

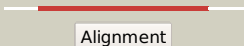

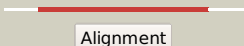







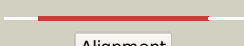




















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0956_(purN)_1067565_1068212
Date	Fri Jul 26 01:50:55 BST 2019
Unique Job ID	85d6c9aa84ea5973

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3dcjA_	 Alignment		100.0	100	PDB header: transferase Chain: A; PDB Molecule: probable 5'-phosphoribosylglycinamide formyltransferase PDBTitle: crystal structure of glycinamide formyltransferase (purn) from2 mycobacterium tuberculosis in complex with 5-methyl-5,6,7,8-3 tetrahydrofolic acid derivative
2	c3aufA_	 Alignment		100.0	42	PDB header: transferase Chain: A; PDB Molecule: glycinamide ribonucleotide transformylase 1; PDBTitle: crystal structure of glycinamide ribonucleotide transformylase 1 from2 symbiobacterium toebii
3	c3tqrA_	 Alignment		100.0	29	PDB header: transferase Chain: A; PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: structure of the phosphoribosylglycinamide formyltransferase (purn) in2 complex with ches from coxiella burnetii
4	c3nrbd_	 Alignment		100.0	28	PDB header: hydrolase Chain: D; PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (puru,2 pp_1943) from pseudomonas putida kt2440 at 2.05 a resolution
5	d1jkxa_	 Alignment		100.0	34	Fold: Formyltransferase Superfamily: Formyltransferase Family: Formyltransferase
6	c3w7bB_	 Alignment		100.0	29	PDB header: hydrolase Chain: B; PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of formyltetrahydrofolate deformylase from thermus2 thermophilus hb8
7	c3n0vD_	 Alignment		100.0	26	PDB header: hydrolase Chain: D; PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (pp_0327)2 from pseudomonas putida kt2440 at 2.25 a resolution
8	c3louB_	 Alignment		100.0	25	PDB header: hydrolase Chain: B; PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of formyltetrahydrofolate deformylase (yp_105254.1)2 from burkholderia mallei atcc 23344 at 1.90 a resolution
9	c3o1lB_	 Alignment		100.0	24	PDB header: hydrolase Chain: B; PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (pspto_4314)2 from pseudomonas syringae pv. tomato str. dc3000 at 2.20 a resolution
10	c3obiC_	 Alignment		100.0	28	PDB header: hydrolase Chain: C; PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (np_949368)2 from rhodopseudomonas palustris cga009 at 1.95 a resolution
11	c2ywrA_	 Alignment		100.0	36	PDB header: transferase Chain: A; PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: crystal structure of gar transformylase from aquifex aeolicus

12	c3p9xB	Alignment		100.0	36	PDB header: transferase Chain: B: PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: crystal structure of phosphoribosylglycinamide formyltransferase from2 bacillus halodurans
13	c3kcgA	Alignment		100.0	33	PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: crystal structure of phosphoribosylglycinamide formyltransferase from2 anaplasma phagocytophilum
14	c3av3A	Alignment		100.0	42	PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: crystal structure of glycine ribonucleotide transformylase 1 from2 geobacillus kaustophilus
15	d1meoa	Alignment		100.0	36	Fold: Formyltransferase Superfamily: Formyltransferase Family: Formyltransferase
16	c4ds3A	Alignment		100.0	43	PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: crystal structure of phosphoribosylglycinamide formyltransferase from2 brucella melitensis
17	c4s1nA	Alignment		100.0	37	PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: the crystal structure of phosphoribosylglycinamide formyltransferase2 from streptococcus pneumoniae tigr4
18	c5cjjA	Alignment		100.0	28	PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: the crystal structure of phosphoribosylglycinamide formyltransferase2 from campylobacter jejuni subsp. jejuni nctc 11168
19	c1z7eC	Alignment		100.0	22	PDB header: hydrolase Chain: C: PDB Molecule: protein arna; PDBTitle: crystal structure of full length arna
20	c1fmtA	Alignment		100.0	25	PDB header: formyltransferase Chain: A: PDB Molecule: methionyl-trna fmet formyltransferase; PDBTitle: methionyl-trnafmet formyltransferase from escherichia coli
21	c3rfoA	Alignment	not modelled	100.0	24	PDB header: transferase Chain: A: PDB Molecule: methionyl-trna formyltransferase; PDBTitle: crystal structure of methionyl-trna formyltransferase from bacillus2 anthracis
22	c3tqqA	Alignment	not modelled	100.0	26	PDB header: transferase Chain: A: PDB Molecule: methionyl-trna formyltransferase; PDBTitle: structure of the methionyl-trna formyltransferase (fmt) from coxiella2 burnetii
23	c3q0iA	Alignment	not modelled	100.0	23	PDB header: transferase Chain: A: PDB Molecule: methionyl-trna formyltransferase; PDBTitle: methionyl-trna formyltransferase from vibrio cholerae
24	c1yrwA	Alignment	not modelled	100.0	22	PDB header: transferase Chain: A: PDB Molecule: protein arna; PDBTitle: crystal structure of e.coli arna transformylase domain
25	d1fmta2	Alignment	not modelled	100.0	25	Fold: Formyltransferase Superfamily: Formyltransferase Family: Formyltransferase
26	c5uaiA	Alignment	not modelled	100.0	29	PDB header: transferase Chain: A: PDB Molecule: methionyl-trna formyltransferase; PDBTitle: crystal structure of methionyl-trna formyltransferase from pseudomonas2 aeruginosa
27	d2blna2	Alignment	not modelled	100.0	22	Fold: Formyltransferase Superfamily: Formyltransferase Family: Formyltransferase
28	c1s3iA	Alignment	not modelled	100.0	23	PDB header: hydrolase, oxidoreductase Chain: A: PDB Molecule: 10-formyltetrahydrofolate dehydrogenase; PDBTitle: crystal structure of the n terminal hydrolase domain of 10-2 formyltetrahydrofolate dehydrogenase
29	d1s3ia2	Alignment	not modelled	100.0	23	Fold: Formyltransferase Superfamily: Formyltransferase Family: Formyltransferase

30	d2bw0a2	Alignment	not modelled	100.0	22	Fold: Formyltransferase Superfamily: Formyltransferase Family: Formyltransferase
31	c5vytD	Alignment	not modelled	100.0	26	PDB header: transferase Chain: D: PDB Molecule: gdp-mannose 4,6-dehydratase / gdp-4-amino-4,6-dideoxy-d- PDBTitle: crystal structure of the wbkc n-formyltransferase (f142a variant) from2 brucella melitensis
32	c5uimB	Alignment	not modelled	100.0	19	PDB header: transferase Chain: B: PDB Molecule: formyltransferase; PDBTitle: x-ray structure of the fdtf n-formyltransferase from salmonella2 enteric o60 in complex with folinic acid and tdp-qui3n
33	c4lxuB	Alignment	not modelled	100.0	17	PDB header: transferase Chain: B: PDB Molecule: wlard, a sugar 3n-formyl transferase; PDBTitle: dtdp-fuc3n and 5-n-formyl-thf
34	c4nv1D	Alignment	not modelled	100.0	15	PDB header: transferase Chain: D: PDB Molecule: formyltransferase; PDBTitle: crystal structure of a 4-n formyltransferase from francisella2 tularensis
35	c6ci2A	Alignment	not modelled	100.0	20	PDB header: transferase Chain: A: PDB Molecule: formyltransferase psej; PDBTitle: crystal structure of the formyltransferase psej from anoxybacillus2 kamchatkensis
36	c4pzuF	Alignment	not modelled	100.0	22	PDB header: transferase Chain: F: PDB Molecule: uncharacterized protein rv3404c/mt3512; PDBTitle: crystal structure of a putative uncharacterize protein rv3404c and2 likely sugar n-formyltransferase from mycobacterium tuberculosis
37	c6nbpA	Alignment	not modelled	100.0	25	PDB header: transferase Chain: A: PDB Molecule: n-formyltransferase; PDBTitle: crystal structure of a sugar n-formyltransferase from the plant2 pathogen pantoea ananatis
38	c4yfvA	Alignment	not modelled	100.0	15	PDB header: transferase Chain: A: PDB Molecule: viof; PDBTitle: x-ray structure of the 4-n-formyltransferase viof from providencia2 alcalifaciens o30
39	d1zgha2	Alignment	not modelled	100.0	15	Fold: Formyltransferase Superfamily: Formyltransferase Family: Formyltransferase
40	c1zghA	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: methionyl-trna formyltransferase; PDBTitle: methionyl-trna formyltransferase from clostridium thermocellum
41	c4xd0A	Alignment	not modelled	99.9	20	PDB header: transferase Chain: A: PDB Molecule: tdp-3-aminoquinovose-n-formyltransferase; PDBTitle: x-ray structure of the n-formyltransferase qdtf from providencia2 alcalifaciens
42	c6culG	Alignment	not modelled	97.9	27	PDB header: transferase Chain: G: PDB Molecule: pyoverdine synthetase f; PDBTitle: pvdf of pyoverdin biosynthesis is a structurally unique n10-2 formyltetrahydrofolate-dependent formyltransferase
43	c5b3uB	Alignment	not modelled	97.0	22	PDB header: transferase Chain: B: PDB Molecule: biliverdin reductase; PDBTitle: crystal structure of biliverdin reductase in complex with nadp+ from2 synechocystis sp. pcc 6803
44	c3db2C	Alignment	not modelled	96.7	19	PDB header: oxidoreductase Chain: C: PDB Molecule: putative nadph-dependent oxidoreductase; PDBTitle: crystal structure of a putative nadph-dependent oxidoreductase2 (dhaf_2064) from desulfitobacterium hafniense dcb-2 at 1.70 a3 resolution
45	c3rbvA	Alignment	not modelled	96.4	20	PDB header: sugar binding protein Chain: A: PDB Molecule: sugar 3-ketoreductase; PDBTitle: crystal structure of kjid10, a 3-ketoreductase from actinomadura2 kijaniata incomplex with nadp
46	c1h6dL	Alignment	not modelled	96.3	21	PDB header: protein translocation Chain: L: PDB Molecule: precursor form of glucose-fructose PDBTitle: oxidized precursor form of glucose-fructose oxidoreductase2 from zymomonas mobilis complexed with glycerol
47	c1ofgF	Alignment	not modelled	96.2	21	PDB header: oxidoreductase Chain: F: PDB Molecule: glucose-fructose oxidoreductase; PDBTitle: glucose-fructose oxidoreductase
48	c6norB	Alignment	not modelled	96.2	20	PDB header: oxidoreductase Chain: B: PDB Molecule: putative nad dependent dehydrogenase; PDBTitle: crystal structure of gend2 from gentamicin a biosynthesis in complex2 with nad
49	c3euwB	Alignment	not modelled	96.2	14	PDB header: oxidoreductase Chain: B: PDB Molecule: myo-inositol dehydrogenase; PDBTitle: crystal structure of a myo-inositol dehydrogenase from corynebacterium2 glutamicum atcc 13032
50	c5uibA	Alignment	not modelled	96.2	20	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase protein; PDBTitle: crystal structure of an oxidoreductase from agrobacterium radiobacter2 in complex with nad+, l-tartaric acid and magnesium
51	c2nvwB	Alignment	not modelled	96.0	11	PDB header: transcription Chain: B: PDB Molecule: galactose/lactose metabolism regulatory protein PDBTitle: crystal sctecture of transcriptional regulator gal80p from2 kluveromyces lactis
52	c4hadD	Alignment	not modelled	95.9	24	PDB header: oxidoreductase Chain: D: PDB Molecule: probable oxidoreductase protein; PDBTitle: crystal structure of probable oxidoreductase protein from rhizobium2 etli cfn 42
53	c3ceaA	Alignment	not modelled	95.9	14	PDB header: oxidoreductase Chain: A: PDB Molecule: myo-inositol 2-dehydrogenase; PDBTitle: crystal structure of myo-inositol 2-dehydrogenase (np_786804.1) from2 lactobacillus plantarum at 2.40 a resolution Fold: NAD(P)-binding Rossmann-fold domains

54	d2nvwa1	Alignment	not modelled	95.7	19	Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
55	c4mkzA	Alignment	not modelled	95.7	18	PDB header: oxidoreductase Chain: A: PDB Molecule: inositol dehydrogenase; PDBTitle: crystal structure of apo scyllo-inositol dehydrogenase from <i>lactobacillus casei</i> at 77k
56	c3ezyB	Alignment	not modelled	95.7	23	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: dehydrogenase; PDBTitle: crystal structure of probable dehydrogenase tm_0414 from <i>thermotoga2 maritima</i>
57	c3e9mC	Alignment	not modelled	95.6	17	PDB header: oxidoreductase Chain: C: PDB Molecule: oxidoreductase, gfo/idh/moca family; PDBTitle: crystal structure of an oxidoreductase from <i>enterococcus2 faecalis</i>
58	c2q4eB	Alignment	not modelled	95.6	19	PDB header: oxidoreductase Chain: B: PDB Molecule: probable oxidoreductase at4g09670; PDBTitle: ensemble refinement of the protein crystal structure of gene product2 from <i>arabidopsis thaliana</i> at4g09670
59	c3nt5B	Alignment	not modelled	95.4	18	PDB header: oxidoreductase Chain: B: PDB Molecule: inositol 2-dehydrogenase/d-chiro-inositol 3-dehydrogenase; PDBTitle: crystal structure of myo-inositol dehydrogenase from <i>bacillus subtilis2</i> with bound cofactor and product inosose
60	c4hktA	Alignment	not modelled	95.3	34	PDB header: oxidoreductase Chain: A: PDB Molecule: inositol 2-dehydrogenase; PDBTitle: crystal structure of a putative myo-inositol dehydrogenase from <i>sinorhizobium meliloti</i> 1021 (target psi-012312)
61	c3e18A	Alignment	not modelled	95.3	22	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of nad-binding protein from <i>listeria innocua</i>
62	c3v5nA	Alignment	not modelled	95.2	19	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase; PDBTitle: the crystal structure of oxidoreductase from <i>sinorhizobium meliloti</i>
63	c3q2kB	Alignment	not modelled	95.1	17	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of the wlbA dehydrogenase from <i>bordetella pertussis2</i> in complex with nadh and udp-glcnaC
64	c2ho3D	Alignment	not modelled	94.9	24	PDB header: oxidoreductase Chain: D: PDB Molecule: oxidoreductase, gfo/idh/moca family; PDBTitle: crystal structure of oxidoreductase, gfo/idh/moca family from <i>streptococcus pneumoniae</i>
65	c3fd8A	Alignment	not modelled	94.9	17	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, gfo/idh/moca family; PDBTitle: crystal structure of an oxidoreductase from <i>enterococcus2 faecalis</i>
66	c3moiA	Alignment	not modelled	94.9	23	PDB header: oxidoreductase Chain: A: PDB Molecule: probable dehydrogenase; PDBTitle: the crystal structure of the putative dehydrogenase from <i>bordetella2 bronchiseptica</i> rb50
67	c3m2tA	Alignment	not modelled	94.8	21	PDB header: oxidoreductase Chain: A: PDB Molecule: probable dehydrogenase; PDBTitle: the crystal structure of dehydrogenase from <i>chromobacterium2 violaceum</i>
68	d1o6ca	Alignment	not modelled	94.7	12	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDP-N-acetylglucosamine 2-epimerase
69	c3ec7C	Alignment	not modelled	94.6	20	PDB header: oxidoreductase Chain: C: PDB Molecule: putative dehydrogenase; PDBTitle: crystal structure of putative dehydrogenase from <i>salmonella2 typhimurium</i> lt2
70	d1f0ka	Alignment	not modelled	94.4	17	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Peptidoglycan biosynthesis glycosyltransferase MurG
71	c3dtyA	Alignment	not modelled	94.2	21	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, gfo/idh/moca family; PDBTitle: crystal structure of an oxidoreductase from <i>pseudomonas2 syringae</i>
72	c1zh8B	Alignment	not modelled	94.2	23	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of oxidoreductase (tm0312) from <i>thermotoga maritima2</i> at 2.50 a resolution
73	c2o48X	Alignment	not modelled	94.1	17	PDB header: oxidoreductase Chain: X: PDB Molecule: dimeric dihydrodiol dehydrogenase; PDBTitle: crystal structure of mammalian dimeric dihydrodiol dehydrogenase
74	c4gqaC	Alignment	not modelled	94.1	21	PDB header: oxidoreductase Chain: C: PDB Molecule: nad binding oxidoreductase; PDBTitle: crystal structure of nad binding oxidoreductase from <i>klebsiella2 pneumoniae</i>
75	c4miyB	Alignment	not modelled	94.1	23	PDB header: oxidoreductase Chain: B: PDB Molecule: inositol 2-dehydrogenase/d-chiro-inositol 3-dehydrogenase; PDBTitle: crystal structure of myo-inositol dehydrogenase from <i>lactobacillus2 casei</i> in complex with nad and myo-inositol
76	d1r0ka2	Alignment	not modelled	94.0	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
77	c3btuD	Alignment	not modelled	93.8	12	PDB header: transcription Chain: D: PDB Molecule: galactose/lactose metabolism regulatory protein PDBTitle: crystal structure of the super-repressor mutant of gal80p2 from <i>saccharomyces cerevisiae</i> ; gal80(s2) [e351k]
78	c2dwcB	Alignment	not modelled	93.8	20	PDB header: transferase Chain: B: PDB Molecule: 433aa long hypothetical phosphoribosylglycinamide formyl PDBTitle: crystal structure of probable phosphoribosylglycinamide formyl2 transferase from <i>pyrococcus horikoshii</i> ot3 complexed with

						adp
79	c5a06E_	Alignment	not modelled	93.7	15	PDB header: oxidoreductase Chain: E: PDB Molecule: aldose-aldose oxidoreductase; PDBTitle: crystal structure of aldose-aldose oxidoreductase from2 caulobacter crescentus complexed with sorbitol
80	c1xeaD_	Alignment	not modelled	93.7	16	PDB header: oxidoreductase Chain: D: PDB Molecule: oxidoreductase, gfo/idh/moca family; PDBTitle: crystal structure of a gfo/idh/moca family oxidoreductase2 from vibrio cholerae
81	c2glxD_	Alignment	not modelled	93.6	19	PDB header: oxidoreductase Chain: D: PDB Molecule: 1,5-anhydro-d-fructose reductase; PDBTitle: crystal structure analysis of bacterial 1,5-af reductase
82	d1h6da1	Alignment	not modelled	93.6	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
83	c3ketA_	Alignment	not modelled	93.2	12	PDB header: transcription/dna Chain: A: PDB Molecule: redox-sensing transcriptional repressor rex; PDBTitle: crystal structure of a rex-family transcriptional regulatory protein2 from streptococcus agalactiae bound to a palindromic operator
84	c3kuxA_	Alignment	not modelled	93.1	17	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: structure of the ypo2259 putative oxidoreductase from yersinia pestis
85	c3beoA_	Alignment	not modelled	92.9	9	PDB header: isomerase Chain: A: PDB Molecule: udp-n-acetylglucosamine 2-epimerase; PDBTitle: a structural basis for the allosteric regulation of non-2 hydrolyzing udp-glcnaC 2-epimerases
86	c1evjC_	Alignment	not modelled	92.9	24	PDB header: oxidoreductase Chain: C: PDB Molecule: glucose-fructose oxidoreductase; PDBTitle: crystal structure of glucose-fructose oxidoreductase (gfor)2 delta1-22 s64d
87	c3wg9D_	Alignment	not modelled	92.9	11	PDB header: transcription Chain: D: PDB Molecule: redox-sensing transcriptional repressor rex; PDBTitle: crystal structure of rsp, a rex-family repressor
88	d1ydwal	Alignment	not modelled	92.9	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
89	c5yabD_	Alignment	not modelled	92.6	25	PDB header: oxidoreductase Chain: D: PDB Molecule: scyllo-inositol dehydrogenase with l-glucose dehydrogenase PDBTitle: crystal structure of scyllo-inositol dehydrogenase with l-glucose2 dehydrogenase activity
90	c4gmfD_	Alignment	not modelled	92.5	18	PDB header: oxidoreductase Chain: D: PDB Molecule: yersiniabactin biosynthetic protein ybtu; PDBTitle: apo structure of a thiazolanyl imine reductase from yersinia2 enterocolitica (irp3)
91	c3uuwB_	Alignment	not modelled	92.5	13	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase with nad(p)-binding rossmann-fold PDBTitle: 1.63 angstrom resolution crystal structure of dehydrogenase (mvim)2 from clostridium difficile.
92	c2axqA_	Alignment	not modelled	92.4	20	PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine dehydrogenase; PDBTitle: apo histidine-tagged saccharopine dehydrogenase (l-glu2 forming) from saccharomyces cerevisiae
93	d1zh8a1	Alignment	not modelled	92.1	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
94	c2ynmD_	Alignment	not modelled	92.0	16	PDB header: oxidoreductase Chain: D: PDB Molecule: light-independent protochlorophyllide reductase subunit b; PDBTitle: structure of the adpxalf3-stabilized transition state of the2 nitrogenase-like dark-operative protochlorophyllide oxidoreductase3 complex from prochlorococcus marinus with its substrate4 protochlorophyllide a
95	c3a14B_	Alignment	not modelled	92.0	24	PDB header: oxidoreductase Chain: B: PDB Molecule: 1-deoxy-d-xylulose 5-phosphate reductoisomerase; PDBTitle: crystal structure of dxr from thermotoga maritima, in complex with2 nadph
96	d2czca2	Alignment	not modelled	91.8	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
97	c3ot5D_	Alignment	not modelled	91.7	16	PDB header: isomerase Chain: D: PDB Molecule: udp-n-acetylglucosamine 2-epimerase; PDBTitle: 2.2 angstrom resolution crystal structure of putative udp-n-2 acetylglucosamine 2-epimerase from listeria monocytogenes
98	c3upyB_	Alignment	not modelled	91.6	17	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of the brucella abortus enzyme catalyzing the first2 committed step of the methylerythritol 4-phosphate pathway.
99	c1r0lD_	Alignment	not modelled	91.5	24	PDB header: oxidoreductase Chain: D: PDB Molecule: 1-deoxy-d-xylulose 5-phosphate reductoisomerase; PDBTitle: 1-deoxy-d-xylulose 5-phosphate reductoisomerase from zymomonas mobilis2 in complex with nadph
100	c1kja_	Alignment	not modelled	91.4	22	PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase 2; PDBTitle: crystal structure of glycnamide ribonucleotide transformylase in2 complex with mg-atp-gamma-s
101	c3evnA_	Alignment	not modelled	90.7	21	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, gfo/idh/moca family; PDBTitle: crystal structure of putative oxidoreductase from

						streptococcus2 agalactiae 2603v/r
102	c1titB_	Alignment	not modelled	90.5	22	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase (virulence factor mvim homolog); PDBTitle: crystal structure of a putative oxidoreductase (virulence factor mvim2 homolog)
103	c4h3vA_	Alignment	not modelled	90.4	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: oxidoreductase domain protein; PDBTitle: crystal structure of oxidoreductase domain protein from kribbella2 flavida
104	c5w8sA_	Alignment	not modelled	90.2	12	PDB header: transferase Chain: A: PDB Molecule: lipid-a-disaccharide synthase; PDBTitle: lipid a disaccharide synthase (lpxb)-7 solubilizing mutations
105	c4zhtB_	Alignment	not modelled	90.1	11	PDB header: isomerase Chain: B: PDB Molecule: bifunctional udp-n-acetylglucosamine 2-epimerase/n- PDBTitle: crystal structure of udp-glcna2-2-epimerase
106	d1b74a1	Alignment	not modelled	89.8	16	Fold: ATC-like Superfamily: Aspartate/glutamate racemase Family: Aspartate/glutamate racemase
107	c3c1aB_	Alignment	not modelled	89.2	19	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase (zp_00056571.1) from2 magnetospirillum magnetotacticum ms-1 at 1.85 a resolution
108	c5zz5D_	Alignment	not modelled	88.9	18	PDB header: gene regulation Chain: D: PDB Molecule: redox-sensing transcriptional repressor rex; PDBTitle: redox-sensing transcriptional repressor rex
109	c3nklA_	Alignment	not modelled	88.7	10	PDB header: oxidoreductase/lyase Chain: A: PDB Molecule: udp-d-quinovosamine 4-dehydrogenase; PDBTitle: crystal structure of udp-d-quinovosamine 4-dehydrogenase from vibrio2 fischeri
110	c2p2sA_	Alignment	not modelled	88.7	16	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of putative oxidoreductase (yp_050235.1) from2 erwinia carotovora atroseptica scri1043 at 1.25 a resolution
111	d1kjq2	Alignment	not modelled	88.5	20	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
112	c3wycB_	Alignment	not modelled	88.3	22	PDB header: oxidoreductase Chain: B: PDB Molecule: meso-diaminopimelate d-dehydrogenase; PDBTitle: structure of a meso-diaminopimelate dehydrogenase in complex with nadp
113	c6g1mA_	Alignment	not modelled	87.7	21	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: amine dehydrogenase from petrotoga mobilis; open and closed form
114	c2ph5A_	Alignment	not modelled	87.4	13	PDB header: transferase Chain: A: PDB Molecule: homospermidine synthase; PDBTitle: crystal structure of the homospermidine synthase hss from legionella2 pneumophila in complex with nad, northeast structural genomics target3 lgr54
115	c1lc3A_	Alignment	not modelled	87.4	18	PDB header: oxidoreductase Chain: A: PDB Molecule: biliverdin reductase a; PDBTitle: crystal structure of a biliverdin reductase enzyme-cofactor2 complex
116	c3uhfB_	Alignment	not modelled	87.2	12	PDB header: isomerase Chain: B: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of glutamate racemase from campylobacter jejuni2 subsp. jejuni
117	d2dt5a2	Alignment	not modelled	87.1	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Transcriptional repressor Rex, C-terminal domain
118	d1ekx2	Alignment	not modelled	87.1	20	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
119	c1b74A_	Alignment	not modelled	86.8	12	PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase; PDBTitle: glutamate racemase from aquifex pyrophilus
120	c2dt5A_	Alignment	not modelled	86.6	13	PDB header: dna binding protein Chain: A: PDB Molecule: at-rich dna-binding protein; PDBTitle: crystal structure of ttha1657 (at-rich dna-binding protein) from2 thermus thermophilus hb8