Phyre2

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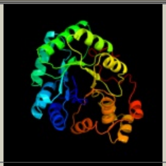
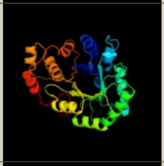
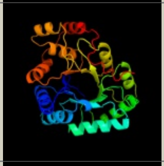
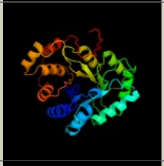
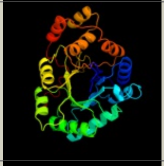
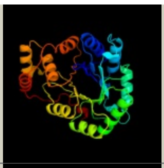
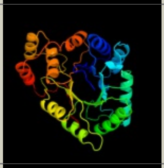
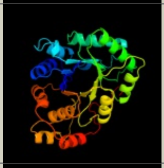
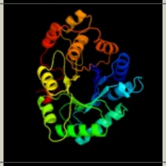
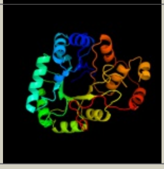
Description	P30863
Date	Thu Jan 5 11:46:39 GMT 2012
Unique Job ID	6a90f760e09424db

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3up8B_	Alignment		100.0	44	**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
2	d1q5ma_	Alignment		100.0	32	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
3	d1frba_	Alignment		100.0	34	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
4	d1hqta_	Alignment		100.0	32	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
5	c3h7uA_	Alignment		100.0	30	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldo-keto reductase; **PDBTitle:** crystal structure of the plant stress-response enzyme akr4c9
6	d1j96a_	Alignment		100.0	33	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
7	c3f7jB_	Alignment		100.0	38	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**yvgn protein; **PDBTitle:** b.subtilis yvgn
8	d2alra_	Alignment		100.0	33	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
9	d1mi3a_	Alignment		100.0	35	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
10	d1ah4a_	Alignment		100.0	36	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
11	d1afsa_	Alignment		100.0	33	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)

12	d1qwka_	Alignment		100.0	36	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
13	d1c9wa_	Alignment		100.0	33	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
14	d1us0a_	Alignment		100.0	35	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
15	d1s1pa_	Alignment		100.0	33	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
16	c2bgsA_	Alignment		100.0	36	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldose reductase; **PDBTitle:** holo aldose reductase from barley
17	c2wztA_	Alignment		100.0	37	**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
18	d1mzra_	Alignment		100.0	38	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
19	c3buvB_	Alignment		100.0	32	**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.
20	c1zgdB_	Alignment		100.0	32	**PDB header:**plant protein **Chain:** B: **PDB Molecule:**chalcone reductase; **PDBTitle:** chalcone reductase complexed with nadp+ at 1.7 angstrom2 resolution
21	c3h7rA_	Alignment	not modelled	100.0	31	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldo-keto reductase; **PDBTitle:** crystal structure of the plant stress-response enzyme akr4c8
22	c3b3dA_	Alignment	not modelled	100.0	37	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative morphine dehydrogenase; **PDBTitle:** b.subtilis ytbe
23	d1vp5a_	Alignment	not modelled	100.0	33	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
24	c1vbjB_	Alignment	not modelled	100.0	32	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**prostaglandin f synthase; **PDBTitle:** the crystal structure of prostaglandin f synthase from2 trypanosoma brucei
25	c3o0kB_	Alignment	not modelled	100.0	37	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aldo/keto reductase; **PDBTitle:** crystal structure of aldo/keto reductase from brucella melitensis
26	d1lqaa_	Alignment	not modelled	100.0	28	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
27	d1hw6a_	Alignment	not modelled	100.0	42	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
28	c3krbB_	Alignment	not modelled	100.0	33	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aldose reductase; **PDBTitle:** structure of aldose reductase from giardia lamblia at 1.75a resolution
						Fold:TIM beta/alpha-barrel

29	d3eaua1	Alignment	not modelled	100.0	27	**Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
30	c3lutA_	Alignment	not modelled	100.0	27	**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
31	d1ur3m_	Alignment	not modelled	100.0	26	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
32	c3erpA_	Alignment	not modelled	100.0	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** structure of idp01002, a putative oxidoreductase from and essential2 gene of salmonella typhimurium
33	d1gvea_	Alignment	not modelled	100.0	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
34	c3n6qF_	Alignment	not modelled	100.0	24	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**yghz aldo-keto reductase; **PDBTitle:** crystal structure of yghz from e. coli
35	d1pyfa_	Alignment	not modelled	100.0	33	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
36	c3n2tA_	Alignment	not modelled	100.0	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** structure of the glycerol dehydrogenase akr11b4 from gluconobacter2 oxydans
37	d1pz1a_	Alignment	not modelled	100.0	28	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
38	c2bp1C_	Alignment	not modelled	100.0	24	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**aflatoxin b1 aldehyde reductase member 2; **PDBTitle:** structure of the aflatoxin aldehyde reductase in complex2 with nadph
39	c1ynpA_	Alignment	not modelled	100.0	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase; **PDBTitle:** aldo-keto reductase akr11c1 from bacillus halodurans (apo form)
40	c3ln3A_	Alignment	not modelled	100.0	30	**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	c3g8rA_	Alignment	not modelled	82.1	15	**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
42	c3ngfA_	Alignment	not modelled	79.8	10	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ap endonuclease, family 2; **PDBTitle:** crystal structure of ap endonuclease, family 2 from brucella2 melitensis
43	c1xuzA_	Alignment	not modelled	68.3	17	**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
44	d1jpma1	Alignment	not modelled	58.6	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
45	d2zdra2	Alignment	not modelled	52.1	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**NeuB-like
46	d1k77a_	Alignment	not modelled	44.0	8	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Hypothetical protein YgbM (EC1530)
47	d1gqna_	Alignment	not modelled	40.8	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
48	c1vliA_	Alignment	not modelled	37.7	8	**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
49	d7odca2	Alignment	not modelled	35.8	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLP-binding barrel **Family:**Alanine racemase-like, N-terminal domain
50	c2ph5A_	Alignment	not modelled	34.5	11	**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
51	d2ijqa1	Alignment	not modelled	33.5	12	**Fold:**Hyaluronidase domain-like **Superfamily:**TTHA0068-like **Family:**TTHA0068-like
52	d2q02a1	Alignment	not modelled	32.3	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**IolI-like
53	d1vp8a_	Alignment	not modelled	29.1	18	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**MTH1675-like

54	c3js3C_	Alignment	not modelled	29.0	14	**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
55	c3l2iB_	Alignment	not modelled	28.6	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** 1.85 angstrom crystal structure of the 3-dehydroquinate dehydratase2 (arod) from salmonella typhimurium lt2.
56	c3aamA_	Alignment	not modelled	27.7	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endonuclease iv; **PDBTitle:** crystal structure of endonuclease iv from thermus thermophilus hb8
57	d3bofa2	Alignment	not modelled	27.0	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Homocysteine S-methyltransferase **Family:**Homocysteine S-methyltransferase
58	d1i27a_	Alignment	not modelled	26.4	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**C-terminal domain of the rap74 subunit of TFIIF
59	d1vlia2	Alignment	not modelled	23.3	8	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**NeuB-like
60	c3cnyA_	Alignment	not modelled	22.0	10	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**inositol catabolism protein iole; **PDBTitle:** crystal structure of a putative inositol catabolism protein iole2 (iole, lp_3607) from lactobacillus plantarum wcfs1 at 1.85 a3 resolution
61	c3oa3A_	Alignment	not modelled	20.5	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**aldolase; **PDBTitle:** crystal structure of a putative deoxyribose-phosphate aldolase from2 coccidioides immitis
62	c3smaD_	Alignment	not modelled	20.3	23	**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
63	d2plca_	Alignment	not modelled	20.0	46	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLC-like phosphodiesterases **Family:**Bacterial PLC
64	d1j5ya2	Alignment	not modelled	20.0	15	**Fold:**HPr-like **Superfamily:**Putative transcriptional regulator TM1602, C-terminal domain **Family:**Putative transcriptional regulator TM1602, C-terminal domain
65	d1r0ma1	Alignment	not modelled	19.9	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
66	c3ic5A_	Alignment	not modelled	19.6	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative saccharopine dehydrogenase; **PDBTitle:** n-terminal domain of putative saccharopine dehydrogenase from ruegeria2 pomeroyi.
67	d1xp3a1	Alignment	not modelled	19.2	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Endonuclease IV
68	d1nu5a1	Alignment	not modelled	18.9	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
69	c3dx5A_	Alignment	not modelled	18.4	11	**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
70	c3ktcB_	Alignment	not modelled	17.8	15	**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
71	d2ptda_	Alignment	not modelled	16.5	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLC-like phosphodiesterases **Family:**Bacterial PLC
72	c2p0oA_	Alignment	not modelled	16.2	11	**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
73	d2gdqa1	Alignment	not modelled	16.2	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
74	c3gpqA_	Alignment	not modelled	15.6	22	**PDB header:**viral protein/rna **Chain:** A: **PDB Molecule:**non-structural protein 3; **PDBTitle:** crystal structure of macro domain of chikungunya virus in complex with2 rna
75	d1fuia2	Alignment	not modelled	15.2	14	**Fold:**FucI/AraA N-terminal and middle domains **Superfamily:**FucI/AraA N-terminal and middle domains **Family:**L-fucose isomerase, N-terminal and second domains
76	d1x87a_	Alignment	not modelled	15.0	15	**Fold:**Urocanase **Superfamily:**Urocanase **Family:**Urocanase
77	d1ub3a_	Alignment	not modelled	14.3	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
78	d1o0ya_	Alignment	not modelled	14.1	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
79	d1pv8a_	Alignment	not modelled	14.0	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**5-aminolaevulinate dehydratase, ALAD (porphobilinogen

						synthase)
80	c2zvrA_	Alignment	not modelled	13.6	15	**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
81	c3kwsB_	Alignment	not modelled	13.5	7	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative sugar isomerase; **PDBTitle:** crystal structure of putative sugar isomerase (yp_001305149.1) from2 parabacteroides distasonis atcc 8503 at 1.68 a resolution
82	c3e4fB_	Alignment	not modelled	12.8	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aminoglycoside n3-acetyltransferase; **PDBTitle:** crystal structure of ba2930- a putative aminoglycoside n3-2 acetyltransferase from bacillus anthracis
83	d1u83a_	Alignment	not modelled	12.4	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**(2r)-phospho-3-sulfolactate synthase ComA **Family:**(2r)-phospho-3-sulfolactate synthase ComA
84	c1u83A_	Alignment	not modelled	12.4	22	**PDB header:**lyase **Chain:** A: **PDB Molecule:**phosphosulfolactate synthase; **PDBTitle:** psl synthase from bacillus subtilis
85	c2cg8B_	Alignment	not modelled	11.7	15	**PDB header:**lyase/transferase **Chain:** B: **PDB Molecule:**dihydroneopterin aldolase 6-hydroxymethyl-7,8- **PDBTitle:** the bifunctional dihydroneopterin aldolase 6-hydroxymethyl-2 7,8-dihydropterin synthase from streptococcus pneumoniae
86	c3dnfB_	Alignment	not modelled	10.9	9	**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
87	d1ulza2	Alignment	not modelled	10.9	31	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
88	d1sjda1	Alignment	not modelled	10.7	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
89	c3gqeA_	Alignment	not modelled	10.6	30	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**non-structural protein 3; **PDBTitle:** crystal structure of macro domain of venezuelan equine encephalitis2 virus
90	d1spva_	Alignment	not modelled	10.2	14	**Fold:**Macro domain-like **Superfamily:**Macro domain-like **Family:**Macro domain
91	d1nexa1	Alignment	not modelled	10.1	17	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
92	c1x7fA_	Alignment	not modelled	10.1	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**outer surface protein; **PDBTitle:** crystal structure of an uncharacterized b. cereus protein
93	d2cp6a1	Alignment	not modelled	9.9	23	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
94	c2fknC_	Alignment	not modelled	9.5	17	**PDB header:**lyase **Chain:** C: **PDB Molecule:**urocanate hydratase; **PDBTitle:** crystal structure of urocanase from bacillus subtilis
95	d2jn6a1	Alignment	not modelled	9.4	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Cgl2762-like
96	d2chra1	Alignment	not modelled	9.4	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
97	c2nx9B_	Alignment	not modelled	9.3	32	**PDB header:**lyase **Chain:** B: **PDB Molecule:**oxaloacetate decarboxylase 2, subunit alpha; **PDBTitle:** crystal structure of the carboxyltransferase domain of the2 oxaloacetate decarboxylase na+ pump from vibrio cholerae
98	d1geqa_	Alignment	not modelled	9.3	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
99	d1uwka_	Alignment	not modelled	9.2	13	**Fold:**Urocanase **Superfamily:**Urocanase **Family:**Urocanase