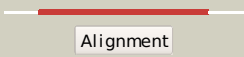
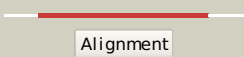
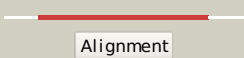
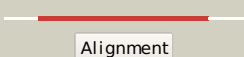
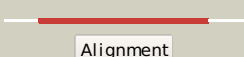
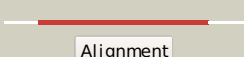
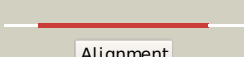
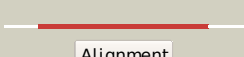
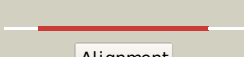
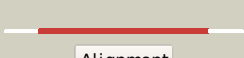


Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P76187
Date	Thu Jan 5 12:20:16 GMT 2012
Unique Job ID	424352f9d9f24080

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ur3m_	 Alignment		100.0	97	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
2	d1lqaa_	 Alignment		100.0	23	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
3	d3eaa1	 Alignment		100.0	22	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
4	c3luta_	 Alignment		100.0	22	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	c3erpA_	 Alignment		100.0	25	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: structure of idp01002, a putative oxidoreductase from and essential2 gene of salmonella typhimurium
6	c3n6qF_	 Alignment		100.0	22	PDB header: oxidoreductase Chain: F: PDB Molecule: yghz aldo-keto reductase; PDBTitle: crystal structure of yghz from e. coli
7	c3n2tA_	 Alignment		100.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: structure of the glycerol dehydrogenase akr11b4 from gluconobacter2 oxydans
8	d1pyfa_	 Alignment		100.0	23	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
9	d1pz1a_	 Alignment		100.0	26	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
10	c3h7uA_	 Alignment		100.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: aldo-keto reductase; PDBTitle: crystal structure of the plant stress-response enzyme akr4c9
11	c1ynpA_	 Alignment		100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase; PDBTitle: aldo-keto reductase akr11c1 from bacillus halodurans (apo form)

12	dlgvea_	Alignment		100.0	20	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
13	dlq5ma_	Alignment		100.0	21	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
14	c3up8B_	Alignment		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
15	c3f7jB_	Alignment		100.0	25	PDB header: oxidoreductase Chain: B: PDB Molecule: yvgn protein; PDBTitle: b.subtilis yvgn
16	d1mi3a_	Alignment		100.0	21	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
17	d1j96a_	Alignment		100.0	22	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
18	d1us0a_	Alignment		100.0	20	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
19	d1qwka_	Alignment		100.0	18	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
20	d1afsa_	Alignment	not modelled	100.0	20	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
21	d1frba_	Alignment	not modelled	100.0	23	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
22	d1hqta_	Alignment	not modelled	100.0	22	PDB header: oxidoreductase Chain: C: PDB Molecule: aflatoxin b1 aldehyde reductase member 2; PDBTitle: structure of the aflatoxin aldehyde reductase in complex2 with nadph
23	c2bp1C_	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
24	c1zgdB_	Alignment	not modelled	100.0	24	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
25	c2wztA_	Alignment	not modelled	100.0	24	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
26	d1mzra_	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	c3h7rA_	Alignment	not modelled	100.0	24	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
28	d1hw6a_	Alignment	not modelled	100.0		

29	c3o0kB	Alignment	not modelled	100.0	27	PDB header: oxidoreductase Chain: B: PDB Molecule: aldo/keto reductase; PDBTitle: crystal structure of aldo/keto reductase from brucella melitensis
30	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.
31	c1vbjB	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: B: PDB Molecule: prostaglandin f synthase; PDBTitle: the crystal structure of prostaglandin f synthase from2 trypanosoma brucei
32	d1s1pa	Alignment	not modelled	100.0	19	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
33	d1ah4a	Alignment	not modelled	100.0	22	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
34	d2alra	Alignment	not modelled	100.0	24	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
35	c3b3dA	Alignment	not modelled	100.0	27	PDB header: oxidoreductase Chain: A: PDB Molecule: putative morphine dehydrogenase; PDBTitle: b.subtilis ytb
36	d1vp5a	Alignment	not modelled	100.0	24	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
37	d1c9wa	Alignment	not modelled	100.0	20	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
38	c2bgsA	Alignment	not modelled	100.0	25	PDB header: oxidoreductase Chain: A: PDB Molecule: aldose reductase; PDBTitle: holo aldose reductase from barley
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	17	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	82.1	12	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	c3l23A	Alignment	not modelled	58.0	11	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
43	d1jpma1	Alignment	not modelled	50.6	15	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
44	d3bofa2	Alignment	not modelled	49.9	9	Fold: TIM beta/alpha-barrel Superfamily: Homocysteine S-methyltransferase Family: Homocysteine S-methyltransferase
45	c3ezxA	Alignment	not modelled	41.7	14	PDB header: transferase Chain: A: PDB Molecule: monomethylamine corrinoid protein 1; PDBTitle: structure of methanosarcina barkeri monomethylamine2 corrinoid protein
46	c2ph5A	Alignment	not modelled	40.3	16	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	d2gjxa1	Alignment	not modelled	30.8	17	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
48	c3g8rA	Alignment	not modelled	30.1	19	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
49	c1jpmB	Alignment	not modelled	29.7	14	PDB header: isomerase Chain: B: PDB Molecule: l-ala-d/l-glu epimerase; PDBTitle: l-ala-d/l-glu epimerase
50	c3a5vA	Alignment	not modelled	25.7	18	PDB header: hydrolase Chain: A: PDB Molecule: alpha-galactosidase; PDBTitle: crystal structure of alpha-galactosidase i from mortierella vinacea
51	c2pz0B	Alignment	not modelled	24.1	8	PDB header: hydrolase Chain: B: PDB Molecule: glycerophosphoryl diester phosphodiesterase; PDBTitle: crystal structure of glycerophosphodiester phosphodiesterase (gdpd)2 from t. tengcongensis
52	c3lmyA	Alignment	not modelled	23.1	17	PDB header: hydrolase Chain: A: PDB Molecule: beta-hexosaminidase subunit beta; PDBTitle: the crystal structure of beta-hexosaminidase b in complex with2 pyrimethamine
53	c1b8hA	Alignment	not modelled	22.7	4	PDB header: transferase Chain: A: PDB Molecule: dna polymerase processivity component; PDBTitle: sliding clamp, dna polymerase
						PDB header: transcription

54	c2k6xA	Alignment	not modelled	22.4	15	Chain: A: PDB Molecule: rna polymerase sigma factor rpod; PDBTitle: autoregulation of a group 1 bacterial sigma factor involves2 the formation of a region 1.1- induced compacted structure
55	c3obeB	Alignment	not modelled	21.4	10	PDB header: isomerase Chain: B: PDB Molecule: sugar phosphate isomerase/epimerase; PDBTitle: crystal structure of a sugar phosphate isomerase/epimerase (bdi_3400)2 from parabacteroides distasonis atcc 8503 at 1.70 a resolution
56	c2zvrA	Alignment	not modelled	21.3	9	PDB header: isomerase Chain: A: PDB Molecule: uncharacterized protein tm_0416; PDBTitle: crystal structure of a d-tagatose 3-epimerase-related2 protein from thermotoga maritima
57	d1qbaa3	Alignment	not modelled	21.1	10	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
58	c2gjxE	Alignment	not modelled	20.9	13	PDB header: hydrolase Chain: E: PDB Molecule: beta-hexosaminidase alpha chain; PDBTitle: crystallographic structure of human beta-hexosaminidase a
59	c2jlhA	Alignment	not modelled	20.2	15	PDB header: protein transport Chain: A: PDB Molecule: yop proteins translocation protein u; PDBTitle: crystal structure of the cytoplasmic domain of yersinia2 pestis yscu n263a mutant
60	c1nouA	Alignment	not modelled	20.1	17	PDB header: hydrolase Chain: A: PDB Molecule: beta-hexosaminidase beta chain; PDBTitle: native human lysosomal beta-hexosaminidase isoform b
61	d1nowa1	Alignment	not modelled	19.8	17	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
62	c3dx5A	Alignment	not modelled	19.6	9	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
63	c1uasA	Alignment	not modelled	19.0	11	PDB header: hydrolase Chain: A: PDB Molecule: alpha-galactosidase; PDBTitle: crystal structure of rice alpha-galactosidase
64	d1yx1a1	Alignment	not modelled	17.7	13	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: KguE-like
65	d2d0oa1	Alignment	not modelled	17.3	12	Fold: The "swivelling" beta/beta/alpha domain Superfamily: Swiveling domain of dehydratase reactivase alpha subunit Family: Swiveling domain of dehydratase reactivase alpha subunit
66	d2nu7a1	Alignment	not modelled	17.0	12	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
67	c2ylaA	Alignment	not modelled	16.9	8	PDB header: hydrolase Chain: A: PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: inhibition of the pneumococcal virulence factor strh and2 molecular insights into n-glycan recognition and3 hydrolysis
68	c1wlzD	Alignment	not modelled	16.8	22	PDB header: unknown function Chain: D: PDB Molecule: cap-binding protein complex interacting protein PDBTitle: crystal structure of djbp fragment which was obtained by2 limited proteolysis
69	d1wlza1	Alignment	not modelled	16.8	22	Fold: EF Hand-like Superfamily: EF-hand Family: EF-hand modules in multidomain proteins
70	d1k77a	Alignment	not modelled	16.1	11	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Hypothetical protein YgbM (EC1530)
71	c3qy6A	Alignment	not modelled	15.6	10	PDB header: hydrolase Chain: A: PDB Molecule: tyrosine-protein phosphatase ywqe; PDBTitle: crystal structures of ywqe from bacillus subtilis and cpsb from2 streptococcus pneumoniae, unique metal-dependent tyrosine3 phosphatases
72	c2wjeA	Alignment	not modelled	15.3	21	PDB header: hydrolase Chain: A: PDB Molecule: tyrosine-protein phosphatase cpsb; PDBTitle: crystal structure of the tyrosine phosphatase cps4b from2 streptococcus pneumoniae tigr4.
73	c3t7yB	Alignment	not modelled	15.2	12	PDB header: protein transport Chain: B: PDB Molecule: yop proteins translocation protein u; PDBTitle: structure of an autocleavage-inactive mutant of the cytoplasmic domain2 of ct091, the yscu homologue of chlamydia trachomatis
74	c3rcnA	Alignment	not modelled	15.0	13	PDB header: hydrolase Chain: A: PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: crystal structure of beta-n-acetylhexosaminidase from arthrobacter2 aurescens
75	c1vliA	Alignment	not modelled	14.8	12	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
76	c3c00B	Alignment	not modelled	14.5	8	PDB header: membrane protein, protein transport Chain: B: PDB Molecule: escu; PDBTitle: crystal structural of the mutated g247t escu/spas c-terminal domain
77	c3nsnA	Alignment	not modelled	14.4	14	PDB header: hydrolase Chain: A: PDB Molecule: n-acetylglucosaminidase; PDBTitle: crystal structure of insect beta-n-acetyl-d-hexosaminidase ofhex12 complexed with tmg-chitotriomycin
78	c2yl8A	Alignment	not modelled	14.4	16	PDB header: hydrolase Chain: A: PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: inhibition of the pneumococcal virulence factor strh

						and2 molecular insights into n-glycan recognition and3 hydrolysis
79	c1t0oA_	Alignment	not modelled	14.3	13	PDB header: hydrolase Chain: A: PDB Molecule: alpha-galactosidase; PDBTitle: the structure of alpha-galactosidase from trichoderma reesei complexed2 with beta-d-galactose
80	c3ic5A_	Alignment	not modelled	14.3	9	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative saccharopine dehydrogenase; PDBTitle: n-terminal domain of putative saccharopine dehydrogenase from ruegeria2 pomeroyi.
81	c3bzaA_	Alignment	not modelled	13.9	8	PDB header: membrane protein, protein transport Chain: A: PDB Molecule: escu; PDBTitle: crystal structure of escu c-terminal domain with n262d mutation, space2 group p 41 21 2
82	d3bzra1	Alignment	not modelled	13.9	8	Fold: EscU C-terminal domain-like Superfamily: EscU C-terminal domain-like Family: EscU C-terminal domain-like
83	c3js3C_	Alignment	not modelled	13.6	17	PDB header: lyase Chain: C: PDB Molecule: 3-dehydroquinate dehydratase; PDBTitle: crystal structure of type i 3-dehydroquinate dehydratase (arod) from2 clostridium difficile with covalent reaction intermediate
84	d1yhta1	Alignment	not modelled	13.1	24	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
85	d1jw2a_	Alignment	not modelled	12.9	13	Fold: Open three-helical up-and-down bundle Superfamily: Hemolysin expression modulating protein HHA Family: Hemolysin expression modulating protein HHA
86	d1qwga_	Alignment	not modelled	12.8	17	Fold: TIM beta/alpha-barrel Superfamily: (2r)-phospho-3-sulfolactate synthase ComA Family: (2r)-phospho-3-sulfolactate synthase ComA
87	d1lk3a_	Alignment	not modelled	12.8	16	Fold: 4-helical cytokines Superfamily: 4-helical cytokines Family: Interferons/Interleukin-10 (IL-10)
88	dlszna2	Alignment	not modelled	12.7	17	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
89	c2p10D_	Alignment	not modelled	12.7	12	PDB header: hydrolase Chain: D: PDB Molecule: mlI9387 protein; PDBTitle: crystal structure of a putative phosphonopyruvate hydrolase (mlI9387)2 from mesorhizobium loti maff303099 at 2.15 a resolution
90	d1bxni_	Alignment	not modelled	12.6	19	Fold: RuBisCO, small subunit Superfamily: RuBisCO, small subunit Family: RuBisCO, small subunit
91	c2vwtA_	Alignment	not modelled	12.4	21	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
92	d1bwvs_	Alignment	not modelled	12.0	13	Fold: RuBisCO, small subunit Superfamily: RuBisCO, small subunit Family: RuBisCO, small subunit
93	c3rpmA_	Alignment	not modelled	11.9	16	PDB header: hydrolase Chain: A: PDB Molecule: beta-n-acetyl-hexosaminidase; PDBTitle: crystal structure of the first gh20 domain of a novel beta-n-acetyl-2 hexosaminidase strh from streptococcus pneumoniae r6
94	d1vlia2	Alignment	not modelled	11.7	10	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: NeuB-like
95	c3pjwA_	Alignment	not modelled	11.6	13	PDB header: lyase Chain: A: PDB Molecule: cyclic dimeric gmp binding protein; PDBTitle: structure of pseudomonas fluorescence lapd ggdef-eal dual domain, i23
96	d2p10a1	Alignment	not modelled	11.4	12	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: MII9387-like
97	c1m04A_	Alignment	not modelled	11.1	4	PDB header: hydrolase Chain: A: PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: mutant streptomyces plicatus beta-hexosaminidase (d313n) in complex2 with product (glcnac)
98	c2ksnA_	Alignment	not modelled	11.0	21	PDB header: signaling protein Chain: A: PDB Molecule: ubiquitin domain-containing protein 2; PDBTitle: solution structure of the n-terminal domain of dc-ubp/ubtd2
99	c1ydnA_	Alignment	not modelled	11.0	20	PDB header: lyase Chain: A: PDB Molecule: hydroxymethylglutaryl-coa lyase; PDBTitle: crystal structure of the hmg-coa lyase from brucella melitensis,2 northeast structural genomics target lr35.