Phyre2

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Description	P0ADI4
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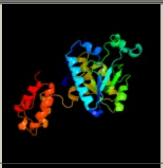
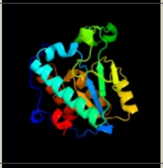
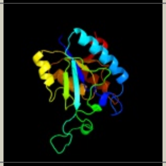
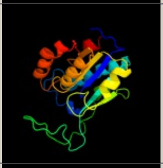
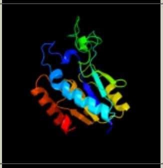
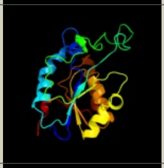
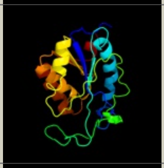
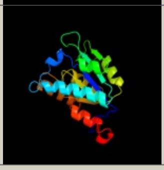
Unique Job ID	1ff44ac2f1478698

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2fq1A_	Alignment		100.0	100	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**isochorismatase; **PDBTitle:** crystal structure of the two-domain non-ribosomal peptide synthetase2 entb containing isochorismate lyase and aryl-carrier protein domains
2	d1nf9a_	Alignment		100.0	47	**Fold:**Isochorismatase-like hydrolases **Superfamily:**Isochorismatase-like hydrolases **Family:**Isochorismatase-like hydrolases
3	d1nbaa_	Alignment		100.0	23	**Fold:**Isochorismatase-like hydrolases **Superfamily:**Isochorismatase-like hydrolases **Family:**Isochorismatase-like hydrolases
4	c3irvA_	Alignment		100.0	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cysteine hydrolase; **PDBTitle:** crystal structure of cysteine hydrolase pspph_2384 from pseudomonas2 syringae pv. phaseolicola 1448a
5	c3ot4F_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**putative isochorismatase; **PDBTitle:** structure and catalytic mechanism of bordetella bronchiseptica nicf
6	d1j2ra_	Alignment		100.0	21	**Fold:**Isochorismatase-like hydrolases **Superfamily:**Isochorismatase-like hydrolases **Family:**Isochorismatase-like hydrolases
7	c3kl2K_	Alignment		100.0	20	**PDB header:**structural genomics, unknown function **Chain:** K: **PDB Molecule:**putative isochorismatase; **PDBTitle:** crystal structure of a putative isochorismatase from streptomyces2 avermitilis
8	c3oqpA_	Alignment		100.0	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative isochorismatase; **PDBTitle:** crystal structure of a putative isochorismatase (bxe_a0706) from2 burkholderia xenovorans lb400 at 1.22 a resolution
9	c3oqpB_	Alignment		100.0	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative isochorismatase; **PDBTitle:** crystal structure of a putative isochorismatase (bxe_a0706) from2 burkholderia xenovorans lb400 at 1.22 a resolution
10	c3hu5B_	Alignment		100.0	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**isochorismatase family protein; **PDBTitle:** crystal structure of isochorismatase family protein from desulfovibrio2 vulgaris subsp. vulgaris str. hildenborough
11	c3mcwA_	Alignment		100.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative hydrolase; **PDBTitle:** crystal structure of an a putative hydrolase of the isochorismatase2 family (cv_1320) from chromobacterium violaceum atcc 12472 at 1.06 a3 resolution

12	c3hb7G_	Alignment		100.0	21	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**isochorismatase hydrolase; **PDBTitle:** the crystal structure of an isochorismatase-like hydrolase from2 alkaliphilus metalliredigens to 2.3a
13	c3eefA_	Alignment		100.0	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**n-carbamoylsarcosine amidase related protein; **PDBTitle:** crystal structure of n-carbamoylsarcosine amidase from thermoplasma2 acidophilum
14	d1im5a_	Alignment		100.0	20	**Fold:**Isochorismatase-like hydrolases **Superfamily:**Isochorismatase-like hydrolases **Family:**Isochorismatase-like hydrolases
15	c3r2jC_	Alignment		100.0	17	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**alpha/beta-hydrolase-like protein; **PDBTitle:** crystal structure of pnc1 from l. infantum in complex with nicotinate
16	c3lqyA_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative isochorismatase hydrolase; **PDBTitle:** crystal structure of putative isochorismatase hydrolase from2 oleispira antarctica
17	c3o93A_	Alignment		100.0	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nicotinamidase; **PDBTitle:** high resolution crystal structures of streptococcus pneumoniae2 nicotinamidase with trapped intermediates provide insights into3 catalytic mechanism and inhibition by aldehydes
18	c2wtaA_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nicotinamidase; **PDBTitle:** acinetobacter baumanii nicotinamidase pyrazinamidease
19	c3gbcA_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pyrazinamidase/nicotinamidas pnca; **PDBTitle:** determination of the crystal structure of the pyrazinamidase from2 m.tuberculosis : a structure-function analysis for prediction3 resistance to pyrazinamide
20	d1yaca_	Alignment		100.0	20	**Fold:**Isochorismatase-like hydrolases **Superfamily:**Isochorismatase-like hydrolases **Family:**Isochorismatase-like hydrolases
21	c2a67C_	Alignment	not modelled	100.0	20	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**isochorismatase family protein; **PDBTitle:** crystal structure of isochorismatase family protein
22	c2b34C_	Alignment	not modelled	100.0	21	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**mar1 ribonuclease; **PDBTitle:** structure of mar1 ribonuclease from caenorhabditis elegans
23	c1yzvA_	Alignment	not modelled	100.0	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** hypothetical protein from trypanosoma cruzi
24	d1x9ga_	Alignment	not modelled	100.0	16	**Fold:**Isochorismatase-like hydrolases **Superfamily:**Isochorismatase-like hydrolases **Family:**Isochorismatase-like hydrolases
25	c2h0rD_	Alignment	not modelled	100.0	18	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**nicotinamidase; **PDBTitle:** structure of the yeast nicotinamidase pnc1p
26	c2cq8A_	Alignment	not modelled	99.6	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**10-formyltetrahydrofolate dehydrogenase; **PDBTitle:** solution structure of rsgi ruh-033, a pp-binding domain of2 10-fthfdh from human cdna
27	c2jgpA_	Alignment	not modelled	99.6	23	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tyrocidine synthetase 3; **PDBTitle:** structure of the tycc5-6 pcp-c bidomain of the tyrocidine2 synthetase tycc
28	c2roqA_	Alignment	not modelled	99.6	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**enterobactin synthetase component f; **PDBTitle:** solution structure of the thiolation-thioesterase di-domain2 of enterobactin synthetase component f

29	c2vsqA_	Alignment	not modelled	99.6	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**surfactin synthetase subunit 3; **PDBTitle:** structure of surfactin a synthetase c (srfa-c), a2 nonribosomal peptide synthetase termination module
30	d2gdwa1	Alignment	not modelled	99.5	27	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**Peptidyl carrier domain
31	c2ju2A_	Alignment	not modelled	99.5	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**erythronolide synthase; **PDBTitle:** minimized mean solution structure of the acyl carrier2 protein domain from module 2 of 6-deoxyerythronolide b3 synthase (debs)
32	c2liuA_	Alignment	not modelled	99.5	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cura; **PDBTitle:** nmr structure of holo-acpi domain from cura module from lyngbya2 majuscula
33	c2afdA_	Alignment	not modelled	99.5	22	**PDB header:**ligand binding protein **Chain:** A: **PDB Molecule:**protein asl1650; **PDBTitle:** solution structure of asl1650, an acyl carrier protein from anabaena2 sp. pcc 7120 with a variant phosphopantetheinylation-site sequence
34	c2kr5A_	Alignment	not modelled	99.3	21	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**aflatoxin biosynthesis polyketide synthase; **PDBTitle:** solution structure of an acyl carrier protein domain from fungal type2 i polyketide synthase
35	d2af8a_	Alignment	not modelled	99.3	22	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**Acyl-carrier protein (ACP)
36	d1or5a_	Alignment	not modelled	99.3	15	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**Acyl-carrier protein (ACP)
37	c2ehtA_	Alignment	not modelled	99.3	19	**PDB header:**lipid transport **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** crystal structure of acyl carrier protein from aquifex aeolicus (form2 2)
38	d1nq4a_	Alignment	not modelled	99.3	17	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**Acyl-carrier protein (ACP)
39	d1vkua_	Alignment	not modelled	99.3	10	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**Acyl-carrier protein (ACP)
40	d1klpa_	Alignment	not modelled	99.3	21	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**Acyl-carrier protein (ACP)
41	d1t8ka_	Alignment	not modelled	99.2	17	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**Acyl-carrier protein (ACP)
42	c1x3oA_	Alignment	not modelled	99.2	16	**PDB header:**lipid transport **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** crystal structure of the acyl carrier protein from thermus2 thermophilus hb8
43	c2fq2A_	Alignment	not modelled	99.2	17	**PDB header:**lipid transport **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** solution structure of minor conformation of holo-acyl2 carrier protein from malaria parasite plasmodium falciparum
44	c2qnwA_	Alignment	not modelled	99.2	15	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** toxoplasma gondii apicoplast-targeted acyl carrier protein
45	c2cgqA_	Alignment	not modelled	99.2	17	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**acyl carrier protein acpa; **PDBTitle:** a putative acyl carrier protein(rv0033) from mycobacterium2 tuberculosis
46	c2l3vA_	Alignment	not modelled	99.2	15	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** nmr structure of acyl carrier protein from brucella melitensis
47	d1f80d_	Alignment	not modelled	99.2	9	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**Acyl-carrier protein (ACP)
48	c2cnrA_	Alignment	not modelled	99.1	17	**PDB header:**lipid transport **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** structural studies on the interaction of scfas acp with2 acps
49	d2pnga1	Alignment	not modelled	99.1	15	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**Acyl-carrier protein (ACP)
50	c3ejbC_	Alignment	not modelled	99.1	17	**PDB header:**oxidoreductase/lipid transport **Chain:** C: **PDB Molecule:**acyl carrier protein; **PDBTitle:** crystal structure of p450bioi in complex with tetradecanoic2 acid ligated acyl carrier protein
51	c2fvfA_	Alignment	not modelled	99.1	12	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** structure of 10:0-acp (protein with docked fatty acid)
52	c2jq4A_	Alignment	not modelled	99.1	20	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**hypothetical protein atu2571; **PDBTitle:** complete resonance assignments and solution structure2 calculation of atc2521 (nesg id: att6) from agrobacterium3 tumefaciens
53	d2jq4a1	Alignment	not modelled	99.1	20	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**Acyl-carrier protein (ACP)
54	c2l9fA_	Alignment	not modelled	99.0	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cale8;

						PDBTitle: nmr solution structure of meacp
55	c2dnwA_	Alignment	not modelled	99.0	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** solution structure of rsgi ruh-059, an acp domain of acyl2 carrier protein, mitochondrial [precursor] from human cdna
56	c2kciA_	Alignment	not modelled	99.0	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative acyl carrier protein; **PDBTitle:** solution nmr structure of gmet_2339 from geobacter2 metallireducens. northeast structural genomics consortium3 target gmr141
57	c2kwlA_	Alignment	not modelled	99.0	18	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** solution structure of acyl carrier protein from borrelia burgdorferi
58	c2l4bA_	Alignment	not modelled	99.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** solution structure of a putative acyl carrier protein from anaplasma2 phagocytophilum. seattle structural genomics center for infectious3 disease target anpha.01018.a
59	d1dv5a_	Alignment	not modelled	98.9	19	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**apo-D-alanyl carrier protein
60	c3lmoA_	Alignment	not modelled	98.7	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**specialized acyl carrier protein; **PDBTitle:** crystal structure of specialized acyl carrier protein2 (rpa2022) from rhodopseudomonas palustris, northeast3 structural genomics consortium target rpr324
61	c3ce7A_	Alignment	not modelled	98.6	10	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**specific mitochodrial acyl carrier protein; **PDBTitle:** crystal structure of toxoplasma specific mitochodrial acyl2 carrier protein, 59.m03510
62	c2vkzC_	Alignment	not modelled	95.4	5	**PDB header:**transferase **Chain:** C: **PDB Molecule:**fatty acid synthase subunit alpha; **PDBTitle:** structure of the cerulenin-inhibited fungal fatty acid2 synthase type i multienzyme complex
63	c2uv8C_	Alignment	not modelled	94.7	5	**PDB header:**transferase **Chain:** C: **PDB Molecule:**fatty acid synthase subunit alpha (fas2); **PDBTitle:** crystal structure of yeast fatty acid synthase with stalled2 acyl carrier protein at 3.1 angstrom resolution
64	c3s8mA_	Alignment	not modelled	92.9	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**enoyl-acp reductase; **PDBTitle:** the crystal structure of fabv
65	c2uv9B_	Alignment	not modelled	89.1	4	**PDB header:**transferase **Chain:** B: **PDB Molecule:**fatty acid synthase alpha subunits; **PDBTitle:** crystal structure of fatty acid synthase from thermomyces2 lanuginosus at 3.1 angstrom resolution. this file contains3 the alpha subunits of the fatty acid synthase. the entire4 crystal structure consists of one heterododecameric fatty5 acid synthase and is described in remark 400
66	d1xp8a1	Alignment	not modelled	77.0	6	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
67	d1cmwa2	Alignment	not modelled	76.6	17	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**5' to 3' exonuclease catalytic domain
68	d1f2da_	Alignment	not modelled	71.9	9	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
69	c1x1qA_	Alignment	not modelled	66.7	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**tryptophan synthase beta chain; **PDBTitle:** crystal structure of tryptophan synthase beta chain from thermus2 thermophilus hb8
70	d2zdra2	Alignment	not modelled	65.8	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**NeuB-like
71	c3bgwD_	Alignment	not modelled	63.6	14	**PDB header:**replication **Chain:** D: **PDB Molecule:**dnab-like replicative helicase; **PDBTitle:** the structure of a dnab-like replicative helicase and its interactions2 with primase
72	c1xuzA_	Alignment	not modelled	62.9	10	**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
73	c2iusB_	Alignment	not modelled	62.6	15	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**dna translocase ftsk; **PDBTitle:** e. coli ftsk motor domain
74	c2iutA_	Alignment	not modelled	59.0	15	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**dna translocase ftsk; **PDBTitle:** p. aeruginosa ftsk motor domain, dimeric
75	c2iuuE_	Alignment	not modelled	58.6	15	**PDB header:**membrane protein **Chain:** E: **PDB Molecule:**dna translocase ftsk; **PDBTitle:** p. aeruginosa ftsk motor domain, hexamer
76	c2recB_	Alignment	not modelled	58.0	11	**PDB header:**helicase **PDB COMPND:**
77	d1ubea1	Alignment	not modelled	56.7	6	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
						Fold: Pyruvate kinase C-terminal domain-like

78	d1vp8a_	Alignment	not modelled	56.2	19	**Superfamily:**PK C-terminal domain-like **Family:**MTH1675-like
79	c3g8rA_	Alignment	not modelled	55.7	12	**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
80	d1vlia2	Alignment	not modelled	55.2	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**NeuB-like
81	c2vyeA_	Alignment	not modelled	53.5	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**replicative dna helicase; **PDBTitle:** crystal structure of the dnac-ssdna complex
82	c1xp8A_	Alignment	not modelled	53.0	6	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**reca protein; **PDBTitle:** "deinococcus radiodurans reca in complex with atp-gamma-s"
83	c3cbwA_	Alignment	not modelled	48.4	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ydht protein; **PDBTitle:** crystal structure of the ydht protein from bacillus subtilis
84	c2ihnA_	Alignment	not modelled	45.9	7	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**ribonuclease h; **PDBTitle:** co-crystal of bacteriophage t4 rnase h with a fork dna2 substrate
85	d1xu9a_	Alignment	not modelled	44.7	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
86	d2ae2a_	Alignment	not modelled	44.6	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
87	c3nugA_	Alignment	not modelled	44.2	8	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-oxoacyl-(acyl-carrier protein) reductase; **PDBTitle:** crystal structure of wild type tetrameric pyridoxal 4-dehydrogenase2 from mesorhizobium loti
88	d1tfra2	Alignment	not modelled	42.3	7	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**5' to 3' exonuclease catalytic domain
89	c3ijrF_	Alignment	not modelled	42.2	17	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**oxidoreductase, short chain dehydrogenase/reductase family; **PDBTitle:** 2.05 angstrom resolution crystal structure of a short chain2 dehydrogenase from bacillus anthracis str. 'ames ancestor' in complex3 with nad+
90	d1ae1a_	Alignment	not modelled	41.8	11	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
91	d1gz6a_	Alignment	not modelled	41.7	10	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
92	d1xsea_	Alignment	not modelled	41.2	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
93	c2cvhB_	Alignment	not modelled	40.4	19	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**dna repair and recombination protein radb; **PDBTitle:** crystal structure of the radb recombinase
94	d2a4ka1	Alignment	not modelled	40.3	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
95	c2pd6D_	Alignment	not modelled	40.2	11	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**estradiol 17-beta-dehydrogenase 8; **PDBTitle:** structure of human hydroxysteroid dehydrogenase type 8, hsd17b8
96	c3ai3A_	Alignment	not modelled	40.2	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadph-sorbose reductase; **PDBTitle:** the crystal structure of l-sorbose reductase from gluconobacter2 frateurii complexed with nadph and l-sorbose
97	c1vliA_	Alignment	not modelled	39.5	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
98	d1mo6a1	Alignment	not modelled	37.2	6	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
99	d1e0ta2	Alignment	not modelled	37.2	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
100	c3bh0A_	Alignment	not modelled	37.0	13	**PDB header:**replication **Chain:** A: **PDB Molecule:**dnab-like replicative helicase; **PDBTitle:** atpase domain of g40p
101	c2nwqA_	Alignment	not modelled	36.8	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable short-chain dehydrogenase; **PDBTitle:** short chain dehydrogenase from pseudomonas aeruginosa
102	c2y8kA_	Alignment	not modelled	35.6	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**carbohydrate binding family 6; **PDBTitle:** structure of ctgh5-cbm6, an arabinoxylan-specific xylanase.
						PDB header:oxidoreductase

103	c2nm0B_	Alignment	not modelled	35.6	19	**Chain:** B: **PDB Molecule:**probable 3-oxacyl-(acyl-carrier-protein) reductase; **PDBTitle:** crystal structure of sco1815: a beta-ketoacyl-acyl carrier protein2 reductase from streptomyces coelicolor a3(2)
104	c3ldaA_	Alignment	not modelled	35.6	22	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna repair protein rad51; **PDBTitle:** yeast rad51 h352y filament interface mutant
105	c3toxG_	Alignment	not modelled	34.3	21	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**short chain dehydrogenase; **PDBTitle:** crystal structure of a short chain dehydrogenase in complex with2 nad(p) from sinorhizobium meliloti 1021
106	c3n7tA_	Alignment	not modelled	33.0	13	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**macrophage binding protein; **PDBTitle:** crystal structure of a macrophage binding protein from coccidioides2 immitis
107	d1pkla2	Alignment	not modelled	32.6	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
108	c2zroA_	Alignment	not modelled	32.1	7	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein reca; **PDBTitle:** msreca adp form iv
109	c3o26A_	Alignment	not modelled	31.3	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**salutaridine reductase; **PDBTitle:** the structure of salutaridine reductase from papaver somniferum.
110	d1wdea_	Alignment	not modelled	31.3	15	**Fold:**Tetrapyrrole methylase **Superfamily:**Tetrapyrrole methylase **Family:**Tetrapyrrole methylase
111	c3enoB_	Alignment	not modelled	30.1	21	**PDB header:**hydrolase/unknown function **Chain:** B: **PDB Molecule:**putative o-sialoglycoprotein endopeptidase; **PDBTitle:** crystal structure of pyrococcus furiosus pcc1 in complex2 with thermoplasma acidophilum kae1
112	d1a3xa2	Alignment	not modelled	30.1	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
113	c2dflA_	Alignment	not modelled	29.9	15	**PDB header:**recombination **Chain:** A: **PDB Molecule:**dna repair and recombination protein rada; **PDBTitle:** crystal structure of left-handed rada filament
114	c2b4qB_	Alignment	not modelled	28.8	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**rhamnolipids biosynthesis 3-oxoacyl-[acyl- **PDBTitle:** pseudomonas aeruginosa rhlg/nadp active-site complex
115	c2amwA_	Alignment	not modelled	28.4	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ne2163; **PDBTitle:** solution nmr structure of protein ne2163 from nitrosomonas europaea.2 northeast structural genomics consortium target net1.
116	c2lkiA_	Alignment	not modelled	28.4	13	**PDB header:**lipid transport **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** solution nmr structure of holo acyl carrier protein ne2163 from2 nitrosomonas europaea. northeast structural genomics consortium3 target net1.
117	d1o4wa_	Alignment	not modelled	28.2	37	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**PIN domain
118	d1qopb_	Alignment	not modelled	28.2	13	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
119	c3sjuA_	Alignment	not modelled	28.2	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**keto reductase; **PDBTitle:** hedamycin polyketide ketoreductase bound to nadph
120	d2pd4a1	Alignment	not modelled	27.8	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases