Phyre2

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Description	RVBD3482c_(-)_3901503_3902285
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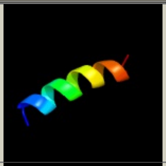
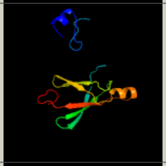
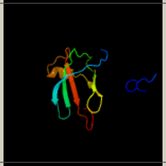
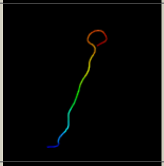
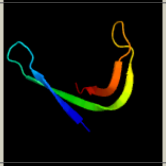
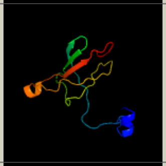
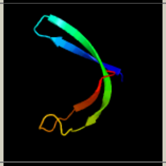
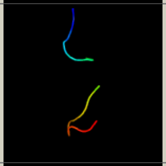
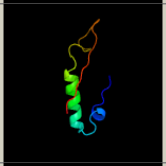
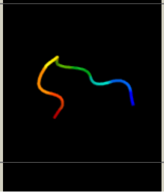
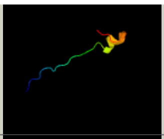
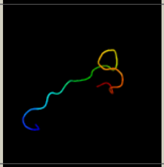
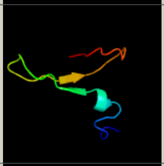
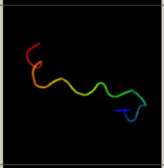
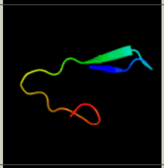
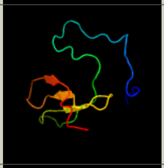
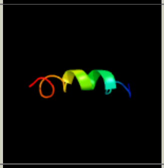
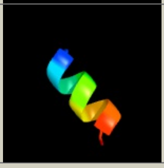
Unique Job ID	dc5314035e5ee511

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2ifoA_	Alignment		66.2	47	**PDB header:**virus **Chain:** A: **PDB Molecule:**inovirus; **PDBTitle:** model-building studies of inovirus: genetic variations on a2 geometric theme
2	c5ogxA_	Alignment		41.7	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome p450 reductase; **PDBTitle:** crystal structure of amycolatopsis cytochrome p450 reductase gcob.
3	c4wqmA_	Alignment		26.5	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**toluene-4-monooxygenase electron transfer component; **PDBTitle:** structure of the toluene 4-monooxygenase nadh oxidoreductase t4mof,2 k270s k271s variant
4	d1neia_	Alignment		22.4	47	**Fold:**Hypothetical protein YoaG **Superfamily:**Hypothetical protein YoaG **Family:**Hypothetical protein YoaG
5	c1wqsA_	Alignment		22.0	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**3c-like protease; **PDBTitle:** crystal structure of norovirus 3c-like protease
6	c1krhA_	Alignment		20.8	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**benzoate 1,2-dioxygenase reductase; **PDBTitle:** x-ray structure of benzoate dioxygenase reductase
7	c6b6iD_	Alignment		20.4	26	**PDB header:**viral protein,protease **Chain:** D: **PDB Molecule:**3c-like protease; **PDBTitle:** 2.4a resolution structure of human norovirus gii.4 protease
8	d1smpi_	Alignment		18.1	40	**Fold:**Streptavidin-like **Superfamily:**beta-Barrel protease inhibitors **Family:**Metalloprotease inhibitor
9	c3uoeB_	Alignment		17.5	50	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**dehydrogenase; **PDBTitle:** the crystal structure of dehydrogenase from sinorhizobium meliloti
10	d1fnoa3	Alignment		12.4	22	**Fold:**Ferredoxin-like **Superfamily:**Bacterial exopeptidase dimerisation domain **Family:**Bacterial exopeptidase dimerisation domain
11	c2y5pB_	Alignment		11.8	56	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**internalin b; **PDBTitle:** b-repeat of listeria monocytogenes inlb (internalin b)

12	c3al0C_	Alignment		11.2	43	**PDB header:**ligase/rna **Chain:** C: **PDB Molecule:**glutamyl-trna(gln) amidotransferase subunit c,linker, **PDBTitle:** crystal structure of the glutamine transamidosome from thermotoga2 maritima in the glutamylation state.
13	d3bmva3	Alignment		10.5	54	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
14	c2vqpA_	Alignment		10.2	35	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**matrix protein; **PDBTitle:** structure of the matrix protein from human respiratory2 syncytial virus
15	c3wolB_	Alignment		10.2	31	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dipeptidyl aminopeptidase bii; **PDBTitle:** crystal structure of the dap bii dipeptide complex i
16	c4l8nA_	Alignment		10.0	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**pdz domain protein; **PDBTitle:** crystal structure of a pdz domain protein (bdi_1242) from2 parabacteroides distasonis atcc 8503 at 2.50 a resolution
17	c5lhxA_	Alignment		9.9	32	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**serine/threonine-protein kinase plk4; **PDBTitle:** pb3 domain of drosophila melanogaster plk4 (sak)
18	c5fjsB_	Alignment		9.8	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glucosylceramidase; **PDBTitle:** bacterial beta-glucosidase reveals the structural and functional2 basis of genetic defects in human glucocerebrosidase 2 (gba2)3 disorders
19	c2hfrA_	Alignment		9.7	42	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**fowlicidin-3; **PDBTitle:** solution structure of antimicrobial peptide fowlicidin 3
20	c6fzoC_	Alignment		9.6	27	**PDB header:**fluorescent protein **Chain:** C: **PDB Molecule:**smurfp; **PDBTitle:** smurfp-y56f mutant
21	c4lj2A_	Alignment	not modelled	9.5	38	**PDB header:**lyase **Chain:** A: **PDB Molecule:**chorismate synthase; **PDBTitle:** crystal structure of chorismate synthase from acinetobacter baumannii2 at 3.15a resolution
22	c4ashB_	Alignment	not modelled	9.2	32	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ns6 protease; **PDBTitle:** crystal structure of the ns6 protease from murine norovirus 1
23	c2wlbB_	Alignment	not modelled	8.8	40	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**electron transfer protein 1, mitochondrial; **PDBTitle:** adrenodoxin-like ferredoxin etp1fd(516-618) of schizosaccharomyces2 pombe mitochondria
24	c5tgtA_	Alignment	not modelled	8.8	44	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamate--trna ligase; **PDBTitle:** crystal structure of glytamyl-trna synthetase glurs from pseudomonas2 aeruginosa
25	c4g5sE_	Alignment	not modelled	8.6	70	**PDB header:**cell cycle/signaling protein **Chain:** E: **PDB Molecule:**g-protein-signaling modulator 2; **PDBTitle:** structure of lgn gl3/galphai3 complex
26	d1b78a_	Alignment	not modelled	8.6	21	**Fold:**Anticodon-binding domain-like **Superfamily:**ITPase-like **Family:**ITPase (Ham1)
27	c4g5sF_	Alignment	not modelled	8.6	70	**PDB header:**cell cycle/signaling protein **Chain:** F: **PDB Molecule:**g-protein-signaling modulator 2; **PDBTitle:** structure of lgn gl3/galphai3 complex
28	c3afhA_	Alignment	not modelled	8.5	56	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamyl-trna synthetase 2; **PDBTitle:** crystal structure of thermotoga maritima nondiscriminating glutamyl-2 trna synthetase in complex with a glutamyl-amp analog
						Fold:beta-Grasp (ubiquitin-like)

29	d1i7ha_	Alignment	not modelled	8.4	31	**Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
30	d1ofza_	Alignment	not modelled	8.2	17	**Fold:**6-bladed beta-propeller **Superfamily:**Fucose-specific lectin **Family:**Fucose-specific lectin
31	d1alla_	Alignment	not modelled	8.1	45	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Phycocyanin-like phycobilisome proteins
32	c4po5E_	Alignment	not modelled	7.9	45	**PDB header:**photosynthesis **Chain:** E: **PDB Molecule:**allophycocyanin subunit alpha-b; **PDBTitle:** crystal structure of allophycocyanin b from synechocystis pcc 6803
33	c2mjdA_	Alignment	not modelled	7.8	40	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**adrenodoxin homolog, mitochondrial; **PDBTitle:** oxidized yeast adrenodoxin homolog 1
34	d2fh1a1	Alignment	not modelled	7.7	28	**Fold:**Gelsolin-like **Superfamily:**Actin depolymerizing proteins **Family:**Gelsolin-like
35	d1e88a3	Alignment	not modelled	7.1	29	**Fold:**FnI-like domain **Superfamily:**FnI-like domain **Family:**Fibronectin type I module
36	c2vmlA_	Alignment	not modelled	7.1	36	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**phycocyanin alpha chain; **PDBTitle:** the monoclinic structure of phycocyanin from gloeobacter violaceus
37	c1l6vA_	Alignment	not modelled	7.0	40	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**adrenodoxin 1; **PDBTitle:** structure of reduced bovine adrenodoxin
38	d1xrha_	Alignment	not modelled	7.0	39	**Fold:**L-sulfolactate dehydrogenase-like **Superfamily:**L-sulfolactate dehydrogenase-like **Family:**L-sulfolactate dehydrogenase-like
39	c5uj5A_	Alignment	not modelled	7.0	60	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**adrenodoxin; **PDBTitle:** solution structure of the oxidized iron-sulfur protein adrenodoxin2 from encephalitozoon cuniculi. seattle structural genomics center for3 infectious disease target encua.00705.a
40	c2k7mA_	Alignment	not modelled	6.9	42	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**gap junction alpha-5 protein; **PDBTitle:** structure of the connexin40 carboxyl terminal domain
41	c4aorE_	Alignment	not modelled	6.9	70	**PDB header:**hydrolase/inhibitor **Chain:** E: **PDB Molecule:**trypsin inhibitor 3; **PDBTitle:** cationic trypsin in complex with the spinacia oleracea trypsin2 inhibitor iii (soti-iii)
42	c4aorF_	Alignment	not modelled	6.9	70	**PDB header:**hydrolase/inhibitor **Chain:** F: **PDB Molecule:**trypsin inhibitor 3; **PDBTitle:** cationic trypsin in complex with the spinacia oleracea trypsin2 inhibitor iii (soti-iii)
43	d1qp3a_	Alignment	not modelled	6.7	61	**Fold:**SH3-like barrel **Superfamily:**Electron transport accessory proteins **Family:**Photosystem I accessory protein E (PsaE)
44	c1g59A_	Alignment	not modelled	6.7	50	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**glutamyl-trna synthetase; **PDBTitle:** glutamyl-trna synthetase complexed with trna(glu).
45	c5onoA_	Alignment	not modelled	6.7	38	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**l-ectoine synthase; **PDBTitle:** crystal structure of ectoine synthase from p. lautus
46	c6r3uA_	Alignment	not modelled	6.5	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycoside hydrolase family 32; **PDBTitle:** endo-levanase bt1760 mutant e221a from bacteroides thetaiotaomicron2 complexed with levantetraose
47	d1b33a_	Alignment	not modelled	6.5	45	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Phycocyanin-like phycobilisome proteins
48	d2bt6a1	Alignment	not modelled	6.5	40	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
49	c3lxfC_	Alignment	not modelled	6.5	50	**PDB header:**metal binding protein **Chain:** C: **PDB Molecule:**ferredoxin; **PDBTitle:** crystal structure of [2fe-2s] ferredoxin arx from novosphingobium2 aromaticivorans
50	d1xlqa1	Alignment	not modelled	6.4	50	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
51	d1kn1a_	Alignment	not modelled	6.2	36	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Phycocyanin-like phycobilisome proteins
52	c3ah7A_	Alignment	not modelled	6.2	28	**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
53	d1psea_	Alignment	not modelled	6.2	45	**Fold:**SH3-like barrel **Superfamily:**Electron transport accessory proteins **Family:**Photosystem I accessory protein E (PsaE)
54	c5frtC_	Alignment	not modelled	6.1	44	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**dimeric (2fe-2s) protein; **PDBTitle:** structure of the fesii (shethna) protein of azotobacter vinelandii
55	d1bg2a_	Alignment	not modelled	5.9	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Motor proteins
						PDB header:ligase

56	c2cfoA_	Alignment	not modelled	5.9	50	**Chain:** A: **PDB Molecule:**glutamyl-trna synthetase; **PDBTitle:** non-discriminating glutamyl-trna synthetase from2 thermosynechococcus elongatus in complex with glu
57	d1e9ma_	Alignment	not modelled	5.9	40	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
58	d1gtra2	Alignment	not modelled	5.9	39	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
59	c4a0tB_	Alignment	not modelled	5.8	42	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**tail fiber protein; **PDBTitle:** structure of the carboxy-terminal domain of bacteriophage t7 fibre2 gp17 containing residues 371-553.
60	c2y5cB_	Alignment	not modelled	5.8	50	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**adrenodoxin-like protein, mitochondrial; **PDBTitle:** structure of human ferredoxin 2 (fdx2)in complex with 2fe2s2 cluster
61	c4agiD_	Alignment	not modelled	5.8	17	**PDB header:**sugar-binding protein **Chain:** D: **PDB Molecule:**fucose-specific lectin flea; **PDBTitle:** crystal structure of fucose binding lectin from aspergillus2 fumigatus (afl) in complex with seleno fucoside.
62	c5m5iC_	Alignment	not modelled	5.8	20	**PDB header:**motor protein **Chain:** C: **PDB Molecule:**kinesin-like protein cut7; **PDBTitle:** pseudo-atomic model of microtubule-bound s.pombe kinesin-5 motor2 domain in the amppnp state (based on cryo-electron microscopy3 experiment): the n-terminus conformation allows formation of a cover4 neck bundle.
63	d1b9ra_	Alignment	not modelled	5.7	60	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
64	c6o2uB_	Alignment	not modelled	5.7	43	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**store-operated calcium entry-associated regulatory factor; **PDBTitle:** crystal structure of the saraf luminal domain
65	d1slqa_	Alignment	not modelled	5.7	29	**Fold:**VP4 membrane interaction domain **Superfamily:**VP4 membrane interaction domain **Family:**VP4 membrane interaction domain
66	c6h9nB_	Alignment	not modelled	5.7	45	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**cell division protein ftsb; **PDBTitle:** complex of the periplasmic domains of bacterial cell division proteins2 ftsq and ftsb
67	d1ekga_	Alignment	not modelled	5.7	22	**Fold:**N domain of copper amine oxidase-like **Superfamily:**Frataxin/Nqo15-like **Family:**Frataxin-like
68	d1uypa2	Alignment	not modelled	5.5	42	**Fold:**5-bladed beta-propeller **Superfamily:**Arabinanase/levansucrase/invertase **Family:**Glycosyl hydrolases family 32 N-terminal domain
69	d1r89a1	Alignment	not modelled	5.4	30	**Fold:**PAP/OAS1 substrate-binding domain **Superfamily:**PAP/OAS1 substrate-binding domain **Family:**Archaeal tRNA CCA-adding enzyme substrate-binding domain
70	c6et5u_	Alignment	not modelled	5.4	26	**PDB header:**photosynthesis **Chain:** U: **PDB Molecule:**light-harvesting protein b-1015 gamma chain; **PDBTitle:** reaction centre light harvesting complex 1 from blc. virids
71	c2mj3A_	Alignment	not modelled	5.4	40	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**iron-sulfur cluster binding protein; **PDBTitle:** backbone 1h, 13c, and 15n chemical shift assignments and structure of2 iron-sulfur cluster binding protein from ehrlichia chaffeensis
72	c6igzE_	Alignment	not modelled	5.4	39	**PDB header:**plant protein **Chain:** E: **PDB Molecule:**psae; **PDBTitle:** structure of psi-lhci
73	c6igzL_	Alignment	not modelled	5.4	20	**PDB header:**plant protein **Chain:** L: **PDB Molecule:**psal; **PDBTitle:** structure of psi-lhci
74	c4proD_	Alignment	not modelled	5.3	42	**PDB header:**serine protease **Chain:** D: **PDB Molecule:**alpha-lytic protease; **PDBTitle:** alpha-lytic protease complexed with pro region
75	c5kz5H_	Alignment	not modelled	5.3	22	**PDB header:**transferase/oxidoreductase **Chain:** H: **PDB Molecule:**frataxin, mitochondrial; **PDBTitle:** architecture of the human mitochondrial iron-sulfur cluster assembly2 machinery: the complex formed by the iron donor, the sulfur donor,3 and the scaffold
76	c2m67A_	Alignment	not modelled	5.3	35	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**merf; **PDBTitle:** full-length mercury transporter protein merf in lipid bilayer2 membranes
77	d1d0na4	Alignment	not modelled	5.2	24	**Fold:**Gelsolin-like **Superfamily:**Actin depolymerizing proteins **Family:**Gelsolin-like
78	c3huiA_	Alignment	not modelled	5.0	50	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**ferredoxin; **PDBTitle:** crystal structure of the mutant a105r of [2fe-2s] ferredoxin in the2 class i cyp199a2 system from rhodopseudomonas palustris
79	c2aezA_	Alignment	not modelled	5.0	37	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**fructan 1-exohydrolase iia; **PDBTitle:** crystal structure of fructan 1-exohydrolase iia (e201q) from cichorium2 intybus in complex with 1-kestose