

Functionally comparable but evolutionarily distinct nucleotide-targeting effectors help identify conserved paradigms across diverse immune systems

## SUPPLEMENTARY MATERIAL

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**<https://aravindlab.github.io/NTdegrade/>**

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## II. Supplementary Data

### A. Genome contextual data

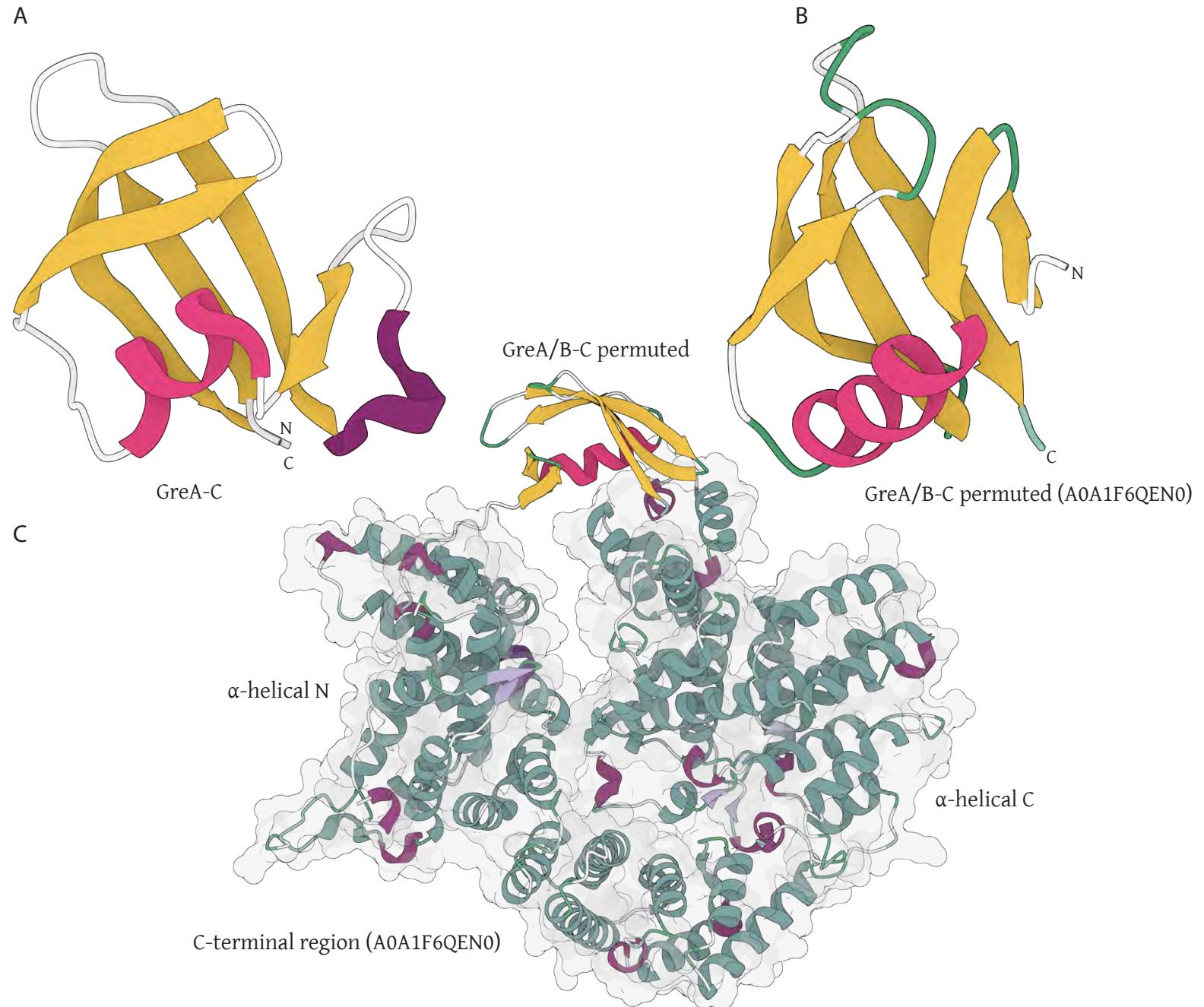
- 1. AEP-1D
- 2. AP-ATPase
- 3. AP-GTPase
- 4. Dynamin
- 5. GreAB-C
- 6. iHD
- 7. HSP70
- 8. HSP90
- 9. ISOCOT
- 10. MNS
- 11. NACHT
- 12. Nadar
- 13. ORC-Cdc6(Calcineurin-CE)
- 14. ORC-Cdc6(HD-CE)
- 15. ORC-Cdc6 (PRTase-CE)
- 16. ORC-Cdc6 (TIR)
- 17. ORC-Cdc6(SIR2)
- 18. ORC-Cdc6(Kinases)
- 19. ORC-Cdc6(Others)
- 20. PUA-like
- 21. ParB-CE
- 22. ParB
- 23. Pepco
- 24. PolBetaCCAA-like
- 25. RVT
- 26. SAMHD1
- 27. nSTAND4
- 28. nSTAND5
- 29. iSTAND3
- 30. iSirtuin
- 31. STAS big protein
- 32. STAS
- 33. Thymidylate synthase
- 34. iThymidylate synthase

### B. Multiple sequence alignments

- 1. Calcineurin-CE
- 2. HD-CE
- 3. PRTase-CE
- 4. PUA-like-CE
- 5. iSirtuin-CE
- 6. Calcineurin-CE+iThymidylate-synthase
- 7. AEP-1D
- 8. REC+Calcineurin-CE
- 9. STAS+HisKin
- 10. STAS+PRTase
- 11. STAS+HisKin+iPRTase+PRTase
- 12. Pepco
- 13. iCalcineurin-CE
- 14. iHD

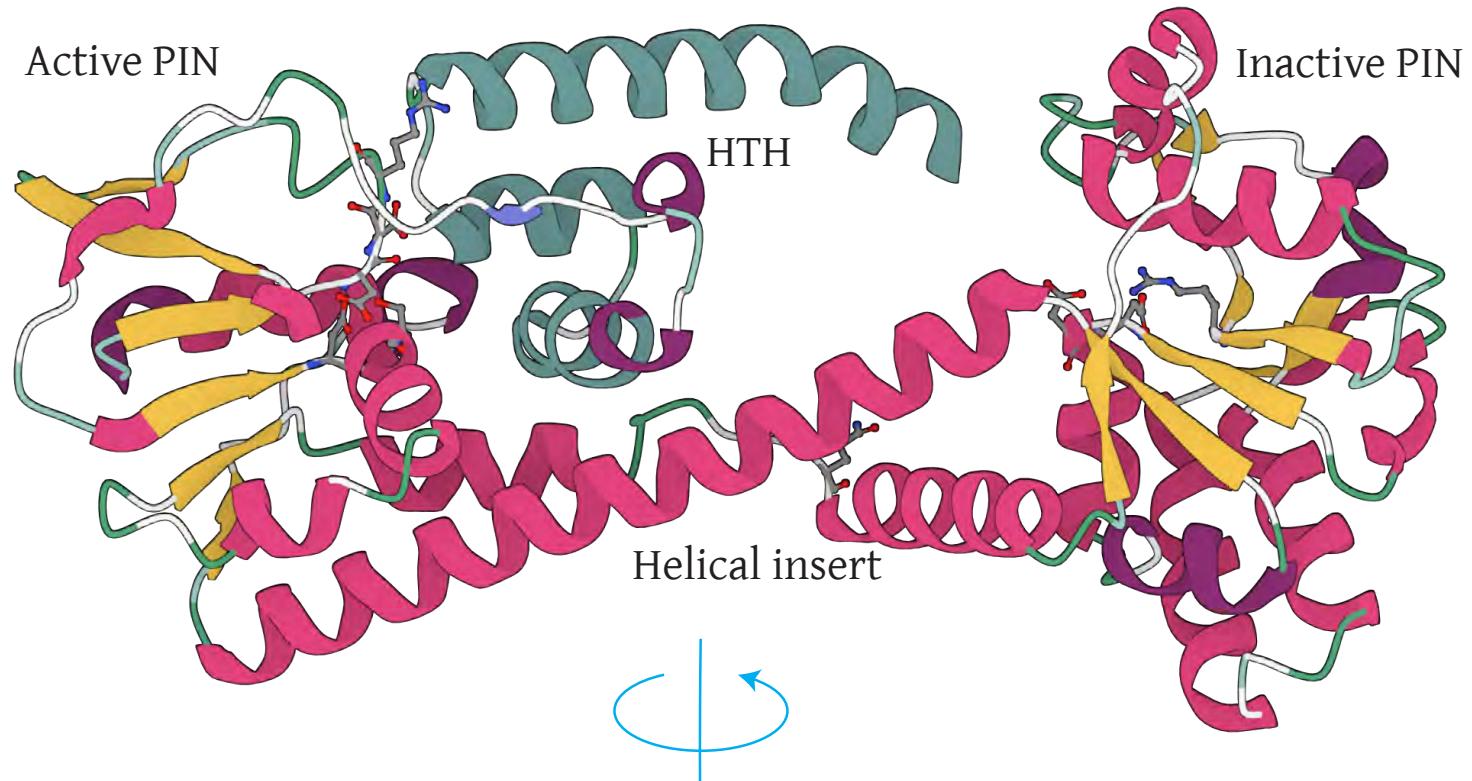
### C. Phylogenetic Tree

- 1. Calcineurin-CE
- 2. HD-CE
- 3. PRTase-CE
- 4. ORC-Cdc6

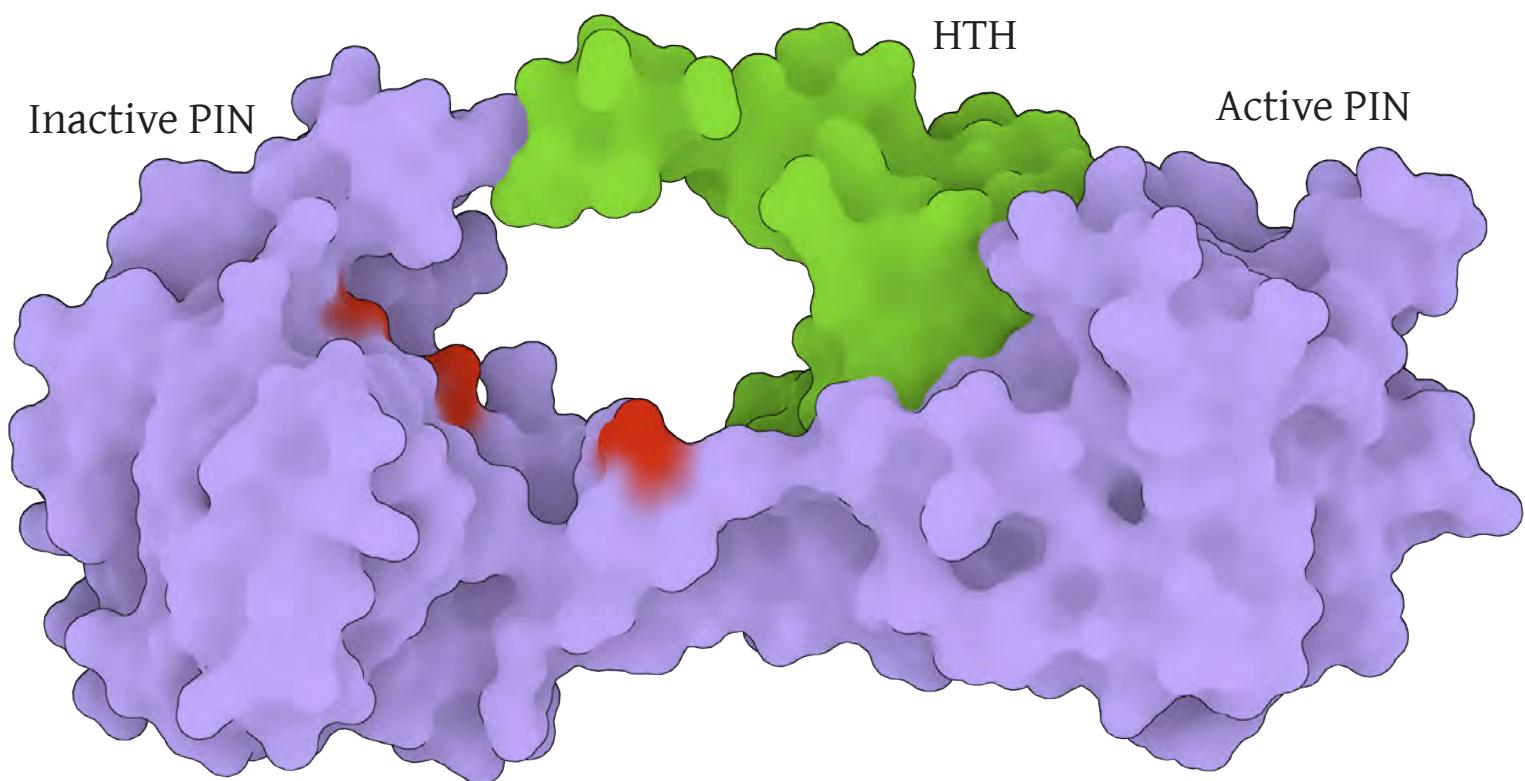


**Supplementary Figure S1. Permuted GreAB-C structure model.** (A) Structure of the previously identified GreAB-C domain. (B) Alphafold model of a permuted GreAB-C domain. (C) Context of the permuted GreAB-C domain embedded in a sequence of divergent TPRs, forming a toroidal structure.

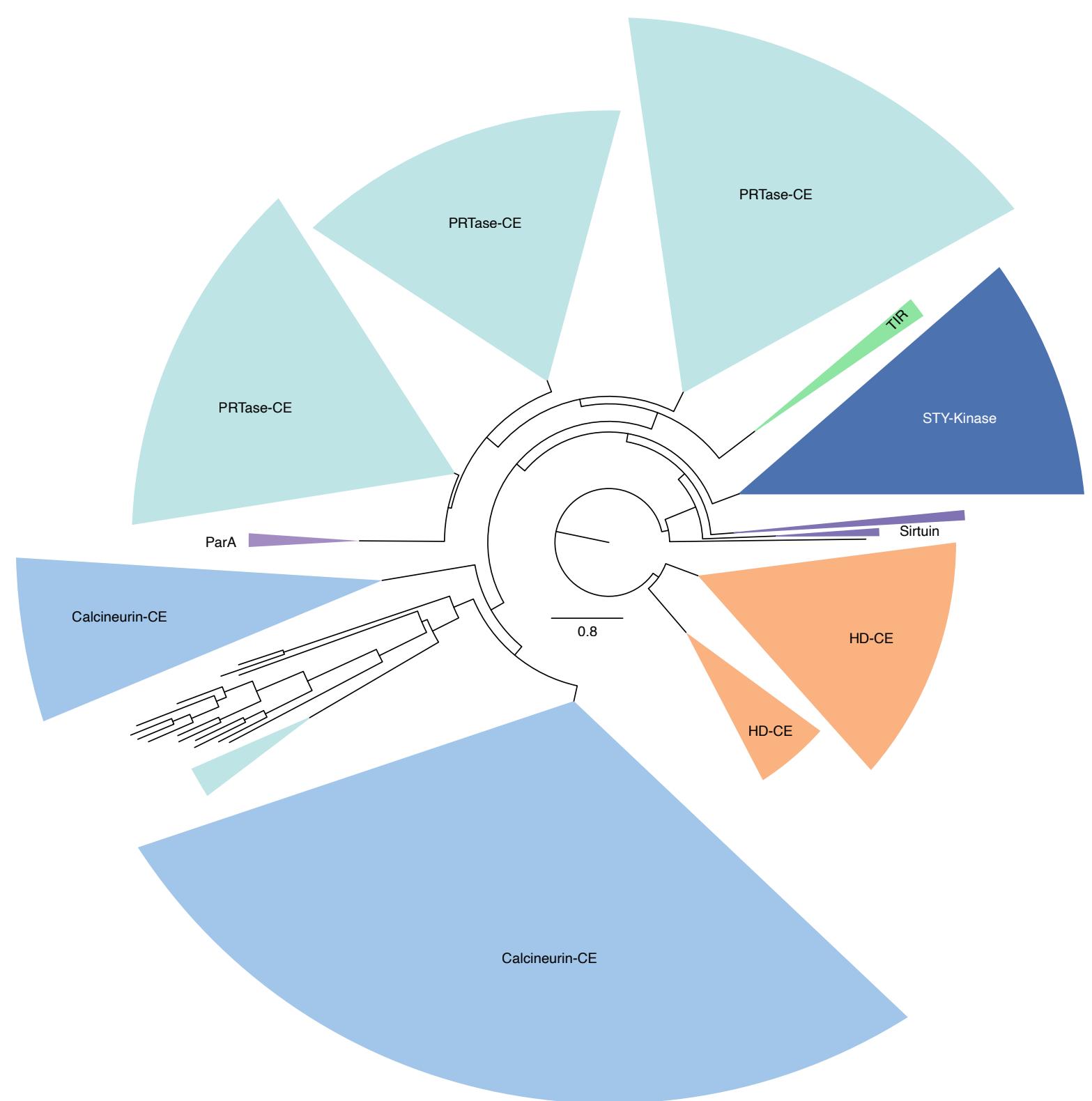
A



B



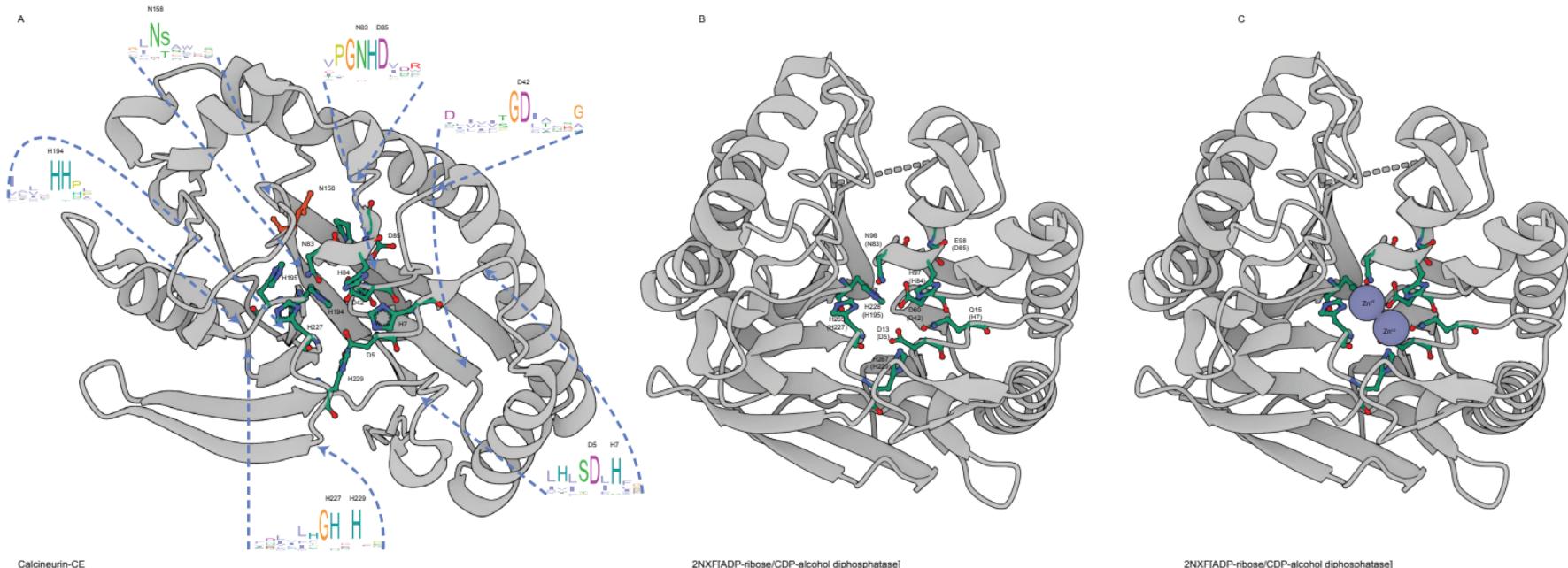
**Supplementary Figure S2. Double PIN structure model.** (A) cartoon representation of the double PIN domain.  $\beta$ -strands are depicted in yellow,  $\alpha$ -helices in dark pink, and the HTH domain in dark cyan. Catalytic residues are shown in ball-and-stick representation. (B) Molecular surface representation demonstrating the occlusion of the active PIN site by the HTH domain. The two PIN domains are represented in purple, the HTH domain in green, and the position of the inactive catalytic residues of the inactive PIN domain is depicted in red.



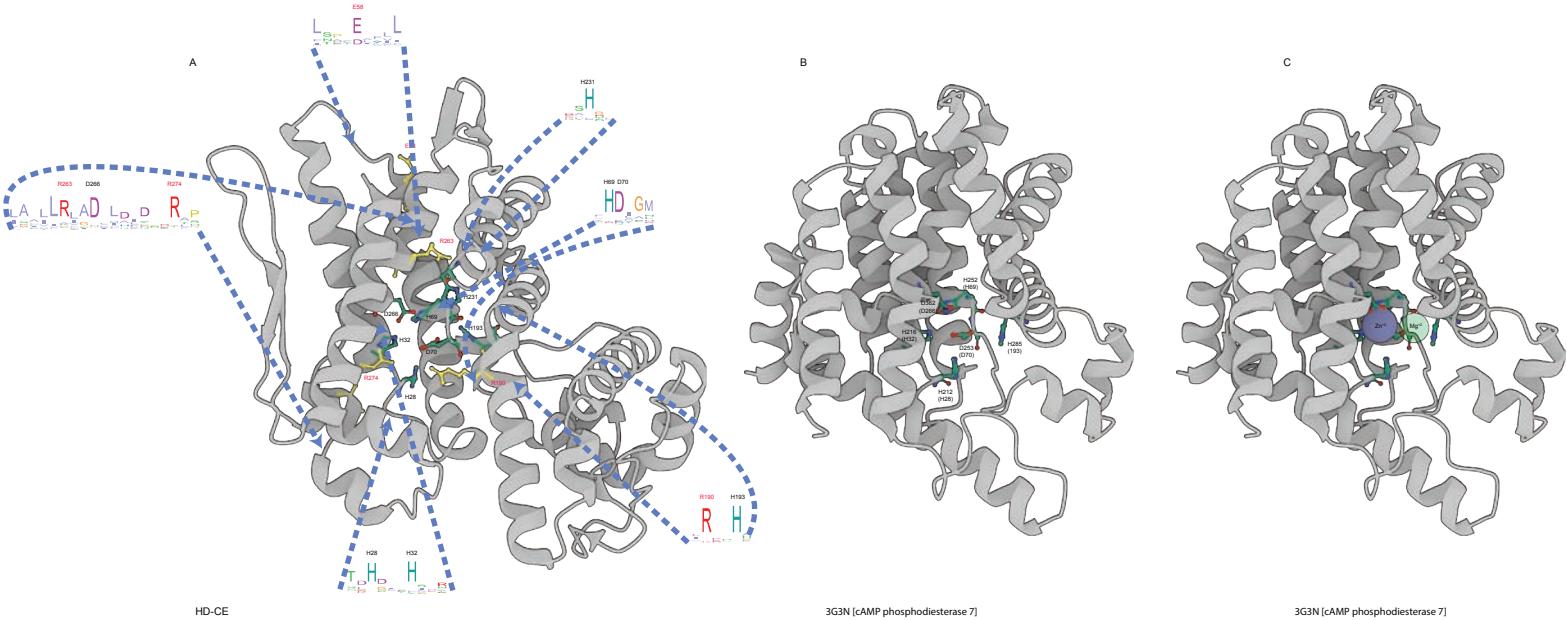
**Supplementary Figure S3. Phylogenetic tree of the Orc/Cdc6-like proteins.** The tree was constructed with IQtree2 using ultrafast bootstrap and SH-aLRT test as support values. The clades are labeled according to associated effector domains present in the genomic neighborhood



**Supplementary Figure S4. Sequence logos of different Calcineurin-like phosphoesterase families.** Sequences from various families of calcineurin-like domains were gathered using previously characterized PDB sequences as seeds. These sequences were aligned using the Mafft local pair algorithm, and the logos representing different families were visualized using the Jalview software. Conserved motifs I-V are depicted with boxes.

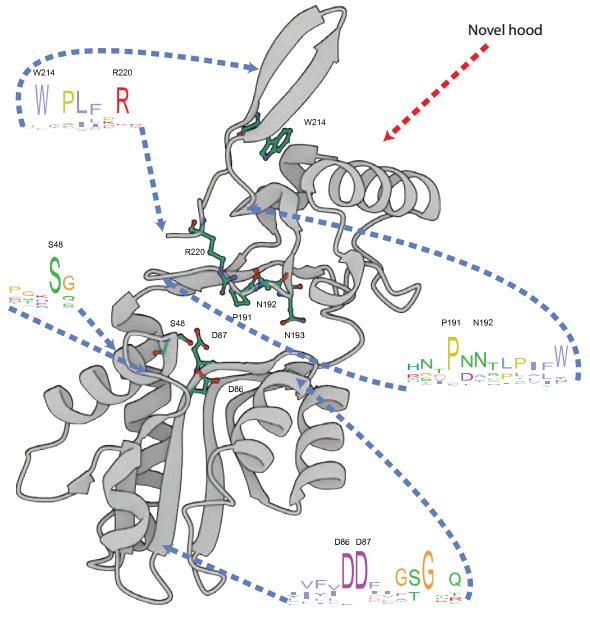


**Supplementary Figure 5. Activity site and conserved residues from the Calcineurin-CE domain. (A)** Alphafold modeling of the Calcineurin-CE domain (WP\_080633877.1). The residues conserved in the activity sites are shown in ball and stick representations. The synapomorphic asparagine is colored in orange. Sequence logos of the conserved regions are shown and the dotted lines indicate the start and end position of the logo in the structural model. (B and C). Activity site of the experimental crystallized ADP-ribose/CDP-alcohol diphosphatase domain from the PDB 2NXF without and with the Zn<sup>+2</sup> ion respectively.



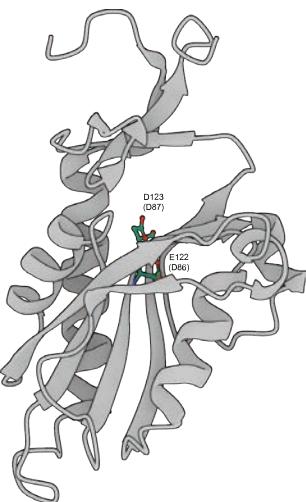
**Supplementary Figure S6. Activity site and conserved residues from the HD-CE domain.** (A) Alphafold modeling of the HD-CE domain (CZQ95560.1). The residues conserved in the activity sites are shown in ball and stick representations. The synapomorphic residues are colored yellow. Sequence logos of the conserved regions are shown and the dotted lines indicate the start and end position of the logo in the structural model. (B and C). Activity site of the experimental crystallized cAMP phosphodiesterase 7 domain from the PDB 3G3N without and with the Zn<sup>+2</sup> and MG<sup>+2</sup> ions respectively.

A



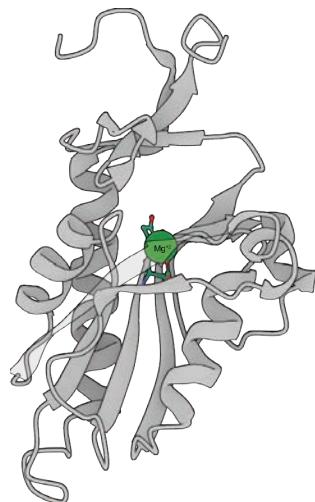
PRTase-CE

B



5KNQ [hypoxanthine guanine PRTase]

C



5KNQ [hypoxanthine guanine PRTase]

**Supplementary Figure S7. Activity site and conserved residues from the PRTase-CE domain.**  
 (A) Alphafold modeling of the PRTase-CE domain (NPV02125.1). The residues conserved in the activity sites are shown in ball and stick representations. Sequence logos of the conserved regions are shown and the dotted lines indicate the start and end position of the logo in the structural model. (B and C). Activity site of the experimental crystallized hypoxanthine guanine PRTase domain from the PDB 5KNQ without and with the Mg<sup>+2</sup> ion respectively.

Figure 3A Calcineurin-CE

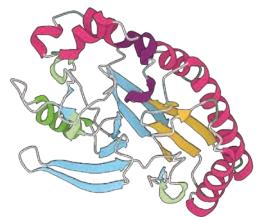
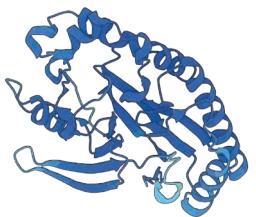


Figure 4G iSirtuin

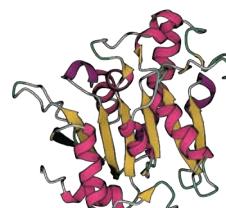
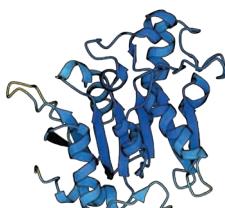


Figure 3B HD-CE

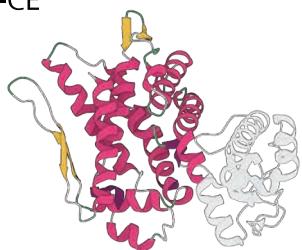
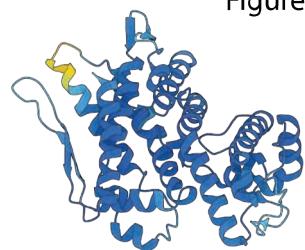


Figure 5G PRTase

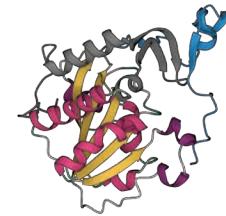
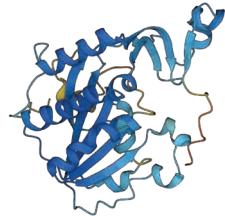


Figure 3C PRTase-CE

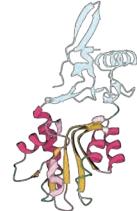


Figure 6B HSP90 system with C-terminal wHTH

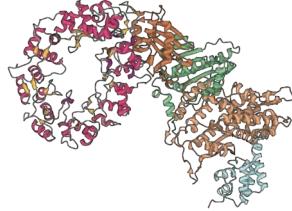
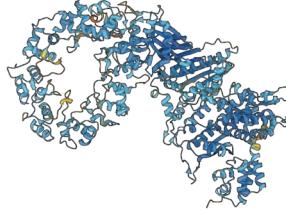


Figure 4B Cdc6-double-CARF•Calcineurin-CE complex

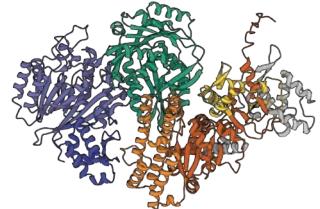
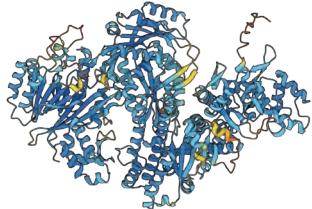


Figure 6E Pepco•Caspase complex



Figure 4D Pua-like

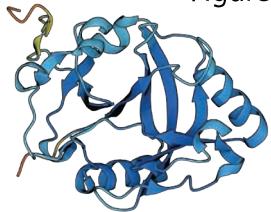
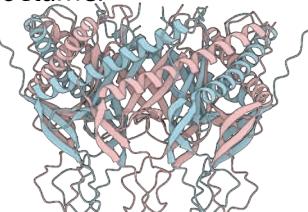
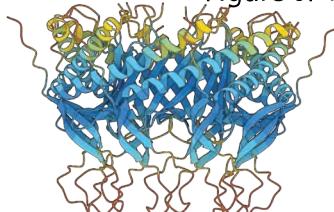


Figure 6F Pepco octamer



Very High (pLDDT > 90)

Confident (90 > pLDDT > 70)

Low (70 > pLDDT > 50)

Very Low(pLDDT < 50)

**Supplementary Figure S8. AlphaFold confidence score for the models produced on the present work.** On the left the structural models are colored by the pLDDT scores. On the right are the structural models as colored in the figures presented in the main text. Dark blue, light blue, yellow and orange represent a very high, confident, low and very low prediction respectively.



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... (content of the file is extremely long and repetitive, containing thousands of entries for various genes and their products)





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WP_051939857.1	TPR_M61t+TPR+TPR	NZ_STRE01000005.1	1:18015-26375	GCF_009811555.1	Spirochaetes	NZ_BGE01000002.1	
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WP_051939857.1	TPR_M61t+TPR+TPR	NZ_STRE01000005.1	1:18015-26375	GCF_009811555.1	Treponema sp. CC77	NZ_BGE01000002.1	
WP_051939857.1	TPR_M61t+TPR+TPR	NZ_STRE01000005.1	1:18015-26375	GCF_009811555.1	Treponemyces sp. LS1784	NZ_BGE01000002.1	
WP_051939857.1	TPR_M61t+TPR+TPR	NZ_STRE01000005.1	1:18015-26375	GCF_009811555.1	Treponomyces sp. MWG1533	NZ_BGE01000002.1	
WP_051							







This block contains the full sequence of the 16S rRNA gene from the provided image, spanning from position 1 to approximately 980. The sequence is presented in a single, long text block with various markers and annotations.

This block contains the full text of the 16S rRNA gene database, which is a collection of 16S rRNA gene sequences from various bacterial species. The database is organized into several sections, including assembly, plasmid, genome, and taxonomic information.



... (The file contains approximately 1000 pages of text, each page starting with a header like 'Mycobacterium tuberculosis' and listing various genes and their functions.)

This block contains the full sequence of the 16S rRNA gene from the provided image, spanning from position 1 to approximately 980.

WP_169631302.1	ORC-CDC6-like	NZ_JABCLX010000258.1:1-326	GCF_012956145.1	108	*ORC-CDC6-like->	Vibrio parahaemolyticus	Gammaproteobacteria	NZ_JABC010000258
WP_162796445.1	ORC-CDC6-like	NZ_QEDE01000009.1:148204-153123	GCF_003347865.1	324	*ORC-CDC6-like->CARF-double->	Vibrio cholerae	Gammaproteobacteria	NZ_QEDE01000009.1
WP_165387721.1	ORC-CDC6-like	NZ_RBZD01000024.1:34261-41182	GCF_004214575.1	206	*ORC-CDC6-like->CARF-double->	Vibrio vulnificus	Gammaproteobacteria	NZ_RBZD01000024.1
WP_123300074.1	ORC-CDC6-like	NZ_RJVD01000001.1:67514-81212	GCF_003751465.1	655	PSE->*ORC-CDC6-like->	Vibrio crassostreiae	Gammaproteobacteria	NZ_RJVD01000001.1
RZP54190.1	ORC-CDC6-like	RZD01000024.1:34261-41081	GCA_004214575.1	173	*ORC-CDC6-like->CARF-double->	Vibrio vulnificus	Gammaproteobacteria	RZD01000024.1
TQP39892.1	ORC-CDC6-like	VIPA01000296.1:53-498	GCA_006802465.1	147	*ORC-CDC6-like->	Vibrio cholerae	Gammaproteobacteria	VIPA01000296.1
ALA88577.1	ORC-CDC6-like	CP011305.1:1884537-1900596	GCA_001274655.1	604	Na+TrkA_N->THF_DHG_CYH+THF_DHG_CYH_C->IMPDH->?->GATase+tRNA_Me_trans+GMP_synt_C->*ORC-CDC6-like->	Stenotrophomonas maltophilia	Gammaproteobacteria	CP011305.1
CAC9623431.1	ORC-CDC6-like	CAIZN01000037.1:54018-94433	GCA_903814045.1	559	PSE->?->SbcC->PSE->PSE->*ORC-CDC6-like->PSE->	uncultured Gammaproteobacteria bacterium	Gammaproteobacteria	CAIZN01000037.1
WP_078485038.1	ORC-CDC6-like	NZ_MPRL01000095.1:5394-12972	GCF_002020875.1	85	S-methyl_trans+Pterin_bind+B12-binding_2+B12-binding+Met_synt_B12->Glycos_transf_2->wHTH->*ORC-CDC6-like->	Solemya pervernica gill symbiont	Gammaproteobacteria	NZ_MPRL01000095.1
MBV8225564.1	ORC-CDC6-like	JAFAIU010000527.1:221-3464	GCA_019236535.1	320	*ORC-CDC6-like->CARF-double->	Verrucomicrobia bacterium	Verrucomicrobia	JAFAIU010000527.1
MBL9159074.1	ORC-CDC6-like	JAEUHI01000058.1:89930-100252	GCA_016795385.1	611	*ORC-CDC6-like->CARF-double->	Verrucomicrobiales bacterium	Verrucomicrobiae	JAEUHI01000058.1
MBL7075605.1	ORC-CDC6-like	JADHWK01000064.1:2665-12761	GCA_016783505.1	663	Phage_integrase->?->REC->*ORC-CDC6-like->?->CARF-double->tRNA->ncRNA->DNA_pol3_delta2+DNA_pol3_gamma3->YbaB_DNA_bd->RecR+Toprim_4->	candidate division KSB1 bacterium	candidate division KSB1	JADHWK01000064.1














KUN35883.1	iHD+HSP90+wHTH+wHTH+wHTH+wHTH	KQ948488.1:155-15702	GCA_001514115.1 1304	HIN-MTH->*iHD+HSP90+wHTH+wHTH+wHTH->PSE->	Streptomyces olivochromogenes	Actinomycetes	<a href="#">KQ948488.1</a>
WP_136738601.1	iHD+HSP90+wHTH+wHTH	NZ_SUMB0100002.1:303168-319727	GCF_005048155.1 1228	*iHD+HSP90+wHTH+wHTH->NTP_transf_9->Calcineurin-CE->	Streptomyces piniterrae	Actinomycetes	<a href="#">NZ_SUMB0100002.1</a>
WP_189865296.1	Peptidase_C14+iHD+HSP90+wHTH	NZ_BMVW0100017.1:154197-172050	GCF_014650915.1 1747	*Peptidase_C14+iHD+HSP90+wHTH->CX2CXnCXCXnH->3TM-2C-EC->	Streptomyces poonensis	Actinomycetes	<a href="#">NZ_BMVW0100017.1</a>

WP_158685720.1	iHD+HSP90+wHTH+wHTH	NZ_KB913030.1:5923635-5938546	GCF_000384175.1	1262	HTH_31->*iHD+HSP90+wHTH+wHTH->ACET->NIR_SIR_ferr+NIR_SIR+NIR_SIR_ferr+NIR_SIR->	Streptomyces purpureus KA281	Actinomycetes	<a href="#">NZ_KB913030.1</a>
WP_058852041.1	CASPASE+iHD+HSP90+wHTH	NZ_LOCL01000062.1:516241-535602	GCF_001482415.1	1664	*CASPASE+iHD+HSP90+wHTH->CX2CXnCXnH->3TM-2C-EC->	Streptomyces silvensis	Actinomycetes	<a href="#">NZ_LOCL01000062.1</a>
WP_074002516.1	iHD+HSP90+wHTH+wHTH+wHTH	NZ_LIPD0100004.1:626946-639328	GCF_001905545.1	1266	?->Cupredoxin->*iHD+HSP90+wHTH+wHTH+wHTH->?->	Streptomyces sp. CB02056	Actinomycetes	<a href="#">NZ_LIPD0100004.1</a>
SCE28337.1	iHD+wHTH+wHTH+wHTH	FML01000350.1:3416-15162	GCA_900091815.1	1257	Gln-synt_N+Gln-synt_C->*iHD+wHTH+wHTH+wHTH->ST-Hiskin->	Streptomyces sp. DfronaAA-171	Actinomycetes	<a href="#">FML01000350.1</a>
WP_210574977.1	CASPASE+iHD+HSP90+wHTH+wHTH	NZ_JAFFSU01000007.1:316080-332134	GCF_017948455.1	1651	Putative_PNPOx->?->*CASPASE+iHD+HSP90+wHTH+wHTH->CX2CXnCXnH->3TM-2C-EC->	Streptomyces sp. GESEQ-4	Actinomycetes	<a href="#">NZ_JAFFSU01000007.1</a>
WP_205018404.1	CASPASE+iHD+HSP90+wHTH+wHTH+wHTH+wHTH+wHTH	NZ_JAFBGA01000001.1:496528-510121	GCF_016909575.1	1720	?->Pepco->*CASPASE+iHD+HSP90+wHTH+wHTH+wHTH+wHTH+wHTH->DoxX->?->	Streptomyces sp. HB132	Actinomycetes	<a href="#">NZ_JAFBGA01000001.1</a>
WP_215132238.1	CASPASE+iHD+HSP90	NZ_JAGGPA01000025.1:28400-40796	GCF_018614035.1	1650	FAD-NAD-dep-oxidoreductase->?->*CASPASE+iHD+HSP90->CX2CXnCXnH->3TM-2C-EC->	Streptomyces sp. ISL-96	Actinomycetes	<a href="#">NZ_JAGGPA01000025.1</a>
SCG03174.1	iHD+HSP90+wHTH+wHTH+wHTH+wHTH+wHTH	FMDK01000769.1:128-7397	GCA_900091995.1	1415	*iHD+HSP90+wHTH+wHTH+wHTH+wHTH+wHTH->	Streptomyces sp. MnatMP-M17	Actinomycetes	<a href="#">FMDK01000769.1</a>
WP_208522032.1	iHD+HSP90+wHTH+wHTH+wHTH+wHTH	NZ_JAGFN001000035.1:56656-78006	GCF_017592595.1	1309	*iHD+HSP90+wHTH+wHTH+wHTH+wHTH->PSE->PSE->PSE->HOP2->?->	Streptomyces sp. NEAU-YJ-81	Actinomycetes	<a href="#">NZ_JAGFN001000035.1</a>
WP_088575546.1	CASPASE+iHD+HSP90+wHTH+wHTH+wHTH+wHTH+wHTH	NZ_FYEJ0100008.1:196782-212294	GCF_900187925.1	1715	Pepco->*CASPASE+iHD+HSP90+wHTH+wHTH+wHTH+wHTH+wHTH->	Streptomyces sp. PgaaA7	Actinomycetes	<a href="#">NZ_FYEJ0100008.1</a>
WP_079045068.1	CASPASE+iHD+HSP90+wHTH	NZ_LMEP0100025.1:330919-344743	GCF_001426405.1	1686	Putative_PNPOx->*CASPASE+iHD+HSP90+wHTH->CX2CXnCXnH->3TM-2C-EC->	Streptomyces sp. Root1304	Actinomycetes	<a href="#">NZ_LMEP0100025.1</a>

WP_164302475.1	CASPASE+iHD+HSP90+wHTH+wHTH	NZ_JAAGMG010000427.1:7544-22927	GCF_010548525.1 1758	Amidohydro_2->Amidohydro_2->*CASPASE+iHD+HSP90+wHTH+wHTH->CX2CXnCXCXnH->3TM-2C-EC->	Actinomycetes	<a href="#">NZ_JAAGMG010000427.1</a>
WP_161166934.1	iHD+HSP90+wHTH+wHTH+wHTH+wHTH+wHTH	NZ_WWHX01000695.1:2227-12485	GCF_009862125.1 1431	*iHD+HSP90+wHTH+wHTH+wHTH+wHTH->	Actinomycetes	<a href="#">NZ_WWHX01000695.1</a>
WP_112472422.1	CASPASE+iHD+HSP90+wHTH	NZ_LXWD01000026.1:9459-24619	GCF_003268555.1 1606	?->*CASPASE+iHD+HSP90+wHTH->CX2CXnCXCXnH->3TM-2C-EC->	Actinomycetes	<a href="#">NZ_LXWD01000026.1</a>
WP_121515784.1	iHD+HSP90+wHTH+wHTH+wHTH+wHTH+wHTH	NZ_RCHV0100002.1:278165-292923	GCF_003665095.1 1327	Lipase_GDSL_2->?->iHD+HSP90+wHTH+wHTH+wHTH+wHTH->Glyco_hydro_130->F5_F8_type_C+DISCOIDIN->	Streptomyces	<a href="#">NZ_RCHV0100002.1</a>
WP_171114306.1	CASPASE+iHD+HSP90+wHTH+wHTH+wHTH+wHTH+wHTH	NZ_CP053109.1:3673245-3686310	GCF_013009255.1 1689	Pepco->*CASPASE+iHD+HSP90+wHTH+wHTH+wHTH+wHTH->	Streptomyces	<a href="#">NZ_CP053109.1</a>
AEM81006.1	CASPASE+iHD+HSP90+wHTH+wHTH+wHTH+wHTH+wHTH	CP002994.1:1079084-1091949	GCA_000147815.3 1694	Flavoprotein->?->*CASPASE+iHD+HSP90+wHTH+wHTH+wHTH+wHTH->	Actinomycetes	<a href="#">CP002994.1</a>
WP_048586600.1	CASPASE+iHD+HSP90	NZ_LGUQ01000198.1:71681-90423	GCF_001270485.1 1706	Rhomboid->Glyco_hydro_46->*CASPASE+iHD+HSP90->CX2CXnCXCXnH->3TM-2C-EC->	Actinomycetes	<a href="#">NZ_LGUQ01000198.1</a>
WP_053200890.1	Trypsin+iHD+HSP90+wHTH+wHTH+wHTH+wHTH+wHTH	NZ_LGUQ01000235.1:923-13630	GCF_001270485.1 1597	PSE->*Trypsin+iHD+HSP90+wHTH+wHTH+wHTH+wHTH+wHTH->	Streptomyces	<a href="#">NZ_LGUQ01000235.1</a>
WP_048586580.1	iHD+HSP90+wHTH+wHTH+wHTH+wHTH+wHTH	NZ_LFNT01000088.1:14244-27534	GCF_001047325.1 1403	*iHD+HSP90+wHTH+wHTH+wHTH+wHTH+wHTH->	Streptomyces	<a href="#">NZ_LFNT01000088.1</a>
MBF0310456.1	REase-ABC-assc+iHD+HSP90+wHTH	JADGAQ01000121.1:5880-12727	GCA_015231925.1 1125	PSE->BrnA_antitoxin->REase-ABC-assc+iHD+HSP90+wHTH->?->Polbeta->	Magnetococcales bacterium	<a href="#">JADGAQ01000121.1</a>
WP_147163312.1	REase-ABC-assc+iHD+HSP90+wHTH+wHTH+wHTH+wHTH+wHTH	NZ_BJZ00100032.1:1918-16799	GCF_007992075.1 1383	Formyl_trans_N->THF_DHG_CYH+THF_DHG_CYH_C->REase-ABC-assc+iHD+HSP90+wHTH+wHTH+wHTH+wHTH->	Pararhodospirillum oryzae	<a href="#">NZ_BJZ00100032.1</a>
WP_198026927.1	Calcineurin-CE+iHD+HSP90+wHTH+wHTH+wHTH+wHTH	NZ_KL448329.1:9368-23540	GCF_000709345.1 1959	*Calcineurin-CE+iHD+HSP90+wHTH+wHTH+wHTH+wHTH->?->	Polaromonas glacialis	<a href="#">NZ_KL448329.1</a>
NQU21064.1	CASPASE+iHD+HSP90+wHTH+wHTH+wHTH+wHTH+wHTH	JABMRB010000306.1:1171-13080	GCA_013202865.1 1490	Pepco->*CASPASE+iHD+HSP90+wHTH+wHTH+wHTH+wHTH+wHTH->	Candidatus Nealsonbacteria bacterium	<a href="#">JABMRB010000306.1</a>
WP_019925848.1	iHD+HSP90+wHTH+wHTH+wHTH+wHTH+wHTH+wHTH	NZ_KB907307.1:986436-999884	GCF_000381925.1 1484	Carnacyltransf->?->iHD+HSP90+wHTH+wHTH+wHTH+wHTH+wHTH->?->PRA-PH->	Nocardia sp. BMG11209	<a href="#">NZ_KB907307.1</a>
WP_190769266.1	CASPASE+iHD+HSP90+wHTH+wHTH+wHTH+wHTH+wHTH	NZ_JACJP001000068.1:1-11535	GCF_014696105.1 1497	Pepco->*CASPASE+iHD+HSP90+wHTH+wHTH+wHTH+wHTH+wHTH->	Microcoleus sp. FACHB-1515	<a href="#">NZ_JACJP001000068.1</a>
WP_215595218.1	REase-ABC-assc+iHD+HSP90	NZ_JAHHN01000023.1:97-6830	GCF_018760735.1 1204	*REase-ABC-assc+iHD+HSP90->	Hymenobacter piscis	<a href="#">NZ_JAHHN01000023.1</a>
WP_054571020.1	TIR_2+CASPASE+iHD+HSP90+wHTH+wHTH+wHTH+wHTH+wHTH+wHTH+wHTH	NZ_LFCW0100012.1:2095-19610	GCF_001306465.1 2227	FtsX->PSE->LuxR-HTH->*TIR_2+CASPASE+iHD+HSP90+wHTH+wHTH+wHTH+wHTH+wHTH+wHTH->	Frankia sp. R43	<a href="#">NZ_LFCW0100012.1</a>
KJE23829.1	TIR_2+CASPASE+iHD+HSP90+wHTH+wHTH+wHTH+wHTH+wHTH+wHTH+wHTH+wHTH	JYFN0100010.1:15162-32152	GCA_000948395.1 2256	Aldo_ket_red->*TIR_2+CASPASE+iHD+HSP90+wHTH+wHTH+wHTH+wHTH+wHTH+wHTH->assembly_gap->	Frankia torreyi	<a href="#">JYFN0100010.1</a>
WP_200285139.1	Peptidase_C14+iHD+HSP90	NZ_NRRS0100065.1:196-13558	GCF_016583795.1 1515	*Peptidase_C14+iHD+HSP90->	Rhabdochromatium marinum	<a href="#">NZ_NRRS0100065.1</a>
WP_232408133.1	Trypsin+iHD+HSP90+wHTH+wHTH+wHTH	NZ_CP089309.1:5516940-5533158	GCF_021228795.1 1617	Lipase_3+Subtilisin+Peptidase_S8->Peptidase_S8->*Trypsin+iHD+HSP90+wHTH+wHTH+wHTH->	Thiocapsa bogorovii	<a href="#">NZ_CP089309.1</a>
WP_231447650.1	CASPASE+iHD+HSP90+wHTH	NZ_JAJOMB01000018.1:165115-178278	GCF_021129305.1 1660	*CASPASE+iHD+HSP90+wHTH->CX2CXnCXCXnH->3TM-2C-EC->	Kineosporia babensis	<a href="#">NZ_JAJOMB01000018.1</a>
MBB2943582.1	CASPASE+iHD+HSP90+wHTH+wHTH+wHTH	JACHWI01000003.1:56643-69844	GCA_014191235.1 1625	*CASPASE+iHD+HSP90+wHTH+wHTH->?->	Actinoplanes lutulentus	<a href="#">JACHWI01000003.1</a>
GIE87618.1	CASPASE+iHD+HSP90+wHTH+wHTH	BOMU0100054.1:22836-41419	GCA_016862355.1 1601	*CASPASE+iHD+HSP90+wHTH->DctM->NMT1_3->	Actinoplanes regularis	<a href="#">BOMU0100054.1</a>
WP_221327876.1	CASPASE+iHD+HSP90+wHTH+wHTH+wHTH	NZ_AP024745.1:3759727-3772618	GCF_019704555.1 1624	Oxidored_FMN->*CASPASE+iHD+HSP90+wHTH+wHTH->CX2CXnCXCXnH->3TM-2C-EC->	Actinoplanes sp. L3-i22	<a href="#">NZ_AP024745.1</a>
WP_015624431.1	CASPASE+iHD+HSP90+wHTH+wHTH+wHTH+wHTH+wHTH	NC_021191.1:7274640-7290164	GCF_000389965.1 1664	TPR_12+FAM70->Pepco->*CASPASE+iHD+HSP90+wHTH+wHTH+wHTH+wHTH+wHTH->GGDEF->TauE->	Actinoplanes sp. N902-109	<a href="#">NC_021191.1</a>
MBT8224903.1	iHD+HSP90+wHTH+wHTH+wHTH+wHTH+wHTH	JAHHJM01000095.1:1-14669	GCA_018680335.1 1323	Peptidase_S26->?->iHD+HSP90+wHTH+wHTH+wHTH+wHTH+wHTH->	Dactylosporangium sp.	<a href="#">JAHHJM01000095.1</a>

#P01276					
MP_12167536.1	Calcaselvina-Cl+15TANDM	nucleotide:ID position	assembly	plan	organism
MP_08495318.1	Calcarinovir-Cl+15TANDM	NZ_CCP33351.1 2996861-2975545	GCF_011707825.1 977	Mesophilobium erdnallii	NZ_CFB33361.1
MP_08495344.1	Calcarinovir-Cl+15TANDM	NZ_AVM9100041.1:2996861-3137427	GCF_00930245.1 1989	Mesophilobium sp. AVM9100041	NZ_CFB33371.1
MP_12808833.1	Calcarinovir-Cl+15TANDM	NZ_CCP33352.1 2996861-2975543	GCF_00930245.1 1989	Mesophilobium sp. AVM9100041	NZ_CFB33381.1
MP_12808833.1	Calcarinovir-Cl+15TANDM	NZ_CCP33372.1 1885812-1985246	GCF_00800895.1 1998	Mesophilobium sp. 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
















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