Phyre^2

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Description	P0ADE2
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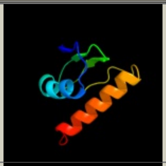
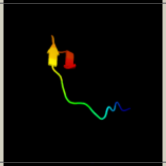
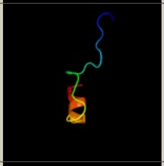
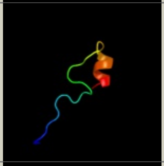
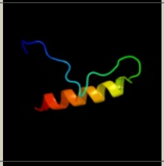
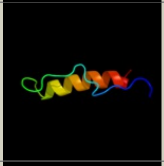
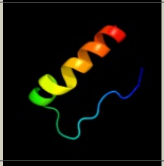
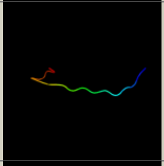
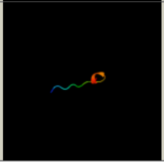
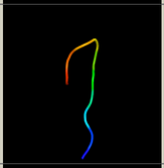
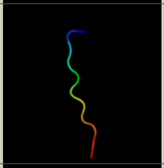
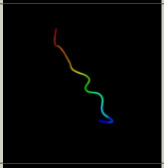
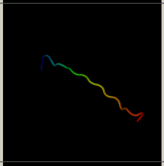
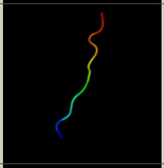
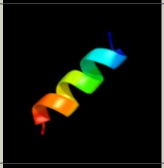
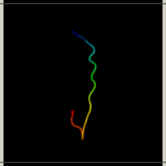
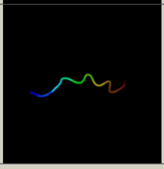
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2jroA_	Alignment		100.0	27	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of so0334 from shewanella oneidensis. northeast2 structural genomics target sor75
2	d1t0hb_	Alignment		36.1	29	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
3	d1njha_	Alignment		24.0	20	**Fold:**Hypothetical protein YojF **Superfamily:**Hypothetical protein YojF **Family:**Hypothetical protein YojF
4	c2ow7A_	Alignment		17.6	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-mannosidase 2; **PDBTitle:** golgi alpha-mannosidase ii complex with (1r,6s,7r,8s)-1-2 thioniabicyclo[4.3.0]nonan-7,8-diol chloride
5	c1htyA_	Alignment		16.0	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-mannosidase ii; **PDBTitle:** golgi alpha-mannosidase ii
6	c1o7dA_	Alignment		13.6	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lysosomal alpha-mannosidase; **PDBTitle:** the structure of the bovine lysosomal a-mannosidase2 suggests a novel mechanism for low ph activation
7	d3bvua3	Alignment		13.5	19	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**alpha-mannosidase
8	d1ve2a1	Alignment		12.5	36	**Fold:**Tetrapyrrole methylase **Superfamily:**Tetrapyrrole methylase **Family:**Tetrapyrrole methylase
9	c2b1kA_	Alignment		12.5	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbe; **PDBTitle:** crystal structure of e. coli ccmg protein
10	c3i0yC_	Alignment		11.6	17	**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
11	c3jx9B_	Alignment		11.2	38	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative phosphoheptose isomerase; **PDBTitle:** crystal structure of putative phosphoheptose isomerase2 (yp_001815198.1) from exiguobacterium sp. 255-15 at 1.95 a resolution

12	d1v3ya_	Alignment		10.9	13	**Fold:**Peptide deformylase **Superfamily:**Peptide deformylase **Family:**Peptide deformylase
13	d1o12a1	Alignment		10.7	45	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**N-acetylglucosamine-6-phosphate deacetylase, NagA
14	c1cbfA_	Alignment		10.4	36	**PDB header:**methyltransferase **Chain:** A: **PDB Molecule:**cobalt-precorrin-4 transmethylase; **PDBTitle:** the x-ray structure of a cobalamin biosynthetic enzyme, cobalt2 precorrin-4 methyltransferase, cbif
15	d1cbfa_	Alignment		10.4	36	**Fold:**Tetrapyrrole methylase **Superfamily:**Tetrapyrrole methylase **Family:**Tetrapyrrole methylase
16	d1oh4a_	Alignment		10.2	21	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Family 27 carbohydrate binding module, CBM27
17	c2e0kA_	Alignment		10.2	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**precorrin-2 c20-methyltransferase; **PDBTitle:** crystal structure of cbil, a methyltransferase involved in anaerobic2 vitamin b12 biosynthesis
18	d1x4ta1	Alignment		10.0	21	**Fold:**Long alpha-hairpin **Superfamily:**ISY1 domain-like **Family:**ISY1 N-terminal domain-like
19	d2gexa1	Alignment		9.9	17	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**SnoaL-like polyketide cyclase
20	c2qbuA_	Alignment		9.8	36	**PDB header:**transferase **Chain:** A: **PDB Molecule:**precorrin-2 methyltransferase; **PDBTitle:** crystal structure of methanothermobacter thermautotrophicus cbil
21	d2geya1	Alignment	not modelled	9.2	28	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**SnoaL-like polyketide cyclase
22	d1zyba1	Alignment	not modelled	9.2	35	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
23	d2k54a1	Alignment	not modelled	8.8	21	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Atu0742-like
24	c1g2cN_	Alignment	not modelled	8.7	30	**PDB header:**viral protein **Chain:** N: **PDB Molecule:**fusion protein (f); **PDBTitle:** human respiratory syncytial virus fusion protein core
25	d1pjqa2	Alignment	not modelled	8.6	20	**Fold:**Tetrapyrrole methylase **Superfamily:**Tetrapyrrole methylase **Family:**Tetrapyrrole methylase
26	c3hh1D_	Alignment	not modelled	8.4	27	**PDB header:**transferase **Chain:** D: **PDB Molecule:**tetrapyrrole methylase family protein; **PDBTitle:** the structure of a tetrapyrrole methylase family protein domain from2 chlorobium tepidum tls
27	c3ff2A_	Alignment	not modelled	8.4	20	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized cystatin fold protein (yp_497570.1) from **PDBTitle:** crystal structure of an uncharacterized cystatin fold protein2 (saro_2299) from novosphingobium aromaticivorans dsm at 1.90 a3 resolution
28	d1s4da_	Alignment	not modelled	7.9	18	**Fold:**Tetrapyrrole methylase **Superfamily:**Tetrapyrrole methylase **Family:**Tetrapyrrole methylase

29	c3f7xA_	Alignment	not modelled	7.7	22	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative polyketide cyclase; **PDBTitle:** crystal structure of a putative polyketide cyclase (pp0894) from2 pseudomonas putida kt2440 at 1.24 a resolution
30	c3k0zB_	Alignment	not modelled	7.5	16	**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
31	c3f14A_	Alignment	not modelled	7.5	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized ntf2-like protein; **PDBTitle:** crystal structure of ntf2-like protein of unknown function2 (yp_680363.1) from cytophaga hutchinsonii atcc 33406 at 1.45 a3 resolution
32	c3f8hA_	Alignment	not modelled	7.5	17	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative polyketide cyclase; **PDBTitle:** crystal structure of a putative polyketide cyclase (tm1040_3560) from2 silicibacter sp. tm1040 at 2.00 a resolution
33	c3myuB_	Alignment	not modelled	7.2	18	**PDB header:**vib binding protein **Chain:** B: **PDB Molecule:**high affinity transport system protein p37; **PDBTitle:** mycoplasma genitalium mg289
34	d1va0a1	Alignment	not modelled	7.1	40	**Fold:**Tetrapyrrole methylase **Superfamily:**Tetrapyrrole methylase **Family:**Tetrapyrrole methylase
35	c2hw2A_	Alignment	not modelled	7.1	55	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rifampin adp-ribosyl transferase; **PDBTitle:** crystal structure of rifampin adp-ribosyl transferase in2 complex with rifampin
36	d1rk8b_	Alignment	not modelled	6.8	35	**Fold:**Mago nashi protein **Superfamily:**Mago nashi protein **Family:**Mago nashi protein
37	c1t3jA_	Alignment	not modelled	6.8	14	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**mitofusin 1; **PDBTitle:** mitofusin domain hr2 v686m/i708m mutant
38	c2zvbA_	Alignment	not modelled	6.6	30	**PDB header:**transferase **Chain:** A: **PDB Molecule:**precorrin-3 c17-methyltransferase; **PDBTitle:** crystal structure of tt0207 from thermus thermophilus hb8
39	c1no1C_	Alignment	not modelled	6.6	36	**PDB header:**replication **Chain:** C: **PDB Molecule:**replisome organizer; **PDBTitle:** structure of truncated variant of b.subtilis spp1 phage g39p helicase2 loader/inhibitor protein
40	d1no1a_	Alignment	not modelled	6.6	36	**Fold:**Replisome organizer (g39p helicase loader/inhibitor protein) **Superfamily:**Replisome organizer (g39p helicase loader/inhibitor protein) **Family:**Replisome organizer (g39p helicase loader/inhibitor protein)
41	d1t3la2	Alignment	not modelled	6.5	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
42	c1r48A_	Alignment	not modelled	6.4	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**proline/betaine transporter; **PDBTitle:** solution structure of the c-terminal cytoplasmic domain2 residues 468-497 of escherichia coli protein prop
43	d2ih2a2	Alignment	not modelled	6.3	33	**Fold:**DNA methylase specificity domain **Superfamily:**DNA methylase specificity domain **Family:**TaqI C-terminal domain-like
44	d2ba0a2	Alignment	not modelled	6.0	20	**Fold:**Barrel-sandwich hybrid **Superfamily:**Ribosomal L27 protein-like **Family:**ECR1 N-terminal domain-like
45	c2l3bA_	Alignment	not modelled	6.0	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved protein found in conjugate transposon; **PDBTitle:** solution nmr structure of the bt_0084 lipoprotein from bacteroides2 thetaiotaomicron, northeast structural genomics consortium target3 btr376
46	c2qg8A_	Alignment	not modelled	5.8	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acyl carrier protein synthase py06285; **PDBTitle:** plasmodium yoelii acyl carrier protein synthase py06285 with adp bound
47	d1w6sb_	Alignment	not modelled	5.7	43	**Fold:**Non-globular all-alpha subunits of globular proteins **Superfamily:**Methanol dehydrogenase subunit **Family:**Methanol dehydrogenase subunit
48	c1w25B_	Alignment	not modelled	5.6	16	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**stalked-cell differentiation controlling protein; **PDBTitle:** response regulator pled in complex with c-digmp
49	c3ot2B_	Alignment	not modelled	5.6	24	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a putative nuclease belonging to duf8202 (ava_3926) from anabaena variabilis atcc 29413 at 1.96 a resolution
50	c3ot2A_	Alignment	not modelled	5.6	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a putative nuclease belonging to duf8202 (ava_3926) from anabaena variabilis atcc 29413 at 1.96 a resolution
51	d2ad6b1	Alignment	not modelled	5.6	35	**Fold:**Non-globular all-alpha subunits of globular proteins **Superfamily:**Methanol dehydrogenase subunit **Family:**Methanol dehydrogenase subunit
52	c3dluA_	Alignment	not modelled	5.5	15	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**signal recognition particle 19 kda protein; **PDBTitle:** structures of srp54 and srp19, the two proteins assembling2 the ribonucleic core of the signal recognition particle3 from the archaeon pyrococcus furiosus.

53	c2rfpA_	Alignment	not modelled	5.5	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative ntp pyrophosphohydrolase; **PDBTitle:** crystal structure of putative ntp pyrophosphohydrolase2 (yp_001813558.1) from exiguobacterium sibiricum 255-15 at 1.74 a3 resolution
54	c1tuhA_	Alignment	not modelled	5.4	32	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical protein egc068; **PDBTitle:** structure of bal32a from a soil-derived mobile gene cassette
55	d1tuha_	Alignment	not modelled	5.4	32	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Hypothetical protein egc068 from a soil-derived mobile gene cassette
56	c2kkmA_	Alignment	not modelled	5.4	27	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation machinery-associated protein 16; **PDBTitle:** solution nmr structure of yeast protein yor252w [residues2 38-178]: northeast structural genomics consortium target3 yt654
57	c3kkgA_	Alignment	not modelled	5.4	22	**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
58	c3e79A_	Alignment	not modelled	5.2	36	**PDB header:**tpp binding protein **Chain:** A: **PDB Molecule:**high affinity transport system protein p37; **PDBTitle:** structure determination of the cancer-associated mycoplasma2 hyorhinis protein mh-p37
59	d1h5oa_	Alignment	not modelled	5.1	41	**Fold:**Defensin-like **Superfamily:**Defensin-like **Family:**Myotoxin
60	d1iw4a_	Alignment	not modelled	5.1	50	**Fold:**Kazal-type serine protease inhibitors **Superfamily:**Kazal-type serine protease inhibitors **Family:**Ovomucoid domain III-like
61	c3hk4B_	Alignment	not modelled	5.1	33	**PDB header:**lyase **Chain:** B: **PDB Molecule:**mlr7391 protein; **PDBTitle:** crystal structure of a putative snoal-like polyketide cyclase2 [carbohydrate phosphatase] (mlr7391) from mesorhizobium loti at 1.963 a resolution