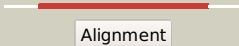



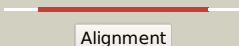

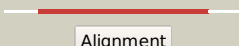

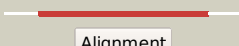

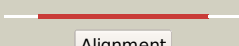

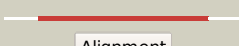











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2692_(ceoC)_3010034_3010696
Date	Wed Aug 7 12:50:34 BST 2019
Unique Job ID	5119bd5e7d77285c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4g65A_			100.0	25	PDB header: transport protein Chain: A: PDB Molecule: trk system potassium uptake protein trka; PDBTitle: potassium transporter peripheral membrane component (trka) from vibrio2 vulnificus
2	c3l4bG_			100.0	27	PDB header: transport protein Chain: G: PDB Molecule: trka k+ channel protien tm1088b; PDBTitle: crystal structure of an octomeric two-subunit trka k+ channel ring2 gating assembly, tm1088a:tm1088b, from thermotoga maritima
3	c4gvlB_			100.0	17	PDB header: transport protein Chain: B: PDB Molecule: trka domain protein; PDBTitle: crystal structure of the gsuk rck domain
4	c4j7cA_			100.0	17	PDB header: transport protein Chain: A: PDB Molecule: ktr system potassium uptake protein a; PDBTitle: ktrab potassium transporter from bacillus subtilis
5	c4gx2B_			100.0	22	PDB header: transport protein Chain: B: PDB Molecule: trka domain protein; PDBTitle: gsuk channel bound to nad
6	c2fy8A_			100.0	19	PDB header: transport protein Chain: A: PDB Molecule: calcium-gated potassium channel mthk; PDBTitle: crystal structure of mthk rck domain in its ligand-free gating-ring2 form
7	c1lnqC_			100.0	19	PDB header: metal transport Chain: C: PDB Molecule: potassium channel related protein; PDBTitle: crystal structure of mthk at 3.3 a
8	c3eywA_			99.9	25	PDB header: transport protein Chain: A: PDB Molecule: c-terminal domain of glutathione-regulated potassium-efflux PDBTitle: crystal structure of the c-terminal domain of e. coli kefc in complex2 with keff
9	c3fwzA_			99.9	17	PDB header: membrane protein Chain: A: PDB Molecule: inner membrane protein ybal; PDBTitle: crystal structure of trka-n domain of inner membrane protein ybal from2 escherichia coli
10	c4hpfB_			99.9	15	PDB header: membrane protein, transport protein Chain: B: PDB Molecule: potassium channel subfamily u member 1; PDBTitle: structure of the human slo3 gating ring
11	d1lssa_			99.9	34	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Potassium channel NAD-binding domain

12	c3u6nC_	Alignment		99.9	16	PDB header: transport protein Chain: C: PDB Molecule: high-conductance ca2+-activated k+ channel protein; PDBTitle: open structure of the bk channel gating ring
13	c4gx5D_	Alignment		99.9	22	PDB header: transport protein Chain: D: PDB Molecule: trka domain protein; PDBTitle: gsuk channel
14	d2hmv1_	Alignment		99.9	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Potassium channel NAD-binding domain
15	d1ld1a_	Alignment		99.9	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Potassium channel NAD-binding domain
16	c5nc8B_	Alignment		99.9	23	PDB header: transport protein Chain: B: PDB Molecule: potassium efflux system protein; PDBTitle: shewanella denitrificans kef ctd in amp bound form
17	c3llvA_	Alignment		99.9	18	PDB header: nad(p) binding protein Chain: A: PDB Molecule: exopolyphosphatase-related protein; PDBTitle: the crystal structure of the nad(p)-binding domain of an2 exopolyphosphatase-related protein from archaeoglobus fulgidus to3 1.7a
18	c3mt5A_	Alignment		99.8	15	PDB header: membrane protein, transport protein Chain: A: PDB Molecule: potassium large conductance calcium-activated channel, PDBTitle: crystal structure of the human bk gating apparatus
19	c2g1uA_	Alignment		99.8	24	PDB header: transport protein Chain: A: PDB Molecule: hypothetical protein tm1088a; PDBTitle: crystal structure of a putative transport protein (tm1088a) from2 thermotoga maritima at 1.50 a resolution
20	d2fy8a1	Alignment		99.8	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Potassium channel NAD-binding domain
21	c3c85A_	Alignment	not modelled	99.8	17	PDB header: transport protein Chain: A: PDB Molecule: putative glutathione-regulated potassium-efflux system PDBTitle: crystal structure of trka domain of putative glutathione-regulated2 potassium-efflux kefb from vibrio parahaemolyticus
22	c5butG_	Alignment	not modelled	99.8	22	PDB header: membrane protein Chain: G: PDB Molecule: ktr system potassium uptake protein a,ktr system potassium PDBTitle: crystal structure of inactive conformation of ktrab k+ transporter
23	c5tj6A_	Alignment	not modelled	99.7	15	PDB header: membrane protein Chain: A: PDB Molecule: high conductance calcium-activated potassium channel; PDBTitle: ca2+ bound aplysia slo1
24	c5a6eC_	Alignment	not modelled	99.7	13	PDB header: transport Chain: C: PDB Molecule: gating ring of potassium channel subfamily t member 1; PDBTitle: cryo-em structure of the slo2.2 na-activated k channel
25	c5u76A_	Alignment	not modelled	99.7	11	PDB header: transport protein Chain: A: PDB Molecule: potassium channel subfamily t member 1; PDBTitle: chicken slo2.2 in a closed conformation vitrified in the presence of2 300 mm nacl
26	c3nafA_	Alignment	not modelled	99.6	16	PDB header: ion transport Chain: A: PDB Molecule: calcium-activated potassium channel subunit alpha-1, PDBTitle: structure of the intracellular gating ring from the human high-2 conductance ca2+ gated k+ channel (bk channel)
27	d1e5qa1	Alignment	not modelled	99.4	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain PDB header: transport protein

28	c3jxoB_	Alignment	not modelled	99.3	30	Chain: B: PDB Molecule: trka-n domain protein; PDBTitle: crystal structure of an octomeric two-subunit trka k+ channel ring2 gating assembly, tm1088a:tm1088b, from thermotoga maritima
29	c4ys2A_	Alignment	not modelled	99.2	31	PDB header: immune system Chain: A: PDB Molecule: na+/h+ antiporter-like protein; PDBTitle: rck domain with cda
30	d1vcta2	Alignment	not modelled	99.0	20	Fold: TrkA C-terminal domain-like Superfamily: TrkA C-terminal domain-like Family: TrkA C-terminal domain-like
31	d2fy8a2	Alignment	not modelled	99.0	21	Fold: TrkA C-terminal domain-like Superfamily: TrkA C-terminal domain-like Family: TrkA C-terminal domain-like
32	c2bknA_	Alignment	not modelled	99.0	19	PDB header: membrane protein Chain: A: PDB Molecule: hypothetical protein ph0236; PDBTitle: structure analysis of unknown function protein
33	c4xttA_	Alignment	not modelled	98.8	19	PDB header: transport protein Chain: A: PDB Molecule: putative potassium transport protein; PDBTitle: structural studies of potassium transport protein ktra regulator of f2 conductance of k+ (rck) c domain in complex with cyclic diadenosine3 monophosphate (c-di-amp)
34	c3ic5A_	Alignment	not modelled	98.7	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative saccharopine dehydrogenase; PDBTitle: n-terminal domain of putative saccharopine dehydrogenase from ruegeria2 pomeroyi.
35	c5zikC_	Alignment	not modelled	98.7	15	PDB header: oxidoreductase Chain: C: PDB Molecule: probable 2-dehydropantoate 2-reductase; PDBTitle: crystal structure of ketopantoate reductase from pseudomonas2 aeruginosa
36	d1pjqa1	Alignment	not modelled	98.7	26	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Siroheme synthase N-terminal domain-like
37	d2f1ka2	Alignment	not modelled	98.6	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
38	c2f1kD_	Alignment	not modelled	98.6	24	PDB header: oxidoreductase Chain: D: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of synechocystis arogonate dehydrogenase
39	c3wfd_	Alignment	not modelled	98.5	19	PDB header: oxidoreductase Chain: D: PDB Molecule: 2-dehydropantoate 2-reductase; PDBTitle: the complex structure of d-mandelate dehydrogenase with nadh
40	c5a9tA_	Alignment	not modelled	98.5	22	PDB header: oxidoreductase Chain: A: PDB Molecule: putative dehydrogenase; PDBTitle: imine reductase from amycolatopsis orientalis in complex2 with (r)-methyltetrahydroisoquinoline
41	d1jaya_	Alignment	not modelled	98.4	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
42	c2x4gA_	Alignment	not modelled	98.4	25	PDB header: isomerase Chain: A: PDB Molecule: nucleoside-diphosphate-sugar epimerase; PDBTitle: crystal structure of pa4631, a nucleoside-diphosphate-sugar epimerase2 from pseudomonas aeruginosa
43	c3qhaB_	Alignment	not modelled	98.4	15	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase from mycobacterium2 avium 104
44	c2vrcD_	Alignment	not modelled	98.4	23	PDB header: oxidoreductase Chain: D: PDB Molecule: triphenylmethane reductase; PDBTitle: crystal structure of the citrobacter sp. triphenylmethane2 reductase complexed with nadp(h)
45	c2ew2B_	Alignment	not modelled	98.4	22	PDB header: oxidoreductase Chain: B: PDB Molecule: 2-dehydropantoate 2-reductase, putative; PDBTitle: crystal structure of the putative 2-dehydropantoate 2-reductase from2 enterococcus faecalis
46	c3egoB_	Alignment	not modelled	98.4	17	PDB header: oxidoreductase Chain: B: PDB Molecule: probable 2-dehydropantoate 2-reductase; PDBTitle: crystal structure of probable 2-dehydropantoate 2-reductase pane from2 bacillus subtilis
47	d1dlja2	Alignment	not modelled	98.4	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
48	c3l6dB_	Alignment	not modelled	98.4	24	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of putative oxidoreductase from pseudomonas putida2 kt2440
49	c2y0dB_	Alignment	not modelled	98.4	18	PDB header: oxidoreductase Chain: B: PDB Molecule: udp-glucose dehydrogenase; PDBTitle: bcec mutation; y10k
50	c4oI9A_	Alignment	not modelled	98.4	16	PDB header: oxidoreductase Chain: A: PDB Molecule: putative 2-dehydropantoate 2-reductase; PDBTitle: crystal structure of putative 2-dehydropantoate 2-reductase pane from2 mycobacterium tuberculosis complexed with nadp and oxamate
51	c2ofpB_	Alignment	not modelled	98.4	19	PDB header: oxidoreductase Chain: B: PDB Molecule: ketopantoate reductase; PDBTitle: crystal structure of escherichia coli ketopantoate2 reductase in a ternary complex with nadp+ and pantoate
52	c5l3zA_	Alignment	not modelled	98.4	22	PDB header: oxidoreductase Chain: A: PDB Molecule: polyketide ketoreductase simc7; PDBTitle: polyketide ketoreductase simc7 - binary complex with nadp+
53	c1ks9A_	Alignment	not modelled	98.4	20	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-dehydropantoate 2-reductase; PDBTitle: ketopantoate reductase from escherichia coli

54	c3gg2B	Alignment	not modelled	98.3	18	PDB header: oxidoreductase Chain: B: PDB Molecule: sugar dehydrogenase, udp-glucose/gdp-mannose dehydrogenase PDBTitle: crystal structure of udp-glucose 6-dehydrogenase from porphyromonas2 gingivalis bound to product udp-glucuronate
55	c3c85D	Alignment	not modelled	98.3	22	PDB header: transport protein Chain: D: PDB Molecule: putative glutathione-regulated potassium-efflux system PDBTitle: crystal structure of trka domain of putative glutathione-regulated2 potassium-efflux kefb from vibrio parahaemolyticus
56	c5ayvB	Alignment	not modelled	98.3	24	PDB header: oxidoreductase Chain: B: PDB Molecule: 2-dehydropantoate 2-reductase; PDBTitle: crystal structure of archaeal ketopantoate reductase complexed with2 coenzyme a and 2-oxopantoate
57	c1e5IA	Alignment	not modelled	98.3	16	PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine reductase; PDBTitle: apo saccharopine reductase from magnaporthe grisea
58	c3ckyA	Alignment	not modelled	98.3	16	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-hydroxymethyl glutarate dehydrogenase; PDBTitle: structural and kinetic properties of a beta-hydroxyacid dehydrogenase2 involved in nicotinate fermentation
59	c1bg6A	Alignment	not modelled	98.3	13	PDB header: oxidoreductase Chain: A: PDB Molecule: n-(1-d-carboxylethyl)-l-norvaline dehydrogenase; PDBTitle: crystal structure of the n-(1-d-carboxylethyl)-l-norvaline2 dehydrogenase from arthrobacter sp. strain 1c
60	c3dttA	Alignment	not modelled	98.3	27	PDB header: oxidoreductase Chain: A: PDB Molecule: nadp oxidoreductase; PDBTitle: crystal structure of a putative f420 dependent nadp-reductase2 (arth_0613) from arthrobacter sp. fb24 at 1.70 a resolution
61	d1ks9a2	Alignment	not modelled	98.3	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
62	d1pgja2	Alignment	not modelled	98.3	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
63	c2gf2B	Alignment	not modelled	98.3	15	PDB header: oxidoreductase Chain: B: PDB Molecule: 3-hydroxyisobutyrate dehydrogenase; PDBTitle: crystal structure of human hydroxyisobutyrate dehydrogenase
64	c3g0oA	Alignment	not modelled	98.3	17	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-hydroxyisobutyrate dehydrogenase; PDBTitle: crystal structure of 3-hydroxyisobutyrate dehydrogenase2 (ygbj) from salmonella typhimurium
65	d2pgda2	Alignment	not modelled	98.3	9	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
66	d1mv8a2	Alignment	not modelled	98.3	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
67	d2c5aa1	Alignment	not modelled	98.3	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
68	c4wb1B	Alignment	not modelled	98.3	21	PDB header: oxidoreductase Chain: B: PDB Molecule: cals8; PDBTitle: crystal structure of cals8 from micromonospora echinospora (p294s2 mutant)
69	c2p5uC	Alignment	not modelled	98.3	18	PDB header: isomerase Chain: C: PDB Molecule: udp-glucose 4-epimerase; PDBTitle: crystal structure of thermus thermophilus hb8 udp-glucose 4-epimerase2 complex with nad
70	d1pjca1	Alignment	not modelled	98.3	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
71	c5y8mA	Alignment	not modelled	98.3	18	PDB header: oxidoreductase Chain: A: PDB Molecule: probable 3-hydroxyisobutyrate dehydrogenase; PDBTitle: mycobacterium tuberculosis 3-hydroxyisobutyrate dehydrogenase2 (mthibadh) + nad + (r)-3-hydroxyisobutyrate (r-hiba)
72	c4tskA	Alignment	not modelled	98.2	19	PDB header: oxidoreductase,isomerase Chain: A: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: ketol-acid reductoisomerase from alicyclobacillus acidocaldarius
73	c4zrmB	Alignment	not modelled	98.2	21	PDB header: isomerase Chain: B: PDB Molecule: udp-glucose 4-epimerase; PDBTitle: crystal structure of udp-glucose 4-epimerase (tm0509) from2 hyperthermophilic eubacterium thermotoga maritima
74	c4d3fB	Alignment	not modelled	98.2	20	PDB header: oxidoreductase Chain: B: PDB Molecule: imiline reductase; PDBTitle: bcisred from bacillus cereus in complex with nadph
75	c3fwnB	Alignment	not modelled	98.2	9	PDB header: oxidoreductase Chain: B: PDB Molecule: 6-phosphogluconate dehydrogenase, decarboxylating; PDBTitle: dimeric 6-phosphogluconate dehydrogenase complexed with 6-2 phosphogluconate and 2'-monophosphoadenosine-5'-diphosphate
76	c3ggpA	Alignment	not modelled	98.2	15	PDB header: oxidoreductase Chain: A: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase from a. aeolicus in2 complex with hydroxyphenyl propionate and nad+
77	d1bg6a2	Alignment	not modelled	98.2	12	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain PDB header: oxidoreductase

78	c4a7pA	Alignment	not modelled	98.2	16	Chain: A: PDB Molecule: udp-glucose dehydrogenase; PDBTitle: se-met derivatized udgd, udp-glucose dehydrogenase from sphingomonas2 elodea
79	c5t57A	Alignment	not modelled	98.2	24	PDB header: oxidoreductase Chain: A: PDB Molecule: semialdehyde dehydrogenase nad-binding protein; PDBTitle: crystal structure of a semialdehyde dehydrogenase nad-binding protein2 from cupriavidus necator in complex with calcium and nad
80	c5ojjA	Alignment	not modelled	98.2	15	PDB header: oxidoreductase Chain: A: PDB Molecule: imine reductase; PDBTitle: imine reductase from aspergillus terreus in complex with nadph4 and2 dibenz[c,e]azepine
81	c2qx7A	Alignment	not modelled	98.2	22	PDB header: plant protein Chain: A: PDB Molecule: eugenol synthase 1; PDBTitle: structure of eugenol synthase from ocimum basilicum
82	c3k96B	Alignment	not modelled	98.2	19	PDB header: oxidoreductase Chain: B: PDB Molecule: glycerol-3-phosphate dehydrogenase [nad(p)+]; PDBTitle: 2.1 angstrom resolution crystal structure of glycerol-3-phosphate2 dehydrogenase (gpsa) from coxiella burnetii
83	d1udca	Alignment	not modelled	98.2	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
84	c3ktdC	Alignment	not modelled	98.2	17	PDB header: oxidoreductase Chain: C: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of a putative prephenate dehydrogenase (cg10226)2 from corynebacterium glutamicum atcc 13032 at 2.60 a resolution
85	c1mv8A	Alignment	not modelled	98.2	21	PDB header: oxidoreductase Chain: A: PDB Molecule: gdp-mannose 6-dehydrogenase; PDBTitle: 1.55 a crystal structure of a ternary complex of gdp-mannose2 dehydrogenase from psuedomonas aeruginosa
86	c6aqjB	Alignment	not modelled	98.2	20	PDB header: isomerase Chain: B: PDB Molecule: ketol-acid reductoisomerase (nadp(+)); PDBTitle: crystal structures of staphylococcus aureus ketol-acid2 reductoisomerase in complex with two transition state analogs that3 have biocidal activity.
87	c3plnA	Alignment	not modelled	98.2	16	PDB header: oxidoreductase Chain: A: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: crystal structure of klebsiella pneumoniae udp-glucose 6-dehydrogenase2 complexed with udp-glucose
88	c2axqA	Alignment	not modelled	98.2	19	PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine dehydrogenase; PDBTitle: apo histidine-tagged saccharopine dehydrogenase (l-glu2 forming) from saccharomyces cerevisiae
89	c3icpA	Alignment	not modelled	98.2	25	PDB header: isomerase Chain: A: PDB Molecule: nad-dependent epimerase/dehydratase; PDBTitle: crystal structure of udp-galactose 4-epimerase
90	c5n2iC	Alignment	not modelled	98.2	24	PDB header: oxidoreductase Chain: C: PDB Molecule: reduced coenzyme f420:nadp oxidoreductase; PDBTitle: f420:nadph oxidoreductase from thermobifida fusca with nadp+ bound
91	c5g6sD	Alignment	not modelled	98.2	16	PDB header: oxidoreductase Chain: D: PDB Molecule: imine reductase; PDBTitle: imine reductase from aspergillus oryzae in complex with nadp(h) and2 (r)-rasagiline
92	c3vtfA	Alignment	not modelled	98.2	20	PDB header: oxidoreductase Chain: A: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: structure of a udp-glucose dehydrogenase from the hyperthermophilic2 archaeon pyrobaculum islandicum
93	c3hwrA	Alignment	not modelled	98.2	23	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-dehydropantoate 2-reductase; PDBTitle: crystal structure of pane/apba family ketopantoate reductase2 (yp_299159.1) from ralstonia eutropha jmp134 at 2.15 a resolution
94	c3dojA	Alignment	not modelled	98.2	19	PDB header: oxidoreductase Chain: A: PDB Molecule: dehydrogenase-like protein; PDBTitle: structure of glyoxylate reductase 1 from arabidopsis (atglyr1)
95	d1txga2	Alignment	not modelled	98.2	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
96	c2z2vA	Alignment	not modelled	98.1	25	PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical protein ph1688; PDBTitle: crystal structure of l-lysine dehydrogenase from2 hyperthermophilic archaeon pyrococcus horikoshii
97	c1txgA	Alignment	not modelled	98.1	27	PDB header: oxidoreductase Chain: A: PDB Molecule: glycerol-3-phosphate dehydrogenase [nad(p)+]; PDBTitle: structure of glycerol-3-phosphate dehydrogenase from archaeoglobus2 fulgidus
98	d1n1ea2	Alignment	not modelled	98.1	12	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
99	c2zcuA	Alignment	not modelled	98.1	24	PDB header: oxidoreductase Chain: A: PDB Molecule: uncharacterized oxidoreductase ytfg; PDBTitle: crystal structure of a new type of nadph-dependent quinone2 oxidoreductase (qor2) from escherichia coli
100	c1i36A	Alignment	not modelled	98.1	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein mth1747; PDBTitle: structure of conserved protein mth1747 of unknown function reveals2 structural similarity with 3-hydroxyacid dehydrogenases
101	c3g17H	Alignment	not modelled	98.1	23	PDB header: structural genomics, unknown function Chain: H: PDB Molecule: similar to 2-dehydropantoate 2-reductase; PDBTitle: structure of putative 2-dehydropantoate 2-reductase from2 staphylococcus aureus

102	c3d1lB_	Alignment	not modelled	98.1	16	PDB header: oxidoreductase Chain: B: PDB Molecule: putative nadp oxidoreductase bf3122; PDBTitle: crystal structure of putative nadp oxidoreductase bf3122 from2 bacteroides fragilis
103	c2g5cD_	Alignment	not modelled	98.1	18	PDB header: oxidoreductase Chain: D: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase from aquifex aeolicus
104	c1dliA_	Alignment	not modelled	98.1	21	PDB header: oxidoreductase Chain: A: PDB Molecule: udp-glucose dehydrogenase; PDBTitle: the first structure of udp-glucose dehydrogenase (udpgdh) reveals the2 catalytic residues necessary for the two-fold oxidation
105	c1pgjA_	Alignment	not modelled	98.1	13	PDB header: oxidoreductase Chain: A: PDB Molecule: 6-phosphogluconate dehydrogenase; PDBTitle: x-ray structure of 6-phosphogluconate dehydrogenase from the protozoan2 parasite t. brucei
106	c3c1oA_	Alignment	not modelled	98.1	22	PDB header: oxidoreductase Chain: A: PDB Molecule: eugenol synthase; PDBTitle: the multiple phenylpropene synthases in both clarkia2 breweri and petunia hybrida represent two distinct lineages
107	c4oqzA_	Alignment	not modelled	98.1	22	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase yfjr; PDBTitle: streptomyces aurantiacus imine reductase
108	c3triB_	Alignment	not modelled	98.1	21	PDB header: oxidoreductase Chain: B: PDB Molecule: pyrroline-5-carboxylate reductase; PDBTitle: structure of a pyrroline-5-carboxylate reductase (proc) from coxiella2 burnetii
109	c5t8xA_	Alignment	not modelled	98.1	18	PDB header: oxidoreductase Chain: A: PDB Molecule: prephenate dehydrogenase 1; PDBTitle: prephenate dehydrogenase from soybean
110	c3cumA_	Alignment	not modelled	98.1	16	PDB header: oxidoreductase Chain: A: PDB Molecule: probable 3-hydroxyisobutyrate dehydrogenase; PDBTitle: crystal structure of a possible 3-hydroxyisobutyrate dehydrogenase2 from pseudomonas aeruginosa pao1
111	d2blla1	Alignment	not modelled	98.1	25	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
112	c4pvcB_	Alignment	not modelled	98.1	17	PDB header: oxidoreductase Chain: B: PDB Molecule: nadph-dependent methylglyoxal reductase gre2; PDBTitle: crystal structure of yeast methylglyoxal/ isovaleraldehyde reductase2 gre2
113	c4gjbB_	Alignment	not modelled	98.1	16	PDB header: oxidoreductase Chain: B: PDB Molecule: 6-phosphogluconate dehydrogenase nad-binding; PDBTitle: crystal structure of nad-binding 6-phosphogluconate dehydrogenase from2 dyadobacter fermentans
114	c3ghyA_	Alignment	not modelled	98.0	24	PDB header: oxidoreductase Chain: A: PDB Molecule: ketopantoate reductase protein; PDBTitle: crystal structure of a putative ketopantoate reductase from ralstonia2 solanacearum molk2
115	c4xdzB_	Alignment	not modelled	98.0	15	PDB header: oxidoreductase Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: holo structure of ketol-acid reductoisomerase from ignisphaera2 aggregans
116	c5ocmA_	Alignment	not modelled	98.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: nad_gly3p_dh, nad-dependent glycerol-3-phosphate PDBTitle: imine reductase from streptosporangium roseum in complex with nadp+2 and 2,2,2-trifluoroacetophenone hydrate
117	c3gpiA_	Alignment	not modelled	98.0	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: nad-dependent epimerase/dehydratase; PDBTitle: structure of putative nad-dependent epimerase/dehydratase from2 methylobacillus flagellatus
118	c2pk3B_	Alignment	not modelled	98.0	25	PDB header: oxidoreductase Chain: B: PDB Molecule: gdp-6-deoxy-d-lyxo-4-hexulose reductase; PDBTitle: crystal structure of a gdp-4-keto-6-deoxy-d-mannose reductase
119	c3dhyC_	Alignment	not modelled	98.0	21	PDB header: hydrolase Chain: C: PDB Molecule: adenosylhomocysteinease; PDBTitle: crystal structures of mycobacterium tuberculosis s-adenosyl-l-2 homocysteine hydrolase in ternary complex with substrate and3 inhibitors
120	c2uyyD_	Alignment	not modelled	98.0	24	PDB header: cytokine Chain: D: PDB Molecule: n-pac protein; PDBTitle: structure of the cytokine-like nuclear factor n-pac