







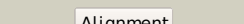

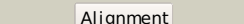

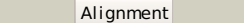



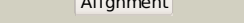

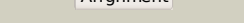

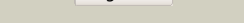









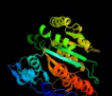










#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1cm7a_	 Alignment		100.0	100	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Dimeric isocitrate & isopropylmalate dehydrogenases
2	d1cnza_	 Alignment		100.0	94	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Dimeric isocitrate & isopropylmalate dehydrogenases
3	d1vlca_	 Alignment		100.0	57	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Dimeric isocitrate & isopropylmalate dehydrogenases
4	c3r8wC_	 Alignment		100.0	52	PDB header: oxidoreductase Chain: C: PDB Molecule: 3-isopropylmalate dehydrogenase 2, chloroplastic; PDBTitle: structure of 3-isopropylmalate dehydrogenase isoform 2 from2 arabidopsis thaliana at 2.2 angstrom resolution
5	d1v53a1	 Alignment		100.0	51	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Dimeric isocitrate & isopropylmalate dehydrogenases
6	d1a05a_	 Alignment		100.0	50	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Dimeric isocitrate & isopropylmalate dehydrogenases
7	c2d1cB_	 Alignment		100.0	34	PDB header: oxidoreductase Chain: B: PDB Molecule: isocitrate dehydrogenase; PDBTitle: crystal structure of tt0538 protein from thermus thermophilus hb8
8	c3u1hA_	 Alignment		100.0	58	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-isopropylmalate dehydrogenase; PDBTitle: crystal structure of ipmdh from the last common ancestor of bacillus
9	c3fmxX_	 Alignment		100.0	36	PDB header: oxidoreductase Chain: X: PDB Molecule: tartrate dehydrogenase/decarboxylase; PDBTitle: crystal structure of tartrate dehydrogenase from pseudomonas2 putida complexed with nadh
10	d1g2ua_	 Alignment		100.0	51	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Dimeric isocitrate & isopropylmalate dehydrogenases
11	d1pb1a_	 Alignment		100.0	27	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Dimeric isocitrate & isopropylmalate dehydrogenases

12	c2d4vD_	Alignment		100.0	29	PDB header: oxidoreductase Chain: D: PDB Molecule: isocitrate dehydrogenase; PDBTitle: crystal structure of nad dependent isocitrate dehydrogenase2 from acidithiobacillus thiooxidans
13	dlxaca_	Alignment		100.0	48	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Dimeric isocitrate & isopropylmalate dehydrogenases
14	dlhgsa_	Alignment		100.0	29	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Dimeric isocitrate & isopropylmalate dehydrogenases
15	c2e0cA_	Alignment		100.0	33	PDB header: oxidoreductase Chain: A: PDB Molecule: 409aa long hypothetical nadp-dependent isocitrate PDBTitle: crystal structure of isocitrate dehydrogenase from sulfolobus tokodaii2 strain7 at 2.0 a resolution
16	dlwpwa_	Alignment		100.0	36	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Dimeric isocitrate & isopropylmalate dehydrogenases
17	c1x0lB_	Alignment		100.0	38	PDB header: oxidoreductase Chain: B: PDB Molecule: homoisocitrate dehydrogenase; PDBTitle: crystal structure of tetrameric homoisocitrate dehydrogenase from an2 extreme thermophile, thermus thermophilus
18	dlw0da_	Alignment		100.0	41	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Dimeric isocitrate & isopropylmalate dehydrogenases
19	c1tyoA_	Alignment		100.0	30	PDB header: oxidoreductase Chain: A: PDB Molecule: isocitrate dehydrogenase; PDBTitle: isocitrate dehydrogenase from the hyperthermophile aeropyrum pernix in2 complex with etheno-nadp
20	c3blxL_	Alignment		100.0	34	PDB header: oxidoreductase Chain: L: PDB Molecule: isocitrate dehydrogenase [nad] subunit 2; PDBTitle: yeast isocitrate dehydrogenase (apo form)
21	c1zorB_	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: B: PDB Molecule: isocitrate dehydrogenase; PDBTitle: isocitrate dehydrogenase from the hyperthermophile thermotoga maritima
22	c3blxM_	Alignment	not modelled	100.0	31	PDB header: oxidoreductase Chain: M: PDB Molecule: isocitrate dehydrogenase [nad] subunit 1; PDBTitle: yeast isocitrate dehydrogenase (apo form)
23	c2uxqB_	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: B: PDB Molecule: isocitrate dehydrogenase native; PDBTitle: isocitrate dehydrogenase from the psychrophilic bacterium2 desulfotalea psychrophila: biochemical properties and3 crystal structure analysis
24	dl1wda_	Alignment	not modelled	100.0	20	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Dimeric isocitrate & isopropylmalate dehydrogenases
25	dl1t0la_	Alignment	not modelled	100.0	21	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Dimeric isocitrate & isopropylmalate dehydrogenases
26	c2qfyE_	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: E: PDB Molecule: isocitrate dehydrogenase [nadp]; PDBTitle: crystal structure of saccharomyces cerevisiae mitochondrial nadp(+)-2 dependent isocitrate dehydrogenase in complex with a-ketoglutarate
27	c3us8A_	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: isocitrate dehydrogenase [nadp]; PDBTitle: crystal structure of an isocitrate dehydrogenase from sinorhizobium2 meliloti 1021
28	c2iv0A_	Alignment	not modelled	100.0	28	PDB header: oxidoreductase Chain: A: PDB Molecule: isocitrate dehydrogenase; PDBTitle: thermal stability of isocitrate dehydrogenase from2

						archaeoglobus fulgidus studied by crystal structure3 analysis and engineering of chimers
29	d1ptma_	Alignment	not modelled	99.0	16	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: PdxA-like
30	c2hi1A_	Alignment	not modelled	99.0	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: 4-hydroxythreonine-4-phosphate dehydrogenase 2; PDBTitle: the structure of a putative 4-hydroxythreonine-4-phosphate2 dehydrogenase from salmonella typhimurium.
31	d1r8ka_	Alignment	not modelled	98.9	15	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: PdxA-like
32	c1yx0B_	Alignment	not modelled	98.3	16	PDB header: oxidoreductase Chain: B: PDB Molecule: 4-hydroxythreonine-4-phosphate dehydrogenase 1; PDBTitle: crystal structure of pyridoxal phosphate biosynthetic protein pdxa2 pa0593
33	c2b0tA_	Alignment	not modelled	89.5	21	PDB header: oxidoreductase Chain: A: PDB Molecule: nadp isocitrate dehydrogenase; PDBTitle: structure of monomeric nadp isocitrate dehydrogenase
34	d1itwa_	Alignment	not modelled	80.9	22	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Monomeric isocitrate dehydrogenase
35	c3s40C_	Alignment	not modelled	61.5	17	PDB header: transferase Chain: C: PDB Molecule: diacylglycerol kinase; PDBTitle: the crystal structure of a diacylglycerol kinases from bacillus2 anthracis str. sterne
36	c1p84E_	Alignment	not modelled	61.1	32	PDB header: oxidoreductase Chain: E: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur PDBTitle: hdbt inhibited yeast cytochrome bc1 complex
37	d2fpoa1	Alignment	not modelled	60.6	13	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: YhhF-like
38	c2fyuE_	Alignment	not modelled	54.7	32	PDB header: oxidoreductase Chain: E: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur subunit; PDBTitle: crystal structure of bovine heart mitochondrial bc1 with jg1442 inhibitor
39	d1riea_	Alignment	not modelled	48.9	32	Fold: ISP domain Superfamily: ISP domain Family: Rieske iron-sulfur protein (ISP)
40	d3thia_	Alignment	not modelled	44.7	16	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
41	d1loria_	Alignment	not modelled	42.8	11	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Arginine methyltransferase
42	d2esra1	Alignment	not modelled	42.3	10	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: YhhF-like
43	c1orhA_	Alignment	not modelled	41.3	14	PDB header: transferase Chain: A: PDB Molecule: protein arginine n-methyltransferase 1; PDBTitle: structure of the predominant protein arginine methyltransferase prmt1
44	d3cx5e1	Alignment	not modelled	40.4	32	Fold: ISP domain Superfamily: ISP domain Family: Rieske iron-sulfur protein (ISP)
45	c2fynO_	Alignment	not modelled	36.5	29	PDB header: oxidoreductase Chain: O: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur PDBTitle: crystal structure analysis of the double mutant rhodobacter2 sphaeroides bc1 complex
46	c3cfxA_	Alignment	not modelled	34.8	19	PDB header: transport protein Chain: A: PDB Molecule: upf0100 protein ma_0280; PDBTitle: crystal structure of m. acetivorans periplasmic binding protein2 moda/wtpa with bound tungstate
47	c2nvgA_	Alignment	not modelled	34.4	26	PDB header: oxidoreductase Chain: A: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur subunit; PDBTitle: soluble domain of rieske iron sulfur protein.
48	d2onsa1	Alignment	not modelled	31.8	11	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
49	c2q62A_	Alignment	not modelled	31.4	10	PDB header: flavoprotein Chain: A: PDB Molecule: arsh; PDBTitle: crystal structure of arsh from sinorhizobium meliloti
50	d2fyt1	Alignment	not modelled	25.2	16	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Arginine methyltransferase
51	d1qapa1	Alignment	not modelled	24.4	18	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: NadC C-terminal domain-like
52	d1jq4a_	Alignment	not modelled	23.0	21	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
53	c3k6wA_	Alignment	not modelled	22.7	19	PDB header: transport protein Chain: A: PDB Molecule: solute-binding protein ma_0280; PDBTitle: apo and ligand bound structures of moda from the archaeon2 methanosarcina acetivorans

54	c3c6kC	 Alignment	not modelled	22.5	10	PDB header: transferase Chain: C: PDB Molecule: spermine synthase; PDBTitle: crystal structure of human spermine synthase in complex2 with spermidine and 5-methylthioadenosine
55	c3cfzA	 Alignment	not modelled	22.5	17	PDB header: transport protein Chain: A: PDB Molecule: upf0100 protein mj1186; PDBTitle: crystal structure of m. jannaschii periplasmic binding2 protein moda/wtpa with bound tungstate
56	d1j08a1	 Alignment	not modelled	22.5	17	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: PDI-like
57	c3ku1E	 Alignment	not modelled	21.1	5	PDB header: transferase Chain: E: PDB Molecule: sam-dependent methyltransferase; PDBTitle: crystal structure of streptococcus pneumoniae sp1610, a2 putative trna (m1a22) methyltransferase, in complex with s-3 adenosyl-l-methionine
58	c2e76D	 Alignment	not modelled	20.8	32	PDB header: photosynthesis Chain: D: PDB Molecule: cytochrome b6-f complex iron-sulfur subunit; PDBTitle: crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus
59	c3l0gD	 Alignment	not modelled	19.3	15	PDB header: transferase Chain: D: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of nicotinate-nucleotide pyrophosphorylase from2 ehrlichia chaffeensis at 2.05a resolution
60	c2esrB	 Alignment	not modelled	18.8	10	PDB header: transferase Chain: B: PDB Molecule: methyltransferase; PDBTitle: conserved hypothetical protein- streptococcus pyogenes
61	d1f3la	 Alignment	not modelled	18.0	16	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Arginine methyltransferase
62	c3lwzC	 Alignment	not modelled	17.9	18	PDB header: lyase Chain: C: PDB Molecule: 3-dehydroquinone dehydratase; PDBTitle: 1.65 angstrom resolution crystal structure of type ii 3-2 dehydroquinone dehydratase (aroq) from yersinia pestis
63	c2pebB	 Alignment	not modelled	17.8	24	PDB header: oxidoreductase Chain: B: PDB Molecule: putative dioxygenase; PDBTitle: crystal structure of a putative dioxygenase (npun_f1925) from nostoc2 punctiforme pcc 73102 at 1.46 a resolution
64	c3p9nA	 Alignment	not modelled	17.8	12	PDB header: transferase Chain: A: PDB Molecule: possible methyltransferase (methylase); PDBTitle: rv2966c of m. tuberculosis is a rsmd-like methyltransferase
65	c3c0kB	 Alignment	not modelled	17.7	15	PDB header: transferase Chain: B: PDB Molecule: upf0064 protein yccw; PDBTitle: crystal structure of a ribosomal rna methyltransferase
66	d1g6q1	 Alignment	not modelled	17.5	10	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Arginine methyltransferase
67	c2huzB	 Alignment	not modelled	16.8	13	PDB header: structural genomics, transferase Chain: B: PDB Molecule: glucosamine 6-phosphate n-acetyltransferase; PDBTitle: crystal structure of gnprn1
68	d1a8la1	 Alignment	not modelled	16.5	12	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: PDI-like
69	c2zkiH	 Alignment	not modelled	15.8	19	PDB header: transcription Chain: H: PDB Molecule: 199aa long hypothetical trp repressor binding PDBTitle: crystal structure of hypothetical trp repressor binding2 protein from sul folobus tokodaii (st0872)
70	c2dumD	 Alignment	not modelled	15.0	8	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: hypothetical protein ph0823; PDBTitle: crystal structure of hypothetical protein, ph0823
71	c3dloC	 Alignment	not modelled	13.2	18	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: universal stress protein; PDBTitle: structure of universal stress protein from archaeoglobus fulgidus
72	d1atia1	 Alignment	not modelled	13.1	16	Fold: Anticodon-binding domain-like Superfamily: Class II aaRS ABD-related Family: Anticodon-binding domain of Class II aaRS
73	d2erya1	 Alignment	not modelled	12.8	35	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
74	c1qpoA	 Alignment	not modelled	12.7	13	PDB header: transferase Chain: A: PDB Molecule: quinolinate acid phosphoribosyl transferase; PDBTitle: quinolinate phosphoribosyl transferase (qaprtase) apo-enzyme from2 mycobacterium tuberculosis
75	d2fhpA1	 Alignment	not modelled	12.7	19	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: YhhF-like
76	c2k4mA	 Alignment	not modelled	12.6	21	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
77	d1q77a	 Alignment	not modelled	12.5	13	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
78	c2qv7A	 Alignment	not modelled	12.5	14	PDB header: transferase Chain: A: PDB Molecule: diacylglycerol kinase dgkb; PDBTitle: crystal structure of diacylglycerol kinase dgkb in

						complex with adp2 and mg PDB header: rna binding protein Chain: B: PDB Molecule: trna uridine 5-carboxymethylaminomethyl modification enzyme PDBTitle: crystal structure of e.coli mnmg (gida), a highly-conserved trna2 modifying enzyme
79	c3cesB_	Alignment	not modelled	11.3	27	PDB header: signaling protein Chain: D: PDB Molecule: universal stress protein tead; PDBTitle: universal stress protein tead from the trap transporter2 teaabc of halomonas elongata
80	c3hgmD_	Alignment	not modelled	11.1	7	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: universal stress protein; PDBTitle: crystal structure of universal stress protein from nitrosomonas2 europaea
81	c2pfsA_	Alignment	not modelled	11.0	12	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Periplasmic domain of cytochrome c oxidase subunit II
82	d1cyxa_	Alignment	not modelled	10.5	10	PDB header: electron transport Chain: A: PDB Molecule: cyoa; PDBTitle: quinol oxidase (periplasmic fragment of subunit ii with2 engineered cu-a binding site)(cyoa)
83	c1cyxA_	Alignment	not modelled	10.5	10	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolate PRTase C-terminal domain-like Family: NadC C-terminal domain-like
84	d1o4ua1	Alignment	not modelled	10.5	18	PDB header: recombination Chain: A: PDB Molecule: replication-associated recombination protein a; PDBTitle: structure and biochemical activities of escherichia coli mgsa
85	c3pvsA_	Alignment	not modelled	10.3	25	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
86	d1yo6a1	Alignment	not modelled	10.0	39	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
87	d1jmva_	Alignment	not modelled	10.0	17	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Periplasmic domain of cytochrome c oxidase subunit II
88	d1fftb1	Alignment	not modelled	9.8	10	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: protein of universal stress protein uspa family; PDBTitle: the crystal structure of an universal stress protein uspa2 family protein from lactobacillus plantarum wcfs1
89	c3fg9B_	Alignment	not modelled	9.8	21	Fold: Ferredoxin-like Superfamily: ACT-like Family: Glycine cleavage system transcriptional repressor
90	d1u8sa1	Alignment	not modelled	9.8	13	PDB header: transferase Chain: A: PDB Molecule: histone-arginine methyltransferase carml; PDBTitle: the 2.55 a crystal structure of the apo catalytic domain of2 coactivator-associated arginine methyl transferase i(carml:28-507,3 residues 28-146 and 479-507 not ordered)
91	c3b3jA_	Alignment	not modelled	9.5	12	Fold: CofD-like Superfamily: CofD-like Family: CofD-like
92	d2ffea1	Alignment	not modelled	9.3	28	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein smu.776; PDBTitle: a putative sam-dependent methyltransferase from2 streptococcus mutans
93	c2b78A_	Alignment	not modelled	9.3	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein pa1789; PDBTitle: the crystal structure of a functionally unknown protein pa1789 from2 pseudomonas aeruginosa pao1
94	c3mt0A_	Alignment	not modelled	9.3	11	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
95	d1xmta_	Alignment	not modelled	8.7	11	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: Synapsin domain
96	d1i7na1	Alignment	not modelled	8.7	16	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
97	d1tq8a_	Alignment	not modelled	8.6	11	Fold: Anticodon-binding domain-like Superfamily: Class II aaRS ABD-related Family: Anticodon-binding domain of Class II aaRS
98	d2g4ca1	Alignment	not modelled	8.5	9	Fold: post-AAA+ oligomerization domain-like Superfamily: post-AAA+ oligomerization domain-like Family: MgsA/YrvN C-terminal domain-like
99	d2r9ga1	Alignment	not modelled	8.3	18	