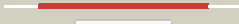



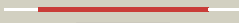



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1121_(zwf1)_1243712_1245112
Date	Wed Jul 31 22:05:20 BST 2019
Unique Job ID	f6c563dc5ac79eda

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4lqvA_	 Alignment		100.0	80	PDB header: oxidoreductase Chain: A: PDB Molecule: glucose-6-phosphate 1-dehydrogenase; PDBTitle: x-ray crystal structure of glucose-6-phosphate 1-dehydrogenase from2 mycobacterium avium
2	c2bhlB_	 Alignment		100.0	33	PDB header: oxidoreductase Chain: B: PDB Molecule: glucose-6-phosphate 1-dehydrogenase; PDBTitle: x-ray crystal structure of human glucose-6-phosphate dehydrogenase (deletion2 variant) complexed with glucose-6-phosphate
3	c1h9aA_	 Alignment		100.0	31	PDB header: oxidoreductase (choh(d) - nad(p)) Chain: A: PDB Molecule: glucose 6-phosphate 1-dehydrogenase; PDBTitle: complex of active mutant (q365->c) of glucose 6-phosphate2 dehydrogenase from I. mesenteroides with coenzyme nadp
4	c1qkiE_	 Alignment		100.0	33	PDB header: oxidoreductase Chain: E: PDB Molecule: glucose-6-phosphate 1-dehydrogenase; PDBTitle: x-ray structure of human glucose 6-phosphate dehydrogenase (variant2 canton r459l) complexed with structural nadp+
5	c4e9iB_	 Alignment		100.0	34	PDB header: oxidoreductase Chain: B: PDB Molecule: glucose-6-phosphate 1-dehydrogenase; PDBTitle: glucose-6-p dehydrogenase (apo form) from trypanosoma cruzi
6	d1qkia2	 Alignment		100.0	35	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Glucose 6-phosphate dehydrogenase-like
7	d1h9aa2	 Alignment		100.0	29	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Glucose 6-phosphate dehydrogenase-like
8	d1h9aa1	 Alignment		100.0	28	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
9	d1qkia1	 Alignment		100.0	28	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
10	c5yabD_	 Alignment		97.9	13	PDB header: oxidoreductase Chain: D: PDB Molecule: scyllo-inositol dehydrogenase with l-glucose dehydrogenase PDBTitle: crystal structure of scyllo-inositol dehydrogenase with l-glucose2 dehydrogenase activity
11	c3kuxA_	 Alignment		97.5	18	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: structure of the ypo2259 putative oxidoreductase from yersinia pestis

12	c3btuD_	Alignment		97.4	16	PDB header: transcription Chain: D: PDB Molecule: galactose/lactose metabolism regulatory protein PDBTitle: crystal structure of the super-repressor mutant of gal80p2 from saccharomyces cerevisiae; gal80(s2) [e351k]
13	c3u3xj_	Alignment		97.3	17	PDB header: oxidoreductase Chain: J: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase from sinorhizobium2 meliloti 1021
14	c5uibA_	Alignment		97.3	15	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase protein; PDBTitle: crystal structure of an oxidoreductase from agrobacterium radiobacter2 in complex with nad+, l-tartaric acid and magnesium
15	c3e18A_	Alignment		97.2	12	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of nad-binding protein from listeria innocua
16	c5b3uB_	Alignment		97.2	19	PDB header: transferase Chain: B: PDB Molecule: biliverdin reductase; PDBTitle: crystal structure of biliverdin reductase in complex with nadp+ from2 synechocystis sp. pcc 6803
17	c3euwB_	Alignment		97.1	13	PDB header: oxidoreductase Chain: B: PDB Molecule: myo-inositol dehydrogenase; PDBTitle: crystal structure of a myo-inositol dehydrogenase from corynebacterium2 glutamicum atcc 13032
18	c3rbvA_	Alignment		97.1	21	PDB header: sugar binding protein Chain: A: PDB Molecule: sugar 3-ketoreductase; PDBTitle: crystal structure of kijd10, a 3-ketoreductase from actinomadura2 kijaniata incomplex with nadp
19	c3db2C_	Alignment		97.1	17	PDB header: oxidoreductase Chain: C: PDB Molecule: putative nadph-dependent oxidoreductase; PDBTitle: crystal structure of a putative nadph-dependent oxidoreductase2 (dhaf_2064) from desulfitobacterium hafniense dcb-2 at 1.70 a3 resolution
20	c4hktA_	Alignment		97.1	18	PDB header: oxidoreductase Chain: A: PDB Molecule: inositol 2-dehydrogenase; PDBTitle: crystal structure of a putative myo-inositol dehydrogenase from2 sinorhizobium meliloti 1021 (target psi-012312)
21	c3qfgB_	Alignment	not modelled	97.0	20	PDB header: oxidoreductase Chain: B: PDB Molecule: uncharacterized oxidoreductase yvaa; PDBTitle: structure of putative oxidoreductase yvaa from bacillus subtilis in2 triclinic form
22	c4hadD_	Alignment	not modelled	96.9	17	PDB header: oxidoreductase Chain: D: PDB Molecule: probable oxidoreductase protein; PDBTitle: crystal structure of probable oxidoreductase protein from rhizobium2 etli cfn 42
23	c1evjC_	Alignment	not modelled	96.9	15	PDB header: oxidoreductase Chain: C: PDB Molecule: glucose-fructose oxidoreductase; PDBTitle: crystal structure of glucose-fructose oxidoreductase (gfor)2 delta1-22 s64d
24	c3nt5B_	Alignment	not modelled	96.9	17	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
25	c1h6dL_	Alignment	not modelled	96.9	16	PDB header: protein translocation Chain: L: PDB Molecule: precursor form of glucose-fructose oxidoreductase2 from zymomonas mobilis complexed with glycerol
26	c4gqaC_	Alignment	not modelled	96.9	15	PDB header: oxidoreductase Chain: C: PDB Molecule: nad binding oxidoreductase; PDBTitle: crystal structure of nad binding oxidoreductase from klebsiella2 pneumoniae
27	c3m2tA_	Alignment	not modelled	96.8	21	PDB header: oxidoreductase Chain: A: PDB Molecule: probable dehydrogenase; PDBTitle: the crystal structure of dehydrogenase from chromobacterium2 violaceum
28	d1h6da1	Alignment	not modelled	96.8	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain

29	c1ofgF_	Alignment	not modelled	96.8	16	PDB header: oxidoreductase Chain: F: PDB Molecule: glucose-fructose oxidoreductase; PDBTitle: glucose-fructose oxidoreductase
30	c4mkzA_	Alignment	not modelled	96.8	17	PDB header: oxidoreductase Chain: A: PDB Molecule: inositol dehydrogenase; PDBTitle: crystal structure of apo scyllo-inositol dehydrogenase from2 lactobacillus casei at 77k
31	c1zh8B_	Alignment	not modelled	96.8	28	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of oxidoreductase (tm0312) from thermotoga maritima2 at 2.50 a resolution
32	c4h3vA_	Alignment	not modelled	96.7	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: oxidoreductase domain protein; PDBTitle: crystal structure of oxidoreductase domain protein from kribbella2 flavida
33	c3ceaA_	Alignment	not modelled	96.6	15	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
34	c3e82A_	Alignment	not modelled	96.6	24	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase from2 klebsiella pneumoniae
35	c3dtyA_	Alignment	not modelled	96.6	15	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, gfo/idh/moca family; PDBTitle: crystal structure of an oxidoreductase from pseudomonas2 syringae
36	c5a06E_	Alignment	not modelled	96.5	15	PDB header: oxidoreductase Chain: E: PDB Molecule: aldose-aldose oxidoreductase; PDBTitle: crystal structure of aldose-aldose oxidoreductase from2 caulobacter crescentus complexed with sorbitol
37	c3ezyB_	Alignment	not modelled	96.4	12	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: dehydrogenase; PDBTitle: crystal structure of probable dehydrogenase tm_0414 from thermotoga2 maritima
38	d2nvwa1	Alignment	not modelled	96.2	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
39	c6a3fB_	Alignment	not modelled	96.2	12	PDB header: oxidoreductase Chain: B: PDB Molecule: putative dehydrogenase; PDBTitle: levoglucosan dehydrogenase, apo form
40	c3e9mC_	Alignment	not modelled	96.1	16	PDB header: oxidoreductase Chain: C: PDB Molecule: oxidoreductase, gfo/idh/moca family; PDBTitle: crystal structure of an oxidoreductase from enterococcus2 faecalis
41	d1zh8a1	Alignment	not modelled	96.0	26	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
42	c2ho3D_	Alignment	not modelled	96.0	17	PDB header: oxidoreductase Chain: D: PDB Molecule: oxidoreductase, gfo/idh/moca family; PDBTitle: crystal structure of oxidoreductase, gfo/idh/moca family from2 streptococcus pneumoniae
43	c2nvwB_	Alignment	not modelled	95.9	17	PDB header: transcription Chain: B: PDB Molecule: galactose/lactose metabolism regulatory protein PDBTitle: crystal sctucture of transcriptional regulator gal80p from2 kluyveromyces lactis
44	c3uuwB_	Alignment	not modelled	95.8	19	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase with nad(p)-binding rossmann-fold PDBTitle: 1.63 angstrom resolution crystal structure of dehydrogenase (mvim)2 from clostridium difficile.
45	c3moiA_	Alignment	not modelled	95.7	18	PDB header: oxidoreductase Chain: A: PDB Molecule: probable dehydrogenase; PDBTitle: the crystal structure of the putative dehydrogenase from bordetella2 bronchiseptica rb50
46	c2glxD_	Alignment	not modelled	95.5	17	PDB header: oxidoreductase Chain: D: PDB Molecule: 1,5-anhydro-d-fructose reductase; PDBTitle: crystal structure analysis of bacterial 1,5-af reductase
47	d1ryda1	Alignment	not modelled	95.5	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
48	c6norB_	Alignment	not modelled	95.4	14	PDB header: oxidoreductase Chain: B: PDB Molecule: putative nad dependent dehydrogenase; PDBTitle: crystal structure of gend2 from gentamicin a biosynthesis in complex2 with nad
49	c2q4eB_	Alignment	not modelled	95.1	14	PDB header: oxidoreductase Chain: B: PDB Molecule: probable oxidoreductase at4g09670; PDBTitle: ensemble refinement of the protein crystal structure of gene product2 from arabidopsis thaliana at4g09670
50	c3c1aB_	Alignment	not modelled	95.0	27	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase (zp_00056571.1) from2 magnetospirillum magnetotacticum ms-1 at 1.85 a resolution
51	c3f4fF_	Alignment	not modelled	95.0	17	PDB header: oxidoreductase Chain: F: PDB Molecule: putative oxidoreductase yhhx; PDBTitle: crystal structure of a probable oxidoreductase yhhx in2 triclinic form. northeast structural genomics target er647
52	c3fhIC_	Alignment	not modelled	94.8	23	PDB header: oxidoreductase Chain: C: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase from bacteroides2 fragilis nctc 9343
53	c3ec7C_	Alignment	not modelled	94.7	16	PDB header: oxidoreductase Chain: C: PDB Molecule: putative dehydrogenase; PDBTitle: crystal structure of putative dehydrogenase from salmonella2 typhimurium lt2
						PDB header: oxidoreductase

54	c2o48X	Alignment	not modelled	94.6	16	Chain: X: PDB Molecule: dimeric dihydrodiol dehydrogenase; PDBTitle: crystal structure of mammalian dimeric dihydrodiol dehydrogenase
55	c3ip3D	Alignment	not modelled	94.5	12	PDB header: oxidoreductase Chain: D: PDB Molecule: oxidoreductase, putative; PDBTitle: structure of putative oxidoreductase (tm_0425) from thermotoga2 maritima
56	c4fb5A	Alignment	not modelled	94.4	12	PDB header: oxidoreductase Chain: A: PDB Molecule: probable oxidoreductase protein; PDBTitle: crystal structure of a probable oxidoreductase protein
57	c6jnkA	Alignment	not modelled	94.1	18	PDB header: oxidoreductase Chain: A: PDB Molecule: l-arabinose 1-dehydrogenase (nad(p)(+)); PDBTitle: crystal structure of azospirillum brasilense l-arabinose 1-2 dehydrogenase (nadp-bound form)
58	c2p2sA	Alignment	not modelled	94.1	18	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of putative oxidoreductase (yp_050235.1) from2 erwinia carotovora atroseptica scri1043 at 1.25 a resolution
59	c1lc3A	Alignment	not modelled	94.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: biliverdin reductase a; PDBTitle: crystal structure of a biliverdin reductase enzyme-cofactor2 complex
60	c1xeaD	Alignment	not modelled	93.9	8	PDB header: oxidoreductase Chain: D: PDB Molecule: oxidoreductase, gfo/idh/moca family; PDBTitle: crystal structure of a gfo/idh/moca family oxidoreductase2 from vibrio cholerae
61	c3oqbF	Alignment	not modelled	93.7	15	PDB header: oxidoreductase Chain: F: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of putative oxidoreductase from bradyrhizobium2 japonicum usda 110
62	c4miyB	Alignment	not modelled	93.6	13	PDB header: oxidoreductase Chain: B: PDB Molecule: inositol 2-dehydrogenase/d-chiro-inositol 3-dehydrogenase; PDBTitle: crystal structure of myo-inositol dehydrogenase from lactobacillus2 casei in complex with nad and myo-inositol
63	d1xea1	Alignment	not modelled	93.4	8	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
64	c3oa2B	Alignment	not modelled	93.4	17	PDB header: oxidoreductase Chain: B: PDB Molecule: wbbp; PDBTitle: crystal structure of the wlba (wbbp) dehydrogenase from pseudomonas2 aeruginosa in complex with nad at 1.5 angstrom resolution
65	d1tita1	Alignment	not modelled	93.2	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
66	c1titB	Alignment	not modelled	93.2	23	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase (virulence factor mvim homolog); PDBTitle: crystal structure of a putative oxidoreductase (virulence factor mvim2 homolog)
67	c3q2kB	Alignment	not modelled	93.0	13	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of the wlba dehydrogenase from bordetella pertussis2 in complex with nadh and udp-glcna
68	c3oa0B	Alignment	not modelled	92.9	16	PDB header: oxidoreductase Chain: B: PDB Molecule: lipopolysaccharide biosynthesis protein wbbp; PDBTitle: crystal structure of the wlba (wbbp) dehydrogenase from thermus2 thermophilus in complex with nad and udp-glcna
69	c2ixaA	Alignment	not modelled	92.9	8	PDB header: hydrolase Chain: A: PDB Molecule: alpha-n-acetylgalactosaminidase; PDBTitle: a-zyme, n-acetylgalactosaminidase
70	d1lc0a1	Alignment	not modelled	92.6	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
71	d1ydw1	Alignment	not modelled	92.3	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
72	c4ew6A	Alignment	not modelled	91.9	17	PDB header: oxidoreductase Chain: A: PDB Molecule: d-galactose-1-dehydrogenase protein; PDBTitle: crystal structure of d-galactose-1-dehydrogenase protein from2 rhizobium etli
73	c3evnA	Alignment	not modelled	90.8	16	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, gfo/idh/moca family; PDBTitle: crystal structure of putative oxidoreductase from streptococcus2 agalactiae 2603v/r
74	c4oo3A	Alignment	not modelled	90.4	10	PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a putative oxidoreductase (parmer_00841) from2 parabacteroides merdae atcc 43184 at 2.23 a resolution
75	d1oi7a1	Alignment	not modelled	90.2	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
76	c3fd8A	Alignment	not modelled	85.6	13	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, gfo/idh/moca family; PDBTitle: crystal structure of an oxidoreductase from enterococcus2 faecalis
77	c5df1A	Alignment	not modelled	85.1	18	PDB header: oxidoreductase Chain: A: PDB Molecule: iridoid synthase; PDBTitle: iridoid synthase from catharanthus roseus - ternary complex with nadp+2 and geranic acid
78	c3v5nA	Alignment	not modelled	84.8	9	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase; PDBTitle: the crystal structure of oxidoreductase from

						sinorhizobium melliloti 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
79	c2zcuA	Alignment	not modelled	84.3	16	
80	d2nu7a1	Alignment	not modelled	82.3	8	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
81	c3wj7B	Alignment	not modelled	78.3	17	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of gox2253
82	c2c20D	Alignment	not modelled	77.4	17	PDB header: isomerase Chain: D: PDB Molecule: udp-glucose 4-epimerase; PDBTitle: crystal structure of udp-glucose 4-epimerase
83	c4idqB	Alignment	not modelled	76.1	18	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
84	d1wvga1	Alignment	not modelled	71.9	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
85	c2vrcD	Alignment	not modelled	71.4	19	PDB header: oxidoreductase Chain: D: PDB Molecule: triphenylmethane reductase; PDBTitle: crystal structure of the citrobacter sp. triphenylmethane2 reductase complexed with nadp(h)
86	c5msuC	Alignment	not modelled	70.4	18	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
87	c2v6gA	Alignment	not modelled	70.1	22	PDB header: oxidoreductase Chain: A: PDB Molecule: progesterone 5-beta-reductase; PDBTitle: structure of progesterone 5beta-reductase from digitalis2 lanata in complex with nadp
88	c4qukA	Alignment	not modelled	66.8	14	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydroflavonol-4-reductase; PDBTitle: crystal structure of cinnamyl-alcohol dehydrogenase 2 mutant k169a
89	c4gmfD	Alignment	not modelled	66.7	12	PDB header: oxidoreductase Chain: D: PDB Molecule: yersiniabactin biosynthetic protein ybtu; PDBTitle: apo structure of a thiazoliny1 imine reductase from yersinia2 enterocolitica (irp3)
90	d1euca1	Alignment	not modelled	66.1	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
91	d1x1na1	Alignment	not modelled	62.9	30	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
92	c1t2aC	Alignment	not modelled	62.8	25	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
93	d1t2aa	Alignment	not modelled	62.8	25	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
94	d1tz7a1	Alignment	not modelled	62.2	40	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
95	c4s3rA	Alignment	not modelled	61.5	35	PDB header: transferase Chain: A: PDB Molecule: 4-alpha-glucanotransferase; PDBTitle: amylomaltase malq from escherichia coli in complex with the pseudo-2 heptasaccharide acarviosine-glucose-acarbose
96	c4pvcB	Alignment	not modelled	59.2	17	PDB header: oxidoreductase Chain: B: PDB Molecule: nadph-dependent methylglyoxal reductase gre2; PDBTitle: crystal structure of yeast methylglyoxal/ isovaleraldehyde reductase2 gre2
97	c6el3A	Alignment	not modelled	59.1	24	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
98	d1eswa	Alignment	not modelled	58.8	40	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
99	c4lw8B	Alignment	not modelled	58.0	22	PDB header: isomerase Chain: B: PDB Molecule: putative epimerase; PDBTitle: crystal structure of a putative epimerase from burkholderia2 cenocepacia j2315
100	c2vz8A	Alignment	not modelled	57.9	18	PDB header: transferase Chain: A: PDB Molecule: fatty acid synthase; PDBTitle: crystal structure of mammalian fatty acid synthase
101	c2z1mC	Alignment	not modelled	57.9	18	PDB header: lyase Chain: C: PDB Molecule: gdp-d-mannose dehydratase; PDBTitle: crystal structure of gdp-d-mannose dehydratase from aquifex aeolicus2 vf5
102	c4j1sA	Alignment	not modelled	57.2	17	PDB header: oxidoreductase Chain: A: PDB Molecule: polyketide synthase pksj; PDBTitle: crystal structure of a ketoreductase domain from the bacillaene2 assembly line
103	c5yylA	Alignment	not modelled	56.3	25	PDB header: signaling protein Chain: A: PDB Molecule: major royal jelly protein 1; PDBTitle: structure of major royal jelly protein 1 oligomer
104	c3mieA	Alignment	not modelled	56.0	11	PDB header: oxidoreductase Chain: A: PDB Molecule: amphb;

104	c5mjsA_	Alignment	not modelled	58.0	11	PDBTitle: structure of a-type ketoreductases from modular polyketide synthase PDB header: oxidoreductase
105	c5l3zA_	Alignment	not modelled	55.6	19	Chain: A; PDB Molecule: polyketide ketoreductase simc7; PDBTitle: polyketide ketoreductase simc7 - binary complex with nadp+
106	c2gn9B_	Alignment	not modelled	55.3	23	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
107	d1a8pa2	Alignment	not modelled	54.7	12	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Reductases
108	c2qx7A_	Alignment	not modelled	53.5	17	PDB header: plant protein Chain: A; PDB Molecule: eugenol synthase 1; PDBTitle: structure of eugenol synthase from ocimum basilicum
109	c5gmoA_	Alignment	not modelled	53.1	17	PDB header: oxidoreductase Chain: A; PDB Molecule: protein induced by osmotic stress; PDBTitle: x-ray structure of carbonyl reductase sscr
110	d1db3a_	Alignment	not modelled	51.9	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
111	d1rkxa_	Alignment	not modelled	51.7	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
112	c4dqvA_	Alignment	not modelled	50.4	19	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
113	c4pivB_	Alignment	not modelled	50.2	12	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
114	c6fn6A_	Alignment	not modelled	49.0	14	PDB header: transferase Chain: A; PDB Molecule: fatty acid synthase 1, isoform a; PDBTitle: modifying region (dh-er-kr) of an insect fatty acid synthase (fas)
115	c5uzhA_	Alignment	not modelled	48.4	21	PDB header: transferase Chain: A; PDB Molecule: nafoa.00085.b; PDBTitle: crystal structure of a gdp-mannose dehydratase from naegleria fowleri
116	c5b68A_	Alignment	not modelled	48.2	50	PDB header: transferase Chain: A; PDB Molecule: 4-alpha-glucanotransferase; PDBTitle: crystal structure of apo amylomaltase from corynebacterium glutamicum
117	c6g1mA_	Alignment	not modelled	47.3	19	PDB header: oxidoreductase Chain: A; PDB Molecule: dihydrodipicolinate reductase; PDBTitle: amine dehydrogenase from petrotoga mobilis; open and closed form
118	d1xgka_	Alignment	not modelled	45.3	11	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
119	c2iodD_	Alignment	not modelled	43.7	17	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
120	c4lisA_	Alignment	not modelled	42.7	18	PDB header: isomerase Chain: A; PDB Molecule: udp-glucose 4-epimerase; PDBTitle: crystal structure of udp-galactose-4-epimerase from aspergillus2 nidulans