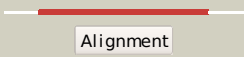

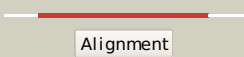

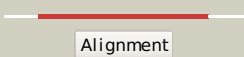

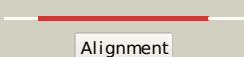

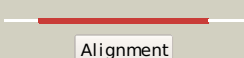

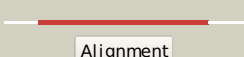

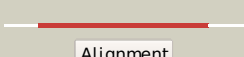

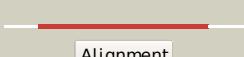

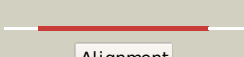

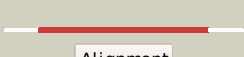





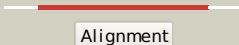



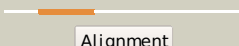
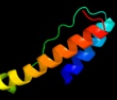
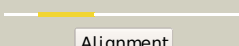
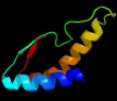
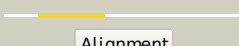

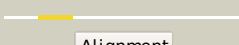


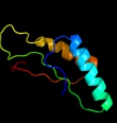
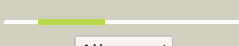

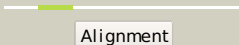
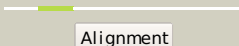
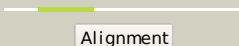
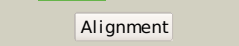
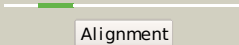

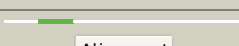
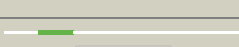
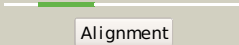
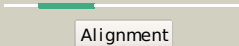
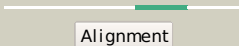

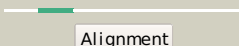
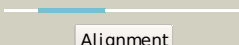




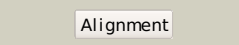

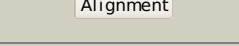
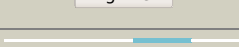

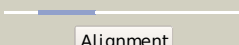

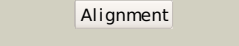
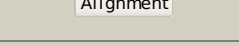
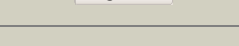
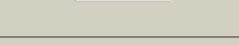
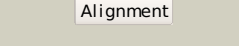
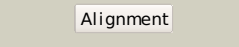
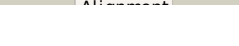



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1emsB_	 Alignment		100.0	30	PDB header: antitumor protein Chain: B; PDB Molecule: nit-fragile histidine triad fusion protein; PDBTitle: crystal structure of the c. elegans nitfhit protein
2	c2vhiG_	 Alignment		100.0	23	PDB header: hydrolase Chain: G; PDB Molecule: cg3027-pa; PDBTitle: crystal structure of a pyrimidine degrading enzyme from <i>Drosophila melanogaster</i>
3	c2w1vA_	 Alignment		100.0	26	PDB header: hydrolase Chain: A; PDB Molecule: nitrilase homolog 2; PDBTitle: crystal structure of mouse nitrilase-2 at 1.4 Å resolution
4	d1uf5a_	 Alignment		100.0	25	Fold: Carbon-nitrogen hydrolase Superfamily: Carbon-nitrogen hydrolase Family: Carbamylase
5	c2e2kC_	 Alignment		100.0	19	PDB header: hydrolase Chain: C; PDB Molecule: formamidase; PDBTitle: <i>Helicobacter pylori</i> formamidase Amif contains a fine-tuned cysteine-2 glutamate-lysine catalytic triad
6	c2plqA_	 Alignment		100.0	21	PDB header: hydrolase Chain: A; PDB Molecule: aliphatic amidase; PDBTitle: crystal structure of the amidase from <i>Geobacillus pallidus</i> rapc8
7	d1emsa2	 Alignment		100.0	31	Fold: Carbon-nitrogen hydrolase Superfamily: Carbon-nitrogen hydrolase Family: Nitrilase
8	c3dlaD_	 Alignment		100.0	19	PDB header: ligase Chain: D; PDB Molecule: glutamine-dependent nad(+) synthetase; PDBTitle: x-ray crystal structure of glutamine-dependent nad+ synthetase from <i>Mycobacterium tuberculosis</i> bound to nad+ and don
9	c2e11B_	 Alignment		100.0	20	PDB header: hydrolase Chain: B; PDB Molecule: hydrolase; PDBTitle: the crystal structure of xc1258 from <i>Xanthomonas campestris</i> : a cn-2 hydrolase superfamily protein with an arsenic adduct in the active site
10	d1f89a_	 Alignment		100.0	25	Fold: Carbon-nitrogen hydrolase Superfamily: Carbon-nitrogen hydrolase Family: Nitrilase
11	d1j31a_	 Alignment		100.0	25	Fold: Carbon-nitrogen hydrolase Superfamily: Carbon-nitrogen hydrolase Family: Carbamylase

12	c3hxA_		Alignment		100.0	24	PDB header: hydrolase Chain: A: PDB Molecule: amidase; PDBTitle: crystal structure analysis of an amidase from nesterenkonia sp.
13	c3n05B_		Alignment		100.0	22	PDB header: ligase Chain: B: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: crystal structure of nh3-dependent nad+ synthetase from streptomyces2 avermitilis
14	c3ilvA_		Alignment		100.0	16	PDB header: ligase Chain: A: PDB Molecule: glutamine-dependent nad(+) synthetase; PDBTitle: crystal structure of a glutamine-dependent nad(+) synthetase2 from cytophaga hutchinsonii
15	c3qxB_		Alignment		82.6	9	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
16	c2hk1D_		Alignment		78.7	6	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
17	d1o60a_		Alignment		77.1	11	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I DAHP synthetase
18	d1s3la_		Alignment		70.5	6	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: YfcE-like
19	d1d9ea_		Alignment		70.3	18	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I DAHP synthetase
20	c2qw5B_		Alignment		69.3	11	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
21	c1s3mA_		Alignment	not modelled	69.3	6	PDB header: phosphodiesterase Chain: A: PDB Molecule: hypothetical protein mj0936; PDBTitle: structural and functional characterization of a novel2 archaeal phosphodiesterase
22	c3qfNA_		Alignment	not modelled	67.7	18	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of streptococcal asymmetric ap4a hydrolase and2 phosphodiesterase spr1479/saph in complex with inorganic phosphate
23	c2zdsB_		Alignment	not modelled	61.2	7	PDB header: dna binding protein Chain: B: PDB Molecule: putative dna-binding protein; PDBTitle: crystal structure of sco6571 from streptomyces coelicolor2 a3(2)
24	d1ydga_		Alignment	not modelled	57.0	11	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: WrbA-like
25	d1uf3a_		Alignment	not modelled	56.2	28	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: TT1561-like
26	d1vlia2		Alignment	not modelled	55.9	14	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: NeuB-like
27	d1su1a_		Alignment	not modelled	55.2	15	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: YfcE-like
28	c1su1A_		Alignment	not modelled	55.2	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein yfce; PDBTitle: structural and biochemical characterization of yfce, a2 phosphoesterase from e. coli

29	c2ou4C_	 Alignment	not modelled	51.7	12	PDB header: isomerase Chain: C: PDB Molecule: d-tagatose 3-epimerase; PDBTitle: crystal structure of d-tagatose 3-epimerase from2 pseudomonas cichorii
30	c3cnyA_	 Alignment	not modelled	48.8	12	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
31	c2nydB_	 Alignment	not modelled	41.0	14	PDB header: unknown function Chain: B: PDB Molecule: upf0135 protein sa1388; PDBTitle: crystal structure of staphylococcus aureus hypothetical protein sa1388
32	c3kwsB_	 Alignment	not modelled	40.8	8	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
33	c2ei9A_	 Alignment	not modelled	40.7	17	PDB header: gene regulation Chain: A: PDB Molecule: non-ltr retrotransposon r1bmks orf2 protein; PDBTitle: crystal structure of r1bm endonuclease domain
34	c3sz8D_	 Alignment	not modelled	39.5	13	PDB header: transferase Chain: D: PDB Molecule: 2-dehydro-3-deoxyphosphooctonate aldolase 2; PDBTitle: crystal structure of 2-dehydro-3-deoxyphosphooctonate aldolase from2 burkholderia pseudomallei
35	c3stgA_	 Alignment	not modelled	38.4	15	PDB header: transferase Chain: A: PDB Molecule: 2-dehydro-3-deoxyphosphooctonate aldolase; PDBTitle: crystal structure of a58p, del(n59), and loop 7 truncated mutant of 3-2 deoxy-d-manno-octulosonate 8-phosphate synthase (kdo8ps) from3 neisseria meningitidis
36	c3o3cD_	 Alignment	not modelled	38.0	12	PDB header: transferase Chain: D: PDB Molecule: glycogen [starch] synthase isoform 2; PDBTitle: glycogen synthase basal state udp complex
37	d1o66a_	 Alignment	not modelled	37.4	16	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Ketopantoate hydroxymethyltransferase PanB
38	d1i60a_	 Alignment	not modelled	37.2	9	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: loli-like
39	d1gsaa1	 Alignment	not modelled	36.4	5	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: Prokaryotic glutathione synthetase, N-terminal domain
40	c3ju2A_	 Alignment	not modelled	35.2	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein smc04130; PDBTitle: crystal structure of protein smc04130 from sinorhizobium meliloti 1021
41	c1gshA_	 Alignment	not modelled	34.6	5	PDB header: glutathione biosynthesis ligase Chain: A: PDB Molecule: glutathione biosynthetic ligase; PDBTitle: structure of escherichia coli glutathione synthetase at ph 7.5
42	d2ngra3	 Alignment	not modelled	31.2	8	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
43	d4pgaa_	 Alignment	not modelled	31.2	13	Fold: Glutaminase/Asparaginase Superfamily: Glutaminase/Asparaginase Family: Glutaminase/Asparaginase
44	d2q02a1	 Alignment	not modelled	30.9	14	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: loli-like
45	c3dx5A_	 Alignment	not modelled	29.6	12	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
46	d1yx1a1	 Alignment	not modelled	29.4	14	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: KguE-like
47	d1wdua_	 Alignment	not modelled	28.6	20	Fold: DNase I-like Superfamily: DNase I-like Family: DNase I-like
48	c2csuB_	 Alignment	not modelled	28.5	11	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: 457aa long hypothetical protein; PDBTitle: crystal structure of ph0766 from pyrococcus horikoshii ot3
49	d1hd7a_	 Alignment	not modelled	28.3	11	Fold: DNase I-like Superfamily: DNase I-like Family: DNase I-like
50	c2zsmA_	 Alignment	not modelled	28.2	25	PDB header: isomerase Chain: A: PDB Molecule: glutamate-1-semialdehyde 2,1-aminomutase; PDBTitle: crystal structure of glutamate-1-semialdehyde 2,1-2 aminomutase from aeropyrum pernix, hexagonal form
51	c1vliA_	 Alignment	not modelled	26.9	14	PDB header: biosynthetic protein Chain: A: PDB Molecule: spore coat polysaccharide biosynthesis protein spse; PDBTitle: crystal structure of spore coat polysaccharide biosynthesis protein2 spse (bsu37870) from bacillus subtilis at 2.38 a resolution
52	d1nmpa_	 Alignment	not modelled	26.4	12	Fold: NIF3 (NGG1p interacting factor 3)-like Superfamily: NIF3 (NGG1p interacting factor 3)-like Family: NIF3 (NGG1p interacting factor 3)-like
53	c3i4iC_	 Alignment	not modelled	25.7	20	PDB header: transferase Chain: C: PDB Molecule: aminotransferase, class iii;

53	c34jc_	Alignment	not modelled	23.7	20	PDBTitle: crystal structure of aminotransferase, class iii from2 deinococcus radiodurans
54	c2o14A_	Alignment	not modelled	24.3	9	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein yxim; PDBTitle: x-ray crystal structure of protein yxim_bacsu from bacillus2 subtilis. northeast structural genomics consortium target3 sr595
55	c3pnxF_	Alignment	not modelled	23.6	10	PDB header: transferase Chain: F: PDB Molecule: putative sulfurtransferase dsre; PDBTitle: crystal structure of a putative sulfurtransferase dsre (swol_2425)2 from syntrophomonas wolfei str. goettingen at 1.92 a resolution
56	dloi7a1	Alignment	not modelled	23.6	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
57	c3pg8B_	Alignment	not modelled	22.4	13	PDB header: transferase Chain: B: PDB Molecule: phospho-2-dehydro-3-deoxyheptonate aldolase; PDBTitle: truncated form of 3-deoxy-d-arabino-heptulosonate 7-phosphate synthase2 from thermotoga maritima
58	d2gx8a1	Alignment	not modelled	22.1	12	Fold: NIF3 (NGG1p interacting factor 3)-like Superfamily: NIF3 (NGG1p interacting factor 3)-like Family: NIF3 (NGG1p interacting factor 3)-like
59	c1zcoA_	Alignment	not modelled	21.7	15	PDB header: lyase Chain: A: PDB Molecule: 2-dehydro-3-deoxyphosphoheptonate aldolase; PDBTitle: crystal structure of pyrococcus furiosus 3-deoxy-d-arabino-2 heptulosonate 7-phosphate synthase
60	c1vs1B_	Alignment	not modelled	20.7	21	PDB header: transferase Chain: B: PDB Molecule: 3-deoxy-7-phosphoheptulonate synthase; PDBTitle: crystal structure of 3-deoxy-d-arabino-heptulosonate-7-2 phosphate synthase (dahp synthase) from aeropyrum pernix3 in complex with mn2+ and pep
61	c3rqzC_	Alignment	not modelled	20.2	13	PDB header: hydrolase Chain: C: PDB Molecule: metallophosphoesterase; PDBTitle: crystal structure of metallophosphoesterase from sphaeobacter2 thermophilus
62	d1k9vf_	Alignment	not modelled	20.0	26	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
63	d2zdra2	Alignment	not modelled	19.9	13	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: NeuB-like
64	c3bleA_	Alignment	not modelled	19.7	11	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
65	d2vgna3	Alignment	not modelled	19.1	15	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: ERF1/Dom34 C-terminal domain-like
66	c3cqkB_	Alignment	not modelled	18.9	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
67	c2wltA_	Alignment	not modelled	18.8	19	PDB header: hydrolase Chain: A: PDB Molecule: l-asparaginase; PDBTitle: the crystal structure of helicobacter pylori l-asparaginase2 at 1.4 a resolution
68	d1s0aa_	Alignment	not modelled	18.4	24	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
69	c3tebA_	Alignment	not modelled	18.2	23	PDB header: hydrolase Chain: A: PDB Molecule: endonuclease/exonuclease/phosphatase; PDBTitle: endonuclease/exonuclease/phosphatase family protein from leptotrichia2 buccalis c-1013-b
70	d2cfba1	Alignment	not modelled	17.8	20	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
71	c2d6fA_	Alignment	not modelled	17.4	16	PDB header: ligase/rna Chain: A: PDB Molecule: glutamyl-trna(gln) amidotransferase subunit d; PDBTitle: crystal structure of glu-trna(gln) amidotransferase in the2 complex with trna(gln)
72	d2d6fa2	Alignment	not modelled	17.2	16	Fold: Glutaminase/Asparaginase Superfamily: Glutaminase/Asparaginase Family: Glutaminase/Asparaginase
73	c3lv2A_	Alignment	not modelled	17.2	19	PDB header: transferase Chain: A: PDB Molecule: adenosyl methionine-8-amino-7-oxononanoate aminotransferase; PDBTitle: crystal structure of mycobacterium tuberculosis 7,8-diaminopelargonic2 acid synthase in complex with substrate analog sinefungin
74	c2gx8B_	Alignment	not modelled	17.1	10	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: nif3-related protein; PDBTitle: the crystal stucture of bacillus cereus protein related to nif3
75	c3qc3B_	Alignment	not modelled	17.0	14	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
76	d1ii7a_	Alignment	not modelled	16.9	13	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: DNA double-strand break repair nuclease
77	c2cy8A_	Alignment	not modelled	16.8	17	PDB header: transferase Chain: A: PDB Molecule: d-phenylglycine aminotransferase; PDBTitle: crystal structure of d-phenylglycine aminotransferase (d-

					phgat) from2 pseudomonas strutzeri st-201
78	d1o7ja_	Alignment	not modelled	16.7	19 Fold: Glutaminase/Asparaginase Superfamily: Glutaminase/Asparaginase Family: Glutaminase/Asparaginase
79	dliuka_	Alignment	not modelled	15.8	9 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
80	d1t70a_	Alignment	not modelled	15.7	10 Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: DR1281-like
81	c3oy2A_	Alignment	not modelled	15.7	10 PDB header: viral protein,transferase Chain: A: PDB Molecule: glycosyltransferase b736l; PDBTitle: crystal structure of a putative glycosyltransferase from paramecium2 bursaria chlorella virus ny2a
82	c3ajxA_	Alignment	not modelled	15.0	16 PDB header: lyase Chain: A: PDB Molecule: 3-hexulose-6-phosphate synthase; PDBTitle: crystal structure of 3-hexulose-6-phosphate synthase
83	c3ngfA_	Alignment	not modelled	14.4	9 PDB header: isomerase Chain: A: PDB Molecule: ap endonuclease, family 2; PDBTitle: crystal structure of ap endonuclease, family 2 from brucella2 melitensis
84	c3dodA_	Alignment	not modelled	14.3	18 PDB header: transferase Chain: A: PDB Molecule: adenosylmethionine-8-amino-7-oxononanoate aminotransferase; PDBTitle: crystal structure of plp bound 7,8-diaminopelargonic acid synthase in2 bacillus subtilis
85	c1zq1B_	Alignment	not modelled	14.1	17 PDB header: lyase Chain: B: PDB Molecule: glutamyl-trna(gln) amidotransferase subunit d; PDBTitle: structure of gatde trna-dependent amidotransferase from2 pyrococcus abyssi
86	d1bxba_	Alignment	not modelled	14.0	12 Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
87	c2yybA_	Alignment	not modelled	13.9	14 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein tha1606; PDBTitle: crystal structure of tha1606 from thermus thermophilus hb8
88	c2zq0B_	Alignment	not modelled	13.9	10 PDB header: hydrolase Chain: B: PDB Molecule: alpha-glucosidase (alpha-glucosidase subb); PDBTitle: crystal structure of subb complexed with acarbose
89	c3ktcB_	Alignment	not modelled	13.9	12 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
90	d1zq1a2	Alignment	not modelled	13.6	17 Fold: Glutaminase/Asparaginase Superfamily: Glutaminase/Asparaginase Family: Glutaminase/Asparaginase
91	c3nb0A_	Alignment	not modelled	13.6	14 PDB header: transferase Chain: A: PDB Molecule: glycogen [starch] synthase isoform 2; PDBTitle: glucose-6-phosphate activated form of yeast glycogen synthase
92	c3navB_	Alignment	not modelled	13.6	8 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
93	d1bxca_	Alignment	not modelled	13.4	10 Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
94	c3bv0A_	Alignment	not modelled	13.3	15 PDB header: transferase Chain: A: PDB Molecule: adenosylmethionine-8-amino-7-oxononanoate aminotransferase; PDBTitle: crystal structure of plp bound 7,8-diaminopelargonic acid synthase in2 mycobacterium tuberculosis
95	d1nnsa_	Alignment	not modelled	13.3	22 Fold: Glutaminase/Asparaginase Superfamily: Glutaminase/Asparaginase Family: Glutaminase/Asparaginase
96	d2gsaa_	Alignment	not modelled	12.6	17 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
97	d1h4pa_	Alignment	not modelled	12.5	13 Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
98	d2yvta1	Alignment	not modelled	12.4	19 Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: TT1561-like
99	c3ct7E_	Alignment	not modelled	12.3	32 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