Phyre2

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Description	P0AEI4
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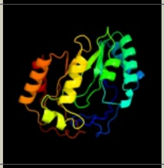
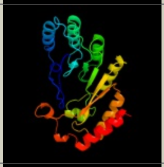
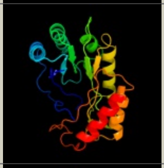
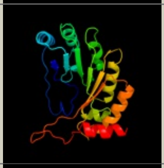
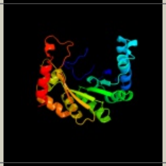
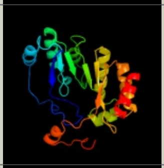
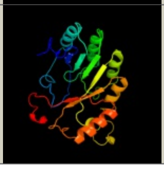
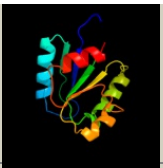
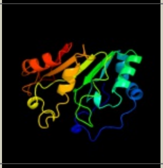
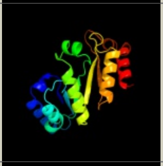
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2qgqF_	Alignment		100.0	37	**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
2	c3cixA_	Alignment		100.0	20	**PDB header:**adomet binding protein **Chain:** A: **PDB Molecule:**fefe-hydrogenase maturase; **PDBTitle:** x-ray structure of the [fefe]-hydrogenase maturase hyde from2 thermotoga maritima in complex with thiocyanate
3	d1olta_	Alignment		100.0	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Radical SAM enzymes **Family:**Oxygen-independent coproporphyrinogen III oxidase HemN
4	c3t7vA_	Alignment		100.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methylornithine synthase pylb; **PDBTitle:** crystal structure of methylornithine synthase (pylb)
5	d1r30a_	Alignment		99.9	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Radical SAM enzymes **Family:**Biotin synthase
6	c1r30A_	Alignment		99.9	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**biotin synthase; **PDBTitle:** the crystal structure of biotin synthase, an s-2 adenosylmethionine-dependent radical enzyme
7	c3rfaA_	Alignment		99.8	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ribosomal rna large subunit methyltransferase n; **PDBTitle:** x-ray structure of rlmn from escherichia coli in complex with s-2 adenosylmethionine
8	d1tv8a_	Alignment		99.7	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Radical SAM enzymes **Family:**MoCo biosynthesis proteins
9	c2yx0A_	Alignment		99.7	15	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**radical sam enzyme; **PDBTitle:** crystal structure of p. horikoshii tyw1
10	c3c8fA_	Alignment		99.5	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pyruvate formate-lyase 1-activating enzyme; **PDBTitle:** 4fe-4s-pyruvate formate-lyase activating enzyme with2 partially disordered adomet
11	c2a5hC_	Alignment		99.3	14	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**l-lysine 2,3-aminomutase; **PDBTitle:** 2.1 angstrom x-ray crystal structure of lysine-2,3-aminomutase from2 clostridium subterminale sb4, with michaelis analog (l-alpha-lysine3 external aldimine form of pyridoxal-5'-phosphate).

12	d7reqa2	Alignment		97.6	18	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
13	d1ccwa_	Alignment		97.2	16	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
14	c2z2uA_	Alignment		96.9	16	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**upf0026 protein mj0257; **PDBTitle:** crystal structure of archaeal tyw1
15	c1y80A_	Alignment		96.7	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**predicted cobalamin binding protein; **PDBTitle:** structure of a corrinoid (factor iiim)-binding protein from2 moorella thermoacetica
16	c3canA_	Alignment		96.6	14	**PDB header:**lyase activator **Chain:** A: **PDB Molecule:**pyruvate-formate lyase-activating enzyme; **PDBTitle:** crystal structure of a domain of pyruvate-formate lyase-activating2 enzyme from bacteroides vulgatus atcc 8482
17	c1e1cA_	Alignment		96.6	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**methylmalonyl-coa mutase alpha chain; **PDBTitle:** methylmalonyl-coa mutase h244a mutant
18	c2yxbA_	Alignment		96.5	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**coenzyme b12-dependent mutase; **PDBTitle:** crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
19	d3bula2	Alignment		96.4	8	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
20	d1fmfa_	Alignment		96.1	19	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
21	c2i2xD_	Alignment	not modelled	95.9	12	**PDB header:**transferase **Chain:** D: **PDB Molecule:**methyltransferase 1; **PDBTitle:** crystal structure of methanol:cobalamin methyltransferase complex2 mtabc from methanosarcina barkeri
22	c3ivuB_	Alignment	not modelled	95.3	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**homocitrate synthase, mitochondrial; **PDBTitle:** homocitrate synthase lys4 bound to 2-og
23	c3ezxA_	Alignment	not modelled	94.6	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**monomethylamine corrinoid protein 1; **PDBTitle:** structure of methanosarcina barkeri monomethylamine2 corrinoid protein
24	c3bicA_	Alignment	not modelled	94.3	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**methylmalonyl-coa mutase, mitochondrial precursor; **PDBTitle:** crystal structure of human methylmalonyl-coa mutase
25	c1bmtB_	Alignment	not modelled	94.0	8	**PDB header:**methyltransferase **Chain:** B: **PDB Molecule:**methionine synthase; **PDBTitle:** how a protein binds b12: a 3.0 angstrom x-ray structure of2 the b12-binding domains of methionine synthase
26	c6reqB_	Alignment	not modelled	92.7	10	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**protein (methylmalonyl-coa mutase); **PDBTitle:** methylmalonyl-coa mutase, 3-carboxypropyl-coa inhibitor complex
27	d1xrsb1	Alignment	not modelled	92.1	17	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
28	d1yvca1	Alignment	not modelled	91.6	26	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**TRAM domain
						Fold:OB-fold

29	d1yeza1	Alignment	not modelled	91.4	30	**Superfamily:**Nucleic acid-binding proteins **Family:**TRAM domain
30	c1xrsB_	Alignment	not modelled	91.3	15	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**d-lysine 5,6-aminomutase beta subunit; **PDBTitle:** crystal structure of lysine 5,6-aminomutase in complex with plp,2 cobalamin, and 5'-deoxyadenosine
31	c2ftpA_	Alignment	not modelled	90.3	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**hydroxymethylglutaryl-coa lyase; **PDBTitle:** crystal structure of hydroxymethylglutaryl-coa lyase from pseudomonas2 aeruginosa
32	c3npgD_	Alignment	not modelled	89.9	16	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**uncharacterized duf364 family protein; **PDBTitle:** crystal structure of a protein with unknown function from duf3642 family (ph1506) from pyrococcus horikoshii at 2.70 a resolution
33	d1ad1a_	Alignment	not modelled	89.7	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
34	c3ewbX_	Alignment	not modelled	89.6	10	**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
35	c3r0jA_	Alignment	not modelled	89.5	17	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**possible two component system response transcriptional **PDBTitle:** structure of phop from mycobacterium tuberculosis
36	c3bleA_	Alignment	not modelled	89.3	12	**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
37	c2bdqA_	Alignment	not modelled	89.3	16	**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.
38	c2cw6B_	Alignment	not modelled	88.3	11	**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
39	d1ajza_	Alignment	not modelled	88.1	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
40	c1k98A_	Alignment	not modelled	87.7	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methionine synthase; **PDBTitle:** adomet complex of meth c-terminal fragment
41	d1nvma2	Alignment	not modelled	87.6	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**HMGL-like
42	d1ys7a2	Alignment	not modelled	87.1	11	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
43	c1nvmG_	Alignment	not modelled	87.0	12	**PDB header:**lyase/oxidoreductase **Chain:** G: **PDB Molecule:**4-hydroxy-2-oxovalerate aldolase; **PDBTitle:** crystal structure of a bifunctional aldolase-dehydrogenase :2 sequestering a reactive and volatile intermediate
44	c3khdC_	Alignment	not modelled	86.4	12	**PDB header:**transferase **Chain:** C: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of pff1300w.
45	d1h4pa_	Alignment	not modelled	86.2	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
46	c3eegB_	Alignment	not modelled	85.9	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**2-isopropylmalate synthase; **PDBTitle:** crystal structure of a 2-isopropylmalate synthase from2 cytophaga hutchinsonii
47	d2h1qa1	Alignment	not modelled	85.9	17	**Fold:**PLP-dependent transferase-like **Superfamily:**Dhaf3308-like **Family:**Dhaf3308-like
48	c1ydnA_	Alignment	not modelled	85.3	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.
49	d1mvoa_	Alignment	not modelled	84.6	15	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
50	c2hk1D_	Alignment	not modelled	84.1	11	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**d-psicose 3-epimerase; **PDBTitle:** crystal structure of d-psicose 3-epimerase (dpease) in the presence of2 d-fructose
51	c3hpxB_	Alignment	not modelled	83.3	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**2-isopropylmalate synthase; **PDBTitle:** crystal structure of mycobacterium tuberculosis leua active site2 domain 1-425 (truncation mutant delta:426-644)
52	d1t3ta2	Alignment	not modelled	82.0	15	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
53	d1eyea_	Alignment	not modelled	79.9	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
54	d2ix0a3	Alignment	not modelled	79.4	26	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like

55	d7reqb2	Alignment	not modelled	78.4	12	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
56	d1k77a_	Alignment	not modelled	78.4	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Hypothetical protein YgbM (EC1530)
57	d1ny5a1	Alignment	not modelled	76.9	19	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
58	c3f6cB_	Alignment	not modelled	75.4	11	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**positive transcription regulator evga; **PDBTitle:** crystal structure of n-terminal domain of positive transcription2 regulator evga from escherichia coli
59	d1f6ya_	Alignment	not modelled	75.0	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Methyltetrahydrofolate-utiluzing methyltransferases
60	c3ct7E_	Alignment	not modelled	74.8	11	**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
61	c3cfyA_	Alignment	not modelled	74.3	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative luxo repressor protein; **PDBTitle:** crystal structure of signal receiver domain of putative luxo2 repressor protein from vibrio parahaemolyticus
62	c3hdvB_	Alignment	not modelled	73.6	20	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator receiver protein from2 pseudomonas putida
63	c2yw3E_	Alignment	not modelled	73.3	21	**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
64	c3cu2A_	Alignment	not modelled	72.5	10	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribulose-5-phosphate 3-epimerase; **PDBTitle:** crystal structure of ribulose-5-phosphate 3-epimerase (yp_718263.1)2 from haemophilus somnus 129pt at 1.91 a resolution
65	d1krwa_	Alignment	not modelled	72.5	12	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
66	c3dx5A_	Alignment	not modelled	71.2	10	**PDB header:**lyase **Chain:** A: **PDB Molecule:**uncharacterized protein asbf; **PDBTitle:** crystal structure of the probable 3-dhs dehydratase asbf involved in2 the petrobactin synthesis from bacillus anthracis
67	c3grcD_	Alignment	not modelled	70.7	15	**PDB header:**transferase **Chain:** D: **PDB Molecule:**sensor protein, kinase; **PDBTitle:** crystal structure of a sensor protein from polaromonas sp.2 js666
68	c3dxiB_	Alignment	not modelled	70.7	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
69	d1x7fa2	Alignment	not modelled	70.5	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Outer surface protein, N-terminal domain
70	d1xima_	Alignment	not modelled	69.0	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
71	d1uwva1	Alignment	not modelled	68.4	17	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**TRAM domain
72	c2zwmA_	Alignment	not modelled	67.3	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulatory protein yycf; **PDBTitle:** crystal structure of yycf receiver domain from bacillus2 subtilis
73	c1x7fA_	Alignment	not modelled	67.3	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**outer surface protein; **PDBTitle:** crystal structure of an uncharacterized b. cereus protein
74	c3lteH_	Alignment	not modelled	67.3	14	**PDB header:**transcription **Chain:** H: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator (signal receiver domain) from2 bermanella marisrubri
75	d1itua_	Alignment	not modelled	67.0	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Renal dipeptidase
76	d1xhfa1	Alignment	not modelled	66.8	16	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
77	d2pb1a1	Alignment	not modelled	65.6	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
78	c2zyfA_	Alignment	not modelled	65.6	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**homocitrate synthase; **PDBTitle:** crystal structure of homocitrate synthase from thermus thermophilus2 complexed with magnesuim ion and alpha-ketoglutarate
79	d1w25a1	Alignment	not modelled	65.4	14	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
80	c2jgqB_	Alignment	not modelled	65.4	8	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**triosephosphate isomerase; **PDBTitle:** kinetics and structural properties of triosephosphate2

						isomerase from helicobacter pylori
81	d1zgza1	Alignment	not modelled	64.5	20	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
82	c2rdmB_	Alignment	not modelled	64.2	18	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of response regulator receiver protein from2 sinorhizobium medicae wsm419
83	d1qmga2	Alignment	not modelled	63.9	29	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
84	d1u2za_	Alignment	not modelled	63.7	23	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Catalytic, N-terminal domain of histone methyltransferase Dot1l
85	d1u0sy_	Alignment	not modelled	63.6	10	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
86	c3itcA_	Alignment	not modelled	63.3	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**renal dipeptidase; **PDBTitle:** crystal structure of sco3058 with bound citrate and glycerol
87	c2yciX_	Alignment	not modelled	63.0	11	**PDB header:**transferase **Chain:** X: **PDB Molecule:**5-methyltetrahydrofolate corrinoid/iron sulfur protein **PDBTitle:** methyltransferase native
88	c3dfuB_	Alignment	not modelled	62.9	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**uncharacterized protein from 6-phosphogluconate **PDBTitle:** crystal structure of a putative rossmann-like dehydrogenase (cgl2689)2 from corynebacterium glutamicum at 2.07 a resolution
89	d2a9pa1	Alignment	not modelled	62.6	17	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
90	c3jteA_	Alignment	not modelled	62.5	15	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of response regulator receiver domain2 protein from clostridium thermocellum
91	d2pl1a1	Alignment	not modelled	62.4	14	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
92	d1nw3a_	Alignment	not modelled	61.7	18	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Catalytic, N-terminal domain of histone methyltransferase Dot1l
93	c1nw3A_	Alignment	not modelled	61.7	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histone methyltransferase dot1l; **PDBTitle:** structure of the catalytic domain of human dot1l, a non-set2 domain nucleosomal histone methyltransferase
94	c3c24A_	Alignment	not modelled	61.4	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of a putative oxidoreductase (yp_511008.1) from2 jannaschia sp. ccs1 at 1.62 a resolution
95	d1liua2	Alignment	not modelled	61.3	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
96	d1peya_	Alignment	not modelled	60.9	15	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
97	d1ka9h_	Alignment	not modelled	60.5	21	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
98	d1eiwa_	Alignment	not modelled	60.4	20	**Fold:**Flavodoxin-like **Superfamily:**Hypothetical protein MTH538 **Family:**Hypothetical protein MTH538
99	d1qopa_	Alignment	not modelled	60.4	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
100	c1zfjA_	Alignment	not modelled	60.1	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**inosine monophosphate dehydrogenase; **PDBTitle:** inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
101	c3hn2A_	Alignment	not modelled	60.1	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2-dehydropantoate 2-reductase; **PDBTitle:** crystal structure of 2-dehydropantoate 2-reductase from geobacter2 metallireducens gs-15
102	c2p10D_	Alignment	not modelled	59.2	20	**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
103	c3tr9A_	Alignment	not modelled	58.8	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydropteroate synthase; **PDBTitle:** structure of a dihydropteroate synthase (folp) in complex with pteroic2 acid from coxiella burnetii
104	d1gpma2	Alignment	not modelled	58.6	13	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
105	c3ktoA_	Alignment	not modelled	58.6	11	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of response regulator receiver protein2 from pseudoalteromonas atlantica

106	c1ydoC_	Alignment	not modelled	57.9	14	**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.
107	d1p2fa2	Alignment	not modelled	57.5	17	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
108	c2rjnA_	Alignment	not modelled	57.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**response regulator receiver:metal-dependent **PDBTitle:** crystal structure of an uncharacterized protein q2bku2 from2 neptuniibacter caesariensis
109	c2nt3A_	Alignment	not modelled	56.5	12	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator homolog; **PDBTitle:** receiver domain from myxococcus xanthus social motility protein frzs2 (y102a mutant)
110	c2ou4C_	Alignment	not modelled	56.4	12	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**d-tagatose 3-epimerase; **PDBTitle:** crystal structure of d-tagatose 3-epimerase from2 pseudomonas cichorii
111	c1u5tA_	Alignment	not modelled	56.3	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**appears to be functionally related to snf7; **PDBTitle:** structure of the escrt-ii endosomal trafficking complex
112	c3fdgA_	Alignment	not modelled	55.9	21	**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
113	d1qkka_	Alignment	not modelled	55.6	16	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
114	c3cqkB_	Alignment	not modelled	55.4	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
115	d1pdza1	Alignment	not modelled	55.2	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**Enolase
116	c2c3yA_	Alignment		55.1	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pyruvate-ferredoxin oxidoreductase; **PDBTitle:** crystal structure of the radical form of2 pyruvate:ferredoxin oxidoreductase from desulfovibrio3 africanus
117	d1tx2a_	Alignment	not modelled	54.5	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
118	c1tx2A_	Alignment	not modelled	54.5	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dhps, dihydropteroate synthase; **PDBTitle:** dihydropteroate synthetase, with bound inhibitor manic, from bacillus2 anthracis
119	d1gvia3	Alignment	not modelled	54.4	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
120	d1muma_	Alignment	not modelled	53.8	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like