



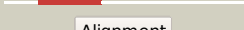








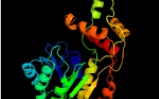


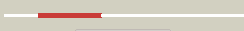







Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2047c (-) _2291970_2294534
Date	Mon Aug 5 13:25:15 BST 2019
Unique Job ID	11fe482a6a6a3b26

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5fbtA_	 Alignment		100.0	19	PDB header: transferase/antibiotic Chain: A: PDB Molecule: phosphoenolpyruvate synthase; PDBTitle: crystal structure of rifampin phosphotransferase rph-lm from listeria2 monocytogenes in complex with rifampin
2	c1z45A_	 Alignment		100.0	21	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	d1i24a_	 Alignment		100.0	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
5	c3oh8A_	 Alignment		100.0	22	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
6	c5df1A_	 Alignment		100.0	19	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	20	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	c6bw1A_	 Alignment		100.0	19	PDB header: lyase Chain: A: PDB Molecule: pal; PDBTitle: x-ray structure of pal from bacillus thuringiensis
9	d2c5aa1	 Alignment		100.0	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
10	c6nbrC_	 Alignment		100.0	20	PDB header: transferase Chain: C: PDB Molecule: kavalactone reductase 1; PDBTitle: crystal structure of piper methysticum kavalactone reductase 1 in2 complex with nadp
11	c3w1vA_	 Alignment		100.0	19	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

12	c5l9aB_	Alignment		100.0	16	PDB header: oxidoreductase Chain: B: PDB Molecule: l-threonine 3-dehydrogenase; PDBTitle: l-threonine dehydrogenase from trypanosoma brucei.
13	d1oc2a_	Alignment		100.0	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
14	d1kewa_	Alignment		100.0	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
15	c4idgB_	Alignment		100.0	23	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
16	c4pvcB_	Alignment		100.0	19	PDB header: oxidoreductase Chain: B: PDB Molecule: nadh-dependent methylglyoxal reductase gre2; PDBTitle: crystal structure of yeast methylglyoxal/ isovaleraldehyde reductase2 gre2
17	c2x4gA_	Alignment		100.0	22	PDB header: isomerase Chain: A: PDB Molecule: nucleoside-diphosphate-sugar epimerase; PDBTitle: crystal structure of pa4631, a nucleoside-diphosphate-sugar epimerase2 from pseudomonas aeruginosa
18	c6el3A_	Alignment		100.0	19	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
19	c3pvzD_	Alignment		100.0	14	PDB header: lyase Chain: D: PDB Molecule: udp-n-acetylglucosamine 4,6-dehydratase; PDBTitle: udp-n-acetylglucosamine 4,6-dehydratase from vibrio fischeri
20	c3m2pD_	Alignment		100.0	21	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
21	d2blla1	Alignment	not modelled	100.0	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
22	c2pk3B_	Alignment	not modelled	100.0	19	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
23	c4j2oD_	Alignment	not modelled	100.0	22	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
24	c1n7gB_	Alignment	not modelled	100.0	15	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.
25	d1e6ua_	Alignment	not modelled	100.0	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
26	c4eqbC_	Alignment	not modelled	100.0	15	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
27	c4zrmB_	Alignment	not modelled	100.0	22	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
28	d1vl0a_	Alignment	not modelled	99.9	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases

29	d1db3a_	Alignment	not modelled	99.9	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
30	d1n2sa_	Alignment	not modelled	99.9	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
31	d1rkxa_	Alignment	not modelled	99.9	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
32	d1r6da_	Alignment	not modelled	99.9	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
33	c3wmxC_	Alignment	not modelled	99.9	18	PDB header: oxidoreductase Chain: C: PDB Molecule: nad dependent epimerase/dehydratase; PDBTitle: gale-like l-threonine dehydrogenase from cupriavidus necator (holo2 form)
34	d1bxka_	Alignment	not modelled	99.9	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
35	c3a1nB_	Alignment	not modelled	99.9	18	PDB header: oxidoreductase Chain: B: PDB Molecule: ndp-sugar epimerase; PDBTitle: crystal structure of l-threonine dehydrogenase from hyperthermophilic2 archaeon thermoplasma volcanium
36	c2z1mC_	Alignment	not modelled	99.9	14	PDB header: lyase Chain: C: PDB Molecule: gdp-d-mannose dehydratase; PDBTitle: crystal structure of gdp-d-mannose dehydratase from aquifex aeolicus2 vf5
37	c2pzlB_	Alignment	not modelled	99.9	21	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
38	c4b8wB_	Alignment	not modelled	99.9	21	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
39	d1wvga1	Alignment	not modelled	99.9	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
40	c5zedA_	Alignment	not modelled	99.9	19	PDB header: isomerase Chain: A: PDB Molecule: uncharacterized protein adh; PDBTitle: crystal structure of kluyveromyces polyspora adh (kpadh) mutant2 (e214v/t215s)
41	c2hunB_	Alignment	not modelled	99.9	16	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
42	c4ej0D_	Alignment	not modelled	99.9	19	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
43	c6aqyD_	Alignment	not modelled	99.9	16	PDB header: oxidoreductase Chain: D: PDB Molecule: gdp-l-fucose synthetase; PDBTitle: crystal structure of a gdp-l-fucose synthetase from naegleria fowleri
44	c2b69A_	Alignment	not modelled	99.9	23	PDB header: lyase Chain: A: PDB Molecule: udp-glucuronate decarboxylase 1; PDBTitle: crystal structure of human udp-glucuronic acid decarboxylase
45	d2b69a1	Alignment	not modelled	99.9	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
46	c2iodD_	Alignment	not modelled	99.9	20	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
47	d1n7ha_	Alignment	not modelled	99.9	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
48	c2q1wC_	Alignment	not modelled	99.9	24	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+
49	c2yy7B_	Alignment	not modelled	99.9	16	PDB header: oxidoreductase Chain: B: PDB Molecule: l-threonine dehydrogenase; PDBTitle: crystal structure of thermolabile l-threonine dehydrogenase from2 flavobacterium frigidimaris kuc-1
50	c3enkB_	Alignment	not modelled	99.9	20	PDB header: isomerase Chain: B: PDB Molecule: udp-glucose 4-epimerase; PDBTitle: 1.9a crystal structure of udp-glucose 4-epimerase from burkholderia2 pseudomallei
51	c2zklA_	Alignment	not modelled	99.9	24	PDB header: isomerase Chain: A: PDB Molecule: capsular polysaccharide synthesis enzyme cap5f; PDBTitle: crystal structure of capsular polysaccharide assembling protein capf2 from staphylococcus aureus
52	c2p5uC_	Alignment	not modelled	99.9	24	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
53	c4b4oA_	Alignment	not modelled	99.9	20	PDB header: isomerase Chain: A: PDB Molecule: epimerase family protein sdr39u1; PDBTitle: crystal structure of human epimerase family protein

					sdr39u1 (isoform2)2 with nadph PDB header: plant protein Chain: X: PDB Molecule: vestitone reductase; PDBTitle: crystal structure of vestitone reductase from alfalfa2 (medicago sativa l.)
54	c2p4hX_	Alignment	not modelled	99.9	23
55	d1rpna_	Alignment	not modelled	99.9	16
56	c5msuC_	Alignment	not modelled	99.9	19
57	c5l3zA_	Alignment	not modelled	99.9	23
58	c6dntA_	Alignment	not modelled	99.9	17
59	c4lw8B_	Alignment	not modelled	99.9	18
60	c5gmoA_	Alignment	not modelled	99.9	17
61	c2q1uA_	Alignment	not modelled	99.9	18
62	c4lisA_	Alignment	not modelled	99.9	20
63	c2c20D_	Alignment	not modelled	99.9	17
64	c4w4tA_	Alignment	not modelled	99.9	17
65	c4lk3A_	Alignment	not modelled	99.9	23
66	c6d2vA_	Alignment	not modelled	99.9	17
67	c2hrzA_	Alignment	not modelled	99.9	21
68	c5uzhA_	Alignment	not modelled	99.9	16
69	c5lnkd_	Alignment	not modelled	99.9	18
70	c4twrA_	Alignment	not modelled	99.9	22
71	d1udca_	Alignment	not modelled	99.9	18
72	c3e48B_	Alignment	not modelled	99.9	20
73	d1gy8a_	Alignment	not modelled	99.9	20
74	d1ek6a_	Alignment	not modelled	99.9	21
75	c3lcpA_	Alignment	not modelled	99.9	21
76	c3sc6F_	Alignment	not modelled	99.9	21
77	c3wj7B_	Alignment	not modelled	99.9	21
					Fold: NAD(P)-binding Rossmann-fold domains

78	d1sb8a_	Alignment	not modelled	99.9	20	Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
79	d1z45a2	Alignment	not modelled	99.9	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
80	c5u4qB_	Alignment	not modelled	99.9	23	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.
81	c6bwcA_	Alignment	not modelled	99.9	20	PDB header: biosynthetic protein Chain: A: PDB Molecule: polysaccharide biosynthesis protein capd; PDBTitle: x-ray structure of pen from bacillus thuringiensis
82	d1t2aa_	Alignment	not modelled	99.9	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
83	c4wpgA_	Alignment	not modelled	99.9	18	PDB header: oxidoreductase Chain: A: PDB Molecule: dtdp-4-dehydrorhamnose reductase; PDBTitle: group a streptococcus gaca is an essential dtdp-4-dehydrorhamnose2 reductase (rmlD)
84	c1t2aC_	Alignment	not modelled	99.9	16	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
85	c4r1sB_	Alignment	not modelled	99.9	22	PDB header: oxidoreductase Chain: B: PDB Molecule: cinnamoyl coa reductase; PDBTitle: crystal structure of petunia hybrida cinnamoyl-coa reductase
86	c5b6kA_	Alignment	not modelled	99.9	19	PDB header: oxidoreductase Chain: A: PDB Molecule: uncharacterized protein cgkr1; PDBTitle: crystal structure of ketoreductase 1 from candida glabrata
87	c2gn9B_	Alignment	not modelled	99.9	17	PDB header: lyase 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
88	c3gpiA_	Alignment	not modelled	99.9	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
89	c3lu1C_	Alignment	not modelled	99.9	22	PDB header: isomerase Chain: C: PDB Molecule: wbgu; PDBTitle: crystal structure analysis of wbgu: a udp-galnac 4-epimerase
90	d1y1pa1	Alignment	not modelled	99.9	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
91	d1orra_	Alignment	not modelled	99.9	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
92	c3eheB_	Alignment	not modelled	99.9	22	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
93	c4qukA_	Alignment	not modelled	99.9	18	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydroflavonol-4-reductase; PDBTitle: crystal structure of cinnamyl-alcohol dehydrogenase 2 mutant k169a
94	c2qx7A_	Alignment	not modelled	99.9	13	PDB header: plant protein Chain: A: PDB Molecule: eugenol synthase 1; PDBTitle: structure of eugenol synthase from ocimum basilicum
95	c5y1dB_	Alignment	not modelled	99.9	16	PDB header: oxidoreductase Chain: B: PDB Molecule: nad dependent epimerase/dehydratase family; PDBTitle: monomeric l-threonine 3-dehydrogenase from metagenome database (apo2 form)
96	c2vrcD_	Alignment	not modelled	99.9	17	PDB header: oxidoreductase Chain: D: PDB Molecule: triphenylmethane reductase; PDBTitle: crystal structure of the citrobacter sp. triphenylmethane2 reductase complexed with nadp(h)
97	d1kbla2	Alignment	not modelled	99.9	28	Fold: The "swivelling" beta/beta/alpha domain Superfamily: Phosphohistidine domain Family: Pyruvate phosphate dikinase, central domain
98	c6gcsE_	Alignment	not modelled	99.9	20	PDB header: oxidoreductase Chain: E: PDB Molecule: nuem subunit; PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
99	c2rh8A_	Alignment	not modelled	99.9	16	PDB header: oxidoreductase Chain: A: PDB Molecule: anthocyanidin reductase; PDBTitle: structure of apo anthocyanidin reductase from vitis vinifera
100	d1vbga2	Alignment	not modelled	99.9	29	Fold: The "swivelling" beta/beta/alpha domain Superfamily: Phosphohistidine domain Family: Pyruvate phosphate dikinase, central domain
101	c2ydyA_	Alignment	not modelled	99.9	17	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
102	c5bjuA_	Alignment	not modelled	99.9	17	PDB header: membrane protein Chain: A: PDB Molecule: wlal protein; PDBTitle: x-ray structure of the pglf dehydratase from campylobacter jejuni in2 complex with udp and nad(h)
103	c5u9cC_	Alignment	not modelled	99.9	18	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

104	c4f6cA_	Alignment	not modelled	99.9	19	PDB header: oxidoreductase Chain: A: PDB Molecule: ausa reductase domain protein; PDBTitle: crystal structure of aureusimine biosynthetic cluster reductase domain
105	c2ggsB_	Alignment	not modelled	99.9	13	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
106	c3slgB_	Alignment	not modelled	99.9	14	PDB header: transferase Chain: B: PDB Molecule: pbgp3 protein; PDBTitle: crystal structure of pbgp3 protein from burkholderia pseudomallei
107	d1h6za2	Alignment	not modelled	99.9	29	Fold: The "swivelling" beta/beta/alpha domain Superfamily: Phosphohistidine domain Family: Pyruvate phosphate dikinase, central domain
108	c4dqvA_	Alignment	not modelled	99.9	20	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
109	c3vpsB_	Alignment	not modelled	99.9	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
110	c2exxB_	Alignment	not modelled	99.9	17	PDB header: unknown function Chain: B: PDB Molecule: hscarg protein; PDBTitle: crystal structure of hscarg from homo sapiens in complex with nadp
111	d1xgka_	Alignment	not modelled	99.9	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
112	c3wmwB_	Alignment	not modelled	99.9	19	PDB header: oxidoreductase Chain: B: PDB Molecule: nad dependent epimerase/dehydratase; PDBTitle: gale-like l-threonine dehydrogenase from cupriavidus necator (apo2 form)
113	c3slgF_	Alignment	not modelled	99.9	14	PDB header: transferase Chain: F: PDB Molecule: pbgp3 protein; PDBTitle: crystal structure of pbgp3 protein from burkholderia pseudomallei
114	c3iusB_	Alignment	not modelled	99.9	15	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
115	c3sxpD_	Alignment	not modelled	99.9	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)
116	d1eq2a_	Alignment	not modelled	99.9	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
117	c4yraD_	Alignment	not modelled	99.9	19	PDB header: oxidoreductase Chain: D: PDB Molecule: l-threonine 3-dehydrogenase, mitochondrial; PDBTitle: mouse tdh in the apo form
118	c2zcuA_	Alignment	not modelled	99.9	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
119	c4qqrB_	Alignment	not modelled	99.9	19	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
120	c2x86K_	Alignment	not modelled	99.9	16	PDB header: isomerase Chain: K: PDB Molecule: adp-l-glycero-d-manno-heptose-6-epimerase; PDBTitle: agme bound to adp-b-mannose