Phyre^2

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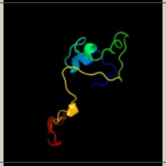
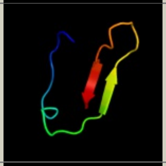
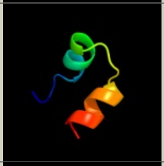
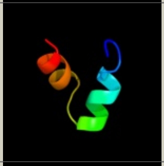
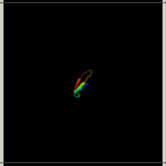
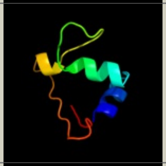
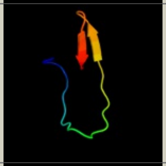
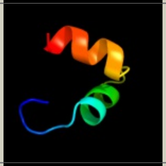
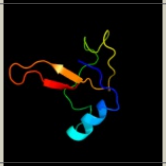
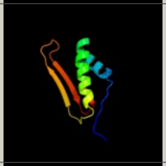
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2gu1A_	Alignment		99.2	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**zinc peptidase; **PDBTitle:** crystal structure of a zinc containing peptidase from2 vibrio cholerae
2	c2l9yA_	Alignment		98.4	13	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**cvnh-lysm lectin; **PDBTitle:** solution structure of the mocvnh-lysm module from the rice blast2 fungus magnaporthe oryzae protein (mgg_03307)
3	c2djpA_	Alignment		98.3	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein sb145; **PDBTitle:** the solution structure of the lysm domain of human2 hypothetical protein sb145
4	d1e0ga_	Alignment		98.3	31	**Fold:**LysM domain **Superfamily:**LysM domain **Family:**LysM domain
5	d1y7ma2	Alignment		98.1	23	**Fold:**LysM domain **Superfamily:**LysM domain **Family:**LysM domain
6	c1y7mB_	Alignment		97.2	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein bsu14040; **PDBTitle:** crystal structure of the b. subtilis ykud protein at 2 a2 resolution
7	c2l55A_	Alignment		58.2	19	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**silb,silver efflux protein, mfp component of the three **PDBTitle:** solution structure of the c-terminal domain of silb from cupriavidus2 metallidurans
8	d1rr7a_	Alignment		55.8	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Middle operon regulator, Mor
9	c1rr7A_	Alignment		55.8	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**middle operon regulator; **PDBTitle:** crystal structure of the middle operon regulator protein of2 bacteriophage mu
10	c1ei5A_	Alignment		53.6	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**d-aminopeptidase; **PDBTitle:** crystal structure of a d-aminopeptidase from ochrobactrum2 anthropi
11	c1vzyA_	Alignment		43.6	19	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**33 kda chaperonin; **PDBTitle:** crystal structure of the bacillus subtilis hsp33

12	d1nera_	Alignment		42.8	16	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
13	d2obpa1	Alignment		42.7	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ReutB4095-like
14	c1zeqX_	Alignment		42.4	17	**PDB header:**metal binding protein **Chain:** X: **PDB Molecule:**cation efflux system protein cusf; **PDBTitle:** 1.5 a structure of apo-cusf residues 6-88 from escherichia2 coli
15	d2jn6a1	Alignment		42.0	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Cgl2762-like
16	c2elhA_	Alignment		40.2	23	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**cg11849-pa; **PDBTitle:** solution structure of the cenp-b n-terminal dna-binding2 domain of fruit fly distal antenna cg11849-pa
17	c2pmzV_	Alignment		38.9	8	**PDB header:**translation, transferase **Chain:** V: **PDB Molecule:**dna-directed rna polymerase subunit h; **PDBTitle:** archaeal rna polymerase from sulfolobus solfataricus
18	c1vq0A_	Alignment		38.8	11	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**33 kda chaperonin; **PDBTitle:** crystal structure of 33 kda chaperonin (heat shock protein 33 homolog)2 (hsp33) (tm1394) from thermotoga maritima at 2.20 a resolution
19	c2r0qF_	Alignment		37.0	15	**PDB header:**recombination/dna **Chain:** F: **PDB Molecule:**putative transposon tn552 dna-invertase bin3; **PDBTitle:** crystal structure of a serine recombinase- dna regulatory2 complex
20	d1hmja_	Alignment		35.5	8	**Fold:**RPB5-like RNA polymerase subunit **Superfamily:**RPB5-like RNA polymerase subunit **Family:**RPB5
21	d1je3a_	Alignment	not modelled	35.2	13	**Fold:**IF3-like **Superfamily:**SirA-like **Family:**SirA-like
22	d1vq0a1	Alignment	not modelled	32.4	11	**Fold:**Hsp33 domain **Superfamily:**Hsp33 domain **Family:**Hsp33 domain
23	c1hw7A_	Alignment	not modelled	31.8	21	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**heat shock protein hsp33; **PDBTitle:** hsp33, heat shock protein with redox-regulated chaperone activity
24	d1hw7a_	Alignment	not modelled	31.8	21	**Fold:**Hsp33 domain **Superfamily:**Hsp33 domain **Family:**Hsp33 domain
25	c3iswA_	Alignment	not modelled	31.5	14	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**filamin-a; **PDBTitle:** crystal structure of filamin-a immunoglobulin-like repeat 21 bound to2 an n-terminal peptide of cftr
26	d1eika_	Alignment	not modelled	31.4	10	**Fold:**RPB5-like RNA polymerase subunit **Superfamily:**RPB5-like RNA polymerase subunit **Family:**RPB5
27	d1vzya1	Alignment	not modelled	30.8	17	**Fold:**Hsp33 domain **Superfamily:**Hsp33 domain **Family:**Hsp33 domain
28	d1uxca_	Alignment	not modelled	29.0	13	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
29	c1i7fA_	Alignment	not modelled	28.9	20	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**heat shock protein 33;

29	c1i7iA_	Alignment	not modelled	28.9	20	**PDBTitle:** crystal structure of the hsp33 domain with constitutive chaperone2 activity
30	d2i6va1	Alignment	not modelled	28.6	22	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**EpsC C-terminal domain-like
31	c3mmlE_	Alignment	not modelled	27.8	29	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**allophanate hydrolase subunit 2; **PDBTitle:** allophanate hydrolase complex from mycobacterium smegmatis, msmeg0435-2 msmeg0436
32	d2i4sa1	Alignment	not modelled	25.0	22	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**EpsC C-terminal domain-like
33	c3cecA_	Alignment	not modelled	24.6	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative antidote protein of plasmid maintenance system; **PDBTitle:** crystal structure of a putative antidote protein of plasmid2 maintenance system (npun_f2943) from nostoc punctiforme pcc 73102 at3 1.60 a resolution
34	d1dzfa2	Alignment	not modelled	24.6	18	**Fold:**RPB5-like RNA polymerase subunit **Superfamily:**RPB5-like RNA polymerase subunit **Family:**RPB5
35	d1dcja_	Alignment	not modelled	24.5	13	**Fold:**IF3-like **Superfamily:**SirA-like **Family:**SirA-like
36	c2ia2D_	Alignment	not modelled	24.3	8	**PDB header:**transcription **Chain:** D: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** the crystal structure of a putative transcriptional regulator rha061952 from rhodococcus sp. rha1
37	d1i7ha_	Alignment	not modelled	23.8	14	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
38	c3hefB_	Alignment	not modelled	23.5	10	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**gene 1 protein; **PDBTitle:** crystal structure of the bacteriophage sf6 terminase small2 subunit
39	d2fug33	Alignment	not modelled	22.8	24	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
40	d1hfua2	Alignment	not modelled	22.7	12	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
41	d1twfc2	Alignment	not modelled	22.6	29	**Fold:**Insert subdomain of RNA polymerase alpha subunit **Superfamily:**Insert subdomain of RNA polymerase alpha subunit **Family:**Insert subdomain of RNA polymerase alpha subunit
42	d1uxda_	Alignment	not modelled	22.5	13	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
43	c2zpmA_	Alignment	not modelled	22.4	6	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**regulator of sigma e protease; **PDBTitle:** crystal structure analysis of pdz domain b
44	d3c8ya2	Alignment	not modelled	22.4	14	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
45	c2gm4B_	Alignment	not modelled	22.2	12	**PDB header:**recombination, dna **Chain:** B: **PDB Molecule:**transposon gamma-delta resolvase; **PDBTitle:** an activated, tetrameric gamma-delta resolvase: hin chimaera bound to2 cleaved dna
46	d2proc1	Alignment	not modelled	22.2	50	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Alpha-lytic protease prodomain **Family:**Alpha-lytic protease prodomain
47	d1y0pa3	Alignment	not modelled	21.9	8	**Fold:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain **Superfamily:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
48	d1d1la_	Alignment	not modelled	21.9	22	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
49	c2pijB_	Alignment	not modelled	21.2	22	**PDB header:**transcription **Chain:** B: **PDB Molecule:**prophage pfl 6 cro; **PDBTitle:** structure of the cro protein from prophage pfl 6 in pseudomonas2 fluorescens pf-5
50	d2q9oa2	Alignment	not modelled	21.2	12	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
51	c2rn7A_	Alignment	not modelled	21.1	9	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**is629 orfa; **PDBTitle:** nmr solution structure of tnpe protein from shigella2 flexneri. northeast structural genomics target sfr125
52	d1wlha1	Alignment	not modelled	20.9	22	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
53	c2brqB_	Alignment	not modelled	20.9	14	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**filamin a; **PDBTitle:** crystal structure of the filamin a repeat 21 complexed with2 the integrin beta7 cytoplasmic tail peptide
54	d1ei5a2	Alignment	not modelled	20.9	24	**Fold:**Streptavidin-like **Superfamily:**D-aminopeptidase, middle and C-terminal domains **Family:**D-aminopeptidase, middle and C-terminal domains
55	c2lcyA	Alignment	not modelled	20.7	13	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**hth-type transcriptional repressor cytr;

		Alignment				**PDBTitle:** structure of the cytidine repressor dna-binding domain; an alternate2 calculation
56	d1v10a2	Alignment	not modelled	20.3	12	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
57	d1fdra1	Alignment	not modelled	20.1	29	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
58	c3fiaA_	Alignment	not modelled	20.1	16	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**intersectin-1; **PDBTitle:** crystal structure of the eh 1 domain from human intersectin-2 1 protein. northeast structural genomics consortium target3 hr3646e.
59	d1kyaa2	Alignment	not modelled	19.9	10	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
60	c2gu3A_	Alignment	not modelled	19.0	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ypmb protein; **PDBTitle:** ypmb protein from bacillus subtilis
61	c3f6vA_	Alignment	not modelled	18.6	13	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**possible transcriptional regulator, arsr family **PDBTitle:** crystal structure of possible transcriptional regulator for2 arsenical resistance
62	d4fxca_	Alignment	not modelled	18.3	7	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
63	c1p0oA_	Alignment	not modelled	18.3	25	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**19-mer peptide from 50s ribosomal protein l1; **PDBTitle:** hp (2-20) substitution of trp for gln and asp at position2 17 and 19 modification in sds-d25 micelles
64	d1aoza2	Alignment	not modelled	18.1	20	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
65	d1a8pa1	Alignment	not modelled	18.1	20	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
66	d1gyca2	Alignment	not modelled	17.8	17	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
67	c2l8nA_	Alignment	not modelled	17.7	12	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional repressor cytr; **PDBTitle:** nmr structure of the cytidine repressor dna binding domain in presence2 of operator half-site dna
68	c3lxfC_	Alignment	not modelled	17.2	28	**PDB header:**metal binding protein **Chain:** C: **PDB Molecule:**ferredoxin; **PDBTitle:** crystal structure of [2fe-2s] ferredoxin arx from novosphingobium2 aromaticivorans
69	d2gu3a1	Alignment	not modelled	16.8	10	**Fold:**Cystatin-like **Superfamily:**Cystatin/monellin **Family:**PepSY-like
70	d4croa_	Alignment	not modelled	16.7	22	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
71	d1awda_	Alignment	not modelled	16.5	10	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
72	d1bw6a_	Alignment	not modelled	16.5	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Centromere-binding
73	d1hlva1	Alignment	not modelled	16.4	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Centromere-binding
74	d2cuaa_	Alignment	not modelled	16.0	20	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Periplasmic domain of cytochrome c oxidase subunit II
75	d2hsga1	Alignment	not modelled	15.8	13	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
76	c3cuoB_	Alignment	not modelled	15.6	17	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**uncharacterized hth-type transcriptional regulator ygav; **PDBTitle:** crystal structure of the predicted dna-binding transcriptional2 regulator from e. coli
77	c2kjpA_	Alignment	not modelled	15.6	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein ylbl; **PDBTitle:** solution structure of protein ylbl (bsu15050) from bacillus2 subtilis, northeast structural genomics consortium target3 sr713a
78	c2xroE_	Alignment	not modelled	15.3	16	**PDB header:**dna-binding protein/dna **Chain:** E: **PDB Molecule:**hth-type transcriptional regulator ttgv; **PDBTitle:** crystal structure of ttgv in complex with its dna operator
79	d1mkma1	Alignment	not modelled	15.1	4	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Transcriptional regulator IclR, N-terminal domain
80	c3h0gE_	Alignment	not modelled	15.0	15	**PDB header:**transcription **Chain:** E: **PDB Molecule:**dna-directed rna polymerases i, ii, and iii **PDBTitle:** rna polymerase ii from schizosaccharomyces pombe
						Fold:EF Hand-like

81	d2jxca1	Alignment	not modelled	15.0	10	**Superfamily:**EF-hand **Family:**Eps15 homology domain (EH domain)
82	d2icta1	Alignment	not modelled	15.0	7	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
83	d1nxza1	Alignment	not modelled	14.9	20	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**YggJ N-terminal domain-like
84	d1zud21	Alignment	not modelled	14.7	13	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
85	d1lcda_	Alignment	not modelled	14.7	12	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
86	c3c19A_	Alignment	not modelled	14.5	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein mk0293; **PDBTitle:** crystal structure of protein mk0293 from methanopyrus kandleri av19
87	d1jiwi_	Alignment	not modelled	14.4	19	**Fold:**Streptavidin-like **Superfamily:**beta-Barrel protease inhibitors **Family:**Metalloprotease inhibitor
88	c1mkmA_	Alignment	not modelled	14.3	4	**PDB header:**transcription **Chain:** A: **PDB Molecule:**iclr transcriptional regulator; **PDBTitle:** crystal structure of the thermotoga maritima iclr
89	d1wxma1	Alignment	not modelled	13.9	13	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ras-binding domain, RBD
90	c2otgA_	Alignment	not modelled	13.9	19	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**myosin heavy chain; **PDBTitle:** rigor-like structures of muscle myosins reveal key2 mechanical elements in the transduction pathways of this3 allosteric motor
91	c3p42D_	Alignment	not modelled	13.7	25	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**predicted protein; **PDBTitle:** structure of gfcc (ymcb), protein encoded by the e. coli group 42 capsule operon
92	d1e9ma_	Alignment	not modelled	13.6	28	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
93	d3orca_	Alignment	not modelled	13.4	26	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
94	d1hh2p4	Alignment	not modelled	13.3	18	**Fold:**Transcription factor NusA, N-terminal domain **Superfamily:**Transcription factor NusA, N-terminal domain **Family:**Transcription factor NusA, N-terminal domain
95	c2kfhA_	Alignment	not modelled	13.3	16	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**eh domain-containing protein 1; **PDBTitle:** structure of the c-terminal domain of ehd1 with fnyestgpftak
96	d1kk8a2	Alignment	not modelled	13.2	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Motor proteins
97	d1d0xa2	Alignment	not modelled	13.1	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Motor proteins
98	c2o0yB_	Alignment	not modelled	13.1	19	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of putative transcriptional regulator rha1_ro069532 (iclr-family) from rhodococcus sp.
99	d1d4ca3	Alignment	not modelled	13.1	27	**Fold:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain **Superfamily:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain