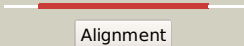

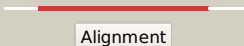

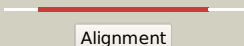







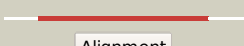


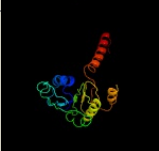

















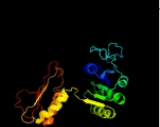













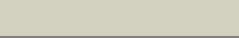


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2953 (-) _3305289_3306545
Date	Thu Aug 8 16:20:11 BST 2019
Unique Job ID	b73375523f252662

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2axqA_	 Alignment		100.0	12	PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine dehydrogenase; PDBTitle: apo histidine-tagged saccharopine dehydrogenase (l-glu2 forming) from saccharomyces cerevisiae
2	c1e5lA_	 Alignment		100.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine reductase; PDBTitle: apo saccharopine reductase from magnaporthe grisea
3	c4rl6A_	 Alignment		100.0	14	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	c5l78A_	 Alignment		100.0	12	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)
5	c4inaA_	 Alignment		100.0	13	PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine dehydrogenase; PDBTitle: crystal structure of the q7mss8_wolsu protein from wolfinella2 succinogenes. northeast structural genomics consortium target wsr35
6	c2z2vA_	 Alignment		100.0	12	PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical protein ph1688; PDBTitle: crystal structure of l-lysine dehydrogenase from2 hyperthermophilic archaeon pyrococcus horikoshii
7	c4plpB_	 Alignment		99.8	13	PDB header: transferase Chain: B: PDB Molecule: homospermidine synthase; PDBTitle: crystal structure of the homospermidine synthase (hss) from2 blastochloris viridis in complex with nad
8	c2ph5A_	 Alignment		99.8	10	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
9	c3ic5A_	 Alignment		99.8	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative saccharopine dehydrogenase; PDBTitle: n-terminal domain of putative saccharopine dehydrogenase from ruegeria2 pomeroyi.
10	d1e5qa1	 Alignment		99.7	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
11	c6iauB_	 Alignment		99.6	14	PDB header: oxidoreductase Chain: B: PDB Molecule: amine dehydrogenase; PDBTitle: amine dehydrogenase from cystobacter fuscus in complex with nadp+ and2 cyclohexylamine

12	c3wgzB_	 Alignment		99.5	14	PDB header: oxidoreductase Chain: B: PDB Molecule: meso-diaminopimelate dehydrogenase; PDBTitle: crystal structure of meso-dapdh q154l/t173i/r199m/p248s/h249n/n276s2 mutant with d-leucine of from clostridium tetani e88
13	c3bioB_	 Alignment		99.4	15	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase, gfo/idh/moca family; PDBTitle: crystal structure of oxidoreductase (gfo/idh/moca family member) from2 porphyromonas gingivalis w83
14	c4ywjB_	 Alignment		99.4	17	PDB header: oxidoreductase Chain: B: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate reductase; PDBTitle: crystal structure of 4-hydroxy-tetrahydrodipicolinate reductase (htpa2 reductase) from pseudomonas aeruginosa
15	c3dapB_	 Alignment		99.4	13	PDB header: oxidoreductase Chain: B: PDB Molecule: diaminopimelic acid dehydrogenase; PDBTitle: c. glutamicum dap dehydrogenase in complex with nadp+ and2 the inhibitor 5s-isoxazoline
16	c3wb9A_	 Alignment		99.4	15	PDB header: oxidoreductase Chain: A: PDB Molecule: diaminopimelate dehydrogenase; PDBTitle: crystal structures of meso-diaminopimelate dehydrogenase from2 symbiobacterium thermophilum
17	c5ugiC_	 Alignment		99.4	15	PDB header: oxidoreductase Chain: C: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate reductase; PDBTitle: crystal structure of htpa reductase from neisseria meningitidis
18	c1drwA_	 Alignment		99.3	14	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: escherichia coli dhpr/nhdh complex
19	c5tenH_	 Alignment		99.3	15	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
20	c5kt0A_	 Alignment		99.3	13	PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate reductase; PDBTitle: dihydrodipicolinate reductase from the industrial and evolutionarily2 important cyanobacteria anabaena variabilis.
21	c4f3yA_	 Alignment	not modelled	99.2	12	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: x-ray crystal structure of dihydrodipicolinate reductase from2 burkholderia thailandensis
22	c6iaqA_	 Alignment	not modelled	99.2	16	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase n-terminus domain-containing PDBTitle: structure of amine dehydrogenase from mycobacterium smegmatis
23	c2zcuA_	 Alignment	not modelled	99.2	20	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
24	c3wycB_	 Alignment	not modelled	99.2	15	PDB header: oxidoreductase Chain: B: PDB Molecule: meso-diaminopimelate d-dehydrogenase; PDBTitle: structure of a meso-diaminopimelate dehydrogenase in complex with nadp
25	c3w1vA_	 Alignment	not modelled	99.1	13	PDB header: lyase Chain: A: PDB Molecule: capsular polysaccharide synthesis enzyme cap8e; PDBTitle: crystal structure of capsular polysaccharide synthesizing enzyme cape2 from staphylococcus aureus in complex with inhibitor
26	d1e5qa2	 Alignment	not modelled	99.1	13	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Homoserine dehydrogenase-like
27	c1luaA_	 Alignment	not modelled	99.1	17	PDB header: oxidoreductase Chain: A: PDB Molecule: methylene tetrahydromethanopterin dehydrogenase; PDBTitle: structure of methylene-tetrahydromethanopterin dehydrogenase from2 methylobacterium extorquens am1 complexed with nadp
28	c5z2fA_	 Alignment	not modelled	99.1	8	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase;

28	c2z1A	Alignment	not modelled	99.1	0	PDBTitle: nadph/pda bound dihydrodipicolinate reductase from paenisporosarcina2 sp. tg-14 PDB header: lyase
29	c2gn9B	Alignment	not modelled	99.1	16	Chain: B: PDB Molecule: udp-glcnac c6 dehydratase; PDBTitle: crystal structure of udp-glcnac inverting 4,6-dehydratase in complex2 with nadp and udp-glc
30	c4j2oD	Alignment	not modelled	99.1	11	PDB header: isomerase Chain: D: PDB Molecule: udp-n-acetylglucosamine 4,6-dehydratase/5-epimerase; PDBTitle: crystal structure of nadp-bound wbjb from a. baumannii community2 strain d1279779
31	c3e48B	Alignment	not modelled	99.0	16	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
32	d1luaa1	Alignment	not modelled	99.0	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
33	c6g1mA	Alignment	not modelled	99.0	11	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: amine dehydrogenase from petrotoga mobilis; open and closed form
34	d1vi2a1	Alignment	not modelled	99.0	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
35	c3pvzD	Alignment	not modelled	99.0	13	PDB header: lyase Chain: D: PDB Molecule: udp-n-acetylglucosamine 4,6-dehydratase; PDBTitle: udp-n-acetylglucosamine 4,6-dehydratase from vibrio fischeri
36	c2qx7A	Alignment	not modelled	99.0	14	PDB header: plant protein Chain: A: PDB Molecule: eugenol synthase 1; PDBTitle: structure of eugenol synthase from ocimum basilicum
37	d1xgka	Alignment	not modelled	99.0	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
38	c2nloA	Alignment	not modelled	99.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate dehydrogenase; PDBTitle: crystal structure of the quinate dehydrogenase from corynebacterium2 glutamicum
39	c2exxB	Alignment	not modelled	99.0	16	PDB header: unknown function Chain: B: PDB Molecule: hscarg protein; PDBTitle: crystal structure of hscarg from homo sapiens in complex with nadp
40	c6bwcA	Alignment	not modelled	99.0	11	PDB header: biosynthetic protein Chain: A: PDB Molecule: polysaccharide biosynthesis protein capd; PDBTitle: x-ray structure of pen from bacillus thuringiensis
41	c1z7eC	Alignment	not modelled	98.9	17	PDB header: hydrolase Chain: C: PDB Molecule: protein arna; PDBTitle: crystal structure of full length arna
42	c2vrcD	Alignment	not modelled	98.9	28	PDB header: oxidoreductase Chain: D: PDB Molecule: triphenylmethane reductase; PDBTitle: crystal structure of the citrobacter sp. triphenylmethane2 reductase complexed with nadp(h)
43	c3nzoB	Alignment	not modelled	98.9	12	PDB header: lyase Chain: B: PDB Molecule: udp-n-acetylglucosamine 4,6-dehydratase; PDBTitle: udp-n-acetylglucosamine 4,6-dehydratase from vibrio fischeri.
44	c4wuvB	Alignment	not modelled	98.9	16	PDB header: oxidoreductase Chain: B: PDB Molecule: 2-hydroxycyclohexanecarboxyl-coa dehydrogenase; PDBTitle: crystal structure of a putative d-mannonate oxidoreductase from2 haemophilus influenza (avi_5165, target efi-513796) with bound nad
45	c5f5nA	Alignment	not modelled	98.9	27	PDB header: oxidoreductase Chain: A: PDB Molecule: monooxygenase; PDBTitle: the structure of monooxygenase ksta11 in complex with nad and its2 substrate
46	d1qyca	Alignment	not modelled	98.9	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
47	c2eggA	Alignment	not modelled	98.9	19	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate 5-dehydrogenase; PDBTitle: crystal structure of shikimate 5-dehydrogenase (aroe) from geobacillus2 kaustophilus
48	c3ijpA	Alignment	not modelled	98.9	11	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: crystal structure of dihydrodipicolinate reductase from bartonella2 henselae at 2.0a resolution
49	c4idgB	Alignment	not modelled	98.9	17	PDB header: oxidoreductase Chain: B: PDB Molecule: short-chain dehydrogenase/reductase; PDBTitle: crystal structure of a short-chain dehydrogenase/reductase superfamily2 protein from agrobacterium tumefaciens (target efi-506441) with bound3 nad, monoclinic form 2
50	d2q46a1	Alignment	not modelled	98.9	10	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
51	c3tozA	Alignment	not modelled	98.9	15	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate dehydrogenase; PDBTitle: 2.2 angstrom crystal structure of shikimate 5-dehydrogenase from2 listeria monocytogenes in complex with nad.
52	c1r0ID	Alignment	not modelled	98.9	25	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

53	c5wo1A	Alignment	not modelled	98.9	14	PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate reductase; PDBTitle: crystal structure of dihydrodipicolinate reductase dapb from coxiella2 burnetii
54	d1dja1	Alignment	not modelled	98.8	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
55	c5l3zA	Alignment	not modelled	98.8	22	PDB header: oxidoreductase Chain: A: PDB Molecule: polyketide ketoreductase simc7; PDBTitle: polyketide ketoreductase simc7 - binary complex with nadp+
56	c3upyB	Alignment	not modelled	98.8	14	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.
57	c1vi2B	Alignment	not modelled	98.8	17	PDB header: oxidoreductase Chain: B: PDB Molecule: shikimate 5-dehydrogenase 2; PDBTitle: crystal structure of shikimate-5-dehydrogenase with nad
58	c5swvC	Alignment	not modelled	98.8	17	PDB header: lyase Chain: C: PDB Molecule: pentafunctional arom polypeptide; PDBTitle: dehydroquinase dehydratase and shikimate dehydrogenase from s. pombe2 arom
59	c4xijA	Alignment	not modelled	98.8	14	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate 5-dehydrogenase; PDBTitle: crystal structure of a shikimate 5-dehydrogenase from mycobacterium2 fortuitum determined by iodide sad phasing
60	c1z45A	Alignment	not modelled	98.8	17	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
61	c2hk8B	Alignment	not modelled	98.8	21	PDB header: oxidoreductase Chain: B: PDB Molecule: shikimate dehydrogenase; PDBTitle: crystal structure of shikimate dehydrogenase from aquifex2 aeolicus at 2.35 angstrom resolution
62	d1db3a	Alignment	not modelled	98.8	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
63	c3a14B	Alignment	not modelled	98.7	21	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
64	c3c1oA	Alignment	not modelled	98.7	15	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
65	d1f06a1	Alignment	not modelled	98.7	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
66	d1mlda1	Alignment	not modelled	98.7	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
67	c3v8bC	Alignment	not modelled	98.7	22	PDB header: oxidoreductase Chain: C: PDB Molecule: putative dehydrogenase, possibly 3-oxoacyl-lacyl-carrier PDBTitle: crystal structure of a 3-ketoacyl-acp reductase from sinorhizobium2 meliloti 1021
68	d2q49a1	Alignment	not modelled	98.7	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
69	c2eghA	Alignment	not modelled	98.7	19	PDB header: oxidoreductase Chain: A: PDB Molecule: 1-deoxy-d-xylulose 5-phosphate reductoisomerase; PDBTitle: crystal structure of 1-deoxy-d-xylulose 5-phosphate reductoisomerase2 complexed with a magnesium ion, nadph and fosmidomycin
70	c1gpiA	Alignment	not modelled	98.7	28	PDB header: reductase Chain: A: PDB Molecule: glutamyl-trna reductase; PDBTitle: glutamyl-trna reductase from methanopyrus kandleri
71	d2pgda2	Alignment	not modelled	98.7	11	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
72	c2x4gA	Alignment	not modelled	98.7	20	PDB header: isomerase Chain: A: PDB Molecule: nucleoside-diphosphate-sugar epimerase; PDBTitle: crystal structure of pa4631, a nucleoside-diphosphate-sugar epimerase2 from pseudomonas aeruginosa
73	c4mkzA	Alignment	not modelled	98.7	16	PDB header: oxidoreductase Chain: A: PDB Molecule: inositol dehydrogenase; PDBTitle: crystal structure of apo scyllo-inositol dehydrogenase from2 lactobacillus casei at 77k
74	d1nvta1	Alignment	not modelled	98.7	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
75	c4pvcB	Alignment	not modelled	98.7	22	PDB header: oxidoreductase Chain: B: PDB Molecule: nadph-dependent methylglyoxal reductase gre2; PDBTitle: crystal structure of yeast methylglyoxal/ isovaleraldehyde reductase2 gre2
76	c4nbwA	Alignment	not modelled	98.7	21	PDB header: oxidoreductase Chain: A: PDB Molecule: short-chain dehydrogenase/reductase sdr; PDBTitle: crystal structure of fabg from plesiocystis pacifica
						Fold: NAD(P)-binding Rossmann-fold domains

77	d1qyda_	Alignment	not modelled	98.7	20	Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
78	c2ixaA_	Alignment	not modelled	98.7	15	PDB header: hydrolase Chain: A: PDB Molecule: alpha-n-acetylgalactosaminidase; PDBTitle: a-zyme, n-acetylgalactosaminidase
79	c5I53A_	Alignment	not modelled	98.7	23	PDB header: oxidoreductase Chain: A: PDB Molecule: (-)-menthone:(+)-neomenthol reductase; PDBTitle: menthone neomenthol reductase from mentha piperita in complex with2 nadp
80	c1nvtA_	Alignment	not modelled	98.7	19	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate 5'-dehydrogenase; PDBTitle: crystal structure of shikimate dehydrogenase (aroe or2 mj1084) in complex with nadp+
81	c3qvoA_	Alignment	not modelled	98.7	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: nmra family protein; PDBTitle: structure of a rossmann-fold nad(p)-binding family protein from2 shigella flexneri.
82	c4omuA_	Alignment	not modelled	98.7	13	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate dehydrogenase; PDBTitle: crystal structure of shikimate dehydrogenase (aroe) from pseudomonas2 putida
83	c4dqvA_	Alignment	not modelled	98.7	21	PDB header: ligase Chain: A: PDB Molecule: probable peptide synthetase nrp (peptide synthase); PDBTitle: crystal structure of reductase (r) domain of non-ribosomal peptide2 synthetase from mycobacterium tuberculosis
84	c3o8qB_	Alignment	not modelled	98.7	15	PDB header: oxidoreductase Chain: B: PDB Molecule: shikimate 5-dehydrogenase i alpha; PDBTitle: 1.45 angstrom resolution crystal structure of shikimate 5-2 dehydrogenase (aroe) from vibrio cholerae
85	d1hdoa_	Alignment	not modelled	98.6	25	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
86	c3enkB_	Alignment	not modelled	98.6	18	PDB header: isomerase Chain: B: PDB Molecule: udp-glucose 4-epimerase; PDBTitle: 1.9a crystal structure of udp-glucose 4-epimerase from burkholderia2 pseudomallei
87	c6nbrC_	Alignment	not modelled	98.6	20	PDB header: transferase Chain: C: PDB Molecule: kavalactone reductase 1; PDBTitle: crystal structure of piper methysticum kavalactone reductase 1 in2 complex with nadp
88	c2ozpA_	Alignment	not modelled	98.6	13	PDB header: oxidoreductase Chain: A: PDB Molecule: n-acetyl-gamma-glutamyl-phosphate reductase; PDBTitle: crystal structure of n-acetyl-gamma-glutamyl-phosphate reductase2 (ttha1904) from thermus thermophilus
89	c3wj7B_	Alignment	not modelled	98.6	25	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of gox2253
90	c1lc3A_	Alignment	not modelled	98.6	16	PDB header: oxidoreductase Chain: A: PDB Molecule: biliverdin reductase a; PDBTitle: crystal structure of a biliverdin reductase enzyme-cofactor2 complex
91	c2q1uA_	Alignment	not modelled	98.6	12	PDB header: sugar binding protein Chain: A: PDB Molecule: putative nucleotide sugar epimerase/dehydratase; PDBTitle: crystal structure of the bordetella bronchiseptica enzyme wbmf in2 complex with nad+ and udp
92	c2z1mC_	Alignment	not modelled	98.6	17	PDB header: lyase Chain: C: PDB Molecule: gdp-d-mannose dehydratase; PDBTitle: crystal structure of gdp-d-mannose dehydratase from aquifex aeolicus2 vf5
93	c4r1sB_	Alignment	not modelled	98.6	18	PDB header: oxidoreductase Chain: B: PDB Molecule: cinnamoyl coa reductase; PDBTitle: crystal structure of petunia hybrida cinnamoyl-coa reductase
94	d1wvga1	Alignment	not modelled	98.6	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
95	c3tumA_	Alignment	not modelled	98.6	26	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate dehydrogenase family protein; PDBTitle: 2.15 angstrom resolution crystal structure of a shikimate2 dehydrogenase family protein from pseudomonas putida kt2440 in3 complex with nad+
96	c3l6dB_	Alignment	not modelled	98.6	18	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of putative oxidoreductase from pseudomonas putida2 kt2440
97	c4nbvA_	Alignment	not modelled	98.6	26	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] reductase putative short- PDBTitle: crystal structure of fabg from cupriavidus taiwanensis
98	d1orra_	Alignment	not modelled	98.6	12	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
99	c6ci9D_	Alignment	not modelled	98.6	21	PDB header: oxidoreductase Chain: D: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] reductase; PDBTitle: rmm microcompartment-associated aminopropanol dehydrogenase nadp +2 aminoacetone holo-structure
100	c5b3uB_	Alignment	not modelled	98.6	12	PDB header: transferase Chain: B: PDB Molecule: biliverdin reductase; PDBTitle: crystal structure of biliverdin reductase in complex with nadp+ from2 synechocystis sp. pcc 6803
101	c4yacA_	Alignment	not modelled	98.6	10	PDB header: oxidoreductase Chain: A: PDB Molecule: c alpha-dehydrogenase; PDBTitle: crystal structure of ligo in complex with nadh from sphingobium sp.2 strain syk-6
102	c3mrtA_	Alignment	not modelled	98.6	14	PDB header: oxidoreductase Chain: A: PDB Molecule: homoserine dehydrogenase;

102	c0m1qA_	Alignment	not modelled	98.6	14	PDBTitle: the crystal structure of a homoserine dehydrogenase from thiobacillus2 denitrificans to 2.15a PDB header: oxidoreductase
103	c6aqyD_	Alignment	not modelled	98.6	15	Chain: D: PDB Molecule: gdp-l-fucose synthetase; PDBTitle: crystal structure of a gdp-l-fucose synthetase from naegleria fowleri
104	d1rkxa_	Alignment	not modelled	98.6	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
105	c4w4tA_	Alignment	not modelled	98.6	21	PDB header: oxidoreductase Chain: A: PDB Molecule: mxaA; PDBTitle: the crystal structure of the terminal r domain from the myxalamid pks-2 nrps biosynthetic pathway
106	c3pgjB_	Alignment	not modelled	98.5	14	PDB header: oxidoreductase Chain: B: PDB Molecule: shikimate dehydrogenase; PDBTitle: 2.49 angstrom resolution crystal structure of shikimate 5-2 dehydrogenase (aroe) from vibrio cholerae o1 biovar eltor str. n169613 in complex with shikimate
107	c1p74B_	Alignment	not modelled	98.5	16	PDB header: oxidoreductase Chain: B: PDB Molecule: shikimate 5-dehydrogenase; PDBTitle: crystal structure of shikimate dehydrogenase (aroe) from haemophilus2 influenzae
108	c1h6dL_	Alignment	not modelled	98.5	15	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
109	c3i5mA_	Alignment	not modelled	98.5	17	PDB header: oxidoreductase Chain: A: PDB Molecule: putative leucoanthocyanidin reductase 1; PDBTitle: structure of the apo form of leucoanthocyanidin reductase from vitis2 vinifera
110	c6gcsE_	Alignment	not modelled	98.5	17	PDB header: oxidoreductase Chain: E: PDB Molecule: nuem subunit; PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
111	c2zklA_	Alignment	not modelled	98.5	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
112	c3nt5B_	Alignment	not modelled	98.5	18	PDB header: oxidoreductase Chain: B: PDB Molecule: inositol 2-dehydrogenase/d-chiro-inositol 3-dehydrogenase; PDBTitle: crystal structure of myo-inositol dehydrogenase from bacillus subtilis2 with bound cofactor and product inosose
113	c3pzwA_	Alignment	not modelled	98.5	17	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate dehydrogenase 3; PDBTitle: crystal structure of an ael1 enzyme from pseudomonas putida
114	c5eesA_	Alignment	not modelled	98.5	15	PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate reductase; PDBTitle: crystal structure of dapb in complex with nadp+ from corynebacterium2 glutamicum
115	d1hyea1	Alignment	not modelled	98.5	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
116	c2gasA_	Alignment	not modelled	98.5	14	PDB header: oxidoreductase Chain: A: PDB Molecule: isoflavone reductase; PDBTitle: crystal structure of isoflavone reductase
117	c3donA_	Alignment	not modelled	98.5	18	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate dehydrogenase; PDBTitle: crystal structure of shikimate dehydrogenase from staphylococcus2 epidermidis
118	c2yy7B_	Alignment	not modelled	98.5	13	PDB header: oxidoreductase Chain: B: PDB Molecule: l-threonine dehydrogenase; PDBTitle: crystal structure of thermolabile l-threonine dehydrogenase from2 flavobacterium frigidimaris kuc-1
119	c2pk3B_	Alignment	not modelled	98.5	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
120	c3dqpA_	Alignment	not modelled	98.5	20	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase ylbe; PDBTitle: crystal structure of the oxidoreductase ylbe from lactococcus lactis,2 northeast structural genomics consortium target kr121.