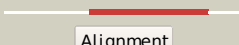



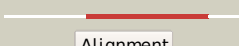

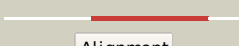











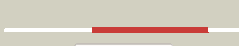





#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3lxqB_	 Alignment		99.1	13	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein vp1736; PDBTitle: the crystal structure of a protein in the alkaline2 phosphatase superfamily from vibrio parahaemolyticus to3 1.95a
2	c2w8dB_	 Alignment		98.9	15	PDB header: transferase Chain: B: PDB Molecule: processed glycerol phosphate lipoteichoic acid synthase 2; PDBTitle: distinct and essential morphogenic functions for wall- and2 lipo-teichoic acids in bacillus subtilis
3	c2w5tA_	 Alignment		98.6	14	PDB header: transferase Chain: A: PDB Molecule: processed glycerol phosphate lipoteichoic acid PDBTitle: structure-based mechanism of lipoteichoic acid synthesis by2 staphylococcus aureus Itas.
4	c3ed4A_	 Alignment		98.2	15	PDB header: transferase Chain: A: PDB Molecule: arylsulfatase; PDBTitle: crystal structure of putative arylsulfatase from escherichia coli
5	c2qzuA_	 Alignment		98.2	14	PDB header: hydrolase Chain: A: PDB Molecule: putative sulfatase yidj; PDBTitle: crystal structure of the putative sulfatase yidj from bacteroides2 fragilis. northeast structural genomics consortium target bfr123
6	d1auka_	 Alignment		98.0	15	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Arylsulfatase
7	d1fsua_	 Alignment		97.8	15	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Arylsulfatase
8	c2vqrA_	 Alignment		97.5	20	PDB header: hydrolase Chain: A: PDB Molecule: putative sulfatase; PDBTitle: crystal structure of a phosphonate monoester hydrolase2 from rhizobium leguminosarum: a new member of the3 alkaline phosphatase superfamily
9	d1hdha_	 Alignment		97.4	18	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Arylsulfatase
10	c2b5qB_	 Alignment		97.1	18	PDB header: hydrolase Chain: B: PDB Molecule: putative sulfatase yidj; PDBTitle: crystal structure of a putative sulfatase (np_810509.1)2 from bacteroides thetaiotaomicron vpi-5482 at 2.40 a3 resolution
11	d1o98a2	 Alignment		96.1	13	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: 2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, catalytic domain

12	c3q3qA_	Alignment		94.8	21	PDB header: hydrolase Chain: A: PDB Molecule: alkaline phosphatase; PDBTitle: crystal structure of spap: an novel alkaline phosphatase from2 bacterium sphingomonas sp. strain bsar-1
13	d1p49a_	Alignment		92.9	13	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Arylsulfatase
14	c2xrgA_	Alignment		92.6	14	PDB header: hydrolase Chain: A: PDB Molecule: ectonucleotide pyrophosphatase/phosphodiesterase family PDBTitle: crystal structure of autotaxin (enpp2) in complex with the2 ha155 boronic acid inhibitor
15	c3szzA_	Alignment		91.8	15	PDB header: hydrolase Chain: A: PDB Molecule: phosphonoacetate hydrolase; PDBTitle: crystal structure of phosphonoacetate hydrolase from sinorhizobium2 meliloti 1021 in complex with acetate
16	d1ei6a_	Alignment		90.7	15	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Phosphonoacetate hydrolase
17	d2i09a1	Alignment		90.1	11	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: DeoB catalytic domain-like
18	c2qsoB_	Alignment		90.0	10	PDB header: hydrolase Chain: B: PDB Molecule: phosphodiesterase-nucleotide pyrophosphatase; PDBTitle: structure of xac nucleotide2 pyrophosphatase/phosphodiesterase in complex with vanadate
19	c2i09A_	Alignment		71.9	13	PDB header: isomerase Chain: A: PDB Molecule: phosphopentomutase; PDBTitle: crystal structure of putative phosphopentomutase from streptococcus2 mutans
20	dlesfa1	Alignment		71.3	26	Fold: OB-fold Superfamily: Bacterial enterotoxins Family: Superantigen toxins, N-terminal domain
21	c2xr9A_	Alignment	not modelled	69.3	16	PDB header: hydrolase Chain: A: PDB Molecule: ectonucleotide pyrophosphatase/phosphodiesterase family PDBTitle: crystal structure of autotaxin (enpp2)
22	d1qhfa_	Alignment	not modelled	68.4	25	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
23	c3f3ka_	Alignment	not modelled	67.9	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein ykr043c; PDBTitle: the structure of uncharacterized protein ykr043c from saccharomyces2 cerevisiae.
24	c3c7tB_	Alignment	not modelled	56.6	21	PDB header: hydrolase Chain: B: PDB Molecule: ecdysteroid-phosphate phosphatase; PDBTitle: crystal structure of the ecdysone phosphate phosphatase, eppase, from2 bombix mori in complex with tungstate
25	c1yxxD_	Alignment	not modelled	52.5	28	PDB header: isomerase, hydrolase Chain: D: PDB Molecule: phosphoglycerate mutase 1; PDBTitle: crystal structure of human b type phosphoglycerate mutase
26	d2hhja1	Alignment	not modelled	43.8	18	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
27	d1klud1	Alignment	not modelled	43.4	24	Fold: OB-fold Superfamily: Bacterial enterotoxins Family: Superantigen toxins, N-terminal domain
28	d2aq2b1	Alignment	not modelled	42.2	24	Fold: OB-fold Superfamily: Bacterial enterotoxins Family: Superantigen toxins, N-terminal domain
						Fold: OB-fold

29	d1ck1a1	Alignment	not modelled	41.6	25	Superfamily: Bacterial enterotoxins Family: Superantigen toxins, N-terminal domain
30	d1xq9a	Alignment	not modelled	40.4	23	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
31	c2ikqA	Alignment	not modelled	38.4	21	PDB header: signaling protein, immune system Chain: A: PDB Molecule: suppressor of t-cell receptor signaling 1; PDBTitle: crystal structure of mouse sts-1 pgm domain in complex with phosphate
32	c3d4iD	Alignment	not modelled	35.4	19	PDB header: hydrolase Chain: D: PDB Molecule: sts-2 protein; PDBTitle: crystal structure of the 2h-phosphatase domain of sts-2
33	d1s0yb	Alignment	not modelled	30.3	26	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: 4-oxalocrotonate tautomerase-like
34	c3ej9D	Alignment	not modelled	29.5	26	PDB header: hydrolase Chain: D: PDB Molecule: beta-subunit of trans-3-chloroacrylic acid dehalogenase; PDBTitle: structural and mechanistic analysis of trans-3-chloroacrylic acid2 dehalogenase activity
35	d1riia	Alignment	not modelled	28.7	23	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
36	d1ugpb	Alignment	not modelled	27.3	9	Fold: SH3-like barrel Superfamily: Electron transport accessory proteins Family: Nitrile hydratase beta chain
37	c3czpA	Alignment	not modelled	27.2	13	PDB header: transferase Chain: A: PDB Molecule: putative polyphosphate kinase 2; PDBTitle: crystal structure of putative polyphosphate kinase 2 from pseudomonas2 aeruginosa pa01
38	d1bifa2	Alignment	not modelled	26.8	24	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
39	c1bplA	Alignment	not modelled	24.6	27	PDB header: glycosyltransferase Chain: A: PDB Molecule: alpha-1,4-glucan-4-glucanohydrolase; PDBTitle: glycosyltransferase
40	d2bvya2	Alignment	not modelled	24.2	19	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
41	d1xbta1	Alignment	not modelled	23.6	32	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Type II thymidine kinase
42	d1e58a	Alignment	not modelled	23.5	20	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
43	c3sr2A	Alignment	not modelled	23.2	23	PDB header: dna binding protein/protein binding Chain: A: PDB Molecule: dna repair protein xrcc4; PDBTitle: crystal structure of human xlf-xrcc4 complex
44	c2bvtB	Alignment	not modelled	23.1	17	PDB header: hydrolase Chain: B: PDB Molecule: beta-1,4-mannanase; PDBTitle: the structure of a modular endo-beta-1,4-mannanase from2 cellulomonas fimi explains the product specificity of3 glycoside hydrolase family 26 mannanases.
45	d1ud2a2	Alignment	not modelled	22.5	23	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
46	d1bxta1	Alignment	not modelled	22.3	30	Fold: OB-fold Superfamily: Bacterial enterotoxins Family: Superantigen toxins, N-terminal domain
47	c3eznB	Alignment	not modelled	22.3	22	PDB header: isomerase Chain: B: PDB Molecule: 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase; PDBTitle: crystal structure of phosphoglyceromutase from burkholderia2 pseudomallei 1710b
48	c3mudA	Alignment	not modelled	21.8	23	PDB header: contractile protein Chain: A: PDB Molecule: dna repair protein xrcc4, tropomyosin alpha-1 chain; PDBTitle: structure of the tropomyosin overlap complex from chicken smooth2 muscle
49	c3k8kB	Alignment	not modelled	21.6	27	PDB header: membrane protein Chain: B: PDB Molecule: alpha-amylase, susg; PDBTitle: crystal structure of susg
50	c1cygA	Alignment	not modelled	21.1	19	PDB header: glycosyltransferase Chain: A: PDB Molecule: cyclodextrin glucanotransferase; PDBTitle: cyclodextrin glucanotransferase (e.c.2.4.1.19) (cgtase)
51	c3ll4B	Alignment	not modelled	20.7	19	PDB header: hydrolase Chain: B: PDB Molecule: uncharacterized protein ykr043c; PDBTitle: structure of the h13a mutant of ykr043c in complex with fructose-1,6-2 bisphosphate
52	c1jd7A	Alignment	not modelled	18.8	12	PDB header: hydrolase Chain: A: PDB Molecule: alpha-amylase; PDBTitle: crystal structure analysis of the mutant k300r of2 pseudoalteromonas haloplantcis alpha-amylase
53	c1k6mA	Alignment	not modelled	18.6	24	PDB header: transferase, hydrolase Chain: A: PDB Molecule: 6-phosphofructo-2-kinase/fructose-2,6- PDBTitle: crystal structure of human liver 6-phosphofructo-2-2 kinase/fructose-2,6-bisphosphatase
54	c1tcmB	Alignment	not modelled	18.3	15	PDB header: glycosyltransferase Chain: B: PDB Molecule: cyclodextrin glycosyltransferase; PDBTitle: cyclodextrin glycosyltransferase w616a mutant from bacillus2 circulans strain 251

55	d1mxga2	Alignment	not modelled	18.2	28	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
56	d1gjwa2	Alignment	not modelled	17.9	23	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
57	d1ob0a2	Alignment	not modelled	17.6	27	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
58	c3qz9D_	Alignment	not modelled	17.4	7	PDB header: lyase Chain: D: PDB Molecule: co-type nitrile hydratase beta subunit; PDBTitle: crystal structure of co-type nitrile hydratase beta-y215f from2 pseudomonas putida.
59	c1mw0A_	Alignment	not modelled	17.4	31	PDB header: hydrolase Chain: A: PDB Molecule: alpha amylase; PDBTitle: crystal structure analysis of the hyperthermostable2 pyrococcus woesei alpha-amylase
60	c2wskA_	Alignment	not modelled	17.2	29	PDB header: hydrolase Chain: A: PDB Molecule: glycogen debranching enzyme; PDBTitle: crystal structure of glycogen debranching enzyme glgx from2 escherichia coli k-12
61	c3rgiA_	Alignment	not modelled	16.3	15	PDB header: transferase Chain: A: PDB Molecule: disd protein; PDBTitle: trans-acting transferase from disorazole synthase
62	c1jaeA_	Alignment	not modelled	16.1	15	PDB header: glycosidase Chain: A: PDB Molecule: alpha-amylase; PDBTitle: structure of tenebrio molitor larval alpha-amylase
63	c1qhoA_	Alignment	not modelled	16.0	31	PDB header: hydrolase Chain: A: PDB Molecule: alpha-amylase; PDBTitle: five-domain alpha-amylase from bacillus stearothermophilus,2 maltose/acarbose complex
64	c2qpuB_	Alignment	not modelled	15.8	24	PDB header: hydrolase Chain: B: PDB Molecule: alpha-amylase type a isozyme; PDBTitle: sugar tongs mutant s378p in complex with acarbose
65	d2fhfa5	Alignment	not modelled	15.8	21	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
66	c3k25B_	Alignment	not modelled	15.7	29	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: slr1438 protein; PDBTitle: crystal structure of slr1438 protein from synechocystis sp. pcc 6803,2 northeast structural genomics consortium target sgr112
67	c3d8hB_	Alignment	not modelled	15.5	19	PDB header: isomerase Chain: B: PDB Molecule: glycolytic phosphoglycerate mutase; PDBTitle: crystal structure of phosphoglycerate mutase from cryptosporidium2 parvum, cgd7_4270
68	d1avaa2	Alignment	not modelled	15.4	23	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
69	d3pgma_	Alignment	not modelled	15.1	24	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
70	c1jdaA_	Alignment	not modelled	14.9	35	PDB header: hydrolase Chain: A: PDB Molecule: 1,4-alpha maltotetrahydrolase; PDBTitle: maltotetraose-forming exo-amylase
71	d1hvx2	Alignment	not modelled	14.6	19	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
72	d1q6za1	Alignment	not modelled	14.6	20	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
73	c1bf2A_	Alignment	not modelled	14.4	31	PDB header: hydrolase Chain: A: PDB Molecule: isoamylase; PDBTitle: structure of pseudomonas isoamylase
74	d1cyga4	Alignment	not modelled	14.2	17	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
75	c3bmWA_	Alignment	not modelled	13.9	19	PDB header: transferase Chain: A: PDB Molecule: cyclomaltoextrin glucanotransferase; PDBTitle: cyclodextrin glycosyl transferase from thermoanaerobacterium2 thermosulfurigenes em1 mutant s77p complexed with a maltoheptaose3 inhibitor
76	c2ya0A_	Alignment	not modelled	13.9	25	PDB header: hydrolase Chain: A: PDB Molecule: putative alkaline amylopullulanase; PDBTitle: catalytic module of the multi-modular glycogen-degrading2 pneumococcal virulence factor spuA
77	c3bv6D_	Alignment	not modelled	13.7	14	PDB header: hydrolase Chain: D: PDB Molecule: metal-dependent hydrolase; PDBTitle: crystal structure of uncharacterized metallo protein from vibrio2 cholerae with beta-lactamase like fold
78	c2i1vB_	Alignment	not modelled	13.6	32	PDB header: transferase, hydrolase Chain: B: PDB Molecule: 6-phosphofructo-2-kinase/fructose-2,6-PDBTitle: crystal structure of pfkfb3 in complex with adp and2 fructose-2,6-bisphosphate
79	c2aaaA_	Alignment	not modelled	13.6	38	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
80	d2gipa2	Alignment	not modelled	13.5	27	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
81	c3fayA_	Alignment	not modelled	13.5	31	PDB header: hydrolase Chain: A: PDB Molecule: reticulocyte binding protein;

81	c3lgaA_	Alignment	not modelled	13.3	31	PDBTitle: the crystal structure of gbs pullulanase sap in complex with2 maltotetraose
82	d2btya1	Alignment	not modelled	13.5	31	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: N-acetyl-l-glutamate kinase
83	c2wcsA_	Alignment	not modelled	13.4	14	PDB header: hydrolase Chain: A: PDB Molecule: alpha amylase, catalytic region; PDBTitle: crystal structure of debranching enzyme from nostoc2 punctiforme (npde)
84	c3blpX_	Alignment	not modelled	13.2	27	PDB header: hydrolase Chain: X: PDB Molecule: alpha-amylase 1; PDBTitle: role of aromatic residues in human salivary alpha-amylase
85	d3bmva4	Alignment	not modelled	13.0	17	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
86	c3q4fG_	Alignment	not modelled	12.9	23	PDB header: dna binding protein/protein binding Chain: G: PDB Molecule: dna repair protein xrcc4; PDBTitle: crystal structure of xrcc4/xf-cernunos complex
87	c2b78A_	Alignment	not modelled	12.4	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein smu.776; PDBTitle: a putative sam-dependent methyltransferase from2 streptococcus mutans
88	d1lv8a2	Alignment	not modelled	12.3	19	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
89	d2io8a1	Alignment	not modelled	12.2	24	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: Glutathionylspermidine synthase substrate-binding domain-like
90	d1e43a2	Alignment	not modelled	12.0	27	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
91	d3bzka5	Alignment	not modelled	11.8	37	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Tex RuvX-like domain-like
92	c1w4rC_	Alignment	not modelled	11.8	40	PDB header: transferase Chain: C: PDB Molecule: thymidine kinase; PDBTitle: structure of a type ii thymidine kinase with bound dttp
93	d2bhua3	Alignment	not modelled	11.8	27	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
94	c3dhuC_	Alignment	not modelled	11.7	24	PDB header: hydrolase Chain: C: PDB Molecule: alpha-amylase; PDBTitle: crystal structure of an alpha-amylase from lactobacillus2 plantarum
95	c3m07A_	Alignment	not modelled	11.7	29	PDB header: unknown function Chain: A: PDB Molecule: putative alpha amylase; PDBTitle: 1.4 angstrom resolution crystal structure of putative alpha2 amylase from salmonella typhimurium.
96	d1k6ma2	Alignment	not modelled	11.5	21	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
97	d1m7xa3	Alignment	not modelled	11.5	27	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
98	c1o7dC_	Alignment	not modelled	11.5	23	PDB header: hydrolase Chain: C: PDB Molecule: lysosomal alpha-mannosidase; PDBTitle: the structure of the bovine lysosomal a-mannosidase2 suggests a novel mechanism for low ph activation
99	c3rhfB_	Alignment	not modelled	11.4	25	PDB header: transferase Chain: B: PDB Molecule: putative polyphosphate kinase 2 family protein; PDBTitle: crystal structure of polyphosphate kinase 2 from arthrobacter2 aureusens tc1