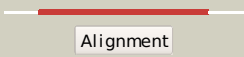
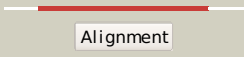
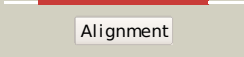
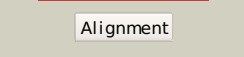
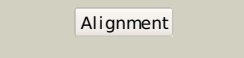
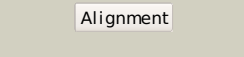
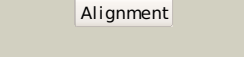
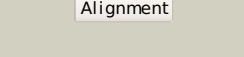
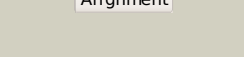
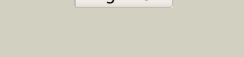
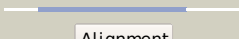
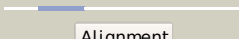
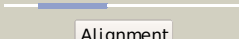
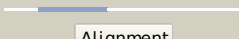
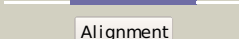
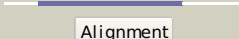
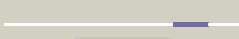
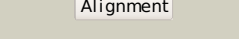
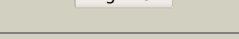


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1lqaa_	 Alignment		100.0	26	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
2	d1pyfa_	 Alignment		100.0	26	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
3	c3erpA_	 Alignment		100.0	22	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: structure of idp01002, a putative oxidoreductase from and essential2 gene of salmonella typhimurium
4	d1pz1a_	 Alignment		100.0	20	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
5	d1ur3m_	 Alignment		100.0	21	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
6	c3n2tA_	 Alignment		100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: structure of the glycerol dehydrogenase akr11b4 from gluconobacter2 oxydans
7	c1ynpA_	 Alignment		100.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase; PDBTitle: aldo-keto reductase akr11c1 from bacillus halodurans (apo form)
8	c3n6qF_	 Alignment		100.0	24	PDB header: oxidoreductase Chain: F: PDB Molecule: yghz aldo-keto reductase; PDBTitle: crystal structure of yghz from e. coli
9	d3eaua1	 Alignment		100.0	25	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
10	c3lutA_	 Alignment		100.0	25	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
11	d1j96a_	 Alignment		100.0	22	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)

12	dlq5ma_	Alignment		100.0	23	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
13	c3up8B_	Alignment		100.0	24	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
14	dlgvea_	Alignment		100.0	25	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
15	c3f7jB_	Alignment		100.0	22	PDB header: oxidoreductase Chain: B: PDB Molecule: yvgn protein; PDBTitle: b.subtilis yvgn
16	c3h7uA_	Alignment		100.0	22	PDB header: oxidoreductase Chain: A: PDB Molecule: aldo-keto reductase; PDBTitle: crystal structure of the plant stress-response enzyme akr4c9
17	dlus0a_	Alignment		100.0	25	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
18	dlafsa_	Alignment		100.0	22	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
19	c2bp1C_	Alignment		100.0	23	PDB header: oxidoreductase Chain: C: PDB Molecule: afatoxin b1 aldehyde reductase member 2; PDBTitle: structure of the afatoxin aldehyde reductase in complex2 with nadph
20	c1vbjB_	Alignment		100.0	22	PDB header: oxidoreductase Chain: B: PDB Molecule: prostaglandin f synthase; PDBTitle: the crystal structure of prostaglandin f synthase from2 trypanosoma brucei
21	c2wztA_	Alignment	not modelled	100.0	21	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
22	c3o0kB_	Alignment	not modelled	100.0	22	PDB header: oxidoreductase Chain: B: PDB Molecule: aldo/keto reductase; PDBTitle: crystal structure of aldo/keto reductase from brucella melitensis
23	dlqwka_	Alignment	not modelled	100.0	22	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
24	dlhqta_	Alignment	not modelled	100.0	22	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
25	dlmi3a_	Alignment	not modelled	100.0	20	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
26	c3h7rA_	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: aldo-keto reductase; PDBTitle: crystal structure of the plant stress-response enzyme akr4c8
27	dlslpa_	Alignment	not modelled	100.0	23	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
28	dlfrba_	Alignment	not modelled	100.0	25	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
						PDB header: oxidoreductase

29	c3b3dA_	Alignment	not modelled	100.0	23	Chain: A: PDB Molecule: putative morphine dehydrogenase; PDBTitle: b.subtilis ytb
30	d1hw6a_	Alignment	not modelled	100.0	25	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
31	d2alra_	Alignment	not modelled	100.0	22	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
32	c1zgdB_	Alignment	not modelled	100.0	21	PDB header: plant protein Chain: B: PDB Molecule: chalcone reductase; PDBTitle: chalcone reductase complexed with nadp+ at 1.7 angstrom2 resolution
33	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.
34	c2bgsA_	Alignment	not modelled	100.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: aldose reductase; PDBTitle: holo aldose reductase from barley
35	d1c9wa_	Alignment	not modelled	100.0	25	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
36	d1vp5a_	Alignment	not modelled	100.0	26	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
37	d1ah4a_	Alignment	not modelled	100.0	26	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
38	d1mzra_	Alignment	not modelled	100.0	22	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
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	21	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	c3ktcB_	Alignment	not modelled	88.5	14	PDB header: isomerase Chain: B: PDB Molecule: xylose isomerase; PDBTitle: crystal structure of putative sugar isomerase (yp_050048.1) from2 erwinia carotovora atroseptica scri1043 at 1.54 a resolution
42	d1jpma1	Alignment	not modelled	73.4	11	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
43	c3g8rA_	Alignment	not modelled	56.9	20	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
44	c2ph5A_	Alignment	not modelled	55.3	17	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
45	c2vc7A_	Alignment	not modelled	38.2	11	PDB header: hydrolase Chain: A: PDB Molecule: aryldialkylphosphatase; PDBTitle: structural basis for natural lactonase and promiscuous2 phosphotriesterase activities
46	c3ik4A_	Alignment	not modelled	37.5	10	PDB header: isomerase Chain: A: PDB Molecule: mandelate racemase/muconate lactonizing protein; PDBTitle: crystal structure of mandelate racemase/muconate lactonizing protein2 from herpetosiphon aurantiacus
47	c3oqbF_	Alignment	not modelled	35.1	12	PDB header: oxidoreductase Chain: F: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of putative oxidoreductase from bradyrhizobium2 japonicum usda 110
48	c6paxA_	Alignment	not modelled	30.9	20	PDB header: gene regulation/dna Chain: A: PDB Molecule: homeobox protein pax-6; PDBTitle: crystal structure of the human pax-6 paired domain-dna2 complex reveals a general model for pax protein-dna3 interactions
49	d2gdqa1	Alignment	not modelled	30.5	10	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
50	d1veya1	Alignment	not modelled	30.2	16	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
51	d1pdnc_	Alignment	not modelled	27.3	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
52	c2k27A_	Alignment	not modelled	24.9	20	PDB header: transcription regulator Chain: A: PDB Molecule: paired box protein pax-8; PDBTitle: solution structure of human pax8 paired box domain
53	d1vp8a_	Alignment	not modelled	24.4	18	Fold: Pyruvate kinase C-terminal domain-like Superfamily: PK C-terminal domain-like Family: MTH1675-like
54	c3noeA_	Alignment	not modelled	23.9	11	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from pseudomonas2 aeruginosa

55	c2qdeA	 Alignment	not modelled	23.8	9	PDB header: lyase Chain: A: PDB Molecule: mandelate racemase/muconate lactonizing enzyme family PDBTitle: crystal structure of mandelate racemase/muconate lactonizing family2 protein from azoarcus sp. ebn1
56	d1k78a1	 Alignment	not modelled	22.7	29	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
57	c3ng3A	 Alignment	not modelled	22.2	21	PDB header: lyase Chain: A: PDB Molecule: deoxyribose-phosphate aldolase; PDBTitle: crystal structure of deoxyribose phosphate aldolase from mycobacterium2 avium 104 in a schiff base with an unknown aldehyde
58	c1xuzA	 Alignment	not modelled	20.8	19	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
59	d1vcva1	 Alignment	not modelled	20.7	18	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
60	d6paxa1	 Alignment	not modelled	20.7	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
61	c3oa3A	 Alignment	not modelled	20.2	14	PDB header: lyase Chain: A: PDB Molecule: aldolase; PDBTitle: crystal structure of a putative deoxyribose-phosphate aldolase from2 coccidioides immitis
62	c1vliA	 Alignment	not modelled	19.9	15	PDB header: biosynthetic protein Chain: A: PDB Molecule: spore coat polysaccharide biosynthesis protein spse; PDBTitle: crystal structure of spore coat polysaccharide biosynthesis protein2 spse (bsu37870) from bacillus subtilis at 2.38 a resolution
63	d1o0ya	 Alignment	not modelled	18.8	17	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
64	c1jpmB	 Alignment	not modelled	18.4	11	PDB header: isomerase Chain: B: PDB Molecule: l-ala-d/l-glu epimerase; PDBTitle: l-ala-d/l-glu epimerase
65	c2yciX	 Alignment	not modelled	17.6	14	PDB header: transferase Chain: X: PDB Molecule: 5-methyltetrahydrofolate corrinoid/iron sulfur protein PDBTitle: methyltransferase native
66	c3ddmD	 Alignment	not modelled	17.0	12	PDB header: lyase Chain: D: PDB Molecule: putative mandelate racemase/muconate lactonizing PDBTitle: crystal structure of mandelate racemase/muconate2 lactonizing enzyme from bordetella bronchiseptica rb50
67	c3l8mA	 Alignment	not modelled	16.9	10	PDB header: transferase Chain: A: PDB Molecule: probable thiamine pyrophosphokinase; PDBTitle: crystal structure of a probable thiamine pyrophosphokinase2 from staphylococcus saprophyticus subsp. saprophyticus.3 northeast structural genomics consortium target id syr86
68	c2oz8B	 Alignment	not modelled	15.6	10	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: ml17089 protein; PDBTitle: crystal structure of putative mandelate racemase from mesorhizobium2 loti
69	d1f6ya	 Alignment	not modelled	15.4	18	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Methyltetrahydrofolate-utilizing methyltransferases
70	c3ngiC	 Alignment	not modelled	14.2	17	PDB header: lyase Chain: C: PDB Molecule: deoxyribose-phosphate aldolase; PDBTitle: crystal structure of a putative deoxyribose-phosphate aldolase from2 entamoeba histolytica
71	c3smaD	 Alignment	not modelled	14.2	18	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
72	d1t57a	 Alignment	not modelled	13.9	21	Fold: Pyruvate kinase C-terminal domain-like Superfamily: PK C-terminal domain-like Family: MTH1675-like
73	d1zata2	 Alignment	not modelled	13.0	13	Fold: L,D-transpeptidase pre-catalytic domain-like Superfamily: L,D-transpeptidase pre-catalytic domain-like Family: L,D-transpeptidase pre-catalytic domain-like
74	c3ic5A	 Alignment	not modelled	12.5	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative saccharopine dehydrogenase; PDBTitle: n-terminal domain of putative saccharopine dehydrogenase from ruegeria2 pomeroyi.
75	d1ydw1	 Alignment	not modelled	12.1	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
76	c3ihkC	 Alignment	not modelled	11.7	15	PDB header: transferase Chain: C: PDB Molecule: thiamin pyrophosphokinase; PDBTitle: crystal structure of thiamin pyrophosphokinase from2 s.mutans, northeast structural genomics consortium target3 smr83
77	c3e4fB	 Alignment	not modelled	11.6	25	PDB header: transferase Chain: B: PDB Molecule: aminoglycoside n3-acetyltransferase; PDBTitle: crystal structure of ba2930- a putative aminoglycoside n3-2 acetyltransferase from bacillus anthracis
78	d1wlza1	 Alignment	not modelled	11.4	22	Fold: EF Hand-like Superfamily: EF-hand Family: EF-hand modules in multidomain proteins
						PDB header: unknown function

79	c1wlzD_	Alignment	not modelled	11.4	22	Chain: D: PDB Molecule: cap-binding protein complex interacting protein PDBTitle: crystal structure of djbp fragment which was obtained by2 limited proteolysis
80	c2p0aA_	Alignment	not modelled	9.6	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein duf871; PDBTitle: crystal structure of a conserved protein from locus ef_2437 in2 enterococcus faecalis with an unknown function
81	d1sjda1	Alignment	not modelled	9.4	15	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
82	d2nu7a1	Alignment	not modelled	8.6	8	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
83	c3ju2A_	Alignment	not modelled	8.6	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein smc04130; PDBTitle: crystal structure of protein smc04130 from sinorhizobium meliloti 1021
84	c2ixaA_	Alignment	not modelled	8.3	17	PDB header: hydrolase Chain: A: PDB Molecule: alpha-n-acetylgalactosaminidase; PDBTitle: a-zyme, n-acetylgalactosaminidase
85	c3dtyA_	Alignment	not modelled	8.2	19	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, gfo/ldh/moca family; PDBTitle: crystal structure of an oxidoreductase from pseudomonas2 syringae
86	c3bjsB_	Alignment	not modelled	8.2	12	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: mandelate racemase/muconate lactonizing enzyme; PDBTitle: crystal structure of a member of enolase superfamily from polaromonas2 sp. js666
87	d1gr0a1	Alignment	not modelled	8.2	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
88	d2ou3a1	Alignment	not modelled	8.2	13	Fold: TerB-like Superfamily: TerB-like Family: COG3793-like
89	c1lc3A_	Alignment	not modelled	7.6	16	PDB header: oxidoreductase Chain: A: PDB Molecule: biliverdin reductase a; PDBTitle: crystal structure of a biliverdin reductase enzyme-cofactor2 complex
90	d1nu5a1	Alignment	not modelled	7.4	8	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
91	d2ijqa1	Alignment	not modelled	7.3	30	Fold: Hyaluronidase domain-like Superfamily: TTHA0068-like Family: TTHA0068-like
92	c3melC_	Alignment	not modelled	7.2	30	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: thiamin pyrophosphokinase family protein; PDBTitle: crystal structure of thiamin pyrophosphokinase family protein from2 enterococcus faecalis, northeast structural genomics consortium3 target efr150
93	d2plca_	Alignment	not modelled	7.2	38	Fold: TIM beta/alpha-barrel Superfamily: PLC-like phosphodiesterases Family: Bacterial PLC
94	c3es8D_	Alignment	not modelled	6.9	11	PDB header: isomerase, lyase Chain: D: PDB Molecule: muconate cycloisomerase; PDBTitle: crystal structure of divergent enolase from oceanobacillus2 ihyensensis complexed with mg and l-malate.
95	d1x87a_	Alignment	not modelled	6.9	13	Fold: Urocanase Superfamily: Urocanase Family: Urocanase
96	d1bxbA_	Alignment	not modelled	6.8	14	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
97	c2wjseA_	Alignment	not modelled	6.7	30	PDB header: hydrolase Chain: A: PDB Molecule: tyrosine-protein phosphatase cpsb; PDBTitle: crystal structure of the tyrosine phosphatase cps4b from2 streptococcus pneumoniae tigr4.
98	d2nyga1	Alignment	not modelled	6.5	18	Fold: TTHA0583/YokD-like Superfamily: TTHA0583/YokD-like Family: Aminoglycoside 3-N-acetyltransferase-like
99	d1mzha_	Alignment	not modelled	6.5	17	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase