Phyre2

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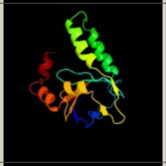
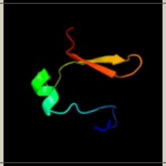
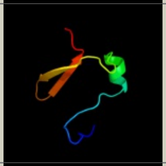
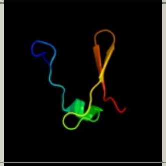
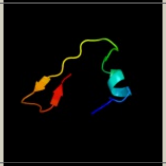
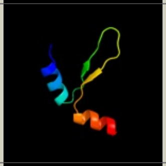
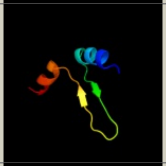
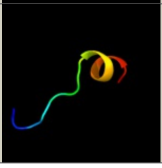
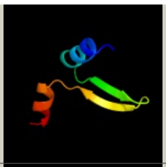
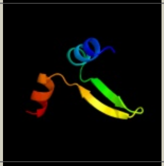
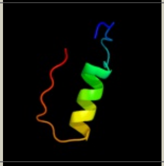
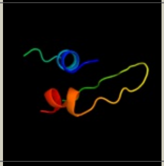
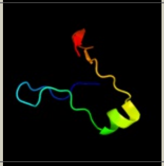
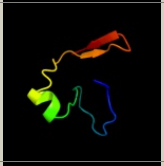
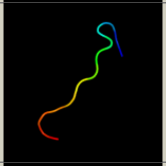
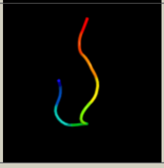
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1n0fF_	Alignment		100.0	25	**PDB header:**biosynthetic protein **Chain:** F: **PDB Molecule:**protein mraz; **PDBTitle:** crystal structure of a cell division and cell wall2 biosynthesis protein upf0040 from mycoplasma pneumoniae:3 indication of a novel fold with a possible new conserved4 sequence motif
2	d1n0ea_	Alignment		100.0	25	**Fold:**Double-split beta-barrel **Superfamily:**AbrB/MazE/MraZ-like **Family:**Hypothetical protein MraZ
3	c2glwA_	Alignment		95.8	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**92aa long hypothetical protein; **PDBTitle:** the solution structure of phs018 from pyrococcus horikoshii
4	c2w1tB_	Alignment		94.4	21	**PDB header:**transcription **Chain:** B: **PDB Molecule:**stage v sporulation protein t; **PDBTitle:** crystal structure of b. subtilis spovt
5	d1yfba1	Alignment		88.9	21	**Fold:**Double-split beta-barrel **Superfamily:**AbrB/MazE/MraZ-like **Family:**AbrB N-terminal domain-like
6	c2ro5B_	Alignment		88.0	21	**PDB header:**transcription **Chain:** B: **PDB Molecule:**stage v sporulation protein t; **PDBTitle:** rdc-refined solution structure of the n-terminal dna2 recognition domain of the bacillus subtilis transition-3 state regulator spovt
7	d2fy9a1	Alignment		87.6	21	**Fold:**Double-split beta-barrel **Superfamily:**AbrB/MazE/MraZ-like **Family:**AbrB N-terminal domain-like
8	c2l66B_	Alignment		50.8	12	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, abrb family; **PDBTitle:** the dna-recognition fold of sso7c4 suggests a new member of spovt-abrb2 superfamily from archaea.
9	c3hs2H_	Alignment		41.5	15	**PDB header:**antitoxin **Chain:** H: **PDB Molecule:**prevent host death protein; **PDBTitle:** crystal structure of phd truncated to residue 57 in an orthorhombic2 space group
10	c3hryA_	Alignment		41.2	15	**PDB header:**antitoxin **Chain:** A: **PDB Molecule:**prevent host death protein; **PDBTitle:** crystal structure of phd in a trigonal space group and partially2 disordered
11	c3nnqA_	Alignment		33.9	21	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**n-terminal domain of moloney murine leukemia virus **PDBTitle:** crystal structure of the n-terminal domain of moloney murine leukemia2 virus integrase, northeast structural genomics consortium target or3

12	d2odka1	Alignment		32.2	18	**Fold:**YefM-like **Superfamily:**YefM-like **Family:**YefM-like
13	c2odkD_	Alignment		30.3	18	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**hypothetical protein; **PDBTitle:** putative prevent-host-death protein from nitrosomonas europaea
14	c3qq5A_	Alignment		27.5	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**small gtp-binding protein; **PDBTitle:** crystal structure of the [fefe]-hydrogenase maturation protein hydf
15	c2k2eA_	Alignment		22.9	32	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein bp2786; **PDBTitle:** solution nmr structure of bordetella pertussis protein2 bp2786, a mth938-like domain. northeast structural3 genomics consortium target ber31
16	c2c45F_	Alignment		21.8	13	**PDB header:**lyase **Chain:** F: **PDB Molecule:**aspartate 1-decarboxylase precursor; **PDBTitle:** native precursor of pyruvoyl dependent aspartate2 decarboxylase
17	c1pt1B_	Alignment		21.1	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**aspartate 1-decarboxylase; **PDBTitle:** unprocessed pyruvoyl dependent aspartate decarboxylase with histidine2 11 mutated to alanine
18	d1ppya_	Alignment		19.6	15	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Pyruvoyl dependent aspartate decarboxylase, ADC
19	d1wida_	Alignment		17.8	23	**Fold:**DNA-binding pseudobarrel domain **Superfamily:**DNA-binding pseudobarrel domain **Family:**B3 DNA binding domain
20	d2zgwa1	Alignment		16.5	44	**Fold:**SH3-like barrel **Superfamily:**C-terminal domain of transcriptional repressors **Family:**Biotin repressor (BirA)
21	d2a6qb1	Alignment	not modelled	15.2	10	**Fold:**YefM-like **Superfamily:**YefM-like **Family:**YefM-like
22	d1s6la1	Alignment	not modelled	15.1	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MerB N-terminal domain-like
23	c3if4C_	Alignment	not modelled	15.1	33	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**integron cassette protein hfx_cass5; **PDBTitle:** structure from the mobile metagenome of north west arm2 sewage outfall: integron cassette protein hfx_cass5
24	c2zcpA_	Alignment	not modelled	15.1	5	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dehydrosqualene synthase; **PDBTitle:** crystal structure of the c(30) carotenoid dehydrosqualene2 synthase from staphylococcus aureus complexed with3 farnesyl thiopyrophosphate
25	d2q4qa1	Alignment	not modelled	14.9	16	**Fold:**MTH938-like **Superfamily:**MTH938-like **Family:**MTH938-like
26	c2gm2A_	Alignment	not modelled	14.0	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** nmr structure of xanthomonas campestris xcc1710: northeast2 structural genomics consortium target xcr35
27	d1d7qa_	Alignment	not modelled	13.7	14	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
28	d2a6qa1	Alignment	not modelled	13.5	10	**Fold:**YefM-like **Superfamily:**YefM-like **Family:**YefM-like
						PDB header:unknown function

29	c2kdnA_	Alignment	not modelled	13.3	13	**Chain:** A: **PDB Molecule:**putative uncharacterized protein pfe0790c; **PDBTitle:** solution structure of pfe0790c, a putative bola-like2 protein from the protozoan parasite plasmodium falciparum.
30	c3dwmA_	Alignment	not modelled	13.0	35	**PDB header:**transferase **Chain:** A: **PDB Molecule:**9.5 kda culture filtrate antigen cfp10a; **PDBTitle:** crystal structure of mycobacterium tuberculosis cyso, an antigen
31	c2oqkA_	Alignment	not modelled	12.2	14	**PDB header:**translation **Chain:** A: **PDB Molecule:**putative translation initiation factor eif-1a; **PDBTitle:** crystal structure of putative cryptosporidium parvum translation2 initiation factor eif-1a
32	d1lpfa2	Alignment	not modelled	12.0	6	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
33	c2dgyA_	Alignment	not modelled	11.9	14	**PDB header:**translation **Chain:** A: **PDB Molecule:**mgc11102 protein; **PDBTitle:** solution structure of the eukaryotic initiation factor 1a2 in mgc11102 protein
34	d2fvta1	Alignment	not modelled	11.2	8	**Fold:**MTH938-like **Superfamily:**MTH938-like **Family:**MTH938-like
35	d1ef4a_	Alignment	not modelled	11.0	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**RNA polymerase subunit RPB10 **Family:**RNA polymerase subunit RPB10
36	d2fi9a1	Alignment	not modelled	10.3	13	**Fold:**MTH938-like **Superfamily:**MTH938-like **Family:**MTH938-like
37	c3errB_	Alignment	not modelled	10.1	24	**PDB header:**ligase **Chain:** B: **PDB Molecule:**fusion protein of microtubule binding domain from **PDBTitle:** microtubule binding domain from mouse cytoplasmic dynein as2 a fusion with seryl-trna synthetase
38	d1m7ja1	Alignment	not modelled	10.0	23	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**D-aminoacylase
39	d2b7oa1	Alignment	not modelled	9.7	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class-II DAHP synthetase
40	c3zvkG_	Alignment	not modelled	9.5	20	**PDB header:**antitoxin/toxin/dna **Chain:** G: **PDB Molecule:**antitoxin of toxin-antitoxin system vapb; **PDBTitle:** crystal structure of vapbc2 from rickettsia felis bound to2 a dna fragment from their promoter
41	c2dq3A_	Alignment	not modelled	9.1	25	**PDB header:**ligase **Chain:** A: **PDB Molecule:**seryl-trna synthetase; **PDBTitle:** crystal structure of aq_298
42	d2j7ja2	Alignment	not modelled	9.1	40	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
43	c2ubpC_	Alignment	not modelled	8.6	16	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**protein (urease alpha subunit); **PDBTitle:** structure of native urease from bacillus pasteurii
44	d1jt8a_	Alignment	not modelled	8.1	14	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
45	c2dq0A_	Alignment	not modelled	7.9	29	**PDB header:**ligase **Chain:** A: **PDB Molecule:**seryl-trna synthetase; **PDBTitle:** crystal structure of seryl-trna synthetase from pyrococcus2 horikoshii complexed with a seryl-adenylate analog
46	d1xova1	Alignment	not modelled	7.9	63	**Fold:**SH3-like barrel **Superfamily:**Prokaryotic SH3-related domain **Family:**Ply C-terminal domain-like
47	d1seta2	Alignment	not modelled	7.9	24	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
48	d1v59a2	Alignment	not modelled	7.6	10	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
49	d1s32d_	Alignment	not modelled	7.5	50	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
50	c3df0C_	Alignment	not modelled	7.5	23	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**calpastatin; **PDBTitle:** calcium-dependent complex between m-calpain and calpastatin
51	c1hzeB_	Alignment	not modelled	7.3	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**riboflavin synthase alpha chain; **PDBTitle:** solution structure of the n-terminal domain of riboflavin synthase2 from e. coli
52	c1i18B_	Alignment	not modelled	7.3	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**riboflavin synthase alpha chain; **PDBTitle:** solution structure of the n-terminal domain of riboflavin synthase2 from e. coli
53	c3h5fB_	Alignment	not modelled	7.3	39	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**coil ser l16l-pen; **PDBTitle:** switching the chirality of the metal environment alters the2 coordination mode in designed peptides.
54	c3h5gA_	Alignment	not modelled	7.3	39	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**coil ser l16d-pen; **PDBTitle:** switching the chirality of the metal environment alters the2 coordination mode in designed peptides.

55	c3h5gC_	Alignment	not modelled	7.3	39	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**coil ser l16d-pen; **PDBTitle:** switching the chirality of the metal environment alters the2 coordination mode in designed peptides.
56	c3h5fA_	Alignment	not modelled	7.3	39	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**coil ser l16l-pen; **PDBTitle:** switching the chirality of the metal environment alters the2 coordination mode in designed peptides.
57	c3h5fC_	Alignment	not modelled	7.3	39	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**coil ser l16l-pen; **PDBTitle:** switching the chirality of the metal environment alters the2 coordination mode in designed peptides.
58	c3h5gB_	Alignment	not modelled	7.3	39	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**coil ser l16d-pen; **PDBTitle:** switching the chirality of the metal environment alters the2 coordination mode in designed peptides.
59	d1eqzb_	Alignment	not modelled	7.2	50	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
60	d1k1da1	Alignment	not modelled	7.2	25	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase)
61	c1sryB_	Alignment	not modelled	7.1	21	**PDB header:**ligase(synthetase) **Chain:** B: **PDB Molecule:**seryl-trna synthetase; **PDBTitle:** refined crystal structure of the seryl-trna synthetase from2 thermus thermophilus at 2.5 angstroms resolution
62	d1tzyb_	Alignment	not modelled	6.9	50	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
63	d2p9ba1	Alignment	not modelled	6.8	30	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**Imidazolonepropionase-like
64	c1e9yB_	Alignment	not modelled	6.5	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**urease subunit beta; **PDBTitle:** crystal structure of helicobacter pylori urease in complex with2 acetohydroxamic acid
65	c3la4A_	Alignment	not modelled	6.5	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**urease; **PDBTitle:** crystal structure of the first plant urease from jack bean (canavalia2 ensiformis)
66	d1kx5d_	Alignment	not modelled	6.5	50	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
67	d1lvla2	Alignment	not modelled	6.4	16	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
68	d2gv8a2	Alignment	not modelled	6.4	22	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
69	d2gf6a1	Alignment	not modelled	6.3	4	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
70	d2ftwa1	Alignment	not modelled	6.3	14	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase)
71	c3jywM_	Alignment	not modelled	6.2	19	**PDB header:**ribosome **Chain:** M: **PDB Molecule:**60s ribosomal protein l16(a); **PDBTitle:** structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
72	d1id3d_	Alignment	not modelled	6.2	42	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
73	c2vlgD_	Alignment	not modelled	6.2	21	**PDB header:**transferase **Chain:** D: **PDB Molecule:**sporulation kinase a; **PDBTitle:** kina pas-a domain, homodimer
74	d2nn6d2	Alignment	not modelled	6.2	23	**Fold:**Ribonuclease PH domain 2-like **Superfamily:**Ribonuclease PH domain 2-like **Family:**Ribonuclease PH domain 2-like
75	d1d6za4	Alignment	not modelled	6.1	10	**Fold:**N domain of copper amine oxidase-like **Superfamily:**Copper amine oxidase, domain N **Family:**Copper amine oxidase, domain N
76	d1ejxc1	Alignment	not modelled	5.9	16	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**alpha-Subunit of urease
77	d1vi7a2	Alignment	not modelled	5.8	14	**Fold:**Ferredoxin-like **Superfamily:**EF-G C-terminal domain-like **Family:**YigZ C-terminal domain-like
78	c2pmzN_	Alignment	not modelled	5.5	19	**PDB header:**translation, transferase **Chain:** N: **PDB Molecule:**dna-directed rna polymerase subunit n; **PDBTitle:** archaeal rna polymerase from sulfolobus solfataricus
79	d2p5zx1	Alignment	not modelled	5.5	23	**Fold:**OB-fold **Superfamily:**gp5 N-terminal domain-like **Family:**gp4 N-terminal domain-like
80	d1wjwa_	Alignment	not modelled	5.5	9	**Fold:**TBP-like **Superfamily:**Phosphoglucomutase, C-terminal domain **Family:**Phosphoglucomutase, C-terminal domain
81	c4a1aI_	Alignment	not modelled	5.4	16	**PDB header:**ribosome **Chain:** I: **PDB Molecule:**60s ribosomal protein l13a; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2

						initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 3.
82	d1ojta2	Alignment	not modelled	5.4	8	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
83	c3ei4D_	Alignment	not modelled	5.4	5	**PDB header:**dna binding protein **Chain:** D: **PDB Molecule:**dna damage-binding protein 2; **PDBTitle:** structure of the hsddb1-hsddb2 complex