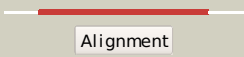
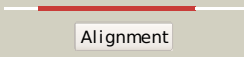
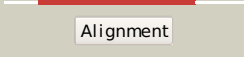
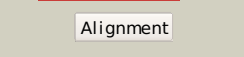
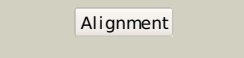
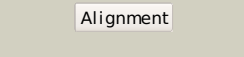
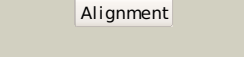
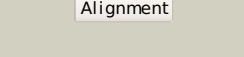
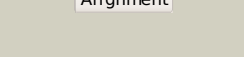
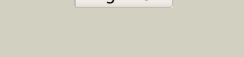
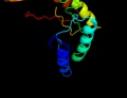


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2fiqa1	 Alignment		100.0	96	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: GatZ-like
2	c3q94B_	 Alignment		99.9	15	PDB header: lyase Chain: B: PDB Molecule: fructose-bisphosphate aldolase, class ii; PDBTitle: the crystal structure of fructose 1,6-bisphosphate aldolase from2 bacillus anthracis str. 'ames ancestor'
3	d1rvga_	 Alignment		99.9	17	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class II FBP aldolase
4	d1dosa_	 Alignment		99.9	15	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class II FBP aldolase
5	d1qvfa_	 Alignment		99.9	16	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class II FBP aldolase
6	c3c52B_	 Alignment		99.9	15	PDB header: lyase Chain: B: PDB Molecule: fructose-bisphosphate aldolase; PDBTitle: class ii fructose-1,6-bisphosphate aldolase from2 helicobacter pylori in complex with3 phosphoglycolohydroxamic acid, a competitive inhibitor
7	c3elfA_	 Alignment		99.9	15	PDB header: lyase Chain: A: PDB Molecule: fructose-bisphosphate aldolase; PDBTitle: structural characterization of tetrameric mycobacterium tuberculosis2 fructose 1,6-bisphosphate aldolase - substrate binding and catalysis3 mechanism of a class iia bacterial aldolase
8	c3qm3C_	 Alignment		99.9	17	PDB header: lyase Chain: C: PDB Molecule: fructose-bisphosphate aldolase; PDBTitle: 1.85 angstrom resolution crystal structure of fructose-bisphosphate2 aldolase (fba) from campylobacter jejuni
9	c2iswB_	 Alignment		99.9	17	PDB header: lyase Chain: B: PDB Molecule: putative fructose-1,6-bisphosphate aldolase; PDBTitle: structure of giardia fructose-1,6-bisphosphate aldolase in2 complex with phosphoglycolohydroxamate
10	c3pm6B_	 Alignment		99.9	16	PDB header: lyase Chain: B: PDB Molecule: putative fructose-bisphosphate aldolase; PDBTitle: crystal structure of a putative fructose-1,6-bisphosphate aldolase from2 coccidioides immitis solved by combined sad mr
11	d1f6ya_	 Alignment		95.8	21	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Methyltetrahydrofolate-utilizing methyltransferases

12	c3bolB_	Alignment		95.8	16	PDB header: transferase Chain: B: PDB Molecule: 5-methyltetrahydrofolate s-homocysteine PDBTitle: cobalamin-dependent methionine synthase (1-566) from2 thermotoga maritima complexed with zn2+
13	d3bofa1	Alignment		95.4	16	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Methyltetrahydrofolate-utilizing methyltransferases
14	c1rr2A_	Alignment		94.8	13	PDB header: transferase Chain: A: PDB Molecule: transcarboxylase 5s subunit; PDBTitle: propionibacterium shermanii transcarboxylase 5s subunit bound to 2-2 ketobutyric acid
15	d1muma_	Alignment		93.7	15	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
16	c2h9aA_	Alignment		93.1	22	PDB header: oxidoreductase Chain: A: PDB Molecule: carbon monoxide dehydrogenase corrinoid/iron- PDBTitle: corrinoid iron-sulfur protein
17	c2yciX_	Alignment		91.9	20	PDB header: transferase Chain: X: PDB Molecule: 5-methyltetrahydrofolate corrinoid/iron sulfur protein PDBTitle: methyltransferase native
18	c3k13A_	Alignment		91.4	21	PDB header: transferase Chain: A: PDB Molecule: 5-methyltetrahydrofolate-homocysteine methyltransferase; PDBTitle: structure of the pterin-binding domain metr of 5-2 methyltetrahydrofolate-homocysteine methyltransferase from3 bacteroides thetaiotaomicron
19	c2dzaA_	Alignment		91.2	21	PDB header: transferase Chain: A: PDB Molecule: dihydropteroate synthase; PDBTitle: crystal structure of dihydropteroate synthase from thermus2 thermophilus hb8 in complex with 4-aminobenzoate
20	c2nx9B_	Alignment		90.8	15	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
21	c2vp8A_	Alignment	not modelled	90.1	18	PDB header: transferase Chain: A: PDB Molecule: dihydropteroate synthase 2; PDBTitle: structure of mycobacterium tuberculosis rv1207
22	c2ze3A_	Alignment	not modelled	89.5	17	PDB header: isomerase Chain: A: PDB Molecule: dfa0005; PDBTitle: crystal structure of dfa0005 complexed with alpha-ketoglutarate: a2 novel member of the icl/pepm superfamily from alkali-tolerant3 deinococcus ficus
23	c2qiwa_	Alignment	not modelled	88.6	14	PDB header: transferase Chain: A: PDB Molecule: pep phosphonmutase; PDBTitle: crystal structure of a putative phosphoenolpyruvate phosphonmutase2 (ncgl1015, cgl1060) from corynebacterium glutamicum atcc 13032 at3 1.80 a resolution
24	c1ps9A_	Alignment	not modelled	86.8	14	PDB header: oxidoreductase Chain: A: PDB Molecule: 2,4-dienoyl-coa reductase; PDBTitle: the crystal structure and reaction mechanism of e. coli 2,4-2 dienoyl coa reductase
25	d1tx2a_	Alignment	not modelled	84.5	17	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
26	c1tx2A_	Alignment	not modelled	84.5	17	PDB header: transferase Chain: A: PDB Molecule: dhps, dihydropteroate synthase; PDBTitle: dihydropteroate synthetase, with bound inhibitor manic, from bacillus2 anthracis
27	c3hf3A_	Alignment	not modelled	83.2	21	PDB header: oxidoreductase Chain: A: PDB Molecule: chromate reductase; PDBTitle: old yellow enzyme from thermus scotoductus sa-01
28	c3b8iF_	Alignment	not modelled	83.0	18	PDB header: lyase Chain: F: PDB Molecule: pa4872 oxaloacetate decarboxylase; PDBTitle: crystal structure of oxaloacetate decarboxylase from

					pseudomonas2 aeruginosa (pa4872) in complex with oxalate and mg2+.
29	c3cqkB_	Alignment	not modelled	83.0	9 PDB header: isomerase Chain: B: PDB Molecule: l-ribulose-5-phosphate 3-epimerase ulae; PDBTitle: crystal structure of l-xylulose-5-phosphate 3-epimerase ulae (form b)2 complex with zn2+ and sulfate
30	dleyea_	Alignment	not modelled	82.4	16 Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
31	dlvhna_	Alignment	not modelled	80.8	17 Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
32	dlps9a1	Alignment	not modelled	79.7	13 Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
33	dlad1a_	Alignment	not modelled	77.9	20 Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
34	c3lhIA_	Alignment	not modelled	77.2	17 PDB header: hydrolase Chain: A: PDB Molecule: putative agmatinase; PDBTitle: crystal structure of a putative agmatinase from clostridium difficile
35	dlz41a1	Alignment	not modelled	75.2	19 Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
36	c3k2gA_	Alignment	not modelled	75.1	13 PDB header: resiniferatoxin binding protein Chain: A: PDB Molecule: resiniferatoxin-binding, phosphotriesterase- PDBTitle: crystal structure of a resiniferatoxin-binding protein from2 rhodobacter sphaeroides
37	dlvyra_	Alignment	not modelled	72.1	17 Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
38	dlajza_	Alignment	not modelled	71.9	19 Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
39	c3d0kA_	Alignment	not modelled	71.5	15 PDB header: hydrolase Chain: A: PDB Molecule: putative poly(3-hydroxybutyrate) depolymerase lpqc; PDBTitle: crystal structure of the lpqc, poly(3-hydroxybutyrate) depolymerase2 from bordetella parapertussis
40	clvraB_	Alignment	not modelled	69.9	23 PDB header: transferase Chain: B: PDB Molecule: arginine biosynthesis bifunctional protein argj; PDBTitle: crystal structure of arginine biosynthesis bifunctional protein argj2 (10175521) from bacillus halodurans at 2.00 a resolution
41	c2y5sA_	Alignment	not modelled	68.3	14 PDB header: transferase Chain: A: PDB Molecule: dihydropteroate synthase; PDBTitle: crystal structure of burkholderia cenocepacia dihydropteroate2 synthase complexed with 7,8-dihydropteroate.
42	c3inpA_	Alignment	not modelled	68.2	14 PDB header: isomerase Chain: A: PDB Molecule: d-ribulose-phosphate 3-epimerase; PDBTitle: 2.05 angstrom resolution crystal structure of d-ribulose-phosphate 3-2 epimerase from francisella tularensis.
43	dlgq6a_	Alignment	not modelled	67.8	19 Fold: Arginase/deacetylase Superfamily: Arginase/deacetylase Family: Arginase-like amidino hydrolases
44	c3it4B_	Alignment	not modelled	67.2	19 PDB header: transferase Chain: B: PDB Molecule: arginine biosynthesis bifunctional protein argj PDBTitle: the crystal structure of ornithine acetyltransferase from2 mycobacterium tuberculosis (rv1653) at 1.7 a
45	c3l5aA_	Alignment	not modelled	67.2	11 PDB header: oxidoreductase Chain: A: PDB Molecule: nadh/flavin oxidoreductase/nadh oxidase; PDBTitle: crystal structure of a probable nadh-dependent flavin oxidoreductase2 from staphylococcus aureus
46	c3nioF_	Alignment	not modelled	66.9	19 PDB header: hydrolase Chain: F: PDB Molecule: guanidinobutyrase; PDBTitle: crystal structure of pseudomonas aeruginosa guanidinobutyrase
47	c2qq8A_	Alignment	not modelled	65.0	14 PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, fmn-binding; PDBTitle: structure of sye1, an oye homologue from s. ondeidensis, in complex2 with p-hydroxyacetophenone
48	dlpq3a_	Alignment	not modelled	63.7	19 Fold: Arginase/deacetylase Superfamily: Arginase/deacetylase Family: Arginase-like amidino hydrolases
49	dlxfka_	Alignment	not modelled	63.6	18 Fold: Arginase/deacetylase Superfamily: Arginase/deacetylase Family: Arginase-like amidino hydrolases
50	d2a0ma1	Alignment	not modelled	62.6	26 Fold: Arginase/deacetylase Superfamily: Arginase/deacetylase Family: Arginase-like amidino hydrolases
51	d2ceva_	Alignment	not modelled	61.4	18 Fold: Arginase/deacetylase Superfamily: Arginase/deacetylase Family: Arginase-like amidino hydrolases
52	d2glka1	Alignment	not modelled	59.4	14 Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
53	c3atyA_	Alignment	not modelled	57.3	19 PDB header: oxidoreductase Chain: A: PDB Molecule: prostaglandin f2a synthase; PDBTitle: crystal structure of tcoye

54	d2iht3	Alignment	not modelled	55.5	27	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
55	c3r4iB	Alignment	not modelled	55.2	6	PDB header: lyase Chain: B: PDB Molecule: citrate lyase; PDBTitle: crystal structure of a citrate lyase (bx_e_b2899) from burkholderia2 xenovorans lb400 at 2.24 a resolution
56	d1woha	Alignment	not modelled	54.4	21	Fold: Arginase/deacetylase Superfamily: Arginase/deacetylase Family: Arginase-like amidino hydrolases
57	c1cqxB	Alignment	not modelled	50.3	25	PDB header: lipid binding protein Chain: B: PDB Molecule: flavo-hemoprotein; PDBTitle: crystal structure of the flavohemoglobin from alcaligenes eutrophus at2 1.75 a resolution
58	d1ujqa	Alignment	not modelled	49.5	17	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
59	d1t4ba1	Alignment	not modelled	48.6	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
60	d2csua1	Alignment	not modelled	47.9	26	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
61	c3nipB	Alignment	not modelled	47.9	16	PDB header: hydrolase Chain: B: PDB Molecule: 3-guanidinopropionase; PDBTitle: crystal structure of pseudomonas aeruginosa guanidinopropionase2 complexed with 1,6-diaminohexane
62	d1qi9a	Alignment	not modelled	47.3	17	Fold: Acid phosphatase/Vanadium-dependent haloperoxidase Superfamily: Acid phosphatase/Vanadium-dependent haloperoxidase Family: Haloperoxidase (bromoperoxidase)
63	d1gwja	Alignment	not modelled	46.9	17	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
64	d1m6ja	Alignment	not modelled	46.4	19	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
65	c3qxbB	Alignment	not modelled	46.1	8	PDB header: isomerase Chain: B: PDB Molecule: putative xylose isomerase; PDBTitle: crystal structure of a putative xylose isomerase (yp_426450.1) from2 rhodospirillum rubrum atcc 11170 at 1.90 a resolution
66	d1yl7a1	Alignment	not modelled	45.7	26	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
67	d1icpa	Alignment	not modelled	45.3	15	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
68	d1h6za1	Alignment	not modelled	43.9	18	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate phosphate dikinase, C-terminal domain
69	d1t9ba3	Alignment	not modelled	43.4	21	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
70	c2h9aB	Alignment	not modelled	43.3	15	PDB header: oxidoreductase Chain: B: PDB Molecule: co dehydrogenase/acetyl-coa synthase, iron- PDBTitle: corrinoide iron-sulfur protein
71	c3gr7A	Alignment	not modelled	43.3	15	PDB header: oxidoreductase Chain: A: PDB Molecule: nadph dehydrogenase; PDBTitle: structure of oye from geobacillus kaustophilus, hexagonal2 crystal form
72	d1vz6a	Alignment	not modelled	42.5	20	Fold: DmpA/Argj-like Superfamily: DmpA/Argj-like Family: Argj-like
73	d1oyaa	Alignment	not modelled	41.9	13	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
74	c2o1tB	Alignment	not modelled	41.6	12	PDB header: chaperone Chain: B: PDB Molecule: endoplasmic; PDBTitle: structure of middle plus c-terminal domains (m+c) of grp94
75	c2vzkD	Alignment	not modelled	41.3	19	PDB header: transferase Chain: D: PDB Molecule: glutamate n-acetyltransferase 2 beta chain; PDBTitle: structure of the acyl-enzyme complex of an n-terminal2 nucleophile (ntn) hydrolase, oat2
76	c2qw5B	Alignment	not modelled	40.0	9	PDB header: isomerase Chain: B: PDB Molecule: xylose isomerase-like tim barrel; PDBTitle: crystal structure of a putative sugar phosphate isomerase/epimerase2 (ava4194) from anabaena variabilis atcc 29413 at 1.78 a resolution
77	c3m1rF	Alignment	not modelled	39.8	32	PDB header: hydrolase Chain: F: PDB Molecule: formimidoyl glutamase; PDBTitle: the crystal structure of formimidoyl glutamase from bacillus subtilis subsp. subtilis str. 168
78	c3no4A	Alignment	not modelled	39.3	16	PDB header: hydrolase Chain: A: PDB Molecule: creatinine amidohydrolase; PDBTitle: crystal structure of a creatinine amidohydrolase (npun_f1913) from2 nostoc punctiforme pcc 73102 at 2.00 a resolution
						PDB header: hydrolase Chain: B: PDB Molecule: formyltetrahydrofolate deformylase;

79	c3o1lB_	Alignment	not modelled	39.0	13	PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (pspto_4314)2 from pseudomonas syringae pv. tomato str. dc3000 at 2.20 a resolution
80	c2gq0B_	Alignment	not modelled	38.1	19	PDB header: chaperone, hydrolase Chain: B: PDB Molecule: chaperone protein htpg; PDBTitle: crystal structure of the middle domain of htpg, the e. coli2 hsp90
81	c1y6zA_	Alignment	not modelled	36.8	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: heat shock protein, putative; PDBTitle: middle domain of plasmodium falciparum putative heat shock protein2 pf14_0417
82	c3dxiB_	Alignment	not modelled	36.3	12	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative aldolase; PDBTitle: crystal structure of the n-terminal domain of a putative2 aldolase (bvu_2661) from bacteroides vulgatus
83	c3tr9A_	Alignment	not modelled	35.3	15	PDB header: transferase Chain: A: PDB Molecule: dihydropteroate synthase; PDBTitle: structure of a dihydropteroate synthase (folp) in complex with pteroi2 acid from coxiella burnetii
84	c3nrbD_	Alignment	not modelled	34.0	21	PDB header: hydrolase Chain: D: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (puru,2 pp_1943) from pseudomonas putida kt2440 at 2.05 a resolution
85	c3mmrA_	Alignment	not modelled	33.6	17	PDB header: hydrolase Chain: A: PDB Molecule: arginase; PDBTitle: structure of plasmodium falciparum arginase in complex with abh
86	c1nofA_	Alignment	not modelled	33.3	11	PDB header: hydrolase Chain: A: PDB Molecule: xylanase; PDBTitle: the first crystallographic structure of a xylanase from2 glycosyl hydrolase family 5: implications for catalysis
87	c3icgD_	Alignment	not modelled	33.3	16	PDB header: hydrolase Chain: D: PDB Molecule: endoglucanase d; PDBTitle: crystal structure of the catalytic and carbohydrate binding domain of2 endoglucanase d from clostridium cellulovorans
88	c3pzlA_	Alignment	not modelled	32.5	19	PDB header: hydrolase Chain: A: PDB Molecule: agmatine ureohydrolase; PDBTitle: the crystal structure of agmatine ureohydrolase of thermoplasma2 volcanium
89	c3obiC_	Alignment	not modelled	31.9	14	PDB header: hydrolase Chain: C: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (np_949368)2 from rhodopseudomonas palustris cga009 at 1.95 a resolution
90	d1vjia_	Alignment	not modelled	31.9	13	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
91	d2aeba1	Alignment	not modelled	31.7	19	Fold: Arginase/deacetylase Superfamily: Arginase/deacetylase Family: Arginase-like amidino hydrolases
92	d1luaa2	Alignment	not modelled	31.1	22	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Methylene-tetrahydromethanopterin dehydrogenase
93	c3i05B_	Alignment	not modelled	30.4	19	PDB header: ligase Chain: B: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: tryptophanyl-trna synthetase from trypanosoma brucei
94	c2cgeD_	Alignment	not modelled	30.3	14	PDB header: chaperone Chain: D: PDB Molecule: atp-dependent molecular chaperone hsp82; PDBTitle: crystal structure of an hsp90-sba1 closed chaperone complex
95	c1gqkB_	Alignment	not modelled	30.2	55	PDB header: hydrolase Chain: B: PDB Molecule: alpha-d-glucuronidase; PDBTitle: structure of pseudomonas cellulosa alpha-d-glucuronidase2 complexed with glucuronic acid
96	c1ydnA_	Alignment	not modelled	29.9	10	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.
97	c1wr2A_	Alignment	not modelled	29.9	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ph1789; PDBTitle: crystal structure of ph1788 from pyrococcus horikoshii ot3
98	c3bleA_	Alignment	not modelled	29.3	18	PDB header: transferase Chain: A: PDB Molecule: citramalate synthase from leptospira interrogans; PDBTitle: crystal structure of the catalytic domain of licms in2 complexed with malonate
99	d1d3va_	Alignment	not modelled	28.2	18	Fold: Arginase/deacetylase Superfamily: Arginase/deacetylase Family: Arginase-like amidino hydrolases
100	d1oy0a_	Alignment	not modelled	28.0	22	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Ketopantoate hydroxymethyltransferase PanB
101	d1zs9a1	Alignment	not modelled	27.8	13	Fold: HAD-like Superfamily: HAD-like Family: Enolase-phosphatase E1
102	c3ih1A_	Alignment	not modelled	27.7	12	PDB header: lyase Chain: A: PDB Molecule: methylisocitrate lyase; PDBTitle: crystal structure of carboxyvinyl-carboxyphosphonate phosphorylmutase2 from bacillus anthracis
103	c3n2tA_	Alignment	not modelled	27.4	19	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: structure of the glycerol dehydrogenase akr11b4 from gluconobacter2 oxydans
						PDB header: hydrolase

104	c3lyeA_	Alignment	not modelled	27.2	14	Chain: A: PDB Molecule: oxaloacetate acetyl hydrolase; PDBTitle: crystal structure of oxaloacetate acetylhydrolase
105	c3epmB_	Alignment	not modelled	27.1	19	PDB header: biosynthetic protein Chain: B: PDB Molecule: thiamine biosynthesis protein thic; PDBTitle: crystal structure of caulobacter crescentus thic
106	c3q6nF_	Alignment	not modelled	27.0	17	PDB header: chaperone Chain: F: PDB Molecule: heat shock protein hsp 90-alpha; PDBTitle: crystal structure of human mc-hsp90 in p21 space group
107	d2p02a1	Alignment	not modelled	26.9	20	Fold: S-adenosylmethionine synthetase Superfamily: S-adenosylmethionine synthetase Family: S-adenosylmethionine synthetase
108	c3opbA_	Alignment	not modelled	24.9	19	PDB header: protein binding Chain: A: PDB Molecule: swi5-dependent ho expression protein 4; PDBTitle: crystal structure of she4p
109	d2hcfa1	Alignment	not modelled	24.8	9	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucosylase-like
110	c3mwdB_	Alignment	not modelled	24.8	14	PDB header: transferase Chain: B: PDB Molecule: atp-citrate synthase; PDBTitle: truncated human atp-citrate lyase with citrate bound
111	c3krsB_	Alignment	not modelled	24.8	16	PDB header: isomerase Chain: B: PDB Molecule: triosephosphate isomerase; PDBTitle: structure of triosephosphate isomerase from cryptosporidium parvum at2 1.55a resolution
112	d1r5ja_	Alignment	not modelled	24.6	14	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Phosphotransacetylase
113	c1vm6B_	Alignment	not modelled	24.5	9	PDB header: oxidoreductase Chain: B: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: crystal structure of dihydrodipicolinate reductase (tm1520) from2 thermotoga maritima at 2.27 a resolution
114	d1qh8b_	Alignment	not modelled	24.3	19	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein
115	c3pryA_	Alignment	not modelled	24.2	14	PDB header: chaperone Chain: A: PDB Molecule: heat shock protein hsp 90-beta; PDBTitle: crystal structure of the middle domain of human hsp90-beta refined at2 2.3 a resolution
116	c3gkaB_	Alignment	not modelled	23.7	17	PDB header: oxidoreductase Chain: B: PDB Molecule: n-ethylmaleimide reductase; PDBTitle: crystal structure of n-ethylmaleimide reductase from2 burkholderia pseudomallei
117	d1rqba2	Alignment	not modelled	23.4	13	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: HMGL-like
118	c3hjca_	Alignment	not modelled	23.0	24	PDB header: chaperone Chain: A: PDB Molecule: heat shock protein 83-1; PDBTitle: crystal structure of the carboxy-terminal domain of hsp90 from2 leishmania major, lmjf33.0312
119	c2v1dA_	Alignment	not modelled	22.7	15	PDB header: oxidoreductase/repressor Chain: A: PDB Molecule: lysine-specific histone demethylase 1; PDBTitle: structural basis of lsd1-corest selectivity in histone h32 recognition
120	c3cyvA_	Alignment	not modelled	22.3	12	PDB header: lyase Chain: A: PDB Molecule: uroporphyrinogen decarboxylase; PDBTitle: crystal structure of uroporphyrinogen decarboxylase from2 shigella flexneri: new insights into its catalytic mechanism