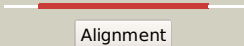

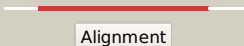

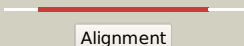







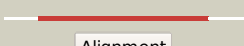











# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3161c_(-)_3529987_3531135
Date	Thu Aug 8 16:20:35 BST 2019
Unique Job ID	eb0043166c8a3556

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3n0qA_</a>	 Alignment		100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative aromatic-ring hydroxylating dioxygenase; <b>PDBTitle:</b> crystal structure of a putative aromatic-ring hydroxylating2 dioxygenase (tm1040_3219) from silicibacter sp. tm1040 at 1.80 a3 resolution
2	<a href="#">c3vcaA_</a>	 Alignment		100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ring-hydroxylating dioxygenase; <b>PDBTitle:</b> quaternary ammonium oxidative demethylation: x-ray crystallographic,2 resonance raman and uv-visible spectroscopic analysis of a rieske-3 type demethylase
3	<a href="#">c2b1xE_</a>	 Alignment		100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> naphthalene dioxygenase large subunit; <b>PDBTitle:</b> crystal structure of naphthalene 1,2-dioxygenase from rhodococcus sp.
4	<a href="#">c1uljA_</a>	 Alignment		100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> biphenyl dioxygenase large subunit; <b>PDBTitle:</b> biphenyl dioxygenase (bpha1a2) in complex with the substrate
5	<a href="#">c1wqlA_</a>	 Alignment		100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> iron-sulfur protein large subunit of cumene dioxygenase; <b>PDBTitle:</b> cumene dioxygenase (cuma1a2) from pseudomonas fluorescens ip01
6	<a href="#">c2hmnA_</a>	 Alignment		100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> naphthalene 1,2-dioxygenase alpha subunit; <b>PDBTitle:</b> crystal structure of the naphthalene 1,2-dioxygenase f352v2 mutant bound to anthracene.
7	<a href="#">c2gbxE_</a>	 Alignment		100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> biphenyl 2,3-dioxygenase alpha subunit; <b>PDBTitle:</b> crystal structure of biphenyl 2,3-dioxygenase from sphingomonas2 yanoikuyae b1 bound to biphenyl
8	<a href="#">c3gteB_</a>	 Alignment		100.0	14	<b>PDB header:</b> electron transport, oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ddmc; <b>PDBTitle:</b> crystal structure of dicamba monooxygenase with non-heme iron
9	<a href="#">c3gkxB_</a>	 Alignment		100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> terminal oxygenase component of carbazole 1,9a-dioxygenase; <b>PDBTitle:</b> terminal oxygenase of carbazole 1,9a-dioxygenase from novosphingobium2 sp. ka1
10	<a href="#">c2zylA_</a>	 Alignment		100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> possible oxidoreductase; <b>PDBTitle:</b> crystal structure of 3-ketosteroid-9-alpha-hydroxylase2 (ksha) from m. tuberculosis
11	<a href="#">c3gcfC_</a>	 Alignment		100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> terminal oxygenase component of carbazole 1,9a-dioxygenase; <b>PDBTitle:</b> terminal oxygenase of carbazole 1,9a-dioxygenase from2 nocardioides aromaticivorans ic177

12	<a href="#">c4qdfA_</a>	Alignment		100.0	14	<b>PDB header:</b> oxidoreductase/oxidoreductase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> 3-ketosteroid 9alpha-hydroxylase oxygenase; <b>PDBTitle:</b> crystal structure of apo ksha5 and ksha1 in complex with 1,4-30q-coa2 from r. rhodochrous
13	<a href="#">c4qdfB_</a>	Alignment		100.0	19	<b>PDB header:</b> oxidoreductase/oxidoreductase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> 3-ketosteroid 9alpha-hydroxylase oxygenase; <b>PDBTitle:</b> crystal structure of apo ksha5 and ksha1 in complex with 1,4-30q-coa2 from r. rhodochrous
14	<a href="#">c2de7B_</a>	Alignment		100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> terminal oxygenase component of carbazole; <b>PDBTitle:</b> the substrate-bound complex between oxygenase and2 ferredoxin in carbazole 1,9a-dioxygenase
15	<a href="#">c1z01D_</a>	Alignment		100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> 2-oxo-1,2-dihydroquinoline 8-monoxygenase, oxygenase <b>PDBTitle:</b> 2-oxoquinoline 8-monoxygenase component: active site modulation by2 rieske-[2fe-2s] center oxidation/reduction
16	<a href="#">d2b1xa1</a>	Alignment		100.0	30	<b>Fold:</b> ISP domain <b>Superfamily:</b> ISP domain <b>Family:</b> Ring hydroxylating alpha subunit ISP domain
17	<a href="#">d1wqla1</a>	Alignment		100.0	32	<b>Fold:</b> ISP domain <b>Superfamily:</b> ISP domain <b>Family:</b> Ring hydroxylating alpha subunit ISP domain
18	<a href="#">d1ulia1</a>	Alignment		100.0	37	<b>Fold:</b> ISP domain <b>Superfamily:</b> ISP domain <b>Family:</b> Ring hydroxylating alpha subunit ISP domain
19	<a href="#">d2bmoa1</a>	Alignment		100.0	28	<b>Fold:</b> ISP domain <b>Superfamily:</b> ISP domain <b>Family:</b> Ring hydroxylating alpha subunit ISP domain
20	<a href="#">d1o7na1</a>	Alignment		100.0	30	<b>Fold:</b> ISP domain <b>Superfamily:</b> ISP domain <b>Family:</b> Ring hydroxylating alpha subunit ISP domain
21	<a href="#">d1z01a1</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> ISP domain <b>Superfamily:</b> ISP domain <b>Family:</b> Ring hydroxylating alpha subunit ISP domain
22	<a href="#">d2de6a1</a>	Alignment	not modelled	100.0	25	<b>Fold:</b> ISP domain <b>Superfamily:</b> ISP domain <b>Family:</b> Ring hydroxylating alpha subunit ISP domain
23	<a href="#">d2bmoa2</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> TBP-like <b>Superfamily:</b> Bet v1-like <b>Family:</b> Ring hydroxylating alpha subunit catalytic domain
24	<a href="#">c3d89A_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> rieske domain-containing protein; <b>PDBTitle:</b> crystal structure of a soluble rieske ferredoxin from mus musculus
25	<a href="#">d1wqla2</a>	Alignment	not modelled	99.9	11	<b>Fold:</b> TBP-like <b>Superfamily:</b> Bet v1-like <b>Family:</b> Ring hydroxylating alpha subunit catalytic domain
26	<a href="#">d2b1xa2</a>	Alignment	not modelled	99.9	21	<b>Fold:</b> TBP-like <b>Superfamily:</b> Bet v1-like <b>Family:</b> Ring hydroxylating alpha subunit catalytic domain
27	<a href="#">d1ulia2</a>	Alignment	not modelled	99.9	10	<b>Fold:</b> TBP-like <b>Superfamily:</b> Bet v1-like <b>Family:</b> Ring hydroxylating alpha subunit catalytic domain
28	<a href="#">d1o7na2</a>	Alignment	not modelled	99.8	18	<b>Fold:</b> TBP-like <b>Superfamily:</b> Bet v1-like <b>Family:</b> Ring hydroxylating alpha subunit catalytic domain
29	<a href="#">d1vm9a_</a>	Alignment	not modelled	99.8	21	<b>Fold:</b> ISP domain <b>Superfamily:</b> ISP domain <b>Family:</b> Rieske iron-sulfur protein (ISP)

30	<a href="#">c2de7E</a>	Alignment	not modelled	99.8	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> ferredoxin component of carbazole; <b>PDBTitle:</b> the substrate-bound complex between oxygenase and2 ferredoxin in carbazole 1,9a-dioxygenase
31	<a href="#">c4aivA</a>	Alignment	not modelled	99.8	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> probable nitrite reductase [nad(p)h] small subunit nird; <b>PDBTitle:</b> crystal structure of putative nadh-dependent nitrite reductase small2 subunit from mycobacterium tuberculosis
32	<a href="#">d2jzaa1</a>	Alignment	not modelled	99.8	19	<b>Fold:</b> ISP domain <b>Superfamily:</b> ISP domain <b>Family:</b> NirD-like
33	<a href="#">c3dqyA</a>	Alignment	not modelled	99.8	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> toluene 1,2-dioxygenase system ferredoxin <b>PDBTitle:</b> crystal structure of toluene 2,3-dioxygenase ferredoxin
34	<a href="#">d1fqta</a>	Alignment	not modelled	99.8	23	<b>Fold:</b> ISP domain <b>Superfamily:</b> ISP domain <b>Family:</b> Rieske iron-sulfur protein (ISP)
35	<a href="#">d3c0da1</a>	Alignment	not modelled	99.8	14	<b>Fold:</b> ISP domain <b>Superfamily:</b> ISP domain <b>Family:</b> NirD-like
36	<a href="#">c3gceA</a>	Alignment	not modelled	99.8	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ferredoxin component of carbazole 1,9a- <b>PDBTitle:</b> ferredoxin of carbazole 1,9a-dioxygenase from nocardioides2 aromaticivorans ic177
37	<a href="#">c2qpzA</a>	Alignment	not modelled	99.8	24	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> naphthalene 1,2-dioxygenase system ferredoxin <b>PDBTitle:</b> naphthalene 1,2-dioxygenase rieske ferredoxin
38	<a href="#">d2jo6a1</a>	Alignment	not modelled	99.8	17	<b>Fold:</b> ISP domain <b>Superfamily:</b> ISP domain <b>Family:</b> NirD-like
39	<a href="#">c2i7fB</a>	Alignment	not modelled	99.8	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ferredoxin component of dioxygenase; <b>PDBTitle:</b> sphingomonas yanoikuyae b1 ferredoxin
40	<a href="#">c5cxmC</a>	Alignment	not modelled	99.7	20	<b>PDB header:</b> metal binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> cytochrome b6/f complex iron-sulfur subunit; <b>PDBTitle:</b> crystal structure of the cyanobacterial plasma membrane rieske protein2 petc3 from synechocystis pcc 6803
41	<a href="#">d1rfsa</a>	Alignment	not modelled	99.6	22	<b>Fold:</b> ISP domain <b>Superfamily:</b> ISP domain <b>Family:</b> Rieske iron-sulfur protein (ISP)
42	<a href="#">d1q90c</a>	Alignment	not modelled	99.5	21	<b>Fold:</b> ISP domain <b>Superfamily:</b> ISP domain <b>Family:</b> Rieske iron-sulfur protein (ISP)
43	<a href="#">d3cx5e1</a>	Alignment	not modelled	99.5	30	<b>Fold:</b> ISP domain <b>Superfamily:</b> ISP domain <b>Family:</b> Rieske iron-sulfur protein (ISP)
44	<a href="#">c4aayH</a>	Alignment	not modelled	99.5	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> H: <b>PDB Molecule:</b> arob; <b>PDBTitle:</b> crystal structure of the arsenite oxidase protein complex2 from rhizobium species strain nt-26
45	<a href="#">d1g8kb</a>	Alignment	not modelled	99.4	16	<b>Fold:</b> ISP domain <b>Superfamily:</b> ISP domain <b>Family:</b> Rieske iron-sulfur protein (ISP)
46	<a href="#">d2e74d1</a>	Alignment	not modelled	99.4	20	<b>Fold:</b> ISP domain <b>Superfamily:</b> ISP domain <b>Family:</b> Rieske iron-sulfur protein (ISP)
47	<a href="#">d1riea</a>	Alignment	not modelled	99.4	24	<b>Fold:</b> ISP domain <b>Superfamily:</b> ISP domain <b>Family:</b> Rieske iron-sulfur protein (ISP)
48	<a href="#">c2nvgA</a>	Alignment	not modelled	99.3	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquinol-cytochrome c reductase iron-sulfur subunit; <b>PDBTitle:</b> soluble domain of rieske iron sulfur protein.
49	<a href="#">d1z01a2</a>	Alignment	not modelled	99.2	15	<b>Fold:</b> TBP-like <b>Superfamily:</b> Bet v1-like <b>Family:</b> Ring hydroxylating alpha subunit catalytic domain
50	<a href="#">d1nyka</a>	Alignment	not modelled	99.1	21	<b>Fold:</b> ISP domain <b>Superfamily:</b> ISP domain <b>Family:</b> Rieske iron-sulfur protein (ISP)
51	<a href="#">c2e76D</a>	Alignment	not modelled	99.1	13	<b>PDB header:</b> photosynthesis <b>Chain:</b> D: <b>PDB Molecule:</b> cytochrome b6-f complex iron-sulfur subunit; <b>PDBTitle:</b> crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus
52	<a href="#">c2fyuE</a>	Alignment	not modelled	99.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> ubiquinol-cytochrome c reductase iron-sulfur subunit, <b>PDBTitle:</b> crystal structure of bovine heart mitochondrial bc1 with jg1442 inhibitor
53	<a href="#">c2fynO</a>	Alignment	not modelled	98.9	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> O: <b>PDB Molecule:</b> ubiquinol-cytochrome c reductase iron-sulfur <b>PDBTitle:</b> crystal structure analysis of the double mutant rhodobacter2 sphaeroides bc1 complex
54	<a href="#">d2de6a2</a>	Alignment	not modelled	98.8	14	<b>Fold:</b> TBP-like <b>Superfamily:</b> Bet v1-like <b>Family:</b> Ring hydroxylating alpha subunit catalytic domain
55	<a href="#">c1n81E</a>	Alignment	not modelled	98.7	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> ubiquinol-cytochrome c reductase iron-

55	<a href="#">c1p84E_</a>	Alignment	not modelled	98.7	30	sulfur subunit; <b>PDBTitle:</b> hdbt inhibited yeast cytochrome bc1 complex
56	<a href="#">c6hwhB_</a>	Alignment	not modelled	97.8	25	<b>PDB header:</b> electron transport <b>Chain:</b> B; <b>PDB Molecule:</b> ubiquinol-cytochrome c reductase iron-sulfur subunit; <b>PDBTitle:</b> structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
57	<a href="#">d1jm1a_</a>	Alignment	not modelled	97.7	25	<b>Fold:</b> ISP domain <b>Superfamily:</b> ISP domain <b>Family:</b> Rieske iron-sulfur protein (ISP)
58	<a href="#">c6fo2R_</a>	Alignment	not modelled	96.1	24	<b>PDB header:</b> membrane protein <b>Chain:</b> R; <b>PDB Molecule:</b> cytochrome b-c1 complex subunit rieske, mitochondrial; <b>PDBTitle:</b> cryoem structure of bovine cytochrome bc1 with no ligand bound
59	<a href="#">c5x2dA_</a>	Alignment	not modelled	68.4	6	<b>PDB header:</b> cell adhesion <b>Chain:</b> A; <b>PDB Molecule:</b> tegumental protein 20.8 kda; <b>PDBTitle:</b> crystal structure of dlc like domain of cstal3 (83-177aa)
60	<a href="#">d1pwka_</a>	Alignment	not modelled	62.2	14	<b>Fold:</b> DLC <b>Superfamily:</b> DLC <b>Family:</b> DLC
61	<a href="#">c5fx0A_</a>	Alignment	not modelled	44.6	9	<b>PDB header:</b> cell adhesion <b>Chain:</b> A; <b>PDB Molecule:</b> calcium binding protein; <b>PDBTitle:</b> fasciola hepatica calcium binding protein fhcabp2: structure of the2 dynein light chain-like domain. p6422 native.
62	<a href="#">c5e7tl_</a>	Alignment	not modelled	37.4	35	<b>PDB header:</b> viral protein <b>Chain:</b> I; <b>PDB Molecule:</b> major structural protein 1; <b>PDBTitle:</b> structure of the tripod (bppuct-a-l) from the baseplate of2 bacteriophage tuc2009
63	<a href="#">c3nwiC_</a>	Alignment	not modelled	37.0	14	<b>PDB header:</b> transport protein <b>Chain:</b> C; <b>PDB Molecule:</b> zinc transport protein zntb; <b>PDBTitle:</b> the soluble domain structure of the zntb zn2+ efflux system
64	<a href="#">c2w3nA_</a>	Alignment	not modelled	35.7	26	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> carbonic anhydrase 2; <b>PDBTitle:</b> structure and inhibition of the co2-sensing carbonic anhydrase can22 from the pathogenic fungus cryptococcus neoformans
65	<a href="#">c4ct0B_</a>	Alignment	not modelled	32.3	13	<b>PDB header:</b> circadian clock protein <b>Chain:</b> B; <b>PDB Molecule:</b> period circadian protein homolog 2; <b>PDBTitle:</b> crystal structure of mouse cryptochrome1 in complex with period2
66	<a href="#">c3fcgB_</a>	Alignment	not modelled	30.1	14	<b>PDB header:</b> membrane protein, protein transport <b>Chain:</b> B; <b>PDB Molecule:</b> f1 capsule-anchoring protein; <b>PDBTitle:</b> crystal structure analysis of the middle domain of the2 caf1a usher
67	<a href="#">c4psiA_</a>	Alignment	not modelled	29.7	12	<b>PDB header:</b> protein binding <b>Chain:</b> A; <b>PDB Molecule:</b> pih1 domain-containing protein 1; <b>PDBTitle:</b> pih1d1/phospho-tel2 complex
68	<a href="#">c5ztpB_</a>	Alignment	not modelled	29.7	29	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> carbonic anhydrase; <b>PDBTitle:</b> carbonic anhydrase from glaciozyma antarctica
69	<a href="#">c3kv0A_</a>	Alignment	not modelled	28.8	29	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> het-c2; <b>PDBTitle:</b> crystal structure of het-c2: a fungal glycolipid transfer protein2 (gltp)
70	<a href="#">c3tenD_</a>	Alignment	not modelled	28.2	33	<b>PDB header:</b> hydrolase <b>Chain:</b> D; <b>PDB Molecule:</b> cs2 hydrolase; <b>PDBTitle:</b> holo form of carbon disulfide hydrolase
71	<a href="#">c4ds1C_</a>	Alignment	not modelled	28.2	9	<b>PDB header:</b> structural protein/transport protein <b>Chain:</b> C; <b>PDB Molecule:</b> dynein light chain 1, cytoplasmic; <b>PDBTitle:</b> the structure of a yeast dyn2-nup159 complex and the molecular basis2 for the dynein light chain - nuclear pore interaction
72	<a href="#">c1ddzA_</a>	Alignment	not modelled	27.9	43	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> carbonic anhydrase; <b>PDBTitle:</b> x-ray structure of a beta-carbonic anhydrase from the red2 alga, porphyridium purpureum r-1
73	<a href="#">c2vpyB_</a>	Alignment	not modelled	27.2	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> nrfc protein; <b>PDBTitle:</b> polysulfide reductase with bound quinone inhibitor,2 pentachlorophenol (pcp)
74	<a href="#">c3lasA_</a>	Alignment	not modelled	27.0	29	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> putative carbonic anhydrase; <b>PDBTitle:</b> crystal structure of carbonic anhydrase from streptococcus mutans to2 1.4 angstrom resolution
75	<a href="#">c4qiwp_</a>	Alignment	not modelled	26.1	21	<b>PDB header:</b> transcription <b>Chain:</b> P; <b>PDB Molecule:</b> dna-directed rna polymerase subunit p; <b>PDBTitle:</b> crystal structure of euryarchaeal rna polymerase from thermococcus2 kodakarensis
76	<a href="#">d1en2a2</a>	Alignment	not modelled	26.1	30	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> Plant lectins/antimicrobial peptides <b>Family:</b> Hevein-like agglutinin (lectin) domain
77	<a href="#">c2z0rA_</a>	Alignment	not modelled	25.7	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> putative uncharacterized protein ttha0547; <b>PDBTitle:</b> crystal structure of hypothetical protein ttha0547
78	<a href="#">c4rxvA_</a>	Alignment	not modelled	25.5	27	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> carbonic anhydrase; <b>PDBTitle:</b> crystal structure of the beta carbonic anhydrase psca3 isolated from2 pseudomonas aeruginosa
79	<a href="#">c3vrkA_</a>	Alignment	not modelled	25.3	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> carbonyl sulfide hydrolase; <b>PDBTitle:</b> crystal structure of thiobacillus thioparus thi115 carbonyl sulfide2 hydrolase / thiocyanate complex
80	<a href="#">d1ehda2</a>	Alignment	not modelled	25.2	30	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> Plant lectins/antimicrobial peptides <b>Family:</b> Hevein-like agglutinin (lectin) domain

81	<a href="#">d1ddza2</a>	Alignment	not modelled	24.8	50	<b>Fold:</b> Resolvase-like <b>Superfamily:</b> beta-carbonic anhydrase, cab <b>Family:</b> beta-carbonic anhydrase, cab
82	<a href="#">c4v36B</a>	Alignment	not modelled	24.6	25	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> lysyl-trna-dependent l-ysyl-phosphatidylglycerol synthase; <b>PDBTitle:</b> the structure of l-pgs from bacillus licheniformis
83	<a href="#">c1y1kA</a>	Alignment	not modelled	22.6	14	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein rv1284/mt1322; <b>PDBTitle:</b> crystal structure of rv1284 from mycobacterium tuberculosis in complex2 with thiocyanate
84	<a href="#">c2c3yA</a>	Alignment	not modelled	20.9	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate-ferredoxin oxidoreductase; <b>PDBTitle:</b> crystal structure of the radical form of f2 pyruvate:ferredoxin oxidoreductase from desulfovibrio3 africanus
85	<a href="#">d1nfga1</a>	Alignment	not modelled	20.8	26	<b>Fold:</b> Composite domain of metallo-dependent hydrolases <b>Superfamily:</b> Composite domain of metallo-dependent hydrolases <b>Family:</b> Hydantoinase (dihydropyrimidinase)
86	<a href="#">d1uhva1</a>	Alignment	not modelled	20.8	28	<b>Fold:</b> Glycosyl hydrolase domain <b>Superfamily:</b> Glycosyl hydrolase domain <b>Family:</b> Composite domain of glycosyl hydrolase families 5, 30, 39 and 51
87	<a href="#">d3e2ba1</a>	Alignment	not modelled	20.6	9	<b>Fold:</b> DLC <b>Superfamily:</b> DLC <b>Family:</b> DLC
88	<a href="#">d1ddza1</a>	Alignment	not modelled	20.3	43	<b>Fold:</b> Resolvase-like <b>Superfamily:</b> beta-carbonic anhydrase, cab <b>Family:</b> beta-carbonic anhydrase, cab
89	<a href="#">d1ei5a2</a>	Alignment	not modelled	20.0	24	<b>Fold:</b> Streptavidin-like <b>Superfamily:</b> D-aminopeptidase, middle and C-terminal domains <b>Family:</b> D-aminopeptidase, middle and C-terminal domains
90	<a href="#">d1cmia</a>	Alignment	not modelled	19.7	9	<b>Fold:</b> DLC <b>Superfamily:</b> DLC <b>Family:</b> DLC
91	<a href="#">c4k8nF</a>	Alignment	not modelled	19.5	60	<b>PDB header:</b> lipid transport <b>Chain:</b> F: <b>PDB Molecule:</b> glycolipid transfer protein domain-containing protein 1; <b>PDBTitle:</b> crystal structure of human ceramide-1-phosphate transfer protein2 (cptp) in complex with 18:1 ceramide-1-phosphate (18:1-c1p)
92	<a href="#">d3orca</a>	Alignment	not modelled	19.1	29	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
93	<a href="#">c5mu4A</a>	Alignment	not modelled	18.8	12	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> tail tubular protein a; <b>PDBTitle:</b> tail tubular protein a of klebsiella pneumoniae bacteriophage kp32
94	<a href="#">c3j20R</a>	Alignment	not modelled	18.8	40	<b>PDB header:</b> ribosome <b>Chain:</b> R: <b>PDB Molecule:</b> 30s ribosomal protein s17p; <b>PDBTitle:</b> promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
95	<a href="#">c5kdiA</a>	Alignment	not modelled	18.7	60	<b>PDB header:</b> lipid transport <b>Chain:</b> A: <b>PDB Molecule:</b> pleckstrin homology domain-containing family a member 8; <b>PDBTitle:</b> how fapp2 selects simple glycosphingolipids using the gltp-fold
96	<a href="#">d1swxa</a>	Alignment	not modelled	18.7	60	<b>Fold:</b> Glycolipid transfer protein, GLTP <b>Superfamily:</b> Glycolipid transfer protein, GLTP <b>Family:</b> Glycolipid transfer protein, GLTP
97	<a href="#">c6gwuB</a>	Alignment	not modelled	18.5	21	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> carbonic anhydrase; <b>PDBTitle:</b> carbonic anhydrase cance103p from candida albicans
98	<a href="#">c3eywA</a>	Alignment	not modelled	18.5	16	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> c-terminal domain of glutathione-regulated potassium-efflux <b>PDBTitle:</b> crystal structure of the c-terminal domain of e. coli kefc in complex2 with keff
99	<a href="#">c3eyxB</a>	Alignment	not modelled	18.3	29	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> carbonic anhydrase; <b>PDBTitle:</b> crystal structure of carbonic anhydrase nce103 from2 saccharomyces cerevisiae