Phyre^2

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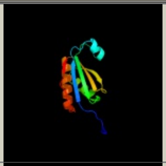
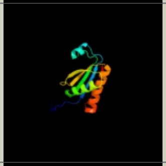
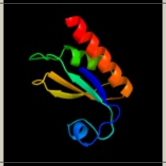
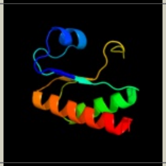
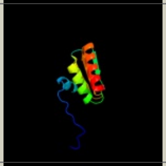
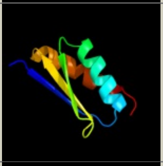
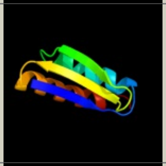
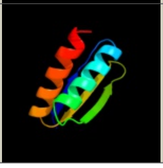
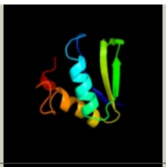
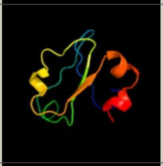
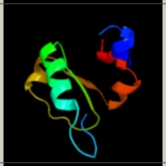
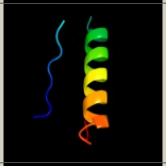
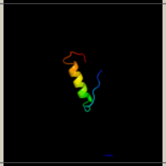
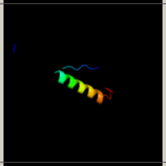
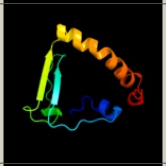
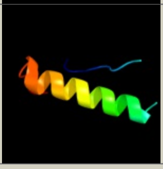
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ia0c_	Alignment		100.0	99	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**ethanolamine utilization protein euts; **PDBTitle:** ethanolamine utilization microcompartment shell subunit,2 euts-g39v mutant
2	c3cgiD_	Alignment		100.0	56	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**propanediol utilization protein pduu; **PDBTitle:** crystal structure of the pduu shell protein from the pdu2 microcompartment
3	c3i82A_	Alignment		99.8	25	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**ethanolamine utilization protein eutl; **PDBTitle:** ethanolamine utilization microcompartment shell subunit, eutl closed2 form
4	c3nwgA_	Alignment		99.4	20	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**microcompartments protein; **PDBTitle:** the crystal structure of a microcomparments protein from2 desulfitobacterium hafniense dcb
5	c3io0A_	Alignment		99.4	31	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**etub protein; **PDBTitle:** crystal structure of etub from clostridium kluyveri
6	c3n79A_	Alignment		99.3	25	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**pdut; **PDBTitle:** pdut c38s mutant from salmonella enterica typhimurium
7	d2ewha1	Alignment		98.7	27	**Fold:**Ferredoxin-like **Superfamily:**CcmK-like **Family:**CcmK-like
8	d2a10a1	Alignment		98.6	23	**Fold:**Ferredoxin-like **Superfamily:**CcmK-like **Family:**CcmK-like
9	c3ngkA_	Alignment		98.6	24	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**propanediol utilization protein pdua; **PDBTitle:** pdua from salmonella enterica typhimurium
10	d2a1ba1	Alignment		98.6	22	**Fold:**Ferredoxin-like **Superfamily:**CcmK-like **Family:**CcmK-like
11	c3i6pF_	Alignment		98.1	24	**PDB header:**structural protein **Chain:** F: **PDB Molecule:**ethanolamine utilization protein eutm; **PDBTitle:** ethanolamine utilization microcompartment shell subunit, eutm

12	c3f56F_	Alignment		93.7	23	**PDB header:**structural protein **Chain:** F: **PDB Molecule:**csos1d; **PDBTitle:** the structure of a previously undetected carboxysome shell2 protein: csos1d from prochlorococcus marinus med4
13	d2r48a1	Alignment		80.5	29	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Fructose specific IIB subunit-like
14	d2r4qa1	Alignment		79.6	32	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Fructose specific IIB subunit-like
15	c2kyrA_	Alignment		77.6	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**fructose-like phosphotransferase enzyme iib component 1; **PDBTitle:** solution structure of enzyme iib subunit of pts system from2 escherichia coli k12. northeast structural genomics consortium target3 er315/ontario center for structural proteomics target ec0544
16	d1qnaa1	Alignment		69.0	23	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
17	d1nh2a1	Alignment		66.5	19	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
18	d1cdwa1	Alignment		61.7	23	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
19	d1qlma_	Alignment		52.0	20	**Fold:**Methenyltetrahydromethanopterin cyclohydrolase **Superfamily:**Methenyltetrahydromethanopterin cyclohydrolase **Family:**Methenyltetrahydromethanopterin cyclohydrolase
20	c3eikB_	Alignment		41.2	26	**PDB header:**transcription **Chain:** B: **PDB Molecule:**tata-box-binding protein; **PDBTitle:** double stranded dna binding protein
21	d1t1ea2	Alignment	not modelled	38.2	18	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Subtilase propeptides/inhibitors
22	c1ngmM_	Alignment	not modelled	36.2	19	**PDB header:**transcription/dna **Chain:** M: **PDB Molecule:**transcription initiation factor tfiid; **PDBTitle:** crystal structure of a yeast brf1-tbp-dna ternary complex
23	c1rm1A_	Alignment	not modelled	36.2	19	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**tata-box binding protein; **PDBTitle:** structure of a yeast tfiia/tbp/tata-box dna complex
24	d1nh2a2	Alignment	not modelled	35.3	23	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
25	c2z8uQ_	Alignment	not modelled	32.6	30	**PDB header:**transcription **Chain:** Q: **PDB Molecule:**tata-box-binding protein; **PDBTitle:** methanococcus jannaschii tbp
26	d1x4ma1	Alignment	not modelled	28.8	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)
27	d1mp9a2	Alignment	not modelled	28.3	33	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
28	c1njjC_	Alignment	not modelled	26.0	10	**PDB header:**lyase **Chain:** C: **PDB Molecule:**ornithine decarboxylase; **PDBTitle:** crystal structure determination of t. brucei ornithine2 decarboxylase bound to d-ornithine and to g418
29	c2hh3A_	Alignment	not modelled	24.5	25	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**kh-type splicing regulatory protein;

						PDBTitle: solution structure of the third kh domain of ksrp
30	d1aisa2	Alignment	not modelled	23.8	31	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
31	d1cdwa2	Alignment	not modelled	23.2	27	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
32	c2hh2A_	Alignment	not modelled	23.0	19	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**kh-type splicing regulatory protein; **PDBTitle:** solution structure of the fourth kh domain of ksrp
33	d1qnaa2	Alignment	not modelled	21.6	27	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
34	d1we8a_	Alignment	not modelled	21.3	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)
35	d1mp9a1	Alignment	not modelled	19.9	27	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
36	c1t1eA_	Alignment	not modelled	18.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**kumamolisin; **PDBTitle:** high resolution crystal structure of the intact pro-2 kumamolisin, a sedolisin type proteinase (previously3 called kumamolysin or kscp)
37	c1ztgD_	Alignment	not modelled	17.5	16	**PDB header:**dna, rna binding protein/dna **Chain:** D: **PDB Molecule:**poly(rc)-binding protein 1; **PDBTitle:** human alpha polyc binding protein kh1
38	c2jzxA_	Alignment	not modelled	16.8	17	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**poly(rc)-binding protein 2; **PDBTitle:** pcbp2 kh1-kh2 domains
39	c1mp9B_	Alignment	not modelled	16.8	31	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**tata-binding protein; **PDBTitle:** tbp from a mesothermophilic archaeon, sulfolobus2 acidocaldarius
40	d1j4wa1	Alignment	not modelled	16.3	22	**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)
41	c3n89B_	Alignment	not modelled	16.2	12	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**defective in germ line development protein 3, isoform a; **PDBTitle:** kh domains
42	d1dtja_	Alignment	not modelled	15.8	17	**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)
43	d1khma_	Alignment	not modelled	14.1	14	**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)
44	d1s99a_	Alignment	not modelled	13.6	13	**Fold:**Ferredoxin-like **Superfamily:**MTH1187/YkoF-like **Family:**Putative thiamin/HMP-binding protein YkoF
45	c1mzjB_	Alignment	not modelled	12.6	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**beta-ketoacylsynthase iii; **PDBTitle:** crystal structure of the priming beta-ketosynthase from the2 r1128 polyketide biosynthetic pathway
46	d2axya1	Alignment	not modelled	12.4	13	**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)
47	c3ipfA_	Alignment	not modelled	12.1	26	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the q251q8_deshy protein from desulfitobacterium2 hafniense. northeast structural genomics consortium target dhr8c.
48	d1ec6a_	Alignment	not modelled	11.8	16	**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)
49	d1zzka1	Alignment	not modelled	11.4	14	**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)
50	d1d7ka2	Alignment	not modelled	11.4	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLP-binding barrel **Family:**Alanine racemase-like, N-terminal domain
51	d2ba0a3	Alignment	not modelled	11.3	19	**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)
52	c3edyA_	Alignment	not modelled	11.2	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tripeptidyl-peptidase 1; **PDBTitle:** crystal structure of the precursor form of human tripeptidyl-peptidase2 1
53	c1iruF_	Alignment	not modelled	10.7	20	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**20s proteasome; **PDBTitle:** crystal structure of the mammalian 20s proteasome at 2.75 a2 resolution
54	d1iruf_	Alignment	not modelled	10.7	20	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
55	d1irug_	Alignment	not modelled	10.5	33	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits

56	d2ctma1	Alignment	not modelled	10.1	22	**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)
57	c3bdmF_	Alignment	not modelled	9.7	27	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**proteasome component c1; **PDBTitle:** yeast 20s proteasome:glidobactin a-complex
58	d1rypg_	Alignment	not modelled	9.7	27	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
59	c3h76A_	Alignment	not modelled	9.7	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pqs biosynthetic enzyme; **PDBTitle:** crystal structure of pqsd, a key enzyme in pseudomonas2 aeruginosa quinolone signal biosynthesis pathway
60	d1irua_	Alignment	not modelled	9.4	31	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
61	c1d3uA_	Alignment	not modelled	9.1	31	**PDB header:**gene regulation/dna **Chain:** A: **PDB Molecule:**tata-binding protein; **PDBTitle:** tata-binding protein/transcription factor (ii)b/bre+tata-2 box complex from pyrococcus woesei
62	d2ooia1	Alignment	not modelled	8.7	6	**Fold:**Chorismate lyase-like **Superfamily:**Chorismate lyase-like **Family:**UTRA domain
63	d1rype_	Alignment	not modelled	8.7	31	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
64	d1x4na1	Alignment	not modelled	8.6	13	**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)
65	d2ctka1	Alignment	not modelled	8.4	18	**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)
66	d1aisa1	Alignment	not modelled	8.3	38	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
67	c2qnxA_	Alignment	not modelled	8.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] synthase 3; **PDBTitle:** crystal structure of the complex between the mycobacterium beta-2 ketoacyl-acyl carrier protein synthase iii (fabh) and 11-3 [(decyloxycarbonyl)dithio]-undecanoic acid
68	c3df7A_	Alignment	not modelled	8.0	36	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative atp-grasp superfamily protein; **PDBTitle:** crystal structure of a putative atp-grasp superfamily2 protein from archaeoglobus fulgidus
69	d1rypf_	Alignment	not modelled	7.7	33	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
70	d1rypb_	Alignment	not modelled	7.7	27	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
71	c2e3uA_	Alignment	not modelled	7.5	11	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**hypothetical protein ph1566; **PDBTitle:** crystal structure analysis of dim2p from pyrococcus horikoshii ot3
72	d1irud_	Alignment	not modelled	7.4	27	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
73	c2kp6A_	Alignment	not modelled	6.8	33	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of protein cv0237 from2 chromobacterium violaceum. northeast structural genomics3 consortium (nesg) target cvt1
74	d1iruc_	Alignment	not modelled	6.8	31	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
75	d1rypa_	Alignment	not modelled	6.6	38	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
76	d1irub_	Alignment	not modelled	6.3	27	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
77	d1nvmb2	Alignment	not modelled	6.0	39	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
78	c3lpeF_	Alignment	not modelled	6.0	35	**PDB header:**transferase **Chain:** F: **PDB Molecule:**dna-directed rna polymerase subunit e''; **PDBTitle:** crystal structure of spt4/5ngn heterodimer complex from methanococcus2 jannaschii
79	d1rypd_	Alignment	not modelled	5.8	38	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
80	d1irue_	Alignment	not modelled	5.8	23	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
81	d2ctla1	Alignment	not modelled	5.8	33	**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)
82	c3krmB_	Alignment	not modelled	5.7	13	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**insulin-like growth factor 2 mrna-binding protein **PDBTitle:** imp1 kh34
83	c3orsD_	Alignment	not modelled	5.7	11	**PDB header:**isomerase,biosynthetic protein **Chain:** D: **PDB Molecule:**n5-carboxyaminoimidazole ribonucleotide mutase; **PDBTitle:** crystal structure of n5-carboxyaminoimidazole ribonucleotide mutase2 from staphylococcus aureus
84	d2ctfa1	Alignment	not modelled	5.5	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)
85	d1rypc_	Alignment	not modelled	5.5	38	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
86	c2pn1A_	Alignment	not modelled	5.5	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**carbamoylphosphate synthase large subunit; **PDBTitle:** crystal structure of carbamoylphosphate synthase large subunit (split2 gene in mj) (zp_00538348.1) from exiguobacterium sp. 255-15 at 2.00 a3 resolution
87	d1wvna1	Alignment	not modelled	5.4	23	**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)
88	c2dgrA_	Alignment	not modelled	5.3	14	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**ring finger and kh domain-containing protein 1; **PDBTitle:** solution structure of the second kh domain in ring finger2 and kh domain containing protein 1
89	c2anrA_	Alignment	not modelled	5.3	9	**PDB header:**rna-binding protein/rna **Chain:** A: **PDB Molecule:**neuro-oncological ventral antigen 1; **PDBTitle:** crystal structure (ii) of nova-1 kh1/kh2 domain tandem with 25nt rna2 hairpin