyanobacteria	Aphanizomenon flos-aquae MDT14a	hypothetical protein AN483_02530 [Aphanizomenon flos-aquae MDT14a].	GCA_001672095.1
OBQ35403.1	LRR-repeats+AP-GTPase+COR*→||<-?<-sGTP+sGTP||?→||<-REC	LRR-repeats+AP-GTPase+COR	799	AN487_15705	Cyanobacteria	Anabaena sp. CRKS33	hypothetical protein AN487_15705, partial [Anabaena sp. CRKS33].	GCA_001672075.1
OBQ36155.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	567	AN484_25870	Cyanobacteria	Aphanizomenon flos-aquae WA102	GTPase, partial [Aphanizomenon flos-aquae WA102].	GCA_001672105.1
OCQ90934.1	LRR-repeats+AP-GTPase+COR→ *LRR-repeats+AP-GTPase+COR*→?→ LRR-repeats+AP-GTPase+COR→	LRR-repeats+AP-GTPase+COR	795	BCR12_04520	Cyanobacteria	Limnothrix sp. P13C2	hypothetical protein BCR12_04520 [Limnothrix sp. P13C2].	GCA_001698445.1
OCQ90935.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	952	BCR12_04525	Cyanobacteria	Limnothrix sp. P13C2	hypothetical protein BCR12_04525 [Limnothrix sp. P13C2].	GCA_001698445.1
OCQ97014.1	TPR-repeats→?→?→ CASPASE+TM+TPR→?→?→?→ LRR-repeats+AP-GTPase+COR+DUF4404*→||<-?<-?||?→||<-?||REC→	LRR-repeats+AP-GTPase+COR+DUF4404	833	BCD64_15615	Cyanobacteria	Nostoc sp. MBR 210	GTP-binding protein [Nostoc sp. MBR 210].	GCA_001698435.1
OCR00628.1	LRR-repeats+AP-GTPase+COR+TM+TM*→||<-?<-?||?→||<-?||?→||<-PRTase<-SIG+TM+TM+TM+TM	LRR-repeats+AP-GTPase+COR+TM+TM	689	BCD67_11660	Cyanobacteria	Oscillatoriales cyanobacterium USR001	GTPase, partial [Oscillatoriales cyanobacterium USR001].	GCA_001698425.1
OCW73618.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	918	A4G24_00320	Bacteroidetes	Elizabethkingia anophelis	hypothetical protein A4G24_00320 [Elizabethkingia anophelis].	GCA_001703835.1
ODG98072.1	LRR-repeats+AP-GTPase+COR+TIR*→||<-CASPASE+TM	LRR-repeats+AP-GTPase+COR+TIR	858	A4S05_10875	Cyanobacteria	Nostoc sp. KVJ20	hypothetical protein A4S05_10875, partial [Nostoc sp. KVJ20].	GCA_001712795.1
ODS35505.1	Cluster846_3clades→ LRR-repeats→ LRR-repeats+AP-GTPase+COR*→?→ VWA→	LRR-repeats+AP-GTPase+COR	644	A7316_10690	DPANN group	Candidatus Altiarchaeales archaeon WOR_SM1_86-2	hypothetical protein A7316_10690 [Candidatus Altiarchaeales archaeon WOR_SM1_86-2].	GCA_001723855.1
ODS40288.1	LRR-repeats+AP-GTPase+CASPASE*→	LRR-repeats+AP-GTPase+CASPASE	811	A7315_09000	DPANN group	Candidatus Altiarchaeales archaeon WOR_SM1_79	hypothetical protein A7315_09000 [Candidatus Altiarchaeales archaeon WOR_SM1_79].	GCA_001723835.1
OED06513.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	666	A9239_11540	Euryarchaeota	Methanosarcina sp. A14	hypothetical protein A9239_11540 [Methanosarcina sp. A14].	GCA_001729375.1
OEU63639.1	LRR-repeats→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	623	BBJ57_05215	Deltaproteobacteria	Desulfobacterales bacterium PC51MH44	hypothetical protein BBJ57_05215 [Desulfobacterales bacterium PC51MH44].	GCA_001751165.1
OFX48341.1	ABC-ATPase→?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	720	A2X10_07060	Bacteroidetes	Bacteroidetes bacterium GWA2_33_15	hypothetical protein A2X10_07060 [Bacteroidetes bacterium GWA2_33_15].	GCA_001769045.1
OFX79107.1	LRR-repeats+AP-GTPase+COR+REase7*→	LRR-repeats+AP-GTPase+COR+REase7	1101	A2X12_10435	Bacteroidetes	Bacteroidetes bacterium GWE2_29_8	hypothetical protein A2X12_10435 [Bacteroidetes bacterium GWE2_29_8].	GCA_001769085.1
OFY84271.1	LRR-repeats→ LRR-repeats+AP-GTPase+COR+REase7*→	LRR-repeats+AP-GTPase+COR+REase7	598	A3F72_14720	Bacteroidetes	Bacteroidetes bacterium RIFC-SPLOWO2_12_FULL_35_15	hypothetical protein A3F72_14720 [Bacteroidetes bacterium RIFC-SPLOWO2_12_FULL_35_15].	GCA_001769385.1

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OGC77574.1	LRR-repeats+AP-GTPase+COR*→?→||<-?<-CCTBP	LRR-repeats+AP-GTPase+COR	975	A2Z27_00115	FCB group	candidate division Zixibacteria bacterium RBG_16_50_21	hypothetical protein A2Z27_00115 [candidate division Zixibacteria bacterium RBG_16_50_21].	GCA_001773465.1
OGH99179.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	572	A2X43_07200	Terrabacteria group	Candidatus Margulisbacteria bacterium GWD2_39_127	hypothetical protein A2X43_07200 [Candidatus Margulisbacteria bacterium GWD2_39_127].	GCA_001783265.1
OGV70404.1	Pkinase+LRR-repeats+AP-GTPase+COR+TM+TM*→	Pkinase+LRR-repeats+AP-GTPase+COR+TM+TM	1157	A2283_19020	Lentisphaerae	Lentisphaerae bacterium RI-FOXYA12_FULL_48_11	hypothetical protein A2283_19020 [Lentisphaerae bacterium RIFOXYA12_FULL_48_11].	GCA_001804885.1
OHB50686.1	S1COLD→ LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	953	A2Y10_02350	Planctomycetes	Planctomycetes bacterium GWF2_41_51	hypothetical protein A2Y10_02350 [Planctomycetes bacterium GWF2_41_51].	GCA_001825665.1
OHB52204.1	LRR-repeats+AP-GTPase+COR*→?→||<-?||SIG+TM→	LRR-repeats+AP-GTPase+COR	1147	A2Y10_11365	Planctomycetes	Planctomycetes bacterium GWF2_41_51	hypothetical protein A2Y10_11365 [Planctomycetes bacterium GWF2_41_51].	GCA_001825665.1
OHB64560.1	REC→ TPR-repeats→||<-?||PSE→||<-?<-?<-?||YBAK→ LRR-repeats+AP-GTPase+COR+DUF4404*→	LRR-repeats+AP-GTPase+COR+DUF4404	740	A2Y76_11060	Planctomycetes	Planctomycetes bacterium RBG_13_60_9	hypothetical protein A2Y76_11060 [Planctomycetes bacterium RBG_13_60_9].	GCA_001824685.1
OHD05988.1	LRR-repeats+AP-GTPase+COR+TM+TM*→ TraJ-RHH→ RelE-ParE→	LRR-repeats+AP-GTPase+COR+TM+TM	1257	A2Z98_10570	Spirochaetes	Spirochaetes bacterium GWB1_27_13	hypothetical protein A2Z98_10570 [Spirochaetes bacterium GWB1_27_13].	GCA_001829125.1
OHD18029.1	MORC→?→?→?→||<-?<-PSE<-?||LRR-repeats+AP-GTPase+COR→*||<-?<-?<-?||?→?→?→?→ REC→||<-LRR-repeats+AP-GTPase+COR+DrHyd*	LRR-repeats+AP-GTPase+COR	1064	A2Z98_11125	Spirochaetes	Spirochaetes bacterium GWB1_27_13	hypothetical protein A2Z98_11125 [Spirochaetes bacterium GWB1_27_13].	GCA_001829125.1
OHD18038.1	LRR-repeats+AP-GTPase+COR+DrHyd*→	LRR-repeats+AP-GTPase+COR+DrHyd	986	A2Z98_11170	Spirochaetes	Spirochaetes bacterium GWB1_27_13	hypothetical protein A2Z98_11170 [Spirochaetes bacterium GWB1_27_13].	GCA_001829125.1
OHD26231.1	LRR-repeats+AP-GTPase+COR+TM+TM*→ TraJ-RHH→ RelE-ParE→	LRR-repeats+AP-GTPase+COR+TM+TM	1234	A2Y34_11235	Spirochaetes	Spirochaetes bacterium GWC1_27_15	hypothetical protein A2Y34_11235 [Spirochaetes bacterium GWC1_27_15].	GCA_001829235.1
OHD42853.1	MORC→?→?→?→||<-?<-PSE<-?||LRR-repeats+AP-GTPase+COR→*||<-?<-?<-?||?→?→?→?→ REC→||<-LRR-repeats+AP-GTPase+COR+DrHyd*	LRR-repeats+AP-GTPase+COR	1020	A2086_15855	Spirochaetes	Spirochaetes bacterium GWD1_27_9	hypothetical protein A2086_15855 [Spirochaetes bacterium GWD1_27_9].	GCA_001830585.1
OIO84219.1	<-XIS-HTH||HTH+HTH→||<-WLM||?→ NACHT+68TM-wHTH→ REase→?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1004	AUK01_09955	Chloroflexi	Anaerolineae bacterium CG2_30_57_67	hypothetical protein AUK01_09955, partial [Anaerolineae bacterium CG2_30_57_67].	GCA_001872455.1
OJJ15121.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1037	BKI52_39320	Bacteroidetes	marine bacterium AO1-C	hypothetical protein BKI52_39320 [marine bacterium AO1-C].	GCA_001890965.1
OJJ19161.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	851	BKI52_20325	Bacteroidetes	marine bacterium AO1-C	hypothetical protein BKI52_20325 [marine bacterium AO1-C].	GCA_001890965.1
OJJ19619.1	LRR-repeats+AP-GTPase+COR*→||<-?<-?<-?<-?<-TetR-HTH	LRR-repeats+AP-GTPase+COR	723	BKI52_22705	Bacteroidetes	marine bacterium AO1-C	hypothetical protein BKI52_22705, partial [marine bacterium AO1-C].	GCA_001890965.1
OJJ19690.1	<-Four-helical-protein<-?<-?<-?<-?||LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1463	BKI52_19350	Bacteroidetes	marine bacterium AO1-C	hypothetical protein BKI52_19350 [marine bacterium AO1-C].	GCA_001890965.1
OJJ20943.1	Cluster2042_2clades→||<-?<-?||?→?→?→||<-?||LRR-repeats+AP-GTPase+COR+EAD11*→||<-PAS+HISKIN	LRR-repeats+AP-GTPase+COR+EAD11	871	BKI52_10210	Bacteroidetes	marine bacterium AO1-C	hypothetical protein BKI52_10210 [marine bacterium AO1-C].	GCA_001890965.1
OJJ21241.1	LRR-repeats+AP-GTPase+COR*→?→||<-?<-cNMPBD	LRR-repeats+AP-GTPase+COR	910	BKI52_11795	Bacteroidetes	marine bacterium AO1-C	hypothetical protein BKI52_11795 [marine bacterium AO1-C].	GCA_001890965.1
OJJ22385.1	<-SIGMA-HTH||?→?→?→?→?→||<-?||LRR-repeats+AP-GTPase+COR*→?→?→?→||<-?<-?<-?<-SIGMA-HTH	LRR-repeats+AP-GTPase+COR	1192	BKI52_06800	Bacteroidetes	marine bacterium AO1-C	hypothetical protein BKI52_06800 [marine bacterium AO1-C].	GCA_001890965.1
OJJ23263.1	D5ATPase→?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1296	BKI52_02595	Bacteroidetes	marine bacterium AO1-C	hypothetical protein BKI52_02595 [marine bacterium AO1-C].	GCA_001890965.1

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OJJ23599.1	SF2-DUF3427A→?→ TRD+TRD→?→?→ LRR-repeats+AP-GTPase+COR*→?→||<-?<-LRR-repeats<-?||cNMPBD→	LRR-repeats+AP-GTPase+COR	1001	BKI52_04350	Bacteroidetes	marine bacterium AO1-C	hypothetical protein BKI52_04350 [marine bacterium AO1-C].	GCA_001890965.1
OKH11101.1	LRR-repeats+AP-GTPase+COR+TM+TM*→	LRR-repeats+AP-GTPase+COR+TM+TM	944	NIES208_17750	Cyanobacteria	Limnothrix rosea IAM M-220	hypothetical protein NIES208_17750 [Limnothrix rosea IAM M-220].	GCA_001904615.1
OKH34496.1	LRR-repeats+AP-GTPase+COR+TM+TM*→||<-CASPASE+TPR	LRR-repeats+AP-GTPase+COR+TM+TM	902	FACHB389_15645	Cyanobacteria	Nostoc calcicola FACHB-389	GTPase [Nostoc calcicola FACHB-389].	GCA_001904715.1
OLE55789.1	<-RFC-AAA<-?<-Trichomonas-DAM<-?<-?<-ISOCOT||LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	862	AUG51_01855	Acidobacteria	Acidobacteria bacterium 13_1_20CM_3_53_8	serine/threonine protein kinase [Acidobacteria bacterium 13_1_20CM_3_53_8].	GCA_001920415.1
OLF12412.1	LRR-repeats+AP-GTPase+COR*→?→?→?→||<-?<-ABC-ATPase+ABC-ATPase	LRR-repeats+AP-GTPase+COR	927	BLA60_09370	Actinobacteria	Actinophytocola xinjiangensis	hypothetical protein BLA60_09370 [Actinophytocola xinjiangensis].	GCA_001921215.1
OQX01793.1	LRR-repeats+AP-GTPase+COR+TIR*→||<-?<-PSE<-?<-PSE<-PSE<-?<-?<-?||PSE→||<-?||ABhydrolase→	LRR-repeats+AP-GTPase+COR+TIR	928	BWK73_44950	Gammaproteobacteria	Thiothrix lacustris	GTP-binding protein [Thiothrix lacustris].	GCA_002083875.1
OQX02054.1	nSTAND3+REase-DUF4143→ LRR-repeats+AP-GTPase+COR*→ TIR→?→||<-Thioredoxin	LRR-repeats+AP-GTPase+COR	784	BWK73_43990	Gammaproteobacteria	Thiothrix lacustris	hypothetical protein BWK73_43990 [Thiothrix lacustris].	GCA_002083875.1
OQX07365.1	LRR-repeats+AP-GTPase+COR+CASPASE*→	LRR-repeats+AP-GTPase+COR+CASPASE	879	BWK80_49550	Deltaproteobacteria	Desulfobacteraceae bacterium IS3	hypothetical protein BWK80_49550 [Desulfobacteraceae bacterium IS3].	GCA_002083955.1
OQX24659.1	LRR-repeats+AP-GTPase+COR→ *Cluster2372_2clades→?→ LRR-repeats+AP-GTPase+COR*→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	881	BWK80_19660	Deltaproteobacteria	Desulfobacteraceae bacterium IS3	hypothetical protein BWK80_19660 [Desulfobacteraceae bacterium IS3].	GCA_002083955.1
OQX24662.1	LRR-repeats+AP-GTPase+COR+TM*→	LRR-repeats+AP-GTPase+COR+TM	925	BWK80_19675	Deltaproteobacteria	Desulfobacteraceae bacterium IS3	hypothetical protein BWK80_19675 [Desulfobacteraceae bacterium IS3].	GCA_002083955.1
OQX24663.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	870	BWK80_19680	Deltaproteobacteria	Desulfobacteraceae bacterium IS3	hypothetical protein BWK80_19680 [Desulfobacteraceae bacterium IS3].	GCA_002083955.1
OQX25920.1	LRR-repeats+AP-GTPase+COR*→?→?→?→?→ ABC-ATPase→ SIG+TM+TM+TM+TM+TM→||<-Cluster968_2clades	LRR-repeats+AP-GTPase+COR	802	BWK80_13160	Deltaproteobacteria	Desulfobacteraceae bacterium IS3	hypothetical protein BWK80_13160 [Desulfobacteraceae bacterium IS3].	GCA_002083955.1
OQY27201.1	LRR-repeats+AP-GTPase+COR*→?→||<-?<-?<-?||TM+TM+TM+TM+TM+TM→	LRR-repeats+AP-GTPase+COR	700	B6244_11350	FCB group	Candidatus Cloacimonetes bacterium 4572_55	hypothetical protein B6244_11350 [Candidatus Cloacimonetes bacterium 4572_55].	GCA_002084765.1
OQY46926.1	LRR-repeats+AP-GTPase+COR*→||<-PSE||?→ LRR-repeats→	LRR-repeats+AP-GTPase+COR	887	B6247_27150	Gammaproteobacteria	Beggiatoa sp. 4572_84	GTPase [Beggiatoa sp. 4572_84].	GCA_002085445.1
OQY52602.1	SIG+TM+TM+TM+TM+TM+TM+TM→?→?→?→?→ LRR-repeats+AP-GTPase+COR→*?→?→?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	429	B6245_23480	Deltaproteobacteria	Desulfobacteraceae bacterium 4572_88	hypothetical protein B6245_23480, partial [Desulfobacteraceae bacterium 4572_88].	GCA_002085455.1
OQY52606.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	933	B6245_23500	Deltaproteobacteria	Desulfobacteraceae bacterium 4572_88	hypothetical protein B6245_23500 [Desulfobacteraceae bacterium 4572_88].	GCA_002085455.1
OQY56003.1	CBS→ PSE→||<-?||?→?→ LRR-repeats→?→ PSE→ LRR-repeats→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	907	B6247_05655	Gammaproteobacteria	Beggiatoa sp. 4572_84	GTPase [Beggiatoa sp. 4572_84].	GCA_002085445.1
OQY58390.1	LRR-repeats+AP-GTPase+COR*→ SIG+DADALIGASE-ATPgrasp→	LRR-repeats+AP-GTPase+COR	791	B6245_12095	Deltaproteobacteria	Desulfobacteraceae bacterium 4572_88	hypothetical protein B6245_12095 [Desulfobacteraceae bacterium 4572_88].	GCA_002085455.1
OSM01684.1	SIGMA-HTH→?→||<-?<-?<-?<-?<-?||LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	876	MAIT1_01702	Alphaproteobacteria	Magnetofaba australis IT-1	putative small GTP-binding protein [Magnetofaba australis IT-1].	GCA_002109495.1
OUC12119.1	LRR-repeats+AP-GTPase+COR+DrHyd*→?→?→ FGS→	LRR-repeats+AP-GTPase+COR+DrHyd	810	B0A82_24265	Cyanobacteria	Alkalinema sp. CACIAM 70d	hypothetical protein B0A82_24265, partial [Alkalinema sp. CACIAM 70d].	GCA_002148405.1
OUC12470.1	<-HISKIN<-?<-?<-PRTase<-?||?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	820	B0A82_22225	Cyanobacteria	Alkalinema sp. CACIAM 70d	hypothetical protein B0A82_22225 [Alkalinema sp. CACIAM 70d].	GCA_002148405.1
OUC13078.1	<-TIR+TM+CHASE2+CHASE2+TM+TM+TM<-SIG+RnaseT2<-?||?→?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	919	B0A82_18905	Cyanobacteria	Alkalinema sp. CACIAM 70d	GTPase [Alkalinema sp. CACIAM 70d].	GCA_002148405.1
OUC15727.1	LRR-repeats+AP-GTPase+COR+DUF4404*→?→||<-Cluster2098_2clades	LRR-repeats+AP-GTPase+COR+DUF4404	969	B0A82_05270	Cyanobacteria	Alkalinema sp. CACIAM 70d	hypothetical protein B0A82_05270, partial [Alkalinema sp. CACIAM 70d].	GCA_002148405.1

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OWK46761.1	<-Aminotran_1_2||LRR-repeats+AP-GTPase+COR+TIR*→||<-?<-?<-?<-DSBH+AraC-HTH+AraC-HTH||?→?→ SIG+TM+TM+TM→	LRR-repeats+AP-GTPase+COR+TIR	1310	FRUB_00460	Planctomycetes	Fimbriiglobus ruber	HtrA protease/chaperone protein [Fimbriiglobus ruber].	GCA_002197845.1
OWK47329.1	<-RelE-ParE<-?||?→ LRR-repeats→||<-?||LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	967	FRUB_01028	Planctomycetes	Fimbriiglobus ruber	putative internalin [Fimbriiglobus ruber].	GCA_002197845.1
OYQ36252.1	<-SIG+TM+TM+TM+HISKIN<-?<-?<-?||?→ LRR-repeats+AP-GTPase+COR+TIR*→ ParA-Soj-PloopNTPase→ ParB→	LRR-repeats+AP-GTPase+COR+TIR	890	CHU95_05565	Alphaproteobacteria	Niveispirillum lacus	hypothetical protein CHU95_05565 [Niveispirillum lacus].	GCA_002251795.1
OYU93091.1	LRR-repeats+AP-GTPase+COR+TM+TM*→	LRR-repeats+AP-GTPase+COR+TM+TM	1040	CFE21_21825	Bacteroidetes	Bacteroidetes bacterium B1(2017)	hypothetical protein CFE21_21825, partial [Bacteroidetes bacterium B1(2017)].	GCA_002256395.1
OYW76150.1	LRR-repeats+AP-GTPase+COR+TIR*→?→||<-?<-WCAK||?→ REC→ REC→	LRR-repeats+AP-GTPase+COR+TIR	996	B7Z37_09950	Verrucomicrobia	Verrucomicrobia bacterium 12-59-8	hypothetical protein B7Z37_09950 [Verrucomicrobia bacterium 12-59-8].	GCA_002279765.1
OYW77555.1	SIG+ABhydrolase→?→ LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	939	B7Z37_03775	Verrucomicrobia	Verrucomicrobia bacterium 12-59-8	hypothetical protein B7Z37_03775 [Verrucomicrobia bacterium 12-59-8].	GCA_002279765.1
OYW78304.1	FGS→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1063	B7Z37_00425	Verrucomicrobia	Verrucomicrobia bacterium 12-59-8	hypothetical protein B7Z37_00425 [Verrucomicrobia bacterium 12-59-8].	GCA_002279765.1
PCI29610.1	LRR-repeats+RNA-Helicase+AP-GTPase+COR+TIR*→?→||<-AraC-HTH||?→?→||<-Cluster1048_2clades<-POLYSACPOLYMERASE	LRR-repeats+RNA-Helicase+AP-GTPase+COR+TIR	1264	COB67_03805	Deltaproteobacteria	SAR324 cluster bacterium	hypothetical protein COB67_03805 [SAR324 cluster bacterium].	GCA_002401295.1
PCK09719.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	908	COA42_02805	Gammaproteobacteria	Alteromonadaceae bacterium	hypothetical protein COA42_02805 [Alteromonadaceae bacterium].	GCA_002746115.1
PHM06637.1	LRR-repeats+AP-GTPase+COR+TM+TM*→	LRR-repeats+AP-GTPase+COR+TM+TM	817	CK516_32280	Cyanobacteria	Nostoc sp. 'Peltigera malacea cyanobiont' DB3992	GTPase [Nostoc sp. 'Peltigera malacea cyanobiont' DB3992].	GCA_002631755.1
PHS08569.1	LRR-repeats+AP-GTPase+COR*→ SIG+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM→	LRR-repeats+AP-GTPase+COR	924	COA88_06290	Bacteroidetes	Kordia sp.	GTP-binding protein [Kordia sp.].	GCA_002733415.1
PID45108.1	Cluster1540_2clades→?→?→?→?→?→?→ tRNA→ LRR-repeats+AP-GTPase+COR*→||<-?<-?||Cluster2057_2clades→	LRR-repeats+AP-GTPase+COR	1016	CSB47_10150	Proteobacteria	Proteobacteria bacterium	hypothetical protein CSB47_10150 [Proteobacteria bacterium].	GCA_002747455.1
PID49971.1	SIG+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM→ LRR-repeats+AP-GTPase+COR+TIR*→?→||<-?<-?<-?<-?<-Cluster1063_3clades<-Cluster1067_3clades	LRR-repeats+AP-GTPase+COR+TIR	916	CR991_03995	Proteobacteria	Proteobacteria bacterium	hypothetical protein CR991_03995 [Proteobacteria bacterium].	GCA_002747435.1
PID58617.1	<-Cluster1581_2clades<-?||NUDIX→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1061	CSB45_03475	Bacteria	candidate division KSB3 bacterium	GTPase [candidate division KSB3 bacterium].	GCA_002747525.1
PIE10915.1	LRR-repeats+AP-GTPase+COR*→||<-?<-tRNA||?→?→ Cluster1995_2clades→	LRR-repeats+AP-GTPase+COR	994	CSA72_05310	Alphaproteobacteria	Rhodobacterales bacterium	hypothetical protein CSA72_05310 [Rhodobacterales bacterium].	GCA_002748265.1
PJB68563.1	<-XIS-HTH||HTH+HTH→||<-WLM||?→ NACHT+68TM-wHTH→ REase→?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	947	CO094_00645	Chloroflexi	Anaerolineae bacterium CG_4_9_14_3_um_filter_57_17	hypothetical protein CO094_00645, partial [Anaerolineae bacterium CG_4_9_14_3_um_filter_57_17].	GCA_002789715.1
PJF39486.1	LRR-repeats+AP-GTPase+COR+TM+TM*→	LRR-repeats+AP-GTPase+COR+TM+TM	751	CUN54_08620	Chloroflexi	Candidatus Thermofonsia Clade 2 bacterium	GTP-binding protein [Candidatus Thermofonsia Clade 2 bacterium].	GCA_002794595.1
PKB73283.1	LRR-repeats+AP-GTPase+COR*→||<-?<-?<-PSE<-SIG+ABhydrolase<-?<-ParA-Soj-PloopNTPase	LRR-repeats+AP-GTPase+COR	593	BZY75_02725	Chloroflexi	SAR202 cluster bacterium Io17-Chloro-G7	hypothetical protein BZY75_02725 [SAR202 cluster bacterium Io17-Chloro-G7].	GCA_002817055.1
PKD18393.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	845	APR41_04380	Bacteroidetes	Salegentibacter salinarum	hypothetical protein APR41_04380 [Salegentibacter salinarum].	GCA_002833365.1
PKN92928.1	UvsW-A18→ LRR-repeats+AP-GTPase+COR→ *NACHT+68TM-wHTH→ LRR-repeats+AP-GTPase+COR→* LRR-repeats+AP-GTPase+COR+DUF4404→*?→?→ Cluster1559_2clades→?→?→||<-?||LRR-repeats+AP-GTPase+COR→*	LRR-repeats+AP-GTPase+COR	769	CVU44_12925	Chloroflexi	Chloroflexi bacterium HGW-Chloroflexi-6	GTP-binding protein [Chloroflexi bacterium HGW-Chloroflexi-6].	GCA_002840685.1
PKN92930.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1044	CVU44_12935	Chloroflexi	Chloroflexi bacterium HGW-Chloroflexi-6	hypothetical protein CVU44_12935 [Chloroflexi bacterium HGW-Chloroflexi-6].	GCA_002840685.1
PKN92931.1	LRR-repeats+AP-GTPase+COR+DUF4404*→	LRR-repeats+AP-GTPase+COR+DUF4404	812	CVU44_12940	Chloroflexi	Chloroflexi bacterium HGW-Chloroflexi-6	hypothetical protein CVU44_12940 [Chloroflexi bacterium HGW-Chloroflexi-6].	GCA_002840685.1
PKN92938.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	673	CVU44_12975	Chloroflexi	Chloroflexi bacterium HGW-Chloroflexi-6	GTP-binding protein [Chloroflexi bacterium HGW-Chloroflexi-6].	GCA_002840685.1

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PKP35889.1	REC→ HISKIN→?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	654	CVU00_00150	Bacteroidetes	Bacteroidetes bacterium HGW-Bacteroidetes-17	hypothetical protein CVU00_00150 [Bacteroidetes bacterium HGW-Bacteroidetes-17].	GCA_002840985.1
PLX96646.1	LRR-repeats+AP-GTPase+COR+DrHyd*→||<-?||?→?→?→||<-?<-?<-SIG+PDZ	LRR-repeats+AP-GTPase+COR+DrHyd	1001	C0622_14350	Deltaproteobacteria	Desulfuromonas sp.	hypothetical protein C0622_14350 [Desulfuromonas sp.].	GCA_002869665.1
PLY10861.1	LRR-repeats+AP-GTPase+COR*→||<-?<-tRNA<-?<-?||Cluster1398_2clades→ ABC-ATPase→	LRR-repeats+AP-GTPase+COR	1225	C0626_04310	Epsilonproteobacteria	Arcobacter sp.	hypothetical protein C0626_04310 [Arcobacter sp.].	GCA_002869535.1
POZ53622.1	REC→||<-?<-?<-?<-?||?→ LRR-repeats+AP-GTPase+COR+DpnII-MboI-NTD+TIR*→	LRR-repeats+AP-GTPase+COR+DpnII-MboI-NTD+TIR	1108	AADEFJLK_00657	Gammaproteobacteria	Methylovulum psychrotolerans	GTP-binding protein [Methylovulum psychrotolerans].	GCA_002923755.1
PPT07796.1	LRR-repeats+AP-GTPase+COR+BactIG*→	LRR-repeats+AP-GTPase+COR+BactIG	726	CKA32_002768	Cyanobacteria	Geitlerinema sp. FC II	Leucine-rich repeat containing protein [Geitlerinema sp. FC II].	GCA_002286845.1
PRQ08092.1	LRR-repeats+AP-GTPase+COR+PNPase*→	LRR-repeats+AP-GTPase+COR+PNPase	933	mtnN	Deltaproteobacteria	Enhygromyxa salina	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase [Enhygromyxa salina].	GCA_002994635.1
PSB34361.1	<-REC||REC→||<-?<-?<-?<-TIR+TM+CHASE2+CHASE2+TM+TM+TM||PSE→ LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1113	C7B82_02520	Cyanobacteria	Stenomitos frigidus ULC18	serine/threonine protein kinase [Stenomitos frigidus ULC18].	GCA_003003795.1
PSM30901.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	431	BVG81_008130	Deltaproteobacteria	Haliangium sp. UPWRP_2	GTPase, partial [Haliangium sp. UPWRP_2].	GCA_002212765.2
PTS96034.1	LRR-repeats+AP-GTPase*→	LRR-repeats+AP-GTPase	357	DBR27_16615	Bacteroidetes	Flavobacterium sp. HMWF030	hypothetical protein DBR27_16615, partial [Flavobacterium sp. HMWF030].	GCA_003061345.1
PWQ95663.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	801	DKT75_11555	Gammaproteobacteria	Leucothrix arctica	GTP-binding protein, partial [Leucothrix arctica].	GCA_003172895.1
PXF61747.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	978	C4B59_02515	Euryarchaeota	ANME-2 cluster archaeon	hypothetical protein C4B59_02515 [ANME-2 cluster archaeon].	GCA_003194445.1
PXX81924.1	<-ACET<-?<-?<-?||?→ HSP70→ DNAJ→ LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	947	DFR34_101153	Betaproteobacteria	Rivicola pingtungensis	internalin A [Rivicola pingtungensis].	GCA_003201855.1
PYI92098.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	882	DME97_11675	Verrucomicrobia	Verrucomicrobia bacterium	hypothetical protein DME97_11675 [Verrucomicrobia bacterium].	GCA_003218375.1
PYQ65591.1	LRR-repeats+AP-GTPase+COR+TIR*→||<-START	LRR-repeats+AP-GTPase+COR+TIR	985	DMF53_05195	Acidobacteria	Acidobacteria bacterium	hypothetical protein DMF53_05195 [Acidobacteria bacterium].	GCA_003223675.1
PZN70482.1	LRR-repeats+AP-GTPase+COR*→ TIR→	LRR-repeats+AP-GTPase+COR	479	DM484_28490	Gammaproteobacteria	Candidatus Methyloumidiphilus alinensis	hypothetical protein DM484_28490 [Candidatus Methyloumidiphilus alinensis].	GCA_003242955.1
PZN77149.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1032	DM484_15240	Gammaproteobacteria	Candidatus Methyloumidiphilus alinensis	hypothetical protein DM484_15240 [Candidatus Methyloumidiphilus alinensis].	GCA_003242955.1
PZN84233.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	820	DM484_03135	Gammaproteobacteria	Candidatus Methyloumidiphilus alinensis	GTP-binding protein [Candidatus Methyloumidiphilus alinensis].	GCA_003242955.1
PZO19892.1	<-SIG+TM+TM+TM||?→?→?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	715	DCF25_07770	Cyanobacteria	Leptolyngbya foveolarum	hypothetical protein DCF25_07770, partial [Leptolyngbya foveolarum].	GCA_003242035.1
PZO41190.1	LRR-repeats+AP-GTPase+COR*→||<-PIN<-PSE||HISKIN→ REC→	LRR-repeats+AP-GTPase+COR	872	DCF19_10445	Cyanobacteria	Pseudanabaena frigida	GTPase [Pseudanabaena frigida].	GCA_003242085.1
PZO43272.1	Cluster53_2clades→ Cluster53_2clades→?→ LRR-repeats+AP-GTPase+COR+CASPASE*→||<-?<-?||?→?→ Cluster944_3clades→||<-tRNA<-NUDIX||REC→	LRR-repeats+AP-GTPase+COR+CASPASE	1158	DCF19_04785	Cyanobacteria	Pseudanabaena frigida	GTPase [Pseudanabaena frigida].	GCA_003242085.1
PZO45083.1	PAS+HISKIN→ REC→ HISKIN→||<-?<-?<-?||LRR-repeats+AP-GTPase+COR*→||<-?||?→||<-?||?→?→?→||<-ABC-ATPase	LRR-repeats+AP-GTPase+COR	1026	DCF19_00905	Cyanobacteria	Pseudanabaena frigida	hypothetical protein DCF19_00905 [Pseudanabaena frigida].	GCA_003242085.1
PZS26024.1	LRR-repeats+AP-GTPase*→	LRR-repeats+AP-GTPase	304	DLM61_19115	Actinobacteria	Pseudonocardiales bacterium	hypothetical protein DLM61_19115 [Pseudonocardiales bacterium].	GCA_003244245.1
PZU97949.1	<-Cluster53_2clades||?→ Cluster53_2clades→ Cluster54_3clades→?→ RelE-ParE→ LRR-repeats+AP-GTPase+COR+DUF4404*→?→?→||<-Cluster1583_2clades<-Cluster1881_2clades<-Cluster1340_2clades	LRR-repeats+AP-GTPase+COR+DUF4404	1125	DCE90_05495	Cyanobacteria	Pseudanabaena sp.	Ras family protein [Pseudanabaena sp.].	GCA_003249015.1

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PZV15467.1	Cluster53_2clades→?→ LRR-repeats+AP-GTPase+COR+TM+TM*→?→||<-?<-?<-ABC-ATPase<-?||PSE→?→ ABC_membrane+ABC_tran→	LRR-repeats+AP-GTPase+COR+TM+TM	966	DCF20_10315	Cyanobacteria	Pseudanabaena sp.	GTP-binding protein [Pseudanabaena sp.].	GCA_003249035.1
PZV19789.1	LRR-repeats+AP-GTPase+COR*→?→ Cluster2508_2clades→	LRR-repeats+AP-GTPase+COR	779	DCF21_06795	Cyanobacteria	Leptolyngbya sp.	GTP-binding protein [Leptolyngbya sp.].	GCA_003249155.1
PZV24423.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	522	DCF12_17370	Cyanobacteria	Snowella sp.	hypothetical protein DCF12_17370 [Snowella sp.].	GCA_003249095.1
PZV25744.1	<-REC||?→?→||<-?<-?||?→ LRR-repeats+AP-GTPase+COR*→||<-DAGKIN||?→ Cluster5_5clades→	LRR-repeats+AP-GTPase+COR	860	DCF12_13370	Cyanobacteria	Snowella sp.	GTP-binding protein [Snowella sp.].	GCA_003249095.1
PZV26136.1	<-Cluster1004_3clades||Cluster1843_2clades→||<-?||Cluster5_5clades→||<-Cluster1306_2clades<-?<-?||LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	885	DCF12_11170	Cyanobacteria	Snowella sp.	GTPase [Snowella sp.].	GCA_003249095.1
PZW23552.1	LRR-repeats→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	813	EI42_04935	Chloroflexi	Thermosporothrix hazakensis	GTPase SAR1 family protein, partial [Thermosporothrix hazakensis].	GCA_003253565.1
QDV38731.1	RelE-ParE→ WCAK→?→||<-Cluster2079_2clades||?→?→?→ LRR-repeats+AP-GTPase+COR+DUF4404*→	LRR-repeats+AP-GTPase+COR+DUF4404	887	slrP	Planctomycetes	Tautonia plasticadhaerens	E3 ubiquitin-protein ligase SlrP [Tautonia plasticadhaerens].	GCA_007752535.1
QEN02468.1	HTH→?→?→ LRR-repeats+AP-GTPase+COR+TIR*→||<-?<-ABC_membrane+ABC_tran||Cyanophycinsyn-ATPgrasp→ Cyanophycinsyn-ATPgrasp→	LRR-repeats+AP-GTPase+COR+TIR	1307	EWH46_18040	Betaproteobacteria	Sphaerotilus natans subsp. sulfidivorans	TIR domain-containing protein [Sphaerotilus natans subsp. sulfidivorans].	GCA_008329925.1
QHA06431.1	LRR-repeats+AP-GTPase+COR*→||<-?||?→||<-?<-SIGMA-HTH<-?<-SIGMA-HTH	LRR-repeats+AP-GTPase+COR	1022	GQF42_26905	Actinobacteria	Streptomyces broussonetiae	GTPase [Streptomyces broussonetiae].	GCA_009796285.1
QKQ77944.1	LRR-repeats+AP-GTPase+COR*→?→||<-?||?→||<-?||?→ ClpABN-AAA+ClpABC-AAA→||<-PSE<-SIG+TPR+TPR+TPR+TPR+TPR+TPR	LRR-repeats+AP-GTPase+COR	894	FBB35_26070	Cyanobacteria	Nostoc sp. TCL240-02	GTPase [Nostoc sp. TCL240-02].	GCA_013343235.1
QLE48778.1	ABhydrolase→?→||<-?||LRR-repeats+AP-GTPase+COR+TIR*→||<-PSE<-?||?→||<-?<-SIG+NUDIX<-?<-?<-Cluster5_5clades	LRR-repeats+AP-GTPase+COR+TIR	1021	FD724_12065	Cyanobacteria	Nostoc sp. C057	TIR domain-containing protein [Nostoc sp. C057].	GCA_013393925.1
QLH39529.1	Cluster850_2clades→?→?→ PRTase→||<-ENDO3+NUDIX<-?||LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	816	HWD60_12020	Alphaproteobacteria	Defluviicoccus sp.	leucine-rich repeat domain-containing protein [Defluviicoccus sp.].	GCA_013414705.1
RAM50807.1	LRR-repeats+AP-GTPase+COR+TIR*→?→||<-SIG+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM	LRR-repeats+AP-GTPase+COR+TIR	849	C6Y22_14980	Cyanobacteria	Hapalosiphonaceae cyanobacterium JJU2	hypothetical protein C6Y22_14980 [Hapalosiphonaceae cyanobacterium JJU2].	GCA_003261315.1
RCJ18019.1	<-Pkinase+Pentapeptide<-?<-?||?→||<-?<-TIR+EAD9<-?||LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	986	A6770_33290	Cyanobacteria	Nostoc minutum NIES-26	GTPase [Nostoc minutum NIES-26].	GCA_003326215.1
RCJ19389.1	LRR-repeats+AP-GTPase+COR*→||<-ClpABN-AAA+ClpABC-AAA<-?||METHYLASE→	LRR-repeats+AP-GTPase+COR	907	A6S26_26810	Cyanobacteria	Nostoc sp. ATCC 43529	GTPase [Nostoc sp. ATCC 43529].	GCA_003326205.1
RCJ25694.1	<-Pkinase+Pentapeptide<-?<-?||?→||<-?||LRR-repeats+AP-GTPase+COR+TIR*→||<-?<-?<-?||?→||<-NUDIX	LRR-repeats+AP-GTPase+COR+TIR	962	A6S26_15250	Cyanobacteria	Nostoc sp. ATCC 43529	GTPase [Nostoc sp. ATCC 43529].	GCA_003326205.1
RCJ30096.1	CR-REase5→ LRR-repeats+AP-GTPase+COR*→?→||<-?||?→||<-?||?→ ClpABN-AAA+ClpABC-AAA→	LRR-repeats+AP-GTPase+COR	894	A6770_21505	Cyanobacteria	Nostoc minutum NIES-26	GTPase [Nostoc minutum NIES-26].	GCA_003326215.1
RCJ30909.1	Cyanophycinsyn-ATPgrasp→||<-Cluster833_2clades<-?||?→||<-?<-Four-helical-protein<-?||LRR-repeats+AP-GTPase+COR+TIR*→||<-ncRNA<-?<-?<-?||?→||<-?||?→ Thioredoxin→	LRR-repeats+AP-GTPase+COR+TIR	928	A6770_20515	Cyanobacteria	Nostoc minutum NIES-26	hypothetical protein A6770_20515 [Nostoc minutum NIES-26].	GCA_003326215.1
RCJ31306.1	METHYLASE→||<-Arginase<-?<-?||LRR-repeats+AP-GTPase+COR+TIR*→?→?→||<-?<-?||?→ Pentapeptide-repeats→	LRR-repeats+AP-GTPase+COR+TIR	1103	A6770_20105	Cyanobacteria	Nostoc minutum NIES-26	GTPase [Nostoc minutum NIES-26].	GCA_003326215.1
RCJ40793.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1079	A6770_10335	Cyanobacteria	Nostoc minutum NIES-26	GTPase [Nostoc minutum NIES-26].	GCA_003326215.1
RCJ41185.1	<-TM||?→||<-?||?→||<-?||?→ LRR-repeats+AP-GTPase+COR+TM+TM*→	LRR-repeats+AP-GTPase+COR+TM+TM	837	A6770_08860	Cyanobacteria	Nostoc minutum NIES-26	hypothetical protein A6770_08860 [Nostoc minutum NIES-26].	GCA_003326215.1
RCV66029.1	LRR-repeats+AP-GTPase+COR→ *?→||<-?<-?||?→||<-?<-?||LRR-repeats→ LRR-repeats+AP-GTPase+COR→*	LRR-repeats+AP-GTPase+COR	640	C5S53_00730	Euryarchaeota	Methanophagales archaeon	GTPase SAR1 family protein [Methanophagales archaeon].	GCA_003336485.1
RCV66037.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	730	C5S53_00775	Euryarchaeota	Methanophagales archaeon	Leucine-rich repeat (LRR) protein [Methanophagales archaeon].	GCA_003336485.1
REJ39442.1	SIG+TM+TM+TM+TM+TM+TM+TM→||<-?||Mbetalac→ SAM-methylase→?→||<-?<-SIG+TPM_phosphatase+TM+TM+TM||PSE→ LRR-repeats+AP-GTPase+COR+TM+TM*→||<-?<-?<-?<-Pro_CA||?→||<-?<-tRNA<-tRNA<-Ferredoxin-betagrasp	LRR-repeats+AP-GTPase+COR+TM+TM	898	DWQ54_21980	Cyanobacteria	Microcystis flos-aquae TF09	GTP-binding protein [Microcystis flos-aquae TF09].	GCA_003390815.1
REJ48778.1	SIG+TM+TM+TM+TM+TM+TM+TM→||<-?||Mbetalac→ SAM-methylase→?→||<-?<-SIG+TPM_phosphatase+TM+TM+TM||PSE→ LRR-repeats+AP-GTPase+COR+TM+TM*→	LRR-repeats+AP-GTPase+COR+TM+TM	852	DWQ53_05035	Cyanobacteria	Microcystis flos-aquae DF17	GTP-binding protein [Microcystis flos-aquae DF17].	GCA_003389435.1
REJ60675.1	SIG+TM+TM+TM+TM+TM+TM+TM→||<-?||Mbetalac→ SAM-methylase→?→||<-?<-SIG+TPM_phosphatase+TM+TM+TM||PSE→ LRR-repeats+AP-GTPase+COR+TM+TM*→||<-?<-?<-?<-Pro_CA||?→||<-?<-tRNA<-tRNA<-Ferredoxin-betagrasp	LRR-repeats+AP-GTPase+COR+TM+TM	826	DWQ56_05670	Cyanobacteria	Microcystis aeruginosa DA14	GTP-binding protein [Microcystis aeruginosa DA14].	GCA_003388675.1

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RFP53135.1	LRR-repeats+AP-GTPase+COR*→||<-?||?→||<-tRNA||?→?→?→ Cluster1088_2clades→	LRR-repeats+AP-GTPase+COR	695	BJG00_017645	Cyanobacteria	Limnothrix sp. CACIAM 69d	hypothetical protein BJG00_017645 [Limnothrix sp. CACIAM 69d].	GCA_001913845.2
RFP63081.1	<-CR-REase5||LRR-repeats+AP-GTPase+COR*→ LRR-repeats→	LRR-repeats+AP-GTPase+COR	886	BJG00_001105	Cyanobacteria	Limnothrix sp. CACIAM 69d	GTPase [Limnothrix sp. CACIAM 69d].	GCA_001913845.2
RIK29270.1	LRR-repeats+AP-GTPase+COR*→||<-?<-?<-?<-Mbetalac<-?<-ABC-ATPase<-TM+TM+TM+TM+TM	LRR-repeats+AP-GTPase+COR	1096	DCC56_13010	Chloroflexi	Anaerolineae bacterium	hypothetical protein DCC56_13010 [Anaerolineae bacterium].	GCA_003577395.1
RJO63533.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1030	C4523_20060	Deltaproteobacteria	Myxococcales bacterium	hypothetical protein C4523_20060 [Myxococcales bacterium].	GCA_003598065.1
RJP51705.1	TM+TM+TM+TM+TM+TM+TM+TM→?→?→||<-?||?→ Cluster1070_2clades→ REase→ LRR-repeats+AP-GTPase+COR*→||<-?||?→?→?→||<-Cluster1854_2clades	LRR-repeats+AP-GTPase+COR	984	C4583_08075	Chloroflexi	Anaerolineaceae bacterium	hypothetical protein C4583_08075 [Anaerolineaceae bacterium].	GCA_003598975.1
RKS02636.1	LRR-repeats+AP-GTPase+COR+TM+TM*→	LRR-repeats+AP-GTPase+COR+TM+TM	1044	C8C84_2360	Bacteroidetes	Flavobacterium sp. 102	RocCOR-like putative regulator of kinase activity [Flavobacterium sp. 102].	GCA_003634615.1
RKZ87118.1	LRR-repeats+AP-GTPase+COR*→ AP-GTPase+COR→ COR→	LRR-repeats+AP-GTPase+COR	159	DRR19_14025	Gammaproteobacteria	Gammaproteobacteria bacterium	hypothetical protein DRR19_14025 [Gammaproteobacteria bacterium].	GCA_003646175.1
RKZ92191.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	778	DRR19_04995	Gammaproteobacteria	Gammaproteobacteria bacterium	hypothetical protein DRR19_04995 [Gammaproteobacteria bacterium].	GCA_003646175.1
RLC02552.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	868	DRI57_29970	Deltaproteobacteria	Deltaproteobacteria bacterium	hypothetical protein DRI57_29970, partial [Deltaproteobacteria bacterium].	GCA_003647425.1
RLC14341.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	442	DRI57_14615	Deltaproteobacteria	Deltaproteobacteria bacterium	hypothetical protein DRI57_14615, partial [Deltaproteobacteria bacterium].	GCA_003647425.1
RLC16559.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	930	DRI57_11050	Deltaproteobacteria	Deltaproteobacteria bacterium	hypothetical protein DRI57_11050 [Deltaproteobacteria bacterium].	GCA_003647425.1
RLD05606.1	UvsW-A18→ LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	759	DRI32_03940	Chloroflexi	Chloroflexi bacterium	GTP-binding protein [Chloroflexi bacterium].	GCA_003648185.1
RLS84177.1	SIG+AP-GTPase+COR+TIR→ *FGS+LRR-repeats+AP-GTPase+COR+TIR→*	SIG+AP-GTPase+COR+TIR	879	DWI04_01885	Planctomycetes	Planctomycetes bacterium	TIR domain-containing protein, partial [Planctomycetes bacterium].	GCA_003669255.1
RLS84178.1	FGS+LRR-repeats+AP-GTPase+COR+TIR*→	FGS+LRR-repeats+AP-GTPase+COR+TIR	1292	DWI04_01890	Planctomycetes	Planctomycetes bacterium	hypothetical protein DWI04_01890, partial [Planctomycetes bacterium].	GCA_003669255.1
RME07294.1	RVT→?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	780	D6816_06800	Bacteroidetes	Bacteroidetes bacterium	hypothetical protein D6816_06800 [Bacteroidetes bacterium].	GCA_003694615.1
RMG75718.1	LRR-repeats+AP-GTPase+COR*→?→ FGS→	LRR-repeats+AP-GTPase+COR	691	D6722_00510	Bacteroidetes	Bacteroidetes bacterium	hypothetical protein D6722_00510 [Bacteroidetes bacterium].	GCA_003696875.1
RPH24755.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	627	EHM93_20250	Bacteroidetes	Bacteroidales bacterium	GTP-binding protein, partial [Bacteroidales bacterium].	GCA_003818205.1
RPI17218.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	944	EHM58_10175	Ignavibacteriae	Ignavibacteriae bacterium	GTP-binding protein [Ignavibacteriae bacterium].	GCA_003820375.1
RPJ19448.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	750	EHM33_30260	Chloroflexi	Chloroflexi bacterium	hypothetical protein EHM33_30260, partial [Chloroflexi bacterium].	GCA_003820175.1
RPJ72349.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	496	EHM20_13865	Alphaproteobacteria	Alphaproteobacteria bacterium	GTP-binding protein, partial [Alphaproteobacteria bacterium].	GCA_003820255.1
RQW02493.1	LRR-repeats+AP-GTPase+COR+DrHyd*→?→?→ Cluster1207_2clades→?→ Cluster2271_2clades→	LRR-repeats+AP-GTPase+COR+DrHyd	763	EH223_12385	Bacteria	candidate division KSB1 bacterium	hypothetical protein EH223_12385, partial [candidate division KSB1 bacterium].	GCA_003854975.1
RUR83995.1	<-Cluster5_5clades||LRR-repeats→ LRR-repeats+AP-GTPase+COR+DUF4404*→||<-?<-ABC-ATPase||?→||<-REC	LRR-repeats+AP-GTPase+COR+DUF4404	746	DSM107007_30530	Cyanobacteria	Nostoc sp. PCC 7120 = FACHB-418	hypothetical protein DSM107007_30530 [Nostoc sp. PCC 7120 = FACHB-418].	GCA_003990585.1
RWX44973.1	<-Cluster1731_2clades<-?<-?||?→?→ LRR-repeats+AP-GTPase+COR*→?→?→||<-Cluster1409_2clades	LRR-repeats+AP-GTPase+COR	648	H206_01140	Deltaproteobacteria	Candidatus Electrothrix aarhusiensis	hypothetical protein H206_01140 [Candidatus Electrothrix aarhusiensis].	GCA_004028505.1

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RWX45664.1	<-S18-HTH<-Cluster1004_3clades<-Cluster2139_2clades<-?<-?<-?||?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	605	H206_01449	Deltaproteobacteria	Candidatus Electrothrix aarhusiensis	hypothetical protein H206_01449 [Candidatus Electrothrix aarhusiensis].	GCA_004028505.1
RWX46469.1	Aminotran_1_2→||<-ABC-ATPase<-?<-?<-?<-?||LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	908	H206_00859	Deltaproteobacteria	Candidatus Electrothrix aarhusiensis	internalin A [Candidatus Electrothrix aarhusiensis].	GCA_004028505.1
RWX47043.1	LRR-repeats+AP-GTPase+COR+TM+TM+TM*→ WCAK→	LRR-repeats+AP-GTPase+COR+TM+TM+TM	873	H206_03377	Deltaproteobacteria	Candidatus Electrothrix aarhusiensis	Ras of Complex, Roc, domain of DAPkinase [Candidatus Electrothrix aarhusiensis].	GCA_004028505.1
RWX51844.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	785	VU01_10733	Deltaproteobacteria	Candidatus Electrothrix marina	hypothetical protein VU01_10733 [Candidatus Electrothrix marina].	GCA_004028495.1
RYD26380.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	442	EOP86_26045	Verrucomicrobia	Verrucomicrobiaceae bacterium	hypothetical protein EOP86_26045, partial [Verrucomicrobiaceae bacterium].	GCA_004143925.1
RYD41313.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	546	EOP85_12890	Verrucomicrobia	Verrucomicrobiaceae bacterium	hypothetical protein EOP85_12890, partial [Verrucomicrobiaceae bacterium].	GCA_004144085.1
RYD45970.1	LRR-repeats+AP-GTPase*→	LRR-repeats+AP-GTPase	529	EOP85_08340	Verrucomicrobia	Verrucomicrobiaceae bacterium	hypothetical protein EOP85_08340, partial [Verrucomicrobiaceae bacterium].	GCA_004144085.1
RYD85024.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	722	EOP84_03815	Verrucomicrobia	Verrucomicrobiaceae bacterium	TIR domain-containing protein, partial [Verrucomicrobiaceae bacterium].	GCA_004144095.1
RYE22211.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	770	EOP45_08535	Bacteroidetes	Sphingobacteriaceae bacterium	GTPase, partial [Sphingobacteriaceae bacterium].	GCA_004144285.1
RYE59584.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1318	EOP48_00430	Bacteroidetes	Sphingobacteriales bacterium	TIR domain-containing protein [Sphingobacteriales bacterium].	GCA_004144425.1
RYF36188.1	LRR-repeats+AP-GTPase*→	LRR-repeats+AP-GTPase	370	EOO38_28030	Bacteroidetes	Cytophagaceae bacterium	hypothetical protein EOO38_28030, partial [Cytophagaceae bacterium].	GCA_004145185.1
RYY12294.1	LRR-repeats+AP-GTPase*→	LRR-repeats+AP-GTPase	540	EOO04_33805	Bacteroidetes	Chitinophagaceae bacterium	hypothetical protein EOO04_33805, partial [Chitinophagaceae bacterium].	GCA_004172945.1
RYZ86256.1	LRR-repeats→ AP-GTPase+COR*→	AP-GTPase+COR	573	EOP04_14245	Proteobacteria	Proteobacteria bacterium	hypothetical protein EOP04_14245, partial [Proteobacteria bacterium].	GCA_004193275.1
RZK07337.1	LRR-repeats+AP-GTPase*→	LRR-repeats+AP-GTPase	262	EOO43_21605	Bacteroidetes	Flavobacterium sp.	hypothetical protein EOO43_21605, partial [Flavobacterium sp.].	GCA_004211555.1
RZK10466.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	421	EOO43_20245	Bacteroidetes	Flavobacterium sp.	hypothetical protein EOO43_20245, partial [Flavobacterium sp.].	GCA_004211555.1
RZN33809.1	pc1599→ Cluster1746_2clades→?→?→ Calcineurin→||<-tRNA||LRR-repeats+AP-GTPase+COR+TM+TM*→?→ Aminotran_1_2→||<-?<-?||Cluster1483_2clades→	LRR-repeats+AP-GTPase+COR+TM+TM	832	EF813_10660	Euryarchaeota	Methanosarcinales archaeon	GTP-binding protein [Methanosarcinales archaeon].	GCA_004211975.1
SCD37814.1	LRR-repeats+AP-GTPase+COR*→||<-NUDIX	LRR-repeats+AP-GTPase+COR	1358	GA0115243_1012136	Actinobacteria	Streptomyces sp. ScaeMP-e83	Leucine-rich repeat (LRR) protein, partial [Streptomyces sp. ScaeMP-e83].	GCA_900091775.1
SDD54826.1	Mbetalac→?→ LRR-repeats+AP-GTPase+COR*→||<-?<-ICLR-HTH||?→?→?→ ABhydrolase→	LRR-repeats+AP-GTPase+COR	887	SAMN05660690_4513	Actinobacteria	Geodermatophilus telluris	Leucine rich repeat-containing protein [Geodermatophilus telluris].	GCA_900102745.1
SEA38734.1	LRR-repeats+AP-GTPase+COR+TIR*→?→?→||<-Thioredoxin||YBAK→	LRR-repeats+AP-GTPase+COR+TIR	849	SAMN05660964_01466	Gammaproteobacteria	Thiothrix caldifontis	Leucine Rich repeat-containing protein [Thiothrix caldifontis].	GCA_900107695.1
SEM73063.1	<-ABC-ATPase<-?||?→?→||<-?||LRR-repeats+AP-GTPase+COR*→?→?→?→||<-?<-?<-SIR2	LRR-repeats+AP-GTPase+COR	717	SAMN05660976_05948	Actinobacteria	Nonomuraea pusilla	GTPase SAR1 family protein [Nonomuraea pusilla].	GCA_900109355.1
SFG01605.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	812	SAMN05216175_102423	Gammaproteobacteria	Neptunomonas qingdaonensis	internalin A, partial [Neptunomonas qingdaonensis].	GCA_900113275.1

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SFL80318.1	LRR-repeats+AP-GTPase+COR+DrHyd*→?→?→?→?→||<-?<-SIG+TM+TM+TM+TM	LRR-repeats+AP-GTPase+COR+DrHyd	738	SAMN05421863_1004142	Betaproteobacteria	Nitrosomonas communis	Ras of Complex, Roc, domain of DAPkinase [Nitrosomonas communis].	GCA_900114745.1
SHH94122.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	756	VA7868_00952	Gammaproteobacteria	Vibrio aerogenes CECT 7868	Ras family protein [Vibrio aerogenes CECT 7868].	GCA_900130105.1
SHI24236.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	954	inlA	Gammaproteobacteria	Vibrio aerogenes CECT 7868	Internalin-A precursor [Vibrio aerogenes CECT 7868].	GCA_900130105.1
SKA94563.1	METHYLASE→?→||<-?||SIG+Trypsin+PDZ→?→ Cluster978_2clades→ LRR-repeats+AP-GTPase+COR+TIR*→?→?→ GDSL→	LRR-repeats+AP-GTPase+COR+TIR	1235	SAMN02745166_02182	Verrucomicrobia	Prosthecobacter debontii	Leucine-rich repeat (LRR) protein [Prosthecobacter debontii].	GCA_900167535.1
SKC31468.1	CI→ CI→?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1108	CZ809_00946	Gammaproteobacteria	Photobacterium piscicola	Ras family protein [Photobacterium piscicola].	GCA_900166965.1
SMS01989.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1190	inlA	Gammaproteobacteria	Vibrio mangrovi	Internalin-A precursor [Vibrio mangrovi].	GCA_900184095.1
SNS86340.1	SIG+Concanavalin-like+SUN→ LRR-repeats+AP-GTPase+COR*→?→?→?→||<-?<-ABC-ATPase	LRR-repeats+AP-GTPase+COR	686	SAMN06264365_12694	Actinobacteria	Actinoplanes regularis	hypothetical protein SAMN06264365_12694 [Actinoplanes regularis].	GCA_900188005.1
SUS04594.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	965	DF3PB_1340002	Alphaproteobacteria	uncultured Defluviicoccus sp.	Leucine-rich repeat (LRR) protein (fragment) [uncultured Defluviicoccus sp.].	GCA_900498315.1
SUS07166.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1031	DF3PB_390011	Alphaproteobacteria	uncultured Defluviicoccus sp.	conserved hypothetical protein [uncultured Defluviicoccus sp.].	GCA_900498315.1
TAA73809.1	<-Cluster1510_2clades<-?<-?||LRR-repeats+AP-GTPase+COR→ *LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	571	CDV28_1587	Deltaproteobacteria	Candidatus Electronema sp. GS	hypothetical protein CDV28_1587 [Candidatus Electronema sp. GS].	GCA_004284765.1
TAA73810.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	678	CDV28_1588	Deltaproteobacteria	Candidatus Electronema sp. GS	hypothetical protein CDV28_1588 [Candidatus Electronema sp. GS].	GCA_004284765.1
TAA74005.1	LRR-repeats+AP-GTPase+COR*→ SIG+TM+TM+TM+TM→	LRR-repeats+AP-GTPase+COR	803	CDV28_14413	Deltaproteobacteria	Candidatus Electronema sp. GS	hypothetical protein CDV28_14413 [Candidatus Electronema sp. GS].	GCA_004284765.1
TAA74213.1	Cluster1147_2clades→?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	680	CDV28_13522	Deltaproteobacteria	Candidatus Electronema sp. GS	hypothetical protein CDV28_13522 [Candidatus Electronema sp. GS].	GCA_004284765.1
TAA75585.1	Cluster2427_2clades→?→ Cluster1969_2clades→ Thioredoxin→?→?→?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	694	CDV28_10542	Deltaproteobacteria	Candidatus Electronema sp. GS	hypothetical protein CDV28_10542 [Candidatus Electronema sp. GS].	GCA_004284765.1
TAA76176.1	<-SIG+HSP70<-?<-?<-?<-?||LRR-repeats+AP-GTPase+COR*→||<-?<-?<-?<-?<-RelE-ParE	LRR-repeats+AP-GTPase+COR	627	CDV28_10174	Deltaproteobacteria	Candidatus Electronema sp. GS	hypothetical protein CDV28_10174 [Candidatus Electronema sp. GS].	GCA_004284765.1
TAD75245.1	RelE-ParE→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	952	EA001_14520	Cyanobacteria	Oscillatoriales cyanobacterium	GTPase [Oscillatoriales cyanobacterium].	GCA_004292515.1
TAD78959.1	HISKIN→?→ LRR-repeats+AP-GTPase+COR*→||<-Cluster971_2clades	LRR-repeats+AP-GTPase+COR	1063	EA001_05550	Cyanobacteria	Oscillatoriales cyanobacterium	GTPase [Oscillatoriales cyanobacterium].	GCA_004292515.1
TAE00317.1	<-Cluster1805_2clades||?→?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	631	EAZ97_06315	Bacteroidetes	Bacteroidetes bacterium	hypothetical protein EAZ97_06315 [Bacteroidetes bacterium].	GCA_004292785.1
TAE06670.1	LRR-repeats→ LRR-repeats+AP-GTPase+COR+DUF4404*→?→?→||<-Pentapeptide-repeats	LRR-repeats+AP-GTPase+COR+DUF4404	900	EAZ94_30300	Cyanobacteria	Oscillatoriales cyanobacterium	GTPase [Oscillatoriales cyanobacterium].	GCA_004292775.1
TAE07007.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	808	EAZ95_18790	Bacteroidetes	Bacteroidetes bacterium	GTP-binding protein [Bacteroidetes bacterium].	GCA_004292795.1
TAE07511.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	774	EAZ95_18335	Bacteroidetes	Bacteroidetes bacterium	hypothetical protein EAZ95_18335 [Bacteroidetes bacterium].	GCA_004292795.1
TAE08557.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	487	EAZ95_17095	Bacteroidetes	Bacteroidetes bacterium	hypothetical protein EAZ95_17095, partial [Bacteroidetes bacterium].	GCA_004292795.1
TAE08925.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	911	EAZ94_23755	Cyanobacteria	Oscillatoriales cyanobacterium	hypothetical protein EAZ94_23755 [Oscillatoriales cyanobacterium].	GCA_004292775.1
TAE12199.1	LRR-repeats+AP-GTPase+COR*→ SIG+TM+TM+TM+TM+TM→ REase→	LRR-repeats+AP-GTPase+COR	811	EAZ95_12720	Bacteroidetes	Bacteroidetes bacterium	hypothetical protein EAZ95_12720, partial [Bacteroidetes bacterium].	GCA_004292795.1

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TAE14819.1	<-Pkinase+TM||?→ PIN→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	769	EAZ95_09495	Bacteroidetes	Bacteroidetes bacterium	GTP-binding protein [Bacteroidetes bacterium].	GCA_004292795.1
TAE15606.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	866	EAZ95_08545	Bacteroidetes	Bacteroidetes bacterium	GTP-binding protein [Bacteroidetes bacterium].	GCA_004292795.1
TAE15646.1	<-CR-REase5<-?<-?||LRR-repeats→?→ PSE→ LRR-repeats+AP-GTPase+COR*→?→?→?→?→||<-?<-PSE<-?||Pentapeptide-repeats→	LRR-repeats+AP-GTPase+COR	1106	EAZ94_03785	Cyanobacteria	Oscillatoriales cyanobacterium	GTP-binding protein [Oscillatoriales cyanobacterium].	GCA_004292775.1
TAE18080.1	<-ABC_membrane+ABC_tran||?→?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	778	EAZ95_05200	Bacteroidetes	Bacteroidetes bacterium	hypothetical protein EAZ95_05200 [Bacteroidetes bacterium].	GCA_004292795.1
TAE30098.1	LRR-repeats→ LRR-repeats+AP-GTPase+COR+DUF4404*→?→?→||<-Pentapeptide-repeats	LRR-repeats+AP-GTPase+COR+DUF4404	1078	EAZ93_01305	Cyanobacteria	Oscillatoriales cyanobacterium	GTPase [Oscillatoriales cyanobacterium].	GCA_004292845.1
TAE37012.1	LRR-repeats+AP-GTPase+COR+DUF4404*→?→?→||<-Pentapeptide-repeats	LRR-repeats+AP-GTPase+COR+DUF4404	1282	EAZ90_27320	Cyanobacteria	Oscillatoriales cyanobacterium	GTPase [Oscillatoriales cyanobacterium].	GCA_004292895.1
TAE38303.1	LRR-repeats+AP-GTPase+COR*→?→?→ PSE→?→ PSE→?→||<-?<-PSE<-?||Pentapeptide-repeats→	LRR-repeats+AP-GTPase+COR	909	EAZ90_25170	Cyanobacteria	Oscillatoriales cyanobacterium	GTP-binding protein [Oscillatoriales cyanobacterium].	GCA_004292895.1
TAE48904.1	LRR-repeats→?→?→?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	695	EAZ88_23370	Cyanobacteria	Oscillatoriales cyanobacterium	GTP-binding protein, partial [Oscillatoriales cyanobacterium].	GCA_004292945.1
TAE51174.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	790	EAZ89_10570	Bacteroidetes	Bacteroidetes bacterium	hypothetical protein EAZ89_10570, partial [Bacteroidetes bacterium].	GCA_004292985.1
TAE53250.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	912	EAZ88_12540	Cyanobacteria	Oscillatoriales cyanobacterium	hypothetical protein EAZ88_12540 [Oscillatoriales cyanobacterium].	GCA_004292945.1
TAE59343.1	LRR-repeats+AP-GTPase+COR+EAD11*→	LRR-repeats+AP-GTPase+COR+EAD11	737	EAZ89_02575	Bacteroidetes	Bacteroidetes bacterium	hypothetical protein EAZ89_02575 [Bacteroidetes bacterium].	GCA_004292985.1
TAE66346.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	742	EAZ85_15975	Bacteroidetes	Bacteroidetes bacterium	GTP-binding protein, partial [Bacteroidetes bacterium].	GCA_004293265.1
TAE67608.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	911	EAZ86_16170	Cyanobacteria	Oscillatoriales cyanobacterium	hypothetical protein EAZ86_16170 [Oscillatoriales cyanobacterium].	GCA_004292955.1
TAE67866.1	FGS→?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	987	EAZ85_14755	Bacteroidetes	Bacteroidetes bacterium	hypothetical protein EAZ85_14755 [Bacteroidetes bacterium].	GCA_004293265.1
TAE68409.1	<-CR-REase5<-?||?→||<-?||LRR-repeats→?→?→ LRR-repeats+AP-GTPase+COR*→?→?→?→ PSE→||<-?<-PSE<-?||Pentapeptide-repeats→	LRR-repeats+AP-GTPase+COR	1061	EAZ86_13565	Cyanobacteria	Oscillatoriales cyanobacterium	GTP-binding protein [Oscillatoriales cyanobacterium].	GCA_004292955.1
TAE73426.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1078	EAZ85_07065	Bacteroidetes	Bacteroidetes bacterium	hypothetical protein EAZ85_07065 [Bacteroidetes bacterium].	GCA_004293265.1
TAE76344.1	LRR-repeats+AP-GTPase+COR*→||<-Cluster1921_2clades	LRR-repeats+AP-GTPase+COR	919	EAZ85_00290	Bacteroidetes	Bacteroidetes bacterium	hypothetical protein EAZ85_00290 [Bacteroidetes bacterium].	GCA_004293265.1
TAE86412.1	LRR-repeats+AP-GTPase+COR+TIR*→||<-?<-Cluster409_3clades	LRR-repeats+AP-GTPase+COR+TIR	1151	EAY81_05595	Bacteroidetes	Bacteroidetes bacterium	TIR domain-containing protein [Bacteroidetes bacterium].	GCA_004293295.1
TAF49891.1	LRR-repeats+AP-GTPase+COR+DUF4404*→	LRR-repeats+AP-GTPase+COR+DUF4404	845	EAZ61_13785	Cyanobacteria	Oscillatoriales cyanobacterium	GTPase, partial [Oscillatoriales cyanobacterium].	GCA_004293855.1
TAF64535.1	LRR-repeats+AP-GTPase+COR+EAD11*→	LRR-repeats+AP-GTPase+COR+EAD11	1108	EAZ55_10760	Bacteroidetes	Cytophagales bacterium	hypothetical protein EAZ55_10760 [Cytophagales bacterium].	GCA_004293905.1
TAF89999.1	GTPase-AIG→?→?→||<-?<-?||LRR-repeats+AP-GTPase+COR+DUF4404*→?→?→||<-Pentapeptide-repeats	LRR-repeats+AP-GTPase+COR+DUF4404	1282	EAZ49_10560	Cyanobacteria	Oscillatoriales cyanobacterium	GTPase [Oscillatoriales cyanobacterium].	GCA_004294035.1
TAF91931.1	<-CR-REase5<-?<-?||LRR-repeats→?→?→ LRR-repeats+AP-GTPase+COR*→?→?→?→ PSE→||<-?<-PSE<-?||Pentapeptide-repeats→	LRR-repeats+AP-GTPase+COR	952	EAZ49_03665	Cyanobacteria	Oscillatoriales cyanobacterium	GTP-binding protein [Oscillatoriales cyanobacterium].	GCA_004294035.1
TAG07081.1	RVT→?→ LRR-repeats+AP-GTPase+COR+ACYC*→?→||<-?<-?<-HISKIN	LRR-repeats+AP-GTPase+COR+ACYC	962	EAZ44_01180	Bacteroidetes	Cytophagia bacterium	hypothetical protein EAZ44_01180 [Cytophagia bacterium].	GCA_004294005.1
TAG17458.1	<-CENPB||?→?→||<-?<-?||Aminotran_1_2→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	975	EAZ38_17395	Bacteroidetes	Cytophagales bacterium	hypothetical protein EAZ38_17395 [Cytophagales bacterium].	GCA_004293585.1
TAG62903.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	778	EAZ28_01955	Cyanobacteria	Oscillatoriales cyanobacterium	hypothetical protein EAZ28_01955, partial [Oscillatoriales cyanobacterium].	GCA_004294275.1

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TAG65048.1	LRR-repeats→?→ PSE→ LRR-repeats+AP-GTPase+COR*→ PSE→?→?→ PSE→||<-?<-PSE<-?||Pentapeptide-repeats→	LRR-repeats+AP-GTPase+COR	939	EAZ25_17645	Cyanobacteria	Oscillatoriales cyanobacterium	GTP-binding protein [Oscillatoriales cyanobacterium].	GCA_004294345.1
TAG86009.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	565	EAZ18_26350	Cyanobacteria	Oscillatoriales cyanobacterium	GTP-binding protein, partial [Oscillatoriales cyanobacterium].	GCA_004294385.1
TAG86671.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	892	EAZ20_12320	Bacteroidetes	Bacteroidetes bacterium	hypothetical protein EAZ20_12320, partial [Bacteroidetes bacterium].	GCA_004294185.1
TAG91526.1	FGS→?→ LRR-repeats+AP-GTPase*→	LRR-repeats+AP-GTPase	279	EAZ20_03245	Bacteroidetes	Bacteroidetes bacterium	hypothetical protein EAZ20_03245, partial [Bacteroidetes bacterium].	GCA_004294185.1
TAG93154.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	935	EAZ19_16680	Cyanobacteria	Oscillatoriales cyanobacterium	hypothetical protein EAZ19_16680 [Oscillatoriales cyanobacterium].	GCA_004293705.1
TAH14728.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	344	EAZ09_26195	Cyanobacteria	Oscillatoriales cyanobacterium	GTP-binding protein, partial [Oscillatoriales cyanobacterium].	GCA_004293745.1
TAH21032.1	Cluster1569_2clades→ ABhydrolase→||<-?||?→?→?→||<-?||LRR-repeats+AP-GTPase*→	LRR-repeats+AP-GTPase	257	EAZ08_04815	Bacteroidetes	Cytophagales bacterium	hypothetical protein EAZ08_04815 [Cytophagales bacterium].	GCA_004294445.1
TAK37700.1	LRR-repeats+AP-GTPase+COR+EAD11*→ Cluster5_5clades→?→ METHYLASE→	LRR-repeats+AP-GTPase+COR+EAD11	783	EPO28_11660	Bacteroidetes	Saprospiraceae bacterium	hypothetical protein EPO28_11660 [Saprospiraceae bacterium].	GCA_004297645.1
TAK50544.1	Cluster1854_2clades→?→?→ PSE→?→||<-Cluster5_5clades||LRR-repeats→ LRR-repeats+AP-GTPase+COR+EAD11*→?→?→?→?→ ABhydrolase→||<-Cluster5_5clades	LRR-repeats+AP-GTPase+COR+EAD11	588	EPO28_00120	Bacteroidetes	Saprospiraceae bacterium	hypothetical protein EPO28_00120 [Saprospiraceae bacterium].	GCA_004297645.1
TAK57982.1	HhH-RADC+JAB→||<-?||?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	666	EPO24_09130	Bacteroidetes	Bacteriodetes bacterium	GTP-binding protein, partial [Bacteriodetes bacterium].	GCA_004322375.1
TAK59812.1	LRR-repeats+AP-GTPase+COR+TIR*→ tRNA→ tRNA→?→?→ Cluster2248_2clades→	LRR-repeats+AP-GTPase+COR+TIR	884	EPO24_07295	Bacteroidetes	Bacteriodetes bacterium	TIR domain-containing protein [Bacteriodetes bacterium].	GCA_004322375.1
TAK63714.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	903	EPO24_03975	Bacteroidetes	Bacteriodetes bacterium	TIR domain-containing protein [Bacteriodetes bacterium].	GCA_004322375.1
TFV86935.1	LRR-repeats+AP-GTPase+COR+DrHyd*→	LRR-repeats+AP-GTPase+COR+DrHyd	783	E4K72_22790	Betaproteobacteria	Oxalobacteraceae bacterium OM1	hypothetical protein E4K72_22790, partial [Oxalobacteraceae bacterium OM1].	GCA_004570315.1
THV28317.1	TM→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1065	E9998_11935	Actinobacteria	Glycomyces paridis	hypothetical protein E9998_11935 [Glycomyces paridis].	GCA_004912155.1
TKJ39119.1	SIGMA-HTH→?→?→||<-?<-?<-?||LRR-repeats+AP-GTPase+COR*→||<-?<-Ferredoxin-RRM	LRR-repeats+AP-GTPase+COR	968	CEE37_11920	FCB group	candidate division LCP-89 bacterium B3_LCP	GTPase [candidate division LCP-89 bacterium B3_LCP].	GCA_005223185.1
TKJ40235.1	HISKIN→?→?→?→?→?→ ACET→ LRR-repeats+AP-GTPase+COR*→?→?→||<-?<-?<-SMPB||?→ Cluster1833_2clades→	LRR-repeats+AP-GTPase+COR	925	CEE37_07880	FCB group	candidate division LCP-89 bacterium B3_LCP	GTPase [candidate division LCP-89 bacterium B3_LCP].	GCA_005223185.1
TKJ41682.1	TPR+TPR→?→?→ RPN10→?→?→ LRR-repeats+AP-GTPase+COR*→||<-?||LRR-repeats+AP-GTPase+COR→||<-?<-tRNA||RADICAL-SAM→||<-tRNA<-MerR-HTH	LRR-repeats+AP-GTPase+COR	1047	CEE37_03700	FCB group	candidate division LCP-89 bacterium B3_LCP	hypothetical protein CEE37_03700 [candidate division LCP-89 bacterium B3_LCP].	GCA_005223185.1
TKZ22725.1	LRR-repeats+AP-GTPase+COR*→||<-?||COR→	LRR-repeats+AP-GTPase+COR	653	EBE85_34345	Cyanobacteria	Hormoscilla sp. GUM007	hypothetical protein EBE85_34345 [Hormoscilla sp. GUM007].	-
TKZ31764.1	Cluster1207_2clades→||<-?<-?<-?<-?<-?<-?||LRR-repeats+AP-GTPase+COR*→ COR→	LRR-repeats+AP-GTPase+COR	424	EBE86_14970	Cyanobacteria	Hormoscilla sp. GUM202	hypothetical protein EBE86_14970, partial [Hormoscilla sp. GUM202].	-
TLU81885.1	Cluster1765_2clades→||<-?<-?||InPase→||<-?||TM→ LRR-repeats+AP-GTPase+COR*→?→?→ ACT→||<-?<-?<-PSE<-DNAJ	LRR-repeats+AP-GTPase+COR	953	FDX21_09980	Chlorobi	Chlorobium sp.	hypothetical protein FDX21_09980 [Chlorobium sp.].	GCA_005862225.1
TLU87350.1	<-FGS<-?||?→||<-?<-?||PSE→?→?→ LRR-repeats+AP-GTPase+COR+TIR*→||<-PSE<-RelE-ParE	LRR-repeats+AP-GTPase+COR+TIR	892	FDX21_00465	Chlorobi	Chlorobium sp.	TIR domain-containing protein [Chlorobium sp.].	GCA_005862225.1
TMQ13801.1	LRR-repeats+AP-GTPase+COR*→ COR+TIR→	LRR-repeats+AP-GTPase+COR	391	E6J90_27900	Deltaproteobacteria	Deltaproteobacteria bacterium	GTP-binding protein, partial [Deltaproteobacteria bacterium].	GCA_005887915.1
TRT70055.1	LRR-repeats+AP-GTPase+COR+TM+TM*→	LRR-repeats+AP-GTPase+COR+TM+TM	710	EWV84_09945	Cyanobacteria	Microcystis sp. M_QC_C_20170808_M3Col	GTP-binding protein, partial [Microcystis sp. M_QC_C_20170808_M3Col].	GCA_007095505.1
TRT86788.1	SIG+TM+TM+TM+TM+TM+TM+TM→||<-?||Mbetalac→ SAM-methylase→?→||<-?<-SIG+TPM_phosphatase+TM+TM+TM||LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	597	EWV66_15420	Cyanobacteria	Microcystis sp. M_OC_Ca_00000000_C217Col	GTP-binding protein, partial [Microcystis sp. M_OC_Ca_00000000_C217Col].	GCA_007095585.1

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TRT92075.1	Mbetalac→ SAM-methylase→?→||<-?||?→||<-SIG+TPM_phosphatase+TM+TM+TM||LRR-repeats+AP-GTPase+COR+TM+TM*→||<-?<-?<-?<-Pro_CA||?→||<-?<-tRNA<-tRNA<-Ferredoxin-betagrasp	LRR-repeats+AP-GTPase+COR+TM+TM	874	EWV65_21090	Cyanobacteria	Microcystis flos-aquae Ma_QC_C_20070823_S18D	GTP-binding protein [Microcystis flos-aquae Ma_QC_C_20070823_S18D].	GCA_007095605.1
TRU14937.1	SIG+TM+TM+TM+TM+TM+TM+TM→||<-?||Mbetalac→ SAM-methylase→?→||<-?<-SIG+TPM_phosphatase+TM+TM+TM||LRR-repeats+AP-GTPase+COR+TM+TM*→||<-?<-?<-?<-Pro_CA||?→||<-?<-tRNA<-tRNA<-Ferredoxin-betagrasp	LRR-repeats+AP-GTPase+COR+TM+TM	874	EWV60_01670	Cyanobacteria	Microcystis sp. Msp_OC_L_20101000_S702	GTP-binding protein [Microcystis sp. Msp_OC_L_20101000_S702].	GCA_007095705.1
TRU25637.1	LRR-repeats+AP-GTPase+COR+TM+TM*→||<-?<-FGS<-?<-?||?→?→ Aminotran_1_2→	LRR-repeats+AP-GTPase+COR+TM+TM	921	EWV79_07400	Cyanobacteria	Microcystis aeruginosa Ma_MB_S_20031200_S102D	GTP-binding protein [Microcystis aeruginosa Ma_MB_S_20031200_S102D].	GCA_007095795.1
TRU29987.1	SIG+TM+TM+TM+TM+TM+TM+TM→||<-?||Mbetalac→ SAM-methylase→?→||<-?<-SIG+TPM_phosphatase+TM+TM+TM||LRR-repeats+AP-GTPase+COR+TM+TM*→||<-?<-?<-?<-?<-Pro_CA	LRR-repeats+AP-GTPase+COR+TM+TM	921	EWV80_03065	Cyanobacteria	Microcystis aeruginosa Ma_QC_B_20070730_S2	GTP-binding protein [Microcystis aeruginosa Ma_QC_B_20070730_S2].	GCA_007095805.1
TRU36579.1	SIG+TM+TM+TM+TM+TM+TM+TM→||<-PSE||Mbetalac→ SAM-methylase→?→||<-?<-SIG+TPM_phosphatase+TM+TM+TM||LRR-repeats+AP-GTPase+COR+TM+TM*→||<-?<-?<-?<-Pro_CA||?→||<-?<-tRNA<-tRNA<-Ferredoxin-betagrasp	LRR-repeats+AP-GTPase+COR+TM+TM	805	EWV78_08805	Cyanobacteria	Microcystis aeruginosa Ma_MB_F_20061100_S20D	GTP-binding protein [Microcystis aeruginosa Ma_MB_F_20061100_S20D].	GCA_007095855.1
TRU47882.1	CHTH→ LRR-repeats+AP-GTPase+COR+TM+TM*→	LRR-repeats+AP-GTPase+COR+TM+TM	874	EWV49_14300	Cyanobacteria	Microcystis aeruginosa Ma_QC_Ch_20071001_S25	GTP-binding protein [Microcystis aeruginosa Ma_QC_Ch_20071001_S25].	GCA_007095935.1
TRU57932.1	CHTH→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	559	EWV56_15605	Cyanobacteria	Microcystis aeruginosa Ma_QC_C_20070823_S13D	GTP-binding protein, partial [Microcystis aeruginosa Ma_QC_C_20070823_S13D].	GCA_007095965.1
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TRU95593.1	Ferredoxin-betagrasp→ tRNA→ tRNA→ SAM-methylase→?→||<-?<-SIG+TPM_phosphatase+TM+TM+TM||LRR-repeats+AP-GTPase+COR+TM+TM*→||<-?<-?<-?<-Pro_CA	LRR-repeats+AP-GTPase+COR+TM+TM	852	EWV73_20055	Cyanobacteria	Microcystis wesenbergii Mw_QC_B_20070930_S4D	GTP-binding protein [Microcystis wesenbergii Mw_QC_B_20070930_S4D].	GCA_007096105.1
TRU97707.1	Ferredoxin-betagrasp→ tRNA→ tRNA→ SAM-methylase→?→||<-?<-SIG+TPM_phosphatase+TM+TM+TM||LRR-repeats+AP-GTPase+COR+TM+TM*→||<-?<-?<-?<-Pro_CA	LRR-repeats+AP-GTPase+COR+TM+TM	943	EWV75_08635	Cyanobacteria	Microcystis wesenbergii Mw_QC_S_20081001_S30D	GTP-binding protein [Microcystis wesenbergii Mw_QC_S_20081001_S30D].	GCA_007096035.1
TRU98843.1	Ferredoxin-betagrasp→ tRNA→ tRNA→ SAM-methylase→?→||<-?<-SIG+TPM_phosphatase+TM+TM+TM||LRR-repeats+AP-GTPase+COR+TM+TM*→||<-?<-?<-?<-Pro_CA	LRR-repeats+AP-GTPase+COR+TM+TM	920	EWV74_15160	Cyanobacteria	Microcystis wesenbergii Mw_QC_S_20081001_S30	GTP-binding protein [Microcystis wesenbergii Mw_QC_S_20081001_S30].	GCA_007096535.1
TRV08313.1	Ferredoxin-betagrasp→ tRNA→ tRNA→ SAM-methylase→?→||<-?<-SIG+TPM_phosphatase+TM+TM+TM||LRR-repeats+AP-GTPase+COR+TM+TM*→?→||<-?<-?<-?||?→||<-Pro_CA	LRR-repeats+AP-GTPase+COR+TM+TM	751	EWV41_10615	Cyanobacteria	Microcystis wesenbergii Mw_MB_S_20031200_S109	GTP-binding protein [Microcystis wesenbergii Mw_MB_S_20031200_S109].	GCA_007096585.1
TRV43292.1	SAM-methylase→?→||<-?<-SIG+TPM_phosphatase+TM+TM+TM||LRR-repeats+AP-GTPase+COR+TM+TM*→||<-?<-?<-?<-Pro_CA||?→||<-?<-tRNA<-tRNA<-Ferredoxin-betagrasp	LRR-repeats+AP-GTPase+COR+TM+TM	874	EWV87_21500	Cyanobacteria	Microcystis panniformis Mp_GB_SS_20050300_S99	GTP-binding protein [Microcystis panniformis Mp_GB_SS_20050300_S99].	GCA_007096815.1
TVP67596.1	LRR-repeats+AP-GTPase+COR+TM+TM*→	LRR-repeats+AP-GTPase+COR+TM+TM	667	EA343_00435	Cyanobacteria	Nodularia sp. (in: Bacteria)	GTPase, partial [Nodularia sp. (in: Bacteria)].	GCA_007692755.1
TVQ58623.1	LRR-repeats+AP-GTPase+COR*→||<-Cluster2343_2clades	LRR-repeats+AP-GTPase+COR	976	EA366_06380	Cyanobacteria	Spirulina sp. DLM2.Bin59	hypothetical protein EA366_06380 [Spirulina sp. DLM2.Bin59].	GCA_007693875.1
TVV43679.1	<-MarR-HTH<-?<-Cluster1077_2clades||Aminotran_1_2→ PSE→||<-?<-?||?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	985	FOT50_08370	Gammaproteobacteria	Thalassolituus sp. C2-1	GTP-binding protein [Thalassolituus sp. C2-1].	GCA_007785795.1
TXI24418.1	LRR-repeats+AP-GTPase+COR+DrHyd*→?→?→?→?→?→?→ Cluster1726_2clades→	LRR-repeats+AP-GTPase+COR+DrHyd	1061	E6Q61_04940	Betaproteobacteria	Nitrosomonas sp.	hypothetical protein E6Q61_04940 [Nitrosomonas sp.].	GCA_008015595.1
TXL81991.1	LRR-repeats+AP-GTPase+COR+CASPASE*→	LRR-repeats+AP-GTPase+COR+CASPASE	1175	FHP25_02680	Alphaproteobacteria	Enhydrobacter sp. CC-CFT640	CHAT domain-containing protein [Enhydrobacter sp. CC-CFT640].	GCA_008039615.1
TYC52188.1	WCAK→?→ LRR-repeats→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	860	FMN50_19470	Alphaproteobacteria	Rhodobacterales bacterium	hypothetical protein FMN50_19470 [Rhodobacterales bacterium].	GCA_008107755.1

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VFJ48800.1	RelE-ParE→?→?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	467	BECKDK2373C_GA0170839_10231	Gammaproteobacteria	Candidatus Kentron sp. DK	Leucine rich repeat-containing protein, partial [Candidatus Kentron sp. DK].	-
VFJ57569.1	RelE-ParE→?→ Cluster54_3clades→?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1027	BECKFW1821A_GA0114235_107219	Gammaproteobacteria	Candidatus Kentron sp. FW	Leucine rich repeat-containing protein [Candidatus Kentron sp. FW].	-
VFJ62833.1	Cluster1147_2clades→?→?→ RelE-ParE→?→?→ LRR-repeats+AP-GTPase+COR*→ Cluster2123_2clades→	LRR-repeats+AP-GTPase+COR	702	BECKDK2373B_GA0170837_111172	Gammaproteobacteria	Candidatus Kentron sp. DK	Leucine rich repeat-containing protein [Candidatus Kentron sp. DK].	-
VFJ65980.1	Cluster1147_2clades→?→?→ RelE-ParE→?→?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	470	BECKDK2373C_GA0170839_113817	Gammaproteobacteria	Candidatus Kentron sp. DK	Leucine rich repeat-containing protein, partial [Candidatus Kentron sp. DK].	-
VFJ75018.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	772	BECKFW1821C_GA0114237_10681	Gammaproteobacteria	Candidatus Kentron sp. FW	Ras of Complex, Roc, domain of DAPkinase [Candidatus Kentron sp. FW].	-
VFJ87041.1	RelE-ParE→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1091	BECKLFY1418B_GA0070995_100545	Gammaproteobacteria	Candidatus Kentron sp. LFY	Leucine rich repeat-containing protein [Candidatus Kentron sp. LFY].	-
VFJ90339.1	RelE-ParE→ LRR-repeats+AP-GTPase+COR*→ COR→	LRR-repeats+AP-GTPase+COR	380	BECKLFY1418A_GA0070994_101124	Gammaproteobacteria	Candidatus Kentron sp. LFY	Leucine rich repeat-containing protein [Candidatus Kentron sp. LFY].	-
VFK39292.1	RelE-ParE→?→ LRR-repeats+AP-GTPase+COR*→?→?→?→ RPN10→	LRR-repeats+AP-GTPase+COR	1088	BECKTC1821E_GA0114239_100479	Gammaproteobacteria	Candidatus Kentron sp. TC	Leucine rich repeat-containing protein [Candidatus Kentron sp. TC].	-
VFK43940.1	Cluster54_3clades→?→ RelE-ParE→ LRR-repeats+AP-GTPase+COR*→?→ Cluster1137_2clades→?→?→ RPN10→	LRR-repeats+AP-GTPase+COR	1017	BECKTC1821D_GA0114238_101924	Gammaproteobacteria	Candidatus Kentron sp. TC	Leucine rich repeat-containing protein [Candidatus Kentron sp. TC].	-
VFK55324.1	RelE-ParE→ LRR-repeats+AP-GTPase+COR*→?→ Cluster1137_2clades→?→?→ RPN10→	LRR-repeats+AP-GTPase+COR	1013	BECKTC1821F_GA0114240_100673	Gammaproteobacteria	Candidatus Kentron sp. TC	Leucine rich repeat-containing protein [Candidatus Kentron sp. TC].	-
VUX45208.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1031	DF3PA_100056	Alphaproteobacteria	Candidatus Defluviicoccus seviourii	conserved hypothetical protein [Candidatus Defluviicoccus seviourii].	GCA_900609035.2
VUX54879.1	<-SIG+Trypsin+PDZ<-?||?→?→||<-?<-?<-?||LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	935	JTBB02_V1_20008	Gammaproteobacteria	uncultured Woeseiaceae bacterium	protein of unknown function [uncultured Woeseiaceae bacterium].	GCA_902167415.1
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WP_002693173.1	<-NUDIX<-?||?→?→ SIG+TM+TM+Calcineurin→||<-?||LRR-repeats+AP-GTPase+COR*→||<-?||?→||<-?||Cluster1843_2clades→	LRR-repeats+AP-GTPase+COR	1282	-	Bacteroidetes	Microscilla marina	leucine-rich repeat protein [Microscilla marina].	GCF_000169175.1
WP_002693833.1	LRR-repeats+AP-GTPase+COR+EAD11*→?→||<-PAS+HISKIN	LRR-repeats+AP-GTPase+COR+EAD11	847	-	Bacteroidetes	Microscilla marina	leucine rich repeat protein [Microscilla marina].	GCF_000169175.1
WP_002694398.1	NUDIX→||<-?<-?<-?<-?||LRR-repeats+AP-GTPase+COR*→?→?→?→||<-?<-?<-SIGMA-HTH	LRR-repeats+AP-GTPase+COR	836	-	Bacteroidetes	Microscilla marina	leucine-rich repeat domain-containing protein [Microscilla marina].	GCF_000169175.1
WP_002703871.1	ABC_membrane+ABC_tran→?→?→ LRR-repeats+AP-GTPase+COR*→?→?→||<-SIG+SecA<-?<-?<-?||SIGMA-HTH→	LRR-repeats+AP-GTPase+COR	966	-	Bacteroidetes	Microscilla marina	leucine-rich repeat domain-containing protein [Microscilla marina].	GCF_000169175.1
WP_002704578.1	<-DAGKIN<-?||?→ LRR-repeats+AP-GTPase+COR*→||<-?||CNMP+CRP-HTH→||<-?||?→ InPase→	LRR-repeats+AP-GTPase+COR	897	-	Bacteroidetes	Microscilla marina	leucine-rich repeat domain-containing protein [Microscilla marina].	GCF_000169175.1

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acc	operon	architecture	len	gen.name	taxend	species	defline	gca
WP_008190613.1	REC→||<-PSE<-HNH<-?||REC→||<-TPR-repeats<-?<-?||LRR-repeats+AP-GTPase+COR+DUF4404*→	LRR-repeats+AP-GTPase+COR+DUF4404	948	-	Cyanobacteria	Moorea producens	leucine-rich repeat domain-containing protein [Moorea producens].	GCF_000211815.1
WP_008231466.1	<-Cluster1131_3clades<-?<-Cluster1163_3clades||?→?→?→ tRNA→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	970	-	Alphaproteobacteria	Roseobacter sp. CCS2	hypothetical protein [Roseobacter sp. CCS2].	GCF_000169435.1
WP_008273960.1	Cluster1550_2clades→?→?→ PIN→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	830	-	Cyanobacteria	Crocosphaera chwakensis	leucine-rich repeat domain-containing protein [Crocosphaera chwakensis].	GCF_000169335.1
WP_008277167.1	<-REC||SIG+TM+TM+TM+TM→||<-?||?→||<-?||?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	974	-	Cyanobacteria	Crocosphaera chwakensis	leucine-rich repeat domain-containing protein [Crocosphaera chwakensis].	GCF_000169335.1
WP_008680517.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1157	-	Planctomycetes	Rhodopirellula sallentina	small GTP-binding protein [Rhodopirellula sallentina].	GCF_000346505.1
WP_009282559.1	LRR-repeats+AP-GTPase+COR+TIR*→||<-?<-?||?→||<-?<-?<-?<-TM+TM+TM+TM+TM	LRR-repeats+AP-GTPase+COR+TIR	925	-	Bacteroidetes	Fibrisoma limi	leucine-rich repeat domain-containing protein [Fibrisoma limi].	GCF_000296815.2
WP_009283610.1	<-McrA-NTD||?→ N-OB→?→?→ LRR-repeats+AP-GTPase+COR+TIR*→ Cluster1088_2clades→?→?→?→||<-SIGMA-HTH	LRR-repeats+AP-GTPase+COR+TIR	1023	-	Bacteroidetes	Fibrisoma limi	leucine-rich repeat protein [Fibrisoma limi].	GCF_000296815.2
WP_009627973.1	LRR-repeats+AP-GTPase+COR+TM+TM*→||<-REC	LRR-repeats+AP-GTPase+COR+TM+TM	945	-	Cyanobacteria	Pseudanabaena biceps	leucine-rich repeat domain-containing protein [Pseudanabaena biceps].	GCF_000332215.1
WP_009964949.1	<-SMS-KaiC<-?<-?<-Cluster1581_2clades||?→?→?→ LRR-repeats+AP-GTPase+COR+TIR*→?→ TIR→?→?→ DrHyd+APATPase+TPR+TPR+TPR→	LRR-repeats+AP-GTPase+COR+TIR	961	-	Verrucomicrobia	Verrucomicrobium spinosum	GTP-binding protein [Verrucomicrobium spinosum].	GCF_000172155.1
WP_010471910.1	<-REC||?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1082	-	Cyanobacteria	Acaryochloris sp. CCMEE 5410	leucine-rich repeat domain-containing protein [Acaryochloris sp. CCMEE 5410].	GCF_000238775.1
WP_010477835.1	<-ABC_membrane+ABC_tran||?→?→||<-?<-?||?→?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1235	-	Cyanobacteria	Acaryochloris sp. CCMEE 5410	leucine-rich repeat domain-containing protein [Acaryochloris sp. CCMEE 5410].	GCF_000238775.1
WP_010933192.1	<-SIG+TM||LRR-repeats+AP-GTPase+COR*→?→?→?→?→ ParA-Soj-PloopNTPase→	LRR-repeats+AP-GTPase+COR	1102	-	Chlorobi	Chlorobaculum tepidum	leucine-rich repeat domain-containing protein [Chlorobaculum tepidum].	GCF_000006985.1
WP_010994301.1	<-Cluster5_5clades||LRR-repeats+AP-GTPase+COR+DUF4404*→||<-?<-PSE<-?||?→||<-REC	LRR-repeats+AP-GTPase+COR+DUF4404	1119	-	Cyanobacteria	Nostocaceae	MULTISPECIES: leucine-rich repeat domain-containing protein [Nostocaceae].	GCF_000009705.1
WP_011022280.1	PAS+HISKIN→||<-?||?→?→?→?→||<-?||LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	631	-	Euryarchaeota	Methanosarcina acetivorans	leucine-rich repeat domain-containing protein [Methanosarcina acetivorans].	-
WP_011307276.1	<-HhH-RADC+JAB||?→ NTP_transf_3→ LRR-repeats+AP-GTPase+COR*→||<-?<-?<-?<-Thioredoxin	LRR-repeats+AP-GTPase+COR	863	-	Euryarchaeota	Methanosarcina barkeri	leucine-rich repeat domain-containing protein [Methanosarcina barkeri].	GCF_000195895.1
WP_011307410.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	886	-	Euryarchaeota	Methanosarcina barkeri	leucine-rich repeat domain-containing protein [Methanosarcina barkeri].	GCF_000195895.1
WP_011308262.1	<-Mbetalac<-PSE<-PSE||?→||<-?||?→?→?→||<-?||LRR-repeats+AP-GTPase+COR*→||<-?||?→||<-?||?→ CHTH→||<-?||ABC-ATPase→	LRR-repeats+AP-GTPase+COR	892	-	Euryarchaeota	Methanosarcina barkeri	leucine-rich repeat domain-containing protein [Methanosarcina barkeri].	GCF_000195895.1
WP_011318314.1	<-Cluster5_5clades||LRR-repeats+AP-GTPase+COR+DUF4404*→||<-?<-ABC-ATPase<-?||?→||<-REC	LRR-repeats+AP-GTPase+COR+DUF4404	1107	-	Cyanobacteria	Trichormus variabilis	leucine-rich repeat domain-containing protein [Trichormus variabilis].	GCF_000204075.1
WP_011361554.1	BACTERIALFRINGE+TM+TM→?→ LRR-repeats+AP-GTPase+COR*→||<-?<-DAGKIN<-?||?→ Cluster881_3clades→?→ Cluster1718_2clades→	LRR-repeats+AP-GTPase+COR	811	-	Chlorobi	Chlorobium chlorochromatii	Rab family protein [Chlorobium chlorochromatii].	-

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
WP_011388592.1	<-ABC_membrane+ABC_tran<-ABC_membrane+ABC_tran<-?<-?<-?<-?||?→ LRR-repeats+AP-GTPase+COR+TIR*→ TM+TM+TM→	LRR-repeats+AP-GTPase+COR+TIR	1085	-	Alphaproteobacteria	Rhodospirillum rubrum	leucine-rich repeat domain-containing protein [Rhodospirillum rubrum].	GCF_000013085.1
WP_011613173.1	<-Cluster1413_2clades<-?||TPR-repeats→||<-?<-?<-PSE||LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1041	-	Cyanobacteria	Trichodesmium erythraeum	leucine-rich repeat domain-containing protein [Trichodesmium erythraeum].	GCF_000014265.1
WP_011712156.1	OmpA→?→||<-?<-?<-?||LRR-repeats+AP-GTPase+COR*→ CNMP+CRP-HTH→||<-?<-Cluster997_2clades<-?<-Thioredoxin<-SIG+RHOD-CDC25<-ARSR-HTH	LRR-repeats+AP-GTPase+COR	761	-	Alphaproteobacteria	Magnetococcus marinus	small GTP-binding protein [Magnetococcus marinus].	GCF_000014865.1
WP_012162488.1	Cluster1052_2clades→ NUDIX→ LRR-repeats+AP-GTPase+COR+TIR*→ TM+TM+TM→	LRR-repeats+AP-GTPase+COR+TIR	842	-	Cyanobacteria	Acaryochloris marina	leucine-rich repeat domain-containing protein [Acaryochloris marina].	GCF_000018105.1
WP_012407958.1	SIG+PBPB→ HISKIN→ HISKIN→ LRR-repeats+AP-GTPase+COR+TIR*→||<-?||?→?→?→||<-?||?→ Pentapeptide-repeats→	LRR-repeats+AP-GTPase+COR+TIR	1185	-	Cyanobacteria	Nostoc punctiforme	leucine-rich repeat domain-containing protein [Nostoc punctiforme].	GCF_000020025.1
WP_012412722.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1124	-	Cyanobacteria	Nostoc punctiforme	leucine-rich repeat domain-containing protein [Nostoc punctiforme].	GCF_000020025.1
WP_012466409.1	<-SF2-DUF3427A+TnsA-REase<-?<-?<-?<-?||?→?→ LRR-repeats+AP-GTPase+COR+TIR*→ TIR→	LRR-repeats+AP-GTPase+COR+TIR	998	-	Chlorobi	Chlorobium limicola	leucine-rich repeat domain-containing protein [Chlorobium limicola].	GCF_000020465.1
WP_012597192.1	Cluster1134_2clades→ REase-4→?→?→?→ HAD→ LRR-repeats+AP-GTPase+COR+TM+TM*→	LRR-repeats+AP-GTPase+COR+TM+TM	937	-	Cyanobacteria	Rippkaea orientalis	GTP-binding protein [Rippkaea orientalis].	GCF_000021805.1
WP_013320928.1	Cluster5_5clades→ LRR-repeats+AP-GTPase+COR*→?→ SIG+GT4→||<-?<-?||Cluster5_5clades→	LRR-repeats+AP-GTPase+COR	876	-	Cyanobacteria	Gloeothece verrucosa	leucine-rich repeat domain-containing protein [Gloeothece verrucosa].	GCF_000147335.1
WP_013323827.1	LRR-repeats+AP-GTPase+COR+TM+TM*→	LRR-repeats+AP-GTPase+COR+TM+TM	857	-	Cyanobacteria	Gloeothece verrucosa	leucine-rich repeat domain-containing protein [Gloeothece verrucosa].	GCF_000147335.1
WP_013762559.1	SIGMA-HTH→?→ SIG+TM→ LRR-repeats+AP-GTPase+COR+TIR*→?→ SIGMA-HTH→?→||<-SIG+TM+TM+TM+HISKIN	LRR-repeats+AP-GTPase+COR+TIR	995	-	Bacteroidetes	Haliscomenobacter hydrossis	leucine-rich repeat domain-containing protein [Haliscomenobacter hydrossis].	GCF_000212735.1
WP_013763674.1	<-ABC_membrane+ABC_tran||FGS→ PSE→ FGS→ LRR-repeats+AP-GTPase+COR+EAD11+CASPASE*→ RNASEII→	LRR-repeats+AP-GTPase+COR+EAD11+CASPASE	1108	-	Bacteroidetes	Haliscomenobacter hydrossis	leucine-rich repeat domain-containing protein [Haliscomenobacter hydrossis].	GCF_000212735.1
WP_013766755.1	LRR-repeats+AP-GTPase+COR+EAD11*→	LRR-repeats+AP-GTPase+COR+EAD11	1448	-	Bacteroidetes	Haliscomenobacter hydrossis	leucine-rich repeat protein [Haliscomenobacter hydrossis].	GCF_000212735.1
WP_013767289.1	<-SIG+ABhydrolase||SIG+7TMR-DISMED1→ FGS→ FGS→ LRR-repeats+AP-GTPase+COR+EAD11*→||<-?<-Cluster1645_2clades	LRR-repeats+AP-GTPase+COR+EAD11	840	-	Bacteroidetes	Haliscomenobacter hydrossis	leucine-rich repeat protein [Haliscomenobacter hydrossis].	GCF_000212735.1
WP_013768874.1	LRR-repeats+AP-GTPase+COR+TIR→ *LRR-repeats+AP-GTPase+COR*→ LRR-repeats+AP-GTPase+COR*→?→?→?→||<-?||?→?→||<-REC	LRR-repeats+AP-GTPase+COR+TIR	741	-	Bacteroidetes	Haliscomenobacter hydrossis	hypothetical protein [Haliscomenobacter hydrossis].	GCF_000212735.1
WP_013768875.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	786	-	Bacteroidetes	Haliscomenobacter hydrossis	hypothetical protein [Haliscomenobacter hydrossis].	GCF_000212735.1
WP_013818452.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	944	-	Gammaproteobacteria	Methylomonas methanica	leucine-rich repeat domain-containing protein [Methylomonas methanica].	GCF_000214665.1
WP_014444162.1	REC→||<-?<-?||?→||<-?<-?<-?||LRR-repeats+AP-GTPase+COR*→||<-?<-7TMR-DISMED1	LRR-repeats+AP-GTPase+COR	979	-	Actinobacteria	Actinoplanes missouriensis	hypothetical protein [Actinoplanes missouriensis].	GCF_000284295.1
WP_014798951.1	LRR-repeats+AP-GTPase+COR*→||<-?<-?<-Pkinase+TM+TPR+TPR	LRR-repeats+AP-GTPase+COR	1071	-	Bacteroidetes	Bernardetia litoralis	leucine-rich repeat domain-containing protein [Bernardetia litoralis].	GCF_000265505.1

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acc	operon	architecture	len	gen.name	taxend	species	defline	gca
WP_016798830.1	CI→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1080	-	Gammaproteobacteria	Vibrio cyclitrophicus	GTP-binding protein [Vibrio cyclitrophicus].	GCF_000256425.1
WP_016860490.1	<-HISKIN||?→?→ LRR-repeats→ LRR-repeats+AP-GTPase+COR+TM+TM*→||<-ABhydrolase	LRR-repeats+AP-GTPase+COR+TM+TM	719	-	Cyanobacteria	Fischerella muscicola	GTP-binding protein [Fischerella muscicola].	GCF_000317245.1
WP_016952822.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	829	-	Cyanobacteria	Anabaena sp. PCC 7108	leucine-rich repeat domain-containing protein [Anabaena sp. PCC 7108].	GCF_000332135.1
WP_017313212.1	Cluster1069__2clades→?→?→||<-?||?→?→ LRR-repeats+AP-GTPase+COR*→||<-?||?→?→?→?→ Mbetalac→	LRR-repeats+AP-GTPase+COR	1085	-	Cyanobacteria	Fischerella sp. PCC 9339	leucine-rich repeat protein [Fischerella sp. PCC 9339].	GCF_000315585.1
WP_017720442.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	852	-	Cyanobacteria	Oscillatoria sp. PCC 10802	leucine-rich repeat domain-containing protein [Oscillatoria sp. PCC 10802].	GCF_000332335.1
WP_017739957.1	Cluster5__5clades→?→||<-Cluster5__5clades||?→ PSE→||<-?<-PSE||?→ LRR-repeats+AP-GTPase+COR+EAD1*→ PSE→?→?→ Cluster2194__2clades→||<-?||Cluster1640__2clades→	LRR-repeats+AP-GTPase+COR+EAD1	965	-	Cyanobacteria	Scytonema hofmannii	leucine-rich repeat domain-containing protein [Scytonema hofmannii].	GCF_000346485.2
WP_018619729.1	<-HISKIN<-?||Cluster1877__2clades→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	925	-	Bacteroidetes	Spirosoma luteum	leucine-rich repeat domain-containing protein [Spirosoma luteum].	GCF_000374065.1
WP_019496026.1	ParB→||<-?<-TM+TM||?→ SIG+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM→?→ EAD1+LRR-repeats+AP-GTPase+COR*→?→?→?→?→ SIG+GT4→||<-PSE||?→ TPR+nSTAND1+BetaPropeller_WD40+BetaPropeller_WD40→	EAD1+LRR-repeats+AP-GTPase+COR	961	-	Cyanobacteria	Calothrix sp. PCC 7103	leucine-rich repeat domain-containing protein [Calothrix sp. PCC 7103].	GCF_000331305.1
WP_019496060.1	Cluster5__5clades→ LRR-repeats+AP-GTPase+COR+EAD1*→ PSE→?→||<-CR-REase5||?→ APATPase+BetaPropeller_WD40-repeats→?→ APATPase+BetaPropeller_WD40-repeats→ APATPase+BetaPropeller_WD40-repeats→	LRR-repeats+AP-GTPase+COR+EAD1	912	-	Cyanobacteria	Calothrix sp. PCC 7103	leucine-rich repeat domain-containing protein [Calothrix sp. PCC 7103].	GCF_000331305.1
WP_019867072.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	856	-	Gammaproteobacteria	Methylovulum miyakonense	TIR domain-containing protein [Methylovulum miyakonense].	GCF_000384075.1
WP_020379418.1	SF2-DUF3427A+TnsA-REase→ DAM→ LRR-repeats+AP-GTPase+COR+TM+TM*→	LRR-repeats+AP-GTPase+COR+TM+TM	1195	-	Actinobacteria	Candidatus Microthrix parvicella	hypothetical protein [Candidatus Microthrix parvicella].	GCF_000299415.1
WP_020396599.1	LRR-repeats+AP-GTPase+COR+TIR*→ TM+TM+TM→	LRR-repeats+AP-GTPase+COR+TIR	767	-	Gammaproteobacteria	Thiolinea disciformis	TIR domain-containing protein, partial [Thiolinea disciformis].	GCF_000371925.1
WP_020483095.1	Cluster1270__2clades→||<-?<-?<-?<-?<-?||?→ LRR-repeats+AP-GTPase+COR*→||<-?<-?<-?<-?||?→ SIGMA-HTH→	LRR-repeats+AP-GTPase+COR	1111	-	Gammaproteobacteria	Methylomonas sp. MK1	leucine-rich repeat domain-containing protein [Methylomonas sp. MK1].	GCF_000365425.1
WP_020496162.1	<-ISOCOT<-?<-?||InPase→||<-?||LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	833	-	Actinobacteria	Sciscionella marina	hypothetical protein [Sciscionella marina].	GCF_000379465.1
WP_020559023.1	Cluster2057__2clades→ LRR-repeats+AP-GTPase+COR+TIR→*?→?→?→?→?→ LRR-repeats+AP-GTPase+COR+TIR*→ Cluster54__3clades→ PSE→||<-TIR+TPR+TPR-S	LRR-repeats+AP-GTPase+COR+TIR	972	-	Gammaproteobacteria	Thiofilum flexile	leucine-rich repeat domain-containing protein [Thiofilum flexile].	GCF_000380185.1
WP_020559030.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	943	-	Gammaproteobacteria	Thiofilum flexile	leucine-rich repeat domain-containing protein [Thiofilum flexile].	GCF_000380185.1
WP_020560643.1	LRR-repeats+AP-GTPase+COR+TIR*→ TM+TM+TM→	LRR-repeats+AP-GTPase+COR+TIR	900	-	Gammaproteobacteria	Thiofilum flexile	TIR domain-containing protein [Thiofilum flexile].	GCF_000380185.1
WP_020570498.1	<-SIG+ABhydrolase<-?<-?<-?||LRR-repeats+AP-GTPase+COR+CASPASE*→?→ FGS→?→ RVT→?→ FGS→	LRR-repeats+AP-GTPase+COR+CASPASE	1039	-	Bacteroidetes	Lewinella persica	CHAT domain-containing protein [Lewinella persica].	GCF_000373105.1
WP_020607470.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	954	-	Bacteroidetes	Spirosoma spitsbergense	leucine-rich repeat domain-containing protein [Spirosoma spitsbergense].	GCF_000374085.1
WP_021020180.1	Polbeta+HEPN→ LRR-repeats→ LRR-repeats+AP-GTPase+COR+TIR*→?→||<-?||?→?→ SIG+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM→ SIG+TM→	LRR-repeats+AP-GTPase+COR+TIR	944	-	Gammaproteobacteria	Vibrio gazogenes	TIR domain-containing protein [Vibrio gazogenes].	GCF_000390165.1
WP_021802668.1	HAD→?→?→?→ Cluster881__3clades→ LRR-repeats+AP-GTPase+COR*→?→?→?→?→?→?→ Cluster1292__2clades→	LRR-repeats+AP-GTPase+COR	936	-	Firmicutes	Clostridium intestinale	GTP-binding protein [Clostridium intestinale].	GCF_013781885.1

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WP_022571049.1	CI→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1095	-	Gammaproteobacteria	Vibrio cyclitrophicus	leucine rich repeat protein [Vibrio cyclitrophicus].	GCF_000473545.1
WP_022589047.1	ABC-ATPase→?→?→||<-Acylphosphatase||?→?→||<-?||LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1264	-	Gammaproteobacteria	Vibrio nigripulchritudo	TIR domain-containing protein [Vibrio nigripulchritudo].	GCF_900067775.1
WP_023074611.1	LRR-repeats+AP-GTPase+COR+TIR*→||<-?||?→||<-?||Cluster1646_2clades→	LRR-repeats+AP-GTPase+COR+TIR	777	-	Cyanobacteria	Leptolyngbya sp. Heron Island J	leucine-rich repeat domain-containing protein, partial [Leptolyngbya sp. Heron Island J].	GCF_000482245.1
WP_023076066.1	Cluster53_2clades→||<-RelE-ParE<-?||LRR-repeats+AP-GTPase+COR+TIR*→||<-?||?→||<-?||?→?→||<-?<-SIG+TM+TM+TM+TM+TM+TM	LRR-repeats+AP-GTPase+COR+TIR	1129	-	Cyanobacteria	Leptolyngbya sp. Heron Island J	leucine-rich repeat domain-containing protein [Leptolyngbya sp. Heron Island J].	GCF_000482245.1
WP_023571556.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1142	-	Bacteroidetes	Flavobacterium cauense	TIR domain-containing protein [Flavobacterium cauense].	GCF_000498475.1
WP_024594403.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	982	-	Gammaproteobacteria	Pseudoalteromonas sp. TB13	GTP-binding protein [Pseudoalteromonas sp. TB13].	GCF_000497915.1
WP_025517521.1	CI→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1105	-	Gammaproteobacteria	Vibrio parahaemolyticus	50S ribosome-binding GTPase [Vibrio parahaemolyticus].	GCF_000489555.1
WP_025605295.1	CI→?→ PSE→ LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1265	-	Gammaproteobacteria	Vibrio parahaemolyticus	TIR domain-containing protein [Vibrio parahaemolyticus].	GCF_000489075.1
WP_026726296.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	698	-	Bacteroidetes	Flavobacterium sasangense	GTP-binding protein [Flavobacterium sasangense].	GCF_000686885.1
WP_028083535.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	993	-	Cyanobacteria	Dolichospermum circinale	leucine-rich repeat domain-containing protein [Dolichospermum circinale].	GCF_000426925.1
WP_028469928.1	LRR-repeats+AP-GTPase+COR*→?→?→ GTPase-AIG→	LRR-repeats+AP-GTPase+COR	697	-	Gammaproteobacteria	Neptunomonas japonica	hypothetical protein [Neptunomonas japonica].	GCF_000422765.1
WP_028667519.1	<-Cluster1063_3clades<-Cluster1067_3clades||?→?→?→?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	798	-	Bacteroidetes	Runella zeae	GTP-binding protein [Runella zeae].	GCF_000423565.1
WP_029631472.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1051	-	Planctomycetes	Zavarzinella formosa	leucine-rich repeat domain-containing protein [Zavarzinella formosa].	GCF_000255705.1
WP_030435343.1	REC→ PSE→?→?→||<-?||?→ Cluster2103_2clades→||<-?||LRR-repeats+AP-GTPase+COR*→ AP-GTPase+COR+TM+TM→||<-REC<-?||ABC-ATPase→	LRR-repeats+AP-GTPase+COR	551	-	Actinobacteria	Actinoplanes subtropicus	GTP-binding protein [Actinoplanes subtropicus].	GCF_000721705.1
WP_030488330.1	LRR-repeats+AP-GTPase+COR*→||<-?<-?||?→?→||<-?||SIG+TM→ REC→	LRR-repeats+AP-GTPase+COR	1088	-	Actinobacteria	Micromonospora chokoriensis	hypothetical protein [Micromonospora chokoriensis].	GCF_000718555.1
WP_031429699.1	CI→?→ PSE→ LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1261	-	Gammaproteobacteria	Vibrio parahaemolyticus	TIR domain-containing protein [Vibrio parahaemolyticus].	GCF_000736345.1
WP_034058880.1	S1COLD→?→||<-?||?→?→||<-?||?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	924	-	Bacteroidetes	Lacinutrix jangbogonensis	leucine-rich repeat domain-containing protein [Lacinutrix jangbogonensis].	GCF_000797445.1
WP_035121352.1	LRR-repeats+AP-GTPase+COR+TIR*→||<-?<-?<-?<-ABC-ATPase	LRR-repeats+AP-GTPase+COR+TIR	1115	-	Cyanobacteria	Fischerella sp. PCC 9431	leucine-rich repeat domain-containing protein [Fischerella sp. PCC 9431].	GCF_000447295.1
WP_035197779.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	914	-	Firmicutes	Calidifontibacillus azotoformans	GTP-binding protein [Calidifontibacillus azotoformans].	GCF_000708505.1
WP_035613546.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1058	-	Verrucomicrobia	Haloferula sp. BvORR071	hypothetical protein [Haloferula sp. BvORR071].	-
WP_035758421.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	956	-	Bacteroidetes	Hugenholtzia roseola	leucine-rich repeat protein, partial [Hugenholtzia roseola].	GCF_000422585.1
WP_038164534.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	793	-	Verrucomicrobia	Verrucomicrobium sp. BvORR106	TIR domain-containing protein [Verrucomicrobium sp. BvORR106].	-
WP_039108669.1	<-Cluster1070_2clades<-ENDO3+NUDIX||HU-IHF→?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	912	-	Bacteroidetes	Flavobacterium sp. AED	leucine-rich repeat domain-containing protein [Flavobacterium sp. AED].	GCF_000812945.1

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WP_039351391.1	LRR-repeats+AP-GTPase+COR*→||<-?||?→||<-RnasePH+RnasePH+KH+S1	LRR-repeats+AP-GTPase+COR	912	-	Bacteroidetes	Chryseobacterium jeonii	GTP-binding protein [Chryseobacterium jeonii].	GCF_000812865.1
WP_039727351.1	SIG+TM+TM+TM+TM+TM+TM→||<-?||?→?→?→ LRR-repeats+AP-GTPase+COR*→?→ PIN→||<-?<-REC+LuxR-HTH<-?<-?<-Cluster1069_2clades	LRR-repeats+AP-GTPase+COR	1075	-	Terrabacteria group	Cyanobacteria	MULTISPECIES: leucine-rich repeat domain-containing protein [Cyanobacteria].	GCF_000817775.2
WP_039983671.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1101	-	Gammaproteobacteria	Vibrio sagamiensis	50S ribosome-binding GTPase [Vibrio sagamiensis].	GCF_000400425.1
WP_040248977.1	LRR-repeats+AP-GTPase+COR*→||<-?<-?<-?||?→?→?→ SIG+TM+TM→	LRR-repeats+AP-GTPase+COR	924	-	Bacteroidetes	Psychroserpens mesophilus	leucine-rich repeat domain-containing protein [Psychroserpens mesophilus].	GCF_000826645.1
WP_044220039.1	FGS→?→ RVT→?→ FGS→?→ LRR-repeats+AP-GTPase+COR+CASPASE*→?→ FGS→	LRR-repeats+AP-GTPase+COR+CASPASE	977	-	Bacteroidetes	Phaeodactylibacter xiamenensis	CHAT domain-containing protein [Phaeodactylibacter xiamenensis].	GCF_000759025.1
WP_044222080.1	REC→ FGS→||<-?||RVT→?→ FGS→ LRR-repeats+AP-GTPase+COR+CASPASE*→?→?→?→ FGS→ FGS→ FGS→	LRR-repeats+AP-GTPase+COR+CASPASE	931	-	Bacteroidetes	Phaeodactylibacter xiamenensis	leucine-rich repeat domain-containing protein [Phaeodactylibacter xiamenensis].	GCF_000759025.1
WP_044448603.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1176	-	Cyanobacteria	Mastigocladus laminosus	leucine-rich repeat domain-containing protein [Mastigocladus laminosus].	-
WP_044448681.1	LRR-repeats+AP-GTPase+COR+DUF4404*→	LRR-repeats+AP-GTPase+COR+DUF4404	806	-	Cyanobacteria	Mastigocladus laminosus	GTP-binding protein [Mastigocladus laminosus].	-
WP_045613052.1	<-Cluster1074_2clades||?→?→?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1105	-	Gammaproteobacteria	Vibrio vulnificus	50S ribosome-binding GTPase [Vibrio vulnificus].	GCF_000960125.1
WP_046355878.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1154	-	Gammaproteobacteria	Pseudoalteromonas luteoviolacea	leucine-rich repeat domain-containing protein [Pseudoalteromonas luteoviolacea].	GCF_001625715.1
WP_047776098.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1055	-	Bacteroidetes	Flavobacterium sp. ABG	leucine-rich repeat domain-containing protein [Flavobacterium sp. ABG].	GCF_001027725.1
WP_047863083.1	Cluster971_2clades→?→||<-?<-?||LRR-repeats+AP-GTPase+COR+TIR*→?→||<-?<-?<-?||?→||<-?<-SIG+Lysozyme	LRR-repeats+AP-GTPase+COR+TIR	921	-	Deltaproteobacteria	Archangium gephyra	GTP-binding protein [Archangium gephyra].	GCF_001027285.1
WP_048040436.1	<-PIN<-?<-SIG+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM||?→?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	935	-	Euryarchaeota	Methanosarcina mazei	leucine-rich repeat domain-containing protein [Methanosarcina mazei].	GCF_000970225.1
WP_048109136.1	<-SIG+TM+VWA+TM<-VWA<-MoxR-AAA||?→ LRR-repeats+AP-GTPase+COR*→?→||<-?||SIG+Calcineurin→?→ PIN→||<-Ferredoxin-RRM	LRR-repeats+AP-GTPase+COR	931	-	Euryarchaeota	Methanosarcina barkeri	leucine-rich repeat domain-containing protein [Methanosarcina barkeri].	GCF_000970305.1
WP_048669264.1	<-ABC_membrane+ABC_tran<-ABC_membrane+ABC_tran<-?||LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	960	-	Gammaproteobacteria	Vibrio crassostreae	GTP-binding protein [Vibrio crassostreae].	GCF_001048475.1
WP_048752807.1	LRR-repeats+AP-GTPase+COR*→||<-PSE<-?||RelE→ CHTH→	LRR-repeats+AP-GTPase+COR	801	-	Cyanobacteria	Crocosphaera watsonii	leucine-rich repeat domain-containing protein, partial [Crocosphaera watsonii].	GCF_001050835.1
WP_049769521.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	662	-	Cyanobacteria	Rippkaea orientalis	GTP-binding protein [Rippkaea orientalis].	GCF_000021805.1
WP_049825328.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	616	-	Cyanobacteria	Rippkaea orientalis	GTP-binding protein [Rippkaea orientalis].	GCF_000024045.1
WP_049875725.1	PAIREDC-HTH→||<-?||LRR-repeats→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	772	-	Actinobacteria	Streptomyces scabiei	hypothetical protein [Streptomyces scabiei].	GCF_000091305.1
WP_049974475.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1267	-	Alphaproteobacteria	Azospirillum sp. B4	leucine-rich repeat domain-containing protein [Azospirillum sp. B4].	GCF_000333275.1
WP_050652657.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1099	-	Gammaproteobacteria	Vibrio sp. J2-17	hypothetical protein [Vibrio sp. J2-17].	GCF_001244075.1

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WP_050710728.1	LRR-repeats+AP-GTPase+COR+DrHyd*→	LRR-repeats+AP-GTPase+COR+DrHyd	1196	-	Bacteroidetes	Dysgonomonas sp. HGC4	leucine-rich repeat domain-containing protein [Dysgonomonas sp. HGC4].	GCF_001261715.1
WP_050857550.1	LRR-repeats+AP-GTPase+COR*→||<-?<-?<-ABC-ATPase	LRR-repeats+AP-GTPase+COR	958	-	Cyanobacteria	Acaryochloris sp. CCMEE 5410	leucine-rich repeat domain-containing protein [Acaryochloris sp. CCMEE 5410].	GCF_000238775.1
WP_051210834.1	SIGMA-HTH→?→?→ LRR-repeats+AP-GTPase+COR*→||<-?<-?<-?<-?<-SIGMA-HTH	LRR-repeats+AP-GTPase+COR	1280	-	Bacteroidetes	Runella zeae	leucine-rich repeat domain-containing protein [Runella zeae].	GCF_000423565.1
WP_051242709.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1043	-	Alphaproteobacteria	Stappia stellulata	leucine-rich repeat domain-containing protein [Stappia stellulata].	GCF_000423705.1
WP_051289443.1	LRR-repeats+AP-GTPase+COR+TM+TM*→||<-PSE||?→?→||<-?<-?||?→||<-?<-ABC-ATPase	LRR-repeats+AP-GTPase+COR+TM+TM	821	-	Cyanobacteria	Dolichospermum circinale	leucine-rich repeat domain-containing protein [Dolichospermum circinale].	GCF_000426925.1
WP_051347554.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	814	-	Cyanobacteria	Dolichospermum circinale	hypothetical protein, partial [Dolichospermum circinale].	GCF_000426905.1
WP_051394619.1	LRR-repeats+AP-GTPase+COR+TM+TM*→	LRR-repeats+AP-GTPase+COR+TM+TM	1004	-	Cyanobacteria	Leptolyngbya sp. Heron Island J	GTP-binding protein [Leptolyngbya sp. Heron Island J].	GCF_000482245.1
WP_051793473.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	946	-	Actinobacteria	Kibdelosporangium aridum	leucine-rich repeat domain-containing protein [Kibdelosporangium aridum].	GCF_003947235.1
WP_051898832.1	InPase→||<-?||LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	833	-	Actinobacteria	Sciscionella sp. SE31	hypothetical protein [Sciscionella sp. SE31].	GCF_000737195.2
WP_051926645.1	LRR-repeats+AP-GTPase+COR*→||<-?||?→||<-?<-SIGMA-HTH<-?<-SIGMA-HTH	LRR-repeats+AP-GTPase+COR	996	-	Actinobacteria	Streptomyces durhamensis	hypothetical protein [Streptomyces durhamensis].	GCF_000725475.1
WP_051937621.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1086	-	Actinobacteria	Streptomyces scabiei	hypothetical protein [Streptomyces scabiei].	GCF_000738715.1
WP_051942852.1	LRR-repeats+AP-GTPase+COR*→||<-?<-?<-Cluster1515_2clades<-?<-ABC-ATPase<-?<-SIG+TM+TM+TM+TM+TM+TM+TM	LRR-repeats+AP-GTPase+COR	1022	-	Actinobacteria	Streptacidiphilus rugosus	hypothetical protein [Streptacidiphilus rugosus].	GCF_000744655.1
WP_052150025.1	LRR-repeats+AP-GTPase+COR*→?→?→||<-?||?→?→?→||<-Pentapeptide	LRR-repeats+AP-GTPase+COR	949	-	Cyanobacteria	Aphanizomenon flos-aquae	leucine-rich repeat domain-containing protein [Aphanizomenon flos-aquae].	GCF_000789435.1
WP_052277881.1	SIG+TM+TM+TM+TM+TM+TM+TM→||<-?||Mbetalac→ SAM-methylase→?→||<-?<-SIG+TPM_phosphatase+TM+TM+TM||LRR-repeats+AP-GTPase+COR+TM+TM*→	LRR-repeats+AP-GTPase+COR+TM+TM	921	-	Cyanobacteria	Microcystis panniformis	leucine-rich repeat domain-containing protein [Microcystis panniformis].	-
WP_052288305.1	<-Hsp10||?→ REC→ Ferretin→||<-Cluster1950_2clades||?→ LRR-repeats+AP-GTPase+COR+TIR*→||<-?<-?||?→?→?→?→ SIG+TM+TM+TM+TM+TM+TM→	LRR-repeats+AP-GTPase+COR+TIR	848	-	Terrabacteria group	Cyanobacteria	MULTISPECIES: TIR domain-containing protein [Cyanobacteria].	GCF_000817775.2
WP_052324486.1	LRR-repeats→ AP-GTPase+COR*→	AP-GTPase+COR	434	-	Bacteroidetes	Haliscomenobacter hydrossis	50S ribosome-binding GTPase [Haliscomenobacter hydrossis].	GCF_000212735.1
WP_052478236.1	LRR-repeats+AP-GTPase+COR*→||<-?||?→||<-?<-?<-Aminotran_1_2	LRR-repeats+AP-GTPase+COR	942	-	Actinobacteria	Kibdelosporangium sp. MJ126-NF4	leucine-rich repeat domain-containing protein [Kibdelosporangium sp. MJ126-NF4].	GCF_000826545.1
WP_052712873.1	<-HhH-RADC+JAB||?→ NTP_transf_3→ LRR-repeats+AP-GTPase+COR*→||<-?<-?||?→||<-?<-?||SIR2→	LRR-repeats+AP-GTPase+COR	926	-	Euryarchaeota	Methanosarcina barkeri	leucine-rich repeat domain-containing protein [Methanosarcina barkeri].	GCF_001027005.1
WP_052718309.1	<-HhH-RADC+JAB||?→ NTP_transf_3→ LRR-repeats+AP-GTPase+COR→*?→ LRR-repeats+AP-GTPase+COR→*	LRR-repeats+AP-GTPase+COR	871	-	Euryarchaeota	Methanosarcina sp. MTP4	leucine-rich repeat domain-containing protein [Methanosarcina sp. MTP4].	GCF_000970045.1

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WP_052718311.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	999	-	Euryarchaeota	Methanosarcina sp. MTP4	leucine-rich repeat domain-containing protein [Methanosarcina sp. MTP4].	GCF_000970045.1
WP_052718346.1	LRR-repeats+AP-GTPase+COR*→?→||<-?<-SIG+TM+TM+TM+TM+TM<-ABC-ATPase	LRR-repeats+AP-GTPase+COR	891	-	Euryarchaeota	Methanosarcina sp. MTP4	leucine-rich repeat domain-containing protein [Methanosarcina sp. MTP4].	GCF_000970045.1
WP_052721594.1	<-HhH-RADC+JAB||?→ NTP__transf_3→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	890	-	Euryarchaeota	Methanosarcina siciliae	leucine-rich repeat domain-containing protein [Methanosarcina siciliae].	GCF_000970085.1
WP_052725465.1	<-HhH-RADC+JAB||?→ NTP__transf_3→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	886	-	Euryarchaeota	Methanosarcina sp. Kolksee	leucine-rich repeat domain-containing protein [Methanosarcina sp. Kolksee].	GCF_000969945.1
WP_052725699.1	<-HhH-RADC+JAB||?→ NTP__transf_3→ LRR-repeats+AP-GTPase+COR*→||<-?<-?||?→||<-?<-?||SIR2→	LRR-repeats+AP-GTPase+COR	926	-	Euryarchaeota	Methanosarcina barkeri	leucine-rich repeat domain-containing protein [Methanosarcina barkeri].	GCF_000970065.1
WP_052725704.1	<-SIG+TPR+TPR+TPR+TPR+TPR+TPR||?→||<-?||?→?→ PSE→?→ LRR-repeats+AP-GTPase+COR*→?→?→ PRTase→	LRR-repeats+AP-GTPase+COR	886	-	Euryarchaeota	Methanosarcina barkeri	leucine-rich repeat domain-containing protein [Methanosarcina barkeri].	GCF_000970065.1
WP_052727304.1	PAS+HISKIN→||<-?||?→?→?→?→||<-PSE||LRR-repeats+AP-GTPase+COR*→||<-?||?→ PSE→||<-?||Cluster1640__2clades→||<-SIG+HIN-HTH	LRR-repeats+AP-GTPase+COR	1010	-	Euryarchaeota	Methanosarcina siciliae	leucine-rich repeat domain-containing protein [Methanosarcina siciliae].	GCF_000970145.1
WP_052727948.1	LRR-repeats+AP-GTPase+COR+TIR*→?→?→?→?→?→ PSE→||<-TPR-repeats	LRR-repeats+AP-GTPase+COR+TIR	877	-	Euryarchaeota	Methanosarcina vacuolata	leucine-rich repeat domain-containing protein [Methanosarcina vacuolata].	GCF_000969905.1
WP_052727973.1	<-HhH-RADC+JAB||?→ NTP__transf_3→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	886	-	Euryarchaeota	Methanosarcina vacuolata	leucine-rich repeat domain-containing protein [Methanosarcina vacuolata].	GCF_000969905.1
WP_052728059.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	930	-	Euryarchaeota	Methanosarcina mazei	leucine-rich repeat domain-containing protein [Methanosarcina mazei].	GCF_000970205.1
WP_052728060.1	<-PIN<-?<-SIG+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM||?→?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	935	-	Euryarchaeota	Methanosarcina mazei	leucine-rich repeat domain-containing protein [Methanosarcina mazei].	GCF_000970205.1
WP_052735402.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	845	-	Euryarchaeota	Methanosarcina sp. 1.H.A.2.2	leucine-rich repeat domain-containing protein [Methanosarcina sp. 1.H.A.2.2].	GCF_000979975.1
WP_052752245.1	LRR-repeats+AP-GTPase+COR*→ TIR→	LRR-repeats+AP-GTPase+COR	1015	-	Betaproteobacteria	Nitrosomonas communis	leucine-rich repeat domain-containing protein [Nitrosomonas communis].	GCF_001007935.1
WP_054015538.1	<-REC||?→||<-?||?→ LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1274	-	Gammaproteobacteria	Pseudoalteromonas sp. R3	TIR domain-containing protein [Pseudoalteromonas sp. R3].	GCF_004014715.1
WP_054015917.1	LRR-repeats+AP-GTPase+COR+TIR*→||<-?<-?<-TM	LRR-repeats+AP-GTPase+COR+TIR	1128	-	Gammaproteobacteria	Pseudoalteromonas sp. R3	leucine-rich repeat domain-containing protein [Pseudoalteromonas sp. R3].	GCF_004014715.1
WP_054961809.1	DSBH+AraC-HTH+AraC-HTH→?→ LRR-repeats+AP-GTPase+COR*→||<-ABC__membrane+ABC__tran	LRR-repeats+AP-GTPase+COR	1057	-	Gammaproteobacteria	Vibrio bivalvicida	hypothetical protein [Vibrio bivalvicida].	GCF_001399455.2
WP_055505179.1	<-ABC-ATPase<-?||?→?→||<-?||LRR-repeats+AP-GTPase+COR*→?→?→?→||<-?<-?<-SIR2	LRR-repeats+AP-GTPase+COR	941	-	Actinobacteria	Nonomuraea pusilla	leucine-rich repeat domain-containing protein [Nonomuraea pusilla].	GCF_001417755.1
WP_057935115.1	SIG+Concanavalin-like+SUN→||<-?||?→ FGS→?→?→?→ LRR-repeats+AP-GTPase+COR+TIR*→?→?→||<-?<-?||?→ TIR→	LRR-repeats+AP-GTPase+COR+TIR	1318	-	Bacteroidetes	Pedobacter ginsenosidimutans	leucine-rich repeat domain-containing protein [Pedobacter ginsenosidimutans].	GCF_001442625.1

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WP_058183692.1	LRR-repeats+AP-GTPase+COR+CASPASE*→ LRR-repeats→	LRR-repeats+AP-GTPase+COR+CASPASE	1194	-	Cyanobacteria	Mastigocoleus testarum	leucine-rich repeat domain-containing protein [Mastigocoleus testarum].	GCF_001456025.1
WP_058183771.1	LRR-repeats+AP-GTPase+COR+EAD1*→	LRR-repeats+AP-GTPase+COR+EAD1	1014	-	Cyanobacteria	Mastigocoleus testarum	leucine-rich repeat domain-containing protein [Mastigocoleus testarum].	GCF_001456025.1
WP_058554438.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	758	-	Gammaproteobacteria	Thiohalocapsa sp. ML1	TIR domain-containing protein [Thiohalocapsa sp. ML1].	GCF_001469165.1
WP_058998621.1	LRR-repeats+AP-GTPase+COR*→?→?→ HNH→	LRR-repeats+AP-GTPase+COR	418	-	Cyanobacteria	Leptolyngbya sp. NIES-2104	leucine-rich repeat domain-containing protein [Leptolyngbya sp. NIES-2104].	GCF_001485215.1
WP_059136441.1	LRR-repeats+AP-GTPase+COR+TIR*→||<-RnasePH+RnasePH+KH+S1	LRR-repeats+AP-GTPase+COR+TIR	1173	-	Bacteroidetes	Chryseobacterium greenlandense	leucine-rich repeat domain-containing protein [Chryseobacterium greenlandense].	GCF_001507325.1
WP_061431817.1	SIG+TM+TM+TM+TM+TM+TM+TM→||<-?||PSE→ PSE→||<-?||SAM-methylase→?→||<-?<-SIG+TPM_phosphatase+TM+TM+TM||PSE→ LRR-repeats+AP-GTPase+COR+TM+TM*→||<-?<-?<-?<-?<-?||?→||<-Classical-AAA+Classical-AAA	LRR-repeats+AP-GTPase+COR+TM+TM	670	-	Cyanobacteria	Microcystis aeruginosa	GTP-binding protein, partial [Microcystis aeruginosa].	GCF_001578075.1
WP_062148002.1	<-TPR-repeats+CASPASE||?→?→ LRR-repeats+AP-GTPase+COR+DUF4404*→	LRR-repeats+AP-GTPase+COR+DUF4404	1474	-	Gammaproteobacteria	Beggiatoa leptomitoformis	leucine-rich repeat domain-containing protein [Beggiatoa leptomitoformis].	GCF_001305575.3
WP_062292830.1	LRR-repeats+AP-GTPase+COR*→||<-?<-Aminotran_1_2<-HU-IHF	LRR-repeats+AP-GTPase+COR	946	-	Cyanobacteria	Nostoc piscinale	leucine-rich repeat domain-containing protein [Nostoc piscinale].	GCF_001298445.1
WP_062689807.1	<-Cluster2368_2clades||?→ ncRNA→?→?→?→?→?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	909	-	Gammaproteobacteria	Photobacterium sanguinicancri	GTP-binding protein [Photobacterium sanguinicancri].	GCF_001563765.1
WP_063362501.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1154	-	Gammaproteobacteria	Pseudoalteromonas luteoviolacea	leucine-rich repeat domain-containing protein [Pseudoalteromonas luteoviolacea].	GCF_001625695.1
WP_064232935.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	699	-	Gammaproteobacteria	Halomonas sp. ALS9	hypothetical protein [Halomonas sp. ALS9].	GCF_001651035.1
WP_065709937.1	LRR-repeats+AP-GTPase+COR*→||<-?<-?||?→ ABC-ATPase→ tRNA→?→||<-?<-Pentapeptide-repeats	LRR-repeats+AP-GTPase+COR	963	-	Cyanobacteria	Synechococcus sp. PCC 7117	leucine-rich repeat domain-containing protein [Synechococcus sp. PCC 7117].	-
WP_066434724.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	276	-	Bacteroidetes	Gelidibacter algens	hypothetical protein [Gelidibacter algens].	GCF_001678675.1
WP_067315083.1	SMPB→?→||<-?||?→||<-?||?→?→ LRR-repeats+AP-GTPase+COR*→||<-SIG+TM+TM+TM||?→||<-?||?→ SIGMA-HTH→	LRR-repeats+AP-GTPase+COR	968	-	Actinobacteria	Streptomyces griseochromogenes	hypothetical protein [Streptomyces griseochromogenes].	GCF_001542625.1
WP_067770734.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1123	-	Cyanobacteria	Nostoc sp. NIES-3756	hypothetical protein [Nostoc sp. NIES-3756].	GCF_001548375.1
WP_068061695.1	7TMR-DISMED1→?→ SIG+Concanavalin-like+SUN→?→?→||<-?||?→ LRR-repeats+AP-GTPase+COR+TIR*→ ABhydrolase+ABhydrolase+CASPASE+TPR-S→?→||<-tRNA<-?<-?<-Cluster2189_2clades	LRR-repeats+AP-GTPase+COR+TIR	1268	-	Gammaproteobacteria	Rheinheimera sp. SA_1	TIR domain-containing protein [Rheinheimera sp. SA_1].	-
WP_068843099.1	LRR-repeats+AP-GTPase+COR*→||<-?||?→?→||<-cNMPBD	LRR-repeats+AP-GTPase+COR	1015	-	Bacteroidetes	Flavobacterium chilense	GTP-binding protein [Flavobacterium chilense].	GCF_900142685.1
WP_068887322.1	LRR-repeats+AP-GTPase+COR+TIR*→ Cluster2230_2clades→?→?→||<-?<-?<-?<-Cluster2322_2clades	LRR-repeats+AP-GTPase+COR+TIR	1168	-	Bacteroidetes	Pedobacter panaciterrae	leucine-rich repeat domain-containing protein [Pedobacter panaciterrae].	GCF_001636695.1
WP_069069853.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1138	-	Cyanobacteria	Nostoc sp. KVJ20	leucine-rich repeat protein [Nostoc sp. KVJ20].	GCF_001712795.1
WP_069070238.1	LRR-repeats+AP-GTPase+COR*→||<-SIG+DADALIGASE-ATPgrasp<-?||?→?→||<-?<-?<-CBS	LRR-repeats+AP-GTPase+COR	1078	-	Cyanobacteria	Nostoc sp. KVJ20	leucine-rich repeat domain-containing protein [Nostoc sp. KVJ20].	GCF_001712795.1

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WP_069474666.1	SIG+TM+TM+TM+TM+TM+TM+TM→||<-?||Mbetalac→ SAM-methylase→?→||<-?<-SIG+TPM_phosphatase+TM+TM+TM||LRR-repeats+AP-GTPase+COR+TM+TM*→||<-?<-?<-?<-Pro_CA||?→||<-?<-tRNA<-tRNA<-Ferredoxin-betagrasp	LRR-repeats+AP-GTPase+COR+TM+TM	897	-	Cyanobacteria	Microcystis aeruginosa	leucine-rich repeat domain-containing protein [Microcystis aeruginosa].	GCF_001725075.1
WP_070392558.1	SIG+PBPI→?→?→ SIG+TM+TM+TM+TM+TM+TM+TM→||<-?||ABC-ATPase→ ABC-ATPase→||<-PSE||LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	909	-	Cyanobacteria	Moorea producens	leucine-rich repeat domain-containing protein [Moorea producens].	GCF_001767235.1
WP_070393924.1	REC→||<-TPR-repeats<-?||LRR-repeats+AP-GTPase+COR+DUF4404*→	LRR-repeats+AP-GTPase+COR+DUF4404	938	-	Cyanobacteria	Moorea producens	leucine-rich repeat domain-containing protein [Moorea producens].	GCF_001767235.1
WP_071837136.1	<-PIN<-?<-PIN<-?<-PIN<-?||LRR-repeats+AP-GTPase+COR+DUF4404*→?→ PSE→||<-Cluster5_5clades<-?<-Cluster2453_2clades	LRR-repeats+AP-GTPase+COR+DUF4404	1008	-	Cyanobacteria	Leptolyngbya sp. NIES-3755	leucine-rich repeat domain-containing protein [Leptolyngbya sp. NIES-3755].	GCF_001548435.1
WP_071987478.1	LRR-repeats+AP-GTPase+COR*→||<-?<-?||RelE→ CHTH→	LRR-repeats+AP-GTPase+COR	725	-	Cyanobacteria	Crocosphaera watsonii	leucine-rich repeat domain-containing protein [Crocosphaera watsonii].	GCF_000235665.1
WP_072015976.1	<-SIG+TM||?→||<-RelE-ParE<-?||LRR-repeats+AP-GTPase+COR*→||<-?||?→?→ COR→	LRR-repeats+AP-GTPase+COR	651	-	Cyanobacteria	Leptolyngbya sp. KIOST-1	hypothetical protein [Leptolyngbya sp. KIOST-1].	GCF_000763385.1
WP_072022104.1	<-ARSR-HTH<-PSE||?→||<-?||?→||<-SIG+Trypsin+PDZ<-?||?→ LRR-repeats+AP-GTPase+COR*→?→||<-RPN10<-?<-?<-Cluster2290_2clades<-Cluster2428_2clades	LRR-repeats+AP-GTPase+COR	838	-	Cyanobacteria	[Scytonema hofmanni] UTEX B 1581	leucine-rich repeat domain-containing protein [[Scytonema hofmanni] UTEX B 1581].	GCF_000582685.1
WP_072061087.1	LRR-repeats+AP-GTPase+COR*→||<-?<-?||RelE→ CHTH→	LRR-repeats+AP-GTPase+COR	725	-	Cyanobacteria	Crocosphaera watsonii	leucine-rich repeat domain-containing protein [Crocosphaera watsonii].	GCF_001039615.1
WP_072926417.1	Mbetalac→ SAM-methylase→?→||<-?<-SIG+TPM_phosphatase+TM+TM+TM||LRR-repeats+AP-GTPase+COR+TM+TM*→	LRR-repeats+AP-GTPase+COR+TM+TM	828	-	Cyanobacteria	Microcystis aeruginosa	leucine-rich repeat domain-containing protein [Microcystis aeruginosa].	GCF_001895325.1
WP_073070049.1	LRR-repeats+AP-GTPase+COR+TM+TM*→	LRR-repeats+AP-GTPase+COR+TM+TM	759	-	Cyanobacteria	Phormidesmis priestleyi	leucine-rich repeat domain-containing protein [Phormidesmis priestleyi].	GCF_001895925.1
WP_073584587.1	<-Aminotran_1_2<-TetR-HTH||Cluster2045_2clades→?→ LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	844	-	Gammaproteobacteria	Vibrio quintilis	TIR domain-containing protein [Vibrio quintilis].	GCF_900143745.1
WP_073604448.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1052	-	Gammaproteobacteria	Vibrio aerogenes	TIR domain-containing protein, partial [Vibrio aerogenes].	GCF_900130105.1
WP_073609490.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1026	-	Cyanobacteria	Phormidium tenue	leucine-rich repeat domain-containing protein [Phormidium tenue].	GCF_014696675.1
WP_073639373.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1122	-	Cyanobacteria	Nostoc calcicola	leucine-rich repeat domain-containing protein [Nostoc calcicola].	GCF_001904715.1
WP_073640743.1	LRR-repeats+AP-GTPase+COR+TIR*→?→||<-Arginase	LRR-repeats+AP-GTPase+COR+TIR	1070	-	Cyanobacteria	Nostoc calcicola	leucine-rich repeat domain-containing protein [Nostoc calcicola].	GCF_014697355.1
WP_073641321.1	<-PIN<-?||?→?→ PIN→ LRR-repeats+AP-GTPase+COR+TIR*→||<-?||?→||<-?||?→?→ RPN10→	LRR-repeats+AP-GTPase+COR+TIR	1188	-	Cyanobacteria	Nostoc calcicola	leucine-rich repeat protein [Nostoc calcicola].	GCF_001904715.1
WP_074191634.1	CI→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1105	-	Gammaproteobacteria	Vibrio antiquarius	50S ribosome-binding GTPase [Vibrio antiquarius].	GCF_001909305.1
WP_074382488.1	<-Cluster1076_2clades<-?||?→||<-?<-?||?→||<-?||LRR-repeats+AP-GTPase+COR+TM+TM*→	LRR-repeats+AP-GTPase+COR+TM+TM	1015	-	Cyanobacteria	Phormidesmis priestleyi	leucine-rich repeat domain-containing protein [Phormidesmis priestleyi].	GCF_001650195.1
WP_075071341.1	<-ABC-ATPase<-?||?→?→?→?→?→ LRR-repeats+AP-GTPase+COR*→ SIG+TM+TM+TM+TM→?→?→||<-?||?→ SIG+TM+TM+TM+TM+TM+TM+TM+TM+TM→	LRR-repeats+AP-GTPase+COR	692	-	Chloroflexi	Levilinea saccharolytica	GTP-binding protein [Levilinea saccharolytica].	GCF_001050255.2

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WP_075170580.1	RNA-Helicase→||<-PSE<-?<-?<-?<-?||?→||<-TM+TM||LRR-repeats+AP-GTPase+COR*→||<-?<-Cluster1726_2clades	LRR-repeats+AP-GTPase+COR	960	-	Gammaproteobacteria	Pseudoalteromonas haloplanktis	GTP-binding protein [Pseudoalteromonas haloplanktis].	GCF_001924935.1
WP_075904287.1	ABC-ATPase→ ABC-ATPase→?→?→||<-?||LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	801	-	Cyanobacteria	Moorea bouillonii	leucine-rich repeat domain-containing protein [Moorea bouillonii].	GCF_001942495.1
WP_076382638.1	<-Polbeta+HEPN<-?||?→ LRR-repeats+AP-GTPase+COR+TIR*→ TIR→ TM+TM+TM→?→?→||<-CNMP+CRP-HTH	LRR-repeats+AP-GTPase+COR+TIR	1349	-	Bacteroidetes	Filimonas lacunae	TIR domain-containing protein [Filimonas lacunae].	GCF_002355595.1
WP_076393053.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	925	-	Bacteroidetes	Chryseobacterium	MULTISPECIES: leucine-rich repeat domain-containing protein [Chryseobacterium].	GCF_900156825.1
WP_076396200.1	LRR-repeats+AP-GTPase+COR*→||<-?||?→ SIG+NUDIX→	LRR-repeats+AP-GTPase+COR	890	-	Bacteroidetes	Chryseobacterium gambrini	hypothetical protein [Chryseobacterium gambrini].	GCF_900156825.1
WP_076994187.1	<-ABC-ATPase<-?||?→?→||<-?||PSE→||<-?||LRR-repeats+AP-GTPase+COR*→||<-?||?→||<-?<-?<-Aminotran_1_2	LRR-repeats+AP-GTPase+COR	942	-	Actinobacteria	Actinosynnema sp. ALI-1.44	hypothetical protein [Actinosynnema sp. ALI-1.44].	GCF_001984155.1
WP_077025618.1	LRR-repeats+AP-GTPase+COR*→?→||<-?<-?||?→||<-?<-?<-ABC-ATPase	LRR-repeats+AP-GTPase+COR	1153	-	Planctomycetes	Fuerstia marisgermanicae	leucine-rich repeat domain-containing protein [Fuerstia marisgermanicae].	GCF_001983935.1
WP_078402495.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	901	-	Bacteroidetes	Elizabethkingia ursingii	leucine-rich repeat domain-containing protein [Elizabethkingia ursingii].	GCF_002022125.1
WP_078608910.1	<-RNA-Helicase||?→?→||<-?||CI→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1012	-	Gammaproteobacteria	Vibrio owensii	GTP-binding protein [Vibrio owensii].	GCF_002021755.1
WP_078814763.1	<-REC||LRR-repeats+AP-GTPase+COR+TIR*→?→?→||<-?||?→||<-?<-NUDIX	LRR-repeats+AP-GTPase+COR+TIR	959	-	Verrucomicrobia	Prosthecobacter debontii	leucine-rich repeat domain-containing protein [Prosthecobacter debontii].	GCF_900167535.1
WP_079184311.1	LRR-repeats+AP-GTPase+COR*→?→||<-?<-SIGMA-HTH	LRR-repeats+AP-GTPase+COR	1056	-	Actinobacteria	Streptomyces uncialis	hypothetical protein [Streptomyces uncialis].	GCF_001905345.1
WP_079712025.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	882	-	Bacteroidetes	Salegentibacter salinarum	hypothetical protein [Salegentibacter salinarum].	GCF_900168115.1
WP_080603599.1	LRR-repeats+AP-GTPase+COR+TM+TM*→	LRR-repeats+AP-GTPase+COR+TM+TM	799	-	Cyanobacteria	Microcystis aeruginosa	leucine-rich repeat protein [Microcystis aeruginosa].	-
WP_080963556.1	Cluster1140_2clades→?→ LRR-repeats+AP-GTPase+COR+TM+TM*→	LRR-repeats+AP-GTPase+COR+TM+TM	830	-	Gammaproteobacteria	Pseudomonas putida	GTP-binding protein [Pseudomonas putida].	GCF_001027965.1
WP_081155426.1	LRR-repeats+AP-GTPase+COR*→||<-?<-?<-?<-?||?→||<-?<-REC	LRR-repeats+AP-GTPase+COR	1088	-	Bacteroidetes	Niastella vici	hypothetical protein [Niastella vici].	GCF_002077945.1
WP_081336246.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1380	-	Actinobacteria	Mycobacteroides chelonae	hypothetical protein [Mycobacteroides chelonae].	GCF_001853965.1
WP_081583858.1	LRR-repeats→ LRR-repeats+AP-GTPase+COR+CASPASE*→	LRR-repeats+AP-GTPase+COR+CASPASE	1375	-	Cyanobacteria	unclassified Tolypothrix	MULTISPECIES: leucine-rich repeat domain-containing protein [unclassified Tolypothrix].	GCF_015207145.1
WP_081656227.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1354	-	Cyanobacteria	Fischerella sp. PCC 9431	leucine-rich repeat domain-containing protein [Fischerella sp. PCC 9431].	-
WP_081983983.1	Ferredoxin-RRM→?→ Cluster1494_2clades→||<-?<-?||?→?→ LRR-repeats+AP-GTPase+COR+DUF4404*→	LRR-repeats+AP-GTPase+COR+DUF4404	971	-	Betaproteobacteria	Massilia sp. JS1662	GTP-binding protein [Massilia sp. JS1662].	GCF_000759615.1
WP_082167682.1	LRR-repeats+AP-GTPase+COR+TIR*→||<-?||Cluster850_2clades→	LRR-repeats+AP-GTPase+COR+TIR	797	-	Alphaproteobacteria	Methylobacterium aquaticum	TIR domain-containing protein, partial [Methylobacterium aquaticum].	GCF_001043915.1
WP_082209748.1	LRR-repeats+AP-GTPase+COR+TCAD4*→||<-Cluster5_5clades<-?||?→?→ Pro_CA→	LRR-repeats+AP-GTPase+COR+TCAD4	714	-	Cyanobacteria	Fischerella sp. PCC 9605	leucine-rich repeat domain-containing protein [Fischerella sp. PCC 9605].	GCF_000517105.1

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WP_082226537.1	LRR-repeats→?→ LRR-repeats+AP-GTPase+COR*→||<-?<-?||?→||<-?<-?<-?||Aminotran_1_2→	LRR-repeats+AP-GTPase+COR	1171	-	Bacteroidetes	Microscilla marina	leucine-rich repeat domain-containing protein [Microscilla marina].	GCF_000169175.1
WP_083250213.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	817	-	Euryarchaeota	Methanosarcina sp. A14	leucine-rich repeat domain-containing protein, partial [Methanosarcina sp. A14].	GCF_001729375.1
WP_083398305.1	LRR-repeats→ LRR-repeats+AP-GTPase+COR+DrHyd*→?→?→?→?→||<-?<-SIG+TM+TM+TM+TM	LRR-repeats+AP-GTPase+COR+DrHyd	751	-	Betaproteobacteria	Nitrosomonas communis	hypothetical protein [Nitrosomonas communis].	GCF_900114745.1
WP_083620324.1	<-SIG+TM+TM+TM+TM+TM+TM<-?||LRR-repeats+AP-GTPase+COR*→?→||<-HNH||Cluster1548_2clades→?→||<-?||CCTBP→	LRR-repeats+AP-GTPase+COR	975	-	Cyanobacteria	Planktothrix paucivesiculata	leucine-rich repeat domain-containing protein [Planktothrix paucivesiculata].	GCF_900009265.2
WP_083622583.1	Cluster1745_2clades→?→?→||<-?||?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1058	-	Cyanobacteria	Planktothrix paucivesiculata	leucine-rich repeat domain-containing protein [Planktothrix paucivesiculata].	GCF_900009265.2
WP_083850172.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1286	-	Deltaproteobacteria	Desulfovibrio sp. U5L	GTP-binding protein [Desulfovibrio sp. U5L].	-
WP_083886975.1	<-SIG+TM||?→||<-?<-?||LRR-repeats→?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	863	-	Cyanobacteria	Nodosilinea nodulosa	hypothetical protein [Nodosilinea nodulosa].	GCF_000309385.1
WP_083887059.1	RelE→ CHTH→ LRR-repeats→ PSE→||<-?||PSE→ LRR-repeats+AP-GTPase+COR*→||<-?<-?||COR+TIR→||<-REase-4	LRR-repeats+AP-GTPase+COR	410	-	Cyanobacteria	Nodosilinea nodulosa	leucine-rich repeat domain-containing protein [Nodosilinea nodulosa].	GCF_000309385.1
WP_083887212.1	Cluster2123_2clades→?→||<-?<-?<-?||PSE→ LRR-repeats→ AP-GTPase*→	AP-GTPase	221	-	Cyanobacteria	Nodosilinea nodulosa	50S ribosome-binding GTPase [Nodosilinea nodulosa].	GCF_000309385.1
WP_083918254.1	LRR-repeats+AP-GTPase+COR+TIR*→||<-?<-?||?→||<-?<-?<-SHS2	LRR-repeats+AP-GTPase+COR+TIR	954	-	Gammaproteobacteria	Methylosarcina fibrata	TIR domain-containing protein [Methylosarcina fibrata].	GCF_000372865.1
WP_084022355.1	<-NUDIX||?→||<-HNH<-?||?→?→?→ LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	850	-	Chlorobi	Chlorobaculum limnaeum	TIR domain-containing protein [Chlorobaculum limnaeum].	GCF_001747405.1
WP_084172951.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	639	-	Cyanobacteria	Phormidium tenue	GTP-binding protein [Phormidium tenue].	GCF_014696675.1
WP_084177732.1	LRR-repeats+AP-GTPase+COR+TM+TM*→||<-CASPASE+TM	LRR-repeats+AP-GTPase+COR+TM+TM	985	-	Cyanobacteria	Nostoc calcicola	leucine-rich repeat domain-containing protein [Nostoc calcicola].	GCF_001904715.1
WP_084227301.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	804	-	Cyanobacteria	Nostoc sp. KVJ20	leucine-rich repeat domain-containing protein [Nostoc sp. KVJ20].	GCF_001712795.1
WP_084428809.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	944	-	Actinobacteria	Kibdelosporangium aridum	hypothetical protein [Kibdelosporangium aridum].	GCF_900176515.1
WP_084630566.1	<-HhH-RADC+JAB||?→ NTP_transf_3→ LRR-repeats+AP-GTPase+COR*→||<-?<-?||?→||<-?||?→||<-Cluster1409_2clades	LRR-repeats+AP-GTPase+COR	906	-	Euryarchaeota	Methanosarcina lacustris	leucine-rich repeat domain-containing protein [Methanosarcina lacustris].	GCF_000970265.1
WP_084713364.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1355	-	Actinobacteria	Streptacidiphilus jeojiense	leucine-rich repeat domain-containing protein [Streptacidiphilus jeojiense].	-
WP_084763145.1	Pentapeptide-repeats→||<-TPR+nSTAND1+BetaPropeller_WD40+BetaPropeller_WD40<-?||?→||<-?||?→||<-?||LRR-repeats+AP-GTPase+COR+CASPASE*→||<-RelE-ParE	LRR-repeats+AP-GTPase+COR+CASPASE	1441	-	Cyanobacteria	[Scytonema hofmanni] UTEX B 1581	leucine-rich repeat domain-containing protein [[Scytonema hofmanni] UTEX B 1581].	GCF_000582685.1
WP_084765096.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	940	-	Firmicutes	Clostridium intestinale	GTP-binding protein [Clostridium intestinale].	-
WP_084967529.1	Cluster1877_2clades→||<-?||Cluster1140_2clades→?→ LRR-repeats+AP-GTPase+COR+TM+TM*→	LRR-repeats+AP-GTPase+COR+TM+TM	830	-	Gammaproteobacteria	Pseudomonas putida	GTP-binding protein [Pseudomonas putida].	GCF_002094785.1

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WP_086488496.1	GTPase-AIG→||<-?||?→?→?→?→ PIN→ LRR-repeats+AP-GTPase+COR+TIR*→?→||<-?<-SIG+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM<-?||?→||<-?<-Cluster1501_2clades	LRR-repeats+AP-GTPase+COR+TIR	936	-	Gammaproteobacteria	Thioflexothrix psekupsii	leucine-rich repeat domain-containing protein [Thioflexothrix psekupsii].	GCF_002149925.1
WP_086489369.1	LRR-repeats+AP-GTPase+COR+HEPN*→ ABC-ATPase→?→?→?→?→ Cluster1668_2clades→	LRR-repeats+AP-GTPase+COR+HEPN	919	-	Gammaproteobacteria	Thioflexothrix psekupsii	leucine-rich repeat domain-containing protein [Thioflexothrix psekupsii].	GCF_002149925.1
WP_086489735.1	<-Cluster1597_2clades<-Cluster1052_2clades<-?||?→?→?→ LRR-repeats+AP-GTPase+COR+HEPN*→ Cluster2027_2clades→?→||<-ABC-ATPase<-MoxR-AAA<-HISKIN	LRR-repeats+AP-GTPase+COR+HEPN	857	-	Gammaproteobacteria	Thioflexothrix psekupsii	leucine-rich repeat domain-containing protein [Thioflexothrix psekupsii].	GCF_002149925.1
WP_086671081.1	SIG+TM+TM+TM+TM→||<-?<-?<-?||?→||<-Cluster2027_2clades<-?||tRNA→ LRR-repeats+AP-GTPase+COR+TM+TM*→||<-?<-?||PSE→||<-?||?→?→||<-?<-SIG+Calcineurin	LRR-repeats+AP-GTPase+COR+TM+TM	937	-	Actinobacteria	Amycolatopsis pretoriensis	GTP-binding protein [Amycolatopsis pretoriensis].	GCF_900107925.1
WP_086685880.1	LRR-repeats+AP-GTPase+COR+DUF4404*→	LRR-repeats+AP-GTPase+COR+DUF4404	1074	-	Cyanobacteria	Nostoc sp. T09	leucine-rich repeat domain-containing protein [Nostoc sp. T09].	GCF_002154695.1
WP_086688381.1	LRR-repeats+AP-GTPase+COR+CASPASE*→||<-?<-?||?→ RelE-ParE→||<-?<-?||Cluster1437_2clades→	LRR-repeats+AP-GTPase+COR+CASPASE	897	-	Cyanobacteria	Nostoc sp. T09	CHAT domain-containing protein, partial [Nostoc sp. T09].	GCF_002154695.1
WP_086688547.1	LRR-repeats+AP-GTPase+COR+TM+TM*→	LRR-repeats+AP-GTPase+COR+TM+TM	883	-	Cyanobacteria	Nostoc sp. T09	leucine-rich repeat domain-containing protein [Nostoc sp. T09].	GCF_002154695.1
WP_086759966.1	LRR-repeats+AP-GTPase+COR+DUF4404*→ TPR-repeats+CASPASE→||<-?||?→ HTH→	LRR-repeats+AP-GTPase+COR+DUF4404	1097	-	Cyanobacteria	Nostoc sp. 106C	leucine-rich repeat domain-containing protein [Nostoc sp. 106C].	GCF_002154725.1
WP_086760374.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1054	-	Cyanobacteria	Nostoc sp. 106C	leucine-rich repeat domain-containing protein [Nostoc sp. 106C].	GCF_002154725.1
WP_086768657.1	RPN10→ Chromo-N+CHROMO→||<-?||LRR-repeats+AP-GTPase+COR+CASPASE*→	LRR-repeats+AP-GTPase+COR+CASPASE	1254	-	Cyanobacteria	Nostoc sp. 106C	leucine-rich repeat domain-containing protein [Nostoc sp. 106C].	GCF_002154725.1
WP_086834293.1	LRR-repeats+AP-GTPase+COR+TM+TM*→	LRR-repeats+AP-GTPase+COR+TM+TM	884	-	Cyanobacteria	Nostoc sp. RF31YmG	leucine-rich repeat domain-containing protein [Nostoc sp. RF31YmG].	GCF_002155185.1
WP_087590341.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	452	-	Cyanobacteria	unicellular cyanobacterium SU3	leucine-rich repeat domain-containing protein [unicellular cyanobacterium SU3].	-
WP_087656332.1	Cluster1742_2clades→ Cluster1685_2clades→?→?→?→?→?→ LRR-repeats+AP-GTPase+COR*→?→ TIR→	LRR-repeats+AP-GTPase+COR	560	-	Betaproteobacteria	Caballeronia terrestris	hypothetical protein [Caballeronia terrestris].	GCF_001544515.1
WP_088134442.1	OmpA→?→ Cluster1633_2clades→||<-?||?→ tRNA→?→ Polbeta+HEPN→ LRR-repeats+AP-GTPase+COR+TIR*→?→||<-?||?→?→ SIG+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM→ SIG+TM→	LRR-repeats+AP-GTPase+COR+TIR	1220	-	Gammaproteobacteria	Vibrio gazogenes	TIR domain-containing protein [Vibrio gazogenes].	GCF_002196515.1
WP_088620375.1	<-Cluster2094_2clades||LRR-repeats+AP-GTPase+COR*→||<-?<-?<-?<-HISKIN||?→||<-REC	LRR-repeats+AP-GTPase+COR	806	-	Gammaproteobacteria	Methylovulum psychrotolerans	GTP-binding protein [Methylovulum psychrotolerans].	GCF_002209385.1
WP_088620603.1	<-ABC-ATPase<-SIG+BLBD<-?<-?||REC→ HISKIN→ REase→ LRR-repeats+AP-GTPase+COR+TIR*→?→?→ Ferredoxin-RRM→	LRR-repeats+AP-GTPase+COR+TIR	1013	-	Gammaproteobacteria	Methylovulum psychrotolerans	TIR domain-containing protein [Methylovulum psychrotolerans].	GCF_002209385.1
WP_088621060.1	LRR-repeats+AP-GTPase+COR+DpnII-MboI-NTD+TIR*→	LRR-repeats+AP-GTPase+COR+DpnII-MboI-NTD+TIR	866	-	Gammaproteobacteria	Methylovulum psychrotolerans	leucine-rich repeat domain-containing protein [Methylovulum psychrotolerans].	GCF_002209385.1
WP_088646515.1	LRR-repeats+AP-GTPase+COR*→||<-?<-?<-?<-?<-Cluster1404_2clades	LRR-repeats+AP-GTPase+COR	987	-	Actinobacteria	Micromonospora wenchangensis	hypothetical protein [Micromonospora wenchangensis].	GCF_002210435.1
WP_088745883.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	863	-	Bacteroidetes	unclassified Sphingobacteriales	MULTISPECIES: GTP-binding protein [unclassified Sphingobacteriales].	-

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WP_088762693.1	TPR-repeats→?→ SIG+Alba→||<-?<-?<-?<-?||LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	851	-	Bacteroidetes	unclassified Sphingobacteriales	MULTISPECIES: GTP-binding protein [unclassified Sphingobacteriales].	-
WP_088764296.1	LRR-repeats+AP-GTPase+COR+TM+TM*→	LRR-repeats+AP-GTPase+COR+TM+TM	969	-	Bacteroidetes	unclassified Sphingobacteriales	MULTISPECIES: leucine-rich repeat domain-containing protein [unclassified Sphingobacteriales].	-
WP_089288360.1	<-SIG+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM<-?||?→ Cluster1974_2clades→?→?→||<-?||LRR-repeats+AP-GTPase+COR+TIR*→||<-?<-ParB<-ParA-Soj-PloopNTPase<-?<-Thioredoxin	LRR-repeats+AP-GTPase+COR+TIR	1212	-	Alphaproteobacteria	unclassified Azospirillum	MULTISPECIES: TIR domain-containing protein [unclassified Azospirillum].	GCF_900188385.1
WP_089298330.1	SIG+Concanavalin-like+SUN→ LRR-repeats+AP-GTPase+COR*→||<-PSE||?→?→?→||<-?<-ABC-ATPase	LRR-repeats+AP-GTPase+COR	908	-	Actinobacteria	Actinoplanes regularis	GTP-binding protein [Actinoplanes regularis].	GCF_016862355.1
WP_089681784.1	LRR-repeats+AP-GTPase+COR*→?→||<-Thioredoxin	LRR-repeats+AP-GTPase+COR	787	-	Bacteroidetes	Catalinimonas alkaloidigena	hypothetical protein [Catalinimonas alkaloidigena].	GCF_900100765.1
WP_089727137.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1009	-	Gammaproteobacteria	Candidatus Thiosymbion oneisti	leucine-rich repeat domain-containing protein [Candidatus Thiosymbion oneisti].	GCF_900092655.1
WP_089824678.1	Cluster1536_2clades→?→||<-tRNA||LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	978	-	Firmicutes	Clostridiales bacterium CHKCI001	leucine-rich repeat domain-containing protein [Clostridiales bacterium CHKCI001].	-
WP_089856669.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	925	-	Bacteroidetes	Chryseobacterium taeanense	leucine-rich repeat domain-containing protein [Chryseobacterium taeanense].	GCF_900099685.1
WP_089938297.1	COR→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	705	-	Nitrospinae/Tectomicrobia group	Candidatus Entotheonella palauensis	hypothetical protein [Candidatus Entotheonella palauensis].	GCF_900079095.1
WP_089941349.1	<-Aminotran_1_2<-Cluster1597_2clades||?→?→?→?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	514	-	Nitrospinae/Tectomicrobia group	Candidatus Entotheonella palauensis	leucine-rich repeat domain-containing protein [Candidatus Entotheonella palauensis].	GCF_900079095.1
WP_090106546.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1148	-	Bacteroidetes	Chitinophaga sp. CF118	leucine-rich repeat domain-containing protein [Chitinophaga sp. CF118].	GCF_900112615.1
WP_090320517.1	LRR-repeats+AP-GTPase+COR*→?→?→ ParA-Soj-PloopNTPase→	LRR-repeats+AP-GTPase+COR	738	-	Betaproteobacteria	Nitrosomonas oligotropha	leucine-rich repeat domain-containing protein [Nitrosomonas oligotropha].	GCF_900106555.1
WP_090640679.1	<-RNA-Helicase||LRR-repeats+AP-GTPase+COR+DrHyd*→||<-CBS	LRR-repeats+AP-GTPase+COR+DrHyd	1059	-	Bacteroidetes	Mucilaginibacter sp. OK283	leucine-rich repeat domain-containing protein [Mucilaginibacter sp. OK283].	GCF_900110415.1
WP_090662001.1	LRR-repeats+AP-GTPase+COR+TIR*→?→||<-?<-?||?→ SIG+FKBP→	LRR-repeats+AP-GTPase+COR+TIR	1182	-	Bacteroidetes	Parafilimonas terrae	leucine-rich repeat domain-containing protein [Parafilimonas terrae].	GCF_900115755.1
WP_091029330.1	TM→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1045	-	Actinobacteria	Glycomyces harbinensis	hypothetical protein [Glycomyces harbinensis].	GCF_900101745.1
WP_091054155.1	<-Cluster2137_2clades<-?<-?||?→||<-?||?→?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1094	-	Actinobacteria	Glycomyces sambucus	hypothetical protein [Glycomyces sambucus].	GCF_900102815.1
WP_091103947.1	<-ABC-ATPase<-?||?→?→||<-?||LRR-repeats+AP-GTPase+COR*→?→?→?→||<-?<-?<-SIR2	LRR-repeats+AP-GTPase+COR	941	-	Actinobacteria	Nonomuraea pusilla	leucine-rich repeat domain-containing protein [Nonomuraea pusilla].	GCF_900109355.1
WP_091133979.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1190	-	Bacteroidetes	Flavobacterium anhuiense	TIR domain-containing protein [Flavobacterium anhuiense].	GCF_900101855.1

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WP_091435026.1	<-Cluster1070_2clades<-ENDO3+NUDIX||HU-IHF→?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	916	-	Bacteroidetes	Flavobacterium degerlachei	leucine-rich repeat domain-containing protein [Flavobacterium degerlachei].	GCF_900106645.1
WP_091506051.1	Cluster944_3clades→||<-?<-?||?→||<-Cluster2045_2clades<-?||LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	997	-	Bacteroidetes	Flexibacter flexilis	leucine-rich repeat domain-containing protein [Flexibacter flexilis].	GCF_900112255.1
WP_091630534.1	<-ABC-ATPase||?→ LRR-repeats+AP-GTPase+COR*→||<-ABC_membrane+ABC_tran	LRR-repeats+AP-GTPase+COR	901	-	Actinobacteria	Micromonospora peucetia	leucine-rich repeat domain-containing protein [Micromonospora peucetia].	GCF_900091625.1
WP_092162518.1	REC→ REC→?→?→?→ LRR-repeats+AP-GTPase+COR*→?→?→ SIG+WWE→?→?→ ABC-ATPase→ ABC-ATPase→	LRR-repeats+AP-GTPase+COR	863	-	Deltaproteobacteria	Maridesulfovibrio ferrireducens	GTP-binding protein [Maridesulfovibrio ferrireducens].	GCF_900101105.1
WP_093066920.1	LRR-repeats+AP-GTPase+COR+TIR*→?→?→||<-Thioredoxin||YBAK→	LRR-repeats+AP-GTPase+COR+TIR	847	-	Gammaproteobacteria	Thiothrix caldifontis	TIR domain-containing protein [Thiothrix caldifontis].	GCF_900107695.1
WP_093070768.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1327	-	Gammaproteobacteria	Thiothrix caldifontis	leucine-rich repeat domain-containing protein [Thiothrix caldifontis].	GCF_900107695.1
WP_094331224.1	Cluster1074_2clades→?→ LRR-repeats+AP-GTPase+COR+DUF4404*→||<-PSE<-?||?→?→ SAM-methylase→	LRR-repeats+AP-GTPase+COR+DUF4404	1016	-	Cyanobacteria	Nostoc sp. 'Peltigera membranacea cyanobiont' 213	leucine-rich repeat domain-containing protein [Nostoc sp. 'Peltigera membranacea cyanobiont' 213].	GCF_002245975.1
WP_094342929.1	<-Arginase<-?||?→ LRR-repeats+AP-GTPase+COR+TIR*→?→||<-?<-?<-ABC_membrane+ABC_tran	LRR-repeats+AP-GTPase+COR+TIR	1126	-	Cyanobacteria	Nostoc sp. 'Peltigera membranacea cyanobiont' 232	leucine-rich repeat domain-containing protein [Nostoc sp. 'Peltigera membranacea cyanobiont' 232].	GCF_002245985.1
WP_094343165.1	LRR-repeats+AP-GTPase+COR+TIR*→?→||<-?<-TIR<-?<-SIG+NUDIX	LRR-repeats+AP-GTPase+COR+TIR	1023	-	Cyanobacteria	Nostoc sp. 'Peltigera membranacea cyanobiont' 232	leucine-rich repeat domain-containing protein [Nostoc sp. 'Peltigera membranacea cyanobiont' 232].	GCF_002245985.1
WP_094350322.1	LRR-repeats+AP-GTPase+COR*→?→?→||<-ABhydrolase<-Cluster1087_2clades	LRR-repeats+AP-GTPase+COR	1217	-	Cyanobacteria	Nostoc sp. 'Peltigera membranacea cyanobiont' 210A	leucine-rich repeat domain-containing protein [Nostoc sp. 'Peltigera membranacea cyanobiont' 210A].	GCF_002246015.1
WP_094350573.1	LRR-repeats+AP-GTPase+COR+DUF4404*→ REC→	LRR-repeats+AP-GTPase+COR+DUF4404	1154	-	Cyanobacteria	Nostoc sp. 'Peltigera membranacea cyanobiont' 210A	leucine-rich repeat domain-containing protein [Nostoc sp. 'Peltigera membranacea cyanobiont' 210A].	GCF_002246015.1
WP_094350736.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	996	-	Cyanobacteria	Nostoc sp. 'Peltigera membranacea cyanobiont' 210A	leucine-rich repeat domain-containing protein [Nostoc sp. 'Peltigera membranacea cyanobiont' 210A].	-
WP_094350925.1	<-TPR+TPR<-?||?→?→ ABhydrolase→?→||<-?||LRR-repeats+AP-GTPase+COR+TIR*→||<-?<-?<-?<-?<-SIG+NUDIX	LRR-repeats+AP-GTPase+COR+TIR	1078	-	Cyanobacteria	Nostoc sp. 'Peltigera membranacea cyanobiont' 210A	leucine-rich repeat domain-containing protein [Nostoc sp. 'Peltigera membranacea cyanobiont' 210A].	GCF_002246015.1
WP_094408510.1	<-ABC-ATPase||ICLR-HTH→ LRR-repeats+AP-GTPase+COR+TIR*→||<-SIG+TM+TM+TM+TM+TM+TM+TM+TM	LRR-repeats+AP-GTPase+COR+TIR	974	-	Alphaproteobacteria	Elstera cyanobacteriorum	leucine-rich repeat domain-containing protein [Elstera cyanobacteriorum].	GCF_014643715.1
WP_094530685.1	LRR-repeats+AP-GTPase+COR*→||<-PSE||?→?→?→||<-ABC-ATPase<-ABC-ATPase<-SIG+TM+TM+TM+TM+TM+TM+TM	LRR-repeats+AP-GTPase+COR	1019	-	Cyanobacteria	Pseudanabaena sp. SR411	leucine-rich repeat domain-containing protein [Pseudanabaena sp. SR411].	GCF_002251945.1

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
WP_094533976.1	Cluster54_3clades→ Cluster1093_2clades→ LRR-repeats+AP-GTPase+COR+TM+TM*→	LRR-repeats+AP-GTPase+COR+TM+TM	1051	-	Cyanobacteria	Pseudanabaena sp. SR411	leucine-rich repeat domain-containing protein [Pseudanabaena sp. SR411].	GCF_002251945.1
WP_095644020.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	774	-	Euryarchaeota	Methanosarcina spelaei	leucine-rich repeat domain-containing protein, partial [Methanosarcina spelaei].	GCF_002287235.1
WP_095644584.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	877	-	Euryarchaeota	Methanosarcina spelaei	leucine-rich repeat domain-containing protein [Methanosarcina spelaei].	GCF_002287235.1
WP_096193484.1	LRR-repeats+AP-GTPase+COR+TIR*→?→||<-FAD-NAD-dep-oxidoreductase<-?<-?<-RNA-Helicase	LRR-repeats+AP-GTPase+COR+TIR	1173	-	Bacteroidetes	Cytophagales bacterium TFI 002	leucine-rich repeat domain-containing protein [Cytophagales bacterium TFI 002].	-
WP_096535168.1	LRR-repeats+AP-GTPase+COR*→||<-ClpABN-AAA+ClpABC-AAA<-?||METHYLASE→	LRR-repeats+AP-GTPase+COR	1018	-	Cyanobacteria	Nostoc linckia	leucine-rich repeat domain-containing protein [Nostoc linckia].	GCF_002368035.1
WP_096538729.1	<-Pkinase+Pentapeptide<-?<-?||?→||<-?||?→ LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1033	-	Cyanobacteria	Nostoc linckia	leucine-rich repeat domain-containing protein [Nostoc linckia].	GCF_002368035.1
WP_096538739.1	LRR-repeats+AP-GTPase+COR+TIR*→?→||<-?||?→?→?→ RPN10→	LRR-repeats+AP-GTPase+COR+TIR	1115	-	Cyanobacteria	Nostoc linckia	leucine-rich repeat domain-containing protein [Nostoc linckia].	GCF_002368035.1
WP_096551538.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	818	-	Cyanobacteria	Nostoc sp. NIES-4103	leucine-rich repeat domain-containing protein [Nostoc sp. NIES-4103].	GCF_002368335.1
WP_096566542.1	HNH→ PSE→ LRR-repeats+AP-GTPase+COR*→?→?→?→||<-?||?→||<-?||PAIREDC-HTH→	LRR-repeats+AP-GTPase+COR	1268	-	Cyanobacteria	Scytonema sp. NIES-4073	leucine-rich repeat protein [Scytonema sp. NIES-4073].	GCF_002368435.1
WP_096579899.1	<-DSBH<-?<-?<-?<-ParA-Soj-PloopNTPase<-?||Cluster5_5clades→ LRR-repeats+AP-GTPase+COR+DUF4404*→	LRR-repeats+AP-GTPase+COR+DUF4404	1153	-	Cyanobacteria	Anabaenopsis circularis	leucine-rich repeat domain-containing protein [Anabaenopsis circularis].	GCF_002367975.1
WP_096585603.1	HISKIN→||<-?<-?||LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	937	-	Cyanobacteria	Anabaenopsis circularis	leucine-rich repeat domain-containing protein [Anabaenopsis circularis].	GCF_002367975.1
WP_096586956.1	<-ABC-ATPase||?→ Pkinase+TM→ Chromo-N+CHROMO→||<-?||LRR-repeats+AP-GTPase+COR+CASPASE*→||<-?<-?||Aminotran_1_2→	LRR-repeats+AP-GTPase+COR+CASPASE	1148	-	Cyanobacteria	Calothrix sp. NIES-2098	leucine-rich repeat domain-containing protein [Calothrix sp. NIES-2098].	GCF_002368175.1
WP_096588412.1	LRR-repeats+AP-GTPase+COR*→ TPR-repeats+CASPASE→	LRR-repeats+AP-GTPase+COR	1066	-	Cyanobacteria	Calothrix sp. NIES-2098	leucine-rich repeat domain-containing protein [Calothrix sp. NIES-2098].	GCF_002368175.1
WP_096598125.1	LRR-repeats+AP-GTPase+COR+DUF4404*→?→||<-?||?→||<-RelE-ParE	LRR-repeats+AP-GTPase+COR+DUF4404	1134	-	Cyanobacteria	Calothrix sp. NIES-2100	leucine-rich repeat domain-containing protein [Calothrix sp. NIES-2100].	GCF_002368195.1
WP_096598883.1	SIG+TM→?→ tRNA→||<-?||LRR-repeats+AP-GTPase+COR+CASPASE*→||<-PSE<-?||?→?→||<-?<-?<-Acylphosphatase	LRR-repeats+AP-GTPase+COR+CASPASE	1108	-	Cyanobacteria	Calothrix sp. NIES-2100	leucine-rich repeat domain-containing protein [Calothrix sp. NIES-2100].	GCF_002368195.1
WP_096598950.1	LRR-repeats+AP-GTPase+COR+TM+TM*→||<-?||?→||<-REC	LRR-repeats+AP-GTPase+COR+TM+TM	929	-	Cyanobacteria	Calothrix sp. NIES-2100	leucine-rich repeat domain-containing protein [Calothrix sp. NIES-2100].	GCF_002368195.1
WP_096621624.1	LRR-repeats→ PSE→ LRR-repeats+AP-GTPase+COR+CASPASE*→	LRR-repeats+AP-GTPase+COR+CASPASE	981	-	Cyanobacteria	Microchaete diplosiphon	CHAT domain-containing protein [Microchaete diplosiphon].	GCF_002368275.1
WP_096658516.1	LRR-repeats+AP-GTPase+COR*→ PSE→?→||<-?||?→||<-?||?→||<-?<-Pentapeptide-repeats	LRR-repeats+AP-GTPase+COR	708	-	Cyanobacteria	Calothrix parasitica	leucine-rich repeat domain-containing protein [Calothrix parasitica].	GCF_002368095.1

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WP_096683758.1	<-TPR-repeats+CASPASE||?→||<-?<-PSE||?→||<-ParB<-ParA-Soj-PloopNTPase||PSE→ LRR-repeats+AP-GTPase+COR+EAD1*→ ParB→||<-NACHT	LRR-repeats+AP-GTPase+COR+EAD1	1112	-	Cyanobacteria	Calothrix sp. NIES-4105	leucine-rich repeat domain-containing protein [Calothrix sp. NIES-4105].	GCF_002368415.1
WP_096729037.1	<-TPR-repeats+CASPASE||?→||<-?<-PSE||?→||<-ParB<-ParA-Soj-PloopNTPase||PSE→ LRR-repeats→ LRR-repeats+AP-GTPase+COR+EAD1*→ ParB→||<-NACHT	LRR-repeats+AP-GTPase+COR+EAD1	885	-	Cyanobacteria	Calothrix sp. NIES-4071	leucine-rich repeat domain-containing protein [Calothrix sp. NIES-4071].	GCF_002368455.1
WP_096789603.1	<-S4<-?||?→?→?→?→?→ LRR-repeats+AP-GTPase+COR*→||<-tRNA<-rRNA<-rRNA<-tRNA<-tRNA<-rRNA<-FAD-NAD-dep-oxidoreductase	LRR-repeats+AP-GTPase+COR	972	-	Alphaproteobacteria	Phaeobacter piscinae	leucine-rich repeat domain-containing protein [Phaeobacter piscinae].	GCF_002407245.1
WP_096793541.1	<-Cluster2127_2clades||?→||<-?||?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	938	-	Gammaproteobacteria	Pseudoalteromonas sp. 1_2015MBL_MicDiv	GTP-binding protein [Pseudoalteromonas sp. 1_2015MBL_MicDiv].	GCF_002407505.1
WP_097126565.1	LRR-repeats+AP-GTPase+COR*→||<-?||?→||<-?||?→||<-?||?→||<-HISKIN	LRR-repeats+AP-GTPase+COR	1103	-	Bacteroidetes	Spirosoma fluviale	leucine-rich repeat domain-containing protein [Spirosoma fluviale].	GCF_900230225.1
WP_097298537.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	802	-	Euryarchaeota	Candidatus Methanoperedens sp. BLZ2	leucine-rich repeat domain-containing protein [Candidatus Methanoperedens sp. BLZ2].	GCF_002487355.1
WP_097998439.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	906	-	Firmicutes	Bacillus cereus	GTP-binding protein [Bacillus cereus].	GCF_002575505.1
WP_098908392.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	934	-	Firmicutes	Bacillus toyonensis	GTP-binding protein [Bacillus toyonensis].	GCF_002551725.1
WP_099009377.1	LRR-repeats+AP-GTPase+COR+EAD11*→	LRR-repeats+AP-GTPase+COR+EAD11	813	-	Bacteroidetes	Lewinellaceae bacterium SD302	leucine-rich repeat domain-containing protein [Lewinellaceae bacterium SD302].	-
WP_099066006.1	LRR-repeats+AP-GTPase+COR+TIR*→||<-PSE<-Arginase||?→||<-?||?→?→?→ Pro_CA→	LRR-repeats+AP-GTPase+COR+TIR	1138	-	Cyanobacteria	Nostoc linckia	leucine-rich repeat domain-containing protein [Nostoc linckia].	GCF_002607965.1
WP_099069019.1	<-Pkinase+Pentapeptide<-?<-?||?→||<-?||LRR-repeats+AP-GTPase+COR+TIR*→?→||<-SIG+TM+TM+TM+TM+TM+TM<-?||?→ Cluster1668_2clades→	LRR-repeats+AP-GTPase+COR+TIR	1053	-	Cyanobacteria	Nostoc linckia	TIR domain-containing protein [Nostoc linckia].	GCF_002607965.1
WP_099076744.1	LRR-repeats+AP-GTPase+COR+TIR*→||<-PSE<-Arginase	LRR-repeats+AP-GTPase+COR+TIR	1138	-	Cyanobacteria	Nostoc linckia	leucine-rich repeat domain-containing protein [Nostoc linckia].	GCF_002608325.1
WP_099103609.1	LRR-repeats+AP-GTPase+COR+TM+TM*→	LRR-repeats+AP-GTPase+COR+TM+TM	825	-	Cyanobacteria	Nostoc sp. ‘Peltigera malacea cyanobiont’ DB3992	leucine-rich repeat domain-containing protein, partial [Nostoc sp. ‘Peltigera malacea cyanobiont’ DB3992].	-
WP_099151645.1	SIG+TM+TM+TM+HISKIN→?→ tRNA→?→?→ LRR-repeats+AP-GTPase+COR+EAD11*→	LRR-repeats+AP-GTPase+COR+EAD11	881	-	Bacteroidetes	Flavilitoribacter nigricans	leucine-rich repeat domain-containing protein [Flavilitoribacter nigricans].	GCF_002646595.1
WP_099285181.1	LRR-repeats+AP-GTPase+COR*→?→||<-?<-SIGMA-HTH	LRR-repeats+AP-GTPase+COR	1056	-	Actinobacteria	unclassified Streptomyces	MULTISPECIES: GTPase [unclassified Streptomyces].	GCF_002705975.1
WP_099426012.1	TPR-repeats→?→?→ tRNA→?→ HNH→ LRR-repeats+AP-GTPase+COR+DUF4404*→?→?→?→ REC→	LRR-repeats+AP-GTPase+COR+DUF4404	1272	-	Cyanobacteria	Tychonema bourrellyi	leucine-rich repeat domain-containing protein [Tychonema bourrellyi].	GCF_002412335.2
WP_099426065.1	GTPase-AIG→?→?→ Cluster53_2clades→?→ LRR-repeats+AP-GTPase+COR+DUF4404*→	LRR-repeats+AP-GTPase+COR+DUF4404	959	-	Cyanobacteria	Tychonema bourrellyi	leucine-rich repeat domain-containing protein [Tychonema bourrellyi].	GCF_002412335.2
WP_099506658.1	ABC_membrane+ABC_tran→||<-?||?→||<-?||PSE→||<-PSE||LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	799	-	Actinobacteria	Streptomyces dengpaensis	hypothetical protein [Streptomyces dengpaensis].	GCF_002946835.1

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
WP_099533140.1	AP-GTPase+COR→?→ LRR-repeats+AP-GTPase+COR*→||<-?||?→||<-tRNA||?→?→ Cluster1088_2clades→||<-?<-tRNA<-BACTERIALFRINGE+TM+TM	LRR-repeats+AP-GTPase+COR	826	-	Cyanobacteria	Limnothrix sp. PR1529	leucine-rich repeat domain-containing protein [Limnothrix sp. PR1529].	GCF_002742025.1
WP_100899585.1	LRR-repeats+AP-GTPase+COR+EAD1*→||<-CASPASE+TM	LRR-repeats+AP-GTPase+COR+EAD1	945	-	Cyanobacteria	Nostoc flagelliforme	leucine-rich repeat domain-containing protein [Nostoc flagelliforme].	GCF_002813575.1
WP_100900079.1	LRR-repeats+AP-GTPase+COR*→ COR→?→||<-?||?→||<-?||?→ ClpABN-AAA+ClpABC-AAA→	LRR-repeats+AP-GTPase+COR	431	-	Cyanobacteria	Nostoc flagelliforme	leucine-rich repeat domain-containing protein [Nostoc flagelliforme].	GCF_002813575.1
WP_100917604.1	<-METHYLASE<-?||?→||<-?||Cluster2515_2clades→ Cluster2268_2clades→ LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	983	-	Gammaproteobacteria	Candidatus Thiodictyon syntrophicum	TIR domain-containing protein [Candidatus Thiodictyon syntrophicum].	GCF_002813775.1
WP_100918672.1	<-Cluster944_3clades<-SIG+PDZ||?→?→||<-ABC-ATPase<-?<-?||LRR-repeats+AP-GTPase+COR+TIR*→||<-ABC-ATPase<-SIG+TM+TM+TM+TM+TM+TM+TM<-?<-SIG+PBPI	LRR-repeats+AP-GTPase+COR+TIR	1095	-	Gammaproteobacteria	Candidatus Thiodictyon syntrophicum	leucine-rich repeat domain-containing protein [Candidatus Thiodictyon syntrophicum].	GCF_002813775.1
WP_101084187.1	<-Cluster1951_2clades||?→ LRR-repeats+AP-GTPase+COR*→?→?→?→?→ Cluster846_3clades→	LRR-repeats+AP-GTPase+COR	1013	-	Gammaproteobacteria	Psychromonas sp. Urea-02u-13	GTP-binding protein [Psychromonas sp. Urea-02u-13].	GCF_002835995.1
WP_101221578.1	SIG+TM+TM+TM+TM+TM+TM+TM→||<-?||?→?→?→ PSE→||<-?<-?||PSE→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	897	-	Firmicutes	Bacillus sp. BA3	GTP-binding protein [Bacillus sp. BA3].	GCF_002835675.1
WP_101309496.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	888	-	Bacteroidetes	Labilibaculum manganireducens	hypothetical protein [Labilibaculum manganireducens].	GCF_002843385.1
WP_101439075.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1694	-	Actinobacteria	Amycolatopsis	MULTISPECIES: leucine-rich repeat domain-containing protein [Amycolatopsis].	GCF_014174495.1
WP_101728686.1	MACRODOMAIN+LRR-repeats+AP-GTPase+COR+TIR*→	MACRODOMAIN+LRR-repeats+AP-GTPase+COR+TIR	1357	-	Bacteroidetes	Emticicia sp. TH156	leucine-rich repeat domain-containing protein [Emticicia sp. TH156].	GCF_002855535.1
WP_101955079.1	<-TM<-WCAK<-?||?→ LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1144	-	Bacteroidetes	Tenacibaculum finnmarkense	leucine-rich repeat domain-containing protein [Tenacibaculum finnmarkense].	GCF_900239185.1
WP_102406975.1	LRR-repeats+AP-GTPase+COR+DrHyd*→	LRR-repeats+AP-GTPase+COR+DrHyd	1169	-	Bacteroidetes	Parabacteroides bouchesdurhonensis	leucine-rich repeat domain-containing protein [Parabacteroides bouchesdurhonensis].	GCF_900186615.1
WP_102484140.1	CI→?→?→ LRR-repeats+AP-GTPase+COR*→?→?→||<-?<-?<-?<-ABC-ATPase	LRR-repeats+AP-GTPase+COR	1107	-	Gammaproteobacteria	Vibrio lentus	GTP-binding protein [Vibrio lentus].	GCF_002874115.1
WP_102498010.1	REC→?→?→?→||<-ABC_membrane+ABC_tran<-ABC_membrane+ABC_tran<-?||LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	960	-	Gammaproteobacteria	Vibrio splendidus	leucine-rich repeat domain-containing protein [Vibrio splendidus].	GCF_002876045.1
WP_102512513.1	CI→ LRR-repeats+AP-GTPase+COR*→?→?→||<-PSE<-?<-?<-?<-ABC-ATPase	LRR-repeats+AP-GTPase+COR	1108	-	Gammaproteobacteria	Vibrio splendidus	GTP-binding protein [Vibrio splendidus].	GCF_002876945.1
WP_102562621.1	CI→ LRR-repeats+AP-GTPase+COR*→||<-?<-?||?→||<-?<-RPN10	LRR-repeats+AP-GTPase+COR	1108	-	Gammaproteobacteria	Vibrio splendidus	50S ribosome-binding GTPase [Vibrio splendidus].	GCF_002878555.1
WP_102571188.1	CI→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1107	-	Gammaproteobacteria	Vibrio splendidus	50S ribosome-binding GTPase [Vibrio splendidus].	GCF_002875585.1
WP_102579518.1	CI→?→ LRR-repeats+AP-GTPase+COR*→?→?→||<-?<-?<-?<-ABC-ATPase	LRR-repeats+AP-GTPase+COR	1106	-	Gammaproteobacteria	Vibrio lentus	GTP-binding protein [Vibrio lentus].	GCF_002876365.1
WP_102756439.1	TM+TM+TM+TM+TM→?→ Cluster2372_2clades→||<-?||?→?→?→ LRR-repeats+AP-GTPase+COR+DrHyd*→	LRR-repeats+AP-GTPase+COR+DrHyd	1054	-	Bacteroidetes	Flavivirga eckloniae	leucine-rich repeat domain-containing protein [Flavivirga eckloniae].	GCF_002886045.1
WP_103111669.1	SIG+TM+TM+TM+TM+TM+TM+TM→||<-?||Mbetalac→ SAM-methylase→?→||<-?<-SIG+TPM_phosphatase+TM+TM+TM||LRR-repeats+AP-GTPase+COR+TM+TM*→||<-?<-?<-?<-Pro_CA||?→||<-?<-tRNA<-tRNA<-Ferredoxin-betagrasp	LRR-repeats+AP-GTPase+COR+TM+TM	851	-	Cyanobacteria	Microcystis aeruginosa	leucine-rich repeat domain-containing protein [Microcystis aeruginosa].	GCF_002897275.1

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
WP_103125147.1	HISKIN→||<-?||LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	889	-	Cyanobacteria	Nostoc cycadae	leucine-rich repeat domain-containing protein [Nostoc cycadae].	GCF_002897135.1
WP_103137712.1	LRR-repeats+AP-GTPase+COR+TIR*→ Cluster1064_2clades→?→||<-?<-?<-?||Arginase→	LRR-repeats+AP-GTPase+COR+TIR	1058	-	Cyanobacteria	Nostoc sp. CENA543	leucine-rich repeat domain-containing protein [Nostoc sp. CENA543].	GCF_002896875.1
WP_103666629.1	<-Cluster1740_2clades<-TM<-?<-?||NACHT→||<-?||LRR-repeats+AP-GTPase+COR+TM+TM*→||<-?||?→?→?→ SIG+TM+TM+TM+TM+TM→	LRR-repeats+AP-GTPase+COR+TM+TM	1164	-	Cyanobacteria	Pseudanabaena sp. BC1403	leucine-rich repeat domain-containing protein [Pseudanabaena sp. BC1403].	GCF_002914585.1
WP_103669449.1	Cluster54_3clades→?→?→?→ PIN→ LRR-repeats+AP-GTPase+COR+TM+TM*→||<-?<-?||ABC-ATPase→	LRR-repeats+AP-GTPase+COR+TM+TM	922	-	Cyanobacteria	Pseudanabaena sp. BC1403	leucine-rich repeat domain-containing protein [Pseudanabaena sp. BC1403].	GCF_002914585.1
WP_103972898.1	LRR-repeatsAP-GTPase+COR+E59-ABC*→	LRR-repeatsAP-GTPase+COR+E59-ABC	953	-	Gammaproteobacteria	Methylovulum psychrotolerans	AAA family ATPase [Methylovulum psychrotolerans].	GCF_002923755.1
WP_103972982.1	<-ABC-ATPase<-SIG+BLBD<-?||REC→ HISKIN→ REase→ LRR-repeats+AP-GTPase+COR*→?→?→?→ Ferredoxin-RRM→	LRR-repeats+AP-GTPase+COR	911	-	Gammaproteobacteria	Methylovulum psychrotolerans	hypothetical protein [Methylovulum psychrotolerans].	GCF_002923755.1
WP_103974058.1	<-PurT-ATPgrasp<-?<-?<-?||?→||<-?<-Cluster1542_2clades||LRR-repeats+AP-GTPase+COR+TIR*→ REase→||<-?<-?<-FKBP<-RHOD-CDC25<-Aminotran_1_2||Cluster2179_2clades→	LRR-repeats+AP-GTPase+COR+TIR	1203	-	Gammaproteobacteria	Methylovulum psychrotolerans	TIR domain-containing protein [Methylovulum psychrotolerans].	GCF_002923755.1
WP_103999297.1	LRR-repeats+AP-GTPase+COR*→?→||<-?<-?<-ABC-ATPase||Cluster995_2clades→	LRR-repeats+AP-GTPase+COR	925	-	Bacteroidetes	Flavobacterium urumqiense	leucine-rich repeat domain-containing protein [Flavobacterium urumqiense].	GCF_900108015.1
WP_104395581.1	SIG+TM+TM+TM+TM+TM+TM+TM→||<-?||Mbetalac→ SAM-methylase→?→||<-?<-SIG+TPM_phosphatase+TM+TM+TM||LRR-repeats+AP-GTPase+COR+TM+TM*→||<-?<-?<-?<-Pro_CA||?→||<-?<-tRNA<-tRNA<-Ferredoxin-betagrasp	LRR-repeats+AP-GTPase+COR+TM+TM	874	-	Cyanobacteria	Microcystis aeruginosa	leucine-rich repeat protein [Microcystis aeruginosa].	GCF_002933835.1
WP_104424498.1	Cluster1018_2clades→?→?→?→ PIN→?→ PIN→ LRR-repeats+AP-GTPase+COR+TIR*→||<-?||Cluster1018_2clades→	LRR-repeats+AP-GTPase+COR+TIR	999	-	Gammaproteobacteria	Methylobacter tundripaludum	TIR domain-containing protein [Methylobacter tundripaludum].	GCF_002934365.1
WP_104900247.1	Cluster1074_2clades→||<-?<-Cluster53_2clades||LRR-repeats+AP-GTPase+COR*→||<-?<-?||?→?→ SAM-methylase→	LRR-repeats+AP-GTPase+COR	1039	-	Cyanobacteria	Nostoc sp. ‘Peltigera membranacea cyanobiont’ N6	leucine-rich repeat domain-containing protein [Nostoc sp. ‘Peltigera membranacea cyanobiont’ N6].	GCF_002949735.1
WP_104904652.1	LRR-repeats+AP-GTPase+COR*→?→?→||<-ABhydrolase<-Cluster1087_2clades	LRR-repeats+AP-GTPase+COR	1097	-	Cyanobacteria	Nostoc sp. ‘Lobaria pulmonaria (5183) cyanobiont’	leucine-rich repeat domain-containing protein [Nostoc sp. ‘Lobaria pulmonaria (5183) cyanobiont’].	GCF_002949795.1
WP_104909847.1	LRR-repeats+AP-GTPase+COR+DUF4404*→	LRR-repeats+AP-GTPase+COR+DUF4404	1125	-	Cyanobacteria	Nostoc sp. ‘Lobaria pulmonaria (5183) cyanobiont’	leucine-rich repeat domain-containing protein [Nostoc sp. ‘Lobaria pulmonaria (5183) cyanobiont’].	-
WP_105041123.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	925	-	Bacteroidetes	Flavipsychrobacter stenotrophus	leucine-rich repeat domain-containing protein [Flavipsychrobacter stenotrophus].	GCF_002954265.1
WP_106089276.1	LRR-repeats+AP-GTPase+COR+PNPase*→	LRR-repeats+AP-GTPase+COR+PNPase	915	-	Deltaproteobacteria	Enhygromyxa salina	50S ribosome-binding GTPase [Enhygromyxa salina].	GCF_002994635.1
WP_106150696.1	LRR-repeats+AP-GTPase+COR+DUF4404*→	LRR-repeats+AP-GTPase+COR+DUF4404	779	-	Cyanobacteria	filamentous cyanobacterium Phorm 46	leucine-rich repeat domain-containing protein, partial [filamentous cyanobacterium Phorm 46].	-
WP_106254335.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	930	-	Cyanobacteria	Stenomitos frigidus	leucine-rich repeat domain-containing protein [Stenomitos frigidus].	GCF_003003795.1
WP_106256414.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	961	-	Cyanobacteria	Stenomitos frigidus	GTPase [Stenomitos frigidus].	GCF_003003795.1

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WP_106289057.1	LRR-repeats+AP-GTPase+COR+DUF4404*→	LRR-repeats+AP-GTPase+COR+DUF4404	918	-	Cyanobacteria	Merismopedia glauca	leucine-rich repeat domain-containing protein [Merismopedia glauca].	GCF_003003775.1
WP_106331563.1	TPR-repeats→?→?→?→ tRNA→||<-PSE<-?||Cluster53_2clades→?→ LRR-repeats+AP-GTPase+COR+DUF4404*→	LRR-repeats+AP-GTPase+COR+DUF4404	1048	-	Cyanobacteria	filamentous cyanobacterium Phorm 6	leucine-rich repeat domain-containing protein [filamentous cyanobacterium Phorm 6].	-
WP_106333130.1	LRR-repeats+AP-GTPase+COR+DUF4404*→?→?→||<-?<-?<-?<-?<-RelE-ParE	LRR-repeats+AP-GTPase+COR+DUF4404	786	-	Cyanobacteria	filamentous cyanobacterium Phorm 6	leucine-rich repeat domain-containing protein, partial [filamentous cyanobacterium Phorm 6].	-
WP_106364139.1	<-ABC-ATPase||?→?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1146	-	Actinobacteria	Glycomyces artemisiae	hypothetical protein [Glycomyces artemisiae].	GCF_003002955.1
WP_106623442.1	LRR-repeats+AP-GTPase+COR+TM+TM*→||<-ABC-ATPase	LRR-repeats+AP-GTPase+COR+TM+TM	970	-	Bacteroidetes	Sphingobacteriales bacterium UPWRP_1	leucine-rich repeat domain-containing protein [Sphingobacteriales bacterium UPWRP_1].	-
WP_106872506.1	RelE-ParE→ LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1126	-	Cyanobacteria	unclassified Cyanobacteria	MULTISPECIES: leucine-rich repeat domain-containing protein [unclassified Cyanobacteria].	-
WP_106922429.1	LRR-repeats+AP-GTPase+COR+TIR*→||<-REase-4	LRR-repeats+AP-GTPase+COR+TIR	826	-	Cyanobacteria	filamentous cyanobacterium CCP3	leucine-rich repeat domain-containing protein [filamentous cyanobacterium CCP3].	-
WP_107346265.1	Arginase→?→||<-?||?→ LRR-repeats+AP-GTPase+COR+TIR*→||<-?<-?<-?<-ABC-ATPase||?→ REC→	LRR-repeats+AP-GTPase+COR+TIR	1173	-	Alphaproteobacteria	Rhodopseudomonas palustris	leucine-rich repeat domain-containing protein [Rhodopseudomonas palustris].	GCF_003031265.1
WP_107357189.1	Arginase→?→||<-?||?→ LRR-repeats+AP-GTPase+COR+TIR*→||<-?<-?<-?<-ABC-ATPase||?→ REC→	LRR-repeats+AP-GTPase+COR+TIR	1173	-	Alphaproteobacteria	Rhodopseudomonas palustris	leucine-rich repeat domain-containing protein [Rhodopseudomonas palustris].	GCF_003031245.1
WP_107867044.1	LRR-repeats+AP-GTPase+COR+GT4*→	LRR-repeats+AP-GTPase+COR+GT4	1510	-	Firmicutes	Agitococcus lubricus	leucine-rich repeat protein [Agitococcus lubricus].	GCF_003051055.1
WP_108091428.1	ABC_membrane+ABC_tran→||<-?||CI→ LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1243	-	Gammaproteobacteria	Vibrio splendidus	TIR domain-containing protein [Vibrio splendidus].	GCF_003050005.1
WP_108099554.1	<-Cluster1756_2clades<-?<-?<-?<-?||?→?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1107	-	Gammaproteobacteria	Vibrio splendidus	50S ribosome-binding GTPase [Vibrio splendidus].	GCF_003050165.1
WP_108112883.1	<-HISKIN<-?||LRR-repeats+AP-GTPase+COR+TIR*→||<-HISKIN<-HISKIN	LRR-repeats+AP-GTPase+COR+TIR	973	-	Bacteroidetes	Kordia periserrulae	leucine-rich repeat domain-containing protein [Kordia periserrulae].	GCF_003054265.1
WP_108114870.1	CHTH→||<-?<-?||RNA-Helicase→?→?→||<-?||LRR-repeats+AP-GTPase+COR+TIR*→||<-?<-?<-?||?→||<-TM+TM+TM	LRR-repeats+AP-GTPase+COR+TIR	1012	-	Bacteroidetes	Kordia periserrulae	leucine-rich repeat domain-containing protein [Kordia periserrulae].	GCF_003054265.1
WP_108176265.1	LRR-repeats+AP-GTPase+COR*→?→ ABC_membrane+ABC_tran→ ABC_membrane+ABC_tran→	LRR-repeats+AP-GTPase+COR	1122	-	Gammaproteobacteria	Vibrio splendidus	hypothetical protein [Vibrio splendidus].	GCF_003050125.1
WP_108207948.1	REC→?→?→?→||<-ABC_membrane+ABC_tran<-ABC_membrane+ABC_tran<-?||LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	960	-	Gammaproteobacteria	Vibrio splendidus	leucine-rich repeat domain-containing protein [Vibrio splendidus].	GCF_003050345.1
WP_108801834.1	<-REC<-?||LRR-repeats+AP-GTPase+COR+TM+TM*→?→?→?→?→||<-?<-SIG+TM+TM+TM+HISKIN	LRR-repeats+AP-GTPase+COR+TM+TM	1086	-	Bacteroidetes	Aquimarina sp. Aq107	leucine-rich repeat domain-containing protein [Aquimarina sp. Aq107].	GCF_900299505.1
WP_109009086.1	ABhydrolase→?→||<-PSE||LRR-repeats+AP-GTPase+COR+TIR*→||<-?<-?<-?<-?<-SIG+NUDIX	LRR-repeats+AP-GTPase+COR+TIR	1078	-	Cyanobacteria	Nostoc commune	leucine-rich repeat domain-containing protein [Nostoc commune].	GCF_003113895.1

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WP_109322545.1	LRR-repeats+AP-GTPase+COR*→?→?→?→ Cluster978_2clades→	LRR-repeats+AP-GTPase+COR	841	-	Bacteroidetes	Allopseudarcicella aquatilis	hypothetical protein [Allopseudarcicella aquatilis].	GCF_003143535.1
WP_109617479.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1124	-	Bacteroidetes	Chryseobacterium oncorhynchi	leucine-rich repeat domain-containing protein [Chryseobacterium oncorhynchi].	GCF_002899895.1
WP_109694822.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1143	-	Bacteroidetes	Chitinophaga deserti	TIR domain-containing protein [Chitinophaga deserti].	-
WP_110392243.1	ABC-ATPase→?→ LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1128	-	Betaproteobacteria	Rivicola pingtungensis	leucine-rich repeat domain-containing protein [Rivicola pingtungensis].	GCF_003201855.1
WP_110578614.1	SIG+TM+TM+TM+TM+TM+TM+TM→||<-PSE||Mbetalac→ SAM-methylase→?→||<-?<-SIG+TPM_phosphatase+TM+TM+TM||LRR-repeats+AP-GTPase+COR+TM+TM*→||<-?<-?<-?<-Pro_CA||?→||<-?<-tRNA<-tRNA<-Ferredoxin-betagrasp	LRR-repeats+AP-GTPase+COR+TM+TM	865	-	Cyanobacteria	Microcystis aeruginosa	leucine-rich repeat domain-containing protein [Microcystis aeruginosa].	GCF_003206555.1
WP_110984619.1	<-Cluster1569_2clades||Mbetalac→||<-?<-?||?→ Mbetalac→||<-?||LRR-repeats+AP-GTPase+COR*→?→ PIN→||<-Cluster1559_2clades	LRR-repeats+AP-GTPase+COR	995	-	Cyanobacteria	Acaryochloris sp. RCC1774	leucine-rich repeat domain-containing protein [Acaryochloris sp. RCC1774].	-
WP_111129223.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	894	-	Bacteroidetes	Mesonia sp. K7	50S ribosome-binding GTPase [Mesonia sp. K7].	GCF_003233725.1
WP_111283162.1	LRR-repeats+AP-GTPase+COR*→||<-?||?→?→||<-?||?→?→||<-cNMPBD	LRR-repeats+AP-GTPase+COR	1144	-	Bacteroidetes	Flavobacterium ginsenosidimutans	leucine-rich repeat domain-containing protein [Flavobacterium ginsenosidimutans].	GCF_003254625.1
WP_111625904.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	846	-	Bacteroidetes	Gelidibacter algens	hypothetical protein [Gelidibacter algens].	GCF_003259265.1
WP_111845807.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	812	-	Bacteroidetes	Aequorivita antarctica	hypothetical protein, partial [Aequorivita antarctica].	-
WP_112086237.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	847	-	Bacteroidetes	Flavobacterium lacus	hypothetical protein [Flavobacterium lacus].	GCF_003268815.1
WP_112134132.1	LRR-repeats+AP-GTPase+COR*→?→||<-?<-?<-?<-REC<-HISKIN	LRR-repeats+AP-GTPase+COR	1186	-	Actinobacteria	Glycomyces dulcitolivorans	leucine-rich repeat domain-containing protein [Glycomyces dulcitolivorans].	GCF_003265355.1
WP_112263949.1	wHTH-4stranded+TPRs+APATPase+TPR-repeats→?→?→?→ ABC_membrane+ABC_tran→?→?→ LRR-repeats+AP-GTPase+COR*→ COR→	LRR-repeats+AP-GTPase+COR	608	-	Actinobacteria	Lentzea terrae	leucine-rich repeat domain-containing protein [Lentzea terrae].	GCF_003265345.1
WP_114082655.1	Cluster5_5clades→ LRR-repeats+AP-GTPase+COR+TM+TM*→||<-CASPASE+TM	LRR-repeats+AP-GTPase+COR+TM+TM	904	-	Cyanobacteria	Nostoc sp. ATCC 53789	leucine-rich repeat domain-containing protein [Nostoc sp. ATCC 53789].	GCF_003326245.1
WP_114084090.1	Pentapeptide-repeats→||<-?<-?||?→?→||<-Arginase<-?||LRR-repeats+AP-GTPase+COR+TIR*→?→||<-?||?→?→?→?→ APATPase+TPR+TPR+TPR→	LRR-repeats+AP-GTPase+COR+TIR	802	-	Cyanobacteria	Nostoc sp. ATCC 53789	leucine-rich repeat domain-containing protein [Nostoc sp. ATCC 53789].	GCF_003326245.1
WP_114085324.1	ABhydrolase→?→||<-?||LRR-repeats+AP-GTPase+COR+TIR*→||<-?<-?<-?<-SIG+NUDIX	LRR-repeats+AP-GTPase+COR+TIR	1069	-	Cyanobacteria	Nostoc sp. ATCC 53789	leucine-rich repeat domain-containing protein [Nostoc sp. ATCC 53789].	GCF_003326245.1
WP_114085448.1	LRR-repeats+AP-GTPase+COR+CASPASE*→?→?→?→ ParA-Soj-PloopNTPase→	LRR-repeats+AP-GTPase+COR+CASPASE	1512	-	Cyanobacteria	Nostoc sp. ATCC 53789	leucine-rich repeat domain-containing protein [Nostoc sp. ATCC 53789].	GCF_003326245.1
WP_114085638.1	<-ParA-Soj-PloopNTPase||LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	881	-	Cyanobacteria	Nostoc sp. ATCC 53789	hypothetical protein [Nostoc sp. ATCC 53789].	GCF_009873495.1
WP_114460382.1	Cluster1398_2clades→?→ LRR-repeats+AP-GTPase*→	LRR-repeats+AP-GTPase	477	-	Bacteroidetes	Runella sp. YX9	leucine-rich repeat domain-containing protein [Runella sp. YX9].	GCF_003339505.1
WP_114694555.1	SIGMA-HTH→?→||<-?||?→?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	865	-	Gammaproteobacteria	Motiliproteus coralliicola	GTP-binding protein [Motiliproteus coralliicola].	GCF_003345655.1

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<tr><td>WP_116857281.1</td><td>LRR-repeats+AP-GTPase+COR+TIR*→</td><td>LRR-repeats+AP-GTPase+COR+TIR</td><td>1379</td><td>-</td><td>Bacteroidetes</td><td>Chitinophaga silvisoli</td><td>leucine-rich repeat domain-containing protein [Chitinophaga silvisoli].</td><td>GCF_003412465.1</td></tr>
<tr><td>WP_116982533.1</td><td>PNPase→?→?→?→?→?→ LRR-repeats+AP-GTPase+COR+TIR*→</td><td>LRR-repeats+AP-GTPase+COR+TIR</td><td>956</td><td>-</td><td>Bacteroidetes</td><td>Emticicia sp. C21</td><td>leucine-rich repeat domain-containing protein [Emticicia sp. C21].</td><td>GCF_003418935.1</td></tr>
<tr><td>WP_117208282.1</td><td><-Aminotran_1_2<-?||?→||<-?||?→?→ LRR-repeats+AP-GTPase+COR*→||<-?<-?<-?<-?<-Cluster2179_2clades<-SIG+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM</td><td>LRR-repeats+AP-GTPase+COR</td><td>905</td><td>-</td><td>Actinobacteria</td><td>Allorhizocola rhizosphaerae</td><td>hypothetical protein [Allorhizocola rhizosphaerae].</td><td>GCF_003426775.1</td></tr>
<tr><td>WP_117882884.1</td><td>REC→||<-?<-?<-?<-?||MORC→?→ LRR-repeats+AP-GTPase+COR*→?→ Cluster1438_2clades→</td><td>LRR-repeats+AP-GTPase+COR</td><td>797</td><td>-</td><td>Bacteroidetes</td><td>Lutibacter sp. SM1352</td><td>GTP-binding protein [Lutibacter sp. SM1352].</td><td>GCF_003449015.1</td></tr>
<tr><td>WP_118170224.1</td><td>Cluster5_5clades→ Cluster5_5clades→||<-?||LRR-repeats+AP-GTPase+COR+TM+TM*→||<-CASPASE+TM||?→||<-?<-?||?→||<-?||Cluster1756_2clades→</td><td>LRR-repeats+AP-GTPase+COR+TM+TM</td><td>962</td><td>-</td><td>Cyanobacteria</td><td>Nostoc sphaeroides</td><td>leucine-rich repeat domain-containing protein [Nostoc sphaeroides].</td><td>GCF_003443655.1</td></tr>
<tr><td>WP_118317581.1</td><td>LRR-repeats+AP-GTPase+COR+DrHyd*→</td><td>LRR-repeats+AP-GTPase+COR+DrHyd</td><td>1169</td><td>-</td><td>Bacteroidetes</td><td>Bacteroidales</td><td>MULTISPECIES: leucine-rich repeat domain-containing protein [Bacteroidales].</td><td>GCF_902364465.1</td></tr>
<tr><td>WP_118840037.1</td><td>ABC_membrane+ABC_tran→||<-Cluster2290_2clades<-Cluster2428_2clades<-?<-DSBH<-?||ClpABN-AAA+ClpABC-AAA→ LRR-repeats+AP-GTPase+COR*→||<-?<-HISKIN<-REC</td><td>LRR-repeats+AP-GTPase+COR</td><td>1051</td><td>-</td><td>Bacteroidetes</td><td>Salinibacter ruber</td><td>leucine-rich repeat domain-containing protein [Salinibacter ruber].</td><td>GCF_003491185.1</td></tr>
<tr><td>WP_119405939.1</td><td>SIG+TM+TM+TM+HISKIN→?→?→||<-?<-PSE||?→?→ TIR+LRR-repeats+AP-GTPase+TIR*→</td><td>TIR+LRR-repeats+AP-GTPase+TIR</td><td>1046</td><td>-</td><td>Bacteroidetes</td><td>Mucilaginibacter sp. HYN0043</td><td>TIR domain-containing protein [Mucilaginibacter sp. HYN0043].</td><td>GCF_003576455.2</td></tr>
<tr><td>WP_119406030.1</td><td>LRR-repeats+AP-GTPase+COR+TIR*→</td><td>LRR-repeats+AP-GTPase+COR+TIR</td><td>885</td><td>-</td><td>Bacteroidetes</td><td>Mucilaginibacter sp. HYN0043</td><td>TIR domain-containing protein [Mucilaginibacter sp. HYN0043].</td><td>GCF_003576455.2</td></tr>
<tr><td>WP_119756574.1</td><td>LRR-repeats+AP-GTPase+COR*→</td><td>LRR-repeats+AP-GTPase+COR</td><td>792</td><td>-</td><td>Bacteroidetes</td><td>Chryseolinea soli</td><td>GTP-binding protein [Chryseolinea soli].</td><td>GCF_003589925.1</td></tr>
<tr><td>WP_120086745.1</td><td>Cluster2248_2clades→?→?→ LRR-repeats+AP-GTPase+COR*→</td><td>LRR-repeats+AP-GTPase+COR</td><td>952</td><td>-</td><td>Actinobacteria</td><td>Pseudonocardiaceae bacterium YIM PH 21723</td><td>leucine-rich repeat domain-containing protein [Pseudonocardiaceae bacterium YIM PH 21723].</td><td>-</td></tr>
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acc	operon	architecture	len	gen.name	taxend	species	defline	gca
WP_120519107.1	<-SIG+TM+TM+TM<-?||Cluster1612_2clades→?→||<-?||?→?→ LRR-repeats+AP-GTPase+COR+REase7*→?→?→||<-?||ABC_membrane+ABC_tran→	LRR-repeats+AP-GTPase+COR+REase7	971	-	Bacteroidetes	Chitinophaga barathri	leucine-rich repeat domain-containing protein [Chitinophaga barathri].	GCF_003614855.1
WP_121068083.1	LRR-repeats+AP-GTPase+COR*→||<-?<-MoxR-AAA	LRR-repeats+AP-GTPase+COR	1055	-	Bacteroidetes	Maribacter vaceletii	50S ribosome-binding GTPase [Maribacter vaceletii].	GCF_003634105.1
WP_121165351.1	SIGMA-HTH→?→?→?→?→?→ LRR-repeats+AP-GTPase+COR+GT4*→?→ ParA-Soj-PloopNTPase→||<-?<-?<-?<-?||Cluster1906_2clades→	LRR-repeats+AP-GTPase+COR+GT4	1488	-	Betaproteobacteria	Nitrosomonas sp. Nm120	leucine-rich repeat domain-containing protein [Nitrosomonas sp. Nm120].	GCF_003664085.1
WP_121968578.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	985	-	Cyanobacteria	Leptolyngbya sp. BC1307	GTPase [Leptolyngbya sp. BC1307].	GCF_002286735.1
WP_122929305.1	Cluster1633_2clades→ Cluster1019_2clades→?→?→ Cluster1131_3clades→ FGS→ LRR-repeats+AP-GTPase+COR+TIR*→ TM+TM+TM→?→?→?→?→ tRNA→?→||<-Cluster1496_2clades	LRR-repeats+AP-GTPase+COR+TIR	943	-	Bacteroidetes	Runella sp. SP2	TIR domain-containing protein [Runella sp. SP2].	GCF_003711225.1
WP_123129115.1	TIR→ LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	802	-	Bacteroidetes	Rufibacter latericius	TIR domain-containing protein [Rufibacter latericius].	GCF_003721515.1
WP_123230450.1	SIG+TM+TM+TM+TM+TM+TM+TM→||<-?||Mbetalac→ SAM-methylase→?→||<-?<-SIG+TPM_phosphatase+TM+TM+TM||LRR-repeats+AP-GTPase+COR+TM+TM*→||<-?<-?<-?<-Pro_CA||?→||<-?<-tRNA<-tRNA<-Ferredoxin-betagrasp	LRR-repeats+AP-GTPase+COR+TM+TM	875	-	Cyanobacteria	Microcystis aeruginosa	leucine-rich repeat domain-containing protein [Microcystis aeruginosa].	GCF_003730145.1
WP_123277931.1	LRR-repeats+AP-GTPase+COR*→?→||<-?<-?<-RFC-AAA	LRR-repeats+AP-GTPase+COR	891	-	Bacteroidetes	Chryseobacterium cucumeris	hypothetical protein [Chryseobacterium cucumeris].	GCF_003729985.1
WP_123852487.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1174	-	Bacteroidetes	Chryseobacterium shandongense	leucine-rich repeat domain-containing protein [Chryseobacterium shandongense].	GCF_003815615.1
WP_123904443.1	LRR-repeats+AP-GTPase+COR+TIR*→ TIR→	LRR-repeats+AP-GTPase+COR+TIR	986	-	Bacteroidetes	Chryseobacterium haifense	leucine-rich repeat domain-containing protein [Chryseobacterium haifense].	GCF_003816015.1
WP_124155292.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	723	-	Cyanobacteria	Okeania hirsuta	leucine-rich repeat domain-containing protein [Okeania hirsuta].	GCF_003838195.1
WP_124898852.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	925	-	Bacteroidetes	Flavobacterium viscosus	GTP-binding protein [Flavobacterium viscosus].	GCF_003858535.1
WP_125246445.1	TM→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1040	-	Actinobacteria	Glycomyces terrestris	hypothetical protein [Glycomyces terrestris].	GCF_003933745.1
WP_125249833.1	<-Cluster1244_2clades||?→?→?→||<-?<-ABC-ATPase||?→ LRR-repeats+AP-GTPase+COR*→?→||<-?<-REC<-HISKIN	LRR-repeats+AP-GTPase+COR	1253	-	Actinobacteria	Glycomyces terrestris	leucine-rich repeat domain-containing protein [Glycomyces terrestris].	GCF_003933745.1
WP_126388556.1	Cluster54_3clades→?→ RelE-ParE→ LRR-repeats+AP-GTPase+COR*→?→?→ Cluster1841_2clades→	LRR-repeats+AP-GTPase+COR	906	-	Cyanobacteria	Pseudanabaena sp. ABRG5-3	leucine-rich repeat domain-containing protein [Pseudanabaena sp. ABRG5-3].	GCF_003967015.1
WP_126389050.1	LRR-repeats→?→?→ LRR-repeats+AP-GTPase+COR+CASPASE*→||<-?||TPR+nSTAND1+BetaPropeller_WD40+BetaPropeller_WD40→?→||<-?||Pentapeptide-repeats→	LRR-repeats+AP-GTPase+COR+CASPASE	1062	-	Cyanobacteria	Pseudanabaena sp. ABRG5-3	leucine-rich repeat domain-containing protein [Pseudanabaena sp. ABRG5-3].	GCF_003967015.1
WP_126391374.1	Pentapeptide-repeats→||<-Cluster5_5clades||Cluster1009_2clades→ Cluster53_2clades→?→ LRR-repeats+AP-GTPase+COR+TM+TM*→||<-?<-?<-?<-?<-?||REC→	LRR-repeats+AP-GTPase+COR+TM+TM	865	-	Cyanobacteria	Pseudanabaena sp. ABRG5-3	GTPase [Pseudanabaena sp. ABRG5-3].	GCF_003967015.1
WP_126618238.1	<-RADICAL-SAM<-?||SIGMA-HTH→?→||<-?||?→?→ LRR-repeats+AP-GTPase+COR+TIR*→?→||<-?||SWACOS→||<-Cluster409_3clades||SIG+RnaseT2→?→ Cluster995_2clades→	LRR-repeats+AP-GTPase+COR+TIR	913	-	Alphaproteobacteria	Azospirillum sp. L-25-5w-1	leucine-rich repeat domain-containing protein [Azospirillum sp. L-25-5w-1].	GCF_003966125.1
WP_127052641.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1083	-	Cyanobacteria	Trichormus variabilis	leucine-rich repeat domain-containing protein [Trichormus variabilis].	GCF_003991935.1
WP_127087241.1	LRR-repeats+AP-GTPase+COR+EAD1*→	LRR-repeats+AP-GTPase+COR+EAD1	929	-	Cyanobacteria	Calothrix desertica	GTPase [Calothrix desertica].	GCF_003991905.1
WP_127498999.1	LRR-repeats+AP-GTPase+COR+TIR*→?→?→||<-?<-?||?→||<-Cluster1023_3clades	LRR-repeats+AP-GTPase+COR+TIR	999	-	Actinobacteria	Actinoplanes sp. LAM7112	TIR domain-containing protein [Actinoplanes sp. LAM7112].	GCF_003999975.1

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WP_127504182.1	LRR-repeats+AP-GTPase+COR*→?→ PSE→||<-?||SIGMA-HTH→	LRR-repeats+AP-GTPase+COR	1080	-	Actinobacteria	Actinoplanes sp. LAM7112	hypothetical protein [Actinoplanes sp. LAM7112].	GCF_003999975.1
WP_127505072.1	Cluster1009_2clades→||<-Cluster1999_2clades<-Cluster2165_2clades<-?<-?<-?||?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1680	-	Actinobacteria	Actinoplanes sp. LAM7112	leucine-rich repeat domain-containing protein [Actinoplanes sp. LAM7112].	GCF_003999975.1
WP_129758774.1	MACRODOMAIN+LRR-repeats+AP-GTPase+COR+TIR*→||<-tRNA<-?<-RNASEII	MACRODOMAIN+LRR-repeats+AP-GTPase+COR+TIR	1357	-	Bacteroidetes	Flavobacterium sp. TCH3-2	leucine-rich repeat domain-containing protein [Flavobacterium sp. TCH3-2].	GCF_004151275.1
WP_129778498.1	Cluster1906_2clades→?→||<-?<-?<-?||?→ LRR-repeats+AP-GTPase+COR*→||<-?<-?||?→?→?→||<-tRNA||SIGMA-HTH→	LRR-repeats+AP-GTPase+COR	1040	-	Gammaproteobacteria	Steroidobacter soli	hypothetical protein [Steroidobacter soli].	GCF_004138485.1
WP_130757642.1	SIG+TM+TM+TM+TM+TM+TM+TM→||<-?||Mbetalac→ SAM-methylase→?→||<-?<-SIG+TPM_phosphatase+TM+TM+TM||LRR-repeats+AP-GTPase+COR+TM+TM*→||<-?<-?<-?<-Pro_CA||?→||<-?<-tRNA<-tRNA<-Ferredoxin-betagrasp	LRR-repeats+AP-GTPase+COR+TM+TM	851	-	Cyanobacteria	Microcystis aeruginosa	leucine-rich repeat domain-containing protein [Microcystis aeruginosa].	GCF_004305995.1
WP_130938329.1	AraC-HTH→?→ SIG+TM+TM+TM→?→?→?→?→ LRR-repeats+AP-GTPase+COR*→?→ ABC_membrane+ABC_tran→||<-?<-?<-?<-?<-Trichomonas-DAM	LRR-repeats+AP-GTPase+COR	925	-	Bacteroidetes	Hyunsoonleella pacifica	leucine-rich repeat domain-containing protein [Hyunsoonleella pacifica].	GCF_014636335.1
WP_131118878.1	HNH→?→||<-?<-PIN<-?||LRR-repeats+AP-GTPase+COR+TIR*→||<-Cluster1077_2clades	LRR-repeats+AP-GTPase+COR+TIR	912	-	Cyanobacteria	Westiellopsis prolifica	leucine-rich repeat domain-containing protein, partial [Westiellopsis prolifica].	GCF_004323185.1
WP_131118899.1	Cluster1069_2clades→?→?→||<-?||?→?→ PSE→ LRR-repeats→ LRR-repeats+AP-GTPase+COR+DUF4404*→||<-?||?→?→?→?→ Mbetalac→	LRR-repeats+AP-GTPase+COR+DUF4404	695	-	Cyanobacteria	Westiellopsis prolifica	GTP-binding protein, partial [Westiellopsis prolifica].	GCF_004323185.1
WP_132561933.1	<-Classical-AAA||?→ LRR-repeats+AP-GTPase+COR+TIR*→?→||<-?<-tRNA||?→||<-tRNA<-?||?→||<-?||ABC-ATPase→	LRR-repeats+AP-GTPase+COR+TIR	1348	-	Bacteroidetes	Niastella sp. CF465	TIR domain-containing protein [Niastella sp. CF465].	GCF_004341975.1
WP_132562618.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1028	-	Bacteroidetes	Niastella sp. CF465	GTP-binding protein [Niastella sp. CF465].	GCF_004341975.1
WP_132566699.1	SIGMA-HTH→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	890	-	Bacteroidetes	Niastella sp. CF465	leucine-rich repeat domain-containing protein [Niastella sp. CF465].	GCF_004341975.1
WP_132835660.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	819	-	Actinobacteria	Streptomyces sp. BK205	hypothetical protein [Streptomyces sp. BK205].	GCF_004341025.1
WP_133504241.1	Cluster2322_2clades→||<-?||PSE→||<-?||LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	764	-	Gammaproteobacteria	Marinomonas balearica	TIR domain-containing protein [Marinomonas balearica].	GCF_004362145.1
WP_133511071.1	Cluster2079_2clades→||<-?||?→||<-SIG+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM<-SIG+TM||PSE→ LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	986	-	Gammaproteobacteria	Candidatus Thiosymbion oneisti	TIR domain-containing protein [Candidatus Thiosymbion oneisti].	GCF_011392785.1
WP_133512972.1	<-PIN<-?||ABC-ATPase→?→?→?→?→ LRR-repeats+AP-GTPase+COR+DrHyd*→	LRR-repeats+AP-GTPase+COR+DrHyd	998	-	Gammaproteobacteria	Candidatus Thiosymbion oneisti	hypothetical protein [Candidatus Thiosymbion oneisti].	GCF_011392785.1
WP_133793944.1	LRR-repeats→ LRR-repeats+AP-GTPase+COR+DUF4404*→	LRR-repeats+AP-GTPase+COR+DUF4404	768	-	Verrucomicrobia	Prosthecobacter fusiformis	GTP-binding protein [Prosthecobacter fusiformis].	GCF_004364345.1
WP_133884327.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	996	-	Actinobacteria	unclassified Glycomyces	MULTISPECIES: leucine-rich repeat domain-containing protein [unclassified Glycomyces].	GCF_000719515.1
WP_133903373.1	Cluster2083_2clades→||<-?||?→||<-?||?→||<-?||LRR-repeats→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1284	-	Actinobacteria	Actinophytocola oryzae	leucine-rich repeat domain-containing protein [Actinophytocola oryzae].	GCF_004364325.1
WP_135106965.1	LRR-repeats+AP-GTPase+COR+DUF4404*→||<-?||?→?→?→?→?→ Mbetalac→	LRR-repeats+AP-GTPase+COR+DUF4404	967	-	Cyanobacteria	Mastigocladus laminosus	leucine-rich repeat domain-containing protein [Mastigocladus laminosus].	GCF_001990805.2
WP_135107787.1	<-PIN<-?||LRR-repeats+AP-GTPase+COR+TIR*→||<-Cluster1077_2clades	LRR-repeats+AP-GTPase+COR+TIR	1167	-	Cyanobacteria	Mastigocladus laminosus	leucine-rich repeat domain-containing protein [Mastigocladus laminosus].	GCF_001990805.2
WP_135191212.1	LRR-repeats+AP-GTPase+COR+DrHyd*→?→?→?→||<-?<-SIG+Phytase-like	LRR-repeats+AP-GTPase+COR+DrHyd	1147	-	Betaproteobacteria	Massilia sp. ONC3	hypothetical protein [Massilia sp. ONC3].	GCF_004614195.1

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
WP_136836096.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1357	-	Bacteroidetes	Pedobacter sp. RP-3-15	leucine-rich repeat domain-containing protein [Pedobacter sp. RP-3-15].	GCF_005116445.1
WP_136929189.1	SIG+TM+TM+TM+TM+TM+TM+TM+TM+TM→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	961	-	Deltaproteobacteria	Polyangium fumosum	GTP-binding protein [Polyangium fumosum].	GCF_005144585.1
WP_137669597.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	272	-	Cyanobacteria	Sphaerospermopsis reniformis	GTP-binding protein, partial [Sphaerospermopsis reniformis].	GCF_005402885.1
WP_137686407.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1152	-	Chloroflexi	Thermosporothrix hazakensis	leucine-rich repeat domain-containing protein [Thermosporothrix hazakensis].	GCF_005402645.1
WP_137908463.1	LRR-repeats+AP-GTPase+COR+TM+TM*→||<-PSE||?→?→||<-PSE<-?||CCTBP→	LRR-repeats+AP-GTPase+COR+TM+TM	875	-	Cyanobacteria	Dolichospermum planctonicum	leucine-rich repeat domain-containing protein [Dolichospermum planctonicum].	GCF_005402965.1
WP_138500060.1	<-Pkinase+Pentapeptide<-?<-?||PSE→||<-?||LRR-repeats+AP-GTPase+COR+TIR*→||<-?<-?<-PSE||?→||<-?||?→?→||<-NUDIX	LRR-repeats+AP-GTPase+COR+TIR	920	-	Cyanobacteria	Nostoc sp. PA-18-2419	leucine-rich repeat domain-containing protein [Nostoc sp. PA-18-2419].	GCF_005869855.1
WP_138503290.1	<-HhH-RADC+JAB||?→?→||<-?||LRR-repeats→ LRR-repeats+AP-GTPase+COR*→||<-?||?→?→||<-PSE<-?||?→?→ PEP-utilisers-C→	LRR-repeats+AP-GTPase+COR	1100	-	Cyanobacteria	Nostoc sp. PA-18-2419	leucine-rich repeat domain-containing protein [Nostoc sp. PA-18-2419].	GCF_005869855.1
WP_138504428.1	<-ABC-ATPase<-?<-?<-?||?→ TM+TM+TM→ LRR-repeats+AP-GTPase+COR+TIR*→ PSE→||<-PSE<-?||PSE→?→?→||<-SIG+TM+TM+TM+TM+TM	LRR-repeats+AP-GTPase+COR+TIR	1019	-	Bacteroidetes	Spirosoma lacussanchae	TIR domain-containing protein [Spirosoma lacussanchae].	GCF_005870035.1
WP_138544765.1	LRR-repeats+AP-GTPase+COR+TIR*→||<-?<-?<-TM	LRR-repeats+AP-GTPase+COR+TIR	1128	-	Gammaproteobacteria	Pseudoalteromonas rubra	leucine-rich repeat domain-containing protein [Pseudoalteromonas rubra].	GCF_005887115.1
WP_138544832.1	<-REC<-?||?→ LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1256	-	Gammaproteobacteria	Pseudoalteromonas rubra	TIR domain-containing protein [Pseudoalteromonas rubra].	GCF_005887115.1
WP_138553289.1	<-REC<-?||?→ LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1255	-	Gammaproteobacteria	Pseudoalteromonas rubra	TIR domain-containing protein [Pseudoalteromonas rubra].	GCF_005887405.1
WP_139281522.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	850	-	Gammaproteobacteria	Vibrio aerogenes	leucine-rich repeat domain-containing protein, partial [Vibrio aerogenes].	GCF_900130105.1
WP_139999876.1	TM+TM+TM→ LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1134	-	Bacteroidetes	Flavobacterium microcysteis	leucine-rich repeat domain-containing protein [Flavobacterium microcysteis].	GCF_006385255.1
WP_140058884.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1265	-	Gammaproteobacteria	Vibrio parahaemolyticus	TIR domain-containing protein [Vibrio parahaemolyticus].	GCF_006376835.1
WP_140063885.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	553	-	Gammaproteobacteria	Vibrio parahaemolyticus	hypothetical protein, partial [Vibrio parahaemolyticus].	GCF_006377025.1
WP_140305225.1	CI→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1113	-	Gammaproteobacteria	Vibrio parahaemolyticus	GTP-binding protein [Vibrio parahaemolyticus].	GCF_006374225.1
WP_140384737.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	829	-	Bacteroidetes	Elizabethkingia anophelis	TIR domain-containing protein, partial [Elizabethkingia anophelis].	GCF_900156995.1
WP_141211867.1	LRR-repeats+AP-GTPase+COR+CASPASE*→||<-?||Cluster1731_2clades→?→||<-Cluster2482_2clades	LRR-repeats+AP-GTPase+COR+CASPASE	835	-	Cyanobacteria	Pseudanabaena sp. SR411	leucine-rich repeat domain-containing protein, partial [Pseudanabaena sp. SR411].	GCF_002251945.1
WP_141954907.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1074	-	Actinobacteria	Actinoallomurus bryophytorum	hypothetical protein [Actinoallomurus bryophytorum].	GCF_006716425.1
WP_142449077.1	LRR-repeats+AP-GTPase+COR+TIR*→ TIR→	LRR-repeats+AP-GTPase+COR+TIR	700	-	Bacteroidetes	Flavobacterium resistens	leucine-rich repeat domain-containing protein [Flavobacterium resistens].	GCF_900182645.1

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WP_142602418.1	LRR-repeats+AP-GTPase+COR*→ PSE→ PSE→||<-?||?→||<-?<-?<-Cluster2042_2clades	LRR-repeats+AP-GTPase+COR	718	-	Cyanobacteria	Pseudanabaena sp. UWO310	leucine-rich repeat domain-containing protein [Pseudanabaena sp. UWO310].	GCF_006861605.1
WP_142653260.1	LRR-repeats→ LRR-repeats+AP-GTPase+COR+CASPASE*→?→?→||<-?<-?<-REC	LRR-repeats+AP-GTPase+COR+CASPASE	1028	-	Cyanobacteria	Pseudanabaena sp. UWO311	leucine-rich repeat domain-containing protein [Pseudanabaena sp. UWO311].	GCF_006937785.1
WP_142654307.1	Cluster54_3clades→?→?→?→ LRR-repeats+AP-GTPase+COR+CASPASE*→?→||<-?<-TPR-repeats+CASPASE<-TPR-repeats+CASPASE	LRR-repeats+AP-GTPase+COR+CASPASE	1096	-	Cyanobacteria	Pseudanabaena sp. UWO311	leucine-rich repeat domain-containing protein [Pseudanabaena sp. UWO311].	GCF_006937785.1
WP_142657357.1	ABC-ATPase→?→?→?→?→ Cluster1009_2clades→ Cluster53_2clades→ LRR-repeats+AP-GTPase+COR*→||<-?||?→?→?→ SIG+TM+TM+TM+TM+TM→	LRR-repeats+AP-GTPase+COR	992	-	Cyanobacteria	Pseudanabaena sp. UWO311	leucine-rich repeat domain-containing protein [Pseudanabaena sp. UWO311].	GCF_006937785.1
WP_142891598.1	LRR-repeats+AP-GTPase+COR+DrHyd*→	LRR-repeats+AP-GTPase+COR+DrHyd	1516	-	Gammaproteobacteria	Aliikangiella sp. M105	hypothetical protein [Aliikangiella sp. M105].	GCF_007004725.1
WP_143234350.1	<-REC<-?||?→ LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	888	-	Actinobacteria	Actinoplanes atraurantiacus	GTPase [Actinoplanes atraurantiacus].	GCF_900215205.1
WP_143288104.1	LRR-repeats+AP-GTPase+COR*→||<-SIG+TM+TM+TM+TM	LRR-repeats+AP-GTPase+COR	716	-	Cyanobacteria	Calothrix rhizosoleniae	GTP-binding protein, partial [Calothrix rhizosoleniae].	GCF_900185595.1
WP_143288141.1	LRR-repeats+AP-GTPase+COR+TM+TM*→	LRR-repeats+AP-GTPase+COR+TM+TM	777	-	Cyanobacteria	Calothrix rhizosoleniae	leucine-rich repeat domain-containing protein, partial [Calothrix rhizosoleniae].	GCF_900185595.1
WP_143301191.1	LRR-repeats+AP-GTPase+COR+DUF4404*→?→||<-RNA-Helicase	LRR-repeats+AP-GTPase+COR+DUF4404	650	-	Nitrospinae/Tectomicrobia group	Candidatus Entotheonella palauensis	GTP-binding protein, partial [Candidatus Entotheonella palauensis].	GCF_900079105.1
WP_143674573.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	802	-	Actinobacteria	Streptomyces sp. HG99	hypothetical protein, partial [Streptomyces sp. HG99].	GCF_002742045.1
WP_143814854.1	SIGMA-HTH→?→||<-?<-?<-?<-?<-?||LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	861	-	Alphaproteobacteria	Magnetofaba australis	hypothetical protein [Magnetofaba australis].	GCF_002109495.1
WP_144282986.1	LRR-repeats+AP-GTPase+COR+TIR*→?→?→?→||<-?<-?<-?<-HISKIN	LRR-repeats+AP-GTPase+COR+TIR	1293	-	Bacteroidetes	Chryseobacterium echinoideorum	leucine-rich repeat domain-containing protein [Chryseobacterium echinoideorum].	GCF_007474535.1
WP_144984133.1	TIR+APATPase+TPR+TPR+TPR→ LRR-repeats+AP-GTPase+COR+TM+TM+TM+TM*→	LRR-repeats+AP-GTPase+COR+TM+TM+TM+TM	1242	-	Planctomycetes	Gimesia aquarii	leucine-rich repeat domain-containing protein [Gimesia aquarii].	GCF_007748195.1
WP_145277465.1	LRR-repeats+AP-GTPase+COR+DUF4404*→	LRR-repeats+AP-GTPase+COR+DUF4404	1013	-	Planctomycetes	Planctomycetes bacterium ElP	leucine-rich repeat domain-containing protein [Planctomycetes bacterium ElP].	-
WP_145532816.1	CI→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1113	-	Gammaproteobacteria	Vibrio sp. ES.045	GTP-binding protein [Vibrio sp. ES.045].	GCF_007827265.1
WP_145988187.1	<-Classical-AAA<-Trichomonas-DAM||LRR-repeats+AP-GTPase*→||<-?<-Cluster1368_2clades<-Cluster2311_2clades	LRR-repeats+AP-GTPase	621	-	Alphaproteobacteria	Blastochloris tepida	leucine-rich repeat domain-containing protein [Blastochloris tepida].	GCF_003966715.1
WP_146033967.1	LRR-repeats+AP-GTPase+COR+DUF4404*→	LRR-repeats+AP-GTPase+COR+DUF4404	700	-	Cyanobacteria	Nostoc cycadae	GTP-binding protein, partial [Nostoc cycadae].	GCF_002897135.1
WP_146129808.1	LRR-repeats→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	715	-	Bacteroidetes	Muricauda pacifica	hypothetical protein [Muricauda pacifica].	GCF_003001695.1
WP_146156812.1	TPR-repeats→?→ SIG+Alba→||<-?<-?<-?<-?||LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	857	-	Bacteroidetes	Sphingobacteriales bacterium UPWRP_1	GTP-binding protein [Sphingobacteriales bacterium UPWRP_1].	-
WP_146201360.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	780	-	Gammaproteobacteria	Leucothrix arctica	TIR domain-containing protein [Leucothrix arctica].	GCF_003172895.1

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WP_146215520.1	LRR-repeats+AP-GTPase+COR+TM+TM+TM*→||<-PSE<-?<-?<-?<-?<-Cluster1270_2clades	LRR-repeats+AP-GTPase+COR+TM+TM+TM	1504	-	Alphaproteobacteria	Hoeflea marina	hypothetical protein [Hoeflea marina].	GCF_003182275.1
WP_146505417.1	LRR-repeats→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	795	-	Chloroflexi	Thermosporothrix hazakensis	GTPase [Thermosporothrix hazakensis].	GCF_003253565.1
WP_146848114.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	846	-	Bacteroidetes	Aequorivita antarctica	hypothetical protein [Aequorivita antarctica].	GCF_007997155.1
WP_146849445.1	SIG+TM→?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1099	-	Verrucomicrobia	Brevifollis gellanilyticus	leucine-rich repeat domain-containing protein [Brevifollis gellanilyticus].	GCF_007992435.1
WP_146856190.1	LRR-repeats+AP-GTPase+COR+DUF4404*→	LRR-repeats+AP-GTPase+COR+DUF4404	944	-	Verrucomicrobia	Brevifollis gellanilyticus	leucine-rich repeat domain-containing protein [Brevifollis gellanilyticus].	GCF_007992435.1
WP_147290429.1	<-Aminotran_1_2<-?||?→?→||<-Arginase||?→ LRR-repeats+AP-GTPase+COR+TIR*→||<-?<-PSE<-?<-?<-?||?→||<-Cluster1063_3clades<-Cluster1067_3clades	LRR-repeats+AP-GTPase+COR+TIR	1134	-	Alphaproteobacteria	Pannonibacter phragmitetus	leucine-rich repeat domain-containing protein [Pannonibacter phragmitetus].	GCF_000382365.1
WP_147864606.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1297	-	Bacteroidetes	Mesonia sp. K4-1	leucine-rich repeat domain-containing protein [Mesonia sp. K4-1].	GCF_008017825.1
WP_148270831.1	35exo→||<-?<-?||?→?→?→ LRR-repeats+AP-GTPase+COR+TIR*→||<-?<-?<-ABC-ATPase+APATPase+ABC-ATPase<-?||SIGMA-HTH→	LRR-repeats+AP-GTPase+COR+TIR	935	-	Bacteroidetes	Haliscomenobacter hydrossis	leucine-rich repeat domain-containing protein [Haliscomenobacter hydrossis].	GCF_000212735.1
WP_148270849.1	LRR-repeats+AP-GTPase+COR+EAD11*→?→?→?→?→?→?→ UvsW-A18→	LRR-repeats+AP-GTPase+COR+EAD11	1113	-	Bacteroidetes	Haliscomenobacter hydrossis	GTP-binding protein [Haliscomenobacter hydrossis].	GCF_000212735.1
WP_148270854.1	MACRODOMAIN→?→ LRR-repeats+AP-GTPase+COR+EAD11*→	LRR-repeats+AP-GTPase+COR+EAD11	1041	-	Bacteroidetes	Haliscomenobacter hydrossis	Miro domain-containing protein [Haliscomenobacter hydrossis].	GCF_000212735.1
WP_148705297.1	<-HhH-RADC+JAB||?→ NTP_transf_3→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1056	-	Euryarchaeota	Methanosarcina siciliae	leucine-rich repeat domain-containing protein [Methanosarcina siciliae].	GCF_000970125.1
WP_149986249.1	SIG+TM+TM+TM+TM+TM+TM+TM→||<-?||Mbetalac→ SAM-methylase→?→||<-?<-SIG+TPM_phosphatase+TM+TM+TM||LRR-repeats+AP-GTPase+COR+TM+TM*→	LRR-repeats+AP-GTPase+COR+TM+TM	829	-	Cyanobacteria	Microcystis aeruginosa	leucine-rich repeat protein [Microcystis aeruginosa].	GCF_008579325.1
WP_150032603.1	Cluster1550_2clades→?→?→?→?→||<-Cluster995_2clades||tRNA→ LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1161	-	Bacteroidetes	Taibaiella sp. KVB11	leucine-rich repeat domain-containing protein [Taibaiella sp. KVB11].	GCF_008629695.1
WP_150875462.1	<-ABC-ATPase<-?<-?||?→?→ LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	976	-	Bacteroidetes	Larkinella sp. MA1	leucine-rich repeat domain-containing protein [Larkinella sp. MA1].	GCF_008727875.1
WP_150977944.1	CHTH→ LRR-repeats+AP-GTPase+COR+TM+TM*→	LRR-repeats+AP-GTPase+COR+TM+TM	796	-	Cyanobacteria	Microcystis aeruginosa	leucine-rich repeat domain-containing protein [Microcystis aeruginosa].	GCF_008757435.1
WP_151015117.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	946	-	Actinobacteria	Micromonospora aurantiaca	leucine-rich repeat domain-containing protein [Micromonospora aurantiaca].	GCF_008806405.1
WP_151968636.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	803	-	Planctomycetes	Planctomycetes bacterium SRT547	leucine-rich repeat domain-containing protein [Planctomycetes bacterium SRT547].	-
WP_152037914.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	919	-	Actinobacteria	Micromonospora sp. B006	leucine-rich repeat domain-containing protein [Micromonospora sp. B006].	GCF_003408515.1
WP_152532113.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	814	-	Cyanobacteria	Leptolyngbya sp. Heron Island J	leucine-rich repeat domain-containing protein [Leptolyngbya sp. Heron Island J].	-

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WP_152589868.1	<-Ferretin<-PSE<-?||?→||<-Ferredoxin-betagrasp<-PSE<-?||LRR-repeats+AP-GTPase+COR*→?→||<-?||?→||<-?||PSE→ PSE→ ClpABN-AAA+ClpABC-AAA→	LRR-repeats+AP-GTPase+COR	993	-	Cyanobacteria	Nostoc sphaeroides	leucine-rich repeat domain-containing protein [Nostoc sphaeroides].	GCF_009372195.1
WP_152648774.1	NUDIX→?→?→ LRR-repeats+AP-GTPase+COR*→?→?→||<-?<-?||?→||<-Cluster2230__2clades	LRR-repeats+AP-GTPase+COR	954	-	Actinobacteria	Streptacidiphilus anmyonensis	hypothetical protein [Streptacidiphilus anmyonensis].	GCF_000787855.1
WP_153009609.1	<-Cluster1102__3clades<-Cluster1102__3clades||?→?→?→||<-Cluster5__5clades<-?||LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	997	-	Cyanobacteria	Mastigocoleus testarum	leucine-rich repeat domain-containing protein [Mastigocoleus testarum].	GCF_001456025.1
WP_153023587.1	TM→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1070	-	Actinobacteria	Glycomyces albidus	leucine-rich repeat domain-containing protein [Glycomyces albidus].	-
WP_153228358.1	<-Cluster5__5clades||LRR-repeats+AP-GTPase+COR+DUF4404*→||<-?<-ABC-ATPase<-?||?→||<-REC	LRR-repeats+AP-GTPase+COR+DUF4404	992	-	Cyanobacteria	Anabaena sp. YBS01	leucine-rich repeat domain-containing protein [Anabaena sp. YBS01].	GCF_009498015.1
WP_153456319.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	992	-	Actinobacteria	Streptomyces sp. RB5	GTPase [Streptomyces sp. RB5].	-
WP_153661567.1	<-cNMPBD<-cNMPBD||?→?→ LRR-repeats+AP-GTPase+COR+TM+TM*→	LRR-repeats+AP-GTPase+COR+TM+TM	1103	-	Bacteroidetes	Chitinophaga sp. SYP-B3965	leucine-rich repeat domain-containing protein [Chitinophaga sp. SYP-B3965].	GCF_009647655.1
WP_155076197.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	899	-	Bacteroidetes	Flavobacterium sp. MC2016-06	GTP-binding protein [Flavobacterium sp. MC2016-06].	GCF_009711165.1
WP_155705093.1	SIG+Trypsin+PDZ→?→?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	951	-	Firmicutes	Paenibacillus psychroresistens	GTP-binding protein [Paenibacillus psychroresistens].	GCF_009728935.1
WP_155743676.1	LRR-repeats+AP-GTPase+COR+EAD1*→||<-PSE||Pkinase→ Pkinase→?→||<-Cluster5__5clades	LRR-repeats+AP-GTPase+COR+EAD1	1152	-	Cyanobacteria	Scytonema sp. UIC 10036	leucine-rich repeat domain-containing protein [Scytonema sp. UIC 10036].	GCF_009725235.1
WP_155746360.1	LRR-repeats→||<-?<-Cluster5__5clades||LRR-repeats→?→ LRR-repeats+AP-GTPase+COR+EAD1*→?→?→ Cluster5__5clades→	LRR-repeats+AP-GTPase+COR+EAD1	988	-	Cyanobacteria	Scytonema sp. UIC 10036	leucine-rich repeat domain-containing protein [Scytonema sp. UIC 10036].	GCF_009725235.1
WP_156420697.1	TetR-HTH→?→||<-?<-?<-?||LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1173	-	Alphaproteobacteria	Sphingopyxis sp. HXXIV	TIR domain-containing protein [Sphingopyxis sp. HXXIV].	GCF_001468305.1
WP_157205648.1	Cluster5__5clades→?→?→ HTH→ LRR-repeats+AP-GTPase+COR+TIR*→ Cluster1019__2clades→?→||<-?<-?<-?||Cluster833__2clades→	LRR-repeats+AP-GTPase+COR+TIR	1096	-	Gammaproteobacteria	Methylomonas koyamae	TIR domain-containing protein [Methylomonas koyamae].	GCF_001644135.1
WP_157310052.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	917	-	Bacteroidetes	Chitinophaga sp. ysch24	leucine-rich repeat protein [Chitinophaga sp. ysch24].	GCF_009758205.1
WP_157453024.1	LRR-repeats+AP-GTPase+COR+DUF4404*→	LRR-repeats+AP-GTPase+COR+DUF4404	1156	-	Cyanobacteria	Coleofasciculus chthonoplastes	leucine-rich repeat domain-containing protein [Coleofasciculus chthonoplastes].	-
WP_157546628.1	<-SIG+TM+TM+TM+TM+TM+TM+TM+TM||?→?→||<-?||?→?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	585	-	Actinobacteria	Hamadaea tsunoensis	leucine-rich repeat domain-containing protein [Hamadaea tsunoensis].	GCF_000428945.1
WP_157584649.1	LRR-repeats+AP-GTPase+COR+TIR*→||<-?||ABC__membrane+ABC__tran→	LRR-repeats+AP-GTPase+COR+TIR	937	-	Bacteroidetes	Spirosoma sp. HMF4905	leucine-rich repeat domain-containing protein [Spirosoma sp. HMF4905].	GCF_009754945.1
WP_157585892.1	LRR-repeats+AP-GTPase+COR+TIR*→ Cluster1510__2clades→	LRR-repeats+AP-GTPase+COR+TIR	1129	-	Bacteroidetes	Spirosoma sp. HMF4905	leucine-rich repeat domain-containing protein [Spirosoma sp. HMF4905].	-
WP_157590734.1	ABhydrolase+ABhydrolase+CASPASE+TPR-S→||<-?||LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1169	-	Bacteroidetes	Spirosoma sp. HMF4905	leucine-rich repeat domain-containing protein [Spirosoma sp. HMF4905].	GCF_009754945.1
WP_157879249.1	LRR-repeats+AP-GTPase+COR+TIR*→||<-PSE<-?<-?<-?<-?<-?<-?<-REC	LRR-repeats+AP-GTPase+COR+TIR	656	-	Alphaproteobacteria	Pararhodospirillum photometricum	hypothetical protein [Pararhodospirillum photometricum].	GCF_000284415.1

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WP_157881522.1	Cluster1792_2clades→?→?→||<-?||?→ LRR-repeats+AP-GTPase+COR*→||<-?||?→ SIG+TM+TM→	LRR-repeats+AP-GTPase+COR	950	-	Actinobacteria	Streptomyces phaeochromogenes	hypothetical protein [Streptomyces phaeochromogenes].	GCF_001418655.1
WP_158043876.1	LRR-repeats+AP-GTPase+COR_TIR*→	LRR-repeats+AP-GTPase+COR_TIR	1167	-	Alphaproteobacteria	Skermanella pratensis	TIR domain-containing protein [Skermanella pratensis].	-
WP_158234411.1	LRR-repeats+AP-GTPase+COR*→ LRR-repeats→ LRR-repeats→	LRR-repeats+AP-GTPase+COR	852	-	Cyanobacteria	Limnothrix sp. PR1529	leucine-rich repeat domain-containing protein [Limnothrix sp. PR1529].	GCF_002742025.1
WP_158281705.1	<-ACET<-?<-?<-?||?→ HSP70→ DNAJ→ LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	944	-	Betaproteobacteria	Rivicola pingtungensis	TIR domain-containing protein [Rivicola pingtungensis].	GCF_003201855.1
WP_158299785.1	TM→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1050	-	Actinobacteria	Glycomyces paridis	hypothetical protein [Glycomyces paridis].	GCF_004912155.1
WP_158592567.1	LRR-repeats+AP-GTPase+COR+TM+TM*→	LRR-repeats+AP-GTPase+COR+TM+TM	1002	-	Bacteroidetes	Flavobacterium sp. 102	50S ribosome-binding GTPase [Flavobacterium sp. 102].	GCF_003634615.1
WP_158623299.1	TPR-repeats→ LRR-repeats+AP-GTPase+COR+TIR*→?→?→?→?→||<-LexA-protease	LRR-repeats+AP-GTPase+COR+TIR	1083	-	Deltaproteobacteria	Corallococcus sp. CA053C	TIR domain-containing protein [Corallococcus sp. CA053C].	GCF_003611675.1
WP_158660235.1	<-SIG+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM<-?<-?<-?<-?||?→?→ LRR-repeats+AP-GTPase+COR+TIR*→||<-ParB<-ParA-Soj-PloopNTPase	LRR-repeats+AP-GTPase+COR+TIR	723	-	Alphaproteobacteria	Niveispirillum cyanobacteriorum	TIR domain-containing protein [Niveispirillum cyanobacteriorum].	GCF_014640215.1
WP_158690560.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1355	-	Actinobacteria	Streptomyces sp. 142MFCol3.1	hypothetical protein, partial [Streptomyces sp. 142MFCol3.1].	GCF_000424945.1
WP_158924018.1	LRR-repeats+AP-GTPase+COR*→||<-?||?→||<-?<-SIGMA-HTH<-?<-SIGMA-HTH	LRR-repeats+AP-GTPase+COR	996	-	Actinobacteria	Streptomyces broussonetiae	GTPase [Streptomyces broussonetiae].	GCF_009796285.1
WP_159021496.1	Cluster1757_2clades→||<-?||LRR-repeats+AP-GTPase+COR*→?→?→?→?→||<-PSE<-PSE<-Cluster1695_2clades	LRR-repeats+AP-GTPase+COR	704	-	Bacteroidetes	Formosa sp. L2A11	GTP-binding protein [Formosa sp. L2A11].	GCF_009796865.1
WP_159170123.1	LRR-repeats+AP-GTPase+COR+DrHyd*→	LRR-repeats+AP-GTPase+COR+DrHyd	855	-	Gammaproteobacteria	Halioglobus japonicus	hypothetical protein [Halioglobus japonicus].	GCF_902705825.1
WP_159248779.1	SIG+TM+TM+TM+TM+TM+TM+TM→||<-?||Mbetalac→ SAM-methylase→?→||<-?<-SIG+TPM_phosphatase+TM+TM+TM||LRR-repeats+AP-GTPase+COR+TM+TM*→||<-?<-?<-?<-Pro_CA||?→||<-?<-tRNA<-tRNA<-Ferredoxin-betagrasp	LRR-repeats+AP-GTPase+COR+TM+TM	805	-	Cyanobacteria	Microcystis aeruginosa	leucine-rich repeat domain-containing protein [Microcystis aeruginosa].	GCF_009811815.1
WP_159254721.1	LRR-repeats+AP-GTPase+COR*→?→?→?→||<-?<-ABC-ATPase	LRR-repeats+AP-GTPase+COR	923	-	Bacteroidetes	Tenacibaculum maritimum	leucine-rich repeat domain-containing protein [Tenacibaculum maritimum].	GCF_902705305.1
WP_159395983.1	LRR-repeats+AP-GTPase+COR*→||<-?||?→||<-?<-SIGMA-HTH<-?<-SIGMA-HTH	LRR-repeats+AP-GTPase+COR	988	-	Actinobacteria	Streptomyces sp. FXJ1.172	GTPase [Streptomyces sp. FXJ1.172].	GCF_001636945.1
WP_159402479.1	ABhydrolase→?→||<-?||LRR-repeats+AP-GTPase+COR+TIR*→||<-?<-?<-?<-SIG+NUDIX	LRR-repeats+AP-GTPase+COR+TIR	1069	-	Cyanobacteria	Nostoc sp. ATCC 53789	leucine-rich repeat domain-containing protein [Nostoc sp. ATCC 53789].	GCF_009873495.1
WP_159402492.1	Pentapeptide-repeats→||<-?<-?||?→?→||<-Arginase<-?||LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	802	-	Cyanobacteria	Nostoc sp. ATCC 53789	leucine-rich repeat domain-containing protein [Nostoc sp. ATCC 53789].	GCF_009873495.1
WP_159402558.1	Cluster5_5clades→ LRR-repeats+AP-GTPase+COR+TM+TM*→||<-CASPASE+TM	LRR-repeats+AP-GTPase+COR+TM+TM	904	-	Cyanobacteria	Nostoc sp. ATCC 53789	leucine-rich repeat domain-containing protein [Nostoc sp. ATCC 53789].	GCF_009873495.1
WP_159402710.1	LRR-repeats+AP-GTPase+COR+CASPASE*→?→?→?→ ParA-Soj-PloopNTPase→	LRR-repeats+AP-GTPase+COR+CASPASE	1535	-	Cyanobacteria	Nostoc sp. ATCC 53789	leucine-rich repeat domain-containing protein [Nostoc sp. ATCC 53789].	GCF_009873495.1
WP_159447934.1	CI→ CI→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1103	-	Gammaproteobacteria	Photobacterium piscicola	GTP-binding protein [Photobacterium piscicola].	GCF_900166965.1
WP_159457453.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1186	-	Gammaproteobacteria	Vibrio mangrovi	leucine-rich repeat domain-containing protein [Vibrio mangrovi].	GCF_900184095.1

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
WP_159789529.1	<-Cluster1921_2clades<-?<-?||?→||<-?||?→?→ LRR-repeats+AP-GTPase+COR*→?→||<-?<-REC	LRR-repeats+AP-GTPase+COR	771	-	Cyanobacteria	Microcoleus sp. IPPAS B-353	leucine-rich repeat domain-containing protein [Microcoleus sp. IPPAS B-353].	GCF_009846485.1
WP_160075537.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1088	-	Bacteroidetes	Saprospirales bacterium GYS_P2D	leucine-rich repeat domain-containing protein [Saprospirales bacterium GYS_P2D].	-
WP_160131147.1	SIGMA-HTH→?→ RADICAL-SAM→ LRR-repeats+AP-GTPase+COR+TIR*→||<-REC<-?<-?<-?||?→ HISKIN→	LRR-repeats+AP-GTPase+COR+TIR	1229	-	Bacteroidetes	Kordia antarctica	leucine-rich repeat domain-containing protein [Kordia antarctica].	GCF_009901525.1
WP_160148531.1	<-SIG+Trypsin+PDZ<-?<-?<-?||?→?→ LRR-repeats+AP-GTPase+COR+TCAD2*→	LRR-repeats+AP-GTPase+COR+TCAD2	919	-	Cyanobacteria	Leptolyngbya sp. PCC 7376	leucine-rich repeat domain-containing protein [Leptolyngbya sp. PCC 7376].	GCF_000316605.1
WP_161144175.1	Cluster1913_2clades→?→?→?→?→ LRR-repeats+AP-GTPase*→	LRR-repeats+AP-GTPase	512	-	Firmicutes	Dorea sp. BIOML-A1	hypothetical protein [Dorea sp. BIOML-A1].	GCF_009875615.1
WP_161213661.1	LRR-repeats+AP-GTPase+COR*→||<-NUDIX	LRR-repeats+AP-GTPase+COR	1340	-	Actinobacteria	unclassified Streptomyces	MULTISPECIES: leucine-rich repeat domain-containing protein [unclassified Streptomyces].	GCF_900091775.1
WP_161967152.1	<-Aminotran_1_2<-?||LRR-repeats+AP-GTPase+COR+TIR*→||<-?<-?<-?<-DSBH+AraC-HTH+AraC-HTH	LRR-repeats+AP-GTPase+COR+TIR	1219	-	Planctomycetes	Fimbriiglobus ruber	hypothetical protein [Fimbriiglobus ruber].	GCF_002197845.1
WP_161967198.1	<-RelE-ParE<-?||?→?→ LRR-repeats→||<-?||LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	915	-	Planctomycetes	Fimbriiglobus ruber	leucine-rich repeat domain-containing protein [Fimbriiglobus ruber].	GCF_002197845.1
WP_162292932.1	LRR-repeats+AP-GTPase+COR*→?→?→?→||<-?<-ABC-ATPase+ABC-ATPase	LRR-repeats+AP-GTPase+COR	1975	-	Actinobacteria	Actinophytocola xinjiangensis	leucine-rich repeat domain-containing protein [Actinophytocola xinjiangensis].	GCF_001921215.1
WP_162399370.1	LRR-repeats+AP-GTPase+COR*→?→||<-?||?→||<-?<-?||?→ ClpABN-AAA+ClpABC-AAA→	LRR-repeats+AP-GTPase+COR	895	-	Cyanobacteria	Nostoc sp. B(2019)	leucine-rich repeat domain-containing protein, partial [Nostoc sp. B(2019)].	GCF_010091925.1
WP_162488066.1	TM+TM→?→||<-?||?→ PSE→||<-?||?→?→ LRR-repeats+AP-GTPase+COR+TIR*→||<-?<-?||ABC_membrane+ABC_tran→?→ Cluster968_2clades→	LRR-repeats+AP-GTPase+COR+TIR	1120	-	Alphaproteobacteria	Azospirillum lipoferum	TIR domain-containing protein [Azospirillum lipoferum].	GCF_000283655.1
WP_162528069.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	781	-	Alphaproteobacteria	Rhodobacterales bacterium	leucine-rich repeat domain-containing protein [Rhodobacterales bacterium].	-
WP_162667694.1	<-Cluster1291_2clades<-?<-PSE<-?||?→?→?→ LRR-repeats+AP-GTPase*→?→||<-?||?→?→ ParB→	LRR-repeats+AP-GTPase	617	-	Planctomycetes	Gemmata massiliana	hypothetical protein [Gemmata massiliana].	GCF_901538265.1
WP_162668063.1	LRR-repeats+AP-GTPase+COR+DUF4404*→||<-?<-?<-?||?→||<-LRR-repeats||REC→	LRR-repeats+AP-GTPase+COR+DUF4404	978	-	Planctomycetes	Gemmata massiliana	leucine-rich repeat domain-containing protein [Gemmata massiliana].	GCF_901538265.1
WP_163431087.1	TIR→ LRR-repeats+AP-GTPase+COR+TIR*→ PSE→?→?→||<-?<-SIG+TM+TM+TM+HISKIN	LRR-repeats+AP-GTPase+COR+TIR	1384	-	Bacteroidetes	unclassified Flavobacterium	MULTISPECIES: leucine-rich repeat domain-containing protein [unclassified Flavobacterium].	GCF_013874595.1
WP_163660644.1	LRR-repeats+AP-GTPase*→	LRR-repeats+AP-GTPase	311	-	Cyanobacteria	Leptolyngbyaceae cyanobacterium CCMR0082	leucine-rich repeat domain-containing protein [Leptolyngbyaceae cyanobacterium CCMR0082].	-
WP_163671600.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	855	-	Cyanobacteria	Leptolyngbyaceae cyanobacterium CCMR0082	leucine-rich repeat domain-containing protein, partial [Leptolyngbyaceae cyanobacterium CCMR0082].	-

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
WP_163671893.1	<-NACHT<-?||LRR-repeats+AP-GTPase+COR+TIR*→||<-?||PSE→||<-NACHT+68TM-wHTH<-?||?→?→||<-?||Cluster53_2clades→	LRR-repeats+AP-GTPase+COR+TIR	726	-	Cyanobacteria	Leptolyngbyaceae cyanobacterium CCMR0082	TIR domain-containing protein [Leptolyngbyaceae cyanobacterium CCMR0082].	-
WP_163697061.1	LRR-repeats+AP-GTPase+COR+TIR*→?→||<-?<-?<-?||?→||<-Cluster1829_2clades	LRR-repeats+AP-GTPase+COR+TIR	1274	-	Cyanobacteria	Leptolyngbyaceae cyanobacterium CCMR0081	leucine-rich repeat domain-containing protein [Leptolyngbyaceae cyanobacterium CCMR0081].	-
WP_163702516.1	<-SIG+DM13||?→?→?→?→?→ PIN→ LRR-repeats+AP-GTPase+COR+TIR*→?→ PSE→?→?→?→||<-?<-SIG+TM+TM+Calcineurin	LRR-repeats+AP-GTPase+COR+TIR	993	-	Cyanobacteria	Leptolyngbyaceae cyanobacterium CCMR0081	leucine-rich repeat domain-containing protein [Leptolyngbyaceae cyanobacterium CCMR0081].	-
WP_163703138.1	SIR2→?→?→?→?→?→?→ LRR-repeats+AP-GTPase+COR+TIR*→ PSE→||<-Pentapeptide	LRR-repeats+AP-GTPase+COR+TIR	830	-	Cyanobacteria	Leptolyngbyaceae cyanobacterium CCMR0081	TIR domain-containing protein [Leptolyngbyaceae cyanobacterium CCMR0081].	-
WP_163833956.1	LRR-repeats+AP-GTPase+COR+DUF4404*→||<-?<-CHTH	LRR-repeats+AP-GTPase+COR+DUF4404	1124	-	Gammaproteobacteria	Spartinivicinus ruber	leucine-rich repeat domain-containing protein [Spartinivicinus ruber].	GCF_011009015.1
WP_163929292.1	LRR-repeats+AP-GTPase+COR+TIR*→||<-?<-?<-TIR<-?<-SIG+NUDIX	LRR-repeats+AP-GTPase+COR+TIR	1024	-	Cyanobacteria	Nostoc sp. UIC 10630	leucine-rich repeat domain-containing protein [Nostoc sp. UIC 10630].	GCF_010747425.1
WP_163938989.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	795	-	Cyanobacteria	Nostoc sp. UIC 10630	leucine-rich repeat domain-containing protein, partial [Nostoc sp. UIC 10630].	GCF_010747425.1
WP_164035239.1	Cluster998_2clades→?→||<-?<-?<-?||SAM-methylase→?→ tRNA→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	858	-	Bacteroidetes	Spirosoma agri	hypothetical protein [Spirosoma agri].	GCF_010747415.1
WP_164490209.1	FGS→ FGS→ FGS→ LRR-repeats+AP-GTPase+COR+CASPASE*→	LRR-repeats+AP-GTPase+COR+CASPASE	976	-	Bacteroidetes	Runella sp. SP2	leucine-rich repeat domain-containing protein [Runella sp. SP2].	GCF_003711225.1
WP_164638795.1	LRR-repeats+AP-GTPase+COR+TIR*→||<-?<-?<-?<-ABC-ATPase||?→ REC→	LRR-repeats+AP-GTPase+COR+TIR	1173	-	Alphaproteobacteria	Rhodopseudomonas sp. BR0G17	leucine-rich repeat domain-containing protein [Rhodopseudomonas sp. BR0G17].	GCF_010907025.1
WP_164714180.1	LRR-repeats+AP-GTPase+COR+TIR*→||<-?<-?||?→ cNMPBD→ SIG+TM+TM+TM→	LRR-repeats+AP-GTPase+COR+TIR	1056	-	Bacteroidetes	Chitinophaga rhizosphaerae	leucine-rich repeat domain-containing protein [Chitinophaga rhizosphaerae].	GCF_003958645.1
WP_165253289.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1053	-	Planctomycetes	Paludisphaera soli	TIR domain-containing protein [Paludisphaera soli].	GCF_011064595.1
WP_165571460.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	871	-	Bacteroidetes	Flavobacterium hydatis	hypothetical protein [Flavobacterium hydatis].	GCF_000737695.1
WP_165772028.1	<-SIG+TM+TM+TM+HISKIN<-?<-?<-?||?→ LRR-repeats+AP-GTPase+COR+TIR*→ ParA-Soj-PloopNTPase→ ParB→	LRR-repeats+AP-GTPase+COR+TIR	674	-	Alphaproteobacteria	Niveispirillum lacus	TIR domain-containing protein [Niveispirillum lacus].	GCF_002251795.1
WP_166124895.1	<-Cluster1501_2clades||?→?→ LRR-repeats+AP-GTPase+COR*→?→ Cluster1023_3clades→?→||<-?||ClpABN-AAA+ClpABC-AAA→	LRR-repeats+AP-GTPase+COR	925	-	Bacteroidetes	unclassified Flavobacterium	MULTISPECIES: leucine-rich repeat domain-containing protein [unclassified Flavobacterium].	GCF_011305415.1
WP_166235797.1	LRR-repeats+AP-GTPase+COR+TM+TM*→	LRR-repeats+AP-GTPase+COR+TM+TM	954	-	Bacteroidetes	Flavobacterium sp. TWA-26	hypothetical protein [Flavobacterium sp. TWA-26].	GCF_011392075.1
WP_166562074.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	931	-	Bacteroidetes	Emticicia sp. CRIBPO	leucine-rich repeat domain-containing protein [Emticicia sp. CRIBPO].	GCF_009905725.1
WP_167031741.1	LRR-repeats+AP-GTPase+COR+TIR*→?→?→ TIR→	LRR-repeats+AP-GTPase+COR+TIR	1295	-	Bacteroidetes	Chryseobacterium sp. Tr-659	leucine-rich repeat domain-containing protein [Chryseobacterium sp. Tr-659].	GCF_011752975.1

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
WP_167211330.1	LRR-repeats+AP-GTPase+COR+TIR*→ TIR→	LRR-repeats+AP-GTPase+COR+TIR	1843	-	Bacteroidetes	Spirosoma aureum	leucine-rich repeat domain-containing protein [Spirosoma aureum].	GCF_011604685.1
WP_167291529.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1060	-	Bacteroidetes	Paraflavitale devenefica	leucine-rich repeat domain-containing protein [Paraflavitale devenefica].	GCF_011759375.1
WP_167387879.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	967	-	Actinobacteria	Streptomyces recifensis	GTPase [Streptomyces recifensis].	GCF_002154615.1
WP_168204481.1	LRR-repeats→ LRR-repeats+AP-GTPase+COR+TM+TM*→	LRR-repeats+AP-GTPase+COR+TM+TM	574	-	Cyanobacteria	Dolichospermum sp. UHCC 0315A	hypothetical protein [Dolichospermum sp. UHCC 0315A].	GCF_008121535.1
WP_168218871.1	LRR-repeats+AP-GTPase+COR*→?→?→||<-?<-?<-?<-?<-PIN	LRR-repeats+AP-GTPase+COR	864	-	Planctomycetes	Limnoglobus roseus	leucine-rich repeat domain-containing protein [Limnoglobus roseus].	GCF_008254045.1
WP_168359257.1	LRR-repeats+AP-GTPase+COR+TM+TM*→	LRR-repeats+AP-GTPase+COR+TM+TM	687	-	Cyanobacteria	Dolichospermum planctonicum	GTP-binding protein, partial [Dolichospermum planctonicum].	GCF_009712075.1
WP_168360389.1	Ferredoxin-betagrasp→?→?→ LRR-repeats→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	682	-	Cyanobacteria	Dolichospermum planctonicum	hypothetical protein, partial [Dolichospermum planctonicum].	GCF_009712075.1
WP_168467214.1	LRR-repeats+AP-GTPase+COR*→ PSE→?→||<-?||?→?→?→||<-Pentapeptide	LRR-repeats+AP-GTPase+COR	692	-	Cyanobacteria	Aphanizomenon sp. UHCC 0183	GTP-binding protein, partial [Aphanizomenon sp. UHCC 0183].	GCF_009712065.1
WP_168493001.1	<-HNH<-?||?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1079	-	Cyanobacteria	Anabaena sp. UHCC 0204	leucine-rich repeat domain-containing protein [Anabaena sp. UHCC 0204].	GCF_009711975.1
WP_168511191.1	NUDIX→?→?→?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1365	-	Actinobacteria	Streptomyces sp. S1D4-11	leucine-rich repeat domain-containing protein [Streptomyces sp. S1D4-11].	-
WP_168644108.1	LRR-repeats+AP-GTPase+COR+TIR*→?→||<-?<-SIG+NUDIX	LRR-repeats+AP-GTPase+COR+TIR	963	-	Cyanobacteria	Dolichospermum sp. UHCC 0259	leucine-rich repeat domain-containing protein [Dolichospermum sp. UHCC 0259].	GCF_009711935.1
WP_169190548.1	<-ABC-ATPase<-?<-?<-?<-?||?→ tRNA→?→ LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1190	-	Bacteroidetes	Chitinophaga sp. Ak27	leucine-rich repeat domain-containing protein [Chitinophaga sp. Ak27].	GCF_012726295.1
WP_169266449.1	LRR-repeats+AP-GTPase+COR+TIR*→||<-?||?→||<-?||NUDIX→	LRR-repeats+AP-GTPase+COR+TIR	936	-	Cyanobacteria	Brasilonema octagenarum	leucine-rich repeat domain-containing protein [Brasilonema octagenarum].	GCF_012912125.1
WP_169315756.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1002	-	Bacteroidetes	Haliscomenobacter hydrossis	leucine-rich repeat domain-containing protein [Haliscomenobacter hydrossis].	GCF_000212735.1
WP_169363874.1	SIG+HIN-HTH→?→?→ LRR-repeats+AP-GTPase+COR+TM+TM*→	LRR-repeats+AP-GTPase+COR+TM+TM	972	-	Cyanobacteria	Pseudanabaena yagii	leucine-rich repeat domain-containing protein [Pseudanabaena yagii].	GCF_012863495.1
WP_169364911.1	TPR-repeats+CASPASE→?→ PSE→ Cluster54_3clades→ Cluster53_2clades→?→ LRR-repeats+AP-GTPase+COR+CASPASE*→||<-?||?→ REC→	LRR-repeats+AP-GTPase+COR+CASPASE	1239	-	Cyanobacteria	Pseudanabaena yagii	leucine-rich repeat domain-containing protein [Pseudanabaena yagii].	GCF_012863495.1
WP_169365210.1	Pentapeptide-repeats→?→ PolB→?→ LRR-repeats→ LRR-repeats+AP-GTPase+COR*→?→?→||<-?||?→?→||<-SIG+TM+TM+TM+TM+TM	LRR-repeats+AP-GTPase+COR	682	-	Cyanobacteria	Pseudanabaena yagii	hypothetical protein [Pseudanabaena yagii].	GCF_012863495.1
WP_169482131.1	LRR-repeats+AP-GTPase+COR*→||<-?||?→||<-?<-?<-?<-?<-Cluster1745_2clades	LRR-repeats+AP-GTPase+COR	965	-	Firmicutes	Paenibacillus sp. SZ31	GTP-binding protein [Paenibacillus sp. SZ31].	GCF_012912005.1
WP_169551474.1	LRR-repeats+AP-GTPase+COR+DrHyd*→||<-?||?→?→||<-TPR-repeats	LRR-repeats+AP-GTPase+COR+DrHyd	1047	-	Bacteroidetes	Spirosoma sp. CJU-R4	hypothetical protein [Spirosoma sp. CJU-R4].	GCF_012849055.1
WP_169617268.1	RelE→ CHTH→?→||<-?<-?<-?<-?||LRR-repeats+AP-GTPase+COR+TIR*→?→||<-?<-?||?→?→||<-?<-RelE-ParE	LRR-repeats+AP-GTPase+COR+TIR	1174	-	Cyanobacteria	Nodosilinea sp. P-1105	leucine-rich repeat domain-containing protein [Nodosilinea sp. P-1105].	GCF_012911975.1

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
WP_169792421.1	<-ABC-ATPase<-?<-?<-?||?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	867	-	Actinobacteria	Actinoplanes rectilineatus	GTP-binding protein [Actinoplanes rectilineatus].	GCF_000962825.1
WP_170065039.1	REC→||<-?<-?<-?<-?||?→ LRR-repeats+AP-GTPase+COR+DpnII-MboI-NTD+TIR*→	LRR-repeats+AP-GTPase+COR+DpnII-MboI-NTD+TIR	992	-	Gammaproteobacteria	Methylovulum psychrotolerans	leucine-rich repeat domain-containing protein [Methylovulum psychrotolerans].	GCF_002923755.1
WP_170200769.1	HNOB→ HISKIN→?→||<-?<-?||LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	921	-	Betaproteobacteria	Ideonella azotifigens	TIR domain-containing protein [Ideonella azotifigens].	GCF_006519715.1
WP_170318945.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	514	-	Actinobacteria	Allorhizocola rhizosphaerae	leucine-rich repeat domain-containing protein, partial [Allorhizocola rhizosphaerae].	GCF_003426775.1
WP_170321800.1	LRR-repeats+AP-GTPase+COR*→?→ Phytase-like→||<-?||?→?→ PSE→ ABC-ATPase→ ABC-ATPase→	LRR-repeats+AP-GTPase+COR	1057	-	Actinobacteria	Acrocarpospora pleiomorpha	leucine-rich repeat domain-containing protein [Acrocarpospora pleiomorpha].	GCF_009687885.1
WP_170944127.1	LRR-repeats+AP-GTPase+COR*→ COR→?→ RelE-ParE→	LRR-repeats+AP-GTPase+COR	216	-	Cyanobacteria	Leptolyngbya sp. BC1307	leucine-rich repeat domain-containing protein, partial [Leptolyngbya sp. BC1307].	GCF_002286735.1
WP_171062796.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	864	-	Bacteroidetes	Larkinella sp. C7	hypothetical protein [Larkinella sp. C7].	GCF_006149005.1
WP_171572097.1	EAD10+VMAP-M1+VMAP-C→?→ VWA+LRR-repeats+AP-GTPase+COR→ *Cluster5_5clades→||<-?<-?<-LRR-repeats+AP-GTPase+COR*<-?<-CASPASE+EAD10<-?<-tRNA||?→?→ Cluster2368_2clades→ Cluster2098_2clades→	VWA+LRR-repeats+AP-GTPase+COR	1320	-	Bacteroidetes	Flavobacterium sp. CLA17	leucine-rich repeat domain-containing protein [Flavobacterium sp. CLA17].	GCF_013112255.1
WP_171572101.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	845	-	Bacteroidetes	Flavobacterium sp. CLA17	leucine-rich repeat domain-containing protein [Flavobacterium sp. CLA17].	GCF_013112255.1
WP_171574279.1	ABC-ATPase→ Ferredoxin-betagrasp→?→?→||<-?||LRR-repeats+AP-GTPase+COR+TM+TM*→ Cluster1136_2clades→ PSE→?→||<-Cluster1782_2clades<-?<-Cluster1583_2clades<-Cluster1881_2clades<-Cluster1340_2clades	LRR-repeats+AP-GTPase+COR+TM+TM	1162	-	Bacteroidetes	Flavobacterium sp. CLA17	leucine-rich repeat domain-containing protein [Flavobacterium sp. CLA17].	GCF_013112255.1
WP_171574361.1	<-SIG+TM+TM+TM+TM+TM+TM<-?||?→||<-SAM-methylase<-Cluster2335_2clades<-SIG+TM||?→ LRR-repeats+AP-GTPase+COR*→?→?→?→?→||<-ISOFLAVOMETHYLASE-HTH	LRR-repeats+AP-GTPase+COR	1103	-	Bacteroidetes	Flavobacterium sp. CLA17	leucine-rich repeat domain-containing protein [Flavobacterium sp. CLA17].	GCF_013112255.1
WP_171626408.1	<-Cluster1969_2clades<-?<-?<-?||?→ LRR-repeats+AP-GTPase+COR+TIR*→||<-?||?→?→ METHYLASE→ ParA-Soj-PloopNTPase→ ParB→	LRR-repeats+AP-GTPase+COR+TIR	1281	-	Gammaproteobacteria	Pseudoalteromonas caenipelagi	leucine-rich repeat protein [Pseudoalteromonas caenipelagi].	GCF_013140855.1
WP_171740721.1	<-SIG+ABhydrolase<-RNA-Helicase||LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	859	-	Bacteroidetes	Spirosoma sp. TS118	hypothetical protein [Spirosoma sp. TS118].	GCF_013127955.1
WP_171801965.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	907	-	Gammaproteobacteria	Vibrio europaeus	GTP-binding protein [Vibrio europaeus].	GCF_013154935.1
WP_171971806.1	LRR-repeats+AP-GTPase+COR+TM+TM*→	LRR-repeats+AP-GTPase+COR+TM+TM	850	-	Cyanobacteria	Limnothrix rosea	leucine-rich repeat domain-containing protein [Limnothrix rosea].	GCF_001904615.1
WP_171976623.1	LRR-repeats+AP-GTPase+COR+TIR*→||<-?||?→||<-?||NUDIX→?→||<-Arginase	LRR-repeats+AP-GTPase+COR+TIR	1029	-	Cyanobacteria	Brasilonema octagenarum	leucine-rich repeat domain-containing protein [Brasilonema octagenarum].	GCF_006968915.1
WP_171977678.1	<-SIG+TM+TM+Calcineurin||?→?→?→ LRR-repeats→ LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	817	-	Cyanobacteria	Brasilonema octagenarum	leucine-rich repeat domain-containing protein [Brasilonema octagenarum].	GCF_006968915.1
WP_171982135.1	LRR-repeats+AP-GTPase+COR+TIR*→||<-?<-?<-MarR-HTH||?→||<-MarR-HTH<-?||Thioredoxin→	LRR-repeats+AP-GTPase+COR+TIR	1247	-	Betaproteobacteria	Aquaspirillum sp. LM1	leucine-rich repeat domain-containing protein [Aquaspirillum sp. LM1].	GCF_002002905.1
WP_171982185.1	<-LexA-protease||?→||<-?<-?||?→ HSP70→ DNAJ→ PSE→ LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	916	-	Betaproteobacteria	Aquaspirillum sp. LM1	leucine-rich repeat domain-containing protein [Aquaspirillum sp. LM1].	GCF_002002905.1

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WP_172187602.1	Chromo-N+CHROMO→||<-RelE-ParE<-?||?→ LRR-repeats+AP-GTPase+COR*→?→ SIG+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM→	LRR-repeats+AP-GTPase+COR	913	-	Cyanobacteria	Microcoleus sp. IPMA8	leucine-rich repeat domain-containing protein [Microcoleus sp. IPMA8].	GCF_013179805.1
WP_172195227.1	LRR-repeats+AP-GTPase+COR+TIR*→||<-?||?→||<-?||NUDIX→?→||<-Arginase	LRR-repeats+AP-GTPase+COR+TIR	1029	-	Cyanobacteria	Brasilonema sennae	leucine-rich repeat domain-containing protein [Brasilonema sennae].	GCF_006968745.1
WP_172195319.1	<-SIG+TM+TM+Calcineurin||?→?→?→ LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1330	-	Cyanobacteria	Brasilonema sennae	leucine-rich repeat domain-containing protein [Brasilonema sennae].	GCF_006968745.1
WP_172621632.1	LRR-repeats+AP-GTPase+COR+TIR*→||<-?||?→?→?→?→||<-?||cNMPBD→	LRR-repeats+AP-GTPase+COR+TIR	975	-	Bacteroidetes	Chitinophaga pinensis	TIR domain-containing protein [Chitinophaga pinensis].	GCF_902167305.1
WP_172622229.1	LRR-repeats+AP-GTPase+COR+TIR*→||<-?||?→?→?→?→||<-?||cNMPBD→	LRR-repeats+AP-GTPase+COR+TIR	975	-	Bacteroidetes	Chitinophaga pinensis	TIR domain-containing protein [Chitinophaga pinensis].	GCF_902167325.1
WP_172632369.1	REC→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1102	-	Chloroflexi	Dictyobacter sp. Uno17	leucine-rich repeat domain-containing protein [Dictyobacter sp. Uno17].	GCF_008326305.1
WP_173012781.1	LRR-repeats+AP-GTPase+COR+TIR*→||<-ParB<-ParA-Soj-PloopNTPase	LRR-repeats+AP-GTPase+COR+TIR	751	-	Alphaproteobacteria	Niveispirillum sp. SYP-B3756	TIR domain-containing protein [Niveispirillum sp. SYP-B3756].	GCF_009495745.1
WP_173037887.1	<-SIG+TM<-?<-ABC-ATPase||?→?→?→?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	981	-	Actinobacteria	Phytohabitans flavus	hypothetical protein [Phytohabitans flavus].	GCF_011764545.1
WP_173124261.1	Cluster1612_2clades→?→?→||<-?<-?||LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1244	-	Actinobacteria	Kibdelosporangium persicum	leucine-rich repeat domain-containing protein [Kibdelosporangium persicum].	GCF_013280595.1
WP_173803276.1	LRR-repeats+AP-GTPase+COR+TIR*→||<-?<-ABC_membrane+ABC_tran||Cyanophycinsyn-ATPgrasp→ Cyanophycinsyn-ATPgrasp→	LRR-repeats+AP-GTPase+COR+TIR	794	-	Betaproteobacteria	Leptothrix sp. C29	TIR domain-containing protein, partial [Leptothrix sp. C29].	GCF_013294065.1
WP_174565117.1	LRR-repeats+AP-GTPase*→	LRR-repeats+AP-GTPase	485	-	Bacteroidetes	Flavobacterium sp. A45	leucine-rich repeat domain-containing protein, partial [Flavobacterium sp. A45].	GCF_002001005.1
WP_174708182.1	PAS+HISKIN→ REC→?→?→ LRR-repeats+AP-GTPase+COR+DUF4404*→||<-?||?→?→ ABC_membrane+ABC_tran→ ABC_membrane+ABC_tran→	LRR-repeats+AP-GTPase+COR+DUF4404	1122	-	Cyanobacteria	Nostoc sp. TCL240-02	leucine-rich repeat domain-containing protein [Nostoc sp. TCL240-02].	GCF_013343235.1
WP_174708278.1	ABhydrolase→?→||<-?||LRR-repeats→ PSE→ LRR-repeats+AP-GTPase+COR+TIR*→?→||<-?<-SIG+NUDIX	LRR-repeats+AP-GTPase+COR+TIR	919	-	Cyanobacteria	Nostoc sp. TCL240-02	leucine-rich repeat domain-containing protein [Nostoc sp. TCL240-02].	GCF_013343235.1
WP_174709624.1	<-Arginase<-?||LRR-repeats+AP-GTPase+COR+TIR→ *LRR-repeats+AP-GTPase+COR+TIR*→?→||<-ABC-ATPase	LRR-repeats+AP-GTPase+COR+TIR	1126	-	Cyanobacteria	Nostoc sp. TCL240-02	leucine-rich repeat domain-containing protein [Nostoc sp. TCL240-02].	GCF_013343235.1
WP_174709625.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1123	-	Cyanobacteria	Nostoc sp. TCL240-02	leucine-rich repeat domain-containing protein [Nostoc sp. TCL240-02].	GCF_013343235.1
WP_174711091.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1189	-	Cyanobacteria	Nostoc sp. TCL240-02	leucine-rich repeat domain-containing protein [Nostoc sp. TCL240-02].	GCF_013343235.1
WP_174712042.1	LRR-repeats+AP-GTPase+COR*→?→||<-?||?→||<-?||?→ ClpABN-AAA+ClpABC-AAA→	LRR-repeats+AP-GTPase+COR	967	-	Cyanobacteria	Nostoc sp. TCL240-02	leucine-rich repeat domain-containing protein [Nostoc sp. TCL240-02].	GCF_013343235.1
WP_175357678.1	Cluster54_3clades→?→ RelE-ParE→ Cluster53_2clades→?→ LRR-repeats+AP-GTPase+COR*→?→?→?→||<-?||?→||<-Pentapeptide-repeats	LRR-repeats+AP-GTPase+COR	928	-	Cyanobacteria	Pseudanabaena biceps	leucine-rich repeat domain-containing protein [Pseudanabaena biceps].	GCF_013361095.1
WP_175471885.1	Mbetalac→?→ LRR-repeats+AP-GTPase+COR*→||<-?<-ICLR-HTH||?→?→?→ ABhydrolase→	LRR-repeats+AP-GTPase+COR	886	-	Actinobacteria	Geodermatophilus telluris	hypothetical protein [Geodermatophilus telluris].	GCF_900102745.1

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WP_175586865.1	<-HISKIN||?→||<-?||?→?→ PSE→||<-?||PSE→||<-?||LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	868	-	Cyanobacteria	Nostoc sp. UIC 10630	leucine-rich repeat domain-containing protein, partial [Nostoc sp. UIC 10630].	GCF_010747425.1
WP_175608776.1	LRR-repeats+AP-GTPase+COR+TIR*→?→?→?→?→?→ TIR→ TM+TM+TM→	LRR-repeats+AP-GTPase+COR+TIR	1128	-	Bacteroidetes	Chryseobacterium gambrini	leucine-rich repeat domain-containing protein [Chryseobacterium gambrini].	GCF_900156825.1
WP_176159351.1	METHYLASE→?→||<-?||SIG+Trypsin+PDZ→?→ Cluster978_2clades→ LRR-repeats+AP-GTPase+COR+TIR*→?→ GDSL→	LRR-repeats+AP-GTPase+COR+TIR	813	-	Verrucomicrobia	Prosthecobacter debontii	TIR domain-containing protein [Prosthecobacter debontii].	GCF_900167535.1
WP_176159465.1	SAM-methylase→?→||<-?<-SIG+ABhydrolase||tRNA→?→ Cluster1685_2clades→||<-?||LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	949	-	Verrucomicrobia	Prosthecobacter debontii	leucine-rich repeat domain-containing protein [Prosthecobacter debontii].	GCF_900167535.1
WP_176722277.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	881	-	Gammaproteobacteria	Candidatus Thiosymbion oneisti	leucine-rich repeat domain-containing protein, partial [Candidatus Thiosymbion oneisti].	GCF_900092655.1
WP_176722477.1	LRR-repeats+AP-GTPase+COR*→?→ PSE→?→?→?→ ABC-ATPase→||<-HTH	LRR-repeats+AP-GTPase+COR	838	-	Gammaproteobacteria	Candidatus Thiosymbion oneisti	hypothetical protein [Candidatus Thiosymbion oneisti].	GCF_900092655.1
WP_177187116.1	LRR-repeats+AP-GTPase+COR*→||<-?||?→||<-RnasePH+RnasePH+KH+S1	LRR-repeats+AP-GTPase+COR	911	-	Bacteroidetes	Chryseobacterium jeonii	GTP-binding protein [Chryseobacterium jeonii].	GCF_900112115.1
WP_177199908.1	PRTase→||<-?<-?<-?||LRR-repeats+AP-GTPase+COR+TIR*→?→?→?→?→ Aminotran_1_2→	LRR-repeats+AP-GTPase+COR+TIR	987	-	Bacteroidetes	Flexibacter flexilis	leucine-rich repeat domain-containing protein [Flexibacter flexilis].	GCF_900112255.1
WP_177201087.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	764	-	Gammaproteobacteria	Neptunomonas qingdaonensis	TIR domain-containing protein [Neptunomonas qingdaonensis].	GCF_900113275.1
WP_178133228.1	LRR-repeats+AP-GTPase+COR+CASPASE*→	LRR-repeats+AP-GTPase+COR+CASPASE	1170	-	Alphaproteobacteria	Enhydrobacter sp. CC-CFT640	CHAT domain-containing protein [Enhydrobacter sp. CC-CFT640].	GCF_008039615.1
WP_178316998.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1450	-	Firmicutes	Lachnospiraceae bacterium	GTP-binding protein [Lachnospiraceae bacterium].	-
WP_179047135.1	ABC-ATPase→||<-?||?→||<-?||LRR-repeats+AP-GTPase+COR+TIR*→?→||<-?<-Cluster1974_2clades||?→?→||<-PSE<-Cluster1515_2clades	LRR-repeats+AP-GTPase+COR+TIR	939	-	Cyanobacteria	Nostoc sp. TCL26-01	leucine-rich repeat domain-containing protein [Nostoc sp. TCL26-01].	GCF_013393945.1
WP_179049659.1	Cluster1081_2clades→?→?→||<-?<-PSE<-?||LRR-repeats+AP-GTPase+COR+TIR*→||<-?<-MoxR-AAA||?→ TPR-repeats→||<-SIG+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM<-SIG+TM	LRR-repeats+AP-GTPase+COR+TIR	1127	-	Cyanobacteria	Nostoc sp. TCL26-01	leucine-rich repeat domain-containing protein [Nostoc sp. TCL26-01].	GCF_013393945.1
WP_179049876.1	<-ACET<-?||Pentapeptide→ Cluster54_3clades→ Cluster1093_2clades→?→||<-?||LRR-repeats+AP-GTPase+COR+TIR*→?→?→ HNH→?→ PSE→||<-?<-?<-Cluster2062_2clades	LRR-repeats+AP-GTPase+COR+TIR	1116	-	Cyanobacteria	Nostoc sp. TCL26-01	leucine-rich repeat domain-containing protein [Nostoc sp. TCL26-01].	GCF_013393945.1
WP_179050104.1	<-ABC_membrane+ABC_tran<-?<-?||?→||<-?<-?||LRR-repeats+AP-GTPase+COR+TIR*→?→||<-?<-?<-?<-?<-Cluster2103_2clades	LRR-repeats+AP-GTPase+COR+TIR	999	-	Cyanobacteria	Nostoc sp. TCL26-01	leucine-rich repeat domain-containing protein [Nostoc sp. TCL26-01].	GCF_013393945.1
WP_179067421.1	REC→ REC→?→||<-?||LRR-repeats+AP-GTPase+COR+DUF4404*→	LRR-repeats+AP-GTPase+COR+DUF4404	1124	-	Cyanobacteria	Nostoc sp. C052	leucine-rich repeat domain-containing protein [Nostoc sp. C052].	GCF_013393905.1
WP_179068637.1	Cluster5_5clades→ Cluster5_5clades→ LRR-repeats+AP-GTPase+COR+TM+TM*→||<-?||Pkinase→	LRR-repeats+AP-GTPase+COR+TM+TM	904	-	Cyanobacteria	Nostoc sp. C052	leucine-rich repeat protein [Nostoc sp. C052].	GCF_013393905.1
WP_179072263.1	TPR-repeats→?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1193	-	Cyanobacteria	Nostoc sp. C057	leucine-rich repeat domain-containing protein [Nostoc sp. C057].	GCF_013393925.1
WP_179072929.1	<-Arginase<-?||?→ LRR-repeats+AP-GTPase+COR+TIR*→?→||<-?||?→?→?→||<-tRNA||Cluster1742_2clades→	LRR-repeats+AP-GTPase+COR+TIR	1009	-	Cyanobacteria	Nostoc sp. C057	leucine-rich repeat domain-containing protein [Nostoc sp. C057].	GCF_013393925.1

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WP_179074744.1	Cluster5_5clades→ Cluster5_5clades→ LRR-repeats+AP-GTPase+COR+TM+TM*→||<-CASPASE+TM	LRR-repeats+AP-GTPase+COR+TM+TM	865	-	Cyanobacteria	Nostoc sp. C057	leucine-rich repeat domain-containing protein [Nostoc sp. C057].	GCF_013393925.1
WP_179212721.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	850	-	Bacteroidetes	Sphingobacteriales bacterium TSM_CSS	GTP-binding protein [Sphingobacteriales bacterium TSM_CSS].	-
WP_180284786.1	<-MarR-HTH||?→ SIG+TM+TM+TM+TM+TM+TM+TM→ SIG+TM+TM+TM+TM+TM+TM+TM→ ABC-ATPase→ ABC-ATPase→?→ LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	709	-	Alphaproteobacteria	Azospirillum oleiclasticum	hypothetical protein [Azospirillum oleiclasticum].	GCF_013423495.1
WP_180287677.1	SbcC→?→ LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	722	-	Alphaproteobacteria	Azospirillum oleiclasticum	hypothetical protein [Azospirillum oleiclasticum].	GCF_013423485.1
WP_180693101.1	LRR-repeats+AP-GTPase+COR+TIR*→||<-?<-ABC_membrane+ABC_tran||Cyanophycinsyn-ATPgrasp→ Cyanophycinsyn-ATPgrasp→	LRR-repeats+AP-GTPase+COR+TIR	904	-	Betaproteobacteria	Sphaerotilus natans	leucine-rich repeat domain-containing protein, partial [Sphaerotilus natans].	GCF_013426975.1
WP_181245610.1	TM→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1035	-	Actinobacteria	Glycomyces artemisiae	leucine-rich repeat domain-containing protein [Glycomyces artemisiae].	GCF_003002955.1
WP_181357317.1	<-REC||REC→||<-?<-?<-?<-TIR+TM+CHASE2+CHASE2+TM+TM+TM||LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1082	-	Cyanobacteria	Stenomitos frigidus	leucine-rich repeat domain-containing protein [Stenomitos frigidus].	GCF_003003795.1
WP_181842201.1	VWA+vWA-L+LRR-repeats+AP-GTPase+COR+TIR*→	VWA+vWA-L+LRR-repeats+AP-GTPase+COR+TIR	1607	-	Bacteroidetes	Emticicia sp. BO119	leucine-rich repeat domain-containing protein [Emticicia sp. BO119].	GCF_013912375.1
WP_181930367.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1084	-	Cyanobacteria	Nostoc edaphicum	leucine-rich repeat domain-containing protein [Nostoc edaphicum].	GCF_014023275.1
WP_181931253.1	<-Pkinase+Pentapeptide<-?<-?<-?||?→ LRR-repeats+AP-GTPase+COR+TIR*→||<-Cluster5_5clades<-Arginase<-?||?→||<-?<-?||Cluster54_3clades→	LRR-repeats+AP-GTPase+COR+TIR	1046	-	Cyanobacteria	Nostoc edaphicum	leucine-rich repeat domain-containing protein [Nostoc edaphicum].	GCF_014023275.1
WP_182043976.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1134	-	Bacteroidetes	Moheibacter sp. BDHS18	leucine-rich repeat domain-containing protein [Moheibacter sp. BDHS18].	GCF_014042165.1
WP_182891755.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	1689	-	Actinobacteria	Amycolatopsis sp. DR6-1	hypothetical protein [Amycolatopsis sp. DR6-1].	GCF_014145675.1
WP_183290945.1	<-SIG+ABhydrolase||?→?→?→?→||<-?<-?||LRR-repeats+AP-GTPase+COR+TIR→ *LRR-repeats+AP-GTPase+COR+TIR*→?→ Cluster1478_2clades→?→ LRR-repeats+AP-GTPase+COR+TIR*→?→ SIGMA-HTH→ SIGMA-HTH→	LRR-repeats+AP-GTPase+COR+TIR	1386	-	Bacteroidetes	Chitinophaga sancti	leucine-rich repeat domain-containing protein [Chitinophaga sancti].	GCF_014190745.1
WP_183290948.1	LRR-repeats+AP-GTPase+COR_TIR*→	LRR-repeats+AP-GTPase+COR_TIR	1378	-	Bacteroidetes	Chitinophaga sancti	TIR domain-containing protein [Chitinophaga sancti].	GCF_014190745.1
WP_183290949.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1391	-	Bacteroidetes	Chitinophaga sancti	hypothetical protein [Chitinophaga sancti].	GCF_014190745.1
WP_183974348.1	FGS→ FGS→ FGS→ LRR-repeats+AP-GTPase+COR+CASPASE*→	LRR-repeats+AP-GTPase+COR+CASPASE	981	-	Bacteroidetes	Runella defluvii	hypothetical protein [Runella defluvii].	GCF_014195535.1
WP_183975497.1	<-SIGMA-HTH||SIG+ABhydrolase→ LRR-repeats+AP-GTPase+COR*→?→||<-?<-?<-?<-?<-?<-SIGMA-HTH	LRR-repeats+AP-GTPase+COR	999	-	Bacteroidetes	Runella defluvii	leucine-rich repeat domain-containing protein [Runella defluvii].	GCF_014195535.1
WP_183978441.1	TIR+TPR+TPR-S→||<-?<-?||?→||<-?||LRR-repeats+AP-GTPase+COR+TIR→*?→ TPR-repeats→?→ TPR-repeats→?→||<-AP-GTPase+COR*<-?<-HTH	LRR-repeats+AP-GTPase+COR+TIR	603	-	Bacteroidetes	Runella defluvii	hypothetical protein [Runella defluvii].	GCF_014195535.1
WP_183978452.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1000	-	Bacteroidetes	Runella defluvii	leucine-rich repeat domain-containing protein [Runella defluvii].	GCF_014195535.1
WP_184494281.1	Cluster1244_2clades→?→ Cluster1291_2clades→ TIR+LRR-repeats+AP-GTPase+TIR*→||<-?<-?<-?||REC→	TIR+LRR-repeats+AP-GTPase+TIR	1102	-	Bacteroidetes	Algoriphagus iocasae	TIR domain-containing protein [Algoriphagus iocasae].	GCF_014206875.1

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
WP_184831163.1	SIG+TM+TM+TM+TM+TM→||<-?||?→?→?→?→ PSE→ LRR-repeats+AP-GTPase+COR*→||<-?<-?||wHTH-4stranded+TPRs+APATPase+TPR-repeats→	LRR-repeats+AP-GTPase+COR	802	-	Actinobacteria	Allocatelliglobosispora scoriae	hypothetical protein [Allocatelliglobosispora scoriae].	GCF_014204945.1
WP_184846103.1	LRR-repeats+AP-GTPase+COR*→||<-?<-?<-?<-BACTERIALFRINGE+TM+TM	LRR-repeats+AP-GTPase+COR	1247	-	Actinobacteria	Allocatelliglobosispora scoriae	leucine-rich repeat domain-containing protein [Allocatelliglobosispora scoriae].	GCF_014204945.1
WP_184892074.1	LRR-repeats+AP-GTPase+COR*→?→?→ REC→ HISKIN→	LRR-repeats+AP-GTPase+COR	1463	-	Actinobacteria	Streptomyces scabiei	leucine-rich repeat domain-containing protein [Streptomyces scabiei].	GCF_014203845.1
WP_184930759.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	954	-	Actinobacteria	Streptomyces sp. SFB5A	hypothetical protein [Streptomyces sp. SFB5A].	GCF_014203895.1
WP_184953474.1	GNTR-HTH→||<-?||REC→ REC→?→ LRR-repeats+AP-GTPase+COR+TIR*→||<-35exo	LRR-repeats+AP-GTPase+COR+TIR	1043	-	Actinobacteria	Actinoplanes abujensis	TIR domain-containing protein [Actinoplanes abujensis].	GCF_016861995.1
WP_185097769.1	LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	901	-	Bacteroidetes	Elizabethkingia anophelis	leucine-rich repeat domain-containing protein [Elizabethkingia anophelis].	GCF_001703835.1
WP_185204695.1	Cluster1364_2clades→?→?→?→?→?→?→ LRR-repeats+AP-GTPase+COR*→||<-Cyanophycinsyn-ATPgrasp	LRR-repeats+AP-GTPase+COR	1038	-	Bacteroidetes	Chryseobacterium sp. C3	leucine-rich repeat protein [Chryseobacterium sp. C3].	GCF_014218905.1
WP_185236942.1	LRR-repeats+AP-GTPase+COR+TM+TM*→	LRR-repeats+AP-GTPase+COR+TM+TM	828	-	Cyanobacteria	Microcystis aeruginosa	leucine-rich repeat protein [Microcystis aeruginosa].	GCF_014218745.1
WP_185240111.1	SAM-methylase→?→||<-?<-SIG+TPM_phosphatase+TM+TM+TM||LRR-repeats+AP-GTPase+COR+TM+TM*→||<-?<-?<-?||?→||<-Pro_CA	LRR-repeats+AP-GTPase+COR+TM+TM	874	-	Cyanobacteria	Microcystis aeruginosa	leucine-rich repeat protein [Microcystis aeruginosa].	GCF_014218765.1
WP_185478866.1	<-Cluster5_5clades||LRR-repeats+AP-GTPase+COR+DUF4404*→	LRR-repeats+AP-GTPase+COR+DUF4404	1084	-	Cyanobacteria	Trichormus variabilis	leucine-rich repeat domain-containing protein [Trichormus variabilis].	GCF_014222125.1
WP_185479669.1	LRR-repeats+AP-GTPase+COR+DUF4404*→||<-?<-ABC-ATPase<-?||?→||<-REC	LRR-repeats+AP-GTPase+COR+DUF4404	866	-	Cyanobacteria	Trichormus variabilis	leucine-rich repeat domain-containing protein, partial [Trichormus variabilis].	GCF_014222155.1
WP_185482851.1	<-Cluster5_5clades||LRR-repeats+AP-GTPase+COR+DUF4404*→||<-?<-ABC-ATPase<-?||?→||<-REC	LRR-repeats+AP-GTPase+COR+DUF4404	1084	-	Cyanobacteria	Trichormus variabilis	leucine-rich repeat domain-containing protein [Trichormus variabilis].	GCF_014222225.1
WP_185499823.1	<-Cluster5_5clades||LRR-repeats+AP-GTPase+COR+DUF4404*→||<-?<-ABC-ATPase<-?||?→||<-REC	LRR-repeats+AP-GTPase+COR+DUF4404	1199	-	Cyanobacteria	Trichormus variabilis	leucine-rich repeat domain-containing protein [Trichormus variabilis].	GCF_014222145.1
WP_185505742.1	<-Cluster5_5clades||LRR-repeats+AP-GTPase+COR+DUF4404*→||<-?<-ABC-ATPase<-?||?→||<-REC	LRR-repeats+AP-GTPase+COR+DUF4404	992	-	Cyanobacteria	Trichormus variabilis	leucine-rich repeat domain-containing protein [Trichormus variabilis].	GCF_014222245.1
WP_185539469.1	LRR-repeats+AP-GTPase+COR+DUF4404*→||<-?<-ABC-ATPase<-?||?→||<-REC	LRR-repeats+AP-GTPase+COR+DUF4404	895	-	Cyanobacteria	Trichormus variabilis	leucine-rich repeat domain-containing protein, partial [Trichormus variabilis].	GCF_014222135.1
WP_185567106.1	LRR-repeats+AP-GTPase+COR+TM+TM*→||<-CASPASE+TM	LRR-repeats+AP-GTPase+COR+TM+TM	862	-	Cyanobacteria	Nostoc sp. 2RC	leucine-rich repeat domain-containing protein [Nostoc sp. 2RC].	GCF_014222165.1
WP_185570121.1	PIN→ LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1020	-	Cyanobacteria	Nostoc sp. 2RC	leucine-rich repeat domain-containing protein [Nostoc sp. 2RC].	GCF_014222165.1
WP_185579937.1	ABhydrolase→?→||<-?||COR+TIR→ LRR-repeats+AP-GTPase+COR+TIR*→?→||<-PIN<-?<-?<-SIG+NUDIX	LRR-repeats+AP-GTPase+COR+TIR	1003	-	Cyanobacteria	unclassified Nostoc	MULTISPECIES: leucine-rich repeat domain-containing protein [unclassified Nostoc].	GCF_014222255.1
WP_185580380.1	Cluster5_5clades→ LRR-repeats+AP-GTPase+COR+TIR*→||<-CASPASE+TM	LRR-repeats+AP-GTPase+COR+TIR	893	-	Cyanobacteria	unclassified Nostoc	MULTISPECIES: leucine-rich repeat domain-containing protein [unclassified Nostoc].	GCF_014222255.1

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
WP_185583983.1	<-PIN<-?<-?||?→?→||<-Arginase<-?||LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	358	-	Cyanobacteria	Nostoc sp. UCD120	leucine-rich repeat domain-containing protein, partial [Nostoc sp. UCD120].	GCF_014222255.1
WP_185584434.1	PAS+HISKIN→ REC→ PSE→?→?→?→ LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1163	-	Cyanobacteria	Nostoc sp. UCD120	leucine-rich repeat domain-containing protein [Nostoc sp. UCD120].	GCF_014222255.1
WP_185591915.1	<-PIN<-?<-?||?→?→||<-Arginase<-?||LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	802	-	Cyanobacteria	Nostoc sp. UCD122	leucine-rich repeat domain-containing protein [Nostoc sp. UCD122].	GCF_014222275.1
WP_185592013.1	ABhydrolase→?→||<-?||COR+TIR→ LRR-repeats+AP-GTPase+COR+TIR*→?→||<-PIN	LRR-repeats+AP-GTPase+COR+TIR	1003	-	Cyanobacteria	Nostoc sp. UCD122	leucine-rich repeat domain-containing protein [Nostoc sp. UCD122].	GCF_014222275.1
WP_185592050.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	859	-	Cyanobacteria	Nostoc sp. UCD122	leucine-rich repeat domain-containing protein, partial [Nostoc sp. UCD122].	GCF_014222275.1
WP_185592512.1	Cluster5_5clades→ LRR-repeats+AP-GTPase+COR+TIR*→||<-CASPASE+TM	LRR-repeats+AP-GTPase+COR+TIR	893	-	Cyanobacteria	Nostoc sp. UCD122	leucine-rich repeat domain-containing protein [Nostoc sp. UCD122].	GCF_014222275.1
WP_185607149.1	<-PIN<-?<-?||?→?→||<-Arginase<-?||LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	825	-	Cyanobacteria	Nostoc sp. UCD121	leucine-rich repeat domain-containing protein [Nostoc sp. UCD121].	GCF_014222285.1
WP_185607288.1	LRR-repeats+AP-GTPase+COR+TIR*→?→?→?→ ABC_membrane+ABC_tran→ ABC_membrane+ABC_tran→	LRR-repeats+AP-GTPase+COR+TIR	917	-	Cyanobacteria	Nostoc sp. UCD121	leucine-rich repeat domain-containing protein, partial [Nostoc sp. UCD121].	GCF_014222285.1
WP_186435859.1	<-Cluster1077_2clades||Aminotran_1_2→?→||<-?<-?||?→ LRR-repeats+AP-GTPase+COR*→	LRR-repeats+AP-GTPase+COR	980	-	Gammaproteobacteria	Thalassolituus sp. C2-1	GTP-binding protein [Thalassolituus sp. C2-1].	GCF_007785795.1
WP_186890728.1	<-Cluster1951_2clades<-?<-?||?→ SIG+TM+TM+TM+HISKIN→?→||<-?||LRR-repeats+AP-GTPase+COR+DrHyd*→||<-?<-REC	LRR-repeats+AP-GTPase+COR+DrHyd	1036	-	Betaproteobacteria	Undibacterium amnicola	hypothetical protein [Undibacterium amnicola].	GCF_014284275.1
WP_186956531.1	LRR-repeats+AP-GTPase+COR+TIR*→	LRR-repeats+AP-GTPase+COR+TIR	1232	-	Betaproteobacteria	Undibacterium sp. NL8W	leucine-rich repeat domain-containing protein [Undibacterium sp. NL8W].	GCF_014284125.1
WP_187308183.1	LRR-repeats+AP-GTPase+COR+TM+TM*→||<-?<-?||?→?→||<-?<-?<-SNF	LRR-repeats+AP-GTPase+COR+TM+TM	720	-	Cyanobacteria	Nostoc cycadae	leucine-rich repeat domain-containing protein, partial [Nostoc cycadae].	GCF_002897135.1
WP_187315132.1	LRR-repeats+AP-GTPase+COR*→?→?→?→||<-?<-tRNA<-?<-?<-Cluster1829_2clades	LRR-repeats+AP-GTPase+COR	914	-	Bacteroidetes	Hymenobacter sp. BT190	GTP-binding protein [Hymenobacter sp. BT190].	GCF_014333525.1
WP_187466435.1	LRR-repeats+AP-GTPase+COR+EAD11→*?→?→ LRR-repeats+AP-GTPase+COR+EAD11*→	LRR-repeats+AP-GTPase+COR+EAD11	1040	-	Bacteroidetes	Lewinella lacunae	leucine-rich repeat domain-containing protein [Lewinella lacunae].	GCF_014349155.1
WP_187466438.1	LRR-repeats+AP-GTPase+COR+EAD11*→	LRR-repeats+AP-GTPase+COR+EAD11	931	-	Bacteroidetes	Lewinella lacunae	leucine-rich repeat domain-containing protein [Lewinella lacunae].	GCF_014349155.1
WP_187467589.1	GTPase-AIG→||<-?||?→?→||<-?<-?<-?||LRR-repeats+AP-GTPase+COR+CASPASE*→?→ FGS→?→ RVT→?→ FGS→	LRR-repeats+AP-GTPase+COR+CASPASE	1063	-	Bacteroidetes	Lewinella lacunae	CHAT domain-containing protein [Lewinella lacunae].	GCF_014349155.1
WP_187560609.1	SIGMA-HTH→?→ RADICAL-SAM→ LRR-repeats+AP-GTPase+COR+TIR*→?→ HISKIN→	LRR-repeats+AP-GTPase+COR+TIR	970	-	Bacteroidetes	Kordia sp. YSTF-M3	leucine-rich repeat domain-containing protein [Kordia sp. YSTF-M3].	GCF_014397005.1
WP_187775535.1	HTH→?→?→ LRR-repeats+AP-GTPase+COR+TIR*→||<-?<-ABC_membrane+ABC_tran||Cyanophycinsyn-ATPgrasp→ Cyanophycinsyn-ATPgrasp→	LRR-repeats+AP-GTPase+COR+TIR	1298	-	Betaproteobacteria	Sphaerotilus natans	leucine-rich repeat domain-containing protein [Sphaerotilus natans].	GCF_008329925.1

Gene neighborhoods and domain architectures of APGTPases whose LRR domains are either absent or not detected

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
AAP36207.1	AP-GTPase*→	AP-GTPase	220	-	-	synthetic construct	Homo sapiens RAB3D, member RAS oncogene family, partial [synthetic construct].	-
AAP36967.1	AP-GTPase*→	AP-GTPase	208	-	-	synthetic construct	Homo sapiens mel transforming oncogene (derived from cell line NK14)- RAB8 homolog, partial [synthetic construct].	-
AAV38505.1	AP-GTPase*→	AP-GTPase	204	-	-	synthetic construct	RAB13, member RAS oncogene family, partial [synthetic construct].	-
AAX32379.1	AP-GTPase*→	AP-GTPase	207	MEL	-	synthetic construct	RAB8A [synthetic construct].	-
AAX36766.1	AP-GTPase*→	AP-GTPase	204	RAB13	-	synthetic construct	RAB13 member RAS oncogene family, partial [synthetic construct].	-
AAX41198.1	AP-GTPase*→	AP-GTPase	203	RAB13	-	synthetic construct	RAB13 member RAS oncogene family [synthetic construct].	-
AAX42776.1	AP-GTPase*→	AP-GTPase	204	RAB13	-	synthetic construct	RAB13 member RAS oncogene family, partial [synthetic construct].	-
ABG50724.1	vWA-L+AP-GTPase+COR*→	vWA-L+AP-GTPase+COR	748	Tery_1428	Cyanobacteria	Trichodesmium erythraeum IMS101	Miro-like [Trichodesmium erythraeum IMS101].	GCA_000014265.1
ABW29719.1	AP-GTPase+ZNR*→	AP-GTPase+ZNR	705	AM1_4747	Cyanobacteria	Acaryochloris marina MBIC11017	conserved hypothetical protein [Acaryochloris marina MBIC11017].	GCA_000018105.1
ACL85629.1	AP-GTPase*→	AP-GTPase	204	Rab10	-	Drosophila melanogaster	Rab10-PA, partial [synthetic construct].	-
ACL86538.1	AP-GTPase*→	AP-GTPase	223	Rab30	-	Drosophila melanogaster	Rab30-PA, partial [synthetic construct].	-
ADQ32831.1	AP-GTPase*→	AP-GTPase	219	RAB3B	-	Homo sapiens	RAB3B, member RAS oncogene family, partial [synthetic construct].	-
AFZ01290.1	<-EAD10+VMAP-M1+VMAP-C||?→ CASPASE+EAD10→ EAD10+VMAP-M1+VMAP-C→?→ VWA+AP-GTPase+COR*→	VWA+AP-GTPase+COR	1196	Cal6303_2274	Cyanobacteria	Calothrix sp. PCC 6303	Miro domain protein [Calothrix sp. PCC 6303].	GCA_000317435.1
AIC55004.1	AP-GTPase*→	AP-GTPase	219	-	-	Homo sapiens	RAB3B, partial [synthetic construct].	-
AIC55612.1	AP-GTPase*→	AP-GTPase	219	-	-	Homo sapiens	RAB3D, partial [synthetic construct].	-
ASF48224.1	AP-GTPase+COR+DUF4404*→	AP-GTPase+COR+DUF4404	879	CEK71_20365	Gammaproteobacteria	Methylovulum psychrotolerans	hypothetical protein CEK71_20365 [Methylovulum psychrotolerans].	GCA_002209385.1
ATO96390.1	AP-GTPase*→	AP-GTPase	207	rab8b	-	Xenopus tropicalis	RAB8B, member RAS oncoprotein family, partial [synthetic construct].	-

acc	operon	architecture	len	gen.name	taxend	species	defline	gca
CCQ62557.1	AP-GTPase+COR*→	AP-GTPase+COR	279	CWATWH0401_4507	Cyanobacteria	Crocosphaera watsonii WH 0401	Leucine-rich repeat [Crocosphaera watsonii WH 0401].	GCA_001039615.1
CCZ82707.1	AP-GTPase+COR*→	AP-GTPase+COR	843	BN709_01979	Bacteroidetes	Odoribacter laneus CAG:561	putative uncharacterized protein [Odoribacter laneus CAG:561].	GCA_000432935.1
HAA12500.1	AP-GTPase+COR*→	AP-GTPase+COR	908	DCE41_12685	Bacteroidetes	Cytophagales bacterium	TPA: hypothetical protein DCE41_12685 [Cytophagales bacterium].	GCA_003444355.1
HAA13307.1	AP-GTPase+COR*→	AP-GTPase+COR	878	DCE41_17110	Bacteroidetes	Cytophagales bacterium	TPA: hypothetical protein DCE41_17110 [Cytophagales bacterium].	GCA_003444355.1
HAC65063.1	DNAJ→ AP-GTPase*→ COR+TM+TM→	AP-GTPase	125	DCF68_16430	Cyanobacteria	Cyanothece sp. UBA12306	TPA: GTPase, partial [Cyanothece sp. UBA12306].	GCA_003448685.1
HAK76392.1	AP-GTPase+COR*→	AP-GTPase+COR	733	DCM71_05675	Bacteroidetes	Runella sp.	TPA: hypothetical protein DCM71_05675, partial [Runella sp.].	GCA_003452005.1
HAO21703.1	AP-GTPase*→	AP-GTPase	569	DCQ37_15290	Deltaproteobacteria	Desulfobacteraceae bacterium	TPA: hypothetical protein DCQ37_15290, partial [Desulfobacteraceae bacterium].	GCA_003456735.1
HAP58612.1	AP-GTPase+COR*→	AP-GTPase+COR	696	DCR93_03550	Bacteroidetes	Cytophagales bacterium	TPA: hypothetical protein DCR93_03550, partial [Cytophagales bacterium].	GCA_003454975.1
HAP62400.1	AP-GTPase+COR*→?→ cNMPBD→ SIG+Phytase-like→	AP-GTPase+COR	744	DCR93_23850	Bacteroidetes	Cytophagales bacterium	TPA: hypothetical protein DCR93_23850 [Cytophagales bacterium].	GCA_003454975.1
HCS91914.1	TIR+BetaPropeller+AP-GTPase*→	TIR+BetaPropeller+AP-GTPase	1236	DIW77_18260	Gammaproteobacteria	Chromatiaceae bacterium	TPA: hypothetical protein DIW77_18260 [Chromatiaceae bacterium].	GCA_003525925.1
HEY83669.1	AP-GTPase+COR*→	AP-GTPase+COR	260	G4N96_00950	Chloroflexi	Chloroflexi bacterium	TPA: hypothetical protein G4N96_00950 [Chloroflexi bacterium].	GCA_011192195.1
HEY85168.1	AP-GTPase*→	AP-GTPase	319	G4N96_08685	Chloroflexi	Chloroflexi bacterium	TPA: hypothetical protein G4N96_08685 [Chloroflexi bacterium].	GCA_011192195.1
HFS11412.1	BetaPropeller+AP-GTPase+TIR*→?→||<-?||?→?→||<-SIG+PSBP	BetaPropeller+AP-GTPase+TIR	1179	ENR14_24625	Cyanobacteria	Anabaena sp.	TPA: TIR domain-containing protein [Anabaena sp.].	GCA_011332035.1
HGZ32338.1	AP-GTPase+COR*→	AP-GTPase+COR	503	ENR17_19310	Bacteroidetes	Bacteroidetes bacterium	TPA: GTPase, partial [Bacteroidetes bacterium].	GCA_011331955.1
HHN34802.1	AP-GTPase*→	AP-GTPase	171	ENM07_01585	Bacteroidetes	Bacteroidetes bacterium	TPA: GTP-binding protein [Bacteroidetes bacterium].	GCA_011375975.1
KAB2958401.1	SIG+AP-GTPase+COR*→	SIG+AP-GTPase+COR	688	F9K13_13725	Bacteria	Candidatus Methylomirabilis oxyfera	hypothetical protein F9K13_13725 [Candidatus Methylomirabilis oxyfera].	GCA_009026205.1
KAF0250167.1	AP-GTPase+COR+Calcineurin+FGS*→	AP-GTPase+COR+Calcineurin+FGS	1237	FD167_433	unclassified Bacteria	bacterium	small GTP-binding protein, partial [bacterium].	GCA_009773835.1
KHD09711.1	AP-GTPase+COR*→	AP-GTPase+COR	530	PN36_20855	Gammaproteobacteria	Candidatus Thiomargarita nelsonii	hypothetical protein PN36_20855 [Candidatus Thiomargarita nelsonii].	GCA_000785145.2
MBC6419378.1	AP-GTPase*→ COR→	AP-GTPase	165	GDA44_11670	Cyanobacteria	Prochloron sp. SP5CPC1	hypothetical protein GDA44_11670 [Prochloron sp. SP5CPC1].	GCA_014323965.1

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NAT10406.1	AP-GTPase*→	AP-GTPase	611	C4E22_02470	Euryarchaeota	ANME-1 cluster archaeon AG-394-G06	hypothetical protein C4E22_02470 [ANME-1 cluster archaeon AG-394-G06].	GCA_009903405.1
NBO93394.1	AP-GTPase+COR*→	AP-GTPase+COR	916	EBV06_13945	Planctomycetes	Planctomycetia bacterium	hypothetical protein EBV06_13945 [Planctomycetia bacterium].	GCA_009918525.1
NBQ70341.1	TIR+AP-GTPase+COR*→	TIR+AP-GTPase+COR	582	EBU46_16510	Betaproteobacteria	Nitrosomonadaceae bacterium	TIR domain-containing protein, partial [Nitrosomonadaceae bacterium].	GCA_009919685.1
NHJ32288.1	AP-GTPase*→	AP-GTPase	230	FK732_05460	Asgard group	Asgard group archaeon	GTP-binding protein [Asgard group archaeon].	GCA_011366225.1
NIM12342.1	TIR+BetaPropeller+AP-GTPase*→	TIR+BetaPropeller+AP-GTPase	1000	GTO81_10200	Bacteria	Candidatus Aminicenantes bacterium	DUF4365 domain-containing protein [Candidatus Aminicenantes bacterium].	GCA_011771225.1
NIM12946.1	TIR+BetaPropeller+AP-GTPase*→	TIR+BetaPropeller+AP-GTPase	1108	GTO81_13270	Bacteria	Candidatus Aminicenantes bacterium	TIR domain-containing protein [Candidatus Aminicenantes bacterium].	GCA_011771225.1
NIR05736.1	TIR+BetaPropeller+AP-GTPase*→ Cluster2387_2clades→ Cluster2274_2clades→||<-Cluster2216_2clades||Cluster2371_2clades→||<-?<-?<-Cluster2251_2clades	TIR+BetaPropeller+AP-GTPase	1004	GTN82_09930	Bacteria	Candidatus Aminicenantes bacterium	DUF4365 domain-containing protein [Candidatus Aminicenantes bacterium].	GCA_011773265.1
NJL71192.1	AP-GTPase*→	AP-GTPase	248	HC888_06030	Gammaproteobacteria	Candidatus Competibacteraceae bacterium	GTP-binding protein [Candidatus Competibacteraceae bacterium].	GCA_012031515.1
NJO13505.1	AP-GTPase*→?→ TIR→	AP-GTPase	144	HC872_08630	Gammaproteobacteria	Gammaproteobacteria bacterium	hypothetical protein HC872_08630 [Gammaproteobacteria bacterium].	GCA_012032615.1
NKB62496.1	AP-GTPase+COR*→	AP-GTPase+COR	274	GKR95_10365	Gammaproteobacteria	Gammaproteobacteria bacterium	hypothetical protein GKR95_10365 [Gammaproteobacteria bacterium].	GCA_012103415.1
NLZ73760.1	AP-GTPase*→	AP-GTPase	202	GX905_08105	Bacteroidetes	Bacteroidales bacterium	hypothetical protein GX905_08105 [Bacteroidales bacterium].	GCA_012800615.1
NMC05010.1	AP-GTPase*→	AP-GTPase	190	GYA24_07360	Asgard group	Candidatus Lokiarchaeota archaeon	GTP-binding protein [Candidatus Lokiarchaeota archaeon].	GCA_012798355.1
NNJ85485.1	AP-GTPase*→	AP-GTPase	345	HKP13_11240	Gammaproteobacteria	Gammaproteobacteria bacterium	hypothetical protein HKP13_11240, partial [Gammaproteobacteria bacterium].	GCA_013042035.1
NOQ28062.1	AP-GTPase+COR*→	AP-GTPase+COR	845	GQ564_22090	Bacteroidetes	Bacteroidales bacterium	hypothetical protein GQ564_22090 [Bacteroidales bacterium].	GCA_013138975.1
NOS87668.1	AP-GTPase+COR+DUF4404*→ REase→	AP-GTPase+COR+DUF4404	775	HOP34_03865	Gammaproteobacteria	Methylococcaceae bacterium	hypothetical protein HOP34_03865, partial [Methylococcaceae bacterium].	GCA_013140465.1
NOT02643.1	AP-GTPase+COR*→	AP-GTPase+COR	1127	HOP29_18715	Planctomycetes	Phycisphaerales bacterium	hypothetical protein HOP29_18715 [Phycisphaerales bacterium].	GCA_013140575.1
NOT61891.1	TIR+BetaPropeller+AP-GTPase*→	TIR+BetaPropeller+AP-GTPase	1134	HOP19_16880	Acidobacteria	Acidobacteria bacterium	TIR domain-containing protein [Acidobacteria bacterium].	GCA_013140935.1

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NOU19042.1	AP-GTPase+COR*→	AP-GTPase+COR	850	HOO91_15910	Bacteroidetes	Bacteroidales bacterium	hypothetical protein HOO91_15910 [Bacteroidales bacterium].	GCA_013141385.1
NOY42283.1	AP-GTPase+COR*→	AP-GTPase+COR	659	GXP26_10655	Planctomycetes	Planctomycetes bacterium	hypothetical protein GXP26_10655 [Planctomycetes bacterium].	GCA_013152205.1
NOY62616.1	AP-GTPase+COR+DUF4404*→	AP-GTPase+COR+DUF4404	555	GXP10_05565	Gammaproteobacteria	Gammaproteobacteria bacterium	hypothetical protein GXP10_05565, partial [Gammaproteobacteria bacterium].	GCA_013152295.1
NPE06693.1	AP-GTPase*→	AP-GTPase	212	GNW80_00285	Asgard group	Asgard group archaeon	GTP-binding protein [Asgard group archaeon].	GCA_013166835.1
NQT13008.1	TIR+BetaPropeller+AP-GTPase*→	TIR+BetaPropeller+AP-GTPase	698	HQ582_09690	Planctomycetes	Planctomycetes bacterium	TIR domain-containing protein, partial [Planctomycetes bacterium].	GCA_013202485.1
NQU22914.1	AP-GTPase*→	AP-GTPase	350	HQ567_16680	Bacteria	Candidatus Nealsonbacteria bacterium	hypothetical protein HQ567_16680 [Candidatus Nealsonbacteria bacterium].	GCA_013202865.1
NQZ10247.1	AP-GTPase+COR*→	AP-GTPase+COR	798	HRT35_24105	Gammaproteobacteria	Algicola sp.	hypothetical protein HRT35_24105 [Algicola sp.].	GCA_013216025.1
NQZ12034.1	AP-GTPase+COR*→	AP-GTPase+COR	875	HRT35_33190	Gammaproteobacteria	Algicola sp.	hypothetical protein HRT35_33190 [Algicola sp.].	GCA_013216025.1
NTV51179.1	SIG+ZetaToxin→ TIR+BetaPropeller+AP-GTPase*→	TIR+BetaPropeller+AP-GTPase	1151	HGA20_16230	Deltaproteobacteria	Geobacteraceae bacterium	TIR domain-containing protein [Geobacteraceae bacterium].	GCA_013336525.1
NUN13817.1	BetaPropeller+AP-GTPase+Calcineurin*→	BetaPropeller+AP-GTPase+Calcineurin	1598	HUU55_09280	Deltaproteobacteria	Myxococcales bacterium	metallophosphoesterase [Myxococcales bacterium].	GCA_013360285.1
NVO09097.1	AP-GTPase+COR*→	AP-GTPase+COR	866	HXX16_03955	Bacteroidetes	Bacteroidales bacterium	50S ribosome-binding GTPase [Bacteroidales bacterium].	GCA_013376985.1
OHD42862.1	AP-GTPase+COR+DrHyd*→	AP-GTPase+COR+DrHyd	671	A2086_15900	Spirochaetes	Spirochaetes bacterium GWD1_27_9	hypothetical protein A2086_15900 [Spirochaetes bacterium GWD1_27_9].	GCA_001830585.1
OLS14677.1	AP-GTPase*→	AP-GTPase	170	RBG13Loki_1719	Asgard group	Candidatus Lokiarchaeota archaeon CR_4	small GTP-binding protein [Candidatus Lokiarchaeota archaeon CR_4].	GCA_001940655.1
OQW99838.1	AP-GTPase+COR*→	AP-GTPase+COR	550	BWK73_49720	Gammaproteobacteria	Thiothrix lacustris	hypothetical protein BWK73_49720 [Thiothrix lacustris].	GCA_002083875.1
OQX07299.1	AP-GTPase*→	AP-GTPase	495	BWK80_49630	Deltaproteobacteria	Desulfobacteraceae bacterium IS3	hypothetical protein BWK80_49630, partial [Desulfobacteraceae bacterium IS3].	GCA_002083955.1
OQX29968.1	AP-GTPase+COR*→	AP-GTPase+COR	659	B0D92_00955	Spirochaetes	Spirochaeta sp. LUC14_002_19_P3	hypothetical protein B0D92_00955, partial [Spirochaeta sp. LUC14_002_19_P3].	GCA_002084135.1
OQY29953.1	AP-GTPase+COR+CASPASE*→	AP-GTPase+COR+CASPASE	1279	B6244_01455	FCB group	Candidatus Cloacimonetes bacterium 4572_55	hypothetical protein B6244_01455 [Candidatus Cloacimonetes bacterium 4572_55].	GCA_002084765.1

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OYW77642.1	AP-GTPase+COR*→	AP-GTPase+COR	915	B7Z37_03570	Verrucomicrobia	Verrucomicrobia bacterium 12-59-8	hypothetical protein B7Z37_03570, partial [Verrucomicrobia bacterium 12-59-8].	GCA_002279765.1
PID37771.1	AP-GTPase+COR*→	AP-GTPase+COR	901	CR966_00525	Gammaproteobacteria	Pseudomonadales bacterium	hypothetical protein CR966_00525 [Pseudomonadales bacterium].	GCA_002746545.1
PIE42009.1	AP-GTPase+COR+DUF4404*→	AP-GTPase+COR+DUF4404	686	CSA47_02360	Gammaproteobacteria	Gammaproteobacteria bacterium	hypothetical protein CSA47_02360 [Gammaproteobacteria bacterium].	GCA_002748595.1
PKL67687.1	BetaPropeller+AP-GTPase+PrimaseZnR+TIR*→	BetaPropeller+AP-GTPase+PrimaseZnR+TIR	1195	CVV28_05310	Euryarchaeota	Methanobacteriales archaeon HGW-Methanobacteriales-1	hypothetical protein CVV28_05310 [Methanobacteriales archaeon HGW-Methanobacteriales-1].	GCA_002839705.1
POZ51526.1	AP-GTPase+COR+DUF4404*→	AP-GTPase+COR+DUF4404	919	AADEFJLK_02392	Gammaproteobacteria	Methylovulum psychrotolerans	GTP-binding protein [Methylovulum psychrotolerans].	GCA_002923755.1
PPD43153.1	AP-GTPase+COR+DUF4404*→	AP-GTPase+COR+DUF4404	914	CTY16_13990	Gammaproteobacteria	Methylobacter sp.	hypothetical protein CTY16_13990 [Methylobacter sp.].	GCA_002929035.1
PPD50180.1	AP-GTPase+COR+DUF4404*→	AP-GTPase+COR+DUF4404	927	CTY13_02150	Gammaproteobacteria	Methylobacter sp.	hypothetical protein CTY13_02150 [Methylobacter sp.].	GCA_002929095.1
PPD50460.1	PolB→ Cluster2355_2clades→ AP-GTPase+COR+DUF4404*→	AP-GTPase+COR+DUF4404	904	CTY16_01515	Gammaproteobacteria	Methylobacter sp.	hypothetical protein CTY16_01515 [Methylobacter sp.].	GCA_002929035.1
QDT95532.1	TIR+APATPase+TPR+TPR+TPR→?→ AP-GTPase+COR+DUF4404*→	AP-GTPase+COR+DUF4404	683	V144x_09770	Planctomycetes	Gimesia aquarii	Miro-like protein [Gimesia aquarii].	GCA_007748195.1
RCJ23846.1	VWA+AP-GTPase+COR+TIR+TIR*→	VWA+AP-GTPase+COR+TIR+TIR	1359	A6770_28940	Cyanobacteria	Nostoc minutum NIES-26	hypothetical protein A6770_28940 [Nostoc minutum NIES-26].	GCA_003326215.1
RHO76387.1	AP-GTPase*→	AP-GTPase	197	DW061_22950	Firmicutes	Ruminococcus sp. AF42-9BH	hypothetical protein DW061_22950, partial [Ruminococcus sp. AF42-9BH].	GCA_003477585.1
RIK66911.1	SIG+AP-GTPase+COR*→	SIG+AP-GTPase+COR	867	DCC65_08160	Planctomycetes	Planctomycetes bacterium	hypothetical protein DCC65_08160 [Planctomycetes bacterium].	GCA_003576905.1
RKZ52796.1	AP-GTPase+COR*→	AP-GTPase+COR	469	DRR00_06990	Gammaproteobacteria	Gammaproteobacteria bacterium	hypothetical protein DRR00_06990 [Gammaproteobacteria bacterium].	GCA_003645185.1
RLI66235.1	AP-GTPase*→	AP-GTPase	176	DRO88_02330	Asgard group	Candidatus Lokiarchaeota archaeon	GTP-binding protein [Candidatus Lokiarchaeota archaeon].	GCA_003662865.1
RLI69359.1	AP-GTPase*→	AP-GTPase	199	DRP02_10785	Asgard group	Candidatus Heimdallarchaeota archaeon	hypothetical protein DRP02_10785 [Candidatus Heimdallarchaeota archaeon].	GCA_003662935.1
RTZ62858.1	AP-GTPase+COR*→	AP-GTPase+COR	577	DSZ29_07625	Aquificae	Aquificaceae bacterium	hypothetical protein DSZ29_07625 [Aquificaceae bacterium].	GCA_003972955.1

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RYE19062.1	AP-GTPase+COR*→	AP-GTPase+COR	577	EOP45_13210	Bacteroidetes	Sphingobacteriaceae bacterium	GTP-binding protein, partial [Sphingobacteriaceae bacterium].	GCA_004144285.1
RZL32479.1	SIG+AP-GTPase+COR*→	SIG+AP-GTPase+COR	392	EOP00_33890	Bacteroidetes	Pedobacter sp.	GTP-binding protein, partial [Pedobacter sp.].	GCA_004211475.1
SEM19691.1	SIG+AP-GTPase+COR*→	SIG+AP-GTPase+COR	929	SAMN04489760_10698	Deltaproteobacteria	Syntrophus gentianae	small GTP-binding protein domain-containing protein [Syntrophus gentianae].	GCA_900109885.1
SKA90036.1	AP-GTPase*→	AP-GTPase	120	SAMN02745166_01647	Verrucomicrobia	Prosthecobacter debontii	hypothetical protein SAMN02745166_01647 [Prosthecobacter debontii].	GCA_900167535.1
SNR48942.1	BetaPropeller+AP-GTPase+TIR*→	BetaPropeller+AP-GTPase+TIR	1008	SAMN06264365_102815	Actinobacteria	Actinoplanes regularis	small GTP-binding protein domain-containing protein [Actinoplanes regularis].	GCA_900188005.1
TAA74167.1	AP-GTPase*→	AP-GTPase	415	CDV28_13720	Deltaproteobacteria	Candidatus Electronema sp. GS	Ras of Complex, Roc, domain of DAPkinase [Candidatus Electronema sp. GS].	GCA_004284765.1
TAN66684.1	AP-GTPase+COR+DUF4404*→	AP-GTPase+COR+DUF4404	912	EPN17_13365	Gammaproteobacteria	Methylobacter sp.	hypothetical protein EPN17_13365 [Methylobacter sp.].	GCA_004299305.1
TET30065.1	AP-GTPase*→	AP-GTPase	212	E3J70_05515	Asgard group	Candidatus Heimdallarchaeota archaeon	GTP-binding protein [Candidatus Heimdallarchaeota archaeon].	GCA_004376455.1
TFF85226.1	AP-GTPase*→	AP-GTPase	173	EU518_01555	Asgard group	Candidatus Lokiarchaeota archaeon	GTP-binding protein [Candidatus Lokiarchaeota archaeon].	GCA_004524075.1
TFF94051.1	AP-GTPase*→	AP-GTPase	179	EU544_04990	Asgard group	Candidatus Lokiarchaeota archaeon	GTP-binding protein [Candidatus Lokiarchaeota archaeon].	GCA_004524325.1
TFG01113.1	AP-GTPase*→	AP-GTPase	173	EU542_07480	Asgard group	Candidatus Lokiarchaeota archaeon	GTP-binding protein [Candidatus Lokiarchaeota archaeon].	GCA_004524355.1
TFG18716.1	AP-GTPase*→	AP-GTPase	217	EU530_08380	Asgard group	Candidatus Lokiarchaeota archaeon	GTP-binding protein [Candidatus Lokiarchaeota archaeon].	GCA_004524545.1
TKG00166.1	AP-GTPase+COR*→	AP-GTPase+COR	467	FCV76_15430	Gammaproteobacteria	Vibrio sp. F13	GTP-binding protein [Vibrio sp. F13].	GCA_005146615.1
TKJ20917.1	AP-GTPase*→	AP-GTPase	192	CEE42_14430	Asgard group	Candidatus Lokiarchaeota archaeon Loki_b31	hypothetical protein CEE42_14430 [Candidatus Lokiarchaeota archaeon Loki_b31].	GCA_005222975.1
TLU87712.1	SIG+ZetaToxin→ TIR+BetaPropeller+AP-GTPase*→	TIR+BetaPropeller+AP-GTPase	1149	FDX21_02485	Chlorobi	Chlorobium sp.	TIR domain-containing protein [Chlorobium sp.].	GCA_005862225.1
TOG86811.1	AP-GTPase+COR*→	AP-GTPase+COR	675	CGI91_22345	Gammaproteobacteria	Vibrio parahaemolyticus	hypothetical protein CGI91_22345 [Vibrio parahaemolyticus].	GCA_006372615.1
TPQ26187.1	AP-GTPase+COR+TM+TM*→	AP-GTPase+COR+TM+TM	752	C2U68_12455	Gammaproteobacteria	Methylomonas koyamae	hypothetical protein C2U68_12455 [Methylomonas koyamae].	GCA_006483455.1
TXT62600.1	AP-GTPase*→	AP-GTPase	178	BAJALOKI3v1_540018	Asgard group	Candidatus Lokiarchaeota archaeon	GTP-binding protein Der [Candidatus Lokiarchaeota archaeon].	GCA_008080735.1

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VFJ44888.1	TIR+BetaPropeller+AP-GTPase*→	TIR+BetaPropeller+AP-GTPase	766	BECKFW1821A_GA0114235_100853	Gammaproteobacteria	Candidatus Kentron sp. FW	WD domain-containing protein, G-beta repeat-containing protein [Candidatus Kentron sp. FW].	-
VFJ45524.1	AP-GTPase+COR+TM+TM*→ AP-GTPase+COR+TM+TM→	AP-GTPase+COR+TM+TM	839	BECKFM1743C_GA0114222_100266	Gammaproteobacteria	Candidatus Kentron sp. FM	Ras of Complex, Roc, domain of DAPkinase [Candidatus Kentron sp. FM].	-
VFJ50707.1	TIR+BetaPropeller+AP-GTPase*→	TIR+BetaPropeller+AP-GTPase	1132	BECKFW1821B_GA0114236_100746	Gammaproteobacteria	Candidatus Kentron sp. FW	WD40 repeat [Candidatus Kentron sp. FW].	-
VFJ53002.1	AP-GTPase+COR+TM+TM*→	AP-GTPase+COR+TM+TM	812	BECKDK2373C_GA0170839_103824	Gammaproteobacteria	Candidatus Kentron sp. DK	Ras of Complex, Roc, domain of DAPkinase [Candidatus Kentron sp. DK].	-
VFJ54602.1	AP-GTPase+COR+TM+TM*→	AP-GTPase+COR+TM+TM	670	BECKDK2373C_GA0170839_10441	Gammaproteobacteria	Candidatus Kentron sp. DK	Ras of Complex, Roc, domain of DAPkinase, partial [Candidatus Kentron sp. DK].	-
VFJ56646.1	AP-GTPase+COR+TM+TM*→	AP-GTPase+COR+TM+TM	841	BECKDK2373B_GA0170837_106011	Gammaproteobacteria	Candidatus Kentron sp. DK	Ras of Complex, Roc, domain of DAPkinase [Candidatus Kentron sp. DK].	-
VFJ57440.1	AP-GTPase*→	AP-GTPase	395	BECKFW1821B_GA0114236_10341	Gammaproteobacteria	Candidatus Kentron sp. FW	Ras of Complex, Roc, domain of DAPkinase, partial [Candidatus Kentron sp. FW].	-
VFJ59594.1	AP-GTPase+COR+CR-ATPase8+CR-REase7+TM+TM+TM*→	AP-GTPase+COR+CR-ATPase8+CR-REase7+TM+TM+TM	1492	BECKFW1821A_GA0114235_109213	Gammaproteobacteria	Candidatus Kentron sp. FW	GTPase SAR1 family protein [Candidatus Kentron sp. FW].	-
VFJ60987.1	AP-GTPase+COR+TM+TM*→	AP-GTPase+COR+TM+TM	889	BECKFM1743C_GA0114222_102852	Gammaproteobacteria	Candidatus Kentron sp. FM	Ras of Complex, Roc, domain of DAPkinase [Candidatus Kentron sp. FM].	-
VFJ61225.1	AP-GTPase+COR+TM+TM*→	AP-GTPase+COR+TM+TM	683	BECKDK2373B_GA0170837_109915	Gammaproteobacteria	Candidatus Kentron sp. DK	Ras of Complex, Roc, domain of DAPkinase, partial [Candidatus Kentron sp. DK].	-
VFJ62038.1	AP-GTPase+COR+TM+TM*→	AP-GTPase+COR+TM+TM	843	BECKFW1821B_GA0114236_106912	Gammaproteobacteria	Candidatus Kentron sp. FW	GTPase SAR1 family protein [Candidatus Kentron sp. FW].	-
VFJ65256.1	AP-GTPase+COR+TM+TM*→	AP-GTPase+COR+TM+TM	523	BECKFW1821A_GA0114235_11961	Gammaproteobacteria	Candidatus Kentron sp. FW	hypothetical protein BECKFW1821A_GA0114235_11961, partial [Candidatus Kentron sp. FW].	-
VFJ68931.1	AP-GTPase+COR+TM+TM*→	AP-GTPase+COR+TM+TM	948	BECKFM1743C_GA0114222_105041	Gammaproteobacteria	Candidatus Kentron sp. FM	Ras of Complex, Roc, domain of DAPkinase [Candidatus Kentron sp. FM].	-
VFJ70290.1	AP-GTPase+COR+TM+TM*→	AP-GTPase+COR+TM+TM	787	BECKFM1743C_GA0114222_105511	Gammaproteobacteria	Candidatus Kentron sp. FM	Ras of Complex, Roc, domain of DAPkinase [Candidatus Kentron sp. FM].	-
VFJ72898.1	AP-GTPase+COR+NACHT*→	AP-GTPase+COR+NACHT	1882	BECKFW1821C_GA0114237_10407	Gammaproteobacteria	Candidatus Kentron sp. FW	Pentapeptide repeat-containing protein [Candidatus Kentron sp. FW].	-
VFJ73192.1	AP-GTPase+COR+TM+TM*→	AP-GTPase+COR+TM+TM	770	BECKFW1821C_GA0114237_104627	Gammaproteobacteria	Candidatus Kentron sp. FW	GTPase SAR1 family protein, partial [Candidatus Kentron sp. FW].	-
VFJ76094.1	AP-GTPase+COR+TM+TM*→	AP-GTPase+COR+TM+TM	834	BECKFW1821C_GA0114237_10987	Gammaproteobacteria	Candidatus Kentron sp. FW	GTPase SAR1 family protein [Candidatus Kentron sp. FW].	-
VFJ95876.1	AP-GTPase+COR+TM+TM*→	AP-GTPase+COR+TM+TM	753	BECKH772A_GA0070896_1009310	Gammaproteobacteria	Candidatus Kentron sp. H	Ras of Complex, Roc, domain of DAPkinase, partial [Candidatus Kentron sp. H].	-

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VFK01091.1	AP-GTPase+COR*→	AP-GTPase+COR	275	BECKLFY1418B_GA0070995_12271	Gammaproteobacteria	Candidatus Kentron sp. LFY	Ras of Complex, Roc, domain of DAPkinase, partial [Candidatus Kentron sp. LFY].	-
VFK03671.1	AP-GTPase*→	AP-GTPase	118	BECKLFY1418A_GA0070994_13111	Gammaproteobacteria	Candidatus Kentron sp. LFY	Ras of Complex, Roc, domain of DAPkinase, partial [Candidatus Kentron sp. LFY].	-
VFK03687.1	AP-GTPase*→	AP-GTPase	118	BECKLFY1418A_GA0070994_13121	Gammaproteobacteria	Candidatus Kentron sp. LFY	Ras of Complex, Roc, domain of DAPkinase, partial [Candidatus Kentron sp. LFY].	-
VFK04035.1	AP-GTPase+COR+TM+TM*→	AP-GTPase+COR+TM+TM	677	BECKH772B_GA0070898_104021	Gammaproteobacteria	Candidatus Kentron sp. H	Ras of Complex, Roc, domain of DAPkinase, partial [Candidatus Kentron sp. H].	-
VFK07263.1	AP-GTPase+COR+TM+TM*→	AP-GTPase+COR+TM+TM	674	BECKH772C_GA0070978_104041	Gammaproteobacteria	Candidatus Kentron sp. H	Ras of Complex, Roc, domain of DAPkinase, partial [Candidatus Kentron sp. H].	-
VFK11049.1	AP-GTPase+COR+TM+TM*→	AP-GTPase+COR+TM+TM	865	BECKLPF1236A_GA0070988_100486	Gammaproteobacteria	Candidatus Kentron sp. LPFa	Ras of Complex, Roc, domain of DAPkinase [Candidatus Kentron sp. LPFa].	-
VFK19789.1	AP-GTPase+COR+TM+TM*→	AP-GTPase+COR+TM+TM	853	BECKLPF1236B_GA0070989_11862	Gammaproteobacteria	Candidatus Kentron sp. LPFa	Ras of Complex, Roc, domain of DAPkinase [Candidatus Kentron sp. LPFa].	-
VFK19871.1	AP-GTPase*→	AP-GTPase	161	BECKLFY1418C_GA0070996_106423	Gammaproteobacteria	Candidatus Kentron sp. LFY	small GTP-binding protein domain-containing protein, partial [Candidatus Kentron sp. LFY].	-
VFK26330.1	AP-GTPase*→	AP-GTPase	116	BECKLFY1418C_GA0070996_13331	Gammaproteobacteria	Candidatus Kentron sp. LFY	Ras of Complex, Roc, domain of DAPkinase, partial [Candidatus Kentron sp. LFY].	-
VFK27413.1	AP-GTPase+COR+TM+TM*→ CR-ATPase8+CR-REase7→ CR-ATPase8+CR-REase7→ CR-ATPase8+CR-REase7→ CR-ATPase8+CR-REase7→?→||<-?<-ParA-Soj-PloopNTPase	AP-GTPase+COR+TM+TM	893	BECKMB1821I_GA0114274_100324	Gammaproteobacteria	Candidatus Kentron sp. MB	Ras of Complex, Roc, domain of DAPkinase [Candidatus Kentron sp. MB].	-
VFK29755.1	AP-GTPase+COR+TM+TM*→ AP-GTPase+COR+TM+TM→	AP-GTPase+COR+TM+TM	840	BECKMB1821G_GA0114241_10537	Gammaproteobacteria	Candidatus Kentron sp. MB	Ras of Complex, Roc, domain of DAPkinase [Candidatus Kentron sp. MB].	-
VFK30623.1	AP-GTPase+COR+TM+TM*→ CR-ATPase8+CR-REase7→ CR-ATPase8+CR-REase7→ CR-ATPase8+CR-REase7→ CR-ATPase8+CR-REase7→?→||<-?<-ParA-Soj-PloopNTPase	AP-GTPase+COR+TM+TM	718	BECKMB1821G_GA0114241_10681	Gammaproteobacteria	Candidatus Kentron sp. MB	hypothetical protein BECKMB1821G_GA0114241_10681, partial [Candidatus Kentron sp. MB].	-
VFK30872.1	AP-GTPase+COR+TM+TM*→	AP-GTPase+COR+TM+TM	680	BECKMB1821G_GA0114241_10721	Gammaproteobacteria	Candidatus Kentron sp. MB	hypothetical protein BECKMB1821G_GA0114241_10721, partial [Candidatus Kentron sp. MB].	-
VFK31841.1	AP-GTPase*→	AP-GTPase	476	BECKMB1821I_GA0114274_102765	Gammaproteobacteria	Candidatus Kentron sp. MB	Ras of Complex, Roc, domain of DAPkinase [Candidatus Kentron sp. MB].	-
VFK32767.1	AP-GTPase+COR+TM+TM*→	AP-GTPase+COR+TM+TM	875	BECKMB1821I_GA0114274_103604	Gammaproteobacteria	Candidatus Kentron sp. MB	Ras of Complex, Roc, domain of DAPkinase [Candidatus Kentron sp. MB].	-
VFK33354.1	AP-GTPase+COR+TM+TM*→	AP-GTPase+COR+TM+TM	844	BECKMB1821I_GA0114274_104404	Gammaproteobacteria	Candidatus Kentron sp. MB	Ras of Complex, Roc, domain of DAPkinase [Candidatus Kentron sp. MB].	-

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VFK39913.1	AP-GTPase+COR+TM+TM*→	AP-GTPase+COR+TM+TM	790	BECKTC1821D_GA0114238_100746	Gammaproteobacteria	Candidatus Kentron sp. TC	Ras of Complex, Roc, domain of DAPkinase [Candidatus Kentron sp. TC].	-
VFK39956.1	RADICAL-SAM→ AP-GTPase+COR*→	AP-GTPase+COR	694	BECKSD772F_GA0070984_105018	Gammaproteobacteria	Candidatus Kentron sp. SD	GTPase SAR1 family protein [Candidatus Kentron sp. SD].	-
VFK40684.1	AP-GTPase+COR+TM+TM*→	AP-GTPase+COR+TM+TM	854	BECKSD772F_GA0070984_10665	Gammaproteobacteria	Candidatus Kentron sp. SD	Ras of Complex, Roc, domain of DAPkinase [Candidatus Kentron sp. SD].	-
VFK42825.1	AP-GTPase+COR+TM+TM*→	AP-GTPase+COR+TM+TM	834	BECKTC1821E_GA0114239_102141	Gammaproteobacteria	Candidatus Kentron sp. TC	Ras of Complex, Roc, domain of DAPkinase [Candidatus Kentron sp. TC].	-
VFK53024.1	AP-GTPase+COR+TM+TM*→	AP-GTPase+COR+TM+TM	852	BECKTUN1418D_GA0071000_101730	Gammaproteobacteria	Candidatus Kentron sp. TUN	Ras of Complex, Roc, domain of DAPkinase [Candidatus Kentron sp. TUN].	-
VFK54740.1	AP-GTPase+COR+TM+TM*→	AP-GTPase+COR+TM+TM	851	BECKTUN1418F_GA0071002_10532	Gammaproteobacteria	Candidatus Kentron sp. TUN	GTPase SAR1 family protein [Candidatus Kentron sp. TUN].	-
VFK54787.1	CR-ATPase8+CR-REase7+AP-GTPase+COR+TM+TM*→	CR-ATPase8+CR-REase7+AP-GTPase+COR+TM+TM	1117	BECKTUN1418F_GA0071002_105513	Gammaproteobacteria	Candidatus Kentron sp. TUN	Ras of Complex, Roc, domain of DAPkinase [Candidatus Kentron sp. TUN].	-
VFK55234.1	AP-GTPase+COR+TM+TM*→	AP-GTPase+COR+TM+TM	870	BECKTUN1418D_GA0071000_102911	Gammaproteobacteria	Candidatus Kentron sp. TUN	GTPase SAR1 family protein [Candidatus Kentron sp. TUN].	-
VFK55404.1	AP-GTPase+COR+TM+TM*→ AP-GTPase+COR+TM+TM→	AP-GTPase+COR+TM+TM	834	BECKTUN1418E_GA0071001_10293	Gammaproteobacteria	Candidatus Kentron sp. TUN	Ras of Complex, Roc, domain of DAPkinase [Candidatus Kentron sp. TUN].	-
VFK57219.1	AP-GTPase+COR+TM+TM*→	AP-GTPase+COR+TM+TM	799	BECKTC1821F_GA0114240_101546	Gammaproteobacteria	Candidatus Kentron sp. TC	Ras of Complex, Roc, domain of DAPkinase [Candidatus Kentron sp. TC].	-
VFK57233.1	AP-GTPase+COR*→	AP-GTPase+COR	1361	BECKTUN1418F_GA0071002_11091	Gammaproteobacteria	Candidatus Kentron sp. TUN	Uncharacterized conserved protein, contains ParB-like and HNH nuclease domains [Candidatus Kentron sp. TUN].	-
VFK58480.1	AP-GTPase+COR*→	AP-GTPase+COR	1384	BECKTUN1418D_GA0071000_10836	Gammaproteobacteria	Candidatus Kentron sp. TUN	Ras of Complex, Roc, domain of DAPkinase [Candidatus Kentron sp. TUN].	-
VFK60758.1	CR-ATPase8+CR-REase7+AP-GTPase*→	CR-ATPase8+CR-REase7+AP-GTPase	877	BECKUNK1418G_GA0071005_101311	Gammaproteobacteria	Candidatus Kentron sp. UNK	PD-(D/E)XK nuclease superfamily protein [Candidatus Kentron sp. UNK].	-
VFK62743.1	AP-GTPase*→	AP-GTPase	337	BECKTUN1418D_GA0071000_11856	Gammaproteobacteria	Candidatus Kentron sp. TUN	Ras of Complex, Roc, domain of DAPkinase, partial [Candidatus Kentron sp. TUN].	-
VFK65329.1	AP-GTPase+COR*→	AP-GTPase+COR	1361	BECKTUN1418E_GA0071001_11051	Gammaproteobacteria	Candidatus Kentron sp. TUN	Uncharacterized conserved protein, contains ParB-like and HNH nuclease domains [Candidatus Kentron sp. TUN].	-
VFK67825.1	BetaPropeller+AP-GTPase*→	BetaPropeller+AP-GTPase	526	BECKUNK1418G_GA0071005_11685	Gammaproteobacteria	Candidatus Kentron sp. UNK	WD domain-containing protein, G-beta repeat-containing protein [Candidatus Kentron sp. UNK].	-
VFK67855.1	AP-GTPase+COR+TM+TM*→	AP-GTPase+COR+TM+TM	598	BECKUNK1418G_GA0071005_11705	Gammaproteobacteria	Candidatus Kentron sp. UNK	Ras of Complex, Roc, domain of DAPkinase [Candidatus Kentron sp. UNK].	-

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VFK77412.1	AP-GTPase+COR+TM+TM*→	AP-GTPase+COR+TM+TM	734	BECKMB1821H_GA0114242_11351	Gammaproteobacteria	Candidatus Kentron sp. MB	Ras of Complex, Roc, domain of DAPkinase, partial [Candidatus Kentron sp. MB].	-
VFK80164.1	AP-GTPase+COR+TM+TM*→	AP-GTPase+COR+TM+TM	872	BECKSD772D_GA0070982_10897	Gammaproteobacteria	Candidatus Kentron sp. SD	Ras of Complex, Roc, domain of DAPkinase [Candidatus Kentron sp. SD].	-
VFM99483.1	AP-GTPase+COR+TM+TM*→	AP-GTPase+COR+TM+TM	725	BECKG1743F_GA0114225_104022	Gammaproteobacteria	Candidatus Kentron sp. G	GTPase SAR1 family protein [Candidatus Kentron sp. G].	GCA_900696175.1
VFM99853.1	AP-GTPase+COR+TM+TM*→	AP-GTPase+COR+TM+TM	744	BECKG1743F_GA0114225_104332	Gammaproteobacteria	Candidatus Kentron sp. G	small GTP-binding protein domain-containing protein [Candidatus Kentron sp. G].	GCA_900696175.1
WP_002684219.1	AP-GTPase+COR+DUF4404*→	AP-GTPase+COR+DUF4404	883	-	Gammaproteobacteria	Beggiatoa alba	Miro-like protein [Beggiatoa alba].	GCF_000245015.1
WP_009138084.1	AP-GTPase+COR*→	AP-GTPase+COR	843	-	Bacteroidetes	Odoribacter laneus	hypothetical protein [Odoribacter laneus].	GCF_902374615.1
WP_012499245.1	AP-GTPase*→	AP-GTPase	394	-	Chlorobi	Chloroherpeton thalassium	Miro domain-containing protein [Chloroherpeton thalassium].	GCF_000020525.1
WP_020559412.1	GTPase-AIG→ ABC-ATPase→ SIG+TM+TM+TM+TM→ AP-GTPase+COR*→	AP-GTPase+COR	833	-	Gammaproteobacteria	Thiofilum flexile	hypothetical protein [Thiofilum flexile].	GCF_000380185.1
WP_027001878.1	AP-GTPase+COR*→	AP-GTPase+COR	754	-	Bacteroidetes	Hugenholtzia roseola	hypothetical protein [Hugenholtzia roseola].	GCF_000422585.1
WP_040612090.1	AP-GTPase+COR*→	AP-GTPase+COR	849	-	Bacteroidetes	Odoribacter laneus	hypothetical protein [Odoribacter laneus].	-
WP_050025079.1	VWA+AP-GTPase+COR+EAD1+Trypsin*→	VWA+AP-GTPase+COR+EAD1+Trypsin	1458	-	Verrucomicrobia	Verrucomicrobium sp. BvORR034	GTP-binding protein [Verrucomicrobium sp. BvORR034].	-
WP_052368940.1	TIR+BetaPropeller+AP-GTPase*→	TIR+BetaPropeller+AP-GTPase	1107	-	Euryarchaeota	Candidatus Methanoperedens nitroreducens	TIR domain-containing protein [Candidatus Methanoperedens nitroreducens].	GCF_000685155.1
WP_071819957.1	TIR+BetaPropeller+AP-GTPase*→||<-?<-?<-?<-?<-?<-RuvB-AAA+RuvB-HTH	TIR+BetaPropeller+AP-GTPase	1449	-	Cyanobacteria	Acaryochloris marina	TIR domain-containing protein [Acaryochloris marina].	GCF_000018105.1
WP_077027722.1	<-Phytase-like||?→?→ tRNA→||<-?<-?<-?||TIR+BetaPropeller+AP-GTPase*→	TIR+BetaPropeller+AP-GTPase	1401	-	Planctomycetes	Fuerstia marisgermanicae	TIR domain-containing protein [Fuerstia marisgermanicae].	GCF_001983935.1
WP_081716878.1	AP-GTPase+COR+TIR*→	AP-GTPase+COR+TIR	722	-	Cyanobacteria	Leptolyngbya sp. Heron Island J	TIR domain-containing protein [Leptolyngbya sp. Heron Island J].	-
WP_081891667.1	AP-GTPase+COR+TIR*→	AP-GTPase+COR+TIR	825	-	Verrucomicrobia	Verrucomicrobium sp. BvORR106	TIR domain-containing protein [Verrucomicrobium sp. BvORR106].	-
WP_083888126.1	AP-GTPase*→	AP-GTPase	116	-	Cyanobacteria	Oscillatoria nigro-viridis	hypothetical protein [Oscillatoria nigro-viridis].	-
WP_093066994.1	AP-GTPase+COR*→	AP-GTPase+COR	857	-	Gammaproteobacteria	Thiothrix caldifontis	hypothetical protein [Thiothrix caldifontis].	GCF_900107695.1
WP_093068668.1	AP-GTPase+COR*→	AP-GTPase+COR	960	-	Gammaproteobacteria	Thiothrix caldifontis	hypothetical protein [Thiothrix caldifontis].	GCF_900107695.1
WP_093882803.1	SIG+AP-GTPase+COR*→	SIG+AP-GTPase+COR	880	-	Deltaproteobacteria	Syntrophus gentianae	hypothetical protein [Syntrophus gentianae].	GCF_900109885.1
WP_103921835.1	HTH→ AP-GTPase+COR*→	AP-GTPase+COR	576	-	Gammaproteobacteria	Thiotrichales bacterium HS_08	hypothetical protein [Thiotrichales bacterium HS_08].	-
WP_129026230.1	AP-GTPase+COR*→	AP-GTPase+COR	431	-	Bacteroidetes	Flavobacterium sp. YO12	hypothetical protein [Flavobacterium sp. YO12].	GCF_004119495.1

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WP_137245090.1	TM+AP-GTPase*→	TM+AP-GTPase	93	-	Actinobacteria	Herbidospora galbida	hypothetical protein [Herbidospora galbida].	GCF_005233835.1
WP_139373135.1	AP-GTPase*→	AP-GTPase	134	-	Verrucomicrobia	Prosthecobacter debontii	hypothetical protein [Prosthecobacter debontii].	GCF_900167535.1
WP_140311973.1	AP-GTPase+COR*→	AP-GTPase+COR	697	-	Gammaproteobacteria	Vibrio parahaemolyticus	GTP-binding protein, partial [Vibrio parahaemolyticus].	GCF_006372615.1
WP_144982131.1	TIR+APATPase+TPR+TPR+TPR→?→ AP-GTPase+COR+DUF4404*→	AP-GTPase+COR+DUF4404	692	-	Planctomycetes	Gimesia aquarii	hypothetical protein [Gimesia aquarii].	GCF_007748195.1
WP_145384506.1	AP-GTPase+COR*→	AP-GTPase+COR	680	-	Planctomycetes	Stieleria neptunia	50S ribosome-binding GTPase [Stieleria neptunia].	GCF_007754155.1
WP_146054573.1	AP-GTPase+COR+DUF4404*→	AP-GTPase+COR+DUF4404	731	-	Gammaproteobacteria	Methylovulum psychrotolerans	hypothetical protein [Methylovulum psychrotolerans].	GCF_002923755.1
WP_147662502.1	AP-GTPase*→	AP-GTPase	204	-	Asgard group	Candidatus Prometheoarchaeum syntrophicum	GTP-binding protein [Candidatus Prometheoarchaeum syntrophicum].	GCF_008000775.1
WP_157679487.1	AP-GTPase+COR+DUF4404*→	AP-GTPase+COR+DUF4404	911	-	Gammaproteobacteria	Methylovulum psychrotolerans	hypothetical protein [Methylovulum psychrotolerans].	GCF_002209385.1
WP_157817021.1	<-EAD10+VMAP-M1+VMAP-C||?→||<-PSE||BetaPropeller+AP-GTPase+Calcineurin+CASPASE+NACHT*→	BetaPropeller+AP-GTPase+Calcineurin+CASPASE+NACHT	1731	-	Cyanobacteria	Nostoc flagelliforme	NACHT domain-containing protein [Nostoc flagelliforme].	GCF_002813575.1
WP_160572809.1	AP-GTPase+COR+DUF4404*→	AP-GTPase+COR+DUF4404	720	-	unclassified Bacteria	bacterium D16-29	GTP-binding protein [bacterium D16-29].	-
WP_162669385.1	AP-GTPase+COR+DUF4404*→	AP-GTPase+COR+DUF4404	615	-	Planctomycetes	Gemmata massiliana	hypothetical protein [Gemmata massiliana].	GCF_901538265.1
WP_170962814.1	AP-GTPase+COR*→	AP-GTPase+COR	453	-	Gammaproteobacteria	Vibrio sp. F13	GTP-binding protein [Vibrio sp. F13].	GCF_005146615.1
WP_173978580.1	TIR+BetaPropeller+AP-GTPase*→	TIR+BetaPropeller+AP-GTPase	1154	-	Alphaproteobacteria	Magnetospirillum sp. UT-4	TIR domain-containing protein [Magnetospirillum sp. UT-4].	GCF_902729435.1
WP_175453917.1	AP-GTPase+COR*→	AP-GTPase+COR	757	-	Firmicutes	Sarcina sp. DSM 11001	GTP-binding protein, partial [Sarcina sp. DSM 11001].	GCF_900101015.1
WP_177428378.1	AP-GTPase+COR+CR-ATPase9*→	AP-GTPase+COR+CR-ATPase9	880	-	Gammaproteobacteria	Thiotrichales bacterium HS_08	hypothetical protein [Thiotrichales bacterium HS_08].	-
WP_179276996.1	BetaPropeller+AP-GTPase+TIR*→	BetaPropeller+AP-GTPase+TIR	996	-	Actinobacteria	Actinoplanes regularis	TIR domain-containing protein [Actinoplanes regularis].	GCF_016862355.1
WP_180983884.1	AP-GTPase+COR*→	AP-GTPase+COR	676	-	Gammaproteobacteria	Vibrio agarivorans	50S ribosome-binding GTPase, partial [Vibrio agarivorans].	GCF_002894965.1
WP_186289598.1	AP-GTPase+COR+TM+TM*→	AP-GTPase+COR+TM+TM	905	-	Gammaproteobacteria	Methylomonas koyamae	hypothetical protein [Methylomonas koyamae].	GCF_006483455.1