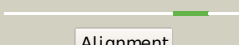
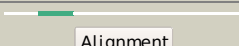
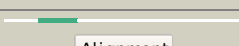
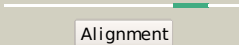
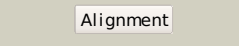
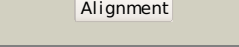
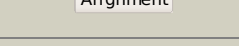
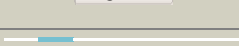
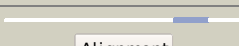
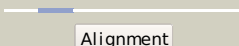
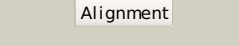
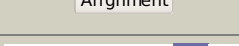
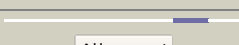
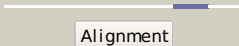
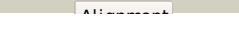
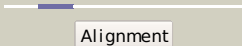
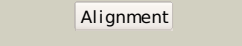
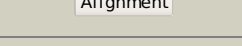
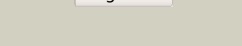
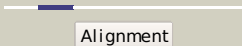
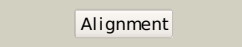
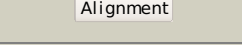
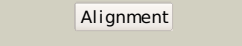
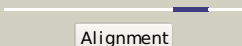
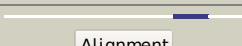


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1otja_	 Alignment		100.0	100	Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: TauD/TfdA-like
2	c3pvjB_	 Alignment		100.0	61	PDB header: oxidoreductase Chain: B: PDB Molecule: alpha-ketoglutarate-dependent taurine dioxygenase; PDBTitle: crystal structure of the fe(ii)/alpha-ketoglutarate dependent taurine2 dioxygenase from pseudomonas putida kt2440
3	d1oiha_	 Alignment		100.0	41	Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: TauD/TfdA-like
4	c3rljB_	 Alignment		100.0	46	PDB header: oxidoreductase Chain: B: PDB Molecule: alpha-ketoglutarate-dependent taurine dioxygenase; PDBTitle: crystal structure of alpha-ketoglutarate-dependent taurine dioxygenase2 from mycobacterium avium, native form
5	c3eatX_	 Alignment		100.0	23	PDB header: oxidoreductase Chain: X: PDB Molecule: pyoverdine biosynthesis protein pvcB; PDBTitle: crystal structure of the pvcB (pa2255) protein from2 pseudomonas aeruginosa
6	d1nx4a_	 Alignment		100.0	18	Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: gamma-Butyrobetaine hydroxylase
7	c3ms5A_	 Alignment		100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: gamma-butyrobetaine dioxygenase; PDBTitle: crystal structure of human gamma-butyrobetaine,2-oxoglutarate2 dioxygenase 1 (bbox1)
8	d1y0za_	 Alignment		100.0	15	Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: gamma-Butyrobetaine hydroxylase
9	d1ds1a_	 Alignment		100.0	18	Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: Clavamate synthase
10	c2og5A_	 Alignment		100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxygenase; PDBTitle: crystal structure of asparagine oxygenase (asno)
11	d1jr7a_	 Alignment		100.0	17	Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: Gab protein (hypothetical protein YgaT)

12	c2wbqA_	Alignment		100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: l-arginine beta-hydroxylase; PDBTitle: crystal structure of vioc in complex with (2s,3s)-2 hydroxyarginine
13	c2opwA_	Alignment		97.9	19	PDB header: oxidoreductase Chain: A: PDB Molecule: phyhd1 protein; PDBTitle: crystal structure of human phytanoyl-coa dioxygenase phyhd1 (apo)
14	c3nnlB_	Alignment		97.4	10	PDB header: biosynthetic protein Chain: B: PDB Molecule: cura; PDBTitle: halogenase domain from cura module (crystal form iii)
15	c2rdsA_	Alignment		96.6	21	PDB header: oxidoreductase Chain: A: PDB Molecule: 1-deoxypentalenic acid 11-beta hydroxylase; fe(ii)/alpha- PDBTitle: crystal structure of pth with fe/oxalylglycine and ent-1-2 deoxypentalenic acid bound
16	d2fcta1	Alignment		96.5	14	Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: PhyH-like
17	c3gjbA_	Alignment		96.1	13	PDB header: biosynthetic protein Chain: A: PDB Molecule: cytc3; PDBTitle: cytc3 with fe(ii) and alpha-ketoglutarate
18	c3emrA_	Alignment		94.9	7	PDB header: oxidoreductase Chain: A: PDB Molecule: ectd; PDBTitle: crystal structure analysis of the ectoine hydroxylase ectd from2 salibacillus salexigens
19	d2a1xa1	Alignment		91.7	10	Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: PhyH-like
20	d1wdia_	Alignment		85.5	11	Fold: QueA-like Superfamily: QueA-like Family: QueA-like
21	c1yy3A_	Alignment	not modelled	85.4	11	PDB header: isomerase Chain: A: PDB Molecule: s-adenosylmethionine:trna ribosyltransferase- PDBTitle: structure of s-adenosylmethionine:trna ribosyltransferase-2 isomerase (quea)
22	d1vkyA_	Alignment	not modelled	83.3	11	Fold: QueA-like Superfamily: QueA-like Family: QueA-like
23	c2ijjA_	Alignment	not modelled	63.7	10	PDB header: hydrolase Chain: A: PDB Molecule: prolyl-4 hydroxylase; PDBTitle: crystal structure of the apo form of chlamydomonas2 reinhardtii prolyl-4 hydroxylase type i
24	d1gp6a_	Alignment	not modelled	59.8	31	Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: Penicillin synthase-like
25	d1dcsa_	Alignment	not modelled	59.5	8	Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: Penicillin synthase-like
26	c2g19A_	Alignment	not modelled	58.3	9	PDB header: oxidoreductase Chain: A: PDB Molecule: egl nine homolog 1; PDBTitle: cellular oxygen sensing: crystal structure of hypoxia-2 inducible factor prolyl hydroxylase (phd2)
27	c3pl0B_	Alignment	not modelled	56.6	21	PDB header: biosynthetic protein Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a bsma homolog (mpe_a2762) from methylobium2 petroleophilum pm1 at 1.91 a resolution
28	d1odma_	Alignment	not modelled	55.8	14	Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: Penicillin synthase-like

29	c3itqB_	 Alignment	not modelled	51.8	8	PDB header: oxidoreductase Chain: B: PDB Molecule: prolyl 4-hydroxylase, alpha subunit domain protein; PDBTitle: crystal structure of a prolyl 4-hydroxylase from bacillus anthracis
30	c3ouiA_	 Alignment	not modelled	49.7	9	PDB header: oxidoreductase Chain: A: PDB Molecule: egl nine homolog 1; PDBTitle: phd2-r717 with 40787422
31	c3on7C_	 Alignment	not modelled	49.3	7	PDB header: oxidoreductase Chain: C: PDB Molecule: oxidoreductase, iron/ascorbate family; PDBTitle: crystal structure of a putative oxygenase (so_2589) from shewanella2 oneidensis at 2.20 a resolution
32	c2fg0B_	 Alignment	not modelled	47.0	10	PDB header: hydrolase Chain: B: PDB Molecule: cog0791: cell wall-associated hydrolases (invasion- PDBTitle: crystal structure of a putative gamma-d-glutamyl-l-diamino acid2 endopeptidase (npun_r0659) from nostoc punctiforme pcc 73102 at 1.793 a resolution
33	d2csga1	 Alignment	not modelled	45.8	12	Fold: Double-stranded beta-helix Superfamily: Clavaminase synthase-like Family: YbiU-like
34	d2evra2	 Alignment	not modelled	42.2	9	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: NlpC/P60
35	d1e5ra_	 Alignment	not modelled	40.5	20	Fold: Double-stranded beta-helix Superfamily: Clavaminase synthase-like Family: Type II Proline 3-hydroxylase (proline oxidase)
36	c2dbiA_	 Alignment	not modelled	37.7	8	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ybiu; PDBTitle: crystal structure of a hypothetical protein jw0805 from2 escherichia coli
37	c3gt2A_	 Alignment	not modelled	34.7	18	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the p60 domain from m. avium2 paratuberculosis antigen map1272c
38	c2xivA_	 Alignment	not modelled	34.2	19	PDB header: structural protein Chain: A: PDB Molecule: hypothetical invasion protein; PDBTitle: structure of rv1477, hypothetical invasion protein of2 mycobacterium tuberculosis
39	d1w9ya1	 Alignment	not modelled	32.2	13	Fold: Double-stranded beta-helix Superfamily: Clavaminase synthase-like Family: Penicillin synthase-like
40	c3npfB_	 Alignment	not modelled	30.6	13	PDB header: hydrolase Chain: B: PDB Molecule: putative dipeptidyl-peptidase vi; PDBTitle: crystal structure of a putative dipeptidyl-peptidase vi (bacova_00612)2 from bacteroides ovatus at 1.72 a resolution
41	c3pbiA_	 Alignment	not modelled	28.2	19	PDB header: hydrolase Chain: A: PDB Molecule: invasion protein; PDBTitle: structure of the peptidoglycan hydrolase ripb (rv1478) from2 mycobacterium tuberculosis at 1.6 resolution
42	c3ghfA_	 Alignment	not modelled	28.1	11	PDB header: cell cycle Chain: A: PDB Molecule: septum site-determining protein minc; PDBTitle: crystal structure of the septum site-determining protein2 minc from salmonella typhimurium
43	d16pka_	 Alignment	not modelled	25.9	20	Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase
44	d1bvp12	 Alignment	not modelled	25.3	21	Fold: Viral protein domain Superfamily: Viral protein domain Family: Top domain of virus capsid protein
45	c2a5hC_	 Alignment	not modelled	24.9	12	PDB header: isomerase Chain: C: PDB Molecule: l-lysine 2,3-aminomutase; PDBTitle: 2.1 angstrom x-ray crystal structure of lysine-2,3-aminomutase from2 clostridium subterminale sb4, with michaelis analog (l-alpha-lysine3 external aldimine form of pyridoxal-5'-phosphate).
46	c1zmrA_	 Alignment	not modelled	22.7	7	PDB header: transferase Chain: A: PDB Molecule: phosphoglycerate kinase; PDBTitle: crystal structure of the e. coli phosphoglycerate kinase
47	d1hdia_	 Alignment	not modelled	20.9	7	Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase
48	d1phpa_	 Alignment	not modelled	20.0	14	Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase
49	d1ltkA_	 Alignment	not modelled	19.3	13	Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase
50	c2nnzA_	 Alignment	not modelled	18.3	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: solution structure of the hypothetical protein af2241 from2 archaeoglobus fulgidus
51	d1fw8a_	 Alignment	not modelled	18.2	14	Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase
52	d1vpea_	 Alignment	not modelled	18.0	7	Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase
53	c2w8iG_	 Alignment	not modelled	16.9	31	PDB header: membrane protein Chain: G: PDB Molecule: putative outer membrane lipoprotein wza; PDBTitle: crystal structure of wza24-345.
54	c3dkoB_	Alignment	not modelled	16.8	8	PDB header: oxidoreductase Chain: B: PDB Molecule: pkhd-type hydroxylase sbal_3634;

54	c3ukqB	Alignment	not modelled	10.8	8	PDBTitle: crystal structure of putative oxygenase (yp_001051978.1) from2 shewanella baltica os155 at 2.26 a resolution
55	d1v6sa	Alignment	not modelled	16.2	14	Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase
56	c2cunA	Alignment	not modelled	16.1	21	PDB header: transferase Chain: A: PDB Molecule: phosphoglycerate kinase; PDBTitle: crystal structure of phosphoglycerate kinase from pyrococcus2 horikoshii o3
57	d2toda1	Alignment	not modelled	15.7	8	Fold: Domain of alpha and beta subunits of F1 ATP synthase-like Superfamily: Alanine racemase C-terminal domain-like Family: Eukaryotic ODC-like
58	c3trrA	Alignment	not modelled	15.5	16	PDB header: isomerase Chain: A: PDB Molecule: probable enoyl-coa hydratase/isomerase; PDBTitle: crystal structure of a probable enoyl-coa hydratase/isomerase from2 mycobacterium abscessus
59	c3q3vA	Alignment	not modelled	14.9	14	PDB header: transferase Chain: A: PDB Molecule: phosphoglycerate kinase; PDBTitle: crystal structure of phosphoglycerate kinase from campylobacter2 jejuni.
60	d1vjda	Alignment	not modelled	14.8	7	Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase
61	d1qpga	Alignment	not modelled	14.6	14	Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase
62	c3cmwA	Alignment	not modelled	14.6	22	PDB header: recombination/dna Chain: A: PDB Molecule: protein reca; PDBTitle: mechanism of homologous recombination from the reca-2 ssdna/dsdna structures
63	c3h41A	Alignment	not modelled	13.8	18	PDB header: hydrolase Chain: A: PDB Molecule: nlp/p60 family protein; PDBTitle: crystal structure of a nlp/p60 family protein (bce_2878) from2 bacillus cereus atcc 10987 at 1.79 a resolution
64	c3bvcA	Alignment	not modelled	13.7	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein ism_01780; PDBTitle: crystal structure of uncharacterized protein ism_01780 from2 roseovarius nubinhibens ism
65	c3cmuA	Alignment	not modelled	13.4	22	PDB header: recombination/dna Chain: A: PDB Molecule: protein reca; PDBTitle: mechanism of homologous recombination from the reca-2 ssdna/dsdna structures
66	c2ej5B	Alignment	not modelled	13.3	12	PDB header: lyase Chain: B: PDB Molecule: enoyl-coa hydratase subunit ii; PDBTitle: crystal structure of gk2038 protein (enoyl-coa hydratase subunit ii)2 from geobacillus kaustophilus
67	c3rcqA	Alignment	not modelled	13.2	11	PDB header: oxidoreductase Chain: A: PDB Molecule: aspartyl/asparaginyl beta-hydroxylase; PDBTitle: crystal structure of human aspartate beta-hydroxylase isoform a
68	c3r38A	Alignment	not modelled	13.1	7	PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine 1-carboxyvinyltransferase 1; PDBTitle: 2.23 angstrom resolution crystal structure of udp-n-acetylglucosamine2 1-carboxyvinyltransferase (mura) from listeria monocytogenes egd-e
69	d1e4cp	Alignment	not modelled	13.1	15	Fold: AraD/HMP-PK domain-like Superfamily: AraD/HMP-PK domain-like Family: AraD-like aldolase/epimerase
70	d7odca1	Alignment	not modelled	12.9	15	Fold: Domain of alpha and beta subunits of F1 ATP synthase-like Superfamily: Alanine racemase C-terminal domain-like Family: Eukaryotic ODC-like
71	c2d40C	Alignment	not modelled	12.5	13	PDB header: oxidoreductase Chain: C: PDB Molecule: putative gentisate 1,2-dioxygenase; PDBTitle: crystal structure of z3393 from escherichia coli o157:h7
72	d1njjb1	Alignment	not modelled	12.4	8	Fold: Domain of alpha and beta subunits of F1 ATP synthase-like Superfamily: Alanine racemase C-terminal domain-like Family: Eukaryotic ODC-like
73	d2fcja1	Alignment	not modelled	12.4	17	Fold: Toprim domain Superfamily: Toprim domain Family: Toprim domain
74	d1zx8a1	Alignment	not modelled	12.4	8	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: TM1367-like
75	d1nzva	Alignment	not modelled	11.6	16	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Crotonase-like
76	c2zpmA	Alignment	not modelled	11.4	21	PDB header: hydrolase Chain: A: PDB Molecule: regulator of sigma e protease; PDBTitle: crystal structure analysis of pdz domain b
77	d16vpa	Alignment	not modelled	10.9	21	Fold: Conserved core of transcriptional regulatory protein vp16 Superfamily: Conserved core of transcriptional regulatory protein vp16 Family: Conserved core of transcriptional regulatory protein vp16
78	c2booA	Alignment	not modelled	10.8	29	PDB header: hydrolase Chain: A: PDB Molecule: uracil-dna glycosylase; PDBTitle: the crystal structure of uracil-dna n-glycosylase (ung)2 from deinococcus radiodurans.
79	d2hxma1	Alignment	not modelled	10.6	29	Fold: Uracil-DNA glycosylase-like Superfamily: Uracil-DNA glycosylase-like Family: Uracil-DNA glycosylase
80	d1ahsa	Alignment	not modelled	10.3	15	Fold: Viral protein domain Superfamily: Viral protein domain Family: Top domain of virus capsid protein

81	d1j5ya2		not modelled	10.3	5	Fold: HPr-like Superfamily: Putative transcriptional regulator TM1602, C-terminal domain Family: Putative transcriptional regulator TM1602, C-terminal domain
82	d2v9va2		not modelled	10.2	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: C-terminal fragment of elongation factor SelB
83	c2k1gA		not modelled	10.1	13	PDB header: lipoprotein Chain: A: PDB Molecule: lipoprotein spr; PDBTitle: solution nmr structure of lipoprotein spr from escherichia coli k12.2 northeast structural genomics target er541-37-162
84	d1okba		not modelled	10.0	29	Fold: Uracil-DNA glycosylase-like Superfamily: Uracil-DNA glycosylase-like Family: Uracil-DNA glycosylase
85	d3euqa		not modelled	9.3	36	Fold: Uracil-DNA glycosylase-like Superfamily: Uracil-DNA glycosylase-like Family: Uracil-DNA glycosylase
86	d3bu7a1		not modelled	9.0	14	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Gentisate 1,2-dioxygenase-like
87	c3bu7A		not modelled	9.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: gentisate 1,2-dioxygenase; PDBTitle: crystal structure and biochemical characterization of gdosp,2 a gentisate 1,2-dioxygenase from silicibacter pomeroyi
88	c2opiB		not modelled	8.6	26	PDB header: lyase Chain: B: PDB Molecule: l-fucose-1-phosphate aldolase; PDBTitle: crystal structure of l-fucose-1-phosphate aldolase from bacteroides2 thetaiotaomicron
89	d1o98a1		not modelled	8.5	38	Fold: 2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain Superfamily: 2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain Family: 2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain
90	c2kvcA		not modelled	8.5	21	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: solution structure of the mycobacterium tuberculosis protein rv0543c,2 a member of the duf3349 superfamily. seattle structural genomics3 center for infectious disease target mytud.17112.a
91	c2i79B		not modelled	8.4	31	PDB header: transferase Chain: B: PDB Molecule: acetyltransferase, gnat family; PDBTitle: the crystal structure of the acetyltransferase of gnat family from2 streptococcus pneumoniae
92	d2phda1		not modelled	8.2	18	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Gentisate 1,2-dioxygenase-like
93	d1f3ta1		not modelled	7.8	8	Fold: Domain of alpha and beta subunits of F1 ATP synthase-like Superfamily: Alanine racemase C-terminal domain-like Family: Eukaryotic ODC-like
94	c3ooxA		not modelled	7.7	16	PDB header: oxidoreductase Chain: A: PDB Molecule: putative 2og-fe(ii) oxygenase family protein; PDBTitle: crystal structure of a putative 2og-fe(ii) oxygenase family protein2 (cc_0200) from caulobacter crescentus at 1.44 a resolution
95	c2zhxG		not modelled	7.6	36	PDB header: hydrolase/hydrolase inhibitor Chain: G: PDB Molecule: uracil-dna glycosylase; PDBTitle: crystal structure of uracil-dna glycosylase from mycobacterium2 tuberculosis in complex with a proteinaceous inhibitor
96	d1dt9a3		not modelled	7.5	15	Fold: N-terminal domain of eukaryotic peptide chain release factor subunit 1, ERF1 Superfamily: N-terminal domain of eukaryotic peptide chain release factor subunit 1, ERF1 Family: N-terminal domain of eukaryotic peptide chain release factor subunit 1, ERF1
97	d1q6za1		not modelled	7.5	13	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
98	c3rrvC		not modelled	7.4	12	PDB header: isomerase Chain: C: PDB Molecule: enoyl-coa hydratase/isomerase; PDBTitle: crystal structure of an enoyl-coa hydratase/isomerase from2 mycobacterium paratuberculosis
99	d1d5ra1		not modelled	7.4	19	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: PLC-like (P variant)