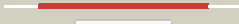
















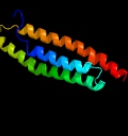

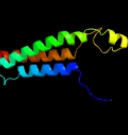













Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2984_(ppk)_3339864_3342092
Date	Thu Aug 8 16:20:15 BST 2019
Unique Job ID	1948d7f27ffba1fd

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1xdoB_	 Alignment		100.0	33	PDB header: transferase Chain: B: PDB Molecule: polyphosphate kinase; PDBTitle: crystal structure of escherichia coli polyphosphate kinase
2	c2o8rA_	 Alignment		100.0	34	PDB header: transferase Chain: A: PDB Molecule: polyphosphate kinase; PDBTitle: crystal structure of polyphosphate kinase from porphyromonas2 gingivalis
3	d2o8ra3	 Alignment		100.0	36	Fold: Phospholipase D/nuclease Superfamily: Phospholipase D/nuclease Family: Polyphosphate kinase C-terminal domain
4	d2o8ra4	 Alignment		100.0	33	Fold: Phospholipase D/nuclease Superfamily: Phospholipase D/nuclease Family: Polyphosphate kinase C-terminal domain
5	d1xdpa4	 Alignment		100.0	32	Fold: Phospholipase D/nuclease Superfamily: Phospholipase D/nuclease Family: Polyphosphate kinase C-terminal domain
6	d1xdpa2	 Alignment		100.0	22	Fold: PHP14-like Superfamily: PHP14-like Family: PPK middle domain-like
7	d1xdpa3	 Alignment		100.0	43	Fold: Phospholipase D/nuclease Superfamily: Phospholipase D/nuclease Family: Polyphosphate kinase C-terminal domain
8	d2o8ra2	 Alignment		100.0	27	Fold: PHP14-like Superfamily: PHP14-like Family: PPK middle domain-like
9	d1xdpa1	 Alignment		100.0	40	Fold: Spectrin repeat-like Superfamily: PPK N-terminal domain-like Family: PPK N-terminal domain-like
10	d2o8ra1	 Alignment		100.0	44	Fold: Spectrin repeat-like Superfamily: PPK N-terminal domain-like Family: PPK N-terminal domain-like
11	c3hsiC_	 Alignment		100.0	12	PDB header: transferase Chain: C: PDB Molecule: phosphatidylserine synthase; PDBTitle: crystal structure of phosphatidylserine synthase haemophilus2 influenzae rd kw20

12	c1v0sA_	Alignment		100.0	25	PDB header: hydrolase Chain: A; PDB Molecule: phospholipase d; PDBTitle: uninhibited form of phospholipase d from streptomyces sp.2 strain pmf
13	c4ggkA_	Alignment		99.6	13	PDB header: hydrolase Chain: A; PDB Molecule: mitochondrial cardiolipin hydrolase; PDBTitle: crystal structure of zucchini from mouse (mzuc / pld6 / mitopl) bound2 to tungstate
14	d1byra_	Alignment		99.5	16	Fold: Phospholipase D/nuclease Superfamily: Phospholipase D/nuclease Family: Nuclease
15	c6ehil_	Alignment		99.5	10	PDB header: dna binding protein Chain: I; PDB Molecule: nuclease nuct; PDBTitle: nuct from helicobacter pylori
16	c4gelA_	Alignment		99.5	19	PDB header: hydrolase Chain: A; PDB Molecule: mitochondrial cardiolipin hydrolase; PDBTitle: crystal structure of zucchini
17	c5lzkB_	Alignment		99.4	18	PDB header: structural genomics Chain: B; PDB Molecule: protein fam83b; PDBTitle: structure of the domain of unknown function duf1669 from human fam83b
18	d1v0wa2	Alignment		99.3	27	Fold: Phospholipase D/nuclease Superfamily: Phospholipase D/nuclease Family: Phospholipase D
19	c4uriA_	Alignment		99.3	16	PDB header: unknown function Chain: A; PDB Molecule: protein fam83a; PDBTitle: crystal structure of human bj-tsa-9
20	d1v0wa1	Alignment		99.2	18	Fold: Phospholipase D/nuclease Superfamily: Phospholipase D/nuclease Family: Phospholipase D
21	c4genA_	Alignment	not modelled	99.1	20	PDB header: hydrolase Chain: A; PDB Molecule: mitochondrial cardiolipin hydrolase; PDBTitle: crystal structure of zucchini (monomer)
22	c5bqtC_	Alignment	not modelled	97.7	9	PDB header: dna binding protein Chain: C; PDB Molecule: putative hth-type transcriptional regulator trmbI2; PDBTitle: structure of trmbI2, an archaeal chromatin protein, shows a novel mode2 of dna binding.
23	c4rctB_	Alignment	not modelled	97.6	13	PDB header: hydrolase Chain: B; PDB Molecule: restriction endonuclease r.ngovii; PDBTitle: crystal structure of r-protein of ngoavii restriction endonuclease
24	c2c1IA_	Alignment	not modelled	94.1	10	PDB header: hydrolase Chain: A; PDB Molecule: restriction endonuclease; PDBTitle: structure of the bfii restriction endonuclease
25	c3qphA_	Alignment	not modelled	91.5	14	PDB header: transcription Chain: A; PDB Molecule: trmb, a global transcription regulator; PDBTitle: the three-dimensional structure of trmb, a global transcriptional2 regulator of the hyperthermophilic archaeon pyrococcus furiosus in3 complex with sucrose
26	c3ecsD_	Alignment	not modelled	90.9	29	PDB header: translation Chain: D; PDB Molecule: translation initiation factor eif-2b subunit alpha; PDBTitle: crystal structure of human eif2b alpha
27	d1vb5a_	Alignment	not modelled	90.3	20	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: !F2B-like
28	c6i7tB_	Alignment	not modelled	89.6	21	PDB header: translation Chain: B; PDB Molecule: translation initiation factor eif-2b subunit alpha;

29	c5b04B_	Alignment	not modelled	88.1	15	PDBTitle: eif2b:eif2 complex PDB header: translation Chain: B: PDB Molecule: translation initiation factor eif-2b subunit alpha; PDBTitle: crystal structure of the eukaryotic translation initiation factor 2b2 from schizosaccharomyces pombe
30	d1zj8a2	Alignment	not modelled	87.8	22	Fold: Ferredoxin-like Superfamily: Nitrite/Sulfite reductase N-terminal domain-like Family: Duplicated SiR/NiR-like domains 1 and 3
31	c4ldrA_	Alignment	not modelled	87.1	14	PDB header: isomerase, cell invasion Chain: A: PDB Molecule: methylthioribose-1-phosphate isomerase; PDBTitle: structure of the s283y mutant of mrdi
32	c2yv2A_	Alignment	not modelled	86.8	20	PDB header: ligase Chain: A: PDB Molecule: succinyl-coa synthetase alpha chain; PDBTitle: crystal structure of succinyl-coa synthetase alpha chain from2 aeropyrum pernix k1
33	d1oy0a_	Alignment	not modelled	86.0	19	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Ketopantoate hydroxymethyltransferase PanB
34	c3r2jC_	Alignment	not modelled	85.2	31	PDB header: hydrolase Chain: C: PDB Molecule: alpha/beta-hydrolase-like protein; PDBTitle: crystal structure of pnc1 from l. infantum in complex with nicotinate
35	c5dboA_	Alignment	not modelled	84.8	23	PDB header: translation Chain: A: PDB Molecule: translation initiation factor eif-2b-like protein; PDBTitle: crystal structure of the tetrameric eif2b-beta2-delta2 complex from c.2 thermophilum
36	d1eucb1	Alignment	not modelled	83.5	20	Fold: Flavodoxin-like Superfamily: Succinyl-CoA synthetase domains Family: Succinyl-CoA synthetase domains
37	c2fpgA_	Alignment	not modelled	82.7	21	PDB header: ligase Chain: A: PDB Molecule: succinyl-coa ligase [gdp-forming] alpha-chain, PDBTitle: crystal structure of pig gtp-specific succinyl-coa synthetase in2 complex with gdp
38	d1jy1a1	Alignment	not modelled	82.0	11	Fold: Phospholipase D/nuclease Superfamily: Phospholipase D/nuclease Family: Tyrosyl-DNA phosphodiesterase TDP1
39	c3a11D_	Alignment	not modelled	81.7	21	PDB header: isomerase Chain: D: PDB Molecule: translation initiation factor eif-2b, delta subunit; PDBTitle: crystal structure of ribose-1,5-bisphosphate isomerase from2 thermococcus kodakaraensis kod1
40	c3gbcA_	Alignment	not modelled	81.0	18	PDB header: hydrolase Chain: A: PDB Molecule: pyrazinamidase/nicotinamidase pnca; PDBTitle: determination of the crystal structure of the pyrazinamidase from2 m.tuberculosis : a structure-function analysis for prediction3 resistance to pyrazinamide
41	d1t9ka_	Alignment	not modelled	80.1	20	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: IF2B-like
42	d1qzqa1	Alignment	not modelled	79.7	11	Fold: Phospholipase D/nuclease Superfamily: Phospholipase D/nuclease Family: Tyrosyl-DNA phosphodiesterase TDP1
43	c6melA_	Alignment	not modelled	79.6	19	PDB header: ligase Chain: A: PDB Molecule: succinate--coa ligase subunit alpha; PDBTitle: succinyl-coa synthase from campylobacter jejuni
44	c5b04C_	Alignment	not modelled	79.4	25	PDB header: translation Chain: C: PDB Molecule: probable translation initiation factor eif-2b subunit beta; PDBTitle: crystal structure of the eukaryotic translation initiation factor 2b2 from schizosaccharomyces pombe
45	d2nu7b1	Alignment	not modelled	79.4	21	Fold: Flavodoxin-like Superfamily: Succinyl-CoA synthetase domains Family: Succinyl-CoA synthetase domains
46	d1t5oa_	Alignment	not modelled	79.1	18	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: IF2B-like
47	c4zemB_	Alignment	not modelled	79.0	19	PDB header: translation Chain: B: PDB Molecule: translation initiation factor eif2b-like protein, PDBTitle: crystal structure of eif2b beta from chaetomium thermophilum
48	c6a34B_	Alignment	not modelled	78.8	12	PDB header: isomerase Chain: B: PDB Molecule: putative methylthioribose-1-phosphate isomerase; PDBTitle: crystal structure of 5-methylthioribose 1-phosphate isomerase from2 pyrococcus horikoshii ot3 - form i
49	c4zeoH_	Alignment	not modelled	78.1	23	PDB header: translation Chain: H: PDB Molecule: translation initiation factor eif-2b-like protein; PDBTitle: crystal structure of eif2b delta from chaetomium thermophilum
50	c5b04G_	Alignment	not modelled	78.0	23	PDB header: translation Chain: G: PDB Molecule: probable translation initiation factor eif-2b subunit PDBTitle: crystal structure of the eukaryotic translation initiation factor 2b2 from schizosaccharomyces pombe
51	c1zj8B_	Alignment	not modelled	77.5	24	PDB header: oxidoreductase Chain: B: PDB Molecule: probable ferredoxin-dependent nitrite reductase nira; PDBTitle: structure of mycobacterium tuberculosis nira protein
52	d1oi7a2	Alignment	not modelled	76.8	20	Fold: Flavodoxin-like Superfamily: Succinyl-CoA synthetase domains Family: Succinyl-CoA synthetase domains

53	c6i3mD_	Alignment	not modelled	75.7	27	PDB header: translation Chain: D: PDB Molecule: translation initiation factor eif-2b subunit delta; PDBTitle: eif2b:eif2 complex, phosphorylated on eif2 alpha serine 52.
54	c6ezoD_	Alignment	not modelled	74.9	24	PDB header: membrane protein Chain: D: PDB Molecule: translation initiation factor eif-2b subunit beta; PDBTitle: eukaryotic initiation factor eif2b in complex with isrib
55	d2akja2	Alignment	not modelled	74.1	29	Fold: Ferredoxin-like Superfamily: Nitrite/Sulfite reductase N-terminal domain-like Family: Duplicated SiR/NiR-like domains 1 and 3
56	c2b34C_	Alignment	not modelled	73.0	18	PDB header: hydrolase Chain: C: PDB Molecule: mar1 ribonuclease; PDBTitle: structure of mar1 ribonuclease from caenorhabditis elegans
57	c2yvka_	Alignment	not modelled	72.2	18	PDB header: isomerase Chain: A: PDB Molecule: methylthioribose-1-phosphate isomerase; PDBTitle: crystal structure of 5-methylthioribose 1-phosphate2 isomerase product complex from bacillus subtilis
58	d1v59a2	Alignment	not modelled	72.0	17	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
59	c6qg0G_	Alignment	not modelled	71.7	26	PDB header: translation Chain: G: PDB Molecule: translation initiation factor eif-2b subunit delta; PDBTitle: structure of eif2b-eif2 (phosphorylated at ser51) complex (model 1)
60	c3b0nA_	Alignment	not modelled	70.1	27	PDB header: oxidoreductase Chain: A: PDB Molecule: nitrite reductase; PDBTitle: q448k mutant of assimilatory nitrite reductase (nii3) from tobacco2 leaf
61	d2a0ua1	Alignment	not modelled	69.7	12	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: IF2B-like
62	c2h0rD_	Alignment	not modelled	68.1	18	PDB header: hydrolase Chain: D: PDB Molecule: nicotinamidase; PDBTitle: structure of the yeast nicotinamidase pnc1p
63	c4davA_	Alignment	not modelled	68.0	23	PDB header: hydrolase/dna Chain: A: PDB Molecule: sugar fermentation stimulation protein homolog; PDBTitle: the structure of pyrococcus furiosus sfsa in complex with dna
64	c5n0sa_	Alignment	not modelled	67.5	9	PDB header: transferase Chain: A: PDB Molecule: peptide n-methyltransferase; PDBTitle: crystal structure of opha-deltac6 mutant y98a in complex with sam
65	c1nopB_	Alignment	not modelled	67.4	11	PDB header: hydrolase/dna Chain: B: PDB Molecule: tyrosyl-dna phosphodiesterase 1; PDBTitle: crystal structure of human tyrosyl-dna phosphodiesterase2 (tdp1) in complex with vanadate, dna and a human3 topoisomerase i-derived peptide
66	d1s4da_	Alignment	not modelled	66.9	19	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase
67	c5h92A_	Alignment	not modelled	66.7	14	PDB header: oxidoreductase/electron transport Chain: A: PDB Molecule: sulfite reductase [ferredoxin], chloroplastic; PDBTitle: crystal structure of the complex between maize sulfite reductase and2 ferredoxin in the form-3 crystal
68	c2nu8D_	Alignment	not modelled	66.5	22	PDB header: ligase Chain: D: PDB Molecule: succinyl-coa ligase [adp-forming] subunit alpha; PDBTitle: c123at mutant of e. coli succinyl-coa synthetase
69	c3mwdB_	Alignment	not modelled	66.4	19	PDB header: transferase Chain: B: PDB Molecule: atp-citrate synthase; PDBTitle: truncated human atp-citrate lyase with citrate bound
70	d2csua2	Alignment	not modelled	66.1	19	Fold: Flavodoxin-like Superfamily: Succinyl-CoA synthetase domains Family: Succinyl-CoA synthetase domains
71	c6g4qB_	Alignment	not modelled	65.9	18	PDB header: ligase Chain: B: PDB Molecule: succinate--coa ligase [adp-forming] subunit beta, PDBTitle: structure of human adp-forming succinyl-coa ligase complex sucg1-2 sucla2
72	c4dapA_	Alignment	not modelled	65.9	23	PDB header: dna binding protein Chain: A: PDB Molecule: sugar fermentation stimulation protein a; PDBTitle: the structure of escherichia coli sfsa
73	c2yboA_	Alignment	not modelled	65.8	20	PDB header: transferase Chain: A: PDB Molecule: methyltransferase; PDBTitle: the x-ray structure of the sam-dependent uroporphyrinogen2 iii methyltransferase nire from pseudomonas aeruginosa in3 complex with sah
74	d1o66a_	Alignment	not modelled	63.1	16	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Ketopantoate hydroxymethyltransferase PanB
75	c4yt2A_	Alignment	not modelled	62.8	42	PDB header: metal binding protein Chain: A: PDB Molecule: h(2)-forming methylenetetrahydromethanopterin PDBTitle: hmd ii from methanocaldococcus jannaschii
76	c3d3kD_	Alignment	not modelled	62.5	15	PDB header: protein binding Chain: D: PDB Molecule: enhancer of mrna-decapping protein 3; PDBTitle: crystal structure of human edc3p
77	c4v34A_	Alignment	not modelled	62.4	16	PDB header: transferase Chain: A: PDB Molecule: alanyl-trna-dependent l-alanyl-phosphatidylglycerol

						PDBTitle: the structure of a-pgs from pseudomonas aeruginosa (semet derivative)
78	d1jy1a2	Alignment	not modelled	61.5	18	Fold: Phospholipase D/nuclease Superfamily: Phospholipase D/nuclease Family: Tyrosyl-DNA phosphodiesterase TDP1
79	c6huxA	Alignment	not modelled	60.6	42	PDB header: oxidoreductase Chain: A: PDB Molecule: h(2)-forming methylenetetrahydromethanopterin PDBTitle: hmdii from methanocaldococcus jannaschii reconstituted with fe-2 guanylylpyridinol (fegp) cofactor and co-crystallized with methenyl-3 tetrahydromethanopterin at 2.5 a resolution
80	c4xp7A	Alignment	not modelled	60.2	10	PDB header: oxidoreductase Chain: A: PDB Molecule: trna-dihydrouridine(20) synthase [nad(p)+]-like; PDBTitle: crystal structure of human trna dihydrouridine synthase 2
81	c1yzvA	Alignment	not modelled	59.5	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: hypothetical protein from trypanosoma cruzi
82	c1eucB	Alignment	not modelled	59.1	20	PDB header: ligase Chain: B: PDB Molecule: succinyl-coa synthetase, beta chain; PDBTitle: crystal structure of dephosphorylated pig heart, gtp-2 specific succinyl-coa synthetase
83	d1vhna	Alignment	not modelled	58.1	14	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
84	c1nvmG	Alignment	not modelled	57.6	10	PDB header: lyase/oxidoreductase Chain: G: PDB Molecule: 4-hydroxy-2-oxovalerate aldolase; PDBTitle: crystal structure of a bifunctional aldolase-dehydrogenase :2 sequestering a reactive and volatile intermediate
85	d1ebda2	Alignment	not modelled	55.4	26	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
86	d1dxla2	Alignment	not modelled	53.6	20	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
87	c4lrtC	Alignment	not modelled	53.3	18	PDB header: lyase/oxidoreductase Chain: C: PDB Molecule: 4-hydroxy-2-oxovalerate aldolase; PDBTitle: crystal and solution structures of the bifunctional enzyme2 (aldolase/aldehyde dehydrogenase) from thermomonospora curvata,3 reveal a cofactor-binding domain motion during nad+ and coa4 accommodation within the shared cofactor-binding site
88	d1euca2	Alignment	not modelled	53.2	21	Fold: Flavodoxin-like Superfamily: Succinyl-CoA synthetase domains Family: Succinyl-CoA synthetase domains
89	d1q32a2	Alignment	not modelled	52.5	20	Fold: Phospholipase D/nuclease Superfamily: Phospholipase D/nuclease Family: Tyrosyl-DNA phosphodiesterase TDP1
90	c6hxiD	Alignment	not modelled	51.7	20	PDB header: lyase Chain: D: PDB Molecule: succinyl-coa ligase (adp-forming) subunit alpha; PDBTitle: structure of atp citrate lyase from methanotrix soehngenii in complex2 with citrate and coenzyme a
91	d1jpmal	Alignment	not modelled	51.7	14	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
92	c2akjA	Alignment	not modelled	51.5	29	PDB header: oxidoreductase Chain: A: PDB Molecule: ferredoxin--nitrite reductase, chloroplast; PDBTitle: structure of spinach nitrite reductase
93	d1j2ra	Alignment	not modelled	50.9	12	Fold: Isochorismatase-like hydrolases Superfamily: Isochorismatase-like hydrolases Family: Isochorismatase-like hydrolases
94	d1x9ga	Alignment	not modelled	49.8	12	Fold: Isochorismatase-like hydrolases Superfamily: Isochorismatase-like hydrolases Family: Isochorismatase-like hydrolases
95	d2nu7a1	Alignment	not modelled	49.6	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
96	c3kwpA	Alignment	not modelled	49.3	14	PDB header: transferase Chain: A: PDB Molecule: predicted methyltransferase; PDBTitle: crystal structure of putative methyltransferase from lactobacillus2 brevis
97	d2nu7a2	Alignment	not modelled	49.2	24	Fold: Flavodoxin-like Superfamily: Succinyl-CoA synthetase domains Family: Succinyl-CoA synthetase domains
98	d1im5a	Alignment	not modelled	48.6	11	Fold: Isochorismatase-like hydrolases Superfamily: Isochorismatase-like hydrolases Family: Isochorismatase-like hydrolases
99	c1oi7A	Alignment	not modelled	47.8	19	PDB header: synthetase Chain: A: PDB Molecule: succinyl-coa synthetase alpha chain; PDBTitle: the crystal structure of succinyl-coa synthetase alpha2 subunit from thermus thermophilus
100	c2rqmA	Alignment	not modelled	47.3	17	PDB header: chaperone Chain: A: PDB Molecule: mesoderm development candidate 2; PDBTitle: nmr solution structure of mesoderm development (mesd) - open2 conformation
101	c2wtaA	Alignment	not modelled	46.6	14	PDB header: hydrolase Chain: A: PDB Molecule: nicotinamidase; PDBTitle: acinetobacter baumannii nicotinamidase pyrazinamidase
102	c3tb4A	Alignment	not modelled	46.6	14	PDB header: hydrolase Chain: A: PDB Molecule: vibriobactin-specific isochorismatase; PDBTitle: crystal structure of the isc domain of vibb

103	c3m4xA	Alignment	not modelled	45.2	13	PDB header: transferase Chain: A: PDB Molecule: no11/nop2/sun family protein; PDBTitle: structure of a ribosomal methyltransferase
104	c5zn8B	Alignment	not modelled	45.1	21	PDB header: metal binding protein Chain: B: PDB Molecule: isochorismatase; PDBTitle: crystal structure of nicotinamidase pnca from bacillus subtilis
105	c1yd2A	Alignment	not modelled	44.9	27	PDB header: dna binding protein Chain: A: PDB Molecule: uvrbc system protein c; PDBTitle: crystal structure of the giy-yig n-terminal endonuclease domain of2 uvrC from thermotoga maritima: point mutant y19f bound to the3 catalytic divalent cation
106	c2csuB	Alignment	not modelled	44.6	21	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: 457aa long hypothetical protein; PDBTitle: crystal structure of ph0766 from pyrococcus horikoshii ot3
107	d1aoga2	Alignment	not modelled	44.2	17	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
108	d3c7bb2	Alignment	not modelled	44.2	25	Fold: Ferredoxin-like Superfamily: Nitrite/Sulfite reductase N-terminal domain-like Family: DsrA/DsrB N-terminal-domain-like
109	c2hxtA	Alignment	not modelled	43.8	22	PDB header: unknown function Chain: A: PDB Molecule: l-fuconate dehydratase; PDBTitle: crystal structure of l-fuconate dehydratase from xanthomonas2 campestris liganded with mg++ and d-erythronhydroxamate
110	d1q32a1	Alignment	not modelled	41.9	12	Fold: Phospholipase D/nuclease Superfamily: Phospholipase D/nuclease Family: Tyrosyl-DNA phosphodiesterase TDP1
111	c2v4jA	Alignment	not modelled	41.7	22	PDB header: oxidoreductase Chain: A: PDB Molecule: sulfite reductase, dissimilatory-type subunit PDBTitle: the crystal structure of desulfovibrio vulgaris2 dissimilatory sulfite reductase bound to dsrC provides3 novel insights into the mechanism of sulfate respiration
112	d1nu5a1	Alignment	not modelled	40.9	23	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
113	c1nu5A	Alignment	not modelled	40.9	26	PDB header: isomerase Chain: A: PDB Molecule: chloromuconate cycloisomerase; PDBTitle: crystal structure of pseudomonas sp. p51 chloromuconate lactonizing2 enzyme
114	c4zhjA	Alignment	not modelled	40.4	19	PDB header: metal binding protein Chain: A: PDB Molecule: mg-chelatase subunit chlH; PDBTitle: crystal structure of the catalytic subunit of magnesium chelatase
115	c2jlaD	Alignment	not modelled	39.8	43	PDB header: transferase Chain: D: PDB Molecule: 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene PDBTitle: crystal structure of e.coli mend, 2-succinyl-5-enolpyruvyl-2 6-hydroxy-3-cyclohexadiene-1-carboxylate synthase - semet3 protein
116	c1pjtB	Alignment	not modelled	39.7	18	PDB header: transferase/oxidoreductase/lyase Chain: B: PDB Molecule: siroheme synthase; PDBTitle: the structure of the ser128ala point-mutant variant of cysg, the2 multifunctional methyltransferase/dehydrogenase/ferrochelatase for3 siroheme synthesis
117	c1yd6A	Alignment	not modelled	39.7	23	PDB header: dna binding protein Chain: A: PDB Molecule: uvrC; PDBTitle: crystal structure of the giy-yig n-terminal endonuclease2 domain of uvrC from bacillus caldotenax
118	c2zzxD	Alignment	not modelled	39.5	8	PDB header: transport protein Chain: D: PDB Molecule: abc transporter, solute-binding protein; PDBTitle: crystal structure of a periplasmic substrate binding protein in2 complex with lactate
119	c3o93A	Alignment	not modelled	39.0	12	PDB header: hydrolase Chain: A: PDB Molecule: nicotinamidase; PDBTitle: high resolution crystal structures of streptococcus pneumoniae2 nicotinamidase with trapped intermediates provide insights into3 catalytic mechanism and inhibition by aldehydes
120	d1lva2	Alignment	not modelled	38.3	24	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains