

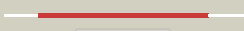
























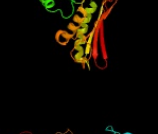
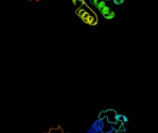
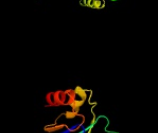
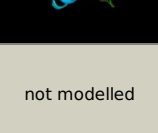


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2449c (-)_2750323_2751582
Date	Wed Aug 7 12:50:07 BST 2019
Unique Job ID	313e6492920d0477

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4rl6A_	 Alignment		100.0	14	PDB header: oxidoreductase Chain: A; PDB Molecule: saccharopine dehydrogenase; PDBTitle: crystal structure of the q04103_strp2 protein from streptococcus2 pneumoniae. northeast structural genomics consortium target spr105
2	c2axqA_	 Alignment		100.0	15	PDB header: oxidoreductase Chain: A; PDB Molecule: saccharopine dehydrogenase; PDBTitle: apo histidine-tagged saccharopine dehydrogenase (l-glu2 forming) from saccharomyces cerevisiae
3	c1e5lA_	 Alignment		100.0	18	PDB header: oxidoreductase Chain: A; PDB Molecule: saccharopine reductase; PDBTitle: apo saccharopine reductase from magnaporthe grisea
4	c5l78A_	 Alignment		100.0	14	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	15	PDB header: oxidoreductase Chain: A; PDB Molecule: saccharopine dehydrogenase; PDBTitle: crystal structure of the q7mss8_wolsu protein from wolinnella2 succinogenes. northeast structural genomics consortium target wsr35
6	c2z2vA_	 Alignment		100.0	13	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	16	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	17	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	16	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		99.4	14	PDB header: oxidoreductase Chain: B: PDB Molecule: meso-diaminopimelate dehydrogenase; PDBTitle: crystal structure of meso-dapdh q154l/t173l/r199m/p248s/h249n/n276s2 mutant with d-leucine of from clostridium tetani e88
13	c3bioB_	Alignment		99.4	14	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	c3dapB_	Alignment		99.4	15	PDB header: oxidoreductase Chain: B: PDB Molecule: diaminopimelic acid dehydrogenase; PDBTitle: c. glutamicum dap dehydrogenase in complex with nadp+ and2 the inhibitor 5s-isoxazoline
15	c3wb9A_	Alignment		99.3	16	PDB header: oxidoreductase Chain: A: PDB Molecule: diaminopimelate dehydrogenase; PDBTitle: crystal structures of meso-diaminopimelate dehydrogenase from2 symbiobacterium thermophilum
16	c4ywjB_	Alignment		99.3	15	PDB header: oxidoreductase Chain: B: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate reductase; PDBTitle: crystal structure of 4-hydroxy-tetrahydrodipicolinate reductase (htpa2 reductase) from pseudomonas aeruginosa
17	c5tenH_	Alignment		99.3	12	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 acid and nadh with intact3 polyhistidine tag
18	c5ugjC_	Alignment		99.3	17	PDB header: oxidoreductase Chain: C: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate reductase; PDBTitle: crystal structure of htpa reductase from neisseria meningitidis
19	c1drwA_	Alignment		99.3	15	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: escherichia coli dhpr/nhdh complex
20	c2zcuA_	Alignment		99.2	22	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
21	c6iaqA_	Alignment	not modelled	99.2	18	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase n-terminus domain-containing PDBTitle: structure of amine dehydrogenase from mycobacterium smegmatis
22	c5kt0A_	Alignment	not modelled	99.1	15	PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate reductase; PDBTitle: dihydrodipicolinate reductase from the industrial and evolutionarily2 important cyanobacteria anabaena variabilis.
23	c1luaA_	Alignment	not modelled	99.1	21	PDB header: oxidoreductase Chain: A: PDB Molecule: methylene tetrahydromethanopterin dehydrogenase; PDBTitle: structure of methylene-tetrahydromethanopterin dehydrogenase from2 methylobacterium extorquens am1 complexed with nadp
24	c4f3yA_	Alignment	not modelled	99.1	14	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: x-ray crystal structure of dihydrodipicolinate reductase from2 burkholderia thailandensis
25	c3w1vA_	Alignment	not modelled	99.1	11	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	c3wycB_	Alignment	not modelled	99.1	16	PDB header: oxidoreductase Chain: B: PDB Molecule: meso-diaminopimelate d-dehydrogenase; PDBTitle: structure of a meso-diaminopimelate dehydrogenase in complex with nadp
27	c2qx7A_	Alignment	not modelled	99.1	13	PDB header: plant protein Chain: A: PDB Molecule: eugenol synthase 1; PDBTitle: structure of eugenol synthase from ocimum basilicum
Fold: NAD(P)-binding Rossmann-fold domains						

28	d1luaa1	Alignment	not modelled	99.1	21	Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
29	c6g1mA	Alignment	not modelled	99.1	10	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: amine dehydrogenase from petrotoga mobilis; open and closed form
30	c1z7eC	Alignment	not modelled	99.0	17	PDB header: hydrolase Chain: C: PDB Molecule: protein arna; PDBTitle: crystal structure of full length arna
31	c3upyB	Alignment	not modelled	99.0	18	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.
32	c3pvzD	Alignment	not modelled	99.0	11	PDB header: lyase Chain: D: PDB Molecule: udp-n-acetylglucosamine 4,6-dehydratase; PDBTitle: udp-n-acetylglucosamine 4,6-dehydratase from vibrio fischeri
33	c4j2oD	Alignment	not modelled	99.0	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
34	c3e48B	Alignment	not modelled	99.0	18	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
35	c2gn9B	Alignment	not modelled	99.0	13	PDB header: lyase Chain: B: PDB Molecule: udp-glcnc c6 dehydratase; PDBTitle: crystal structure of udp-glcnc inverting 4,6-dehydratase in complex2 with nadp and udp-glc
36	c2exxB	Alignment	not modelled	99.0	18	PDB header: unknown function Chain: B: PDB Molecule: hscarg protein; PDBTitle: crystal structure of hscarg from homo sapiens in complex with nadp
37	c5z2fA	Alignment	not modelled	99.0	12	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: nadph/pda bound dihydrodipicolinate reductase from paenisporsarcina2 sp. tg-14
38	c2vrcD	Alignment	not modelled	99.0	26	PDB header: oxidoreductase Chain: D: PDB Molecule: triphenylmethane reductase; PDBTitle: crystal structure of the citrobacter sp. triphenylmethane2 reductase complexed with nadp(h)
39	d2q46a1	Alignment	not modelled	98.9	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
40	d1e5qa2	Alignment	not modelled	98.9	10	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Homoserine dehydrogenase-like
41	c4idgB	Alignment	not modelled	98.9	15	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
42	c4wuvB	Alignment	not modelled	98.9	18	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
43	c5f5nA	Alignment	not modelled	98.9	29	PDB header: oxidoreductase Chain: A: PDB Molecule: monooxygenase; PDBTitle: the structure of monooxygenase ksta11 in complex with nad and its2 substrate
44	c1r0ID	Alignment	not modelled	98.9	20	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
45	c5l3zA	Alignment	not modelled	98.8	24	PDB header: oxidoreductase Chain: A: PDB Molecule: polyketide ketoreductase simc7; PDBTitle: polyketide ketoreductase simc7 - binary complex with nadp+
46	d1vi2a1	Alignment	not modelled	98.8	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
47	c3nzoB	Alignment	not modelled	98.8	10	PDB header: lyase Chain: B: PDB Molecule: udp-n-acetylglucosamine 4,6-dehydratase; PDBTitle: udp-n-acetylglucosamine 4,6-dehydratase from vibrio fischeri.
48	d1mlda1	Alignment	not modelled	98.8	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
49	c2nloA	Alignment	not modelled	98.8	22	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate dehydrogenase; PDBTitle: crystal structure of the quinate dehydrogenase from corynebacterium2 glutamicum
50	d1qyca	Alignment	not modelled	98.8	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
51	d1xgka	Alignment	not modelled	98.8	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
52	d1qyda	Alignment	not modelled	98.8	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains

						Family: Tyrosine-dependent oxidoreductases
53	c3v8bC_	Alignment	not modelled	98.8	25	PDB header: oxidoreductase Chain: C: PDB Molecule: putative dehydrogenase, possibly 3-oxoacyl-lacyl-carrier PDBTitle: crystal structure of a 3-ketoacyl-acyl reductase from sinorhizobium2 meliloti 1021
54	d1f06a1	Alignment	not modelled	98.8	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
55	c2eggA_	Alignment	not modelled	98.8	20	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate 5-dehydrogenase; PDBTitle: crystal structure of shikimate 5-dehydrogenase (aroe) from geobacillus2 kaustophilus
56	c6bwcA_	Alignment	not modelled	98.8	14	PDB header: biosynthetic protein Chain: A: PDB Molecule: polysaccharide biosynthesis protein capd; PDBTitle: x-ray structure of pen from bacillus thuringiensis
57	c3c1oA_	Alignment	not modelled	98.8	13	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
58	c2ixaA_	Alignment	not modelled	98.8	14	PDB header: hydrolase Chain: A: PDB Molecule: alpha-n-acetylgalactosaminidase; PDBTitle: a-zyme, n-acetylgalactosaminidase
59	c3jipA_	Alignment	not modelled	98.7	11	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: crystal structure of dihydrodipicolinate reductase from bartonella2 henselae at 2.0a resolution
60	d1db3a_	Alignment	not modelled	98.7	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
61	c2x4gA_	Alignment	not modelled	98.7	19	PDB header: isomerase Chain: A: PDB Molecule: nucleoside-diphosphate-sugar epimerase; PDBTitle: crystal structure of pa4631, a nucleoside-diphosphate-sugar epimerase2 from pseudomonas aeruginosa
62	c4pvcB_	Alignment	not modelled	98.7	19	PDB header: oxidoreductase Chain: B: PDB Molecule: nadph-dependent methylglyoxal reductase gre2; PDBTitle: crystal structure of yeast methylglyoxal/ isovaleraldehyde reductase2 gre2
63	c4mkzA_	Alignment	not modelled	98.7	14	PDB header: oxidoreductase Chain: A: PDB Molecule: inositol dehydrogenase; PDBTitle: crystal structure of apo scyllo-inositol dehydrogenase from2 lactobacillus casei at 77k
64	c5swvC_	Alignment	not modelled	98.7	18	PDB header: lyase Chain: C: PDB Molecule: pentafunctional arom polypeptide; PDBTitle: dehydroquinate dehydratase and shikimate dehydrogenase from s. pombe2 arom
65	d1diha1	Alignment	not modelled	98.7	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
66	c4nbwA_	Alignment	not modelled	98.7	24	PDB header: oxidoreductase Chain: A: PDB Molecule: short-chain dehydrogenase/reductase sdr; PDBTitle: crystal structure of fabg from plesiocystis pacifica
67	d2pgda2	Alignment	not modelled	98.7	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
68	c6nbrC_	Alignment	not modelled	98.7	18	PDB header: transferase Chain: C: PDB Molecule: kavalactone reductase 1; PDBTitle: crystal structure of piper methysticum kavalactone reductase 1 in2 complex with nadp
69	c5I53A_	Alignment	not modelled	98.7	27	PDB header: oxidoreductase Chain: A: PDB Molecule: (-)-menthone:(+)-neomenthol reductase; PDBTitle: menthone neomenthol reductase from mentha piperita in complex with2 nadp
70	c4xijA_	Alignment	not modelled	98.7	15	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
71	c2eghA_	Alignment	not modelled	98.7	18	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
72	c2ozpA_	Alignment	not modelled	98.7	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
73	d2q49a1	Alignment	not modelled	98.7	10	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
74	c3a14B_	Alignment	not modelled	98.7	18	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
75	d1orra_	Alignment	not modelled	98.7	11	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
76	d1hyea1	Alignment	not modelled	98.7	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
77	c1lc3A_	Alignment	not modelled	98.7	14	PDB header: oxidoreductase Chain: A: PDB Molecule: biliverdin reductase a;

77	c1t3A	Alignment	not modelled	98.7	14	PDBTitle: crystal structure of a biliverdin reductase enzyme-cofactor2 complex 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 PDB header: protein translocation
78	c4dqvA	Alignment	not modelled	98.7	23	Chain: L: PDB Molecule: precursor form of glucose-fructose oxidoreductase2 from zymomonas mobilis complexed with glycerol PDB header: oxidoreductase
79	c1h6dL	Alignment	not modelled	98.7	13	Chain: A: PDB Molecule: shikimate dehydrogenase; PDBTitle: 2.2 angstrom crystal structure of shikimate 5-dehydrogenase from2 listeria monocytogenes in complex with nad.
80	c3tozA	Alignment	not modelled	98.6	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
81	d1pjca1	Alignment	not modelled	98.6	20	PDB header: oxidoreductase Chain: F: PDB Molecule: glucose-fructose oxidoreductase; PDBTitle: glucose-fructose oxidoreductase
82	c1ofgF	Alignment	not modelled	98.6	13	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
83	c4yacA	Alignment	not modelled	98.6	10	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
84	c1z45A	Alignment	not modelled	98.6	18	PDB header: oxidoreductase Chain: A: PDB Molecule: myo-inositol 2-dehydrogenase; PDBTitle: crystal structure of myo-inositol 2-dehydrogenase (np_786804.1) from2 lactobacillus plantarum at 2.40 a resolution
85	c3ceaA	Alignment	not modelled	98.6	15	PDB header: oxidoreductase Chain: A: PDB Molecule: probable dehydrogenase; PDBTitle: the crystal structure of the putative dehydrogenase from bordetella2 bronchiseptica rb50
86	c3moiA	Alignment	not modelled	98.6	17	PDB header: isomerase Chain: A: PDB Molecule: capsular polysaccharide synthesis enzyme cap5f; PDBTitle: crystal structure of capsular polysaccharide assembling protein capf2 from staphylococcus aureus
87	c2zkIA	Alignment	not modelled	98.6	21	PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate reductase; PDBTitle: crystal structure of dihydrodipicolinate reductase dapb from coxiella2 burnetii
88	c5woIA	Alignment	not modelled	98.6	17	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of gox2253
89	c3wj7B	Alignment	not modelled	98.6	32	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
90	d2c5aa1	Alignment	not modelled	98.6	16	PDB header: oxidoreductase Chain: B: PDB Molecule: shikimate dehydrogenase; PDBTitle: crystal structure of shikimate dehydrogenase from aquifex2 aeolicus at 2.35 angstrom resolution
91	c2hk8B	Alignment	not modelled	98.6	19	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.
92	c3qvoA	Alignment	not modelled	98.6	15	PDB header: lyase Chain: A: PDB Molecule: pal; PDBTitle: x-ray structure of pal from bacillus thuringiensis
93	c6bwIA	Alignment	not modelled	98.6	10	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
94	d1gega	Alignment	not modelled	98.6	24	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
95	c4w4tA	Alignment	not modelled	98.6	22	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
96	c2pk3B	Alignment	not modelled	98.6	17	PDB header: oxidoreductase Chain: G: PDB Molecule: short chain dehydrogenase; PDBTitle: crystal structure of a short chain dehydrogenase in complex with2 nad(p) from sinorhizobium meliloti 1021
97	c3toxG	Alignment	not modelled	98.6	14	PDB header: lyase Chain: C: PDB Molecule: gdp-d-mannose dehydratase; PDBTitle: crystal structure of gdp-d-mannose dehydratase from aquifex aeolicus2 vf5
98	c2z1mC	Alignment	not modelled	98.6	18	PDB header: oxidoreductase Chain: A: PDB Molecule: polyketide synthase pksj; PDBTitle: crystal structure of a ketoreductase domain from the bacillaene2 assembly line
99	c4jlSA	Alignment	not modelled	98.6	24	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	c6ci9D	Alignment	not modelled	98.6	15	PDB header: oxidoreductase Chain: B: PDB Molecule: shikimate 5-dehydrogenase 2; PDBTitle: crystal structure of shikimate-5-dehydrogenase with nad
101	c1vi2B	Alignment	not modelled	98.6	16	PDB header: oxidoreductase Chain: A: PDB Molecule: mlne; PDBTitle: crystal structure of an n-terminal ketoreductase from
102	c5d2eA	Alignment	not modelled	98.6	16	

						macrolactin2 assembly line
103	c3oh8A_	Alignment	not modelled	98.6	17	PDB header: isomerase Chain: A: PDB Molecule: nucleoside-diphosphate sugar epimerase (sula family); PDBTitle: crystal structure of the nucleoside-diphosphate sugar epimerase from2 corynebacterium glutamicum. northeast structural genomics consortium3 target cgr91
104	c3mtjA_	Alignment	not modelled	98.6	17	PDB header: oxidoreductase Chain: A: PDB Molecule: homoserine dehydrogenase; PDBTitle: the crystal structure of a homoserine dehydrogenase from thiobacillus2 denitrificans to 2.15a
105	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
106	c6aqyD_	Alignment	not modelled	98.6	12	PDB header: oxidoreductase Chain: D: PDB Molecule: gdp-l-fucose synthetase; PDBTitle: crystal structure of a gdp-l-fucose synthetase from naegleria fowleri
107	c1gpiA_	Alignment	not modelled	98.6	25	PDB header: reductase Chain: A: PDB Molecule: glutamyl-trna reductase; PDBTitle: glutamyl-trna reductase from methanopyrus kandleri
108	c3nt5B_	Alignment	not modelled	98.6	16	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
109	c2hunB_	Alignment	not modelled	98.6	12	PDB header: lyase Chain: B: PDB Molecule: 336aa long hypothetical dtdp-glucose 4,6-dehydratase; PDBTitle: crystal structure of hypothetical protein ph0414 from pyrococcus2 horikoshii ot3
110	d1nvtA1	Alignment	not modelled	98.6	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
111	c2nvwB_	Alignment	not modelled	98.6	14	PDB header: transcription Chain: B: PDB Molecule: galactose/lactose metabolism regulatory protein PDBTitle: crystal sctucture of transcriptional regulator gal80p from2 kluveromyces lactis
112	c2q1wC_	Alignment	not modelled	98.6	14	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+
113	c5ig2B_	Alignment	not modelled	98.6	20	PDB header: oxidoreductase Chain: B: PDB Molecule: short-chain dehydrogenase/reductase sdr; PDBTitle: crystal structure of a short chain dehydrogenase/reductase sdr from2 burkholderia phymatum in complex with nad
114	c3i5mA_	Alignment	not modelled	98.6	19	PDB header: oxidoreductase Chain: A: PDB Molecule: putative leucoanthocyanidin reductase 1; PDBTitle: structure of the apo form of leucoanthocyanidin reductase from vitis2 vinifera
115	c3e18A_	Alignment	not modelled	98.6	10	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of nad-binding protein from listeria innocua
116	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
117	c5k9zB_	Alignment	not modelled	98.5	20	PDB header: oxidoreductase Chain: B: PDB Molecule: putative short-chain dehydrogenase/reductase; PDBTitle: crystal structure of putative short-chain dehydrogenase/reductase from2 burkholderia xenovorans lb400
118	c2yy7B_	Alignment	not modelled	98.5	12	PDB header: oxidoreductase Chain: B: PDB Molecule: l-threonine dehydrogenase; PDBTitle: crystal structure of thermolabile l-threonine dehydrogenase from2 flavobacterium frigidimaris kuc-1
119	c3dqpA_	Alignment	not modelled	98.5	21	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.
120	c4pivB_	Alignment	not modelled	98.5	19	PDB header: transferase/transferase inhibitor Chain: B: PDB Molecule: fatty acid synthase; PDBTitle: human fatty acid synthase psi/kr tri-domain with nadph and gsk2194069