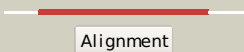

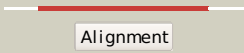







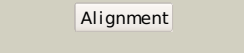

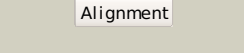

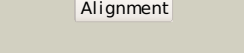



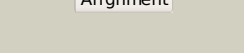

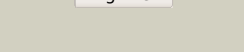








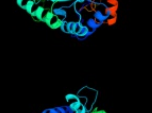
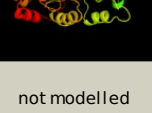


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1lqaa_	 Alignment		100.0	100	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
2	c3erpA_	 Alignment		100.0	31	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: structure of idp01002, a putative oxidoreductase from and essential2 gene of salmonella typhimurium
3	d3eaa1	 Alignment		100.0	32	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
4	c3luta_	 Alignment		100.0	32	PDB header: membrane protein Chain: A: PDB Molecule: voltage-gated potassium channel subunit beta-2; PDBTitle: a structural model for the full-length shaker potassium channel kv1.2
5	d1pyfa_	 Alignment		100.0	29	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
6	c3n2tA_	 Alignment		100.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: structure of the glycerol dehydrogenase akr11b4 from gluconobacter2 oxydans
7	d1pz1a_	 Alignment		100.0	30	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
8	d1gvea_	 Alignment		100.0	23	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
9	c3n6qF_	 Alignment		100.0	31	PDB header: oxidoreductase Chain: F: PDB Molecule: yghz aldo-keto reductase; PDBTitle: crystal structure of yghz from e. coli
10	d1ur3m_	 Alignment		100.0	23	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
11	c2bp1C_	 Alignment		100.0	25	PDB header: oxidoreductase Chain: C: PDB Molecule: aflatoxin b1 aldehyde reductase member 2; PDBTitle: structure of the aflatoxin aldehyde reductase in complex2 with nadph

12	dlq5ma_	Alignment		100.0	25	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
13	dlj96a_	Alignment		100.0	23	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
14	clynpA_	Alignment		100.0	33	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase; PDBTitle: aldo-keto reductase akr11c1 from bacillus halodurans (apo form)
15	c3h7uA_	Alignment		100.0	29	PDB header: oxidoreductase Chain: A: PDB Molecule: aldo-keto reductase; PDBTitle: crystal structure of the plant stress-response enzyme akr4c9
16	dlafsa_	Alignment		100.0	20	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
17	dlus0a_	Alignment		100.0	23	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
18	dlmi3a_	Alignment		100.0	26	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
19	dlfrba_	Alignment		100.0	24	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
20	dls1pa_	Alignment		100.0	23	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
21	dlqwka_	Alignment	not modelled	100.0	24	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
22	dlhqta_	Alignment	not modelled	100.0	25	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
23	c3buVB_	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: B: PDB Molecule: 3-oxo-5-beta-steroid 4-dehydrogenase; PDBTitle: crystal structure of human delta(4)-3-ketosteroid 5-beta-reductase in2 complex with nadp and hepes. resolution: 1.35 a.
24	c3f7jB_	Alignment	not modelled	100.0	32	PDB header: oxidoreductase Chain: B: PDB Molecule: yvgn protein; PDBTitle: b.subtilis yvgn
25	c3up8B_	Alignment	not modelled	100.0	27	PDB header: oxidoreductase Chain: B: PDB Molecule: putative 2,5-diketo-d-gluconic acid reductase b; PDBTitle: crystal structure of a putative 2,5-diketo-d-gluconic acid reductase b
26	c3h7rA_	Alignment	not modelled	100.0	27	PDB header: oxidoreductase Chain: A: PDB Molecule: aldo-keto reductase; PDBTitle: crystal structure of the plant stress-response enzyme akr4c8
27	clzgdB_	Alignment	not modelled	100.0	24	PDB header: plant protein Chain: B: PDB Molecule: chalcone reductase; PDBTitle: chalcone reductase complexed with nadp+ at 1.7 angstrom2 resolution
28	dlah4a_	Alignment	not modelled	100.0	23	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)

29	d1c9wa_	Alignment	not modelled	100.0	24	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
30	d2alra_	Alignment	not modelled	100.0	25	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
31	c2wztA_	Alignment	not modelled	100.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: aldo-keto reductase; PDBTitle: crystal structure of a mycobacterium aldo-keto reductase in2 its apo and liganded form
32	d1mzra_	Alignment	not modelled	100.0	29	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
33	c2bgsA_	Alignment	not modelled	100.0	24	PDB header: oxidoreductase Chain: A: PDB Molecule: aldose reductase; PDBTitle: holo aldose reductase from barley
34	d1vp5a_	Alignment	not modelled	100.0	23	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
35	c3o0kB_	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: B: PDB Molecule: aldo/keto reductase; PDBTitle: crystal structure of aldo/keto reductase from brucella melitensis
36	d1hw6a_	Alignment	not modelled	100.0	27	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
37	c3b3dA_	Alignment	not modelled	100.0	29	PDB header: oxidoreductase Chain: A: PDB Molecule: putative morphine dehydrogenase; PDBTitle: b.subtilis ytb
38	c1vbjB_	Alignment	not modelled	100.0	25	PDB header: oxidoreductase Chain: B: PDB Molecule: prostaglandin f synthase; PDBTitle: the crystal structure of prostaglandin f synthase from2 trypanosoma brucei
39	c3krbB_	Alignment	not modelled	100.0	25	PDB header: oxidoreductase Chain: B: PDB Molecule: aldose reductase; PDBTitle: structure of aldose reductase from giardia lamblia at 1.75a resolution
40	c3ln3A_	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodiol dehydrogenase; PDBTitle: crystal structure of putative reductase (np_038806.2) from2 mus musculus at 1.18 a resolution
41	d1olta_	Alignment	not modelled	64.4	17	Fold: TIM beta/alpha-barrel Superfamily: Radical SAM enzymes Family: Oxygen-independent coproporphyrinogen III oxidase HemN
42	d2aeba1	Alignment	not modelled	55.7	10	Fold: Arginase/deacetylase Superfamily: Arginase/deacetylase Family: Arginase-like amidino hydrolases
43	d1rioa_	Alignment	not modelled	46.4	20	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
44	c3l23A_	Alignment	not modelled	45.3	10	PDB header: isomerase Chain: A: PDB Molecule: sugar phosphate isomerase/epimerase; PDBTitle: crystal structure of sugar phosphate isomerase/epimerase2 (yp_001303399.1) from parabacteroides distasonis atcc 8503 at 1.70 a3 resolution
45	c3oqbF_	Alignment	not modelled	45.0	10	PDB header: oxidoreductase Chain: F: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of putative oxidoreductase from bradyrhizobium2 japonicum usda 110
46	c2ph5A_	Alignment	not modelled	43.5	21	PDB header: transferase Chain: A: PDB Molecule: homospermidine synthase; PDBTitle: crystal structure of the homospermidine synthase hss from legionella2 pneumophila in complex with nad, northeast structural genomics target3 lgr54
47	c2v5jB_	Alignment	not modelled	41.0	6	PDB header: lyase Chain: B: PDB Molecule: 2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase; PDBTitle: apo class ii aldolase hpch
48	c2vwtA_	Alignment	not modelled	41.0	10	PDB header: lyase Chain: A: PDB Molecule: yfau, 2-keto-3-deoxy sugar aldolase; PDBTitle: crystal structure of yfau, a metal ion dependent class ii2 aldolase from escherichia coli k12 - mg-pyruvate product3 complex
49	c3f6wE_	Alignment	not modelled	40.7	16	PDB header: dna binding protein Chain: E: PDB Molecule: xre-family like protein; PDBTitle: xre-family like protein from pseudomonas syringae pv. tomato str.2 dc3000
50	c3bdkB_	Alignment	not modelled	40.5	17	PDB header: lyase Chain: B: PDB Molecule: d-mannonate dehydratase; PDBTitle: crystal structure of streptococcus suis mannonate2 dehydratase complexed with substrate analogue
51	d1lmb3_	Alignment	not modelled	40.0	21	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
52	c3lmyA_	Alignment	not modelled	38.9	21	PDB header: hydrolase Chain: A: PDB Molecule: beta-hexosaminidase subunit beta; PDBTitle: the crystal structure of beta-hexosaminidase b in complex with2 pyrimethamine
53	c3n2oA_	Alignment	not modelled	38.2	17	PDB header: lyase Chain: A: PDB Molecule: biosynthetic arginine decarboxylase; PDBTitle: x-ray crystal structure of arginine decarboxylase complexed with2 arginine from vibrio vulnificus
54	d1nowa1	Alignment	not modelled	36.1	21	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
						PDB header: dna binding protein

55	c3eusB	Alignment	not modelled	34.5	16	Chain: B: PDB Molecule: dna-binding protein; PDBTitle: the crystal structure of the dna binding protein from silicibacter2 pomeroyi
56	c3g8rA	Alignment	not modelled	34.3	16	PDB header: biosynthetic protein Chain: A: PDB Molecule: probable spore coat polysaccharide biosynthesis protein e; PDBTitle: crystal structure of putative spore coat polysaccharide biosynthesis2 protein e from chromobacterium violaceum atcc 12472
57	d1lilb	Alignment	not modelled	33.5	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
58	c1ydoC	Alignment	not modelled	33.3	13	PDB header: lyase Chain: C: PDB Molecule: hmg-coa lyase; PDBTitle: crystal structure of the bacillus subtilis hmg-coa lyase, northeast2 structural genomics target sr181.
59	d1r0ma1	Alignment	not modelled	31.7	19	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
60	c2hk1D	Alignment	not modelled	31.6	9	PDB header: isomerase Chain: D: PDB Molecule: d-psicose 3-epimerase; PDBTitle: crystal structure of d-psicose 3-epimerase (dpease) in the presence of 2 d-fructose
61	d1rvka1	Alignment	not modelled	31.6	15	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
62	d1jpma1	Alignment	not modelled	31.2	17	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
63	c2l8nA	Alignment	not modelled	30.6	14	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional repressor cytr; PDBTitle: nmr structure of the cytidine repressor dna binding domain in presence2 of operator half-site dna
64	c3bolB	Alignment	not modelled	30.4	9	PDB header: transferase Chain: B: PDB Molecule: 5-methyltetrahydrofolate s-homocysteine PDBTitle: cobalamin-dependent methionine synthase (1-566) from2 thermotoga maritima complexed with zn2+
65	d1pq3a	Alignment	not modelled	30.3	7	Fold: Arginase/deacetylase Superfamily: Arginase/deacetylase Family: Arginase-like amidino hydrolases
66	d1x87a	Alignment	not modelled	29.8	21	Fold: Urocanase Superfamily: Urocanase Family: Urocanase
67	c3ik4A	Alignment	not modelled	29.7	15	PDB header: isomerase Chain: A: PDB Molecule: mandelate racemase/muconate lactonizing protein; PDBTitle: crystal structure of mandelate racemase/muconate lactonizing protein2 from herpetosiphon aurantiacus
68	c1nouA	Alignment	not modelled	29.1	21	PDB header: hydrolase Chain: A: PDB Molecule: beta-hexosaminidase beta chain; PDBTitle: native human lysosomal beta-hexosaminidase isoform b
69	d1jfla1	Alignment	not modelled	27.3	15	Fold: ATC-like Superfamily: Aspartate/glutamate racemase Family: Aspartate/glutamate racemase
70	d2ceva	Alignment	not modelled	27.2	8	Fold: Arginase/deacetylase Superfamily: Arginase/deacetylase Family: Arginase-like amidino hydrolases
71	c1xuzA	Alignment	not modelled	27.0	16	PDB header: biosynthetic protein Chain: A: PDB Molecule: polysialic acid capsule biosynthesis protein siac; PDBTitle: crystal structure analysis of sialic acid synthase (neub)from2 neisseria meningitidis, bound to mn2+, phosphoenolpyruvate, and n-3 acetyl mannosaminitol
72	c2nqlB	Alignment	not modelled	26.9	12	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: isomerase/lactonizing enzyme; PDBTitle: crystal structure of a member of the enolase superfamily from2 agrobacterium tumefaciens
73	c3dx5A	Alignment	not modelled	26.6	13	PDB header: lyase Chain: A: PDB Molecule: uncharacterized protein asbf; PDBTitle: crystal structure of the probable 3-dhs dehydratase asbf involved in2 the petrobactin synthesis from bacillus anthracis
74	d1d3va	Alignment	not modelled	26.3	10	Fold: Arginase/deacetylase Superfamily: Arginase/deacetylase Family: Arginase-like amidino hydrolases
75	c2lcvA	Alignment	not modelled	26.3	14	PDB header: transcription regulator Chain: A: PDB Molecule: hth-type transcriptional repressor cytr; PDBTitle: structure of the cytidine repressor dna-binding domain; an alternate2 calculation
76	d1uwka	Alignment	not modelled	25.5	26	Fold: Urocanase Superfamily: Urocanase Family: Urocanase
77	c3pg8B	Alignment	not modelled	25.4	15	PDB header: transferase Chain: B: PDB Molecule: phospho-2-dehydro-3-deoxyheptonate aldolase; PDBTitle: truncated form of 3-deoxy-d-arabino-heptulosonate 7-phosphate synthase2 from thermotoga maritima
78	c3b7hA	Alignment	not modelled	24.7	12	PDB header: structural protein Chain: A: PDB Molecule: prophage lp1 protein 11; PDBTitle: crystal structure of the prophage lp1 protein 11
79	c3mmrA	Alignment	not modelled	24.2	4	PDB header: hydrolase Chain: A: PDB Molecule: arginase; PDBTitle: structure of plasmodium falciparum arginase in complex with abh
						PDB header: hydrolase Chain: A: PDB Molecule: haloacid dehalogenase/epoxide

80	c2pr7A_	Alignment	not modelled	24.0	10	hydrolase family; PDBTitle: crystal structure of uncharacterized protein (np_599989.1) from2 corynebacterium glutamicum atcc 13032 kitasato at 1.44 a resolution
81	c1sjaA_	Alignment	not modelled	23.7	16	PDB header: lyase, isomerase Chain: A: PDB Molecule: n-acylamino acid racemase; PDBTitle: x-ray structure of o-succinylbenzoate synthase complexed2 with n-acetyl methionine
82	d1wuea1	Alignment	not modelled	23.6	17	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
83	c3dnfB_	Alignment	not modelled	23.4	14	PDB header: oxidoreductase Chain: B: PDB Molecule: 4-hydroxy-3-methylbut-2-enyl diphosphate reductase; PDBTitle: structure of (e)-4-hydroxy-3-methyl-but-2-enyl diphosphate reductase,2 the terminal enzyme of the non-mevalonate pathway
84	c3m1rF_	Alignment	not modelled	22.6	11	PDB header: hydrolase Chain: F: PDB Molecule: formimidoyl glutamase; PDBTitle: the crystal structure of formimidoyl glutamase from bacillus2 subtilis subsp. subtilis str. 168
85	d1nu5a1	Alignment	not modelled	22.6	14	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
86	d2hsqa1	Alignment	not modelled	20.4	20	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
87	c1qbaA_	Alignment	not modelled	20.3	23	PDB header: glycosyl hydrolase Chain: A: PDB Molecule: chitinase; PDBTitle: bacterial chitinase, glycosyl hydrolase family 20
88	c3t76A_	Alignment	not modelled	20.2	9	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator vanug; PDBTitle: crystal structure of transcriptional regulator vanug, form ii
89	d1y9qa1	Alignment	not modelled	20.2	14	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Probable transcriptional regulator VC1968, N-terminal domain
90	c2fknC_	Alignment	not modelled	20.2	27	PDB header: lyase Chain: C: PDB Molecule: urocanate hydratase; PDBTitle: crystal structure of urocanase from bacillus subtilis
91	d2a6ca1	Alignment	not modelled	19.9	21	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354
92	d1lizca_	Alignment	not modelled	19.9	13	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: HpCh/HpaI aldolase
93	c1lizCA_	Alignment	not modelled	19.9	13	PDB header: lyase Chain: A: PDB Molecule: macrophomate synthase intermolecular diels-alderase; PDBTitle: crystal structure analysis of macrophomate synthase
94	c3smaD_	Alignment	not modelled	19.0	20	PDB header: transferase Chain: D: PDB Molecule: frbf; PDBTitle: a new n-acetyltransferase fold in the structure and mechanism of the2 phosphonate biosynthetic enzyme frbf
95	c2ovlA_	Alignment	not modelled	19.0	18	PDB header: isomerase Chain: A: PDB Molecule: putative racemase; PDBTitle: crystal structure of a racemase from streptomyces2 coelicolor a3(2)
96	c3nsnA_	Alignment	not modelled	19.0	10	PDB header: hydrolase Chain: A: PDB Molecule: n-acetylglucosaminidase; PDBTitle: crystal structure of insect beta-n-acetyl-d-hexosaminidase ofhex12 complexed with tmg-chitotriomycin
97	d2chra1	Alignment	not modelled	18.8	15	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
98	c3nzqB_	Alignment	not modelled	17.9	17	PDB header: lyase Chain: B: PDB Molecule: biosynthetic arginine decarboxylase; PDBTitle: crystal structure of biosynthetic arginine decarboxylase adc (spea)2 from escherichia coli, northeast structural genomics consortium3 target er600
99	d1f6ya_	Alignment	not modelled	17.7	15	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Methyltetrahydrofolate-utilizing methyltransferases