Phyre2

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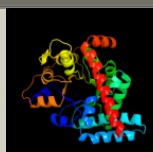
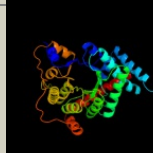
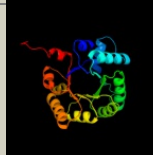
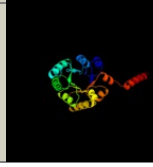
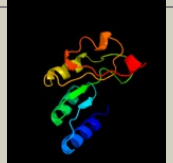
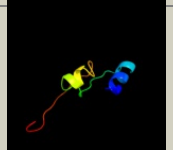
Description	P0A870
Date	Thu Jan 5 11:07:02 GMT 2012
Unique Job ID	1606c35c02d4306e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1onra_	Alignment		100.0	100	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
2	d1f05a_	Alignment		100.0	60	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
3	d2e1da1	Alignment		100.0	60	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
4	c3m16A_	Alignment		100.0	61	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transaldolase; **PDBTitle:** structure of a transaldolase from oleispira antarctica
5	c3igxA_	Alignment		100.0	48	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transaldolase; **PDBTitle:** 1.85 angstrom resolution crystal structure of transaldolase b (tala)2 from francisella tularensis.
6	c3hjzA_	Alignment		100.0	53	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transaldolase b; **PDBTitle:** the structure of an aldolase from prochlorococcus marinus
7	c3cq0B_	Alignment		100.0	53	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative transaldolase ygr043c; **PDBTitle:** crystal structure of tal2_yeast
8	c3clmA_	Alignment		100.0	23	**PDB header:**lyase **Chain:** A: **PDB Molecule:**transaldolase; **PDBTitle:** crystal structure of transaldolase (yp_208650.1) from neisseria2 gonorrhoeae fa 1090 at 1.14 a resolution
9	c3s1vD_	Alignment		100.0	37	**PDB header:**transferase **Chain:** D: **PDB Molecule:**probable transaldolase; **PDBTitle:** transaldolase from thermoplasma acidophilum in complex with d-fructose2 6-phosphate schiff-base intermediate
10	d1wx0a1	Alignment		100.0	32	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
11	d1vpxa_	Alignment		100.0	39	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase

12	d1l6wa_	Alignment		100.0	30	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
13	d1xm3a_	Alignment		96.0	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**ThiG-like **Family:**ThiG-like
14	c2htmB_	Alignment		95.0	18	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**thiazole biosynthesis protein thig; **PDBTitle:** crystal structure of ttha0676 from thermus thermophilus hb8
15	c2p10D_	Alignment		92.5	17	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**mll9387 protein; **PDBTitle:** crystal structure of a putative phosphonopyruvate hydrolase (mll9387)2 from mesorhizobium loti maff303099 at 2.15 a resolution
16	d1o4ua1	Alignment		87.2	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Nicotinate/Quinolinate PRTase C-terminal domain-like **Family:**NadC C-terminal domain-like
17	c1o4uA_	Alignment		85.1	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**type ii quinolic acid phosphoribosyltransferase; **PDBTitle:** crystal structure of a nicotinate nucleotide pyrophosphorylase2 (tm1645) from thermotoga maritima at 2.50 a resolution
18	d2p10a1	Alignment		84.8	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Mll9387-like
19	c3labA_	Alignment		83.8	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative kdpg (2-keto-3-deoxy-6-phosphogluconate) **PDBTitle:** crystal structure of a putative kdpg (2-keto-3-deoxy-6-2 phosphogluconate) aldolase from oleispira antarctica
20	c3gk0H_	Alignment		80.6	28	**PDB header:**transferase **Chain:** H: **PDB Molecule:**pyridoxine 5'-phosphate synthase; **PDBTitle:** crystal structure of pyridoxal phosphate biosynthetic2 protein from burkholderia pseudomallei
21	d1ea0a2	Alignment	not modelled	77.6	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
22	d1m5wa_	Alignment	not modelled	75.8	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Pyridoxine 5'-phosphate synthase **Family:**Pyridoxine 5'-phosphate synthase
23	d1o66a_	Alignment	not modelled	72.1	26	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Ketopantoate hydroxymethyltransferase PanB
24	c3ez4B_	Alignment	not modelled	70.4	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**3-methyl-2-oxobutanoate hydroxymethyltransferase; **PDBTitle:** crystal structure of 3-methyl-2-oxobutanoate2 hydroxymethyltransferase from burkholderia pseudomallei
25	c2jbmA_	Alignment	not modelled	70.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** qprtase structure from human
26	c3o6cA_	Alignment	not modelled	69.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyridoxine 5'-phosphate synthase; **PDBTitle:** pyridoxal phosphate biosynthetic protein pdxj from campylobacter2 jejuni
27	d1nkua_	Alignment	not modelled	65.8	23	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**3-Methyladenine DNA glycosylase I (Tag)
28	d1wa3a1	Alignment	not modelled	64.3	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase

29	d1nu5a1	Alignment	not modelled	64.1	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
30	d1ofda2	Alignment	not modelled	64.0	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
31	d1cjca2	Alignment	not modelled	62.0	19	**Fold:**Nucleotide-binding domain **Superfamily:**Nucleotide-binding domain **Family:**N-terminal domain of adrenodoxin reductase-like
32	d1kbia1	Alignment	not modelled	60.9	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
33	c2yw3E_	Alignment	not modelled	60.8	25	**PDB header:**lyase **Chain:** E: **PDB Molecule:**4-hydroxy-2-oxoglutarate aldolase/2-deydro-3- **PDBTitle:** crystal structure analysis of the 4-hydroxy-2-oxoglutarate aldolase/2-2 deydro-3-deoxyphosphogluconate aldolase from tthb1
34	d1wbha1	Alignment	not modelled	59.4	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
35	c3oa3A_	Alignment	not modelled	59.4	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**aldolase; **PDBTitle:** crystal structure of a putative deoxyribose-phosphate aldolase from2 coccidioides immitis
36	c2p0iA_	Alignment	not modelled	59.0	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**l-rhamnonate dehydratase; **PDBTitle:** crystal structure of l-rhamnonate dehydratase from gibberella zeae
37	c2hxtA_	Alignment	not modelled	58.1	16	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**l-fuconate dehydratase; **PDBTitle:** crystal structure of l-fuconate dehydratase from xanthomonas2 campestris liganded with mg++ and d-erythronohydroxamate
38	d1mzha_	Alignment	not modelled	56.1	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
39	c2jg6A_	Alignment	not modelled	55.7	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dna-3-methyladenine glycosidase; **PDBTitle:** crystal structure of a 3-methyladenine dna glycosylase i2 from staphylococcus aureus
40	c2b7pA_	Alignment	not modelled	54.2	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** crystal structure of quinolinic acid phosphoribosyltransferase from2 helicobacter pylori
41	d1wv2a_	Alignment	not modelled	52.8	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**ThiG-like **Family:**ThiG-like
42	c1kbiB_	Alignment	not modelled	52.3	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**cytochrome b2; **PDBTitle:** crystallographic study of the recombinant flavin-binding domain of2 baker's yeast flavocytochrome b2: comparison with the intact wild-3 type enzyme
43	c3ffsC_	Alignment	not modelled	50.8	16	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**inosine-5-monophosphate dehydrogenase; **PDBTitle:** the crystal structure of cryptosporidium parvum inosine-5'-2 monophosphate dehydrogenase
44	d1pv8a_	Alignment	not modelled	50.6	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
45	d1iyna_	Alignment	not modelled	50.5	21	**Fold:**Heme-dependent peroxidases **Superfamily:**Heme-dependent peroxidases **Family:**CCP-like
46	c3pajA_	Alignment	not modelled	49.6	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase, carboxylating; **PDBTitle:** 2.00 angstrom resolution crystal structure of a quinolinate2 phosphoribosyltransferase from vibrio cholerae o1 biovar eltor str.3 n16961
47	c1zfjA_	Alignment	not modelled	49.6	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**inosine monophosphate dehydrogenase; **PDBTitle:** inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
48	c1lm1A_	Alignment	not modelled	49.4	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ferredoxin-dependent glutamate synthase; **PDBTitle:** structural studies on the synchronization of catalytic centers in2 glutamate synthase: native enzyme
49	c1cjcA_	Alignment	not modelled	46.3	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein (adrenodoxin reductase); **PDBTitle:** structure of adrenodoxin reductase of mitochondrial p4502 systems
50	c3cxoA_	Alignment	not modelled	43.6	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative galactonate dehydratase; **PDBTitle:** crystal structure of l-rhamnonate dehydratase from2 salmonella typhimurium complexed with mg and 3-deoxy-l-3 rhamnonate
51	d2euta1	Alignment	not modelled	43.5	23	**Fold:**Heme-dependent peroxidases **Superfamily:**Heme-dependent peroxidases **Family:**CCP-like
52	c3rcyC_	Alignment	not modelled	42.7	13	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**mandelate racemase/muconate lactonizing enzyme-like **PDBTitle:** crystal structure of mandelate racemase/muconate

						lactonizing enzyme-2 like protein from roseovarius sp. tm1035
53	c2v3aA_	Alignment	not modelled	40.7	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**rubredoxin reductase; **PDBTitle:** crystal structure of rubredoxin reductase from pseudomonas2 aeruginosa.
54	d1j5ta_	Alignment	not modelled	40.1	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
55	d1vc4a_	Alignment	not modelled	40.0	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
56	d1vhna_	Alignment	not modelled	39.9	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
57	d1eepa_	Alignment	not modelled	39.7	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
58	d1d7ya2	Alignment	not modelled	39.6	21	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
59	c2oz3F_	Alignment	not modelled	39.6	15	**PDB header:**lyase **Chain:** F: **PDB Molecule:**mandelate racemase/muconate lactonizing enzyme; **PDBTitle:** crystal structure of l-rhamnonate dehydratase from azotobacter2 vinelandii
60	d1vhca_	Alignment	not modelled	39.1	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
61	c3l0gD_	Alignment	not modelled	37.1	23	**PDB header:**transferase **Chain:** D: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** crystal structure of nicotinate-nucleotide pyrophosphorylase from2 ehrlichia chaffeensis at 2.05a resolution
62	c3ef6A_	Alignment	not modelled	37.1	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**toluene 1,2-dioxygenase system ferredoxin--nad(+) **PDBTitle:** crystal structure of toluene 2,3-dioxygenase reductase
63	d1bd3a_	Alignment	not modelled	37.0	10	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
64	d1p0ka_	Alignment	not modelled	36.6	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
65	c3dg7B_	Alignment	not modelled	36.2	14	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**muconate cycloisomerase; **PDBTitle:** crystal structure of muconate lactonizing enzyme from mucobacterium2 smegmatis complexed with muconolactone
66	d2e39a1	Alignment	not modelled	35.8	18	**Fold:**Heme-dependent peroxidases **Superfamily:**Heme-dependent peroxidases **Family:**CCP-like
67	d1mxsa_	Alignment	not modelled	35.7	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
68	c3n4eA_	Alignment	not modelled	35.4	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**mandelate racemase/muconate lactonizing enzyme, c-terminal **PDBTitle:** crystal structure of mandelate racemase/muconate lactonizing protein2 from paracoccus denitrificans pd1222
69	c3llvA_	Alignment	not modelled	35.0	10	**PDB header:**nad(p) binding protein **Chain:** A: **PDB Molecule:**exopolyphosphatase-related protein; **PDBTitle:** the crystal structure of the nad(p)-binding domain of an2 exopolyphosphatase-related protein from archaeoglobus fulgidus to3 1.7a
70	c3gr7A_	Alignment	not modelled	34.8	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadph dehydrogenase; **PDBTitle:** structure of oye from geobacillus kaustophilus, hexagonal2 crystal form
71	c2gr2A_	Alignment	not modelled	34.5	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ferredoxin reductase; **PDBTitle:** crystal structure of ferredoxin reductase, bpha4 (oxidized form)
72	d1qpoa1	Alignment	not modelled	33.4	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Nicotinate/Quinolinate PRTase C-terminal domain-like **Family:**NadC C-terminal domain-like
73	c2v82A_	Alignment	not modelled	33.1	23	**PDB header:**lyase **Chain:** A: **PDB Molecule:**2-dehydro-3-deoxy-6-phosphogalactonate aldolase; **PDBTitle:** kdpgal complexed to kdpgal
74	c2qq6B_	Alignment	not modelled	32.2	12	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**mandelate racemase/muconate lactonizing enzyme- **PDBTitle:** crystal structure of mandelate racemase/muconate2 lactonizing enzyme-like protein from rubrobacter3 xylanophilus dsm 9941
75	c3gkaB_	Alignment	not modelled	32.2	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**n-ethylmaleimide reductase; **PDBTitle:** crystal structure of n-ethylmaleimidine reductase from2 burkholderia pseudomallei
76	d1vyra_	Alignment	not modelled	32.1	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
77	c2pp1C_	Alignment	not modelled	31.5	17	**PDB header:**lyase **Chain:** C: **PDB Molecule:**l-talarate/galactarate dehydratase; **PDBTitle:** crystal structure of l-talarate/galactarate dehydratase

						from2 salmonella typhimurium lt2 liganded with mg and l-lyxarohydroxamate
78	c1x1oC_	Alignment	not modelled	30.7	16	**PDB header:**transferase **Chain:** C: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** crystal structure of project id tt0268 from thermus thermophilus hb8
79	d2gdqa1	Alignment	not modelled	30.5	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
80	c2ox4E_	Alignment	not modelled	29.8	17	**PDB header:**isomerase **Chain:** E: **PDB Molecule:**putative mandelate racemase; **PDBTitle:** crystal structure of putative dehydratase from zymomonas mobilis zm4
81	d1z41a1	Alignment	not modelled	29.5	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
82	c3hyxC_	Alignment	not modelled	29.0	19	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**sulfide-quinone reductase; **PDBTitle:** 3-d x-ray structure of the sulfide:quinone oxidoreductase from aquifex2 aeolicus in complex with aurachin c
83	c3px5A_	Alignment	not modelled	28.5	14	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**enzyme of enolase superfamily; **PDBTitle:** structure of efi enolase target en500555, a putative dipeptide2 epimerase: apo structure
84	c3q3uA_	Alignment	not modelled	28.4	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**lignin peroxidase; **PDBTitle:** trametes cervina lignin peroxidase
85	c2vdcF_	Alignment	not modelled	28.1	24	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**glutamate synthase [nadph] large chain; **PDBTitle:** the 9.5 a resolution structure of glutamate synthase from2 cryo-electron microscopy and its oligomerization behavior3 in solution: functional implications.
86	c3t6cB_	Alignment	not modelled	27.5	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative mand family dehydratase; **PDBTitle:** crystal structure of an enolase from pantoea ananatis (efi target efi-2 501676) with bound d-gluconate and mg
87	c3riwA_	Alignment	not modelled	27.3	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ascorbate peroxidase; **PDBTitle:** the crystal structure of leishmania major peroxidase mutant c197t
88	d2dw4a2	Alignment	not modelled	27.1	27	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
89	d1n7ka_	Alignment	not modelled	27.0	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
90	d1goxa_	Alignment	not modelled	27.0	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
91	c1tv5A_	Alignment	not modelled	26.8	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydroorotate dehydrogenase homolog, mitochondrial; **PDBTitle:** plasmodium falciparum dihydroorotate dehydrogenase with a bound2 inhibitor
92	d1tv5a1	Alignment	not modelled	26.8	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
93	d1i5za1	Alignment	not modelled	26.7	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
94	c1qpoA_	Alignment	not modelled	26.7	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**quinolinate acid phosphoribosyl transferase; **PDBTitle:** quinolinate phosphoribosyl transferase (qaprtase) apo-enzyme from2 mycobacterium tuberculosis
95	c3lxdA_	Alignment	not modelled	26.7	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fad-dependent pyridine nucleotide-disulphide **PDBTitle:** crystal structure of ferredoxin reductase arr from novosphingobium2 aromaticivorans
96	d1f61a_	Alignment	not modelled	26.2	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like
97	c2rusB_	Alignment	not modelled	26.0	19	**PDB header:**lyase(carbon-carbon) **Chain:** B: **PDB Molecule:**rubisco (ribulose-1,5-bisphosphate **PDBTitle:** crystal structure of the ternary complex of ribulose-1,5-2 bisphosphate carboxylase, mg(ii), and activator co2 at 2.3-3 angstroms resolution
98	c3fg2P_	Alignment	not modelled	25.8	25	**PDB header:**oxidoreductase **Chain:** P: **PDB Molecule:**putative rubredoxin reductase; **PDBTitle:** crystal structure of ferredoxin reductase for the cyp199a2 system from2 rhodopseudomonas palustris
99	c1qapA_	Alignment	not modelled	25.8	12	**PDB header:**glycosyltransferase **Chain:** A: **PDB Molecule:**quinolinic acid phosphoribosyltransferase; **PDBTitle:** quinolinic acid phosphoribosyltransferase with bound2 quinolinic acid
100	c3fwzA_	Alignment	not modelled	25.6	10	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**inner membrane protein ybal; **PDBTitle:** crystal structure of trka-n domain of inner membrane protein ybal from2 escherichia coli
101	c3h12B_	Alignment	not modelled	25.3	13	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**mandelate racemase; **PDBTitle:** crystal structure of putative mandelate racemase from bordetella2 bronchiseptica rb50

102	d1vkfa_	Alignment	not modelled	25.3	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**GlpP-like **Family:**GlpP-like
103	c3bw2A_	Alignment	not modelled	25.1	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2-nitropropane dioxygenase; **PDBTitle:** crystal structures and site-directed mutagenesis study of nitroalkane2 oxidase from streptomyces ansochromogenes
104	c1yqzA_	Alignment	not modelled	25.0	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**coenzyme a disulfide reductase; **PDBTitle:** structure of coenzyme a-disulfide reductase from2 staphylococcus aureus refined at 1.54 angstrom resolution
105	c2ehjA_	Alignment	not modelled	24.5	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uracil phosphoribosyltransferase; **PDBTitle:** structure of uracil phosphoribosyl transferase
106	c1q1wA_	Alignment	not modelled	24.2	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putidaredoxin reductase; **PDBTitle:** crystal structure of putidaredoxin reductase from2 pseudomonas putida
107	d1nhpa2	Alignment	not modelled	24.1	24	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
108	d1itza3	Alignment	not modelled	24.0	27	**Fold:**TK C-terminal domain-like **Superfamily:**TK C-terminal domain-like **Family:**Transketolase C-terminal domain-like
109	c2zrvC_	Alignment	not modelled	23.8	17	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**isopentenyl-diphosphate delta-isomerase; **PDBTitle:** crystal structure of sulfolobus shibatae isopentenyl2 diphosphate isomerase in complex with reduced fmn.
110	d1tb3a1	Alignment	not modelled	23.8	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
111	c3ivuB_	Alignment	not modelled	23.8	25	**PDB header:**transferase **Chain:** B: **PDB Molecule:**homocitrate synthase, mitochondrial; **PDBTitle:** homocitrate synthase lys4 bound to 2-og
112	d1uuma_	Alignment	not modelled	23.7	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
113	d1o5oa_	Alignment	not modelled	23.7	16	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
114	c3sqsA_	Alignment	not modelled	23.5	7	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**mandelate racemase/muconate lactonizing protein; **PDBTitle:** crystal structure of a putative mandelate racemase/muconate2 lactonizing protein from dinoroseobacter shibae dfl 12
115	c1rcxH_	Alignment	not modelled	23.4	21	**PDB header:**lyase (carbon-carbon) **Chain:** H: **PDB Molecule:**ribulose bisphosphate carboxylase/oxygenase; **PDBTitle:** non-activated spinach rubisco in complex with its substrate2 ribulose-1,5-bisphosphate
116	d1p4ca_	Alignment	not modelled	23.1	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
117	d2chra1	Alignment	not modelled	22.7	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
118	d1v9sa1	Alignment	not modelled	22.7	14	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
119	c1me9A_	Alignment	not modelled	22.6	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**inosine-5'-monophosphate dehydrogenase; **PDBTitle:** inosine monophosphate dehydrogenase (impdh) from2 tritrichomonas foetus with imp bound
120	d2gl5a1	Alignment	not modelled	21.9	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like