







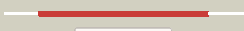














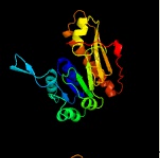
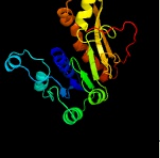

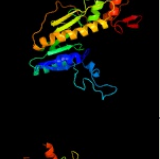
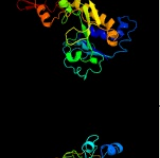
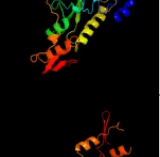
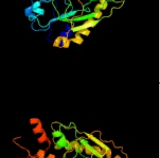
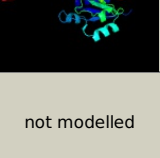


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1406_fmt_1582172_1583110
Date	Wed Jul 31 22:05:51 BST 2019
Unique Job ID	0d9805f18d6d9738

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5uaiA_</a>	 Alignment		100.0	37	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methionyl-trna formyltransferase; <b>PDBTitle:</b> crystal structure of methionyl-trna formyltransferase from pseudomonas2 aeruginosa
2	<a href="#">c3rfoA_</a>	 Alignment		100.0	31	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methionyl-trna formyltransferase; <b>PDBTitle:</b> crystal structure of methionyl-trna formyltransferase from bacillus2 anthracis
3	<a href="#">c1fmtA_</a>	 Alignment		100.0	36	<b>PDB header:</b> formyltransferase <b>Chain:</b> A: <b>PDB Molecule:</b> methionyl-trna fmet formyltransferase; <b>PDBTitle:</b> methionyl-trnafmet formyltransferase from escherichia coli
4	<a href="#">c3q0iA_</a>	 Alignment		100.0	34	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methionyl-trna formyltransferase; <b>PDBTitle:</b> methionyl-trna formyltransferase from vibrio cholerae
5	<a href="#">c3tqqA_</a>	 Alignment		100.0	35	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methionyl-trna formyltransferase; <b>PDBTitle:</b> structure of the methionyl-trna formyltransferase (fmt) from coxiella2 burnetii
6	<a href="#">c1z7eC_</a>	 Alignment		100.0	28	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> protein arna; <b>PDBTitle:</b> crystal structure of full length arna
7	<a href="#">c1yrwA_</a>	 Alignment		100.0	28	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein arna; <b>PDBTitle:</b> crystal structure of e.coli arna transformylase domain
8	<a href="#">c1s3iA_</a>	 Alignment		100.0	25	<b>PDB header:</b> hydrolase, oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 10-formyltetrahydrofolate dehydrogenase; <b>PDBTitle:</b> crystal structure of the n terminal hydrolase domain of 10-2 formyltetrahydrofolate dehydrogenase
9	<a href="#">c4lxuB_</a>	 Alignment		100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> wlward, a sugar 3n-formyl transferase; <b>PDBTitle:</b> dtdp-fuc3n and 5-n-formyl-thf
10	<a href="#">c5vytD_</a>	 Alignment		100.0	24	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> gdp-mannose 4,6-dehydratase / gdp-4-amino-4,6-dideoxy-d- <b>PDBTitle:</b> crystal structure of the wbkc n-formyltransferase (f142a variant) from2 brucella melitensis
11	<a href="#">c5uimB_</a>	 Alignment		100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> formyltransferase; <b>PDBTitle:</b> x-ray structure of the fdtf n-formyltransferase from salmonella2 enteric o60 in complex with folinic acid and tdp-qui3n

12	<a href="#">d2blna2</a>	Alignment		100.0	30	<b>Fold:</b> Formyltransferase <b>Superfamily:</b> Formyltransferase <b>Family:</b> Formyltransferase
13	<a href="#">d1fmta2</a>	Alignment		100.0	40	<b>Fold:</b> Formyltransferase <b>Superfamily:</b> Formyltransferase <b>Family:</b> Formyltransferase
14	<a href="#">d1s3ia2</a>	Alignment		100.0	26	<b>Fold:</b> Formyltransferase <b>Superfamily:</b> Formyltransferase <b>Family:</b> Formyltransferase
15	<a href="#">d2bw0a2</a>	Alignment		100.0	26	<b>Fold:</b> Formyltransferase <b>Superfamily:</b> Formyltransferase <b>Family:</b> Formyltransferase
16	<a href="#">c4nv1D</a>	Alignment		100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> formyltransferase; <b>PDBTitle:</b> crystal structure of a 4-n formyltransferase from francisella2 tularensis
17	<a href="#">c4yfvA</a>	Alignment		100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> viof; <b>PDBTitle:</b> x-ray structure of the 4-n-formyltransferase viof from providencia2 alcalifaciens o30
18	<a href="#">c1zghA</a>	Alignment		100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methionyl-trna formyltransferase; <b>PDBTitle:</b> methionyl-trna formyltransferase from clostridium thermocellum
19	<a href="#">c4pzuF</a>	Alignment		100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> uncharacterized protein rv3404c/mt3512; <b>PDBTitle:</b> crystal structure of a putative uncharacterize protein rv3404c and2 likely sugar n-formyltransferase from mycobacterium tuberculosis
20	<a href="#">c6nbpA</a>	Alignment		100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> n-formyltransferase; <b>PDBTitle:</b> crystal structure of a sugar n-formyltransferase from the plant2 pathogen pantoea ananatis
21	<a href="#">c3kcaA</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylglycinamide formyltransferase; <b>PDBTitle:</b> crystal structure of phosphoribosylglycinamide formyltransferase from2 anaplasma phagocytophilum
22	<a href="#">d1jkaA</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> Formyltransferase <b>Superfamily:</b> Formyltransferase <b>Family:</b> Formyltransferase
23	<a href="#">c2ywrA</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylglycinamide formyltransferase; <b>PDBTitle:</b> crystal structure of gar transformylase from aquifex aeolicus
24	<a href="#">c3dcjA</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable 5'-phosphoribosylglycinamide formyltransferase <b>PDBTitle:</b> crystal structure of glycinamide formyltransferase (purn) from2 mycobacterium tuberculosis in complex with 5-methyl-5,6,7,8-3 tetrahydrofolic acid derivative
25	<a href="#">c3aufA</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glycinamide ribonucleotide transformylase 1; <b>PDBTitle:</b> crystal structure of glycinamide ribonucleotide transformylase 1 from2 symbiobacterium toebii
26	<a href="#">c3tqrA</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylglycinamide formyltransferase; <b>PDBTitle:</b> structure of the phosphoribosylglycinamide formyltransferase (purn) in2 complex with ches from coxiella burnetii
						<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoribosylglycinamide

27	<a href="#">c3p9xB_</a>	Alignment	not modelled	100.0	25	formyltransferase; <b>PDBTitle:</b> crystal structure of phosphoribosylglycinamide formyltransferase from2 bacillus halodurans <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylglycinamide formyltransferase; <b>PDBTitle:</b> crystal structure of glycinamide ribonucleotide transformylase 1 from2 geobacillus kaustophilus <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylglycinamide formyltransferase; <b>PDBTitle:</b> the crystal structure of phosphoribosylglycinamide formyltransferase2 from streptococcus pneumoniae tigr4
28	<a href="#">c3av3A_</a>	Alignment	not modelled	100.0	25	<b>Fold:</b> Formyltransferase <b>Superfamily:</b> Formyltransferase <b>Family:</b> Formyltransferase
29	<a href="#">c4s1nA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylglycinamide formyltransferase; <b>PDBTitle:</b> crystal structure of phosphoribosylglycinamide formyltransferase from2 brucella melitensis
30	<a href="#">d1meoa_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylglycinamide formyltransferase; <b>PDBTitle:</b> crystal structure of phosphoribosylglycinamide formyltransferase from2 brucella melitensis
31	<a href="#">c4ds3A_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylglycinamide formyltransferase; <b>PDBTitle:</b> crystal structure of phosphoribosylglycinamide formyltransferase from2 brucella melitensis
32	<a href="#">c6ci2A_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> formyltransferase psej; <b>PDBTitle:</b> crystal structure of the formyltransferase psej from anoxybacillus2 kamchatkensis
33	<a href="#">c5cjjA_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylglycinamide formyltransferase; <b>PDBTitle:</b> the crystal structure of phosphoribosylglycinamide formyltransferase2 from campylobacter jejuni subsp. jejuni nctc 11168
34	<a href="#">c3n0vD_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> formyltetrahydrofolate deformylase; <b>PDBTitle:</b> crystal structure of a formyltetrahydrofolate deformylase (pp_0327)2 from pseudomonas putida kt2440 at 2.25 a resolution
35	<a href="#">c3w7bB_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> formyltetrahydrofolate deformylase; <b>PDBTitle:</b> crystal structure of formyltetrahydrofolate deformylase from thermus2 thermophilus hb8
36	<a href="#">c3o1lB_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> formyltetrahydrofolate deformylase; <b>PDBTitle:</b> crystal structure of a formyltetrahydrofolate deformylase (pspto_4314)2 from pseudomonas syringae pv. tomato str. dc3000 at 2.20 a resolution
37	<a href="#">c3louB_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> formyltetrahydrofolate deformylase; <b>PDBTitle:</b> crystal structure of formyltetrahydrofolate deformylase (yp_105254.1)2 from burkholderia mallei atcc 23344 at 1.90 a resolution
38	<a href="#">c3obiC_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> formyltetrahydrofolate deformylase; <b>PDBTitle:</b> crystal structure of a formyltetrahydrofolate deformylase (np_949368)2 from rhodopseudomonas palustris cga009 at 1.95 a resolution
39	<a href="#">c3nrbD_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> formyltetrahydrofolate deformylase; <b>PDBTitle:</b> crystal structure of a formyltetrahydrofolate deformylase (puru_2 pp_1943) from pseudomonas putida kt2440 at 2.05 a resolution
40	<a href="#">c4xd0A_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> tdp-3-aminoquinovose-n-formyltransferase; <b>PDBTitle:</b> x-ray structure of the n-formyltransferase qdtf from providencia2 alcalifaciens
41	<a href="#">d1zgaha2</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> Formyltransferase <b>Superfamily:</b> Formyltransferase <b>Family:</b> Formyltransferase
42	<a href="#">d1fmta1</a>	Alignment	not modelled	99.9	30	<b>Fold:</b> FMT C-terminal domain-like <b>Superfamily:</b> FMT C-terminal domain-like <b>Family:</b> Post formyltransferase domain
43	<a href="#">d2blna1</a>	Alignment	not modelled	99.9	22	<b>Fold:</b> FMT C-terminal domain-like <b>Superfamily:</b> FMT C-terminal domain-like <b>Family:</b> Post formyltransferase domain
44	<a href="#">d2bw0a1</a>	Alignment	not modelled	99.9	20	<b>Fold:</b> FMT C-terminal domain-like <b>Superfamily:</b> FMT C-terminal domain-like <b>Family:</b> Post formyltransferase domain
45	<a href="#">d1s3ia1</a>	Alignment	not modelled	99.9	22	<b>Fold:</b> FMT C-terminal domain-like <b>Superfamily:</b> FMT C-terminal domain-like <b>Family:</b> Post formyltransferase domain
46	<a href="#">c6culG_</a>	Alignment	not modelled	96.5	27	<b>PDB header:</b> transferase <b>Chain:</b> G: <b>PDB Molecule:</b> pyoverdine synthetase f; <b>PDBTitle:</b> pvdf of pyoverdin biosynthesis is a structurally unique n10-2 formyltetrahydrofolate-dependent formyltransferase
47	<a href="#">c5b3uB_</a>	Alignment	not modelled	96.5	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> biliverdin reductase; <b>PDBTitle:</b> crystal structure of biliverdin reductase in complex with nadp+ from2 synechocystis sp. pcc 6803
48	<a href="#">c3ezyB_</a>	Alignment	not modelled	96.4	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> dehydrogenase; <b>PDBTitle:</b> crystal structure of probable dehydrogenase tm_0414 from thermotoga2 maritima
49	<a href="#">c3euwB_</a>	Alignment	not modelled	96.3	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> myo-inositol dehydrogenase; <b>PDBTitle:</b> crystal structure of a myo-inositol dehydrogenase from corynebacterium2 glutamicum atcc 13032
50	<a href="#">c3db2C_</a>	Alignment	not modelled	96.3	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> putative nadph-dependent oxidoreductase; <b>PDBTitle:</b> crystal structure of a putative nadph-dependent

						oxidoreductase2 (dhaf_2064) from desulfitobacterium hafniense dcb-2 at 1.70 a3 resolution
51	<a href="#">c6norB_</a>	Alignment	not modelled	96.1	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative nad dependent dehydrogenase; <b>PDBTitle:</b> crystal structure of gend2 from gentamicin a biosynthesis in complex2 with nad
52	<a href="#">c3rbvA_</a>	Alignment	not modelled	96.0	20	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> sugar 3-ketoreductase; <b>PDBTitle:</b> crystal structure of kjid10, a 3-ketoreductase from actinomadura2 kijaniata incomplex with nadp
53	<a href="#">c5uibA_</a>	Alignment	not modelled	95.8	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase protein; <b>PDBTitle:</b> crystal structure of an oxidoreductase from agrobacterium radiobacter2 in complex with nad+, l-tartaric acid and magnesium
54	<a href="#">c4hktA_</a>	Alignment	not modelled	95.8	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> inositol 2-dehydrogenase; <b>PDBTitle:</b> crystal structure of a putative myo-inositol dehydrogenase from2 sinorhizobium meliloti 1021 (target psi-012312)
55	<a href="#">c4mkzA_</a>	Alignment	not modelled	95.7	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> inositol dehydrogenase; <b>PDBTitle:</b> crystal structure of apo scyllo-inositol dehydrogenase from2 lactobacillus casei at 77k
56	<a href="#">c2ho3D_</a>	Alignment	not modelled	95.6	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> oxidoreductase, gfo/idh/moca family; <b>PDBTitle:</b> crystal structure of oxidoreductase, gfo/idh/moca family from2 streptococcus pneumoniae
57	<a href="#">c3ec7C_</a>	Alignment	not modelled	95.6	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> putative dehydrogenase; <b>PDBTitle:</b> crystal structure of putative dehydrogenase from salmonella2 typhimurium lt2
58	<a href="#">c4hadD_</a>	Alignment	not modelled	95.5	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> probable oxidoreductase protein; <b>PDBTitle:</b> crystal structure of probable oxidoreductase protein from rhizobium2 etli cfn 42
59	<a href="#">d1zgah1</a>	Alignment	not modelled	95.5	15	<b>Fold:</b> FMT C-terminal domain-like <b>Superfamily:</b> FMT C-terminal domain-like <b>Family:</b> Post formyltransferase domain
60	<a href="#">c3e9mC_</a>	Alignment	not modelled	95.4	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> oxidoreductase, gfo/idh/moca family; <b>PDBTitle:</b> crystal structure of an oxidoreductase from enterococcus2 faecalis
61	<a href="#">c2ynmD_</a>	Alignment	not modelled	95.3	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> light-independent protochlorophyllide reductase subunit b; <b>PDBTitle:</b> structure of the adpxalf3-stabilized transition state of the2 nitrogenase-like dark-operative protochlorophyllide oxidoreductase3 complex from prochlorococcus marinus with its substrate4 protochlorophyllide a
62	<a href="#">c2glxD_</a>	Alignment	not modelled	95.2	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> 1,5-anhydro-d-fructose reductase; <b>PDBTitle:</b> crystal structure analysis of bacterial 1,5-af reductase
63	<a href="#">c3e18A_</a>	Alignment	not modelled	95.2	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase; <b>PDBTitle:</b> crystal structure of nad-binding protein from listeria innocua
64	<a href="#">c3nt5B_</a>	Alignment	not modelled	95.1	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> inositol 2-dehydrogenase/d-chiro-inositol 3-dehydrogenase; <b>PDBTitle:</b> crystal structure of myo-inositol dehydrogenase from bacillus subtilis2 with bound cofactor and product inosose
65	<a href="#">c4miyB_</a>	Alignment	not modelled	95.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> inositol 2-dehydrogenase/d-chiro-inositol 3-dehydrogenase; <b>PDBTitle:</b> crystal structure of myo-inositol dehydrogenase from lactobacillus2 casei in complex with nad and myo-inositol
66	<a href="#">c3eywA_</a>	Alignment	not modelled	94.9	17	<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
67	<a href="#">d1lssa_</a>	Alignment	not modelled	94.9	12	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Potassium channel NAD-binding domain
68	<a href="#">c3mojA_</a>	Alignment	not modelled	94.8	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> probable dehydrogenase; <b>PDBTitle:</b> the crystal structure of the putative dehydrogenase from bordetella2 bronchiseptica rb50
69	<a href="#">c3wqzB_</a>	Alignment	not modelled	94.6	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> meso-diaminopimelate dehydrogenase; <b>PDBTitle:</b> crystal structure of meso-dapdh q154/t173i/r199m/p248s/h249n/n276s2 mutant with d-leucine of from clostridium tetani e88
70	<a href="#">c3ceaA_</a>	Alignment	not modelled	94.6	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> myo-inositol 2-dehydrogenase; <b>PDBTitle:</b> crystal structure of myo-inositol 2-dehydrogenase (np_786804.1) from2 lactobacillus plantarum at 2.40 a resolution
71	<a href="#">c2ynmC_</a>	Alignment	not modelled	94.6	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> light-independent protochlorophyllide reductase subunit n; <b>PDBTitle:</b> structure of the adpxalf3-stabilized transition state of the2 nitrogenase-like dark-operative protochlorophyllide oxidoreductase3 complex from prochlorococcus marinus with its substrate4 protochlorophyllide a
72	<a href="#">c3q2kB_</a>	Alignment	not modelled	94.5	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> oxidoreductase; <b>PDBTitle:</b> crystal structure of the wlbA dehydrogenase from bordetella pertussis2 in complex with nadh and udp-glcna
73	<a href="#">c3q4kB_</a>	Alignment	not modelled	94.4	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> probable oxidoreductase at4g09670;

73	<a href="#">c2q4eB</a>	Alignment	not modelled	94.4	19	<b>PDBTitle:</b> ensemble refinement of the protein crystal structure of gene product2 from arabidopsis thaliana at4g09670 <b>PDB header:</b> oxidoreductase
74	<a href="#">c2o48X</a>	Alignment	not modelled	94.4	23	<b>Chain:</b> X: <b>PDB Molecule:</b> dimeric dihydrodiol dehydrogenase; <b>PDBTitle:</b> crystal structure of mammalian dimeric dihydrodiol dehydrogenase
75	<a href="#">c3v5nA</a>	Alignment	not modelled	94.3	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase; <b>PDBTitle:</b> the crystal structure of oxidoreductase from sinorhizobium meliloti
76	<a href="#">d1qh8b</a>	Alignment	not modelled	94.3	16	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> "Helical backbone" metal receptor <b>Family:</b> Nitrogenase iron-molybdenum protein
77	<a href="#">c3nk1A</a>	Alignment	not modelled	94.2	14	<b>PDB header:</b> oxidoreductase/lyase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-d-quinovosamine 4-dehydrogenase; <b>PDBTitle:</b> crystal structure of udp-d-quinovosamine 4-dehydrogenase from vibrio2 fischeri
78	<a href="#">c4amuB</a>	Alignment	not modelled	94.1	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> ornithine carbamoyltransferase, catabolic; <b>PDBTitle:</b> structure of ornithine carbamoyltransferase from mycoplasma2 penetrans with a p321 space group
79	<a href="#">d1pvva2</a>	Alignment	not modelled	94.0	22	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
80	<a href="#">c1zh8B</a>	Alignment	not modelled	93.9	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> oxidoreductase; <b>PDBTitle:</b> crystal structure of oxidoreductase (tm0312) from thermotoga maritima2 at 2.50 a resolution
81	<a href="#">d1a9xa4</a>	Alignment	not modelled	93.8	13	<b>Fold:</b> PreATP-grasp domain <b>Superfamily:</b> PreATP-grasp domain <b>Family:</b> BC N-terminal domain-like
82	<a href="#">d1kewa</a>	Alignment	not modelled	93.8	14	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
83	<a href="#">c3m2tA</a>	Alignment	not modelled	93.8	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> probable dehydrogenase; <b>PDBTitle:</b> the crystal structure of dehydrogenase from chromobacterium2 violaceum
84	<a href="#">d1m1nb</a>	Alignment	not modelled	93.7	18	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> "Helical backbone" metal receptor <b>Family:</b> Nitrogenase iron-molybdenum protein
85	<a href="#">d1miob</a>	Alignment	not modelled	93.7	15	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> "Helical backbone" metal receptor <b>Family:</b> Nitrogenase iron-molybdenum protein
86	<a href="#">c3uuwB</a>	Alignment	not modelled	93.7	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative oxidoreductase with nad(p)-binding rossmann-fold <b>PDBTitle:</b> 1.63 angstrom resolution crystal structure of dehydrogenase (mvim)2 from clostridium difficile.
87	<a href="#">c3wb9A</a>	Alignment	not modelled	93.6	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> diaminopimelate dehydrogenase; <b>PDBTitle:</b> crystal structures of meso-diaminopimelate dehydrogenase from2 symbiobacterium thermophilum
88	<a href="#">c3ic5A</a>	Alignment	not modelled	93.6	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative saccharopine dehydrogenase; <b>PDBTitle:</b> n-terminal domain of putative saccharopine dehydrogenase from ruegeria2 pomeroyi.
89	<a href="#">c4g65A</a>	Alignment	not modelled	93.6	10	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> trk system potassium uptake protein trka; <b>PDBTitle:</b> potassium transporter peripheral membrane component (trka) from vibrio2 vulnificus
90	<a href="#">c5z2fA</a>	Alignment	not modelled	93.4	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate reductase; <b>PDBTitle:</b> nadph/pda bound dihydrodipicolinate reductase from paenisporosarcina2 sp. tg-14
91	<a href="#">d1ydw1</a>	Alignment	not modelled	93.3	18	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
92	<a href="#">d1vlva2</a>	Alignment	not modelled	93.2	20	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
93	<a href="#">c5kojD</a>	Alignment	not modelled	93.2	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> nitrogenase femo beta subunit protein nifk; <b>PDBTitle:</b> nitrogenase mofep protein in the ids oxidized state
94	<a href="#">c3i4bG</a>	Alignment	not modelled	93.2	12	<b>PDB header:</b> transport protein <b>Chain:</b> G: <b>PDB Molecule:</b> trka k+ channel protien tm1088b; <b>PDBTitle:</b> crystal structure of an octomeric two-subunit trka k+ channel ring2 gating assembly, tm1088a:tm1088b, from thermotoga maritima
95	<a href="#">c4gmfD</a>	Alignment	not modelled	93.2	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> yersiniabactin biosynthetic protein ybtu; <b>PDBTitle:</b> apo structure of a thiazolanyl imine reductase from yersinia2 enterocolitica (irp3)
96	<a href="#">c2axqA</a>	Alignment	not modelled	93.1	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> saccharopine dehydrogenase; <b>PDBTitle:</b> apo histidine-tagged saccharopine dehydrogenase (l-glu2 forming) from saccharomyces cerevisiae
97	<a href="#">c1ofgF</a>	Alignment	not modelled	93.1	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> glucose-fructose oxidoreductase; <b>PDBTitle:</b> glucose-fructose oxidoreductase
98	<a href="#">c3fd8A</a>	Alignment	not modelled	93.1	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase, gfo/idh/moca family; <b>PDBTitle:</b> crystal structure of an oxidoreductase from enterococcus2 faecalis
						<b>PDB header:</b> protein translocation

99	<a href="#">c1h6dL_</a>	Alignment	not modelled	93.0	15	<b>Chain:</b> L: <b>PDB Molecule:</b> precursor form of glucose-fructose <b>PDBTitle:</b> oxidized precursor form of glucose-fructose oxidoreductase2 from zymomonas mobilis complexed with glycerol
100	<a href="#">c1drwA_</a>	Alignment	not modelled	93.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate reductase; <b>PDBTitle:</b> escherichia coli dhpr/nhdh complex
101	<a href="#">c4gqaC_</a>	Alignment	not modelled	92.9	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> nad binding oxidoreductase; <b>PDBTitle:</b> crystal structure of nad binding oxidoreductase from klebsiella2 pneumoniae
102	<a href="#">c5yabD_</a>	Alignment	not modelled	92.9	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> scyllo-inositol dehydrogenase with l-glucose dehydrogenase <b>PDBTitle:</b> crystal structure of scyllo-inositol dehydrogenase with l-glucose2 dehydrogenase activity
103	<a href="#">c3ijpA_</a>	Alignment	not modelled	92.8	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate reductase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate reductase from bartonella2 henselae at 2.0a resolution
104	<a href="#">d1ml4a2</a>	Alignment	not modelled	92.8	13	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
105	<a href="#">c5n6yD_</a>	Alignment	not modelled	92.7	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> nitrogenase vanadium-iron protein alpha chain; <b>PDBTitle:</b> azotobacter vinelandii vanadium nitrogenase
106	<a href="#">c6g1mA_</a>	Alignment	not modelled	92.7	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate reductase; <b>PDBTitle:</b> amine dehydrogenase from petrotoga mobilis; open and closed form
107	<a href="#">c2p5uC_</a>	Alignment	not modelled	92.7	15	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> udp-glucose 4-epimerase; <b>PDBTitle:</b> crystal structure of thermus thermophilus hb8 udp-glucose 4-epimerase2 complex with nad
108	<a href="#">d1qh8a_</a>	Alignment	not modelled	92.6	12	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> "Helical backbone" metal receptor <b>Family:</b> Nitrogenase iron-molybdenum protein
109	<a href="#">d1m1na_</a>	Alignment	not modelled	92.4	12	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> "Helical backbone" metal receptor <b>Family:</b> Nitrogenase iron-molybdenum protein
110	<a href="#">c2p2sA_</a>	Alignment	not modelled	92.4	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> crystal structure of putative oxidoreductase (yp_050235.1) from2 erwinia carotovora atroseptica scri1043 at 1.25 a resolution
111	<a href="#">c3evnA_</a>	Alignment	not modelled	92.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase, gfo/idh/moca family; <b>PDBTitle:</b> crystal structure of putative oxidoreductase from streptococcus2 agalactiae 2603v/r
112	<a href="#">c5wolA_</a>	Alignment	not modelled	91.9	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-hydroxy-tetrahydrodipicolinate reductase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate reductase dapb from coxiella2 burnetii
113	<a href="#">c2pk3B_</a>	Alignment	not modelled	91.9	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> gdp-6-deoxy-d-lyxo-4-hexulose reductase; <b>PDBTitle:</b> crystal structure of a gdp-4-keto-6-deoxy-d-mannose reductase
114	<a href="#">c3pdiG_</a>	Alignment	not modelled	91.8	12	<b>PDB header:</b> protein binding <b>Chain:</b> G: <b>PDB Molecule:</b> nitrogenase mofe cofactor biosynthesis protein nife; <b>PDBTitle:</b> precursor bound nifen
115	<a href="#">c5ugjC_</a>	Alignment	not modelled	91.8	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> 4-hydroxy-tetrahydrodipicolinate reductase; <b>PDBTitle:</b> crystal structure of htpa reductase from neisseria meningitidis
116	<a href="#">c5kt0A_</a>	Alignment	not modelled	91.7	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-hydroxy-tetrahydrodipicolinate reductase; <b>PDBTitle:</b> dihydrodipicolinate reductase from the industrial and evolutionarily2 important cyanobacteria anabaena variabilis.
117	<a href="#">c2ph5A_</a>	Alignment	not modelled	91.5	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> homospermidine synthase; <b>PDBTitle:</b> crystal structure of the homospermidine synthase hss from legionella2 pneumophila in complex with nad, northeast structural genomics target3 lgr54
118	<a href="#">c3aerC_</a>	Alignment	not modelled	91.4	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> light-independent protochlorophyllide reductase subunit n; <b>PDBTitle:</b> structure of the light-independent protochlorophyllide reductase2 catalyzing a key reduction for greening in the dark
119	<a href="#">c3kuxA_</a>	Alignment	not modelled	91.4	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> structure of the ypo2259 putative oxidoreductase from yersinia pestis
120	<a href="#">c5a06E_</a>	Alignment	not modelled	91.1	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> aldose-aldose oxidoreductase; <b>PDBTitle:</b> crystal structure of aldose-aldose oxidoreductase from2 caulobacter crescentus complexed with sorbitol