Phyre2

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Description	P0AEZ1
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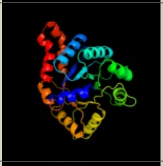
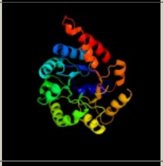
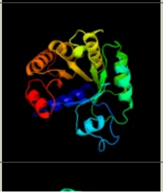
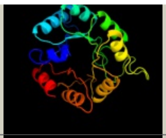
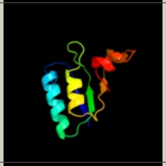
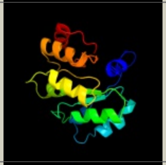
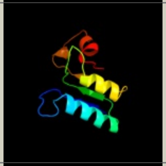
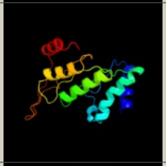
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1b5ta_	Alignment		100.0	100	**Fold:**TIM beta/alpha-barrel **Superfamily:**FAD-linked oxidoreductase **Family:**Methylenetetrahydrofolate reductase
2	d1v93a_	Alignment		100.0	36	**Fold:**TIM beta/alpha-barrel **Superfamily:**FAD-linked oxidoreductase **Family:**Methylenetetrahydrofolate reductase
3	c2fmoA_	Alignment		100.0	99	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**5,10-methylenetetrahydrofolate reductase; **PDBTitle:** ala177val mutant of e. coli methylenetetrahydrofolate2 reductase
4	c3ijdB_	Alignment		100.0	19	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** uncharacterized protein cthe_2304 from clostridium2 thermocellum binds two copies of 5-methyl-5,6,7,8-3 tetrahydrofolic acid
5	d1xcfa_	Alignment		97.7	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
6	c2ekcA_	Alignment		96.9	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**tryptophan synthase alpha chain; **PDBTitle:** structural study of project id aq_1548 from aquifex aeolicus vf5
7	d1rd5a_	Alignment		96.6	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
8	d1ujpa_	Alignment		96.5	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
9	c3navB_	Alignment		96.3	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**tryptophan synthase alpha chain; **PDBTitle:** crystal structure of an alpha subunit of tryptophan synthase from2 vibrio cholerae o1 biovar el tor str. n16961
10	d1qopa_	Alignment		96.1	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
11	c2p10D_	Alignment		95.8	13	**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

12	c3igsB_	Alignment		92.4	10	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**n-acetylmannosamine-6-phosphate 2-epimerase 2; **PDBTitle:** structure of the salmonella enterica n-acetylmannosamine-6-phosphate2 2-epimerase
13	d1x7fa2	Alignment		91.8	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Outer surface protein, N-terminal domain
14	d1j5ta_	Alignment		91.4	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
15	d1tqja_	Alignment		91.1	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
16	c3daqB_	Alignment		90.6	11	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from methicillin-2 resistant staphylococcus aureus
17	c1x7fA_	Alignment		90.2	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**outer surface protein; **PDBTitle:** crystal structure of an uncharacterized b. cereus protein
18	c2hmcA_	Alignment		89.9	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** the crystal structure of dihydrodipicolinate synthase dapa from2 agrobacterium tumefaciens
19	c2y85D_	Alignment		89.9	15	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**phosphoribosyl isomerase a; **PDBTitle:** crystal structure of mycobacterium tuberculosis phosphoribosyl2 isomerase with bound rcdrp
20	c2c3zA_	Alignment		89.3	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**indole-3-glycerol phosphate synthase; **PDBTitle:** crystal structure of a truncated variant of indole-3-2 glycerol phosphate synthase from sulfolobus solfataricus
21	c2yw3E_	Alignment	not modelled	89.2	14	**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
22	d1yxya1	Alignment	not modelled	88.9	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**NanE-like
23	c3thaB_	Alignment	not modelled	88.8	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**tryptophan synthase alpha chain; **PDBTitle:** tryptophan synthase subunit alpha from campylobacter jejuni.
24	d1h1ya_	Alignment	not modelled	88.1	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
25	c3cprB_	Alignment	not modelled	87.2	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthetase; **PDBTitle:** the crystal structure of corynebacterium glutamicum2 dihydrodipicolinate synthase to 2.2 a resolution
26	d2p10a1	Alignment	not modelled	86.9	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Mll9387-like
27	c3fluD_	Alignment	not modelled	86.0	15	**PDB header:**lyase **Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from the pathogen2 neisseria meningitidis
28	c3ct7E_	Alignment	not modelled	86.0	14	**PDB header:**isomerase **Chain:** E: **PDB Molecule:**d-allulose-6-phosphate 3-epimerase; **PDBTitle:** crystal structure of d-allulose 6-phosphate 3-epimerase2 from escherichia coli k-12
						PDB header:isomerase

29	c2oemA_	Alignment	not modelled	85.7	14	**Chain:** A: **PDB Molecule:**2,3-diketo-5-methylthiopentyl-1-phosphate enolase; **PDBTitle:** crystal structure of a rubisco-like protein from geobacillus2 kaustophilus liganded with mg2+ and 2,3-diketohexane 1-phosphate
30	d1xxxa1	Alignment	not modelled	85.6	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
31	c3s5oA_	Alignment	not modelled	84.9	10	**PDB header:**lyase **Chain:** A: **PDB Molecule:**4-hydroxy-2-oxoglutarate aldolase, mitochondrial; **PDBTitle:** crystal structure of human 4-hydroxy-2-oxoglutarate aldolase bound to2 pyruvate
32	c2rfgB_	Alignment	not modelled	83.9	17	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from hahella2 chejuensis at 1.5a resolution
33	c3pueA_	Alignment	not modelled	82.9	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of the complex of dhydrodipicolinate synthase from2 acinetobacter baumannii with lysine at 2.6a resolution
34	c3gr7A_	Alignment	not modelled	82.6	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadph dehydrogenase; **PDBTitle:** structure of oye from geobacillus kaustophilus, hexagonal2 crystal form
35	d1rpxa_	Alignment	not modelled	82.5	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
36	c3bi8A_	Alignment	not modelled	82.0	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** structure of dihydrodipicolinate synthase from clostridium2 botulinum
37	c1rr2A_	Alignment	not modelled	80.7	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transcarboxylase 5s subunit; **PDBTitle:** propionibacterium shermanii transcarboxylase 5s subunit bound to 2-2 ketobutyric acid
38	c3e96B_	Alignment	not modelled	80.4	10	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 bacillus clausii
39	c3na8A_	Alignment	not modelled	80.0	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative dihydrodipicolinate synthetase; **PDBTitle:** crystal structure of a putative dihydrodipicolinate synthetase from2 pseudomonas aeruginosa
40	c2nx9B_	Alignment	not modelled	79.8	17	**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
41	d1geqa_	Alignment	not modelled	79.6	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
42	c3labA_	Alignment	not modelled	79.6	12	**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
43	c3qjaA_	Alignment	not modelled	78.8	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**indole-3-glycerol phosphate synthase; **PDBTitle:** crystal structure of the mycobacterium tuberculosis indole-3-glycerol2 phosphate synthase (trpc) in apo form
44	d1mkza_	Alignment	not modelled	78.7	10	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
45	d1rvga_	Alignment	not modelled	76.6	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class II FBP aldolase
46	d2a6na1	Alignment	not modelled	75.8	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
47	c3d0cB_	Alignment	not modelled	75.4	17	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 oceanobacillus iheyensis at 1.9 a resolution
48	d1y5ea1	Alignment	not modelled	75.0	11	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
49	d1vc4a_	Alignment	not modelled	74.8	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
50	c3bolB_	Alignment	not modelled	74.2	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**5-methyltetrahydrofolate s-homocysteine **PDBTitle:** cobalamin-dependent methionine synthase (1-566) from2 thermotoga maritima complexed with zn2+
51	c2qgqF_	Alignment	not modelled	73.4	9	**PDB header:**structural genomics, unknown function **Chain:** F: **PDB Molecule:**protein tm_1862; **PDBTitle:** crystal structure of tm_1862 from thermotoga maritima.2 northeast structural genomics consortium target vr77
52	d1vzwa1	Alignment	not modelled	73.4	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
53	c3g0sA_	Alignment	not modelled	72.2	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** dihydrodipicolinate synthase from salmonella typhimurium lt2
						PDB header:unknown function

54	c3kwlA_	Alignment	not modelled	70.8	10	**Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a hypothetical protein from helicobacter pylori
55	c1kwgA_	Alignment	not modelled	70.7	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-galactosidase; **PDBTitle:** crystal structure of thermus thermophilus a4 beta-galactosidase
56	d2flia1	Alignment	not modelled	70.2	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
57	c3qfeB_	Alignment	not modelled	70.0	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative dihydrodipicolinate synthase family protein; **PDBTitle:** crystal structures of a putative dihydrodipicolinate synthase family2 protein from coccidioides immitis
58	d1a9xa4	Alignment	not modelled	68.5	20	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
59	d1mxsa_	Alignment	not modelled	67.9	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
60	c3lciA_	Alignment	not modelled	67.0	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**n-acetylneuraminate lyase; **PDBTitle:** the d-sialic acid aldolase mutant v251w
61	c3rfqC_	Alignment	not modelled	65.5	14	**PDB header:**biosynthetic protein **Chain:** C: **PDB Molecule:**pterin-4-alpha-carbinolamine dehydratase moab2; **PDBTitle:** crystal structure of pterin-4-alpha-carbinolamine dehydratase moab22 from mycobacterium marinum
62	d1vyra_	Alignment	not modelled	65.4	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
63	c3inpA_	Alignment	not modelled	64.7	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**d-ribulose-phosphate 3-epimerase; **PDBTitle:** 2.05 angstrom resolution crystal structure of d-ribulose-phosphate 3-2 epimerase from francisella tularensis.
64	d1xkya1	Alignment	not modelled	64.6	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
65	c2vc6A_	Alignment	not modelled	64.2	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** structure of mosa from s. meliloti with pyruvate bound
66	c1zlpA_	Alignment	not modelled	64.0	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**petal death protein; **PDBTitle:** petal death protein psr132 with cysteine-linked glutaraldehyde forming2 a thiohemiacetal adduct
67	c3ih1A_	Alignment	not modelled	63.7	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**methylisocitrate lyase; **PDBTitle:** crystal structure of carboxyvinyl-carboxyphosphonate phosphorylmutase2 from bacillus anthracis
68	c2r8wB_	Alignment	not modelled	63.2	8	**PDB header:**lyase **Chain:** B: **PDB Molecule:**agr_c_1641p; **PDBTitle:** the crystal structure of dihydrodipicolinate synthase (atu0899) from2 agrobacterium tumefaciens str. c58
69	c3dxiB_	Alignment	not modelled	62.8	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
70	c3eb2A_	Alignment	not modelled	61.6	10	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative dihydrodipicolinate synthetase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 rhodopseudomonas palustris at 2.0a resolution
71	d1muma_	Alignment	not modelled	59.9	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like
72	d1piia2	Alignment	not modelled	59.8	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
73	c3o8nA_	Alignment	not modelled	58.8	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**6-phosphofructokinase, muscle type; **PDBTitle:** structure of phosphofructokinase from rabbit skeletal muscle
74	d1rbla1	Alignment	not modelled	58.5	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**RuBisCo, C-terminal domain **Family:**RuBisCo, large subunit, C-terminal domain
75	c2zviB_	Alignment	not modelled	57.8	14	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**2,3-diketo-5-methylthiopentyl-1-phosphate **PDBTitle:** crystal structure of 2,3-diketo-5-methylthiopentyl-1-2 phosphate enolase from bacillus subtilis
76	d1yx1a1	Alignment	not modelled	57.4	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**KguE-like
77	c3e05B_	Alignment	not modelled	56.1	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**precorrin-6y c5,15-methyltransferase (decarboxylating); **PDBTitle:** crystal structure of precorrin-6y c5,15-methyltransferase from2 geobacter metallireducens gs-15
78	c2ftpA_	Alignment	not modelled	54.6	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**hydroxymethylglutaryl-coa lyase; **PDBTitle:** crystal structure of hydroxymethylglutaryl-coa lyase from pseudomonas2 aeruginosa
79	c2yxgD_	Alignment	not modelled	54.4	17	**PDB header:**lyase **Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihyrodipicolinate synthase (dapa)

80	c3b9bA_	Alignment	not modelled	54.3	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sarcoplasmic/endoplasmic reticulum calcium **PDBTitle:** structure of the e2 beryllium fluoride complex of the serca2 ca2+-atpase
81	c3ivuB_	Alignment	not modelled	53.3	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**homocitrate synthase, mitochondrial; **PDBTitle:** homocitrate synthase lys4 bound to 2-og
82	c2vcbA_	Alignment	not modelled	53.3	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-n-acetylglucosaminidase; **PDBTitle:** family 89 glycoside hydrolase from clostridium perfringens2 in complex with pugnac
83	d1w3ia_	Alignment	not modelled	52.0	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
84	c2cw6B_	Alignment	not modelled	51.3	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**hydroxymethylglutaryl-coa lyase, mitochondrial; **PDBTitle:** crystal structure of human hmg-coa lyase: insights into2 catalysis and the molecular basis for3 hydroxymethylglutaric aciduria
85	c3qc3B_	Alignment	not modelled	50.9	13	**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
86	c2wamB_	Alignment	not modelled	50.8	17	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**conserved hypothetical alanine and leucine rich **PDBTitle:** crystal structure of mycobacterium tuberculosis unknown2 function protein rv2714
87	c2nuxB_	Alignment	not modelled	49.8	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**2-keto-3-deoxygluconate/2-keto-3-deoxy-6-phospho gluconate **PDBTitle:** 2-keto-3-deoxygluconate aldolase from sulfolobus acidocaldarius,2 native structure in p6522 at 2.5 a resolution
88	c3qfwB_	Alignment	not modelled	49.7	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**ribulose-1,5-bisphosphate carboxylase/oxygenase large **PDBTitle:** crystal structure of rubisco-like protein from rhodopseudomonas2 palustris
89	c3t7vA_	Alignment	not modelled	49.5	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methylornithine synthase pylb; **PDBTitle:** crystal structure of methylornithine synthase (pylb)
90	d1xi8a3	Alignment	not modelled	49.5	16	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
91	c1m6vE_	Alignment	not modelled	47.9	17	**PDB header:**ligase **Chain:** E: **PDB Molecule:**carbamoyl phosphate synthetase large chain; **PDBTitle:** crystal structure of the g359f (small subunit) point mutant of2 carbamoyl phosphate synthetase
92	c1yadD_	Alignment	not modelled	47.6	10	**PDB header:**transcription **Chain:** D: **PDB Molecule:**regulatory protein teni; **PDBTitle:** structure of teni from bacillus subtilis
93	d2b6fa1	Alignment	not modelled	46.8	15	**Fold:**ParB/Sulfiredoxin **Superfamily:**ParB/Sulfiredoxin **Family:**Sulfiredoxin-like
94	c1ydoC_	Alignment	not modelled	44.9	12	**PDB header:**lyase **Chain:** C: **PDB Molecule:**hmg-coa lyase; **PDBTitle:** crystal structure of the bacillis subtilis hmg-coa lyase, northeast2 structural genomics target sr181.
95	c2is8A_	Alignment	not modelled	43.7	16	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**molybdopterin biosynthesis enzyme, moab; **PDBTitle:** crystal structure of the molybdopterin biosynthesis enzyme moab2 (ttha0341) from thermus theromophilus hb8
96	c3sdsA_	Alignment	not modelled	43.5	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase, mitochondrial; **PDBTitle:** crystal structure of a mitochondrial ornithine carbamoyltransferase2 from coccidioides immitis
97	c1rldB_	Alignment	not modelled	43.4	11	**PDB header:**lyase(carbon-carbon) **Chain:** B: **PDB Molecule:**ribulose 1,5 bisphosphate carboxylase/oxygenase (large **PDBTitle:** solid-state phase transition in the crystal structure of ribulose 1,5-2 biphosphate carboxylase(slash)oxygenase
98	c2bdqA_	Alignment	not modelled	43.2	11	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**copper homeostasis protein cutc; **PDBTitle:** crystal structure of the putative copper homeostasis2 protein cutc from streptococcus agalactiae, northeast3 strucural genomics target sar15.
99	c2h6rG_	Alignment	not modelled	42.9	16	**PDB header:**isomerase **Chain:** G: **PDB Molecule:**triosephosphate isomerase; **PDBTitle:** crystal structure of triosephosphate isomerase (tim) from2 methanocaldococcus jannaschii
100	c2v9dB_	Alignment	not modelled	42.8	9	**PDB header:**lyase **Chain:** B: **PDB Molecule:**yage; **PDBTitle:** crystal structure of yage, a prophage protein belonging to2 the dihydrodipicolinic acid synthase family from e. coli3 k12
101	c3kc2A_	Alignment	not modelled	40.9	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized protein ykr070w; **PDBTitle:** crystal structure of mitochondrial had-like phosphatase from2 saccharomyces cerevisiae
102	c1ydnA_	Alignment	not modelled	40.5	16	**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.
						PDB header:hydrolase

103	c3b8cB_	Alignment	not modelled	39.9	14	**Chain:** B: **PDB Molecule:**atpase 2, plasma membrane-type; **PDBTitle:** crystal structure of a plasma membrane proton pump
104	c2p0oA_	Alignment	not modelled	39.9	10	**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
105	c3bleA_	Alignment	not modelled	39.4	8	**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
106	c1xc6A_	Alignment	not modelled	39.3	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-galactosidase; **PDBTitle:** native structure of beta-galactosidase from penicillium sp. in complex2 with galactose
107	d1s2wa_	Alignment	not modelled	38.7	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like
108	c3e0vB_	Alignment	not modelled	38.7	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of pyruvate kinase from leishmania mexicana in2 complex with sulphate ions
109	c3gaaB_	Alignment	not modelled	38.5	12	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein ta1441; **PDBTitle:** the crystal structure of the protein with unknown function from2 thermoplasma acidophilum
110	d1q6oa_	Alignment	not modelled	38.3	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Decarboxylase
111	d1to3a_	Alignment	not modelled	37.7	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
112	d2gdwa1	Alignment	not modelled	37.4	11	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**Peptidyl carrier domain
113	c3fk4A_	Alignment	not modelled	36.6	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**rubisco-like protein; **PDBTitle:** crystal structure of rubisco-like protein from bacillus2 cereus atcc 14579
114	c1u83A_	Alignment	not modelled	36.5	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**phosphosulfolactate synthase; **PDBTitle:** psl synthase from bacillus subtilis
115	d1u83a_	Alignment	not modelled	36.5	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(2r)-phospho-3-sulfolactate synthase ComA **Family:**(2r)-phospho-3-sulfolactate synthase ComA
116	d2tpsa_	Alignment	not modelled	36.1	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Thiamin phosphate synthase **Family:**Thiamin phosphate synthase
117	d2o3aa1	Alignment	not modelled	35.9	27	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**AF0751-like
118	c2ejaB_	Alignment	not modelled	35.0	8	**PDB header:**lyase **Chain:** B: **PDB Molecule:**uroporphyrinogen decarboxylase; **PDBTitle:** crystal structure of uroporphyrinogen decarboxylase from2 aquifex aeolicus
119	c3ewbX_	Alignment	not modelled	34.7	9	**PDB header:**transferase **Chain:** X: **PDB Molecule:**2-isopropylmalate synthase; **PDBTitle:** crystal structure of n-terminal domain of putative 2-2 isopropylmalate synthase from listeria monocytogenes
120	d1pkla2	Alignment	not modelled	34.5	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase