Phyre^2

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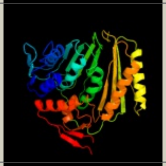
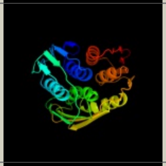
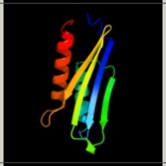
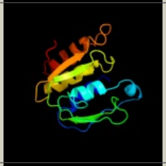
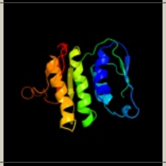
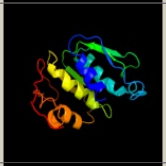
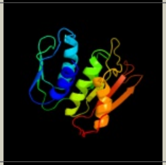
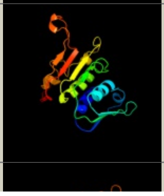
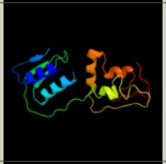
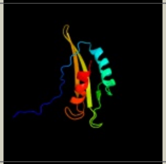
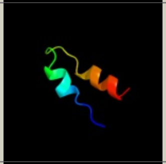
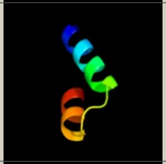
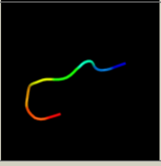
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1qmiC_	Alignment		100.0	99	**PDB header:**rna 3'-terminal phosphate cyclase **Chain:** C: **PDB Molecule:**rna 3'-terminal phosphate cyclase; **PDBTitle:** crystal structure of rna 3'-terminal phosphate cyclase, an2 ubiquitous enzyme with unusual topology
2	c3pqvD_	Alignment		100.0	18	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**rcl1 protein; **PDBTitle:** cyclase homolog
3	d1qmha2	Alignment		100.0	100	**Fold:**IF3-like **Superfamily:**EPT/RTPC-like **Family:**RNA 3'-terminal phosphate cyclase, RPTC
4	d1qmha1	Alignment		99.9	100	**Fold:**Thioredoxin fold **Superfamily:**RNA 3'-terminal phosphate cyclase, RPTC, insert domain **Family:**RNA 3'-terminal phosphate cyclase, RPTC, insert domain
5	d1p88a_	Alignment		95.7	15	**Fold:**IF3-like **Superfamily:**EPT/RTPC-like **Family:**Enolpyruvate transferase, EPT
6	c2o0zA_	Alignment		94.7	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-phosphoshikimate 1-carboxyvinyltransferase; **PDBTitle:** mycobacterium tuberculosis epsp synthase in complex with2 product (eps)
7	d1uaea_	Alignment		94.5	17	**Fold:**IF3-like **Superfamily:**EPT/RTPC-like **Family:**Enolpyruvate transferase, EPT
8	d1g6sa_	Alignment		93.0	21	**Fold:**IF3-like **Superfamily:**EPT/RTPC-like **Family:**Enolpyruvate transferase, EPT
9	c2pqdA_	Alignment		92.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-phosphoshikimate 1-carboxyvinyltransferase; **PDBTitle:** a100g cp4 epsps liganded with (r)-difluoromethyl tetrahedral reaction2 intermediate analog
10	c3roiA_	Alignment		91.8	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-phosphoshikimate 1-carboxyvinyltransferase; **PDBTitle:** 2.20 angstrom resolution structure of 3-phosphoshikimate 1-2 carboxyvinyltransferase (aroa) from coxiella burnetii
11	c3rmtB_	Alignment		91.7	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**3-phosphoshikimate 1-carboxyvinyltransferase 1; **PDBTitle:** crystal structure of putative 5-enolpyruvoylshikimate-3-phosphate2 synthase from bacillus halodurans c-125

12	c2yvwA_	Alignment		87.1	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine 1-carboxyvinyltransferase; **PDBTitle:** crystal structure of udp-n-acetylglucosamine 1-carboxyvinyltransferase2 from aquifex aeolicus vf5
13	d1ejda_	Alignment		81.4	17	**Fold:**IF3-like **Superfamily:**EPT/RTPC-like **Family:**Enolpyruvate transferase, EPT
14	c3r38A_	Alignment		73.0	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine 1-carboxyvinyltransferase 1; **PDBTitle:** 2.23 angstrom resolution crystal structure of udp-n-acetylglucosamine2 1-carboxyvinyltransferase (mura) from listeria monocytogenes egd-e
15	d1rf6a_	Alignment		69.6	13	**Fold:**IF3-like **Superfamily:**EPT/RTPC-like **Family:**Enolpyruvate transferase, EPT
16	d1ul7a_	Alignment		46.3	14	**Fold:**TBP-like **Superfamily:**KA1-like **Family:**Kinase associated domain 1, KA1
17	c3cvoA_	Alignment		34.5	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methyltransferase-like protein of unknown function; **PDBTitle:** crystal structure of a methyltransferase-like protein (spo2022) from2 silicibacter pomeroyi dss-3 at 1.80 a resolution
18	c2uwjE_	Alignment		34.3	24	**PDB header:**chaperone **Chain:** E: **PDB Molecule:**type iii export protein psce; **PDBTitle:** structure of the heterotrimeric complex which regulates2 type iii secretion needle formation
19	c1hskA_	Alignment		28.2	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**udp-n-acetylenolpyruvoylglucosamine reductase; **PDBTitle:** crystal structure of s. aureus murb
20	d2e1ba1	Alignment		26.7	75	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**AlaX-M N-terminal domain-like
21	d1hska2	Alignment	not modelled	23.6	23	**Fold:**Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain **Superfamily:**Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain **Family:**Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain
22	d1f46a_	Alignment	not modelled	22.2	12	**Fold:**TBP-like **Superfamily:**Cell-division protein ZipA, C-terminal domain **Family:**Cell-division protein ZipA, C-terminal domain
23	c2e1bA_	Alignment	not modelled	16.0	75	**PDB header:**ligase, hydrolase **Chain:** A: **PDB Molecule:**216aa long hypothetical alanyl-trna synthetase; **PDBTitle:** crystal structure of the alax-m trans-editing enzyme from2 pyrococcus horikoshii
24	c2q1kA_	Alignment	not modelled	13.2	29	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**asce; **PDBTitle:** cyrstal structure of asce from aeromonas hydrophilla
25	d2q07a3	Alignment	not modelled	11.4	38	**Fold:**Cystatin-like **Superfamily:**Pre-PUA domain **Family:**AF0587 pre C-terminal domain-like
26	d1h72c1	Alignment	not modelled	10.9	16	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**GHMP Kinase, N-terminal domain
27	d2od4a1	Alignment	not modelled	10.9	21	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Marine metagenome family DABB2
28	d1mp9a1	Alignment	not modelled	10.7	23	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain

29	d1hh2p3	Alignment	not modelled	9.9	5	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Prokaryotic type KH domain (KH-domain type II) **Family:**Prokaryotic type KH domain (KH-domain type II)
30	d2zdra1	Alignment	not modelled	9.8	12	**Fold:**beta-clip **Superfamily:**AFP III-like domain **Family:**AFP III-like domain
31	d1nh2a1	Alignment	not modelled	9.4	28	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
32	c2xi5D_	Alignment	not modelled	9.4	13	**PDB header:**transferase **Chain:** D: **PDB Molecule:**rna polymerase l; **PDBTitle:** n-terminal endonuclease domain of la crosse virus l-protein
33	c2xi7B_	Alignment	not modelled	9.3	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**rna polymerase l; **PDBTitle:** n-terminal endonuclease domain of la crosse virus l-protein
34	d2a9sa1	Alignment	not modelled	9.3	5	**Fold:**Anticodon-binding domain-like **Superfamily:**CinA-like **Family:**CinA-like
35	d1ul1x1	Alignment	not modelled	9.1	12	**Fold:**SAM domain-like **Superfamily:**5' to 3' exonuclease, C-terminal subdomain **Family:**5' to 3' exonuclease, C-terminal subdomain
36	d1nwpa_	Alignment	not modelled	9.0	21	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
37	d1cuoa_	Alignment	not modelled	8.3	13	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
38	c2ch4A_	Alignment	not modelled	7.8	18	**PDB header:**transferase/chemotaxis **Chain:** A: **PDB Molecule:**chemotaxis protein chea; **PDBTitle:** complex between bacterial chemotaxis histidine kinase chea2 domains p4 and p5 and receptor-adaptor protein chew
39	d1cf2o2	Alignment	not modelled	7.4	36	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
40	d1rkra_	Alignment	not modelled	7.3	21	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
41	d1qnaa1	Alignment	not modelled	7.3	20	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
42	c1fwlD_	Alignment	not modelled	7.0	16	**PDB header:**transferase **Chain:** D: **PDB Molecule:**homoserine kinase; **PDBTitle:** crystal structure of homoserine kinase
43	d1aisa1	Alignment	not modelled	6.7	26	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
44	c1gmuB_	Alignment	not modelled	6.6	31	**PDB header:**metallochaperone **Chain:** B: **PDB Molecule:**uree; **PDBTitle:** structure of uree
45	d1cc3a_	Alignment	not modelled	6.4	17	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
46	d1mp9a2	Alignment	not modelled	5.8	14	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
47	c2rrnA_	Alignment	not modelled	5.8	14	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**probable secdf protein-export membrane protein; **PDBTitle:** solution structure of secdf periplasmic domain p4
48	d1cdwa1	Alignment	not modelled	5.4	18	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
49	d1gmua2	Alignment	not modelled	5.3	30	**Fold:**Ferredoxin-like **Superfamily:**Urease metallochaperone UreE, C-terminal domain **Family:**Urease metallochaperone UreE, C-terminal domain