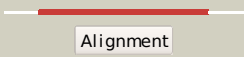

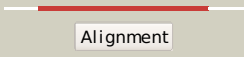

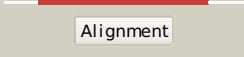
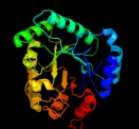
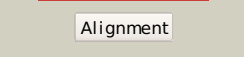

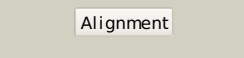

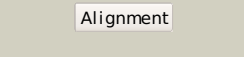

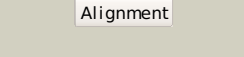

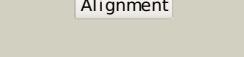

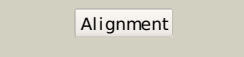

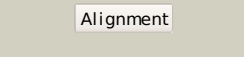

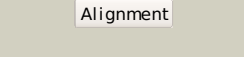












#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1qtwA_	 Alignment		100.0	100	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Endonuclease IV
2	c2x7vA_	 Alignment		100.0	32	PDB header: hydrolase Chain: A: PDB Molecule: probable endonuclease 4; PDBTitle: crystal structure of thermotoga maritima endonuclease iv in2 the presence of zinc
3	d1xp3a1	 Alignment		100.0	30	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Endonuclease IV
4	c3aamA_	 Alignment		100.0	35	PDB header: hydrolase Chain: A: PDB Molecule: endonuclease iv; PDBTitle: crystal structure of endonuclease iv from thermus thermophilus hb8
5	c3qxbB_	 Alignment		100.0	10	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
6	c2hk1D_	 Alignment		100.0	16	PDB header: isomerase Chain: D: PDB Molecule: d-psicose 3-epimerase; PDBTitle: crystal structure of d-psicose 3-epimerase (dpease) in the presence of2 d-fructose
7	c2qw5B_	 Alignment		100.0	16	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
8	c3cqkB_	 Alignment		100.0	11	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
9	d1i60a_	 Alignment		100.0	15	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: lolI-like
10	c2ou4C_	 Alignment		100.0	16	PDB header: isomerase Chain: C: PDB Molecule: d-tagatose 3-epimerase; PDBTitle: crystal structure of d-tagatose 3-epimerase from2 pseudomonas cichorii
11	c3kwsB_	 Alignment		100.0	12	PDB header: isomerase Chain: B: PDB Molecule: putative sugar isomerase; PDBTitle: crystal structure of putative sugar isomerase (yp_001305149.1) from2 parabacteroides distasonis atcc 8503 at 1.68 a resolution

12	c3ktcB	Alignment		100.0	16	PDB header: isomerase Chain: B: PDB Molecule: xylose isomerase; PDBTitle: crystal structure of putative sugar isomerase (yp_050048.1) from2 erwinia carotovora atroseptica scri1043 at 1.54 a resolution
13	c2zvrA	Alignment		100.0	16	PDB header: isomerase Chain: A: PDB Molecule: uncharacterized protein tm_0416; PDBTitle: crystal structure of a d-tagatose 3-epimerase-related2 protein from thermotoga maritima
14	c2zdsB	Alignment		100.0	18	PDB header: dna binding protein Chain: B: PDB Molecule: putative dna-binding protein; PDBTitle: crystal structure of sco6571 from streptomyces coelicolor2 a3(2)
15	c3ju2A	Alignment		100.0	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein smc04130; PDBTitle: crystal structure of protein smc04130 from sinorhizobium meliloti 1021
16	d1k77a	Alignment		100.0	16	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Hypothetical protein YgbM (EC1530)
17	c3dx5A	Alignment		100.0	13	PDB header: lyase Chain: A: PDB Molecule: uncharacterized protein asbf; PDBTitle: crystal structure of the probable 3-dhs dehydratase asbf involved in2 the petrobactin synthesis from bacillus anthracis
18	c3ngfA	Alignment		100.0	14	PDB header: isomerase Chain: A: PDB Molecule: ap endonuclease, family 2; PDBTitle: crystal structure of ap endonuclease, family 2 from brucella2 melitensis
19	c3cnyA	Alignment		100.0	13	PDB header: biosynthetic protein Chain: A: PDB Molecule: inositol catabolism protein iole; PDBTitle: crystal structure of a putative inositol catabolism protein iole2 (iole, lp_3607) from lactobacillus plantarum wcfs1 at 1.85 a3 resolution
20	c3obeB	Alignment		100.0	13	PDB header: isomerase Chain: B: PDB Molecule: sugar phosphate isomerase/epimerase; PDBTitle: crystal structure of a sugar phosphate isomerase/epimerase (bdi_3400)2 from parabacteroides distasonis atcc 8503 at 1.70 a resolution
21	c3l23A	Alignment	not modelled	100.0	13	PDB header: isomerase Chain: A: PDB Molecule: sugar phosphate isomerase/epimerase; PDBTitle: crystal structure of sugar phosphate isomerase/epimerase2 (yp_001303399.1) from parabacteroides distasonis atcc 8503 at 1.70 a3 resolution
22	d2g0wa1	Alignment	not modelled	100.0	13	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: loli-like
23	d2q02a1	Alignment	not modelled	100.0	13	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: loli-like
24	c3lmzA	Alignment	not modelled	100.0	17	PDB header: isomerase Chain: A: PDB Molecule: putative sugar isomerase; PDBTitle: crystal structure of putative sugar isomerase. (yp_001305105.1) from2 parabacteroides distasonis atcc 8503 at 1.44 a resolution
25	c3p6lA	Alignment	not modelled	100.0	15	PDB header: isomerase Chain: A: PDB Molecule: sugar phosphate isomerase/epimerase; PDBTitle: crystal structure of a sugar phosphate isomerase/epimerase (bdi_1903)2 from parabacteroides distasonis atcc 8503 at 1.85 a resolution
26	d1xima	Alignment	not modelled	100.0	18	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
27	d1yx1a1	Alignment	not modelled	100.0	15	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: KguE-like
28	d1tz9a	Alignment	not modelled	100.0	13	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: UxuA-like

29	d1muwa_	Alignment	not modelled	100.0	16	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
30	d1qt1a_	Alignment	not modelled	100.0	18	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
31	d2glka1	Alignment	not modelled	100.0	16	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
32	d1bxba_	Alignment	not modelled	99.9	17	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
33	d1bxca_	Alignment	not modelled	99.9	16	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
34	c3bdkB_	Alignment	not modelled	99.9	14	PDB header: lyase Chain: B: PDB Molecule: d-mannonate dehydratase; PDBTitle: crystal structure of streptococcus suis mannonate2 dehydratase complexed with substrate analogue
35	d1x1ma_	Alignment	not modelled	99.9	16	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
36	c3bzjA_	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: A: PDB Molecule: uv endonuclease; PDBTitle: uvde k229l
37	d1a0ea_	Alignment	not modelled	99.7	11	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
38	d1a0da_	Alignment	not modelled	99.7	11	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
39	c2i56A_	Alignment	not modelled	99.7	15	PDB header: isomerase, metal-binding protein Chain: A: PDB Molecule: l-rhamnose isomerase; PDBTitle: crystal structure of l-rhamnose isomerase from pseudomonas2 stutzeri with l-rhamnose
40	d1a0ca_	Alignment	not modelled	99.7	14	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
41	c3bwwA_	Alignment	not modelled	99.0	16	PDB header: metal binding protein Chain: A: PDB Molecule: protein of unknown function duf692/cog3220; PDBTitle: crystal structure of a duf692 family protein (hs_1138) from2 haemophilus somnus 129pt at 2.20 a resolution
42	d1d8wa_	Alignment	not modelled	98.4	12	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: L-rhamnose isomerase
43	c3p14C_	Alignment	not modelled	98.1	14	PDB header: isomerase Chain: C: PDB Molecule: l-rhamnose isomerase; PDBTitle: crystal structure of l-rhamnose isomerase with a novel high thermo-2 stability from bacillus halodurans
44	d1qwga_	Alignment	not modelled	97.5	11	Fold: TIM beta/alpha-barrel Superfamily: (2r)-phospho-3-sulfolactate synthase ComA Family: (2r)-phospho-3-sulfolactate synthase ComA
45	c1rr2A_	Alignment	not modelled	96.8	10	PDB header: transferase Chain: A: PDB Molecule: transcarboxylase 5s subunit; PDBTitle: propionibacterium shermanii transcarboxylase 5s subunit bound to 2-2 ketobutyric acid
46	c2ftpA_	Alignment	not modelled	96.2	15	PDB header: lyase Chain: A: PDB Molecule: hydroxymethylglutaryl-coa lyase; PDBTitle: crystal structure of hydroxymethylglutaryl-coa lyase from pseudomonas2 aeruginosa
47	c2nx9B_	Alignment	not modelled	95.7	12	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
48	c3bg3B_	Alignment	not modelled	95.5	11	PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase, mitochondrial; PDBTitle: crystal structure of human pyruvate carboxylase (missing2 the biotin carboxylase domain at the n-terminus)
49	c1ydoC_	Alignment	not modelled	95.3	15	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.
50	d1rqba2	Alignment	not modelled	94.5	14	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: HMGL-like
51	d1u83a_	Alignment	not modelled	93.6	10	Fold: TIM beta/alpha-barrel Superfamily: (2r)-phospho-3-sulfolactate synthase ComA Family: (2r)-phospho-3-sulfolactate synthase ComA
52	c1u83A_	Alignment	not modelled	93.6	10	PDB header: lyase Chain: A: PDB Molecule: phosphosulfolactate synthase; PDBTitle: psl synthase from bacillus subtilis
53	c2zyfA_	Alignment	not modelled	93.2	13	PDB header: transferase Chain: A: PDB Molecule: homocitrate synthase; PDBTitle: crystal structure of homocitrate synthase from thermus thermophilus2 complexed with magnesuim ion and alpha-ketoglutarate
54	c3hf3A_	Alignment	not modelled	93.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: chromate reductase; PDBTitle: old yellow enzyme from thermus scotoductus sa-01
						PDB header: biosynthetic protein

55	c3btnA	Alignment	not modelled	92.8	11	Chain: A: PDB Molecule: antizyme inhibitor 1; PDBTitle: crystal structure of antizyme inhibitor, an ornithine2 decarboxylase homologous protein
56	c2i2xO	Alignment	not modelled	92.6	16	PDB header: transferase Chain: O: PDB Molecule: methyltransferase 1; PDBTitle: crystal structure of methanol:cobalamin methyltransferase complex2 mtabc from methanosarcina barkeri
57	c2cw6B	Alignment	not modelled	92.6	13	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
58	c1ydnA	Alignment	not modelled	92.1	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.
59	c3ogrA	Alignment	not modelled	92.1	8	PDB header: hydrolase Chain: A: PDB Molecule: beta-galactosidase; PDBTitle: complex structure of beta-galactosidase from trichoderma reesei with2 galactose
60	d1z41a1	Alignment	not modelled	91.9	12	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
61	c2dh3A	Alignment	not modelled	91.8	15	PDB header: transport protein, signaling protein Chain: A: PDB Molecule: 4f2 cell-surface antigen heavy chain; PDBTitle: crystal structure of human ed-4f2hc
62	c3ivuB	Alignment	not modelled	91.1	11	PDB header: transferase Chain: B: PDB Molecule: homocitrate synthase, mitochondrial; PDBTitle: homocitrate synthase lys4 bound to 2-og
63	d1f3ta2	Alignment	not modelled	90.6	10	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel Family: Alanine racemase-like, N-terminal domain
64	c3gk0H	Alignment	not modelled	90.4	12	PDB header: transferase Chain: H: PDB Molecule: pyridoxine 5'-phosphate synthase; PDBTitle: crystal structure of pyridoxal phosphate biosynthetic2 protein from burkholderia pseudomallei
65	d1ps9a1	Alignment	not modelled	89.9	16	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
66	c1gcyA	Alignment	not modelled	89.6	10	PDB header: hydrolase Chain: A: PDB Molecule: glucan 1,4-alpha-maltotetrahydrolase; PDBTitle: high resolution crystal structure of maltotetraose-forming2 exo-amylase
67	c1d7kB	Alignment	not modelled	88.9	15	PDB header: lyase Chain: B: PDB Molecule: human ornithine decarboxylase; PDBTitle: crystal structure of human ornithine decarboxylase at 2.12 angstroms resolution
68	c2hmaA	Alignment	not modelled	88.5	16	PDB header: transferase Chain: A: PDB Molecule: probable trna (5-methylaminomethyl-2-thiouridylate)- PDBTitle: the crystal structure of trna (5-methylaminomethyl-2-thiouridylate)-2 methyltransferase trmu from streptococcus pneumoniae
69	d1d7ka2	Alignment	not modelled	88.3	11	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel Family: Alanine racemase-like, N-terminal domain
70	d1x7fa2	Alignment	not modelled	87.9	12	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Outer surface protein, N-terminal domain
71	c2h90A	Alignment	not modelled	86.9	12	PDB header: oxidoreductase Chain: A: PDB Molecule: xenobiotic reductase a; PDBTitle: xenobiotic reductase a in complex with coumarin
72	d1ujpa	Alignment	not modelled	85.9	9	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
73	c1j0yD	Alignment	not modelled	85.2	11	PDB header: hydrolase Chain: D: PDB Molecule: beta-amylase; PDBTitle: beta-amylase from bacillus cereus var. mycoides in complex2 with glucose
74	d1vyra	Alignment	not modelled	85.0	12	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
75	c1sr9A	Alignment	not modelled	85.0	12	PDB header: transferase Chain: A: PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of leua from mycobacterium tuberculosis
76	d7odca2	Alignment	not modelled	84.5	11	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel Family: Alanine racemase-like, N-terminal domain
77	c2aaaA	Alignment	not modelled	84.4	9	PDB header: glycosidase Chain: A: PDB Molecule: alpha-amylase; PDBTitle: calcium binding in alpha-amylases: an x-ray diffraction2 study at 2.1 angstroms resolution of two enzymes from3 aspergillus
78	d1e43a2	Alignment	not modelled	84.3	22	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
79	c2on3A	Alignment	not modelled	83.7	11	PDB header: lyase Chain: A: PDB Molecule: ornithine decarboxylase; PDBTitle: a structural insight into the inhibition of human and2 leishmania donovani ornithine decarboxylases by 3-aminoxy-3 1-aminopropane
80	d1rh9a1	Alignment	not modelled	83.5	14	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases

					Family:beta-glycanases
81	c2xioA_	Alignment	not modelled	83.2	12 PDB header: hydrolase Chain: A: PDB Molecule: putative deoxyribonuclease tatdn1; PDBTitle: structure of putative deoxyribonuclease tatdn1 isoform a
82	c3aysA_	Alignment	not modelled	82.0	9 PDB header: hydrolase Chain: A: PDB Molecule: endoglucanase; PDBTitle: gh5 endoglucanase from a ruminal fungus in complex with cellobiose
83	c3u7vA_	Alignment	not modelled	81.9	7 PDB header: hydrolase Chain: A: PDB Molecule: beta-galactosidase; PDBTitle: the structure of a putative beta-galactosidase from caulobacter2 crescentus cb15.
84	d1vema2	Alignment	not modelled	81.7	11 Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
85	c2ekcA_	Alignment	not modelled	81.6	21 PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: structural study of project id aq_1548 from aquifex aeolicus vf5
86	c1ud8A_	Alignment	not modelled	81.5	17 PDB header: hydrolase Chain: A: PDB Molecule: amylase; PDBTitle: crystal structure of amyk38 with lithium ion
87	c1qhoA_	Alignment	not modelled	80.5	15 PDB header: hydrolase Chain: A: PDB Molecule: alpha-amylase; PDBTitle: five-domain alpha-amylase from bacillus stearothermophilus,2 maltose/acarbose complex
88	d1nvma2	Alignment	not modelled	79.5	11 Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: HMGL-like
89	c2taaA_	Alignment	not modelled	79.1	11 PDB header: hydrolase (o-glycosyl) Chain: A: PDB Molecule: taka-amylase a; PDBTitle: structure and possible catalytic residues of taka-amylase a
90	c2by0A_	Alignment	not modelled	79.1	14 PDB header: hydrolase Chain: A: PDB Molecule: maltooligosyltrehalose trehalohydrolase; PDBTitle: is radiation damage dependent on the dose-rate used during2 macromolecular crystallography data collection
91	d1q45a_	Alignment	not modelled	79.0	18 Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
92	c3b0vD_	Alignment	not modelled	79.0	17 PDB header: oxidoreductase/rna Chain: D: PDB Molecule: trna-dihydrouridine synthase; PDBTitle: trna-dihydrouridine synthase from thermus thermophilus in complex with2 trna
93	c1xc6A_	Alignment	not modelled	78.8	10 PDB header: hydrolase Chain: A: PDB Molecule: beta-galactosidase; PDBTitle: native structure of beta-galactosidase from penicillium sp. in complex2 with galactose
94	c1x7fA_	Alignment	not modelled	78.6	14 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: outer surface protein; PDBTitle: crystal structure of an uncharacterized b. cereus protein
95	c3dhuC_	Alignment	not modelled	78.3	13 PDB header: hydrolase Chain: C: PDB Molecule: alpha-amylase; PDBTitle: crystal structure of an alpha-amylase from lactobacillus2 plantarum
96	d1oyaa_	Alignment	not modelled	78.3	16 Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
97	c2bdqA_	Alignment	not modelled	77.9	14 PDB header: metal transport Chain: A: PDB Molecule: copper homeostasis protein cutc; PDBTitle: crystal structure of the putative copper homeostasis2 protein cutc from streptococcus agalactiae, northeast3 strucural genomics target sar15.
98	c3mi6A_	Alignment	not modelled	77.7	9 PDB header: hydrolase Chain: A: PDB Molecule: alpha-galactosidase; PDBTitle: crystal structure of the alpha-galactosidase from lactobacillus2 brevis, northeast structural genomics consortium target lbr11.
99	d1gjwa2	Alignment	not modelled	77.3	11 Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
100	d2bhua3	Alignment	not modelled	77.3	14 Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
101	c1bagA_	Alignment	not modelled	77.2	18 PDB header: alpha-amylase Chain: A: PDB Molecule: alpha-1,4-glucan-4-glucanohydrolase; PDBTitle: alpha-amylase from bacillus subtilis complexed with2 maltopentaose
102	c3thaB_	Alignment	not modelled	77.0	19 PDB header: lyase Chain: B: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: tryptophan synthase subunit alpha from campylobacter jejuni.
103	d1avaa2	Alignment	not modelled	76.2	12 Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
104	d1icpa_	Alignment	not modelled	75.1	18 Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
105	c3l5aA_	Alignment	not modelled	74.6	14 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
106	c3owhY_	Alignment	not modelled	74.5	13 PDB header: transferase Chain: X: PDB Molecule: 2-isopropylmalate synthase;

106	c3ewvA_	Alignment	not modelled	74.3	13	PDBTitle: crystal structure of n-terminal domain of putative 2-2 isopropylmalate synthase from listeria monocytogenes PDB header: lyase
107	c2qjhH_	Alignment	not modelled	74.3	13	Chain: H: PDB Molecule: putative aldolase mj0400; PDBTitle: m. jannaschii adh synthase covalently bound to2 dihydroxyacetone phosphate
108	c3lciA_	Alignment	not modelled	74.2	8	PDB header: lyase Chain: A: PDB Molecule: n-acetylneuraminate lyase; PDBTitle: the d-sialic acid aldolase mutant v251w
109	d1ua7a2	Alignment	not modelled	74.0	18	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
110	c1njjC_	Alignment	not modelled	73.7	11	PDB header: lyase Chain: C: PDB Molecule: ornithine decarboxylase; PDBTitle: crystal structure determination of t. brucei ornithine2 decarboxylase bound to d-ornithine and to g418
111	c1jd7A_	Alignment	not modelled	73.5	8	PDB header: hydrolase Chain: A: PDB Molecule: alpha-amylase; PDBTitle: crystal structure analysis of the mutant k300r of2 pseudoalteromonas haloplantis alpha-amylase
112	d1hx0a2	Alignment	not modelled	73.3	2	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
113	d1vjia_	Alignment	not modelled	73.0	23	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
114	c2derA_	Alignment	not modelled	73.0	20	PDB header: transferase/rna Chain: A: PDB Molecule: trna-specific 2-thiouridylase mnma; PDBTitle: cocrystal structure of an rna sulfuration enzyme mnma and2 trna-glu in the initial trna binding state
115	c3qc3B_	Alignment	not modelled	72.8	11	PDB header: isomerase Chain: B: PDB Molecule: d-ribulose-5-phosphate-3-epimerase; PDBTitle: crystal structure of a d-ribulose-5-phosphate-3-epimerase (np_954699)2 from homo sapiens at 2.20 a resolution
116	c1ehaA_	Alignment	not modelled	72.8	9	PDB header: hydrolase Chain: A: PDB Molecule: glycosyltrehalose trehalohydrolase; PDBTitle: crystal structure of glycosyltrehalose trehalohydrolase2 from sulfolobus solfataricus
117	d1hvx2	Alignment	not modelled	72.4	19	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
118	d1djq1	Alignment	not modelled	72.4	13	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
119	c3k8kB_	Alignment	not modelled	71.7	9	PDB header: membrane protein Chain: B: PDB Molecule: alpha-amylase, susg; PDBTitle: crystal structure of susg
120	c3eegB_	Alignment	not modelled	71.5	13	PDB header: transferase Chain: B: PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of a 2-isopropylmalate synthase from2 cytophaga hutchinsonii