Phyre2

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Description	P39405
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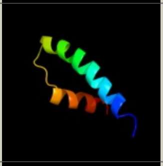
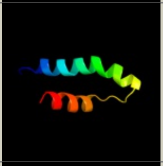
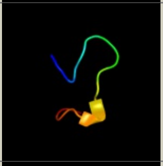
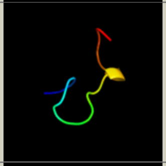
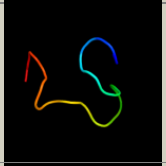
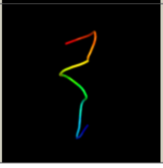
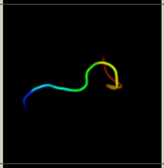
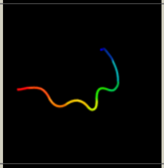
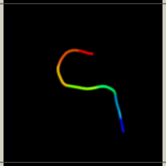
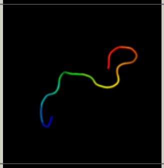
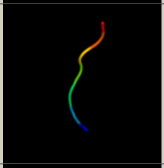
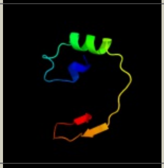
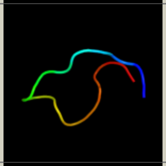
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ffeB_	Alignment		97.5	13	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**acsd; **PDBTitle:** structure of achromobactin synthetase protein d, (acsd)
2	c2w02A_	Alignment		97.4	12	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**acsd; **PDBTitle:** co-complex structure of achromobactin synthetase protein d (2 acsd) with atp from pectobacterium chrysanthemi
3	c2x0oA_	Alignment		96.7	14	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**alcaligin biosynthesis protein; **PDBTitle:** apo structure of the alcaligin biosynthesis protein c (alcc)2 from bordetella bronchiseptica
4	d1r2aa_	Alignment		66.4	31	**Fold:**Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit **Superfamily:**Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit **Family:**Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit
5	d2hwna1	Alignment		65.3	31	**Fold:**Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit **Superfamily:**Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit **Family:**Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit
6	d1kg2a_	Alignment		35.3	24	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Mismatch glycosylase
7	d1keaa_	Alignment		33.9	24	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Mismatch glycosylase
8	d2abka_	Alignment		25.3	29	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Endonuclease III
9	c1rrqA_	Alignment		24.8	24	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**muty; **PDBTitle:** muty adenine glycosylase in complex with dna containing an2 a:oxog pair
10	d1rrqa1	Alignment		22.3	24	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Mismatch glycosylase
11	d1orna_	Alignment		18.1	33	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Endonuclease III

12	c3kk4B_	Alignment		13.8	71	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein bp1543; **PDBTitle:** uncharacterized protein bp1543 from bordetella pertussis tohama i
13	c3n5nX_	Alignment		13.4	25	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**a/g-specific adenine dna glycosylase; **PDBTitle:** crystal structure analysis of the catalytic domain and interdomain2 connector of human muty homologue
14	d2o8ra4	Alignment		11.7	38	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Polyphosphate kinase C-terminal domain
15	c2dcvA_	Alignment		11.3	57	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**tachystatin-b1; **PDBTitle:** the solution structure of horseshoe crab antimicrobial2 peptide tachystatin b with the inhibitory cystine-knot3 motif
16	d1xdpa4	Alignment		11.0	27	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Polyphosphate kinase C-terminal domain
17	d1xn7a_	Alignment		10.7	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Hypothetical protein YhgG
18	c2i9wA_	Alignment		10.5	17	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a sec-c motif containing protein (psyc_2064) from2 psychrobacter arcticus at 1.75 a resolution
19	c3gj4D_	Alignment		10.3	25	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**nuclear pore complex protein nup153; **PDBTitle:** crystal structure of human rangdp-nup153znf3 complex
20	d1hlqa_	Alignment		9.1	31	**Fold:**HIPIP (high potential iron protein) **Superfamily:**HIPIP (high potential iron protein) **Family:**HIPIP (high potential iron protein)
21	d1hpia_	Alignment	not modelled	9.0	29	**Fold:**HIPIP (high potential iron protein) **Superfamily:**HIPIP (high potential iron protein) **Family:**HIPIP (high potential iron protein)
22	c2eqeA_	Alignment	not modelled	9.0	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tumor necrosis factor, alpha-induced protein 3; **PDBTitle:** solution structure of the fourth a20-type zinc finger2 domain from human tumor necrosis factor, alpha-induced3 protein3
23	d1b24a1	Alignment	not modelled	8.6	32	**Fold:**Homing endonuclease-like **Superfamily:**Homing endonucleases **Family:**Group I mobile intron endonuclease
24	d1u55a_	Alignment	not modelled	7.9	14	**Fold:**Ligand-binding domain in the NO signalling and Golgi transport **Superfamily:**Ligand-binding domain in the NO signalling and Golgi transport **Family:**H-NOX domain
25	d2nz1d1	Alignment	not modelled	7.9	50	**Fold:**IL8-like **Superfamily:**Interleukin 8-like chemokines **Family:**Interleukin 8-like chemokines
26	d1lghb_	Alignment	not modelled	7.8	6	**Fold:**Light-harvesting complex subunits **Superfamily:**Light-harvesting complex subunits **Family:**Light-harvesting complex subunits
27	d1b8ta1	Alignment	not modelled	7.7	38	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
28	d1b0ya_	Alignment	not modelled	7.5	24	**Fold:**HIPIP (high potential iron protein) **Superfamily:**HIPIP (high potential iron protein) **Family:**HIPIP (high potential iron protein)

29	d1q5na_	Alignment	not modelled	7.4	17	**Fold:**L-aspartase-like **Superfamily:**L-aspartase-like **Family:**L-aspartase/fumarase
30	c1pyaD_	Alignment	not modelled	7.3	20	**PDB header:**carboxy-lyase **Chain:** D: **PDB Molecule:**pyruvoyl-dependent histidine decarboxylase (l- **PDBTitle:** refined structure of the pyruvoyl-dependent histidine2 decarboxylase from lactobacillus 30a
31	c2o8rA_	Alignment	not modelled	7.3	38	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polyphosphate kinase; **PDBTitle:** crystal structure of polyphosphate kinase from2 porphyromonas gingivalis
32	d1otka_	Alignment	not modelled	6.8	24	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ribonucleotide reductase-like
33	c2o0cB_	Alignment	not modelled	6.8	12	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**alr2278 protein; **PDBTitle:** crystal structure of the h-nox domain from nostoc sp. pcc 71202 complexed to no
34	c3mkyP_	Alignment	not modelled	6.6	26	**PDB header:**dna binding protein/dna **Chain:** P: **PDB Molecule:**protein sopb; **PDBTitle:** structure of sopb(155-323)-18mer dna complex, i23 form
35	d3hipa_	Alignment	not modelled	6.6	24	**Fold:**HIPIP (high potential iron protein) **Superfamily:**HIPIP (high potential iron protein) **Family:**HIPIP (high potential iron protein)
36	c2kilA_	Alignment	not modelled	6.4	14	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** nmr structure of the h103g mutant so2144 h-nox domain from2 shewanella oneidensis in the fe(ii)co ligation state
37	c2hgoA_	Alignment	not modelled	6.3	50	**PDB header:**toxin **Chain:** A: **PDB Molecule:**cassiicolin; **PDBTitle:** nmr structure of cassiicolin
38	c2e2fA_	Alignment	not modelled	6.3	19	**PDB header:**antifungal protein **Chain:** A: **PDB Molecule:**diapausin; **PDBTitle:** solution structure of dsp
39	d1uzka3	Alignment	not modelled	6.0	18	**Fold:**TB module/8-cys domain **Superfamily:**TB module/8-cys domain **Family:**TB module/8-cys domain
40	d3ceda1	Alignment	not modelled	5.9	23	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**NIL domain-like
41	d2v4jb1	Alignment	not modelled	5.8	60	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
42	d1fxia_	Alignment	not modelled	5.8	25	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
43	d1f1oa_	Alignment	not modelled	5.7	11	**Fold:**L-aspartase-like **Superfamily:**L-aspartase-like **Family:**L-aspartase/fumarase
44	d2qeec1	Alignment	not modelled	5.7	7	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Uronate isomerase-like
45	d1js2a_	Alignment	not modelled	5.5	24	**Fold:**HIPIP (high potential iron protein) **Superfamily:**HIPIP (high potential iron protein) **Family:**HIPIP (high potential iron protein)
46	d1i7ha_	Alignment	not modelled	5.5	25	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
47	d2qswa1	Alignment	not modelled	5.4	2	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**NIL domain-like
48	d1re5a_	Alignment	not modelled	5.4	17	**Fold:**L-aspartase-like **Superfamily:**L-aspartase-like **Family:**L-aspartase/fumarase
49	d1rooa_	Alignment	not modelled	5.4	43	**Fold:**Crisp domain-like **Superfamily:**Crisp domain-like **Family:**Sea anemone toxin k
50	d1wwia1	Alignment	not modelled	5.2	17	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Bacterial histone-fold protein
51	c2odmA_	Alignment	not modelled	5.2	71	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**upf0358 protein mw0995; **PDBTitle:** crystal structure of s. aureus ylan, an essential leucine rich protein2 involved in the control of cell shape
52	d1xhja_	Alignment	not modelled	5.2	43	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Fe-S cluster assembly (FSCA) domain-like **Family:**NifU C-terminal domain-like
53	c3ah7A_	Alignment	not modelled	5.1	38	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**[2fe-2s]ferredoxin; **PDBTitle:** crystal structure of the isc-like [2fe-2s] ferredoxin (fdxb) from2 pseudomonas putida jcm 20004
54	d1kf6b2	Alignment	not modelled	5.1	38	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
55	c1wrgA_	Alignment	not modelled	5.0	12	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**light-harvesting protein b-880, beta chain; **PDBTitle:** light-harvesting complex 1 beta subunit from wild-type2