Phyre^2

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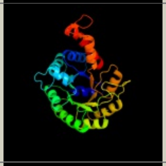
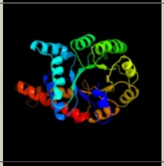
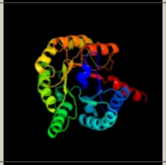
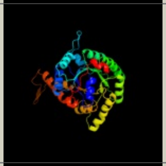
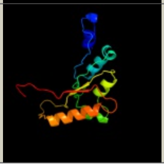
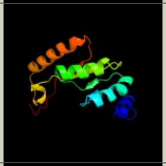
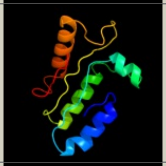
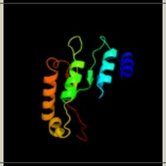
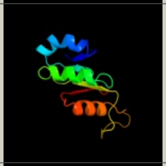
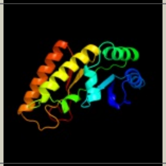
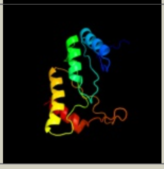
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2fiqa1	Alignment		100.0	53	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**GatZ-like
2	c3q94B_	Alignment		99.9	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**fructose-bisphosphate aldolase, class ii; **PDBTitle:** the crystal structure of fructose 1,6-bisphosphate aldolase from2 bacillus anthracis str. 'ames ancestor'
3	d1rvga_	Alignment		99.8	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class II FBP aldolase
4	d1dosa_	Alignment		99.8	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class II FBP aldolase
5	d1gvfa_	Alignment		99.8	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class II FBP aldolase
6	c3qm3C_	Alignment		99.8	18	**PDB header:**lyase **Chain:** C: **PDB Molecule:**fructose-bisphosphate aldolase; **PDBTitle:** 1.85 angstrom resolution crystal structure of fructose-bisphosphate2 aldolase (fba) from campylobacter jejuni
7	c3c52B_	Alignment		99.8	18	**PDB header:**lyase **Chain:** B: **PDB Molecule:**fructose-bisphosphate aldolase; **PDBTitle:** class ii fructose-1,6-bisphosphate aldolase from2 helicobacter pylori in complex with3 phosphoglycolohydroxamic acid, a competitive inhibitor
8	c3pm6B_	Alignment		99.8	20	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative fructose-bisphosphate aldolase; **PDBTitle:** crystal structure of a putative fructose-1,6-biphosphate aldolase from2 coccidioides immitis solved by combined sad mr
9	c3elfA_	Alignment		99.8	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**fructose-bisphosphate aldolase; **PDBTitle:** structural characterization of tetrameric mycobacterium tuberculosis2 fructose 1,6-bisphosphate aldolase - substrate binding and catalysis3 mechanism of a class iia bacterial aldolase
10	c2iswB_	Alignment		99.8	17	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative fructose-1,6-bisphosphate aldolase; **PDBTitle:** structure of giardia fructose-1,6-biphosphate aldolase in2 complex with phosphoglycolohydroxamate
11	d1f6ya_	Alignment		95.8	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Methyltetrahydrofolate-utiluzing methyltransferases

12	c3bolB_	Alignment		94.8	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**5-methyltetrahydrofolate s-homocysteine **PDBTitle:** cobalamin-dependent methionine synthase (1-566) from2 thermotoga maritima complexed with zn2+
13	d3bofa1	Alignment		93.6	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Methyltetrahydrofolate-utiluzing methyltransferases
14	c1rr2A_	Alignment		93.2	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transcarboxylase 5s subunit; **PDBTitle:** propionibacterium shermanii transcarboxylase 5s subunit bound to 2-2 ketobutyric acid
15	c3k13A_	Alignment		92.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**5-methyltetrahydrofolate-homocysteine methyltransferase; **PDBTitle:** structure of the pterin-binding domain metr of 5-2 methyltetrahydrofolate-homocysteine methyltransferase from3 bacteroides thetaiotaomicron
16	c2yciX_	Alignment		91.6	14	**PDB header:**transferase **Chain:** X: **PDB Molecule:**5-methyltetrahydrofolate corrinoid/iron sulfur protein **PDBTitle:** methyltransferase native
17	c2h9aA_	Alignment		91.6	33	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**carbon monoxide dehydrogenase corrinoid/iron- **PDBTitle:** corrinoid iron-sulfur protein
18	c2nx9B_	Alignment		91.3	13	**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
19	c3cqkB_	Alignment		87.7	11	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**l-ribulose-5-phosphate 3-epimerase ulae; **PDBTitle:** crystal structure of l-xylulose-5-phosphate 3-epimerase ulae (form b)2 complex with zn2+ and sulfate
20	c3k2gA_	Alignment		86.7	21	**PDB header:**resiniferatoxin binding protein **Chain:** A: **PDB Molecule:**resiniferatoxin-binding, phosphotriesterase- **PDBTitle:** crystal structure of a resiniferatoxin-binding protein from2 rhodobacter sphaeroides
21	c2vp8A_	Alignment	not modelled	86.5	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydropteroate synthase 2; **PDBTitle:** structure of mycobacterium tuberculosis rv1207
22	c2dzaA_	Alignment	not modelled	85.8	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydropteroate synthase; **PDBTitle:** crystal structure of dihydropteroate synthase from thermus2 thermophilus hb8 in complex with 4-aminobenzoate
23	c3lhlA_	Alignment	not modelled	85.1	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative agmatinase; **PDBTitle:** crystal structure of a putative agmatinase from clostridium difficile
24	c2ze3A_	Alignment	not modelled	83.6	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**dfa0005; **PDBTitle:** crystal structure of dfa0005 complexed with alpha-ketoglutarate: a2 novel member of the icl/pepm superfamily from alkali-tolerant3 deinococcus ficus
25	d1eyea_	Alignment	not modelled	82.4	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
26	d1muma_	Alignment	not modelled	81.4	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like
27	d1ad1a_	Alignment	not modelled	81.3	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
28	c2uvaI_	Alignment	not modelled	79.4	25	**PDB header:**transferase **Chain:** I: **PDB Molecule:**fatty acid synthase beta subunits; **PDBTitle:** crystal structure of fatty acid synthase from thermomyces2 lanuginosus at 3.1 angstrom resolution. this file contains3 the beta subunits of the fatty acid synthase. the entire4

						crystal structure consists of one heterododecameric fatty5 acid synthase and is described in remark 400
29	d2a0ma1	Alignment	not modelled	79.0	20	**Fold:**Arginase/deacetylase **Superfamily:**Arginase/deacetylase **Family:**Arginase-like amidino hydrolases
30	d1xfka_	Alignment	not modelled	77.8	20	**Fold:**Arginase/deacetylase **Superfamily:**Arginase/deacetylase **Family:**Arginase-like amidino hydrolases
31	c3o1lB_	Alignment	not modelled	77.3	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (pspto_4314)2 from pseudomonas syringae pv. tomato str. dc3000 at 2.20 a resolution
32	d2ceva_	Alignment	not modelled	77.1	24	**Fold:**Arginase/deacetylase **Superfamily:**Arginase/deacetylase **Family:**Arginase-like amidino hydrolases
33	c2vkzH_	Alignment	not modelled	76.9	20	**PDB header:**transferase **Chain:** H: **PDB Molecule:**fatty acid synthase subunit beta; **PDBTitle:** structure of the cerulenin-inhibited fungal fatty acid2 synthase type i multienzyme complex
34	d1gq6a_	Alignment	not modelled	76.4	18	**Fold:**Arginase/deacetylase **Superfamily:**Arginase/deacetylase **Family:**Arginase-like amidino hydrolases
35	c3nioF_	Alignment	not modelled	76.3	20	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**guanidinobutyrase; **PDBTitle:** crystal structure of pseudomonas aeruginosa guanidinobutyrase
36	c3nrbD_	Alignment	not modelled	76.0	16	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (puru,2 pp_1943) from pseudomonas putida kt2440 at 2.05 a resolution
37	d1vhna_	Alignment	not modelled	75.8	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
38	d1t4ba1	Alignment	not modelled	74.2	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
39	d1pq3a_	Alignment	not modelled	73.0	17	**Fold:**Arginase/deacetylase **Superfamily:**Arginase/deacetylase **Family:**Arginase-like amidino hydrolases
40	c2y5sA_	Alignment	not modelled	70.3	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydropteroate synthase; **PDBTitle:** crystal structure of burkholderia cenocepacia dihydropteroate2 synthase complexed with 7,8-dihydropteroate.
41	d1ajza_	Alignment	not modelled	69.8	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
42	d1tx2a_	Alignment	not modelled	67.6	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
43	c1tx2A_	Alignment	not modelled	67.6	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dhps, dihydropteroate synthase; **PDBTitle:** dihydropteroate synthetase, with bound inhibitor manic, from bacillus2 anthracis
44	c2hjpA_	Alignment	not modelled	66.9	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphonopyruvate hydrolase; **PDBTitle:** crystal structure of phosphonopyruvate hydrolase complex with2 phosphonopyruvate and mg++
45	c3obiC_	Alignment	not modelled	66.0	18	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (np_949368)2 from rhodopseudomonas palustris cga009 at 1.95 a resolution
46	c2qiwA_	Alignment	not modelled	66.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pep phosphonomutase; **PDBTitle:** crystal structure of a putative phosphoenolpyruvate phosphonomutase2 (ncgl1015, cgl1060) from corynebacterium glutamicum atcc 13032 at3 1.80 a resolution
47	c3nipB_	Alignment	not modelled	65.5	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**3-guanidinopropionase; **PDBTitle:** crystal structure of pseudomonas aeruginosa guanidinopropionase2 complexed with 1,6-diaminohexane
48	d1woha_	Alignment	not modelled	64.6	20	**Fold:**Arginase/deacetylase **Superfamily:**Arginase/deacetylase **Family:**Arginase-like amidino hydrolases
49	c3mmrA_	Alignment	not modelled	62.8	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**arginase; **PDBTitle:** structure of plasmodium falciparum arginase in complex with abh
50	c3louB_	Alignment	not modelled	62.4	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of formyltetrahydrofolate deformylase (yp_105254.1)2 from burkholderia mallei atcc 23344 at 1.90 a resolution
51	c3n0vD_	Alignment	not modelled	62.2	21	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (pp_0327)2 from pseudomonas putida kt2440 at 2.25 a resolution
52	d1aw1a_	Alignment	not modelled	61.2	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
53	c1vraB	Alignment	not modelled	58.4	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**arginine biosynthesis bifunctional protein argj;

		Alignment				**PDBTitle:** crystal structure of arginine biosynthesis bifunctional protein argj2 (10175521) from bacillus halodurans at 2.00 a resolution
54	c1ydnA_	Alignment	not modelled	58.3	12	**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.
55	c3it4B_	Alignment	not modelled	58.1	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**arginine biosynthesis bifunctional protein argj **PDBTitle:** the crystal structure of ornithine acetyltransferase from2 mycobacterium tuberculosis (rv1653) at 1.7 a
56	d2ihta3	Alignment	not modelled	56.6	31	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase PP module
57	c3r4iB_	Alignment	not modelled	56.3	4	**PDB header:**lyase **Chain:** B: **PDB Molecule:**citrate lyase; **PDBTitle:** crystal structure of a citrate lyase (bxe_b2899) from burkholderia2 xenovorans lb400 at 2.24 a resolution
58	c3lerA_	Alignment	not modelled	55.1	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 campylobacter jejuni subsp. jejuni nctc 11168
59	c1cqxB_	Alignment	not modelled	55.0	19	**PDB header:**lipid binding protein **Chain:** B: **PDB Molecule:**flavohemoprotein; **PDBTitle:** crystal structure of the flavohemoglobin from alcaligenes eutrophus at2 1.75 a resolution
60	d1pqua1	Alignment	not modelled	54.7	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
61	d2aeba1	Alignment	not modelled	52.4	22	**Fold:**Arginase/deacetylase **Superfamily:**Arginase/deacetylase **Family:**Arginase-like amidino hydrolases
62	c3pzlA_	Alignment	not modelled	51.9	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**agmatine ureohydrolase; **PDBTitle:** the crystal structure of agmatine ureohydrolase of thermoplasma2 volcanium
63	c3d0kA_	Alignment	not modelled	50.9	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative poly(3-hydroxybutyrate) depolymerase lpqc; **PDBTitle:** crystal structure of the lpqc, poly(3-hydroxybutyrate) depolymerase2 from bordetella parapertussis
64	d1mb4a1	Alignment	not modelled	49.7	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
65	c3dxiB_	Alignment	not modelled	48.8	12	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative aldolase; **PDBTitle:** crystal structure of the n-terminal domain of a putative2 aldolase (bvu_2661) from bacteroides vulgatus
66	d1yl7a1	Alignment	not modelled	48.5	24	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
67	c3m1rF_	Alignment	not modelled	48.3	23	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**formimidoylglutamase; **PDBTitle:** the crystal structure of formimidoylglutamase from bacillus2 subtilis subsp. subtilis str. 168
68	d1ujqa_	Alignment	not modelled	48.2	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like
69	d1d3va_	Alignment	not modelled	48.1	20	**Fold:**Arginase/deacetylase **Superfamily:**Arginase/deacetylase **Family:**Arginase-like amidino hydrolases
70	c3fdgA_	Alignment	not modelled	45.6	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dipeptidase ac. metallo peptidase. merops family m19; **PDBTitle:** the crystal structure of the dipeptidase ac, metallo peptidase. merops2 family m19
71	c3ez4B_	Alignment	not modelled	44.6	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**3-methyl-2-oxobutanoate hydroxymethyltransferase; **PDBTitle:** crystal structure of 3-methyl-2-oxobutanoate2 hydroxymethyltransferase from burkholderia pseudomallei
72	d1f16a_	Alignment	not modelled	43.7	15	**Fold:**Toxins' membrane translocation domains **Superfamily:**Bcl-2 inhibitors of programmed cell death **Family:**Bcl-2 inhibitors of programmed cell death
73	d1m6ja_	Alignment	not modelled	43.0	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
74	c3ai9X_	Alignment	not modelled	40.7	17	**PDB header:**transferase **Chain:** X: **PDB Molecule:**upf0217 protein mj1640; **PDBTitle:** crystal structure of duf358 protein reveals a putative spout-class2 rrna methyltransferase
75	c3gvgA_	Alignment	not modelled	40.3	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**triosephosphate isomerase; **PDBTitle:** crystal structure of triosephosphate isomerase from mycobacterium2 tuberculosis
76	c2vzkD_	Alignment	not modelled	40.1	18	**PDB header:**transferase **Chain:** D: **PDB Molecule:**glutamate n-acetyltransferase 2 beta chain; **PDBTitle:** structure of the acyl-enzyme complex of an n-terminal2 nucleophile (ntn) hydrolase, oat2
77	c3b8iF_	Alignment	not modelled	39.9	18	**PDB header:**lyase **Chain:** F: **PDB Molecule:**pa4872 oxaloacetate decarboxylase; **PDBTitle:** crystal structure of oxaloacetate decarboxylase from pseudomonas2 aeruginosa (pa4872) in complex with oxalate and mg2+.

78	c3bleA_	Alignment	not modelled	39.5	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**citramalate synthase from leptospira interrogans; **PDBTitle:** crystal structure of the catalytic domain of licms in2 complexed with malonate
79	c2h31A_	Alignment	not modelled	38.5	17	**PDB header:**ligase, lyase **Chain:** A: **PDB Molecule:**multifunctional protein ade2; **PDBTitle:** crystal structure of human paics, a bifunctional carboxylase and2 synthetase in purine biosynthesis
80	d2p02a1	Alignment	not modelled	38.5	16	**Fold:**S-adenosylmethionine synthetase **Superfamily:**S-adenosylmethionine synthetase **Family:**S-adenosylmethionine synthetase
81	d1trea_	Alignment	not modelled	37.7	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
82	c3tr9A_	Alignment	not modelled	37.6	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydropteroate synthase; **PDBTitle:** structure of a dihydropteroate synthase (folp) in complex with pteroic2 acid from coxiella burnetii
83	c1zorB_	Alignment	not modelled	36.6	10	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**isocitrate dehydrogenase; **PDBTitle:** isocitrate dehydrogenase from the hyperthermophile thermotoga maritima
84	c2gq0B_	Alignment	not modelled	36.3	16	**PDB header:**chaperone, hydrolase **Chain:** B: **PDB Molecule:**chaperone protein htpg; **PDBTitle:** crystal structure of the middle domain of htpg, the e. coli2 hsp90
85	c3gndC_	Alignment	not modelled	36.0	15	**PDB header:**lyase **Chain:** C: **PDB Molecule:**aldolase lsrf; **PDBTitle:** crystal structure of e. coli lsrf in complex with ribulose-5-phosphate
86	c1k87A_	Alignment	not modelled	35.5	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**proline dehydrogenase; **PDBTitle:** crystal structure of e.coli puta (residues 1-669)
87	c1y6zA_	Alignment	not modelled	35.2	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**heat shock protein, putative; **PDBTitle:** middle domain of plasmodium falciparum putative heat shock protein2 pf14_0417
88	c2h9aB_	Alignment	not modelled	33.8	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**co dehydrogenase/acetyl-coa synthase, iron- **PDBTitle:** corrinoid iron-sulfur protein
89	c2o1tB_	Alignment	not modelled	33.5	16	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**endoplasmin; **PDBTitle:** structure of middle plus c-terminal domains (m+c) of grp94
90	d1mxaa1	Alignment	not modelled	33.1	14	**Fold:**S-adenosylmethionine synthetase **Superfamily:**S-adenosylmethionine synthetase **Family:**S-adenosylmethionine synthetase
91	c2v1dA_	Alignment	not modelled	32.0	15	**PDB header:**oxidoreductase/repressor **Chain:** A: **PDB Molecule:**lysine-specific histone demethylase 1; **PDBTitle:** structural basis of lsd1-corest selectivity in histone h32 recognition
92	c3h7uA_	Alignment	not modelled	31.8	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldo-keto reductase; **PDBTitle:** crystal structure of the plant stress-response enzyme akr4c9
93	d1qm4a1	Alignment	not modelled	31.3	18	**Fold:**S-adenosylmethionine synthetase **Superfamily:**S-adenosylmethionine synthetase **Family:**S-adenosylmethionine synthetase
94	d1xima_	Alignment	not modelled	30.4	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
95	d2al1a1	Alignment	not modelled	30.3	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**Enolase
96	d2af4c1	Alignment	not modelled	30.2	12	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Phosphotransacetylase
97	d1vz6a_	Alignment	not modelled	30.1	17	**Fold:**DmpA/ArgJ-like **Superfamily:**DmpA/ArgJ-like **Family:**ArgJ-like
98	c4a1aH_	Alignment	not modelled	30.0	24	**PDB header:**ribosome **Chain:** H: **PDB Molecule:**60s ribosomal protein l10; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 3.
99	c3qc3B_	Alignment	not modelled	29.8	28	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**d-ribulose-5-phosphate-3-epimerase; **PDBTitle:** crystal structure of a d-ribulose-5-phosphate-3-epimerase (np_954699)2 from homo sapiens at 2.20 a resolution
100	d1t9ba3	Alignment	not modelled	29.7	19	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase PP module
101	c1yl7F_	Alignment	not modelled	29.5	24	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**dihydrodipicolinate reductase; **PDBTitle:** the crystal structure of mycobacterium tuberculosis2 dihydrodipicolinate reductase (rv2773c) in complex with nadh (crystal3 form c)
102	d1n8fa_	Alignment	not modelled	29.4	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I DAHP synthetase
103	d3clsc1	Alignment	not modelled	28.3	15	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits

104	c1vm6B_	Alignment	not modelled	28.2	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**dihydrodipicolinate reductase; **PDBTitle:** crystal structure of dihydrodipicolinate reductase (tm1520) from2 thermotoga maritima at 2.27 a resolution
105	c3ih1A_	Alignment	not modelled	28.1	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**methylisocitrate lyase; **PDBTitle:** crystal structure of carboxyvinyl-carboxyphosphonate phosphorylmutase2 from bacillus anthracis
106	d1s2wa_	Alignment	not modelled	28.0	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like
107	d1ixka_	Alignment	not modelled	27.4	29	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**NOL1/NOP2/sun
108	c1nofA_	Alignment	not modelled	27.2	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**xylanase; **PDBTitle:** the first crystallographic structure of a xylanase from2 glycosyl hydrolase family 5: implications for catalysis
109	c3m4xA_	Alignment	not modelled	26.9	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nol1/nop2/sun family protein; **PDBTitle:** structure of a ribosomal methyltransferase
110	c3v7nA_	Alignment	not modelled	26.4	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**threonine synthase; **PDBTitle:** crystal structure of threonine synthase (thrc) from from burkholderia2 thailandensis
111	c2qb5B_	Alignment	not modelled	25.8	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**inositol-tetrakisphosphate 1-kinase; **PDBTitle:** crystal structure of human inositol 1,3,4-trisphosphate 5/6-kinase2 (itpk1) in complex with adp and mn2+
112	d1e0ta2	Alignment	not modelled	25.6	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
113	d1oy0a_	Alignment	not modelled	25.3	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Ketopantoate hydroxymethyltransferase PanB
114	d2fyma1	Alignment	not modelled	25.3	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**Enolase
115	c3so4C_	Alignment	not modelled	25.2	14	**PDB header:**transferase **Chain:** C: **PDB Molecule:**methionine-adenosyltransferase; **PDBTitle:** methionine-adenosyltransferase from entamoeba histolytica
116	c1rg9D_	Alignment	not modelled	24.8	14	**PDB header:**transferase **Chain:** D: **PDB Molecule:**s-adenosylmethionine synthetase; **PDBTitle:** s-adenosylmethionine synthetase complexed with sam and ppnp
117	d1azta1	Alignment	not modelled	24.7	15	**Fold:**Transducin (alpha subunit), insertion domain **Superfamily:**Transducin (alpha subunit), insertion domain **Family:**Transducin (alpha subunit), insertion domain
118	d2ebna_	Alignment	not modelled	24.6	26	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Type II chitinase
119	c2e1mC_	Alignment	not modelled	24.1	18	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**l-glutamate oxidase; **PDBTitle:** crystal structure of l-glutamate oxidase from streptomyces sp. x-119-6
120	d1vm6a3	Alignment	not modelled	24.0	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain