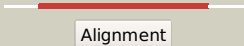

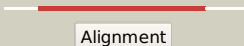

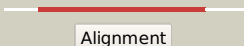







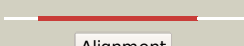









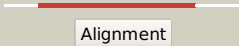

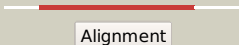

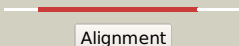



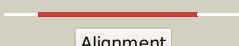

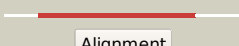

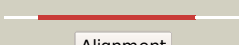





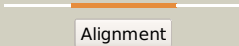
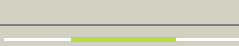
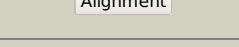
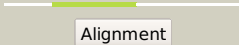

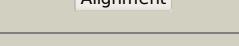
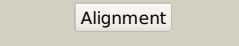


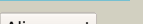


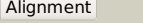
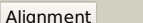
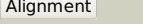
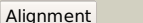
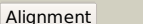
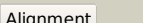
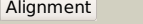
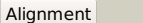
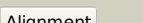
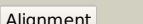
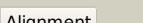
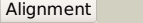
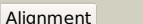





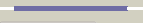


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3146_(nuoB)_3512074_3512628
Date	Thu Aug 8 16:20:33 BST 2019
Unique Job ID	5085c8b094409490

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6humK_	 Alignment		100.0	43	PDB header: proton transport Chain: K; PDB Molecule: nad(p)h-quinone oxidoreductase subunit k; PDBTitle: structure of the photosynthetic complex i from thermosynechococcus2 elongatus
2	c6gcsK_	 Alignment		100.0	51	PDB header: oxidoreductase Chain: K; PDB Molecule: psst subunit (nukm); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
3	c5lc5B_	 Alignment		100.0	53	PDB header: oxidoreductase Chain: B; PDB Molecule: nadh dehydrogenase [ubiquinone] iron-sulfur protein 7, PDBTitle: structure of mammalian respiratory complex i, class2
4	d2fug61	 Alignment		100.0	66	Fold: HydA/Nqo6-like Superfamily: HydA/Nqo6-like Family: NqO6-like
5	c6cfwJ_	 Alignment		100.0	36	PDB header: membrane protein Chain: J; PDB Molecule: probable membrane-bound hydrogenase subunit mbhj; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase
6	c5xf9G_	 Alignment		99.9	26	PDB header: oxidoreductase Chain: G; PDB Molecule: nad-reducing hydrogenase; PDBTitle: crystal structure of nad+-reducing [nife]-hydrogenase in the air-2 oxidized state
7	c5odiE_	 Alignment		99.9	25	PDB header: oxidoreductase Chain: E; PDB Molecule: methyl-viologen reducing hydrogenase, subunit g; PDBTitle: heterodisulfide reductase / [nife]-hydrogenase complex from2 methanothermococcus thermolithotrophicus cocrystallized with com-sh
8	d1frfs_	 Alignment		99.9	22	Fold: HydA/Nqo6-like Superfamily: HydA/Nqo6-like Family: Nickel-iron hydrogenase, small subunit
9	d1e3da_	 Alignment		99.9	19	Fold: HydA/Nqo6-like Superfamily: HydA/Nqo6-like Family: Nickel-iron hydrogenase, small subunit
10	c6ehqT_	 Alignment		99.9	21	PDB header: oxidoreductase Chain: T; PDB Molecule: hydrogenase-2 small chain; PDBTitle: e. coli hydrogenase-2 (as isolated form).
11	d1wuis1	 Alignment		99.9	21	Fold: HydA/Nqo6-like Superfamily: HydA/Nqo6-like Family: Nickel-iron hydrogenase, small subunit

12	c1h2aS_	 Alignment		99.9	21	PDB header: oxidoreductase Chain: S: PDB Molecule: hydrogenase; PDBTitle: single crystals of hydrogenase from desulfovibrio vulgaris
13	c3zfsB_	 Alignment		99.9	22	PDB header: oxidoreductase Chain: B: PDB Molecule: f420-reducing hydrogenase, subunit gamma; PDBTitle: cryo-em structure of the f420-reducing nife-hydrogenase from a2 methanogenic archaeon with bound substrate
14	c3rgwS_	 Alignment		99.9	26	PDB header: oxidoreductase/oxidoreductase Chain: S: PDB Molecule: membrane-bound hydrogenase (nife) small subunit hoX; PDBTitle: crystal structure at 1.5 a resolution of an h2-reduced, o2-tolerant2 hydrogenase from ralstonia eutropha unmasks a novel iron-sulfur3 cluster
15	c3myrE_	 Alignment		99.8	27	PDB header: oxidoreductase Chain: E: PDB Molecule: hydrogenase (nife) small subunit hyda; PDBTitle: crystal structure of [nife] hydrogenase from allochromatium vinosum in2 its ni-a state
16	d1yq9a1	 Alignment		99.8	19	Fold: HydA/Nqo6-like Superfamily: HydA/Nqo6-like Family: Nickel-iron hydrogenase, small subunit
17	d1cc1s_	 Alignment		99.8	21	Fold: HydA/Nqo6-like Superfamily: HydA/Nqo6-like Family: Nickel-iron hydrogenase, small subunit
18	c4gd3T_	 Alignment		99.8	25	PDB header: oxidoreductase/electron transport Chain: T: PDB Molecule: hydrogenase-1 small chain; PDBTitle: structure of e. coli hydrogenase-1 in complex with cytochrome b
19	c2wpaA_	 Alignment		99.8	20	PDB header: oxidoreductase Chain: A: PDB Molecule: periplasmic [nifese] hydrogenase, small subunit; PDBTitle: structure of the oxidised, as-isolated nifese hydrogenase from d.2 vulgaris hildenborough
20	c5aa5D_	 Alignment		99.4	25	PDB header: oxidoreductase Chain: D: PDB Molecule: nife-hydrogenase small subunit, hofk; PDBTitle: actinobacterial-type nife-hydrogenase from ralstonia eutropha h16 at2 2.85 angstrom resolution
21	c2v4jA_	 Alignment	not modelled	83.5	9	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
22	c1zj8B_	 Alignment	not modelled	63.1	19	PDB header: oxidoreductase Chain: B: PDB Molecule: probable ferredoxin-dependent nitrite reductase nira; PDBTitle: structure of mycobacterium tuberculosis nira protein
23	c4jc0B_	 Alignment	not modelled	62.9	12	PDB header: transferase Chain: B: PDB Molecule: ribosomal protein s12 methylthiotransferase rimo; PDBTitle: crystal structure of thermotoga maritima holo rimo in complex with2 pentasulfide, northeast structural genomics consortium target vr77
24	d1sqsa_	 Alignment	not modelled	55.3	14	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Hypothetical protein SP1951
25	c3c7bA_	 Alignment	not modelled	51.2	16	PDB header: oxidoreductase Chain: A: PDB Molecule: sulfite reductase, dissimilatory-type subunit alpha; PDBTitle: structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
26	c5aopA_	 Alignment	not modelled	48.5	19	PDB header: oxidoreductase Chain: A: PDB Molecule: sulfite reductase hemoprotein; PDBTitle: sulfite reductase structure reduced with crii edta, 5-coordinate2 siroheme, siroheme feii, [4fe-4s] +1
27	c3rl4A_	 Alignment	not modelled	44.9	8	PDB header: hydrolase Chain: A: PDB Molecule: metallophosphoesterase mpped2; PDBTitle: rat metallophosphodiesterase mpped2 g252h mutant

28	c1ychD	 Alignment	not modelled	38.3	18	PDB header: oxidoreductase Chain: D: PDB Molecule: nitric oxide reductase; PDBTitle: x-ray crystal structures of moorella thermoacetica fpra. novel diiron2 site structure and mechanistic insights into a scavenging nitric3 oxide reductase
29	c2z1dA	 Alignment	not modelled	36.6	27	PDB header: metal binding protein Chain: A: PDB Molecule: hydrogenase expression/formation protein hypd; PDBTitle: crystal structure of [nife] hydrogenase maturation protein, hypd from2 thermococcus kodakaraensis
30	c2d3yA	 Alignment	not modelled	34.9	19	PDB header: hydrolase Chain: A: PDB Molecule: uracil-dna glycosylase; PDBTitle: crystal structure of uracil-dna glycosylase from thermus thermophilus2 hb8
31	c3fhcB	 Alignment	not modelled	34.7	9	PDB header: transport protein/hydrolase Chain: B: PDB Molecule: atp-dependent rna helicase ddx19b; PDBTitle: crystal structure of human dbp5 in complex with nup214
32	c2d0iC	 Alignment	not modelled	33.8	20	PDB header: oxidoreductase Chain: C: PDB Molecule: dehydrogenase; PDBTitle: crystal structure ph0520 protein from pyrococcus horikoshii ot3
33	c2akjA	 Alignment	not modelled	33.4	24	PDB header: oxidoreductase Chain: A: PDB Molecule: ferredoxin--nitrite reductase, chloroplast; PDBTitle: structure of spinach nitrite reductase
34	c3b0nA	 Alignment	not modelled	32.2	21	PDB header: oxidoreductase Chain: A: PDB Molecule: nitrite reductase; PDBTitle: q448k mutant of assimilatory nitrite reductase (nii3) from tobacc02 leaf
35	d2dlda2	 Alignment	not modelled	28.0	11	Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like Family: Formate/glycerate dehydrogenases, substrate-binding domain
36	c3ca8B	 Alignment	not modelled	27.7	26	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: protein ydcf; PDBTitle: crystal structure of escherichia coli ydcf, an s-adenosyl-l-methionine2 utilizing enzyme
37	d1fmfa	 Alignment	not modelled	24.2	18	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
38	d2dlda1	 Alignment	not modelled	23.1	10	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
39	d1e5da1	 Alignment	not modelled	22.2	18	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
40	c3c7bE	 Alignment	not modelled	22.0	14	PDB header: oxidoreductase Chain: E: PDB Molecule: sulfite reductase, dissimilatory-type subunit beta; PDBTitle: structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
41	c2pi1C	 Alignment	not modelled	21.9	18	PDB header: oxidoreductase Chain: C: PDB Molecule: d-lactate dehydrogenase; PDBTitle: crystal structure of d-lactate dehydrogenase from aquifex2 aeolicus complexed with nad and lactic acid
42	c5mp4C	 Alignment	not modelled	21.2	11	PDB header: oxidoreductase Chain: C: PDB Molecule: protoplast secreted protein 2; PDBTitle: the structure of pst2p from saccharomyces cerevisiae
43	c2v4jE	 Alignment	not modelled	21.2	15	PDB header: oxidoreductase Chain: E: 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
44	c3aerC	 Alignment	not modelled	19.8	16	PDB header: oxidoreductase Chain: C: PDB Molecule: light-independent protochlorophyllide reductase subunit n; PDBTitle: structure of the light-independent protochlorophyllide reductase2 catalyzing a key reduction for greening in the dark
45	c5h92A	 Alignment	not modelled	19.4	19	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
46	c1m46B	 Alignment	not modelled	18.6	33	PDB header: cell cycle protein Chain: B: PDB Molecule: iq4 motif from myo2p, a class v myosin; PDBTitle: crystal structure of mlc1p bound to iq4 of myo2p, a class v2 myosin
47	d1ygya2	 Alignment	not modelled	18.4	18	Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like Family: Formate/glycerate dehydrogenases, substrate-binding domain
48	d1j4aa1	 Alignment	not modelled	18.2	10	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
49	c6h0cA	 Alignment	not modelled	17.8	13	PDB header: oxidoreductase Chain: A: PDB Molecule: putative diflavin flavoprotein a 3; PDBTitle: flv1 flavodiiron core from synechocystis sp. pcc6803
50	c3mgIA	 Alignment	not modelled	17.2	19	PDB header: transport protein Chain: A: PDB Molecule: sulfate permease family protein; PDBTitle: crystal structure of permease family protein from vibrio cholerae
51	c5n6yD	 Alignment	not modelled	17.1	15	PDB header: oxidoreductase Chain: D: PDB Molecule: nitrogenase vanadium-iron protein alpha chain; PDBTitle: azotobacter vinelandii vanadium nitrogenase

52	d1m1la_	Alignment	not modelled	16.8	26	Fold: Suppressor of Fused, N-terminal domain Superfamily: Suppressor of Fused, N-terminal domain Family: Suppressor of Fused, N-terminal domain
53	c3ikbB_	Alignment	not modelled	15.9	19	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized conserved protein; PDBTitle: the structure of a conserved protein from streptococcus2 mutans ua159.
54	c2gn0A_	Alignment	not modelled	15.1	8	PDB header: lyase Chain: A: PDB Molecule: threonine dehydratase catabolic; PDBTitle: crystal structure of dimeric biodegradative threonine deaminase (tdcb)2 from salmonella typhimurium at 1.7 a resolution (triclinic form with3 one complete subunit built in alternate conformation)
55	c4iciA_	Alignment	not modelled	14.6	9	PDB header: flavoprotein Chain: A: PDB Molecule: putative flavoprotein; PDBTitle: crystal structure of a putative flavoprotein (bacegg_01620) from2 bacteroides eggerthii dsm 20697 at 1.40 a resolution
56	c3fn4A_	Alignment	not modelled	14.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: nad-dependent formate dehydrogenase; PDBTitle: apo-form of nad-dependent formate dehydrogenase from bacterium2 moraxella sp.c-1 in closed conformation
57	c2is8A_	Alignment	not modelled	13.7	22	PDB header: structural protein Chain: A: PDB Molecule: molybdopterin biosynthesis enzyme, moab; PDBTitle: crystal structure of the molybdopterin biosynthesis enzyme moab2 (ttha0341) from thermus thermophilus hb8
58	c4ehtA_	Alignment	not modelled	11.9	20	PDB header: electron transport Chain: A: PDB Molecule: activator of 2-hydroxyisocaproyl-coa dehydratase; PDBTitle: activator of the 2-hydroxyisocaproyl-coa dehydratase from clostridium2 difficile with bound adp
59	c2q9uB_	Alignment	not modelled	11.2	10	PDB header: oxidoreductase Chain: B: PDB Molecule: a-type flavoprotein; PDBTitle: crystal structure of the flavodiiron protein from giardia2 intestinalis
60	c3fw2A_	Alignment	not modelled	10.7	3	PDB header: oxidoreductase Chain: A: PDB Molecule: thiol-disulfide oxidoreductase; PDBTitle: c-terminal domain of putative thiol-disulfide oxidoreductase from2 bacteroides thetaiotaomicron.
61	d2fug71	Alignment	not modelled	10.6	57	Fold: N domain of copper amine oxidase-like Superfamily: Frataxin/Nqo15-like Family: Nqo15-like
62	c3k1yE_	Alignment	not modelled	10.2	14	PDB header: oxidoreductase Chain: E: PDB Molecule: oxidoreductase; PDBTitle: x-ray structure of oxidoreductase from corynebacterium diphtheriae.2 orthorombic crystal form, northeast structural genomics consortium3 target cdr100d
63	c3d3kD_	Alignment	not modelled	10.1	12	PDB header: protein binding Chain: D: PDB Molecule: enhancer of mrna-decapping protein 3; PDBTitle: crystal structure of human edc3p
64	c5n6yC_	Alignment	not modelled	10.0	22	PDB header: oxidoreductase Chain: C: PDB Molecule: nitrogenase vanadium-iron protein delta chain; PDBTitle: azotobacter vinelandii vanadium nitrogenase
65	c5cd6C_	Alignment	not modelled	9.9	19	PDB header: unknown function Chain: C: PDB Molecule: tpr-domain containing protein; PDBTitle: crystal structure of a tpr-domain containing protein (bdi_1685) from2 parabacteroides distazonis atcc 8503 at 2.26 a resolution
66	c2d16B_	Alignment	not modelled	9.8	24	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein ph1918; PDBTitle: crystal structure of ph1918 protein from pyrococcus horikoshii ot3
67	d1mx3a2	Alignment	not modelled	9.7	14	Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like Family: Formate/glycerate dehydrogenases, substrate-binding domain
68	d1xm7a_	Alignment	not modelled	9.6	12	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Hypothetical protein aq 1666
69	c4qeZC_	Alignment	not modelled	9.6	14	PDB header: hydrolase Chain: C: PDB Molecule: 5'-methylthioadenosine/s-adenosylhomocysteine nucleosidase; PDBTitle: crystal structure of 5'-methylthioadenosine/s-adenosylhomocysteine2 nucleosidase from bacillus anthracis
70	d1m1na_	Alignment	not modelled	9.6	14	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein
71	d3cxeb1	Alignment	not modelled	9.6	71	Fold: 4-helical cytokines Superfamily: 4-helical cytokines Family: Short-chain cytokines
72	d1ygya1	Alignment	not modelled	9.5	10	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
73	c5ykjA_	Alignment	not modelled	9.2	17	PDB header: transferase Chain: A: PDB Molecule: peroxiredoxin prx1, mitochondrial; PDBTitle: structural basis of the thiol resolving mechanism in yeast2 mitochondrial 1-cys peroxiredoxin via glutathione/thioredoxin systems
74	d1ycga1	Alignment	not modelled	8.8	23	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
75	c4njmA_	Alignment	not modelled	8.7	6	PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase, putative; PDBTitle: crystal structure of phosphoglycerate bound 3-

						phosphoglycerate2 dehydrogenase in entamoeba histolytica
76	d1fyja_	Alignment	not modelled	8.5	71	Fold: S15/NS1 RNA-binding domain Superfamily: S15/NS1 RNA-binding domain Family: a tRNA synthase domain
77	d2naca2	Alignment	not modelled	8.5	16	Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like Family: Formate/glycerate dehydrogenases, substrate-binding domain
78	c4l0mA_	Alignment	not modelled	8.4	14	PDB header: hydrolase Chain: A: PDB Molecule: putative 5'-methylthioadenosine/s-adenosylhomocysteine PDBTitle: crystal structure of a putative 5'-methylthioadenosine/s-2 adenosylhomocysteine nucleosidase from borrelia burgdorferi b31 bound3 to adenine (target nysgrc-029268)
79	c5n6yE_	Alignment	not modelled	8.3	4	PDB header: oxidoreductase Chain: E: PDB Molecule: nitrogenase vanadium-iron protein beta chain; PDBTitle: azotobacter vinelandii vanadium nitrogenase
80	d1sc6a1	Alignment	not modelled	8.3	2	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
81	c3pdiG_	Alignment	not modelled	8.3	21	PDB header: protein binding Chain: G: PDB Molecule: nitrogenase mofe cofactor biosynthesis protein nife; PDBTitle: precursor bound nifen
82	d2cv4a1	Alignment	not modelled	8.2	14	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
83	d1dxya1	Alignment	not modelled	8.1	10	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
84	c1geaA_	Alignment	not modelled	8.1	33	PDB header: neuropeptide Chain: A: PDB Molecule: pituitary adenylate cyclase activating PDBTitle: receptor-bound conformation of pacap21
85	c3edoA_	Alignment	not modelled	8.0	16	PDB header: flavoprotein Chain: A: PDB Molecule: putative trp repressor binding protein; PDBTitle: crystal structure of flavoprotein in complex with fmn (yp_193882.1)2 from lactobacillus acidophilus ncfm at 1.20 a resolution
86	c1e5dA_	Alignment	not modelled	7.8	19	PDB header: oxidoreductase Chain: A: PDB Molecule: rubredoxin\;oxygen oxidoreductase; PDBTitle: rubredoxin oxygen:oxidoreductase (roo) from anaerobe desulfovibrio2 gigas
87	c6feuj_	Alignment	not modelled	7.5	14	PDB header: oxidoreductase Chain: J: PDB Molecule: peroxiredoxin; PDBTitle: prxq2, a 1-cys peroxiredoxin of the thermo-acidophilic archaeon2 sulfobolus islandicus
88	d1qh8a_	Alignment	not modelled	7.5	11	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein
89	c3bsfB_	Alignment	not modelled	7.5	11	PDB header: hydrolase Chain: B: PDB Molecule: at4g34840; PDBTitle: crystal structure of the mta/sah nucleosidase
90	c3lkIB_	Alignment	not modelled	7.4	15	PDB header: transport protein Chain: B: PDB Molecule: antisigma-factor antagonist stas; PDBTitle: crystal structure of the c-terminal domain of anti-sigma factor2 antagonist stas from rhodobacter sphaeroides
91	c1q14A_	Alignment	not modelled	7.4	45	PDB header: hydrolase Chain: A: PDB Molecule: hst2 protein; PDBTitle: structure and autoregulation of the yeast hst2 homolog of sir2
92	c4wj3E_	Alignment	not modelled	7.3	26	PDB header: ligase/rna Chain: E: PDB Molecule: aspartyl/glutamyl-trna(asn/gln) amidotransferase subunit b; PDBTitle: crystal structure of the asparagine transamidosome from pseudomonas2 aeruginosa
93	c4wj3K_	Alignment	not modelled	7.3	26	PDB header: ligase/rna Chain: K: PDB Molecule: aspartyl/glutamyl-trna(asn/gln) amidotransferase subunit b; PDBTitle: crystal structure of the asparagine transamidosome from pseudomonas2 aeruginosa
94	c4wj3H_	Alignment	not modelled	7.3	26	PDB header: ligase/rna Chain: H: PDB Molecule: aspartyl/glutamyl-trna(asn/gln) amidotransferase subunit b; PDBTitle: crystal structure of the asparagine transamidosome from pseudomonas2 aeruginosa
95	d1zj8a3	Alignment	not modelled	7.3	22	Fold: Nitrite and sulphite reductase 4Fe-4S domain-like Superfamily: Nitrite and sulphite reductase 4Fe-4S domain-like Family: Nitrite and sulphite reductase 4Fe-4S domain-like
96	c4wj3B_	Alignment	not modelled	7.3	26	PDB header: ligase/rna Chain: B: PDB Molecule: aspartyl/glutamyl-trna(asn/gln) amidotransferase subunit b; PDBTitle: crystal structure of the asparagine transamidosome from pseudomonas2 aeruginosa
97	c2r47C_	Alignment	not modelled	7.3	19	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: uncharacterized protein mth_862; PDBTitle: crystal structure of mth_862 protein of unknown function from2 methanothermobacter thermautotrophicus
98	d1prxa_	Alignment	not modelled	7.3	14	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
99	c2rmzA_	Alignment	not modelled	7.2	43	PDB header: cell adhesion Chain: A: PDB Molecule: integrin beta-3; PDBTitle: bicelle-embedded integrin beta3 transmembrane segment