Phyre^2

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Description	P0ACW2
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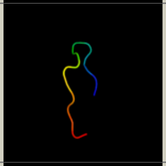
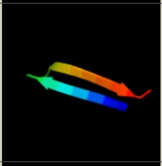
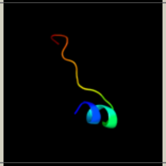
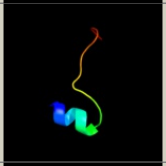
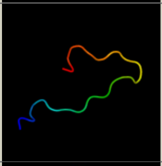
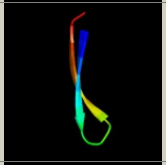
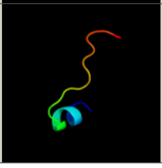
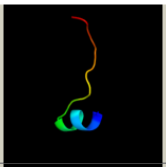
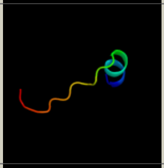
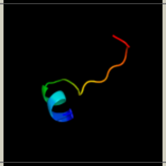
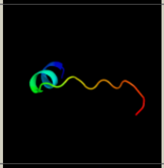
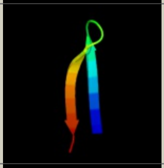
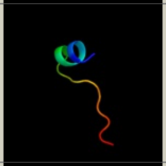
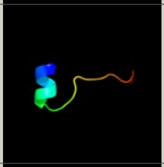
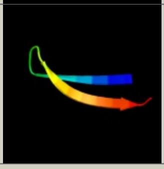
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3k0zB_	Alignment		28.2	22	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative polyketide cyclase; **PDBTitle:** crystal structure of putative polyketide cyclase (np_977253.1) from2 bacillus cereus atcc 10987 at 1.91 a resolution
2	c3hwpA_	Alignment		25.1	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phlg; **PDBTitle:** crystal structure and computational analyses provide insights into the2 catalytic mechanism of 2, 4-diacetylphloroglucinol hydrolase phlg3 from pseudomonas fluorescens
3	d1ewsa_	Alignment		24.9	38	**Fold:**Defensin-like **Superfamily:**Defensin-like **Family:**Defensin
4	d2geya1	Alignment		19.8	11	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**SnoaL-like polyketide cyclase
5	d1wk1a_	Alignment		19.6	32	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**C-type lectin domain
6	d2coha2	Alignment		19.6	17	**Fold:**Double-stranded beta-helix **Superfamily:**cAMP-binding domain-like **Family:**cAMP-binding domain
7	d1rdl1_	Alignment		17.7	21	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**C-type lectin domain
8	d1zhva1	Alignment		15.2	19	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Atu0741-like
9	c3ehcA_	Alignment		15.2	11	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**snoal-like polyketide cyclase; **PDBTitle:** crystal structure of a snoal-like polyketide cyclase (atu3018) from2 agrobacterium tumefaciens str. c58 at 2.12 a resolution
10	c3dlmA_	Alignment		14.3	31	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histone-lysine n-methyltransferase setdb1; **PDBTitle:** crystal structure of tudor domain of human histone-lysine n-2 methyltransferase setdb1
11	d3bdwa1	Alignment		13.7	26	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**C-type lectin domain

12	d1mpua_	Alignment		13.3	21	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**C-type lectin domain
13	c3kkgA_	Alignment		12.3	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative snoal-like polyketide cyclase; **PDBTitle:** crystal structure of putative snoal-like polyketide cyclase2 (yp_509242.1) from jannaschia sp. ccs1 at 1.40 a resolution
14	c1hupA_	Alignment		12.1	21	**PDB header:**c-type lectin **Chain:** A: **PDB Molecule:**mannose-binding protein; **PDBTitle:** human mannose binding protein carbohydrate recognition domain2 trimerizes through a triple alpha-helical coiled-coil
15	d1r13a1	Alignment		11.3	26	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**C-type lectin domain
16	d1hupa1	Alignment		11.2	21	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**C-type lectin domain
17	d2f99a1	Alignment		10.5	17	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**SnoaL-like polyketide cyclase
18	d1fifa1	Alignment		10.3	24	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**C-type lectin domain
19	d1ja3a_	Alignment		10.2	21	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**C-type lectin domain
20	c3f9sB_	Alignment		9.8	0	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative polyketide cyclase; **PDBTitle:** crystal structure of a putative polyketide cyclase (lferr_0659) from2 acidithiobacillus ferrooxidans atcc at 1.76 a resolution
21	d1egga_	Alignment	not modelled	9.7	21	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**C-type lectin domain
22	c1v91A_	Alignment	not modelled	9.7	44	**PDB header:**toxin **Chain:** A: **PDB Molecule:**delta-palutoxin it2; **PDBTitle:** solution structure of insectidal toxin delta-paluit2-nh2
23	c3cfwA_	Alignment	not modelled	9.6	12	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**l-selectin; **PDBTitle:** l-selectin lectin and egf domains
24	d2msba_	Alignment	not modelled	9.4	24	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**C-type lectin domain
25	d2gexa1	Alignment	not modelled	9.4	11	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**SnoaL-like polyketide cyclase
26	c3ff7C_	Alignment	not modelled	9.4	16	**PDB header:**cell adhesion/immunue system **Chain:** C: **PDB Molecule:**killer cell lectin-like receptor subfamily g **PDBTitle:** structure of nk cell receptor klrg1 bound to e-cadherin
27	c3fh1A_	Alignment	not modelled	9.3	10	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized ntf2-like protein; **PDBTitle:** crystal structure of a ntf2-like protein of unknown function (mll8193)2 from mesorhizobium loti at 1.60 a resolution
28	d1pwba1	Alignment	not modelled	8.9	29	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**C-type lectin domain
29	d1g1ta1	Alignment	not modelled	8.9	16	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like

						Family:C-type lectin domain
30	d1byfa_	Alignment	not modelled	8.9	21	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**C-type lectin domain
31	d1rjha_	Alignment	not modelled	8.5	26	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**C-type lectin domain
32	c3m9zA_	Alignment	not modelled	8.4	21	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**killer cell lectin-like receptor subfamily b member 1a; **PDBTitle:** crystal structure of extracellular domain of mouse nkr-p1a
33	d1g1sa1	Alignment	not modelled	7.9	12	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**C-type lectin domain
34	d1id0a_	Alignment	not modelled	7.5	10	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**Histidine kinase
35	d1sjwa_	Alignment	not modelled	7.4	12	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**SnoaL-like polyketide cyclase
36	c3g12A_	Alignment	not modelled	7.1	26	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative lactoylglutathione lyase; **PDBTitle:** crystal structure of a putative lactoylglutathione lyase2 from bdellovibrio bacteriovorus
37	c1r13A_	Alignment	not modelled	7.1	29	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**pulmonary surfactant-associated protein a; **PDBTitle:** carbohydrate recognition and neck domains of surfactant protein a (sp-2 a)
38	c1kwwC_	Alignment	not modelled	7.0	24	**PDB header:**immune system, sugar binding protein **Chain:** C: **PDB Molecule:**mannose-binding protein a; **PDBTitle:** rat mannose protein a complexed with a-me-fuc.
39	c2vuvA_	Alignment	not modelled	7.0	21	**PDB header:**sugar-binding protein **Chain:** A: **PDB Molecule:**codakine; **PDBTitle:** crystal structure of codakine at 1.3a resolution
40	c1eslA_	Alignment	not modelled	6.8	18	**PDB header:**cell adhesion protein **Chain:** A: **PDB Molecule:**human e-selectin; **PDBTitle:** insight into e-selectin(slash)ligand interaction from the2 crystal structure and mutagenesis of the lec(slash)egf3 domains
41	c1twcF_	Alignment	not modelled	6.5	33	**PDB header:**transcription **Chain:** F: **PDB Molecule:**dna-directed rna polymerases i, ii, and iii 23 **PDBTitle:** rna polymerase ii complexed with gtp
42	d1twff_	Alignment	not modelled	6.4	33	**Fold:**RPB6/omega subunit-like **Superfamily:**RPB6/omega subunit-like **Family:**RPB6
43	c3g0kA_	Alignment	not modelled	6.4	7	**PDB header:**ca-binding protein **Chain:** A: **PDB Molecule:**putative membrane protein; **PDBTitle:** crystal structure of a protein of unknown function with a cystatin-2 like fold (saro_2880) from novosphingobium aromaticivorans dsm at3 1.30 a resolution
44	c3g8zA_	Alignment	not modelled	6.3	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein of unknown function with cystatin-like fold; **PDBTitle:** crystal structure of protein of unknown function with cystatin-like2 fold (np_639274.1) from xanthomonas campestris at 1.90 a resolution
45	c3bc6D_	Alignment	not modelled	5.9	16	**PDB header:**immune system **Chain:** D: **PDB Molecule:**c-type lectin domain family 4 member k; **PDBTitle:** the carbohydrate recognition domain of langerin reveals high2 structural similarity with the one of dc-sign but an additional,3 calcium-independent sugar-binding site
46	d1wqjb1	Alignment	not modelled	5.8	42	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Growth factor receptor domain **Family:**Growth factor receptor domain
47	d1hq8a_	Alignment	not modelled	5.7	21	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**C-type lectin domain
48	d1qo3d_	Alignment	not modelled	5.6	21	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**C-type lectin domain
49	c3i0yC_	Alignment	not modelled	5.6	6	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**putative polyketide cyclase; **PDBTitle:** crystal structure of a putative polyketide cyclase (xcc0381) from2 xanthomonas campestris pv. campestris at 1.50 a resolution
50	c3g8lD_	Alignment	not modelled	5.6	21	**PDB header:**immune system **Chain:** D: **PDB Molecule:**lectin-related nk cell receptor ly49l1; **PDBTitle:** crystal structure of murine natural killer cell receptor,2 ly49l4
51	d3c8ja1	Alignment	not modelled	5.5	26	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**C-type lectin domain
52	c1zhvA_	Alignment	not modelled	5.5	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein atu0741; **PDBTitle:** x-ray crystal structure protein atu0741 from agobacterium tumefaciens.2 northeast structural genomics consortium target atr8.
53	c1fm5A_	Alignment	not modelled	5.4	24	**PDB header:**immune system **Chain:** A: **PDB Molecule:**early activation antigen cd69; **PDBTitle:** crystal structure of human cd69

54	d2c2aa2	Alignment	not modelled	5.4	14	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**Histidine kinase
55	d1ua7a1	Alignment	not modelled	5.2	33	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
56	c2qg7A_	Alignment	not modelled	5.1	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ethanolamine kinase pv091845; **PDBTitle:** plasmodium vivax ethanolamine kinase pv091845
57	d1jaea1	Alignment	not modelled	5.1	50	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
58	d1xpha1	Alignment	not modelled	5.1	16	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**C-type lectin domain
59	c3c22B_	Alignment	not modelled	5.1	16	**PDB header:**immune system, sugar binding protein **Chain:** B: **PDB Molecule:**c-type lectin domain family 4 member k; **PDBTitle:** crystal structure of the carbohydrate recognition domain of2 human langerin