Phyre2

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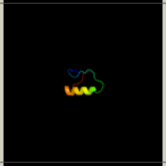
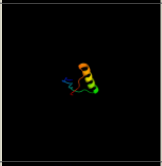
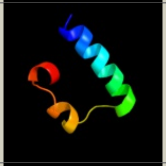
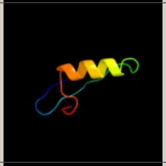
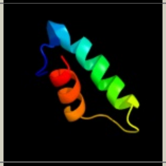
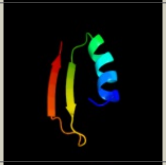
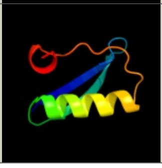
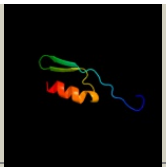
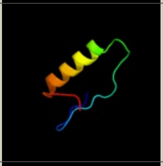
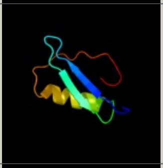
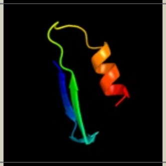
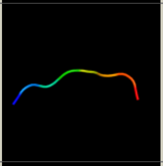
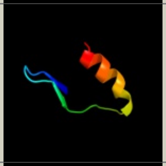
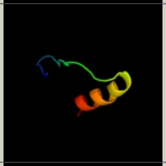
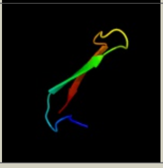
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2owlA_	Alignment		100.0	96	**PDB header:**recombination **Chain:** A: **PDB Molecule:**recombination-associated protein rdgc; **PDBTitle:** crystal structure of e. coli rdgc
2	c2owyB_	Alignment		100.0	49	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**recombination-associated protein rdgc; **PDBTitle:** the recombination-associated protein rdgc adopts a novel toroidal2 architecture for dna binding
3	d2cfua2	Alignment		89.8	26	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Alkylsulfatase-like
4	c2cfuA_	Alignment		86.2	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sdsa1; **PDBTitle:** crystal structure of sdsa1, an alkylsulfatase from2 pseudomonas aeruginosa, in complex with 1-decane-sulfonic-3 acid.
5	c2kmuA_	Alignment		63.1	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent dna helicase q4; **PDBTitle:** recql4 amino-terminal domain
6	d1vmea2	Alignment		31.3	11	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**ROO N-terminal domain-like
7	c2l09A_	Alignment		27.5	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**asr4154 protein; **PDBTitle:** solution nmr structure of protein asr4154 from nostoc sp. pcc71202 northeast structural genomics consortium target id nsr143
8	c2kruA_	Alignment		27.4	8	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**light-independent protochlorophyllide reductase **PDBTitle:** solution nmr structure of the pcp_red domain of light-2 independent protochlorophyllide reductase subunit b from3 chlorobium tepidum. northeast structural genomics4 consortium target ctr69a (casp target)
9	c1yd2A_	Alignment		26.0	9	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**uvrabc system protein c; **PDBTitle:** crystal structure of the giy-yig n-terminal endonuclease domain of2 uvrc from thermotoga maritima: point mutant y19f bound to the3 catalytic divalent cation
10	d1asua_	Alignment		21.7	12	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
11	c3nf9A_	Alignment		21.1	21	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** structural basis for a new mechanism of inhibition of hiv integrase2 identified by fragment screening and structure based design

12	d1ztca1	Alignment		19.2	10	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**TM0894-like
13	c2ohiB_	Alignment		17.7	10	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**type a flavoprotein fpra; **PDBTitle:** crystal structure of coenzyme f420h2 oxidase (fpra), a diiron2 flavoprotein, reduced state
14	d1c6va_	Alignment		17.5	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
15	c3hleA_	Alignment		15.2	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transesterase; **PDBTitle:** simvastatin synthase (lovd), from aspergillus terreus, s5 mutant, s76a2 mutant, complex with monacolin j acid
16	c1v1cA_	Alignment		14.4	50	**PDB header:**sh3-domain **Chain:** A: **PDB Molecule:**obscurin; **PDBTitle:** solution structure of the sh3 domain of obscurin
17	c3spuB_	Alignment		13.6	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-lactamase ndm-1; **PDBTitle:** apo ndm-1 crystal structure
18	d2aioa1	Alignment		13.4	17	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
19	d2gmna1	Alignment		13.3	29	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
20	c1yd6A_	Alignment		13.1	15	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**uvrc; **PDBTitle:** crystal structure of the giy-yig n-terminal endonuclease2 domain of uvrc from bacillus caldotenax
21	d1hyva_	Alignment	not modelled	13.1	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
22	d1cxqa_	Alignment	not modelled	13.0	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
23	c2yz3B_	Alignment	not modelled	11.8	30	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**metallo-beta-lactamase; **PDBTitle:** crystallographic investigation of inhibition mode of the2 vim-2 metallo-beta-lactamase from pseudomonas aeruginosa3 with mercaptocarboxylate inhibitor
24	d1ycga2	Alignment	not modelled	11.0	14	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**ROO N-terminal domain-like
25	d1e5da2	Alignment	not modelled	10.9	8	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**ROO N-terminal domain-like
26	d1p5zb_	Alignment	not modelled	10.7	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
27	c3au5B_	Alignment	not modelled	10.6	14	**PDB header:**motor protein **Chain:** B: **PDB Molecule:**myosin-x; **PDBTitle:** structure of the human myosin-x myth4-ferm cassette
28	c1vmeB_	Alignment	not modelled	10.5	9	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**flavoprotein; **PDBTitle:** crystal structure of flavoprotein (tm0755) from thermotoga maritima at2 1.80 a resolution
						PDB header:oxidoreductase

29	c2q9uB_	Alignment	not modelled	10.5	10	**Chain:** B: **PDB Molecule:**a-type flavoprotein; **PDBTitle:** crystal structure of the flavodiiron protein from giardia2 intestinalis
30	c3lw8G_	Alignment	not modelled	10.1	28	**PDB header:**signaling protein/rhoa-binding protein **Chain:** G: **PDB Molecule:**ipgb2; **PDBTitle:** shigella ipgb2 in complex with human rhoa, gdp and mg2+ (complex a)
31	d2cowa1	Alignment	not modelled	10.1	10	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
32	c3ewgA_	Alignment	not modelled	9.8	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative transcription antitermination protein nusg; **PDBTitle:** crystal structure of the n-terminal domain of nusg (ngn) from2 methanocaldococcus jannaschii
33	c1c0mA_	Alignment	not modelled	9.8	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (integrase); **PDBTitle:** crystal structure of rsv two-domain integrase
34	d1whma_	Alignment	not modelled	9.8	19	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
35	d1rw2a_	Alignment	not modelled	9.6	11	**Fold:**alpha-alpha superhelix **Superfamily:**C-terminal domain of Ku80 **Family:**C-terminal domain of Ku80
36	c2d3o1_	Alignment	not modelled	9.4	24	**PDB header:**ribosome **Chain:** 1: **PDB Molecule:**trigger factor; **PDBTitle:** structure of ribosome binding domain of the trigger factor2 on the 50s ribosomal subunit from d. radiodurans
37	d1ixda_	Alignment	not modelled	9.0	33	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
38	c2b7fD_	Alignment	not modelled	8.8	24	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** D: **PDB Molecule:**htlv protease; **PDBTitle:** crystal structure of human t-cell leukemia virus protease, a novel2 target for anti-cancer design
39	c1ychD_	Alignment	not modelled	8.6	15	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**nitric oxide reductase; **PDBTitle:** x-ray crystal structures of moorella thermoacetica fpra.2 novel diiron site structure and mechanistic insights into3 a scavenging nitric oxide reductase
40	c3s6eB_	Alignment	not modelled	8.5	18	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**rna-binding protein 39; **PDBTitle:** crystal structure of a rna binding motif protein 39 (rbm39) from mus2 musculus at 0.95 a resolution
41	d1x8ha_	Alignment	not modelled	8.4	17	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
42	d1knwa2	Alignment	not modelled	8.4	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLP-binding barrel **Family:**Alanine racemase-like, N-terminal domain
43	c3f9uA_	Alignment	not modelled	8.2	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative exported cytochrome c biogenesis-related protein; **PDBTitle:** crystal structure of c-terminal domain of putative exported cytochrome2 c biogenesis-related protein from bacteroides fragilis
44	c2ja9A_	Alignment	not modelled	8.1	20	**PDB header:**rna-binding protein **Chain:** A: **PDB Molecule:**exosome complex exonuclease rrp40; **PDBTitle:** structure of the n-terminal deletion of yeast exosome2 component rrp40
45	c3lvzA_	Alignment	not modelled	8.1	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**blr6230 protein; **PDBTitle:** new refinement of the crystal structure of bjp-1, a subclass b32 metallo-beta-lactamase of bradyrhizobium japonicum
46	d2eyqa2	Alignment	not modelled	7.8	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
47	d1tova_	Alignment	not modelled	7.8	13	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
48	d1ul7a_	Alignment	not modelled	7.8	25	**Fold:**TBP-like **Superfamily:**KA1-like **Family:**Kinase associated domain 1, KA1
49	c1bw8A_	Alignment	not modelled	7.7	23	**PDB header:**peptide binding protein **Chain:** A: **PDB Molecule:**protein (mu2 adaptin subunit); **PDBTitle:** mu2 adaptin subunit (ap50) of ap2 adaptor (second domain),2 complexed with egfr internalization peptide fyralm
50	c3sd9B_	Alignment	not modelled	7.5	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-lactamase; **PDBTitle:** crystal structure of serratia fonticola sfh-i: source of the2 nucleophile in the catalytic mechanism of mono-zinc metallo-beta-3 lactamases
51	d1y88a1	Alignment	not modelled	7.4	44	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**Hypothetical protein AF1548, C-terminal domain
52	c2joiA_	Alignment	not modelled	7.2	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ta0095; **PDBTitle:** nmr solution structure of hypothetical protein ta0095 from2 thermoplasma acidophilum
53	d2cp2a1	Alignment	not modelled	7.2	11	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
54	c1w26B_	Alignment	not modelled	7.1	17	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**trigger factor;

54	c1w26B_	Alignment	not modelled	7.1	17	**PDBTitle:** trigger factor in complex with the ribosome forms a2 molecular cradle for nascent proteins
55	d1tp6a_	Alignment	not modelled	7.1	19	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**PA1314-like
56	d1exqa_	Alignment	not modelled	7.0	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
57	d1mk0a_	Alignment	not modelled	6.7	25	**Fold:**GIY-YIG endonuclease **Superfamily:**GIY-YIG endonuclease **Family:**GIY-YIG endonuclease
58	d1xs8a_	Alignment	not modelled	6.7	18	**Fold:**YggX-like **Superfamily:**YggX-like **Family:**YggX-like
59	c3p8bB_	Alignment	not modelled	6.6	15	**PDB header:**transferase/transcription **Chain:** B: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** x-ray crystal structure of pyrococcus furiosus transcription2 elongation factor spt4/5
60	c1ex4A_	Alignment	not modelled	6.5	21	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** hiv-1 integrase catalytic core and c-terminal domain
61	c1tf2A_	Alignment	not modelled	6.4	20	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**preprotein translocase seca subunit; **PDBTitle:** crystal structure of seca:adp in an open conformation from2 bacillus subtilis
62	c2qdoC_	Alignment	not modelled	6.4	54	**PDB header:**photosynthesis **Chain:** C: **PDB Molecule:**nbla protein; **PDBTitle:** nbla protein from t. vulcanus
63	d2cp5a1	Alignment	not modelled	6.3	11	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
64	d1whja_	Alignment	not modelled	6.2	19	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
65	c2bh8B_	Alignment	not modelled	6.1	20	**PDB header:**transcription **Chain:** B: **PDB Molecule:**1b11; **PDBTitle:** combinatorial protein 1b11
66	c1k8wA_	Alignment	not modelled	6.1	12	**PDB header:**lyase/rna **Chain:** A: **PDB Molecule:**trna pseudouridine synthase b; **PDBTitle:** crystal structure of the e. coli pseudouridine synthase2 trub bound to a t stem-loop rna
67	c3rkjA_	Alignment	not modelled	6.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-lactamase ndm-1; **PDBTitle:** crystal structure of new delhi metallo-beta-lactamase-1 from2 klebsiella pnueumoniae
68	d1t11a2	Alignment	not modelled	5.8	28	**Fold:**Ribosome binding domain-like **Superfamily:**Trigger factor ribosome-binding domain **Family:**Trigger factor ribosome-binding domain
69	d1znba_	Alignment	not modelled	5.6	16	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
70	d2q0ia1	Alignment	not modelled	5.5	16	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**PqsE-like
71	c2nn6G_	Alignment	not modelled	5.5	20	**PDB header:**hydrolase/transferase **Chain:** G: **PDB Molecule:**exosome complex exonuclease rrp40; **PDBTitle:** structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40
72	c3camB_	Alignment	not modelled	5.4	25	**PDB header:**gene regulation **Chain:** B: **PDB Molecule:**cold-shock domain family protein; **PDBTitle:** crystal structure of the cold shock domain protein from neisseria2 meningitidis
73	c1vsqC_	Alignment	not modelled	5.3	23	**PDB header:**transferase **Chain:** C: **PDB Molecule:**mannose-specific phosphotransferase enzyme iib **PDBTitle:** solution nmr structure of the productive complex between2 iiamannose and iibmannose of the mannose transporter of3 the e. coli phosphotransferase system
74	d2nn6g3	Alignment	not modelled	5.2	21	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
75	c3nadB_	Alignment	not modelled	5.2	36	**PDB header:**lyase **Chain:** B: **PDB Molecule:**ferulate decarboxylase; **PDBTitle:** crystal structure of phenolic acid decarboxylase from bacillus pumilus2 ui-670
76	c1yf2A_	Alignment	not modelled	5.2	16	**PDB header:**hydrolase regulator **Chain:** A: **PDB Molecule:**type i restriction-modification enzyme, s subunit; **PDBTitle:** three-dimensional structure of dna sequence specificity (s) subunit of2 a type i restriction-modification enzyme and its functional3 implications