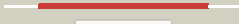



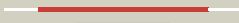



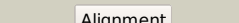
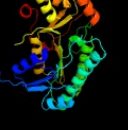
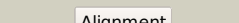

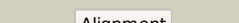











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2216 (-)_2483634_2484539
Date	Mon Aug 5 13:25:34 BST 2019
Unique Job ID	a023d9c534a89f13

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4b4oA_	 Alignment		100.0	32	PDB header: isomerase Chain: A: PDB Molecule: epimerase family protein sdr39u1; PDBTitle: crystal structure of human epimerase family protein sdr39u1 (isoform2)2 with nadph
2	c1z45A_	 Alignment		100.0	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
3	c1z7eC_	 Alignment		100.0	16	PDB header: hydrolase Chain: C: PDB Molecule: protein arna; PDBTitle: crystal structure of full length arna
4	c3oh8A_	 Alignment		100.0	36	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
5	d1i24a_	 Alignment		100.0	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
6	c5df1A_	 Alignment		100.0	12	PDB header: oxidoreductase Chain: A: PDB Molecule: iridoid synthase; PDBTitle: iridoid synthase from catharanthus roseus - ternary complex with nadp+2 and geranic acid
7	c2v6gA_	 Alignment		100.0	13	PDB header: oxidoreductase Chain: A: PDB Molecule: progesterone 5-beta-reductase; PDBTitle: structure of progesterone 5beta-reductase from digitalis2 lanata in complex with nadp
8	c4j2oD_	 Alignment		100.0	13	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
9	c3pvzD_	 Alignment		100.0	12	PDB header: lyase Chain: D: PDB Molecule: udp-n-acetylglucosamine 4,6-dehydratase; PDBTitle: udp-n-acetylglucosamine 4,6-dehydratase from vibrio fischeri
10	c6dntA_	 Alignment		100.0	15	PDB header: sugar binding protein Chain: A: PDB Molecule: nad-dependent epimerase/dehydratase; PDBTitle: udp-n-acetylglucosamine 4-epimerase from methanobrevibacter2 ruminantium m1 in complex with udp-n-acetylmuramic acid
11	c2x4gA_	 Alignment		100.0	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

12	d1e6ua_	Alignment		100.0	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
13	c6d2vA_	Alignment		100.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: terb oxidoreductase; PDBTitle: apo structure of terb, an nadp dependent oxidoreductase in the2 terfestatin biosynthesis pathway
14	c5u9cC_	Alignment		100.0	14	PDB header: hydrolase,oxidoreductase Chain: C: PDB Molecule: dtdp-4-dehydrorhamnose reductase; PDBTitle: 1.9 angstrom resolution crystal structure of dtdp-4-dehydrorhamnose2 reductase from yersinia enterocolitica
15	c3enkB_	Alignment		100.0	17	PDB header: isomerase Chain: B: PDB Molecule: udp-glucose 4-epimerase; PDBTitle: 1.9a crystal structure of udp-glucose 4-epimerase from burkholderia2 pseudomallei
16	c2z1mC_	Alignment		100.0	12	PDB header: lyase Chain: C: PDB Molecule: gdp-d-mannose dehydratase; PDBTitle: crystal structure of gdp-d-mannose dehydratase from aquifex aeolicus2 vf5
17	c4r1sB_	Alignment		100.0	14	PDB header: oxidoreductase Chain: B: PDB Molecule: cinnamoyl coa reductase; PDBTitle: crystal structure of petunia hydrida cinnamoyl-coa reductase
18	c3iusB_	Alignment		100.0	17	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized conserved protein; PDBTitle: the structure of a functionally unknown conserved protein2 from silicibacter pomeroyi dss
19	d1oc2a_	Alignment		100.0	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
20	c5gmoA_	Alignment		100.0	12	PDB header: oxidoreductase Chain: A: PDB Molecule: protein induced by osmotic stress; PDBTitle: x-ray structure of carbonyl reductase sscr
21	c3w1vA_	Alignment	not modelled	100.0	16	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
22	d1db3a_	Alignment	not modelled	100.0	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
23	c2b69A_	Alignment	not modelled	100.0	18	PDB header: lyase Chain: A: PDB Molecule: udp-glucuronate decarboxylase 1; PDBTitle: crystal structure of human udp-glucuronic acid decarboxylase
24	d2b69a1	Alignment	not modelled	100.0	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
25	c1n7gB_	Alignment	not modelled	100.0	14	PDB header: lyase Chain: B: PDB Molecule: gdp-d-mannose-4,6-dehydratase; PDBTitle: crystal structure of the gdp-mannose 4,6-dehydratase2 ternary complex with nadph and gdp-rhamnose.
26	c4wpgA_	Alignment	not modelled	100.0	12	PDB header: oxidoreductase Chain: A: PDB Molecule: dtdp-4-dehydrorhamnose reductase; PDBTitle: group a streptococcus gaca is an essential dtdp-4-dehydrorhamnose2 reductase (rmlD)
27	c2hunB_	Alignment	not modelled	100.0	14	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
28	c2c20D_	Alignment	not modelled	100.0	16	PDB header: isomerase Chain: D: PDB Molecule: udp-glucose 4-epimerase; PDBTitle: crystal structure of udp-glucose 4-epimerase

29	c6nbrC_	Alignment	not modelled	100.0	11	PDB header: transferase Chain: C: PDB Molecule: kavalactone reductase 1; PDBTitle: crystal structure of piper methysticum kavalactone reductase 1 in2 complex with nadp
30	c6el3A_	Alignment	not modelled	100.0	12	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-oxo-delta(4,5)-steroid 5-beta-reductase; PDBTitle: structure of progesterone 5beta-reductase from arabidopsis thaliana in2 complex with nadp
31	c2hrzA_	Alignment	not modelled	100.0	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: nucleoside-diphosphate-sugar epimerase; PDBTitle: the crystal structure of the nucleoside-diphosphate-sugar epimerase2 from agrobacterium tumefaciens
32	c5msuC_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: C: PDB Molecule: carboxylic acid reductase; PDBTitle: structure of the r domain of carboxylic acid reductase (car) from2 mycobacterium marinum in complex with nadp, p21 form
33	c3sc6F_	Alignment	not modelled	100.0	12	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
34	c5bjuA_	Alignment	not modelled	100.0	16	PDB header: membrane protein Chain: A: PDB Molecule: wlal protein; PDBTitle: x-ray struture of the pglf dehydratase from campylobacter jejuni in2 complex with udp and nad(h)
35	d1ek6a_	Alignment	not modelled	100.0	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
36	c4w4tA_	Alignment	not modelled	100.0	17	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
37	c6aqyD_	Alignment	not modelled	100.0	13	PDB header: oxidoreductase Chain: D: PDB Molecule: gdp-l-fucose synthetase; PDBTitle: crystal structure of a gdp-l-fucose synthetase from naegleria fowleri
38	c5l9aB_	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: B: PDB Molecule: l-threonine 3-dehydrogenase; PDBTitle: l-threonine dehydrogenase from trypanosoma brucei.
39	c2p4hX_	Alignment	not modelled	100.0	16	PDB header: plant protein Chain: X: PDB Molecule: vestitone reductase; PDBTitle: crystal structure of vestitone reductase from alfalfa2 (medicago sativa l.)
40	c3gpiA_	Alignment	not modelled	100.0	17	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
41	d1z45a2	Alignment	not modelled	100.0	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
42	d2c5aa1	Alignment	not modelled	100.0	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
43	d1t2aa_	Alignment	not modelled	100.0	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
44	c2gn9B_	Alignment	not modelled	100.0	13	PDB header: lyase Chain: B: PDB Molecule: udp-glcnaC 6 dehydratase; PDBTitle: crystal structure of udp-glcnaC inverting 4,6-dehydratase in complex2 with nadp and udp-glc
45	d1n7ha_	Alignment	not modelled	100.0	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
46	d1y1pa1	Alignment	not modelled	100.0	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
47	c2yy7B_	Alignment	not modelled	100.0	13	PDB header: oxidoreductase Chain: B: PDB Molecule: l-threonine dehydrogenase; PDBTitle: crystal structure of thermolabile l-threonine dehydrogenase from2 flavobacterium frigidimaris kuc-1
48	c3wj7B_	Alignment	not modelled	100.0	14	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of gox2253
49	c4lisA_	Alignment	not modelled	100.0	19	PDB header: isomerase Chain: A: PDB Molecule: udp-glucose 4-epimerase; PDBTitle: crystal structure of udp-galactose-4-epimerase from aspergillus2 nidulans
50	c4eqbC_	Alignment	not modelled	100.0	14	PDB header: lyase Chain: C: PDB Molecule: dtdp-glucose 4,6-dehydratase; PDBTitle: 3.0 angstrom resolution crystal structure of dtdp-glucose 4,6-2 dehydratase (rfbb) from bacillus anthracis str. ames in complex with3 nad
51	c1t2aC_	Alignment	not modelled	100.0	13	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
52	c4idgB_	Alignment	not modelled	100.0	19	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
53	c4twrA_	Alignment	not modelled	100.0	18	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

54	d1rkxa_	Alignment	not modelled	100.0	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
55	c6bwcA_	Alignment	not modelled	100.0	14	PDB header: biosynthetic protein Chain: A: PDB Molecule: polysaccharide biosynthesis protein capd; PDBTitle: x-ray structure of pen from bacillus thuringiensis
56	c2iodD_	Alignment	not modelled	100.0	14	PDB header: oxidoreductase Chain: D: PDB Molecule: dihydroflavonol 4-reductase; PDBTitle: binding of two substrate analogue molecules to2 dihydroflavonol-4-reductase alters the functional geometry3 of the catalytic site
57	c3m2pD_	Alignment	not modelled	100.0	13	PDB header: isomerase Chain: D: PDB Molecule: udp-n-acetylglucosamine 4-epimerase; PDBTitle: the crystal structure of udp-n-acetylglucosamine 4-epimerase2 from bacillus cereus
58	c5uzhA_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: A: PDB Molecule: nafoa.00085.b; PDBTitle: crystal structure of a gdp-mannose dehydratase from naegleria fowleri
59	c3eheB_	Alignment	not modelled	100.0	16	PDB header: isomerase Chain: B: PDB Molecule: udp-glucose 4-epimerase (gale-1); PDBTitle: crystal structure of udp-glucose 4 epimerase (gale-1) from2 archaeoglobus fulgidus
60	c4ej0D_	Alignment	not modelled	100.0	16	PDB header: isomerase Chain: D: PDB Molecule: adp-l-glycero-d-manno-heptose-6-epimerase; PDBTitle: crystal structure of adp-l-glycero-d-manno-heptose-6-epimerase from2 burkholderia thailandensis
61	c4lw8B_	Alignment	not modelled	100.0	15	PDB header: isomerase Chain: B: PDB Molecule: putative epimerase; PDBTitle: crystal structure of a putative epimerase from burkholderia2 cenocepacia j2315
62	c3lu1C_	Alignment	not modelled	100.0	14	PDB header: isomerase Chain: C: PDB Molecule: wbgu; PDBTitle: crystal structure analysis of wbgu: a udp-galnac 4-epimerase
63	d1wvga1	Alignment	not modelled	100.0	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
64	d1rpna_	Alignment	not modelled	100.0	12	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
65	d1vl0a_	Alignment	not modelled	100.0	12	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
66	c5lnkd_	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: D: PDB Molecule: PDBTitle: entire ovine respiratory complex i
67	d1n2sa_	Alignment	not modelled	100.0	12	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
68	c4pvcB_	Alignment	not modelled	100.0	13	PDB header: oxidoreductase Chain: B: PDB Molecule: nadph-dependent methylglyoxal reductase gre2; PDBTitle: crystal structure of yeast methylglyoxal/ isovaleraldehyde reductase2 gre2
69	c2pk3B_	Alignment	not modelled	100.0	12	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
70	d1r6da_	Alignment	not modelled	100.0	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
71	c6bw1A_	Alignment	not modelled	100.0	12	PDB header: lyase Chain: A: PDB Molecule: pal; PDBTitle: x-ray structure of pal from bacillus thuringiensis
72	c5zedA_	Alignment	not modelled	100.0	10	PDB header: isomerase Chain: A: PDB Molecule: uncharacterized protein adh; PDBTitle: crystal structure of kluyveromyces polyspora adh (kpadh) mutant2 (e214v/t215s)
73	d1kewa_	Alignment	not modelled	100.0	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
74	c3wmxC_	Alignment	not modelled	100.0	14	PDB header: oxidoreductase Chain: C: PDB Molecule: nad dependent epimerase/dehydratase; PDBTitle: gale-like l-threonine dehydrogenase from cupriavidus necator (holo2 form)
75	c4zrmB_	Alignment	not modelled	100.0	15	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
76	c2p5uC_	Alignment	not modelled	100.0	19	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
77	c2q1uA_	Alignment	not modelled	100.0	16	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
78	c2pzb_	Alignment	not modelled	100.0	14	PDB header: sugar binding protein Chain: B: PDB Molecule: putative nucleotide sugar epimerase/dehydratase; PDBTitle: crystal structure of the bordetella bronchiseptica enzyme wbmj in2 complex with nad and udp PDB header: oxidoreductase

79	c4f6cA_	Alignment	not modelled	100.0	12	Chain: A: PDB Molecule: ausa reductase domain protein; PDBTitle: crystal structure of aureusimine biosynthetic cluster reductase domain
80	c2q1wC_	Alignment	not modelled	100.0	17	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+
81	d1bxka_	Alignment	not modelled	100.0	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
82	c2ydyA_	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: methionine adenosyltransferase 2 subunit beta; PDBTitle: crystal structure of human s-adenosylmethionine synthetase 2, beta2 subunit in orthorhombic crystal form
83	c5b6kA_	Alignment	not modelled	100.0	13	PDB header: oxidoreductase Chain: A: PDB Molecule: uncharacterized protein cgkr1; PDBTitle: crystal structure of ketoreductase 1 from candida glabrata
84	c4dqvA_	Alignment	not modelled	100.0	17	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
85	c4qukA_	Alignment	not modelled	100.0	13	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydroflavonol-4-reductase; PDBTitle: crystal structure of cinnamyl-alcohol dehydrogenase 2 mutant k169a
86	c3a1nB_	Alignment	not modelled	100.0	11	PDB header: oxidoreductase Chain: B: PDB Molecule: ndp-sugar epimerase; PDBTitle: crystal structure of l-threonine dehydrogenase from hyperthermophilic2 archaeon thermoplasma volcanium
87	d1gy8a_	Alignment	not modelled	100.0	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
88	c2rh8A_	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: anthocyanidin reductase; PDBTitle: structure of apo anthocyanidin reductase from vitis vinifera
89	d1sb8a_	Alignment	not modelled	100.0	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
90	c2qx7A_	Alignment	not modelled	100.0	16	PDB header: plant protein Chain: A: PDB Molecule: eugenol synthase 1; PDBTitle: structure of eugenol synthase from ocimum basilicum
91	c4qqrB_	Alignment	not modelled	100.0	14	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
92	c4b8wB_	Alignment	not modelled	100.0	13	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
93	c5u4qB_	Alignment	not modelled	100.0	16	PDB header: lipid-binding protein Chain: B: PDB Molecule: dtdp-glucose 4,6-dehydratase; PDBTitle: 1.5 angstrom resolution crystal structure of nad-dependent epimerase2 from klebsiella pneumoniae in complex with nad.
94	c2ggsB_	Alignment	not modelled	100.0	12	PDB header: oxidoreductase Chain: B: PDB Molecule: 273aa long hypothetical dtdp-4-dehydrorhamnose PDBTitle: crystal structure of hypothetical dtdp-4-dehydrorhamnose2 reductase from sulfolobus tokodaii
95	c3sxpD_	Alignment	not modelled	100.0	14	PDB header: isomerase Chain: D: PDB Molecule: adp-l-glycero-d-mannoheptose-6-epimerase; PDBTitle: crystal structure of helicobacter pylori adp-l-glycero-d-manno-2 heptose-6-epimerase (rfad, hp0859)
96	c2zklA_	Alignment	not modelled	100.0	18	PDB header: isomerase Chain: A: PDB Molecule: capsular polysaccharide synthesis enzyme cap5f; PDBTitle: crystal structure of capsular polysaccharide assembling protein capf2 from staphylococcus aureus
97	c3slgB_	Alignment	not modelled	100.0	12	PDB header: transferase Chain: B: PDB Molecule: pbgp3 protein; PDBTitle: crystal structure of pbgp3 protein from burkholderia pseudomallei
98	d2blla1	Alignment	not modelled	100.0	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
99	c3icpA_	Alignment	not modelled	100.0	15	PDB header: isomerase Chain: A: PDB Molecule: nad-dependent epimerase/dehydratase; PDBTitle: crystal structure of udp-galactose 4-epimerase
100	d1udca_	Alignment	not modelled	100.0	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
101	d1orra_	Alignment	not modelled	100.0	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
102	c3slgF_	Alignment	not modelled	100.0	13	PDB header: transferase Chain: F: PDB Molecule: pbgp3 protein; PDBTitle: crystal structure of pbgp3 protein from burkholderia pseudomallei
103	c6gcsE_	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: E: PDB Molecule: nuem subunit; PDBTitle: cryo-em structure of respiratory complex i from yarrowia

					lipolytica
104	c3vpsB_	Alignment	not modelled	100.0	17 PDB header: transferase Chain: B: PDB Molecule: nad-dependent epimerase/dehydratase; PDBTitle: structure of a novel nad dependent-ndp-hexosamine 5,6-dehydratase,2 tuna, involved in tunicamycin biosynthesis
105	d1qyda_	Alignment	not modelled	100.0	14 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
106	c3c1oA_	Alignment	not modelled	100.0	12 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	c4lk3A_	Alignment	not modelled	100.0	19 PDB header: lyase Chain: A: PDB Molecule: udp-glucuronic acid decarboxylase 1; PDBTitle: crystal structure of human udp-xylose synthase r236a substitution
108	c4yraD_	Alignment	not modelled	100.0	13 PDB header: oxidoreductase Chain: D: PDB Molecule: l-threonine 3-dehydrogenase, mitochondrial; PDBTitle: mouse tdh in the apo form
109	c5y1dB_	Alignment	not modelled	100.0	12 PDB header: oxidoreductase Chain: B: PDB Molecule: nad dependent epimerase/dehydratase family; PDBTitle: monomeric l-threonine 3-dehydrogenase from metagenome database (apo2 form)
110	c5z76D_	Alignment	not modelled	100.0	13 PDB header: oxidoreductase Chain: D: PDB Molecule: artificial l-threonine 3-dehydrogenase; PDBTitle: artificial l-threonine 3-dehydrogenase designed by full consensus2 design
111	d1eq2a_	Alignment	not modelled	100.0	16 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
112	d1xgka_	Alignment	not modelled	100.0	16 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
113	c2exxB_	Alignment	not modelled	100.0	13 PDB header: unknown function Chain: B: PDB Molecule: hscarg protein; PDBTitle: crystal structure of hscarg from homo sapiens in complex with nadp
114	c2x86K_	Alignment	not modelled	100.0	15 PDB header: isomerase Chain: K: PDB Molecule: adp-l-glycero-d-manno-heptose-6-epimerase; PDBTitle: agme bound to adp-b-mannose
115	c3i5mA_	Alignment	not modelled	100.0	17 PDB header: oxidoreductase Chain: A: PDB Molecule: putative leucoanthocyanidin reductase 1; PDBTitle: structure of the apo form of leucoanthocyanidin reductase from vitis2 vinifera
116	c3e48B_	Alignment	not modelled	100.0	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
117	d1qyca_	Alignment	not modelled	100.0	16 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
118	c5f5nA_	Alignment	not modelled	100.0	20 PDB header: oxidoreductase Chain: A: PDB Molecule: monooxygenase; PDBTitle: the structure of monooxygenase ksta11 in complex with nad and its2 substrate
119	c2gasA_	Alignment	not modelled	100.0	16 PDB header: oxidoreductase Chain: A: PDB Molecule: isoflavone reductase; PDBTitle: crystal structure of isoflavone reductase
120	c4tqgA_	Alignment	not modelled	100.0	13 PDB header: sugar binding protein Chain: A: PDB Molecule: putative dtdp-d-glucose 4 6-dehydratase; PDBTitle: crystal structure of megavirus udp-glcnac 4,6-dehydratase, 5-epimerase2 mg534