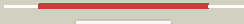











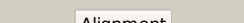


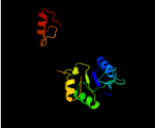








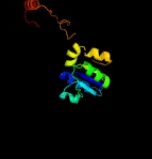
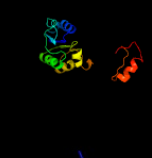
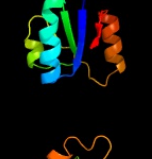



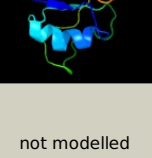


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2070c_(cobK)_2327499_2328233
Date	Mon Aug 5 13:25:18 BST 2019
Unique Job ID	a6277094f5cc34b4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5c4nD_	 Alignment		100.0	40	PDB header: oxidoreductase Chain: D: PDB Molecule: precorrin-6a reductase; PDBTitle: cobk precorrin-6a reductase
2	c4inaA_	 Alignment		97.6	20	PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine dehydrogenase; PDBTitle: crystal structure of the q7mss8_wolsu protein from wolinella2 succinogenes. northeast structural genomics consortium target wsr35
3	c4rl6A_	 Alignment		97.4	17	PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine dehydrogenase; PDBTitle: crystal structure of the q04l03_strp2 protein from streptococcus2 pneumoniae. northeast structural genomics consortium target spr105
4	c2qx7A_	 Alignment		97.2	16	PDB header: plant protein Chain: A: PDB Molecule: eugenol synthase 1; PDBTitle: structure of eugenol synthase from ocimum basilicum
5	c2dwcB_	 Alignment		97.2	18	PDB header: transferase Chain: B: PDB Molecule: 433aa long hypothetical phosphoribosylglycinamide formyl PDBTitle: crystal structure of probable phosphoribosylglycinamide formyl2 transferase from pyrococcus horikoshii ot3 complexed with adp
6	c1gsoA_	 Alignment		97.0	21	PDB header: ligase Chain: A: PDB Molecule: protein (glycinamide ribonucleotide synthetase); PDBTitle: glycinamide ribonucleotide synthetase (gar-syn) from e.2 coli.
7	c5z2fA_	 Alignment		97.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: nadph/pda bound dihydrodipicolinate reductase from paenisporosarcina2 sp. tg-14
8	c2qk4A_	 Alignment		97.0	20	PDB header: ligase Chain: A: PDB Molecule: trifunctional purine biosynthetic protein adenosine-3; PDBTitle: human glycinamide ribonucleotide synthetase
9	c4ywjB_	 Alignment		97.0	18	PDB header: oxidoreductase Chain: B: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate reductase; PDBTitle: crystal structure of 4-hydroxy-tetrahydrodipicolinate reductase (htpa2 reductase) from pseudomonas aeruginosa
10	c2z2vA_	 Alignment		96.9	15	PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical protein ph1688; PDBTitle: crystal structure of l-lysine dehydrogenase from2 hyperthermophilic archaeon pyrococcus horikoshii
11	c1kjaA_	 Alignment		96.9	23	PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase 2; PDBTitle: crystal structure of glycinamide ribonucleotide transformylase in2 complex with mg-atp-gamma-s

12	c3lp8A_	Alignment		96.9	10	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylamine-glycine ligase; PDBTitle: crystal structure of phosphoribosylamine-glycine ligase from2 ehrlichia chaffeensis
13	c2ip4A_	Alignment		96.8	21	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylamine-glycine ligase; PDBTitle: crystal structure of glycinamide ribonucleotide synthetase from2 thermus thermophilus hb8
14	c2xd4A_	Alignment		96.8	12	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylamine-glycine ligase; PDBTitle: nucleotide-bound structures of bacillus subtilis glycinamide2 ribonucleotide synthetase
15	c2yyaB_	Alignment		96.7	16	PDB header: ligase Chain: B: PDB Molecule: phosphoribosylamine-glycine ligase; PDBTitle: crystal structure of gar synthetase from aquifex aeolicus
16	d1gsoa2	Alignment		96.5	25	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
17	c3e48B_	Alignment		96.4	11	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative nucleoside-diphosphate-sugar epimerase; PDBTitle: crystal structure of a nucleoside-diphosphate-sugar epimerase2 (sav0421) from staphylococcus aureus, northeast structural genomics3 consortium target zr319
18	c3ic5A_	Alignment		96.4	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.
19	c4dimA_	Alignment		96.3	16	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylglycinamide synthetase; PDBTitle: crystal structure of phosphoribosylglycinamide synthetase from2 anaerococcus prevotii
20	c5ugiC_	Alignment		96.3	21	PDB header: oxidoreductase Chain: C: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate reductase; PDBTitle: crystal structure of htpa reductase from neisseria meningitidis
21	c5tenH_	Alignment	not modelled	96.3	18	PDB header: oxidoreductase Chain: H: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate reductase; PDBTitle: structure of 4-hydroxy-tetrahydrodipicolinate reductase from vibrio2 vulnificus with 2,5 furan dicarboxylic and nadh with intact3 polyhistidine tag
22	c5vevB_	Alignment	not modelled	96.3	15	PDB header: ligase Chain: B: PDB Molecule: phosphoribosylamine-glycine ligase; PDBTitle: crystal structure of phosphoribosylamine-glycine ligase from neisseria2 gonorrhoeae
23	d1m1nb_	Alignment	not modelled	96.2	19	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein
24	c5kt0A_	Alignment	not modelled	96.2	18	PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate reductase; PDBTitle: dihydrodipicolinate reductase from the industrial and evolutionarily2 important cyanobacteria anabaena variabilis.
25	c2ys6A_	Alignment	not modelled	96.2	13	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylglycinamide synthetase; PDBTitle: crystal structure of gar synthetase from geobacillus kaustophilus
26	c1e5IA_	Alignment	not modelled	96.1	14	PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine reductase; PDBTitle: apo saccharopine reductase from magnaporthe grisea
27	c3c1oA_	Alignment	not modelled	96.1	16	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
						PDB header: isomerase, lyase Chain: A: PDB Molecule: nad-dependent epimerase/dehydratase;

28	c3dhnA	Alignment	not modelled	96.0	13	PDBTitle: crystal structure of the putative epimerase q89z24_bactn from2 bacteroides thetaiotaomicron. northeast structural genomics3 consortium target btr310.
29	d1qh8b	Alignment	not modelled	96.0	14	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein
30	c5ua0B	Alignment	not modelled	96.0	22	PDB header: oxidoreductase Chain: B: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate reductase 2, PDBTitle: dimeric crystal structure of htpa reductase from arabidopsis thaliana
31	c5kojD	Alignment	not modelled	95.9	16	PDB header: oxidoreductase Chain: D: PDB Molecule: nitrogenase femo beta subunit protein nifk; PDBTitle: nitrogenase mofep protein in the ids oxidized state
32	c2axqA	Alignment	not modelled	95.8	16	PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine dehydrogenase; PDBTitle: apo histidine-tagged saccharopine dehydrogenase (l-glu2 forming) from saccharomyces cerevisiae
33	d1e6ua	Alignment	not modelled	95.8	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
34	d1i24a	Alignment	not modelled	95.7	27	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
35	c5mlkA	Alignment	not modelled	95.7	14	PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase; PDBTitle: biotin dependent carboxylase acca3 dimer from mycobacterium2 tuberculosis (rv3285)
36	c4ffnA	Alignment	not modelled	95.7	14	PDB header: ligase/substrate Chain: A: PDB Molecule: pylc; PDBTitle: pylc in complex with d-ornithine and amppnp
37	c3i5mA	Alignment	not modelled	95.5	23	PDB header: oxidoreductase Chain: A: PDB Molecule: putative leucoanthocyanidin reductase 1; PDBTitle: structure of the apo form of leucoanthocyanidin reductase from vitis2 vinifera
38	c2dzdB	Alignment	not modelled	95.5	16	PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of the biotin carboxylase domain of pyruvate2 carboxylase
39	c2q1wC	Alignment	not modelled	95.4	18	PDB header: sugar binding protein Chain: C: PDB Molecule: putative nucleotide sugar epimerase/ dehydratase; PDBTitle: crystal structure of the bordetella bronchiseptica enzyme wbmh in2 complex with nad+
40	c5ffqA	Alignment	not modelled	95.4	16	PDB header: unknown function Chain: A: PDB Molecule: shuy-like protein; PDBTitle: chuy: an anaerobillin reductase from escherichia coli o157:h7
41	c5I78A	Alignment	not modelled	95.4	20	PDB header: oxidoreductase Chain: A: PDB Molecule: alpha-aminoadipic semialdehyde synthase, mitochondrial; PDBTitle: crystal structure of human aminoadipate semialdehyde synthase,2 saccharopine dehydrogenase domain (in nad+ bound form)
42	c3ouzA	Alignment	not modelled	95.4	10	PDB header: ligase Chain: A: PDB Molecule: biotin carboxylase; PDBTitle: crystal structure of biotin carboxylase-adp complex from campylobacter2 jejuni
43	d1qyca	Alignment	not modelled	95.3	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
44	c5I3zA	Alignment	not modelled	95.3	18	PDB header: oxidoreductase Chain: A: PDB Molecule: polyketide ketoreductase simc7; PDBTitle: polyketide ketoreductase simc7 - binary complex with nadp+
45	c2gpwC	Alignment	not modelled	95.2	7	PDB header: ligase Chain: C: PDB Molecule: biotin carboxylase; PDBTitle: crystal structure of the biotin carboxylase subunit, f363a2 mutant, of acetyl-coa carboxylase from escherichia coli.
46	d1m1na	Alignment	not modelled	95.2	15	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein
47	c3nklA	Alignment	not modelled	95.2	16	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
48	c1yl7F	Alignment	not modelled	95.2	20	PDB header: oxidoreductase Chain: F: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: the crystal structure of mycobacterium tuberculosis2 dihydrodipicolinate reductase (rv2773c) in complex with nadh (crystal3 form c)
49	c1drwA	Alignment	not modelled	95.2	22	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: escherichia coli dhpr/nhdh complex
50	c4f3yA	Alignment	not modelled	95.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: x-ray crystal structure of dihydrodipicolinate reductase from2 burkholderia thailandensis
51	c3sc6F	Alignment	not modelled	94.9	19	PDB header: oxidoreductase Chain: F: PDB Molecule: dtdp-4-dehydrorhamnose reductase; PDBTitle: 2.65 angstrom resolution crystal structure of dtdp-4-dehydrorhamnose2 reductase (rfbd) from bacillus anthracis str. ames in complex with3 nadp
52	c2yy7B	Alignment	not modelled	94.9	14	PDB header: oxidoreductase Chain: B: PDB Molecule: l-threonine dehydrogenase; PDBTitle: crystal structure of thermolabile l-threonine dehydrogenase from2 flavobacterium frigidimaris kuc-1

53	c4wpgA_	Alignment	not modelled	94.8	14	PDB header: oxidoreductase Chain: A: PDB Molecule: ddtp-4-dehydrorhamnose reductase; PDBTitle: group a streptococcus gaca is an essential dtdp-4-dehydrorhamnose2 reductase (rmid)
54	c3g8cB_	Alignment	not modelled	94.8	8	PDB header: ligase Chain: B: PDB Molecule: biotin carboxylase; PDBTitle: crystal structure of biotin carboxylase in complex with biotin,2 bicarbonate, adp and mg ion
55	d1qh8a_	Alignment	not modelled	94.8	18	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein
56	c2ph5A_	Alignment	not modelled	94.7	16	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
57	d1kjq2_	Alignment	not modelled	94.6	22	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
58	d1xgka_	Alignment	not modelled	94.6	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
59	c4plpB_	Alignment	not modelled	94.5	17	PDB header: transferase Chain: B: PDB Molecule: homospermidine synthase; PDBTitle: crystal structure of the homospermidine synthase (hss) from2 blastochloris viridis in complex with nad
60	d1bxka_	Alignment	not modelled	94.4	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
61	c1ulzA_	Alignment	not modelled	94.4	15	PDB header: ligase Chain: A: PDB Molecule: pyruvate carboxylase n-terminal domain; PDBTitle: crystal structure of the biotin carboxylase subunit of pyruvate2 carboxylase
62	c1z7eC_	Alignment	not modelled	94.4	24	PDB header: hydrolase Chain: C: PDB Molecule: protein arna; PDBTitle: crystal structure of full length arna
63	c4qqrB_	Alignment	not modelled	94.3	16	PDB header: oxidoreductase Chain: B: PDB Molecule: 3,5-epimerase/4-reductase; PDBTitle: structural insight into nucleotide rhamnose synthase/epimerase-2 reductase from arabidopsis thaliana
64	d1hdoa_	Alignment	not modelled	94.3	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
65	c1tcvB_	Alignment	not modelled	94.2	29	PDB header: transferase Chain: B: PDB Molecule: purine-nucleoside phosphorylase; PDBTitle: crystal structure of the purine nucleoside phosphorylase2 from schistosoma mansoni in complex with non-detergent3 sulfobetaine 195 and acetate
66	c4jgbB_	Alignment	not modelled	94.2	16	PDB header: protein binding Chain: B: PDB Molecule: putative exported protein; PDBTitle: crystal structure of putative exported protein from burkholderia2 pseudomallei
67	c3jipA_	Alignment	not modelled	94.2	17	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: crystal structure of dihydrodipicolinate reductase from bartonella2 henselae at 2.0a resolution
68	c5l9aB_	Alignment	not modelled	94.2	16	PDB header: oxidoreductase Chain: B: PDB Molecule: l-threonine 3-dehydrogenase; PDBTitle: l-threonine dehydrogenase from trypanosoma brucei.
69	c4b8wB_	Alignment	not modelled	94.1	15	PDB header: oxidoreductase Chain: B: PDB Molecule: gdp-l-fucose synthase; PDBTitle: crystal structure of human gdp-l-fucose synthase with bound nadp and2 gdp, tetragonal crystal form
70	c3ax6C_	Alignment	not modelled	94.0	13	PDB header: ligase Chain: C: PDB Molecule: phosphoribosylaminoimidazole carboxylase, atpase subunit; PDBTitle: crystal structure of n5-carboxyaminoimidazole ribonucleotide2 synthetase from thermotoga maritima
71	c3wmxC_	Alignment	not modelled	94.0	14	PDB header: oxidoreductase Chain: C: PDB Molecule: nad dependent epimerase/dehydratase; PDBTitle: gale-like l-threonine dehydrogenase from cupriavidus necator (holo2 form)
72	c5wo1A_	Alignment	not modelled	94.0	22	PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate reductase; PDBTitle: crystal structure of dihydrodipicolinate reductase dapb from coxiella2 burnetii
73	d1pjqa1	Alignment	not modelled	94.0	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Siroheme synthase N-terminal domain-like
74	c5cxsA_	Alignment	not modelled	94.0	24	PDB header: transferase Chain: A: PDB Molecule: purine nucleoside phosphorylase; PDBTitle: crystal structure of isoform 2 of purine nucleoside phosphorylase2 complexed with mes
75	c2ynmD_	Alignment	not modelled	93.9	18	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
76	c3u9sA_	Alignment	not modelled	93.8	15	PDB header: ligase Chain: A: PDB Molecule: methylcrotonyl-coa carboxylase, alpha-subunit; PDBTitle: crystal structure of p. aeruginosa 3-methylcrotonyl-coa carboxylase2 (mcc) 750 kd holoenzyme, coa complex Fold: NAD(P)-binding Rossmann-fold domains

77	d2c5aa1	Alignment	not modelled	93.8	9	Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
78	d1yl7a1	Alignment	not modelled	93.8	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
79	c6aqyD_	Alignment	not modelled	93.6	18	PDB header: oxidoreductase Chain: D: PDB Molecule: gdp-l-fucose synthetase; PDBTitle: crystal structure of a gdp-l-fucose synthetase from naegleria fowleri
80	d1mioa_	Alignment	not modelled	93.5	18	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein
81	c2zklA_	Alignment	not modelled	93.5	19	PDB header: isomerase Chain: A: PDB Molecule: capsular polysaccharide synthesis enzyme cap5f; PDBTitle: crystal structure of capsular polysaccharide assembling protein capf2 from staphylococcus aureus
82	c3jzfA_	Alignment	not modelled	93.5	7	PDB header: ligase Chain: A: PDB Molecule: biotin carboxylase; PDBTitle: crystal structure of biotin carboxylase from e. coli in2 complex with benzimidazoles series
83	c3gidB_	Alignment	not modelled	93.5	12	PDB header: ligase Chain: B: PDB Molecule: acetyl-coa carboxylase 2; PDBTitle: the biotin carboxylase (bc) domain of human acetyl-coa carboxylase 22 (acc2) in complex with soraphen a
84	c5us6L_	Alignment	not modelled	93.5	21	PDB header: oxidoreductase Chain: L: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate reductase; PDBTitle: structure of dihydrodipicolinate reductase from vibrio vulnificus2 bound to nadh and 2,6 pyridine dicarboxylic acid with intact3 polyhistidine tag
85	c2p5uC_	Alignment	not modelled	93.5	22	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
86	c2z1mC_	Alignment	not modelled	93.4	19	PDB header: lyase Chain: C: PDB Molecule: gdp-d-mannose dehydratase; PDBTitle: crystal structure of gdp-d-mannose dehydratase from aquifex aeolicus2 vf5
87	c1yr3A_	Alignment	not modelled	93.4	22	PDB header: transferase Chain: A: PDB Molecule: xanthosine phosphorylase; PDBTitle: escherichia coli purine nucleoside phosphorylase ii, the product of2 the xapa gene
88	c3pdiB_	Alignment	not modelled	93.3	21	PDB header: protein binding Chain: B: PDB Molecule: nitrogenase mofe cofactor biosynthesis protein nifn; PDBTitle: precursor bound nifen
89	c5ifkC_	Alignment	not modelled	93.2	18	PDB header: transferase Chain: C: PDB Molecule: purine nucleoside phosphorylase; PDBTitle: purine nucleoside phosphorylase
90	c4qlfA_	Alignment	not modelled	93.1	15	PDB header: transferase Chain: A: PDB Molecule: rsfp; PDBTitle: crystal structure of methylthioadenosine phosphorylase sourced from an2 antarctic soil metagenomic library
91	c2pk3B_	Alignment	not modelled	93.1	18	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
92	c3rggA_	Alignment	not modelled	93.1	10	PDB header: hydrolase Chain: A: PDB Molecule: protein-tyrosine phosphatase mitochondrial 1; PDBTitle: crystal structure of ptpmt1 in complex with pi(5)p
93	c5eesA_	Alignment	not modelled	92.9	20	PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate reductase; PDBTitle: crystal structure of dapb in complex with nadp+ from corynebacterium2 glutamicum
94	d1n7ha_	Alignment	not modelled	92.7	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
95	c4twrA_	Alignment	not modelled	92.7	19	PDB header: isomerase Chain: A: PDB Molecule: nad binding site:nad-dependent epimerase/dehydratase:udp- PDBTitle: structure of udp-glucose 4-epimerase from brucella abortus
96	c6f2cK_	Alignment	not modelled	92.7	12	PDB header: lyase Chain: K: PDB Molecule: methylglyoxal synthase; PDBTitle: methylglyoxal synthase mgsa from bacillus subtilis
97	d2q46a1	Alignment	not modelled	92.7	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
98	c1z45A_	Alignment	not modelled	92.6	20	PDB header: isomerase Chain: A: PDB Molecule: gal10 bifunctional protein; PDBTitle: crystal structure of the gal10 fusion protein galactose2 mutarotase/udp-galactose 4-epimerase from saccharomyces cerevisiae3 complexed with nad, udp-glucose, and galactose
99	d1kyqa1	Alignment	not modelled	92.6	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Siroheme synthase N-terminal domain-like
100	c4eggD_	Alignment	not modelled	92.5	25	PDB header: ligase Chain: D: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: crystal structure of d-alanine-d-alanine ligase b from burkholderia2 pseudomallei
101	d1db3a_	Alignment	not modelled	92.5	26	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases

102	d1wo8a1	Alignment	not modelled	92.2	16	Fold: Methylglyoxal synthase-like Superfamily: Methylglyoxal synthase-like Family: Methylglyoxal synthase, MgsA
103	c3etjB	Alignment	not modelled	92.0	16	PDB header: lyase Chain: B: PDB Molecule: phosphoribosylaminoimidazole carboxylase atpase PDBTitle: crystal structure e. coli purk in complex with mg, adp, and2 pi
104	c4egjD	Alignment	not modelled	91.9	25	PDB header: ligase Chain: D: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: crystal structure of d-alanine-d-alanine ligase from burkholderia2 xenovorans
105	d1vl0a	Alignment	not modelled	91.8	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
106	d1kewa	Alignment	not modelled	91.8	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
107	c3ew7A	Alignment	not modelled	91.7	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lmo0794 protein; PDBTitle: crystal structure of the lmo0794 protein from listeria2 monocytogenes. northeast structural genomics consortium3 target lmr162.
108	d1oc2a	Alignment	not modelled	91.7	11	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
109	d1dih1	Alignment	not modelled	91.7	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
110	c2p4sA	Alignment	not modelled	91.6	18	PDB header: transferase Chain: A: PDB Molecule: purine nucleoside phosphorylase; PDBTitle: structure of purine nucleoside phosphorylase from anopheles gambiae in2 complex with dadme-immh
111	c4zrmB	Alignment	not modelled	91.4	12	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
112	c2yvqA	Alignment	not modelled	91.4	17	PDB header: ligase Chain: A: PDB Molecule: carbamoyl-phosphate synthase; PDBTitle: crystal structure of mgs domain of carbamoyl-phosphate2 synthetase from homo sapiens
113	c3tw6B	Alignment	not modelled	91.1	9	PDB header: ligase/activator Chain: B: PDB Molecule: pyruvate carboxylase protein; PDBTitle: structure of rhizobium etli pyruvate carboxylase t882a with the2 allosteric activator, acetyl coenzyme-a
114	c3hblA	Alignment	not modelled	91.1	16	PDB header: ligase Chain: A: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of s. aureus pyruvate carboxylase t908a mutant
115	c1t2aC	Alignment	not modelled	90.9	17	PDB header: structural genomics,lyase Chain: C: PDB Molecule: gdp-mannose 4,6 dehydratase; PDBTitle: crystal structure of human gdp-d-mannose 4,6-dehydratase
116	d1t2aa	Alignment	not modelled	90.9	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
117	c3k5iB	Alignment	not modelled	90.9	23	PDB header: lyase Chain: B: PDB Molecule: phosphoribosyl-aminoimidazole carboxylase; PDBTitle: crystal structure of n5-carboxyaminoimidazole synthase from2 aspergillus clavatus in complex with adp and 5-aminoimidazole3 ribonucleotide
118	d2fmu1	Alignment	not modelled	90.9	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
119	c4yraD	Alignment	not modelled	90.8	21	PDB header: oxidoreductase Chain: D: PDB Molecule: l-threonine 3-dehydrogenase, mitochondrial; PDBTitle: mouse tdh in the apo form
120	c2xdqB	Alignment	not modelled	90.7	15	PDB header: oxidoreductase Chain: B: PDB Molecule: light-independent protochlorophyllide reductase subunit b; PDBTitle: dark operative protochlorophyllide oxidoreductase (chl-chlb)2 complex