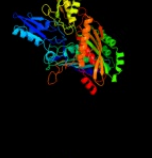
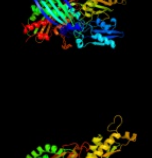
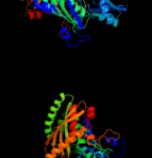
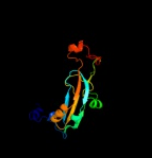
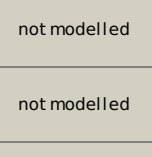
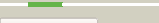
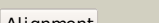
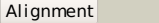
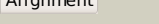
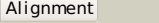
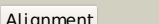
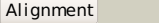
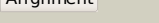
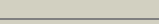
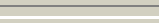
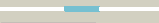


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1ffvB_	 Alignment		100.0	27	PDB header: hydrolase Chain: B: PDB Molecule: cutl, molybdoprotein of carbon monoxide PDBTitle: carbon monoxide dehydrogenase from hydrogenophaga2 pseudoflava
2	c1sb3D_	 Alignment		100.0	33	PDB header: oxidoreductase Chain: D: PDB Molecule: 4-hydroxybenzoyl-coa reductase alpha subunit; PDBTitle: structure of 4-hydroxybenzoyl-coa reductase from thauera2 aromatica
3	c1n62E_	 Alignment		100.0	26	PDB header: oxidoreductase Chain: E: PDB Molecule: carbon monoxide dehydrogenase large chain; PDBTitle: crystal structure of the mo,cu-co dehydrogenase (codh), n-2 butylisocyanide-bound state
4	c1t3qB_	 Alignment		100.0	28	PDB header: oxidoreductase Chain: B: PDB Molecule: quinoline 2-oxidoreductase large subunit; PDBTitle: crystal structure of quinoline 2-oxidoreductase from pseudomonas2 putida 86
5	c2w54F_	 Alignment		100.0	25	PDB header: oxidoreductase Chain: F: PDB Molecule: xanthine dehydrogenase; PDBTitle: crystal structure of xanthine dehydrogenase from2 rhodobacter capsulatus in complex with bound inhibitor3 pterin-6-aldehyde
6	c1wygA_	 Alignment		100.0	25	PDB header: oxidoreductase Chain: A: PDB Molecule: xanthine dehydrogenase/oxidase; PDBTitle: crystal structure of a rat xanthine dehydrogenase triple mutant2 (c535a, c992r and c1324s)
7	c3eubL_	 Alignment		100.0	25	PDB header: oxidoreductase Chain: L: PDB Molecule: xanthine dehydrogenase/oxidase; PDBTitle: crystal structure of desulfo-xanthine oxidase with xanthine
8	c1vlbA_	 Alignment		100.0	27	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde oxidoreductase; PDBTitle: structure refinement of the aldehyde oxidoreductase from2 desulfovibrio gigas at 1.28 a
9	c1dgiA_	 Alignment		100.0	25	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde oxidoreductase; PDBTitle: crystal structure of the aldehyde oxidoreductase from2 desulfovibrio desulfuricans atcc 27774
10	d1rm6a2	 Alignment		100.0	33	Fold: Molybdenum cofactor-binding domain Superfamily: Molybdenum cofactor-binding domain Family: Molybdenum cofactor-binding domain
11	d1n62b2	 Alignment		100.0	24	Fold: Molybdenum cofactor-binding domain Superfamily: Molybdenum cofactor-binding domain Family: Molybdenum cofactor-binding domain

12	d1ffvb2	Alignment		100.0	26	Fold: Molybdenum cofactor-binding domain Superfamily: Molybdenum cofactor-binding domain Family: Molybdenum cofactor-binding domain
13	d1jrob2	Alignment		100.0	25	Fold: Molybdenum cofactor-binding domain Superfamily: Molybdenum cofactor-binding domain Family: Molybdenum cofactor-binding domain
14	d1t3qb2	Alignment		100.0	26	Fold: Molybdenum cofactor-binding domain Superfamily: Molybdenum cofactor-binding domain Family: Molybdenum cofactor-binding domain
15	d1v97a5	Alignment		100.0	24	Fold: Molybdenum cofactor-binding domain Superfamily: Molybdenum cofactor-binding domain Family: Molybdenum cofactor-binding domain
16	d1vlba4	Alignment		100.0	27	Fold: Molybdenum cofactor-binding domain Superfamily: Molybdenum cofactor-binding domain Family: Molybdenum cofactor-binding domain
17	d1dgja4	Alignment		100.0	25	Fold: Molybdenum cofactor-binding domain Superfamily: Molybdenum cofactor-binding domain Family: Molybdenum cofactor-binding domain
18	c3hrdE	Alignment		100.0	32	PDB header: oxidoreductase Chain: E: PDB Molecule: nicotinate dehydrogenase large molybdopterin PDBTitle: crystal structure of nicotinate dehydrogenase
19	c3hrdF	Alignment		100.0	28	PDB header: oxidoreductase Chain: F: PDB Molecule: nicotinate dehydrogenase medium molybdopterin PDBTitle: crystal structure of nicotinate dehydrogenase
20	d1t3qb1	Alignment		100.0	37	Fold: alpha/beta-Hammerhead Superfamily: CO dehydrogenase molybdoprotein N-domain-like Family: CO dehydrogenase molybdoprotein N-domain-like
21	d1ffvb1	Alignment	not modelled	100.0	34	Fold: alpha/beta-Hammerhead Superfamily: CO dehydrogenase molybdoprotein N-domain-like Family: CO dehydrogenase molybdoprotein N-domain-like
22	d1v97a3	Alignment	not modelled	100.0	26	Fold: alpha/beta-Hammerhead Superfamily: CO dehydrogenase molybdoprotein N-domain-like Family: CO dehydrogenase molybdoprotein N-domain-like
23	d1n62b1	Alignment	not modelled	100.0	32	Fold: alpha/beta-Hammerhead Superfamily: CO dehydrogenase molybdoprotein N-domain-like Family: CO dehydrogenase molybdoprotein N-domain-like
24	d3b9jc1	Alignment	not modelled	100.0	26	Fold: alpha/beta-Hammerhead Superfamily: CO dehydrogenase molybdoprotein N-domain-like Family: CO dehydrogenase molybdoprotein N-domain-like
25	d1rm6a1	Alignment	not modelled	100.0	37	Fold: alpha/beta-Hammerhead Superfamily: CO dehydrogenase molybdoprotein N-domain-like Family: CO dehydrogenase molybdoprotein N-domain-like
26	d1jrob1	Alignment	not modelled	100.0	30	Fold: alpha/beta-Hammerhead Superfamily: CO dehydrogenase molybdoprotein N-domain-like Family: CO dehydrogenase molybdoprotein N-domain-like
27	d1vlba3	Alignment	not modelled	100.0	27	Fold: alpha/beta-Hammerhead Superfamily: CO dehydrogenase molybdoprotein N-domain-like Family: CO dehydrogenase molybdoprotein N-domain-like
28	d1dgja3	Alignment	not modelled	100.0	24	Fold: alpha/beta-Hammerhead Superfamily: CO dehydrogenase molybdoprotein N-domain-like Family: CO dehydrogenase molybdoprotein N-domain-like
29	d1knwa2	Alignment	not modelled	52.5	16	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel

						Family: Alanine racemase-like, N-terminal domain
30	c2rghA_	 Alignment	not modelled	52.3	15	PDB header: oxidoreductase Chain: A: PDB Molecule: alpha-glycerophosphate oxidase; PDBTitle: structure of alpha-glycerophosphate oxidase from2 streptococcus sp.: a template for the mitochondrial alpha-3 glycerophosphate dehydrogenase
31	c2kwpA_	 Alignment	not modelled	49.4	23	PDB header: transcription Chain: A: PDB Molecule: transcription elongation protein nusa; PDBTitle: solution structure of the aminoterminal domain of e. coli nusa
32	d1hh2p4	 Alignment	not modelled	48.4	18	Fold: Transcription factor NusA, N-terminal domain Superfamily: Transcription factor NusA, N-terminal domain Family: Transcription factor NusA, N-terminal domain
33	c3n2oA_	 Alignment	not modelled	47.4	20	PDB header: lyase Chain: A: PDB Molecule: biosynthetic arginine decarboxylase; PDBTitle: x-ray crystal structure of arginine decarboxylase complexed with2 arginine from vibrio vulnificus
34	d1otfa_	 Alignment	not modelled	46.0	22	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: 4-oxalocrotonate tautomerase-like
35	c1vraA_	 Alignment	not modelled	43.8	31	PDB header: transferase Chain: A: PDB Molecule: arginine biosynthesis bifunctional protein argj; PDBTitle: crystal structure of arginine biosynthesis bifunctional protein argj2 (10175521) from bacillus halodurans at 2.00 a resolution
36	c2op8A_	 Alignment	not modelled	42.7	14	PDB header: isomerase Chain: A: PDB Molecule: probable tautomerase ywhb; PDBTitle: crystal structure of ywhb- homologue of 4-oxalocrotonate tautomerase
37	c3abfB_	 Alignment	not modelled	41.4	28	PDB header: isomerase Chain: B: PDB Molecule: 4-oxalocrotonate tautomerase; PDBTitle: crystal structure of a 4-oxalocrotonate tautomerase homologue2 (tthb242)
38	d2aala1	 Alignment	not modelled	40.7	13	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: MSAD-like
39	d1mwwa_	 Alignment	not modelled	39.6	8	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: Hypothetical protein HI1388.1
40	d1uiza_	 Alignment	not modelled	39.4	14	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: MIF-related
41	c2xczA_	 Alignment	not modelled	39.0	18	PDB header: immune system Chain: A: PDB Molecule: possible atls1-like light-inducible protein; PDBTitle: crystal structure of macrophage migration inhibitory factor2 homologue from prochlorococcus marinus
42	c2ormA_	 Alignment	not modelled	38.1	16	PDB header: isomerase Chain: A: PDB Molecule: probable tautomerase hp0924; PDBTitle: crystal structure of the 4-oxalocrotonate tautomerase homologue dmpi2 from helicobacter pylori.
43	d2cpqa1	 Alignment	not modelled	37.8	37	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
44	c3gacD_	 Alignment	not modelled	37.7	16	PDB header: cytokine Chain: D: PDB Molecule: macrophage migration inhibitory factor-like PDBTitle: structure of mif with hpp
45	c3mlcC_	 Alignment	not modelled	37.4	22	PDB header: isomerase Chain: C: PDB Molecule: fg41 malonate semialdehyde decarboxylase; PDBTitle: crystal structure of fg41msad inactivated by 3-chloropropionate
46	c3m20A_	 Alignment	not modelled	37.3	16	PDB header: isomerase Chain: A: PDB Molecule: 4-oxalocrotonate tautomerase, putative; PDBTitle: crystal structure of dmpi from archaeoglobus fulgidus determined to2 2.37 angstroms resolution
47	d1yh5a1	 Alignment	not modelled	37.2	13	Fold: YggU-like Superfamily: YggU-like Family: YggU-like
48	c3mb2G_	 Alignment	not modelled	37.1	37	PDB header: isomerase Chain: G: PDB Molecule: 4-oxalocrotonate tautomerase family enzyme - alpha subunit; PDBTitle: kinetic and structural characterization of a heterohexamer 4-2 oxalocrotonate tautomerase from chloroflexus aurantiacus j-10-fl:3 implications for functional and structural diversity in the4 tautomerase superfamily
49	c2lfcA_	 Alignment	not modelled	36.8	35	PDB header: oxidoreductase Chain: A: PDB Molecule: fumarate reductase, flavoprotein subunit; PDBTitle: solution nmr structure of fumarate reductase flavoprotein subunit from2 lactobacillus plantarum, northeast structural genomics consortium3 target lpr145j
50	d1t0aa_	 Alignment	not modelled	36.4	18	Fold: Bacillus chorismate mutase-like Superfamily: lpsF-like Family: lpsF-like
51	d1bjpa_	 Alignment	not modelled	36.1	24	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: 4-oxalocrotonate tautomerase-like
52	c3fwtA_	 Alignment	not modelled	36.1	15	PDB header: cytokine Chain: A: PDB Molecule: macrophage migration inhibitory factor-like PDBTitle: crystal structure of leishmania major mif2
53	c3nzqB_	 Alignment	not modelled	35.8	20	PDB header: lyase Chain: B: PDB Molecule: biosynthetic arginine decarboxylase; PDBTitle: crystal structure of biosynthetic arginine decarboxylase

77	c3f0gA_	Alignment	not modelled	23.4	26	Chain: A: PDB Molecule: 2-c-methyl-d-erythritol 2,4-cyclodiphosphate synthase; PDBTitle: co-crystal structure of 2c-methyl-d-erythritol 2,4-cyclodiphosphate2 synthase with cmp
78	c2os5C_	Alignment	not modelled	23.3	12	PDB header: cytokine Chain: C: PDB Molecule: acemif; PDBTitle: macrophage migration inhibitory factor from ancylostoma ceylanicum
79	d1d7ka2	Alignment	not modelled	23.3	17	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel Family: Alanine racemase-like, N-terminal domain
80	c3re3B_	Alignment	not modelled	23.1	17	PDB header: lyase Chain: B: PDB Molecule: 2-c-methyl-d-erythritol 2,4-cyclodiphosphate synthase; PDBTitle: crystal structure of 2-c-methyl-d-erythritol 2,4-cyclodiphosphate2 synthase from francisella tularensis
81	d1gx1a_	Alignment	not modelled	21.8	17	Fold: Bacillus chorismate mutase-like Superfamily: lpsF-like Family: lpsF-like
82	d1up7a2	Alignment	not modelled	20.6	13	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: AglA-like glucosidase
83	c2on3A_	Alignment	not modelled	20.2	19	PDB header: lyase Chain: A: PDB Molecule: ornithine decarboxylase; PDBTitle: a structural insight into the inhibition of human and2 leishmania donovani ornithine decarboxylases by 3-aminoxy-3 1-aminopropane
84	c3b6nA_	Alignment	not modelled	19.4	26	PDB header: lyase Chain: A: PDB Molecule: 2-c-methyl-d-erythritol 2,4-cyclodiphosphate PDBTitle: crystal structure of 2c-methyl-d-erythritol 2,4-2 cyclodiphosphate synthase pv003920 from plasmodium vivax
85	d1s6ya2	Alignment	not modelled	19.4	22	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: AglA-like glucosidase
86	c1m8pB_	Alignment	not modelled	19.0	21	PDB header: transferase Chain: B: PDB Molecule: sulfate adenyllyltransferase; PDBTitle: crystal structure of p. chrysogenum atp sulfurylase in the t-state
87	d2g0ta1	Alignment	not modelled	18.8	27	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
88	c3ketA_	Alignment	not modelled	18.3	24	PDB header: transcription/dna Chain: A: PDB Molecule: redox-sensing transcriptional repressor rex; PDBTitle: crystal structure of a rex-family transcriptional regulatory protein2 from streptococcus agalactiae bound to a palindromic operator
89	d7odca2	Alignment	not modelled	17.4	20	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel Family: Alanine racemase-like, N-terminal domain
90	d1f3ta2	Alignment	not modelled	17.3	10	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel Family: Alanine racemase-like, N-terminal domain
91	c3a1yF_	Alignment	not modelled	16.1	28	PDB header: ribosomal protein Chain: F: PDB Molecule: 50s ribosomal protein p1 (l12p); PDBTitle: the structure of protein complex
92	c3e0mB_	Alignment	not modelled	15.9	18	PDB header: oxidoreductase Chain: B: PDB Molecule: peptide methionine sulfoxide reductase msra/msrb PDBTitle: crystal structure of fusion protein of msra and msrb
93	d1l0oc_	Alignment	not modelled	15.8	35	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
94	c1l0oC_	Alignment	not modelled	15.8	35	PDB header: protein binding Chain: C: PDB Molecule: sigma factor; PDBTitle: crystal structure of the bacillus stearothermophilus anti-2 sigma factor spoiiab with the sporulation sigma factor3 sigmaf
95	d1f80d_	Alignment	not modelled	15.8	20	Fold: Acyl carrier protein-like Superfamily: ACP-like Family: Acyl-carrier protein (ACP)
96	c2hlhA_	Alignment	not modelled	15.6	21	PDB header: transferase Chain: A: PDB Molecule: nodulation fucosyltransferase; PDBTitle: crystal structure of fucosyltransferase nodz from bradyrhizobium
97	c2jxuA_	Alignment	not modelled	15.4	39	PDB header: unknown function Chain: A: PDB Molecule: terb; PDBTitle: nmr solution structure of kp-terb, a tellurite resistance2 protein from klebsiella pneumoniae
98	c3mt1B_	Alignment	not modelled	15.3	19	PDB header: lyase Chain: B: PDB Molecule: putative carboxynorspermidine decarboxylase protein; PDBTitle: crystal structure of putative carboxynorspermidine decarboxylase2 protein from sinorhizobium meliloti
99	d2p3ra2	Alignment	not modelled	14.2	25	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glycerol kinase