



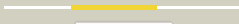

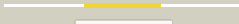





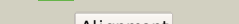

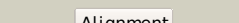

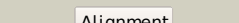


























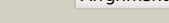






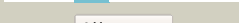
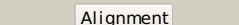
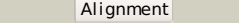
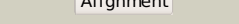
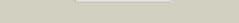

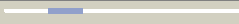

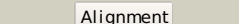

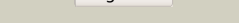
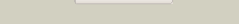
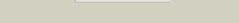

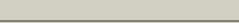

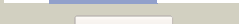
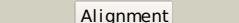
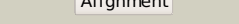
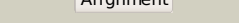
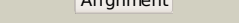




#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2qs0A_	 Alignment		100.0	39	PDB header: biosynthetic protein Chain: A: PDB Molecule: quinolinate synthetase a; PDBTitle: quinolinate synthase from pyrococcus furiosus
2	d1wzua1	 Alignment		100.0	40	Fold: NadA-like Superfamily: NadA-like Family: NadA-like
3	c3dmpD_	 Alignment		74.2	23	PDB header: transferase Chain: D: PDB Molecule: uracil phosphoribosyltransferase; PDBTitle: 2.6 a crystal structure of uracil phosphoribosyltransferase2 from burkholderia pseudomallei
4	d2nx2a1	 Alignment		70.1	10	Fold: MCP/YpsA-like Superfamily: MCP/YpsA-like Family: YpsA-like
5	c2e55D_	 Alignment		61.9	21	PDB header: transferase Chain: D: PDB Molecule: uracil phosphoribosyltransferase; PDBTitle: structure of aq2163 protein from aquifex aeolicus
6	c2ekcA_	 Alignment		59.5	25	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: structural study of project id aq_1548 from aquifex aeolicus vf5
7	c3fn9B_	 Alignment		57.9	16	PDB header: hydrolase Chain: B: PDB Molecule: putative beta-galactosidase; PDBTitle: crystal structure of putative beta-galactosidase from bacteroides2 fragilis
8	c3cmgA_	 Alignment		55.2	23	PDB header: hydrolase Chain: A: PDB Molecule: putative beta-galactosidase; PDBTitle: crystal structure of putative beta-galactosidase from bacteroides2 fragilis
9	d16pka_	 Alignment		52.6	21	Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase
10	d1xhja_	 Alignment		51.4	12	Fold: Alpha-lytic protease prodomain-like Superfamily: Fe-S cluster assembly (FSCA) domain-like Family: NifU C-terminal domain-like
11	c3gm8A_	 Alignment		48.1	20	PDB header: hydrolase Chain: A: PDB Molecule: glycoside hydrolase family 2, candidate beta-glycosidase; PDBTitle: crystal structure of a beta-glycosidase from bacteroides vulgatus

12	d2tpsa_	 Alignment		47.2	16	Fold: TIM beta/alpha-barrel Superfamily: Thiamin phosphate synthase Family: Thiamin phosphate synthase
13	dlj97a_	 Alignment		46.8	13	Fold: HAD-like Superfamily: HAD-like Family: Phosphoserine phosphatase
14	dljbqa_	 Alignment		46.7	20	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
15	cljbqD_	 Alignment		46.7	20	PDB header: lyase Chain: D: PDB Molecule: cystathionine beta-synthase; PDBTitle: structure of human cystathionine beta-synthase: a unique pyridoxal 5'-2 phosphate dependent hemeprotein
16	dlybha1	 Alignment		45.6	20	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
17	c3iz6A_	 Alignment		45.1	15	PDB header: ribosome Chain: A: PDB Molecule: 40s ribosomal protein sa (s2p); PDBTitle: localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
18	c3k7pA_	 Alignment		42.0	20	PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase; PDBTitle: structure of mutant of ribose 5-phosphate isomerase type b from2 trypanosoma cruzi.
19	dlvhca_	 Alignment		41.1	19	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
20	d2ez9a1	 Alignment		40.1	18	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
21	c3m1pA_	 Alignment	not modelled	39.5	20	PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase; PDBTitle: structure of ribose 5-phosphate isomerase type b from trypanosoma2 cruzi, soaked with alllose-6-phosphate
22	c3p04B_	 Alignment	not modelled	39.4	15	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized bcr; PDBTitle: crystal structure of the bcr protein from corynebacterium glutamicum.2 northeast structural genomics consortium target cgr8
23	dl0jra_	 Alignment	not modelled	38.7	7	Fold: AraD/HMP-PK domain-like Superfamily: AraD/HMP-PK domain-like Family: AraD-like aldolase/epimerase
24	c2pcjB_	 Alignment	not modelled	38.5	11	PDB header: hydrolase Chain: B: PDB Molecule: lipoprotein-releasing system atp-binding protein Iold; PDBTitle: crystal structure of abc transporter (aq_297) from aquifex aeolicus2 vf5
25	c3p9zA_	 Alignment	not modelled	37.6	19	PDB header: ligase Chain: A: PDB Molecule: uroporphyrinogen iii cosynthase (hemd); PDBTitle: crystal structure of uroporphyrinogen-iii synthetase from helicobacter2 pylori 26695
26	dljr2a_	 Alignment	not modelled	37.4	19	Fold: HemD-like Superfamily: HemD-like Family: HemD-like
27	cljr2A_	 Alignment	not modelled	37.4	19	PDB header: lyase Chain: A: PDB Molecule: uroporphyrinogen-iii synthase; PDBTitle: structure of uroporphyrinogen iii synthase
28	cls1hB_	 Alignment	not modelled	37.3	18	PDB header: ribosome Chain: B: PDB Molecule: 40s ribosomal protein s0-a; PDBTitle: structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and

						protein3 components into a 11.7 a cryo-em map. this file, 1s1h,4 contains 40s subunit. the 60s ribosomal subunit is in file5 1s1i.
29	c2ejaB_	 Alignment	not modelled	33.3	14	PDB header: lyase Chain: B: PDB Molecule: uroporphyrinogen decarboxylase; PDBTitle: crystal structure of uroporphyrinogen decarboxylase from2 aquifex aeolicus
30	c1zq1B_	 Alignment	not modelled	33.2	26	PDB header: lyase Chain: B: PDB Molecule: glutamyl-trna(gln) amidotransferase subunit d; PDBTitle: structure of gatde trna-dependent amidotransferase from2 pyrococcus abyssi
31	d1zbra1	 Alignment	not modelled	32.5	20	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Porphyromonas-type peptidylarginine deiminase
32	c3p04A_	 Alignment	not modelled	32.1	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized bcr; PDBTitle: crystal structure of the bcr protein from corynebacterium glutamicum.2 northeast structural genomics consortium target cgr8
33	c2infB_	 Alignment	not modelled	31.7	13	PDB header: lyase Chain: B: PDB Molecule: uroporphyrinogen decarboxylase; PDBTitle: crystal structure of uroporphyrinogen decarboxylase from2 bacillus subtilis
34	c3bg3B_	 Alignment	not modelled	31.3	22	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)
35	d1hrua_	 Alignment	not modelled	29.8	15	Fold: YrdC/RibB Superfamily: YrdC/RibB Family: YrdC-like
36	c1d7kB_	 Alignment	not modelled	29.7	17	PDB header: lyase Chain: B: PDB Molecule: human ornithine decarboxylase; PDBTitle: crystal structure of human ornithine decarboxylase at 2.12 angstroms resolution
37	d1veha_	 Alignment	not modelled	29.4	9	Fold: Alpha-lytic protease prodomain-like Superfamily: Fe-S cluster assembly (FSCA) domain-like Family: NifU C-terminal domain-like
38	d1zqla2	 Alignment	not modelled	29.3	26	Fold: Glutaminase/Asparaginase Superfamily: Glutaminase/Asparaginase Family: Glutaminase/Asparaginase
39	c1oidA_	 Alignment	not modelled	28.8	15	PDB header: hydrolase Chain: A: PDB Molecule: protein usha; PDBTitle: 5'-nucleotidase (e. coli) with an engineered disulfide2 bridge (s228c, p513c)
40	d1bd3a_	 Alignment	not modelled	28.6	21	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
41	d2awna2	 Alignment	not modelled	28.5	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
42	d1bw0a_	 Alignment	not modelled	28.2	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
43	c2p5tA_	 Alignment	not modelled	27.6	30	PDB header: transcription regulator Chain: A: PDB Molecule: putative transcriptional regulator peza; PDBTitle: molecular and structural characterization of the pezat chromosomal2 toxin-antitoxin system of the human pathogen streptococcus pneumoniae
44	d2pjuA1	 Alignment	not modelled	27.5	17	Fold: Chelatase-like Superfamily: PrpR receptor domain-like Family: PrpR receptor domain-like
45	c3dwgA_	 Alignment	not modelled	26.5	15	PDB header: transferase Chain: A: PDB Molecule: cysteine synthase b; PDBTitle: crystal structure of a sulfur carrier protein complex found in the2 cysteine biosynthetic pathway of mycobacterium tuberculosis
46	d1agxa_	 Alignment	not modelled	26.4	29	Fold: Glutaminase/Asparaginase Superfamily: Glutaminase/Asparaginase Family: Glutaminase/Asparaginase
47	d1xkna_	 Alignment	not modelled	26.2	16	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Porphyromonas-type peptidylarginine deiminase
48	d1pvda1	 Alignment	not modelled	26.2	21	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
49	d1wbha1	 Alignment	not modelled	25.4	15	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
50	d1v9sa1	 Alignment	not modelled	25.1	24	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
51	d1pswa_	 Alignment	not modelled	25.0	14	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: ADP-heptose LPS heptosyltransferase II
52	c2xznB_	 Alignment	not modelled	24.8	19	PDB header: ribosome Chain: B: PDB Molecule: rps0e; PDBTitle: crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
53	d1b0ua_	 Alignment	not modelled	24.2	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
						Fold: Phosphoglycerate kinase

54	d1phpa_	Alignment	not modelled	24.1	17	Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase
55	c3hbmA_	Alignment	not modelled	23.9	11	PDB header: hydrolase Chain: A: PDB Molecule: udp-sugar hydrolase; PDBTitle: crystal structure of pseg from campylobacter jejuni
56	c3nm3D_	Alignment	not modelled	23.3	14	PDB header: transferase Chain: D: PDB Molecule: thiamine biosynthetic bifunctional enzyme; PDBTitle: the crystal structure of candida glabrata thi6, a bifunctional enzyme2 involved in thiamin biosynthesis of eukaryotes
57	d1jcua_	Alignment	not modelled	22.9	10	Fold: YrdC/RibB Superfamily: YrdC/RibB Family: YrdC-like
58	c2yswB_	Alignment	not modelled	22.8	9	PDB header: lyase Chain: B: PDB Molecule: 3-dehydroquinate dehydratase; PDBTitle: crystal structure of the 3-dehydroquinate dehydratase from aquifex2 aeolicus vf5
59	c2htmB_	Alignment	not modelled	22.8	23	PDB header: biosynthetic protein Chain: B: PDB Molecule: thiazole biosynthesis protein thig; PDBTitle: crystal structure of ttha0676 from thermus thermophilus hb8
60	d1g2912	Alignment	not modelled	22.0	12	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
61	c2ehhE_	Alignment	not modelled	20.3	19	PDB header: lyase Chain: E: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 aquifex aeolicus
62	c3tovB_	Alignment	not modelled	20.0	13	PDB header: transferase Chain: B: PDB Molecule: glycosyl transferase family 9; PDBTitle: the crystal structure of the glycosyl transferase family 9 from2 veillonella parvula dsm 2008
63	c3bchA_	Alignment	not modelled	19.9	14	PDB header: cell adhesion, ribosomal protein Chain: A: PDB Molecule: 40s ribosomal protein sa; PDBTitle: crystal structure of the human laminin receptor precursor
64	d1i5ea_	Alignment	not modelled	19.7	20	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
65	c3bgaB_	Alignment	not modelled	19.3	31	PDB header: hydrolase Chain: B: PDB Molecule: beta-galactosidase; PDBTitle: crystal structure of beta-galactosidase from bacteroides2 thetaiotaomicron vpi-5482
66	c3il0B_	Alignment	not modelled	17.7	14	PDB header: hydrolase Chain: B: PDB Molecule: aminopeptidase p; xaa-pro aminopeptidase; PDBTitle: the crystal structure of the aminopeptidase p, xaa-pro aminopeptidase2 from streptococcus thermophilus
67	c2yz2B_	Alignment	not modelled	17.5	12	PDB header: hydrolase Chain: B: PDB Molecule: putative abc transporter atp-binding protein tm_0222; PDBTitle: crystal structure of the abc transporter in the cobalt transport2 system
68	d1usha2	Alignment	not modelled	17.4	16	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: 5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain
69	c3jyfb_	Alignment	not modelled	17.2	11	PDB header: hydrolase Chain: B: PDB Molecule: 2',3'-cyclic nucleotide 2'-phosphodiesterase/3'- PDBTitle: the crystal structure of a 2,3-cyclic nucleotide 2-2 phosphodiesterase/3-nucleotidase bifunctional periplasmic precursor3 protein from klebsiella pneumoniae subsp. pneumoniae mgh 78578
70	c2jnvA_	Alignment	not modelled	16.8	14	PDB header: metal transport Chain: A: PDB Molecule: nifu-like protein 1, chloroplast; PDBTitle: solution structure of c-terminal domain of nifu-like2 protein from oryza sativa
71	d3dhwc1	Alignment	not modelled	16.7	7	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
72	d2d6fa2	Alignment	not modelled	16.4	24	Fold: Glutaminase/Asparaginase Superfamily: Glutaminase/Asparaginase Family: Glutaminase/Asparaginase
73	c3nxkE_	Alignment	not modelled	16.3	29	PDB header: hydrolase Chain: E: PDB Molecule: cytoplasmic l-asparaginase; PDBTitle: crystal structure of probable cytoplasmic l-asparaginase from2 campylobacter jejuni
74	c1zmrA_	Alignment	not modelled	16.3	15	PDB header: transferase Chain: A: PDB Molecule: phosphoglycerate kinase; PDBTitle: crystal structure of the e. coli phosphoglycerate kinase
75	d1r3sa_	Alignment	not modelled	16.1	16	Fold: TIM beta/alpha-barrel Superfamily: UROD/MeE-like Family: Uroporphyrinogen decarboxylase, UROD
76	d2ocda1	Alignment	not modelled	16.1	24	Fold: Glutaminase/Asparaginase Superfamily: Glutaminase/Asparaginase Family: Glutaminase/Asparaginase
77	d2vzsa5	Alignment	not modelled	16.0	20	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
78	c2k4mA_	Alignment	not modelled	16.0	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0146 protein mth_1000; PDBTitle: solution nmr structure of m. thermoautotrophicum protein2 mth_1000, northeast structural genomics consortium

					target3 tr8
79	c3pihA_	Alignment	not modelled	16.0	20 PDB header: hydrolase/dna Chain: A: PDB Molecule: uvrabc system protein a; PDBTitle: t. maritima uvra in complex with fluorescein-modified dna
80	c1zfjA_	Alignment	not modelled	15.8	14 PDB header: oxidoreductase Chain: A: PDB Molecule: inosine monophosphate dehydrogenase; PDBTitle: inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
81	c2e0kA_	Alignment	not modelled	15.6	8 PDB header: transferase Chain: A: PDB Molecule: precorrin-2 c20-methyltransferase; PDBTitle: crystal structure of cbil, a methyltransferase involved in anaerobic2 vitamin b12 biosynthesis
82	c2vzvB_	Alignment	not modelled	15.6	20 PDB header: hydrolase Chain: B: PDB Molecule: exo-beta-d-glucosaminidase; PDBTitle: substrate complex of amycolatopsis orientalis exo-2 chitosanase csxa e541a with chitosan
83	c1q1bD_	Alignment	not modelled	15.5	21 PDB header: transport protein Chain: D: PDB Molecule: maltose/maltodextrin transport atp-binding protein malk; PDBTitle: crystal structure of e. coli malk in the nucleotide-free form
84	c2r8zC_	Alignment	not modelled	15.4	30 PDB header: hydrolase Chain: C: PDB Molecule: 3-deoxy-d-manno-octulosonate 8-phosphate phosphatase; PDBTitle: crystal structure of yrbi phosphatase from escherichia coli in complex2 with a phosphate and a calcium ion
85	d1pvta_	Alignment	not modelled	15.4	10 Fold: AraD/HMP-PK domain-like Superfamily: AraD/HMP-PK domain-like Family: AraD-like aldolase/epimerase
86	c2i4rA_	Alignment	not modelled	15.3	18 PDB header: hydrolase Chain: A: PDB Molecule: v-type atp synthase subunit f; PDBTitle: crystal structure of the v-type atp synthase subunit f from2 archaeoglobus fulgidus. nesg target gr52a.
87	c2kg4A_	Alignment	not modelled	15.2	32 PDB header: cell cycle Chain: A: PDB Molecule: growth arrest and dna-damage-inducible protein PDBTitle: three-dimensional structure of human gadd45alpha in2 solution by nmr
88	c1wnfA_	Alignment	not modelled	15.2	26 PDB header: hydrolase Chain: A: PDB Molecule: l-asparaginase; PDBTitle: crystal structure of ph0066 from pyrococcus horikoshii
89	c2d3wB_	Alignment	not modelled	15.1	13 PDB header: biosynthetic protein Chain: B: PDB Molecule: probable atp-dependent transporter sufcc; PDBTitle: crystal structure of escherichia coli sufcc, an atpase2 compenent of the suf iron-sulfur cluster assembly machinery
90	c3m1yA_	Alignment	not modelled	15.0	15 PDB header: hydrolase Chain: A: PDB Molecule: phosphoserine phosphatase (serb); PDBTitle: crystal structure of a phosphoserine phosphatase (serb) from2 helicobacter pylori
91	c1nm3B_	Alignment	not modelled	14.7	24 PDB header: electron transport Chain: B: PDB Molecule: protein hi0572; PDBTitle: crystal structure of heamophilus influenza hybrid-prx5
92	c2yxgD_	Alignment	not modelled	14.7	13 PDB header: lyase Chain: D: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase (dapa)
93	c2olkD_	Alignment	not modelled	14.7	12 PDB header: hydrolase Chain: D: PDB Molecule: amino acid abc transporter; PDBTitle: abc protein artp in complex with adp-beta-s
94	c2o7qA_	Alignment	not modelled	14.7	15 PDB header: oxidoreductase,transferase Chain: A: PDB Molecule: bifunctional 3-dehydroquinate dehydratase/shikimate PDBTitle: crystal structure of the a. thaliana dhq-dehydroshikimate-sdh-2 shikimate-nadp(h)
95	d1ji0a_	Alignment	not modelled	14.7	11 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
96	d1g6ha_	Alignment	not modelled	14.6	9 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
97	c3eebB_	Alignment	not modelled	14.6	25 PDB header: toxin Chain: B: PDB Molecule: rtx toxin rtxa; PDBTitle: structure of the v. cholerae rtx cysteine protease domain
98	c3mc3A_	Alignment	not modelled	14.5	17 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: dsre/dsrf-like family protein; PDBTitle: crystal structure of dsre/dsrf-like family protein (np_342589.1) from2 sulfolobus solfataricus at 1.49 a resolution
99	d1wsaa_	Alignment	not modelled	14.3	24 Fold: Glutaminase/Asparaginase Superfamily: Glutaminase/Asparaginase Family: Glutaminase/Asparaginase