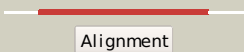

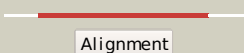

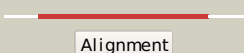

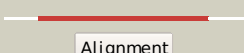



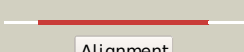

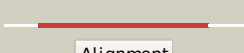

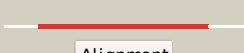









#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3sqliB_	 Alignment		100.0	28	PDB header: hydrolase Chain: B: PDB Molecule: glycosyl hydrolase family 3; PDBTitle: crystal structure of glycoside hydrolase from synechococcus
2	d1tr9a_	 Alignment		100.0	55	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: NagZ-like
3	c3bmxB_	 Alignment		100.0	26	PDB header: hydrolase Chain: B: PDB Molecule: uncharacterized lipoprotein ybbd; PDBTitle: beta-n-hexosaminidase (ybbd) from bacillus subtilis
4	c3lk6A_	 Alignment		100.0	26	PDB header: hydrolase Chain: A: PDB Molecule: lipoprotein ybbd; PDBTitle: beta-n-hexosaminidase n318d mutant (ybbd_n318d) from bacillus subtilis
5	c3tevA_	 Alignment		100.0	28	PDB header: hydrolase Chain: A: PDB Molecule: glycosyl hydrolase, family 3; PDBTitle: the crystal structure of glycosyl hydrolase from deinococcus2 radiodurans r1
6	d1x38a1	 Alignment		100.0	20	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: NagZ-like
7	c1ex1A_	 Alignment		100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: protein (beta-d-glucan exohydrolase isoenzyme exo1); PDBTitle: beta-d-glucan exohydrolase from barley
8	c3f93D_	 Alignment		100.0	20	PDB header: hydrolase Chain: D: PDB Molecule: beta-glucosidase; PDBTitle: crystal structure of exo-1,3/1,4-beta-glucanase (exop) from2 pseudoalteromonas sp. bb1
9	c2x41A_	 Alignment		100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: beta-glucosidase; PDBTitle: structure of beta-glucosidase 3b from thermotoga neapolitana2 in complex with glucose
10	c3ac0B_	 Alignment		100.0	22	PDB header: hydrolase Chain: B: PDB Molecule: beta-glucosidase i; PDBTitle: crystal structure of beta-glucosidase from kluyveromyces marxianus in2 complex with glucose
11	d1o4ua1	 Alignment		78.2	22	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: NadC C-terminal domain-like

12	c3mmrA_		Alignment		69.1	13	PDB header: hydrolase Chain: A: PDB Molecule: arginase; PDBTitle: structure of plasmodium falciparum arginase in complex with abh
13	c1o4uA_		Alignment		60.7	20	PDB header: transferase Chain: A: PDB Molecule: type ii quinolic acid phosphoribosyltransferase; PDBTitle: crystal structure of a nicotinate nucleotide pyrophosphorylase2 (tm1645) from thermotoga maritima at 2.50 a resolution
14	d1vqon1		Alignment		50.2	15	Fold: Ribonuclease H-like motif Superfamily: Translational machinery components Family: Ribosomal protein L18 and S11
15	c2y69X_		Alignment		45.1	15	PDB header: electron transport Chain: X: PDB Molecule: cytochrome c oxidase polypeptide 7b; PDBTitle: bovine heart cytochrome c oxidase re-refined with molecular2 oxygen
16	d1v54k_		Alignment		45.1	15	Fold: Single transmembrane helix Superfamily: Mitochondrial cytochrome c oxidase subunit VIIb Family: Mitochondrial cytochrome c oxidase subunit VIIb
17	c3o3nA_		Alignment		36.4	12	PDB header: lyase Chain: A: PDB Molecule: alpha-subunit 2-hydroxyisocaproyl-coa dehydratase; PDBTitle: (r)-2-hydroxyisocaproyl-coa dehydratase in complex with its substrate2 (r)-2-hydroxyisocaproyl-coa
18	c4a1aM_		Alignment		29.4	21	PDB header: ribosome Chain: M: PDB Molecule: 60s ribosomal protein l5; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 3.
19	d1t9ha2		Alignment		28.8	12	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
20	d2a0ma1		Alignment		28.6	17	Fold: Arginase/deacetylase Superfamily: Arginase/deacetylase Family: Arginase-like amidino hydrolases
21	c3m1rF_		Alignment	not modelled	26.1	12	PDB header: hydrolase Chain: F: PDB Molecule: formimidoylglutamate; PDBTitle: the crystal structure of formimidoylglutamate from bacillus2 subtilis subsp. subtilis str. 168
22	d1nmpa_		Alignment	not modelled	22.3	8	Fold: NIF3 (NGG1p interacting factor 3)-like Superfamily: NIF3 (NGG1p interacting factor 3)-like Family: NIF3 (NGG1p interacting factor 3)-like
23	c1iq8B_		Alignment	not modelled	22.2	17	PDB header: transferase Chain: B: PDB Molecule: archaeosine trna-guanine transglycosylase; PDBTitle: crystal structure of archaeosine trna-guanine2 transglycosylase from pyrococcus horikoshii
24	d1eaka1		Alignment	not modelled	19.5	6	Fold: PGBD-like Superfamily: PGBD-like Family: MMP N-terminal domain
25	c3bolB_		Alignment	not modelled	19.3	17	PDB header: transferase Chain: B: PDB Molecule: 5-methyltetrahydrofolate s-homocysteine PDBTitle: cobalamin-dependent methionine synthase (1-566) from2 thermotoga maritima complexed with zn2+
26	d1cf2o2		Alignment	not modelled	19.3	20	Fold: FwdE/GAPDH domain-like Superfamily: Glycerol dehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
27	c3kruC_		Alignment	not modelled	18.8	14	PDB header: oxidoreductase Chain: C: PDB Molecule: nadh:flavin oxidoreductase/nadh oxidase; PDBTitle: crystal structure of the thermostable old yellow enzyme from2 thermoanaerobacter pseudethanolicus e39
28	c3guzB_		Alignment	not modelled	18.2	19	PDB header: ligase Chain: B: PDB Molecule: pantothenate synthetase; PDBTitle: structural and substrate-binding studies of

						pantothenate2 synthenate (ps)provide insights into homotropic inhibition3 by pantoate in ps's
29	d2vcha1	Alignment	not modelled	18.1	10	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like
30	d2czca1	Alignment	not modelled	18.0	20	Fold: FwdE/GAPDH domain-like Superfamily: Glyceroldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
31	c2eivH_	Alignment	not modelled	17.1	17	PDB header: hydrolase Chain: H: PDB Molecule: arginase; PDBTitle: crystal structure of the arginase from thermus thermophilus
32	d1yira1	Alignment	not modelled	17.1	28	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: Monomeric nicotinate phosphoribosyltransferase C-terminal domain
33	d1xi3a_	Alignment	not modelled	16.8	17	Fold: TIM beta/alpha-barrel Superfamily: Thiamin phosphate synthase Family: Thiamin phosphate synthase
34	c3itcA_	Alignment	not modelled	16.7	18	PDB header: hydrolase Chain: A: PDB Molecule: renal dipeptidase; PDBTitle: crystal structure of sco3058 with bound citrate and glycerol
35	c3os4A_	Alignment	not modelled	16.1	28	PDB header: transferase Chain: A: PDB Molecule: nicotinate phosphoribosyltransferase; PDBTitle: the crystal structure of nicotinate phosphoribosyltransferase from2 yersinia pestis
36	d1ybea1	Alignment	not modelled	16.0	31	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: Monomeric nicotinate phosphoribosyltransferase C-terminal domain
37	c2htmB_	Alignment	not modelled	15.4	18	PDB header: biosynthetic protein Chain: B: PDB Molecule: thiazole biosynthesis protein thig; PDBTitle: crystal structure of ttha0676 from thermus thermophilus hb8
38	c3ihjA_	Alignment	not modelled	14.7	14	PDB header: transferase Chain: A: PDB Molecule: alanine aminotransferase 2; PDBTitle: human alanine aminotransferase 2 in complex with plp
39	d1pv8a_	Alignment	not modelled	14.5	18	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
40	c2nydB_	Alignment	not modelled	14.0	11	PDB header: unknown function Chain: B: PDB Molecule: upf0135 protein sa1388; PDBTitle: crystal structure of staphylococcus aureus hypothetical protein sa1388
41	c1t9hA_	Alignment	not modelled	13.2	12	PDB header: hydrolase Chain: A: PDB Molecule: probable gtpase engc; PDBTitle: the crystal structure of yloq, a circularly permuted gtpase.
42	d1l5oa_	Alignment	not modelled	12.7	19	Fold: Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) Superfamily: Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) Family: Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT)
43	d1vlpa2	Alignment	not modelled	12.6	16	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: Monomeric nicotinate phosphoribosyltransferase C-terminal domain
44	d1vhna_	Alignment	not modelled	12.3	19	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
45	d1ihoa_	Alignment	not modelled	12.2	17	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Pantothenate synthetase (Pantoate-beta-alanine ligase, PanC)
46	c1ybeA_	Alignment	not modelled	11.9	31	PDB header: transferase Chain: A: PDB Molecule: nicotinate phosphoribosyltransferase; PDBTitle: crystal structure of a nicotinate phosphoribosyltransferase
47	c2x4bA_	Alignment	not modelled	11.9	14	PDB header: hydrolase Chain: A: PDB Molecule: limit dextrinase; PDBTitle: barley limit dextrinase in complex with beta-cyclodextrin
48	c2l1nA_	Alignment	not modelled	11.4	54	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of the protein yp_399305.1
49	c2im5C_	Alignment	not modelled	11.1	31	PDB header: transferase Chain: C: PDB Molecule: nicotinate phosphoribosyltransferase; PDBTitle: crystal structure of nicotinate phosphoribosyltransferase2 from porphyromonas gingivalis
50	c3izcQ_	Alignment	not modelled	10.9	25	PDB header: ribosome Chain: Q: PDB Molecule: 60s ribosomal protein rp15 (l18p); PDBTitle: localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
51	c1y80A_	Alignment	not modelled	10.8	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: predicted cobalamin binding protein; PDBTitle: structure of a corrinoid (factor iim)-binding protein from2 moorella thermoacetica
52	d2g2ca1	Alignment	not modelled	10.2	13	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
						Fold: FomD barrel-like

53	d2p12a1	Alignment	not modelled	10.1	6	Superfamily: FomD-like Family: FomD-like
54	c2qgaF_	Alignment	not modelled	10.0	10	PDB header: structural genomics, unknown function Chain: F: PDB Molecule: protein tm 1862; PDBTitle: crystal structure of tm_1862 from thermotoga maritima.2 northeast structural genomics consortium target vr77
55	d2bz1a1	Alignment	not modelled	9.9	17	Fold: RibA-like Superfamily: RibA-like Family: RibA-like
56	d1tifa_	Alignment	not modelled	9.7	19	Fold: beta-Grasp (ubiquitin-like) Superfamily: Translation initiation factor IF3, N-terminal domain Family: Translation initiation factor IF3, N-terminal domain
57	c2yybA_	Alignment	not modelled	9.6	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein tha1606; PDBTitle: crystal structure of tha1606 from thermus thermophilus hb8
58	d1fj2a_	Alignment	not modelled	9.5	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
59	d2gx8a1	Alignment	not modelled	9.4	10	Fold: NIF3 (NGG1p interacting factor 3)-like Superfamily: NIF3 (NGG1p interacting factor 3)-like Family: NIF3 (NGG1p interacting factor 3)-like
60	d1litua_	Alignment	not modelled	9.3	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Renal dipeptidase
61	d2gycm1	Alignment	not modelled	8.7	14	Fold: Ribonuclease H-like motif Superfamily: Translational machinery components Family: Ribosomal protein L18 and S11
62	d2c1ha1	Alignment	not modelled	8.5	17	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
63	c3gmiA_	Alignment	not modelled	8.4	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0348 protein mj0951; PDBTitle: crystal structure of a protein of unknown function from2 methanocaldococcus jannaschii
64	c2h90A_	Alignment	not modelled	8.4	12	PDB header: oxidoreductase Chain: A: PDB Molecule: xenobiotic reductase a; PDBTitle: xenobiotic reductase a in complex with coumarin
65	c3qfeB_	Alignment	not modelled	8.3	14	PDB header: lyase Chain: B: PDB Molecule: putative dihydrodipicolinate synthase family protein; PDBTitle: crystal structures of a putative dihydrodipicolinate synthase family2 protein from coccidioides immitis
66	d2c1xa1	Alignment	not modelled	8.3	19	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like
67	d1lj8a3	Alignment	not modelled	8.2	26	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: Mannitol 2-dehydrogenase
68	c3innB_	Alignment	not modelled	8.0	20	PDB header: ligase Chain: B: PDB Molecule: pantothenate synthetase; PDBTitle: crystal structure of pantoate-beta-alanine-ligase in complex2 with atp at low occupancy at 2.1 a resolution
69	c3qy6A_	Alignment	not modelled	8.0	11	PDB header: hydrolase Chain: A: PDB Molecule: tyrosine-protein phosphatase ywqe; PDBTitle: crystal structures of ywqe from bacillus subtilis and cpsb from2 streptococcus pneumoniae, unique metal-dependent tyrosine3 phosphatases
70	c2gx8B_	Alignment	not modelled	7.9	10	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: nif3-related protein; PDBTitle: the crystal structure of bacillus cereus protein related to nif3
71	d3gcba_	Alignment	not modelled	7.6	11	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Papain-like
72	d1r5ya_	Alignment	not modelled	7.5	18	Fold: TIM beta/alpha-barrel Superfamily: tRNA-guanine transglycosylase Family: tRNA-guanine transglycosylase
73	d1hfel1	Alignment	not modelled	7.5	21	Fold: Fe-only hydrogenase Superfamily: Fe-only hydrogenase Family: Fe-only hydrogenase
74	c3u5eL_	Alignment	not modelled	7.5	13	PDB header: ribosome Chain: L: PDB Molecule: 60s ribosomal protein l13-a; PDBTitle: the structure of the eukaryotic ribosome at 3.0 resolution
75	c1ps9A_	Alignment	not modelled	7.3	12	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
76	d1iq8a1	Alignment	not modelled	7.3	17	Fold: TIM beta/alpha-barrel Superfamily: tRNA-guanine transglycosylase Family: tRNA-guanine transglycosylase
77	d1d3va_	Alignment	not modelled	7.3	13	Fold: Arginase/deacetylase Superfamily: Arginase/deacetylase Family: Arginase-like amidino hydrolases
78	c4a18U_	Alignment	not modelled	7.2	22	PDB header: ribosome Chain: U: PDB Molecule: rpl13; PDBTitle: t.thermophila 60s ribosomal subunit in complex with initiation2 factor 6. this file contains 26s rrna and proteins of molecule 1
						Fold: TIM beta/alpha-barrel

79	d2p10a1	Alignment	not modelled	7.1	18	Superfamily: Phosphoenolpyruvate/pyruvate domain Family: MI19387-like
80	c3obkH	Alignment	not modelled	6.6	20	PDB header: lyase Chain: H: PDB Molecule: delta-aminolevulinic acid dehydratase; PDBTitle: crystal structure of delta-aminolevulinic acid dehydratase2 (porphobilinogen synthase) from toxoplasma gondii me49 in complex3 with the reaction product porphobilinogen
81	d1ps9a1	Alignment	not modelled	6.6	12	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
82	d1i5ga	Alignment	not modelled	6.5	15	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
83	c2p10D	Alignment	not modelled	6.2	18	PDB header: hydrolase Chain: D: PDB Molecule: ml19387 protein; PDBTitle: crystal structure of a putative phosphonopyruvate hydrolase (ml19387)2 from mesorhizobium loti maff303099 at 2.15 a resolution
84	d1o66a	Alignment	not modelled	6.1	19	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Ketopantoate hydroxymethyltransferase PanB
85	c3g0tA	Alignment	not modelled	5.9	10	PDB header: transferase Chain: A: PDB Molecule: putative aminotransferase; PDBTitle: crystal structure of putative aspartate aminotransferase (np_905498.1)2 from porphyromonas gingivalis w83 at 1.75 a resolution
86	c2wskA	Alignment	not modelled	5.8	20	PDB header: hydrolase Chain: A: PDB Molecule: glycogen debranching enzyme; PDBTitle: crystal structure of glycogen debranching enzyme glgx from2 escherichia coli k-12
87	d1zt2a1	Alignment	not modelled	5.7	17	Fold: Prim-pol domain Superfamily: Prim-pol domain Family: PriA-like
88	d2aeba1	Alignment	not modelled	5.7	13	Fold: Arginase/deacetylase Superfamily: Arginase/deacetylase Family: Arginase-like amidino hydrolases
89	c2waqG	Alignment	not modelled	5.6	57	PDB header: transcription Chain: G: PDB Molecule: dna-directed rna polymerase rpo8 subunit; PDBTitle: the complete structure of the archaeal 13-subunit dna-2 directed rna polymerase
90	c3s9xA	Alignment	not modelled	5.4	26	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: asch domain; PDBTitle: high resolution crystal structure of asch domain from lactobacillus2 crispatus jv v101
91	d1mkya3	Alignment	not modelled	5.4	13	Fold: Alpha-lytic protease prodomain-like Superfamily: Probable GTPase Der, C-terminal domain Family: Probable GTPase Der, C-terminal domain
92	d1a3xa2	Alignment	not modelled	5.4	14	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase
93	d1tqyb1	Alignment	not modelled	5.3	8	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
94	c1m7xC	Alignment	not modelled	5.3	19	PDB header: transferase Chain: C: PDB Molecule: 1,4-alpha-glucan branching enzyme; PDBTitle: the x-ray crystallographic structure of branching enzyme
95	d1x2ga2	Alignment	not modelled	5.3	7	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: LplA-like
96	d1v33a	Alignment	not modelled	5.2	33	Fold: Prim-pol domain Superfamily: Prim-pol domain Family: PriA-like
97	c2pc4B	Alignment	not modelled	5.1	19	PDB header: lyase Chain: B: PDB Molecule: fructose-bisphosphate aldolase; PDBTitle: crystal structure of fructose-bisphosphate aldolase from plasmodium2 falciparum in complex with trap-tail determined at 2.4 angstrom3 resolution
98	d3tata	Alignment	not modelled	5.1	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
99	d1bj4a	Alignment	not modelled	5.1	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like