
















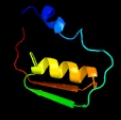






Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0976c_(-)_1088497_1090179
Date	Wed Jul 31 22:05:04 BST 2019
Unique Job ID	4c576cca7dbd8f49

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3gndC_	 Alignment		94.4	14	PDB header: lyase Chain: C: PDB Molecule: aldolase lsrf; PDBTitle: crystal structure of e. coli lsrf in complex with ribulose-5-phosphate
2	d1ojxa_	 Alignment		93.3	15	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
3	c2qjhH_	 Alignment		87.7	17	PDB header: lyase Chain: H: PDB Molecule: putative aldolase mj0400; PDBTitle: m. jannaschii adh synthase covalently bound to2 dihydroxyacetone phosphate
4	c1rr2A_	 Alignment		86.0	15	PDB header: transferase Chain: A: PDB Molecule: transcarboxylase 5s subunit; PDBTitle: propionibacterium shermanii transcarboxylase 5s subunit bound to 2-2 ketobutyric acid
5	c5n2pA_	 Alignment		85.5	15	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: sulfolobus solfataricus tryptophan synthase a
6	c5kzmA_	 Alignment		84.2	25	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha-beta chain complex from2 francisella tularensis
7	c4lrtC_	 Alignment		83.3	27	PDB header: lyase/oxidoreductase Chain: C: PDB Molecule: 4-hydroxy-2-oxovalerate aldolase; PDBTitle: crystal and solution structures of the bifunctional enzyme2 (aldolase/aldehyde dehydrogenase) from thermomonospora curvata,3 reveal a cofactor-binding domain motion during nad+ and coa4 accommodation within the shared cofactor-binding site
8	c3tfxB_	 Alignment		81.8	17	PDB header: lyase Chain: B: PDB Molecule: orotidine 5'-phosphate decarboxylase; PDBTitle: crystal structure of orotidine 5'-phosphate decarboxylase from2 lactobacillus acidophilus
9	c4euhA_	 Alignment		81.5	26	PDB header: oxidoreductase Chain: A: PDB Molecule: putative reductase ca_c0462; PDBTitle: crystal structure of clostridium acetobutlicum trans-2-enoyl-coa2 reductase apo form
10	c5ks8F_	 Alignment		79.2	20	PDB header: ligase Chain: F: PDB Molecule: pyruvate carboxylase subunit beta; PDBTitle: crystal structure of two-subunit pyruvate carboxylase from2 methylobacillus flagellatus
11	c3bg3A_	 Alignment		76.5	26	PDB header: ligase Chain: A: PDB Molecule: pyruvate carboxylase, mitochondrial; PDBTitle: crystal structure of human pyruvate carboxylase (missing the biotin2 carboxylase domain at the n-terminus)

12	d1o94c_	 Alignment		74.6	15	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
13	c4jn6C_	 Alignment		74.1	24	PDB header: lyase/oxidoreductase Chain: C: PDB Molecule: 4-hydroxy-2-oxoalate aldolase; PDBTitle: crystal structure of the aldolase-dehydrogenase complex from 2 mycobacterium tuberculosis hrv37
14	c5ey5A_	 Alignment		73.8	19	PDB header: lyase Chain: A: PDB Molecule: lbcats-a; PDBTitle: lbcats
15	c1ydoC_	 Alignment		70.7	23	PDB header: lyase Chain: C: PDB Molecule: hmg-coa lyase; PDBTitle: crystal structure of the bacillus subtilis hmg-coa lyase, northeast2 structural genomics target sr181.
16	d1t1ra2	 Alignment		70.1	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
17	c3bg3B_	 Alignment		70.0	14	PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase, mitochondrial; PDBTitle: crystal structure of human pyruvate carboxylase (missing the biotin2 carboxylase domain at the n-terminus)
18	d1efpb_	 Alignment		69.9	18	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
19	c4nu7C_	 Alignment		69.4	18	PDB header: isomerase Chain: C: PDB Molecule: ribulose-phosphate 3-epimerase; PDBTitle: 2.05 angstrom crystal structure of ribulose-phosphate 3-epimerase from 2 toxoplasma gondii.
20	c3h75A_	 Alignment		68.3	20	PDB header: sugar binding protein Chain: A: PDB Molecule: periplasmic sugar-binding domain protein; PDBTitle: crystal structure of a periplasmic sugar-binding protein from the 2 pseudomonas fluorescens
21	c1k5hB_	 Alignment	not modelled	67.5	15	PDB header: oxidoreductase Chain: B: PDB Molecule: 1-deoxy-d-xylulose-5-phosphate reductoisomerase; PDBTitle: 1-deoxy-d-xylulose-5-phosphate reductoisomerase
22	d2fywa1	 Alignment	not modelled	67.5	23	Fold: NIF3 (NGG1p interacting factor 3)-like Superfamily: NIF3 (NGG1p interacting factor 3)-like Family: NIF3 (NGG1p interacting factor 3)-like
23	c3ct7E_	 Alignment	not modelled	66.7	16	PDB header: isomerase Chain: E: PDB Molecule: d-allulose-6-phosphate 3-epimerase; PDBTitle: crystal structure of d-allulose 6-phosphate 3-epimerase2 from escherichia coli k-12
24	c4go4E_	 Alignment	not modelled	66.4	21	PDB header: oxidoreductase Chain: E: PDB Molecule: putative gamma-hydroxymuconic semialdehyde dehydrogenase; PDBTitle: crystal structure of pnpe in complex with nicotinamide adenine2 dinucleotide
25	d1tqxa_	 Alignment	not modelled	66.3	12	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
26	c2ekcA_	 Alignment	not modelled	66.2	18	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: structural study of project id aq_1548 from aquifex aeolicus vf5
27	d1qopa_	 Alignment	not modelled	65.7	20	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
28	c4kpuB_	 Alignment	not modelled	65.3	17	PDB header: electron transport Chain: B: PDB Molecule: electron transfer flavoprotein alpha/beta-subunit; PDBTitle: electron transferring flavoprotein of acidaminococcus

						fermentans:2 towards a mechanism of flavin-based electron bifurcation
29	c3zu3A_	Alignment	not modelled	65.0	28	PDB header: oxidoreductase Chain: A: PDB Molecule: putative reductase ypo4104/y4119/yp_4011; PDBTitle: structure of the enoyl-acp reductase fabv from yersinia pestis with2 the cofactor nadh (mr, cleaved histag)
30	c3ed6B_	Alignment	not modelled	64.1	22	PDB header: oxidoreductase Chain: B: PDB Molecule: betaine aldehyde dehydrogenase; PDBTitle: 1.7 angstrom resolution crystal structure of betaine aldehyde2 dehydrogenase (betb) from staphylococcus aureus
31	c5ks8D_	Alignment	not modelled	64.1	19	PDB header: ligase Chain: D: PDB Molecule: pyruvate carboxylase subunit beta; PDBTitle: crystal structure of two-subunit pyruvate carboxylase from2 methylobacillus flagellatus
32	c3a9iA_	Alignment	not modelled	63.9	21	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: homocitrate synthase; PDBTitle: crystal structure of homocitrate synthase from thermus thermophilus2 complexed with lys
33	c3bfjK_	Alignment	not modelled	63.8	25	PDB header: oxidoreductase Chain: K: PDB Molecule: 1,3-propanediol oxidoreductase; PDBTitle: crystal structure analysis of 1,3-propanediol oxidoreductase
34	c4k05B_	Alignment	not modelled	63.0	24	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: conserved hypothetical exported protein; PDBTitle: crystal structure of a duf1343 family protein (bf0371) from2 bacteroides fragilis nctc 9343 at 1.65 a resolution
35	c4qslC_	Alignment	not modelled	62.2	20	PDB header: ligase Chain: C: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of listeria monocytogenes pyruvate carboxylase
36	d1h1ya_	Alignment	not modelled	61.9	12	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
37	c5xi0B_	Alignment	not modelled	61.6	31	PDB header: oxidoreductase Chain: B: PDB Molecule: enoyl-[acyl-carrier-protein] reductase [nadh]; PDBTitle: crystal structure of fabv, a new class of enyl-acyl carrier protein2 reductase from vibrio fischeri
38	d1rqba2	Alignment	not modelled	60.8	19	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: HMGL-like
39	c3navB_	Alignment	not modelled	59.8	25	PDB header: lyase Chain: B: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of an alpha subunit of tryptophan synthase from2 vibrio cholerae o1 biovar el tor str. n16961
40	c3i44A_	Alignment	not modelled	59.8	19	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde dehydrogenase; PDBTitle: crystal structure of aldehyde dehydrogenase from bartonella2 henselae at 2.0a resolution
41	c5kqoA_	Alignment	not modelled	58.2	17	PDB header: oxidoreductase Chain: A: PDB Molecule: 1-deoxy-d-xylulose 5-phosphate reductoisomerase; PDBTitle: 1-deoxy-d-xylulose 5-phosphate reductoisomerase from vibrio vulnificus
42	d1pvda1	Alignment	not modelled	57.3	13	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
43	d1r0ka2	Alignment	not modelled	56.5	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
44	c3lvuB_	Alignment	not modelled	55.9	20	PDB header: transport protein Chain: B: PDB Molecule: abc transporter, periplasmic substrate-binding protein; PDBTitle: crystal structure of abc transporter, periplasmic substrate-binding2 protein spo2066 from silicibacter pomeroyi
45	d1xcfa_	Alignment	not modelled	55.8	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
46	c5ol2E_	Alignment	not modelled	55.6	17	PDB header: flavoprotein Chain: E: PDB Molecule: electron transfer flavoprotein small subunit; PDBTitle: the electron transferring flavoprotein/butyryl-coa dehydrogenase2 complex from clostridium difficile
47	c4ov9A_	Alignment	not modelled	55.0	19	PDB header: transferase Chain: A: PDB Molecule: isopropylmalate synthase; PDBTitle: structure of isopropylmalate synthase binding with alpha-2 isopropylmalate
48	c3thaB_	Alignment	not modelled	54.9	15	PDB header: lyase Chain: B: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: tryptophan synthase subunit alpha from campylobacter jejuni.
49	c3rmjB_	Alignment	not modelled	54.8	19	PDB header: transferase Chain: B: PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of truncated alpha-isopropylmalate synthase from2 neisseria meningitidis
50	d1dvja_	Alignment	not modelled	54.3	22	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
51	c3zs6A_	Alignment	not modelled	54.2	16	PDB header: peptide binding protein Chain: A: PDB Molecule: periplasmic oligopeptide-binding protein; PDBTitle: the structural characterization of burkholderia pseudomallei oppa.
52	d1rd5a_	Alignment	not modelled	53.4	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
						PDB header: lyase Chain: C: PDB Molecule: orotidine 5'-phosphate decarboxylase;

53	c3ru6C_	Alignment	not modelled	53.2	13	PDBTitle: 1.8 angstrom resolution crystal structure of orotidine 5'-phosphate2 decarboxylase (pyrf) from campylobacter jejuni subsp. jejuni nctc3 11168
54	c4qslE_	Alignment	not modelled	52.9	19	PDB header: ligase Chain: E; PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of listeria monocytogenes pyruvate carboxylase
55	d1nvma2	Alignment	not modelled	52.7	16	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: HMGL-like
56	c3l55B_	Alignment	not modelled	52.7	9	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: b-1,4-endoglucanase/cellulase; PDBTitle: crystal structure of a putative beta-1,4-endoglucanase / cellulase2 from prevotella bryantii
57	d2amxa1	Alignment	not modelled	51.7	18	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Adenosine/AMP deaminase
58	c3rmsA_	Alignment	not modelled	50.7	27	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein svir_20580 from2 saccharomonospora viridis
59	d3clsc1	Alignment	not modelled	50.4	14	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
60	c2d4eB_	Alignment	not modelled	50.3	25	PDB header: oxidoreductase Chain: B; PDB Molecule: 5-carboxymethyl-2-hydroxyuconate semialdehyde PDBTitle: crystal structure of the hpcc from thermus thermophilus hb8
61	d1x7fa2	Alignment	not modelled	50.0	14	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Outer surface protein, N-terminal domain
62	c3p96A_	Alignment	not modelled	49.9	24	PDB header: hydrolase Chain: A; PDB Molecule: phosphoserine phosphatase serb; PDBTitle: crystal structure of phosphoserine phosphatase serb from mycobacterium2 avium, native form
63	d1gyta2	Alignment	not modelled	49.7	21	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Leucine aminopeptidase, C-terminal domain
64	d1vlja_	Alignment	not modelled	49.4	17	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
65	c1r0lD_	Alignment	not modelled	49.2	19	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
66	c3ivuB_	Alignment	not modelled	48.3	20	PDB header: transferase Chain: B; PDB Molecule: homocitrate synthase, mitochondrial; PDBTitle: homocitrate synthase lys4 bound to 2-og
67	c1ta9A_	Alignment	not modelled	47.8	13	PDB header: oxidoreductase Chain: A; PDB Molecule: glycerol dehydrogenase; PDBTitle: crystal structure of glycerol dehydrogenase from schizosaccharomyces2 pombe
68	c1mwoA_	Alignment	not modelled	47.5	30	PDB header: hydrolase Chain: A; PDB Molecule: alpha amylase; PDBTitle: crystal structure analysis of the hyperthermostable2 pyrococcus woesei alpha-amylase
69	c2cw6B_	Alignment	not modelled	46.2	16	PDB header: lyase Chain: B; PDB Molecule: hydroxymethylglutaryl-coa lyase, mitochondrial; PDBTitle: crystal structure of human hmg-coa lyase: insights into2 catalysis and the molecular basis for3 hydroxymethylglutaric aciduria
70	c1ydnA_	Alignment	not modelled	46.2	25	PDB header: lyase Chain: A; PDB Molecule: hydroxymethylglutaryl-coa lyase; PDBTitle: crystal structure of the hmg-coa lyase from brucella melitensis,2 northeast structural genomics target lr35.
71	c2nx9B_	Alignment	not modelled	46.0	19	PDB header: lyase Chain: B; PDB Molecule: oxaloacetate decarboxylase 2, subunit alpha; PDBTitle: crystal structure of the carboxyltransferase domain of the2 oxaloacetate decarboxylase na+ pump from vibrio cholerae
72	d1uuqa_	Alignment	not modelled	45.8	29	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
73	c1uz4A_	Alignment	not modelled	45.8	29	PDB header: hydrolase Chain: A; PDB Molecule: man5a; PDBTitle: common inhibition of beta-glucosidase and beta-mannosidase2 by isofagomine lactam reflects different conformational3 itineraries for glucoside and mannoside hydrolysis
74	c4hnbV_	Alignment	not modelled	45.8	20	PDB header: ligase Chain: B; PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of r54e mutant of s. aureus pyruvate carboxylase
75	d1efvb_	Alignment	not modelled	45.8	19	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
76	d1dbta_	Alignment	not modelled	45.5	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Decarboxylase
77	c3qr3B_	Alignment	not modelled	45.4	17	PDB header: hydrolase Chain: B; PDB Molecule: endoglucanase eg-ii; PDBTitle: crystal structure of cel5a (eg2) from hypocrea jecorina (trichoderma2 reesei) PDB header: hydrolase

78	c3icgD	Alignment	not modelled	45.2	19	Chain: D: PDB Molecule: endoglucanase d; PDBTitle: crystal structure of the catalytic and carbohydrate binding domain of2 endoglucanase d from clostridium cellulovorans
79	c2oylB	Alignment	not modelled	45.1	26	PDB header: hydrolase Chain: B: PDB Molecule: endoglycoceramidase ii; PDBTitle: endo-glycoceramidase ii from rhodococcus sp.: cellobiose-like2 imidazole complex
80	c3ff4A	Alignment	not modelled	45.0	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein chu_1412
81	c6gl2A	Alignment	not modelled	44.8	15	PDB header: hydrolase Chain: A: PDB Molecule: endoglucanase, family gh5; PDBTitle: structure of zgegagh5_4 wild type at 1.2 angstrom resolution
82	c3ox4D	Alignment	not modelled	44.5	23	PDB header: oxidoreductase Chain: D: PDB Molecule: alcohol dehydrogenase 2; PDBTitle: structures of iron-dependent alcohol dehydrogenase 2 from zymomonas2 mobilis zm4 complexed with nad cofactor
83	c3iwkB	Alignment	not modelled	44.1	18	PDB header: oxidoreductase Chain: B: PDB Molecule: aminoaldehyde dehydrogenase; PDBTitle: crystal structure of aminoaldehyde dehydrogenase 1 from pisum sativum2 (psamadh1)
84	c5vbfH	Alignment	not modelled	43.9	17	PDB header: oxidoreductase Chain: H: PDB Molecule: nad-dependent succinate-semialdehyde dehydrogenase; PDBTitle: crystal structure of succinate semialdehyde dehydrogenase from2 burkholderia vietnamiensis
85	d1q6za1	Alignment	not modelled	43.9	18	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
86	c4zn6B	Alignment	not modelled	43.7	14	PDB header: oxidoreductase Chain: B: PDB Molecule: 1-deoxy-d-xylulose 5-phosphate reductoisomerase; PDBTitle: x-ray crystal structure of 1-deoxy-d-xylulose 5-phosphate2 reductoisomerase (ispc) from acinetobacter baumannii
87	c4dbeB	Alignment	not modelled	43.6	14	PDB header: lyase/lyase inhibitor Chain: B: PDB Molecule: orotidine 5'-phosphate decarboxylase; PDBTitle: crystal structure of orotidine 5'-monophosphate decarboxylase from2 sulfolobus solfataricus complexed with inhibitor bmp
88	c4df1B	Alignment	not modelled	43.4	38	PDB header: lyase/lyase inhibitor Chain: B: PDB Molecule: orotidine 5'-phosphate decarboxylase; PDBTitle: crystal structure of orotidine 5'-monophosphate decarboxylase from2 thermoproteus neutrophilus complexed with inhibitor bmp
89	d1rrma	Alignment	not modelled	43.4	18	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
90	d1wa3a1	Alignment	not modelled	43.3	19	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
91	c1nvmG	Alignment	not modelled	43.2	16	PDB header: lyase/oxidoreductase Chain: G: PDB Molecule: 4-hydroxy-2-oxovalerate aldolase; PDBTitle: crystal structure of a bifunctional aldolase-dehydrogenase :2 sequestering a reactive and volatile intermediate
92	c5e09A	Alignment	not modelled	42.8	19	PDB header: hydrolase Chain: A: PDB Molecule: cellulase; PDBTitle: structural insight of a trimodular halophilic cellulase with a family2 46 carbohydrate-binding module
93	c3ncoA	Alignment	not modelled	42.8	16	PDB header: hydrolase Chain: A: PDB Molecule: endoglucanase fncel5a; PDBTitle: crystal structure of fncel5a from f. nodosum rt17-b1
94	d2djia1	Alignment	not modelled	41.9	18	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
95	c3vndD	Alignment	not modelled	41.9	20	PDB header: lyase Chain: D: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha-subunit from the2 psychrophile shewanella frigidimarina k14-2
96	c2q5cA	Alignment	not modelled	41.6	18	PDB header: transcription Chain: A: PDB Molecule: ntrc family transcriptional regulator; PDBTitle: crystal structure of ntrc family transcriptional regulator from2 clostridium acetobutylicum
97	d1rxwa2	Alignment	not modelled	41.5	7	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
98	c5ow0B	Alignment	not modelled	41.4	22	PDB header: electron transport Chain: B: PDB Molecule: electron transfer flavoprotein, beta subunit; PDBTitle: crystal structure of an electron transfer flavoprotein from2 geobacillus metallireducens
99	d1qhoa4	Alignment	not modelled	41.3	26	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
100	c3a24A	Alignment	not modelled	41.2	24	PDB header: hydrolase Chain: A: PDB Molecule: alpha-galactosidase; PDBTitle: crystal structure of bt1871 retaining glycosidase
101	c2yytA	Alignment	not modelled	40.8	31	PDB header: lyase Chain: A: PDB Molecule: orotidine 5'-phosphate decarboxylase; PDBTitle: crystal structure of uncharacterized conserved protein from2 geobacillus kaustophilus
102	c3dmyA	Alignment	not modelled	40.7	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein fdra; PDBTitle: crystal structure of a predicated acyl-coa synthetase from e.coli
						PDB header: transferase

103	c2vp8A_	Alignment	not modelled	40.5	18	Chain: A: PDB Molecule: dihydropteroate synthase 2; PDBTitle: structure of mycobacterium tuberculosis rv1207
104	d1losc_	Alignment	not modelled	40.4	20	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
105	c4yztA_	Alignment	not modelled	40.4	19	PDB header: hydrolase Chain: A: PDB Molecule: cellulose hydrolase; PDBTitle: crystal structure of a tri-modular gh5 (subfamily 4) endo-beta-1, 4-2 glucanase from bacillus licheniformis complexed with cellotetraose
106	c3igfB_	Alignment	not modelled	40.4	17	PDB header: atp binding protein Chain: B: PDB Molecule: all4481 protein; PDBTitle: crystal structure of the all4481 protein from nostoc sp. pcc 7120,2 northeast structural genomics consortium target nsr300
107	c5ccuA_	Alignment	not modelled	40.1	15	PDB header: hydrolase Chain: A: PDB Molecule: putative secreted endoglycosylceramidase; PDBTitle: crystal structure of endoglycosylceramidase i from rhodococcus equi
108	c3ldvB_	Alignment	not modelled	40.0	31	PDB header: lyase Chain: B: PDB Molecule: orotidine 5'-phosphate decarboxylase; PDBTitle: 1.77 angstrom resolution crystal structure of orotidine 5'-phosphate2 decarboxylase from vibrio cholerae o1 biovar eltor str. n16961
109	c3urkA_	Alignment	not modelled	39.6	16	PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxy-3-methylbut-2-enyl diphosphate reductase; PDBTitle: isph in complex with propynyl diphosphate (1061)
110	c3ke8A_	Alignment	not modelled	39.6	16	PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxy-3-methylbut-2-enyl diphosphate reductase; PDBTitle: crystal structure of isph:hmbpp-complex
111	c2eghA_	Alignment	not modelled	39.6	14	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
112	c3pamB_	Alignment	not modelled	39.4	24	PDB header: transport protein Chain: B: PDB Molecule: transmembrane protein; PDBTitle: crystal structure of a domain of transmembrane protein of abc-type2 oligopeptide transport system from bartonella henselae str. houston-1
113	d1lovma1	Alignment	not modelled	39.4	15	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
114	d1mkza_	Alignment	not modelled	39.4	18	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
115	c3jr2D_	Alignment	not modelled	39.4	22	PDB header: biosynthetic protein Chain: D: PDB Molecule: hexulose-6-phosphate synthase sgbh; PDBTitle: x-ray crystal structure of the mg-bound 3-keto-l-gulonate-6-phosphate2 decarboxylase from vibrio cholerae o1 biovar el tor str. n16961
116	c3mmwB_	Alignment	not modelled	39.0	18	PDB header: hydrolase Chain: B: PDB Molecule: endoglucanase; PDBTitle: crystal structure of endoglucanase cel5a from the hyperthermophilic2 thermotoga maritima
117	c4v2xA_	Alignment	not modelled	38.9	19	PDB header: hydrolase Chain: A: PDB Molecule: endo-beta-1,4-glucanase (cellulase b); PDBTitle: high resolution structure of the full length tri-modular2 endo-beta-1,4-glucanase b (cel5b) from bacillus halodurans
118	c6hlxA_	Alignment	not modelled	38.2	19	PDB header: transport protein Chain: A: PDB Molecule: agaa; PDBTitle: structure of the pbp agaa in complex with agropinic acid from2 a.tumefaciens r10
119	c2fpgA_	Alignment	not modelled	38.2	14	PDB header: ligase Chain: A: PDB Molecule: succinyl-coa ligase [gdp-forming] alpha-chain, PDBTitle: crystal structure of pig gtp-specific succinyl-coa synthetase in2 complex with gdp
120	c2zunB_	Alignment	not modelled	38.0	19	PDB header: hydrolase Chain: B: PDB Molecule: 458aa long hypothetical endo-1,4-beta-glucanase; PDBTitle: functional analysis of hyperthermophilic endocellulase from2 the archaeon pyrococcus horikoshii