Phyre^2

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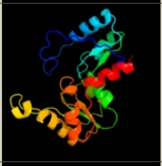
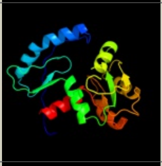
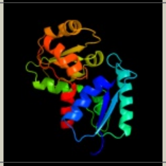
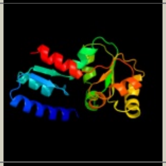
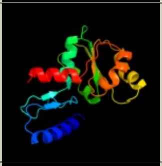
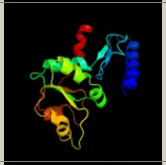
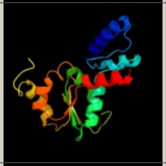
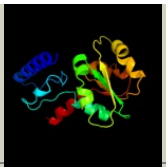
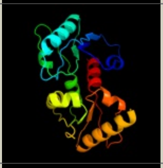
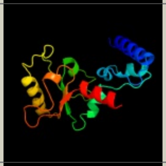
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2vlbC_	Alignment		99.4	19	**PDB header:**lyase **Chain:** C: **PDB Molecule:**arylmalonate decarboxylase; **PDBTitle:** structure of unliganded arylmalonate decarboxylase
2	c3qvjB_	Alignment		98.8	13	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative hydantoin racemase; **PDBTitle:** allantoin racemase from klebsiella pneumoniae
3	c2dgdD_	Alignment		98.8	16	**PDB header:**lyase **Chain:** D: **PDB Molecule:**223aa long hypothetical arylmalonate decarboxylase; **PDBTitle:** crystal structure of st0656, a function unknown protein from2 sulfolobus tokodaii
4	c2eq5D_	Alignment		98.6	18	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**228aa long hypothetical hydantoin racemase; **PDBTitle:** crystal structure of hydantoin racemase from pyrococcus horikoshii ot3
5	c2xecD_	Alignment		98.5	15	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**putative maleate isomerase; **PDBTitle:** nocardia farcinica maleate cis-trans isomerase bound to2 tris
6	c2gzmB_	Alignment		97.9	17	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of the glutamate racemase from bacillus2 anthracis
7	c3outC_	Alignment		97.9	16	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of glutamate racemase from francisella tularensis2 subsp. tularensis schu s4 in complex with d-glutamate.
8	c2dwuA_	Alignment		97.8	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of glutamate racemase isoform race1 from bacillus2 anthracis
9	c1b74A_	Alignment		97.8	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase; **PDBTitle:** glutamate racemase from aquifex pyrophilus
10	c2jfoB_	Alignment		97.7	13	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of enterococcus faecalis glutamate2 racemase in complex with d- and l-glutamate
11	c3s81A_	Alignment		97.7	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative aspartate racemase; **PDBTitle:** crystal structure of putative aspartate racemase from salmonella2 typhimurium

12	c3hfrA_	Alignment		97.5	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of glutamate racemase from listeria monocytogenes
13	c2jfqA_	Alignment		97.5	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of staphylococcus aureus glutamate2 racemase in complex with d-glutamate
14	c1zuwA_	Alignment		97.3	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase 1; **PDBTitle:** crystal structure of b.subtilis glutamate racemase (race) with d-glu
15	c2ohoA_	Alignment		97.2	20	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase; **PDBTitle:** structural basis for glutamate racemase inhibitor
16	c2jfzB_	Alignment		96.8	11	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of helicobacter pylori glutamate racemase2 in complex with d-glutamate and an inhibitor
17	c3ojcD_	Alignment		96.6	20	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**putative aspartate/glutamate racemase; **PDBTitle:** crystal structure of a putative asp/glu racemase from yersinia pestis
18	c2dx7B_	Alignment		96.4	14	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**aspartate racemase; **PDBTitle:** crystal structure of pyrococcus horikoshii ot3 aspartate racemase2 complex with citric acid
19	c2zskA_	Alignment		96.1	15	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**226aa long hypothetical aspartate racemase; **PDBTitle:** crystal structure of ph1733, an aspartate racemase2 homologue, from pyrococcus horikoshii ot3
20	c2jfnA_	Alignment		95.5	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of escherichia coli glutamate racemase2 in complex with l-glutamate and activator udp-murnac-ala
21	c3bg3B_	Alignment	not modelled	93.2	15	**PDB header:**ligase **Chain:** B: **PDB Molecule:**pyruvate carboxylase, mitochondrial; **PDBTitle:** crystal structure of human pyruvate carboxylase (missing2 the biotin carboxylase domain at the n-terminus)
22	c3ez4B_	Alignment	not modelled	91.3	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**3-methyl-2-oxobutanoate hydroxymethyltransferase; **PDBTitle:** crystal structure of 3-methyl-2-oxobutanoate2 hydroxymethyltransferase from burkholderia pseudomallei
23	d1oy0a_	Alignment	not modelled	90.4	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Ketopantoate hydroxymethyltransferase PanB
24	d1m3ua_	Alignment	not modelled	90.4	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Ketopantoate hydroxymethyltransferase PanB
25	c1nvmG_	Alignment	not modelled	88.6	18	**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
26	d1jfla1	Alignment	not modelled	88.3	26	**Fold:**ATC-like **Superfamily:**Aspartate/glutamate racemase **Family:**Aspartate/glutamate racemase
27	d1nvma2	Alignment	not modelled	88.0	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**HMGL-like
28	c2hqbA_	Alignment	not modelled	86.8	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional activator of comk gene; **PDBTitle:** crystal structure of a transcriptional activator of comk2 gene from bacillus halodurans

29	c3bleA_	Alignment	not modelled	86.1	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
30	d1jfla2	Alignment	not modelled	84.0	20	**Fold:**ATC-like **Superfamily:**Aspartate/glutamate racemase **Family:**Aspartate/glutamate racemase
31	d1muma_	Alignment	not modelled	83.6	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like
32	d2dx7a1	Alignment	not modelled	81.6	19	**Fold:**ATC-like **Superfamily:**Aspartate/glutamate racemase **Family:**Aspartate/glutamate racemase
33	d1j8yf2	Alignment	not modelled	81.3	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
34	d1sr9a2	Alignment	not modelled	80.3	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**HMGL-like
35	d2ajta2	Alignment	not modelled	78.4	11	**Fold:**FucI/AraA N-terminal and middle domains **Superfamily:**FucI/AraA N-terminal and middle domains **Family:**AraA N-terminal and middle domain-like
36	c3s5oA_	Alignment	not modelled	77.5	15	**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
37	c3a23A_	Alignment	not modelled	74.4	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative secreted alpha-galactosidase; **PDBTitle:** crystal structure of beta-l-arabinopyranosidase complexed with d-2 galactose
38	c2og2A_	Alignment	not modelled	71.2	16	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**putative signal recognition particle receptor; **PDBTitle:** crystal structure of chloroplast ftsy from arabidopsis2 thaliana
39	c2ftpA_	Alignment	not modelled	70.2	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**hydroxymethylglutaryl-coa lyase; **PDBTitle:** crystal structure of hydroxymethylglutaryl-coa lyase from pseudomonas2 aeruginosa
40	c3dhyC_	Alignment	not modelled	69.4	22	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**adenosylhomocysteinase; **PDBTitle:** crystal structures of mycobacterium tuberculosis s-adenosyl-l-2 homocysteine hydrolase in ternary complex with substrate and3 inhibitors
41	c2wdfA_	Alignment	not modelled	69.3	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sulfur oxidation protein soxb; **PDBTitle:** termus thermophilus sulfate thiohydrolase soxb
42	d2p10a1	Alignment	not modelled	68.9	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Mll9387-like
43	d1tqja_	Alignment	not modelled	68.9	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
44	c1ydnA_	Alignment	not modelled	66.3	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.
45	c2vc6A_	Alignment	not modelled	65.2	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** structure of mosa from s. meliloti with pyruvate bound
46	d1b74a2	Alignment	not modelled	64.9	11	**Fold:**ATC-like **Superfamily:**Aspartate/glutamate racemase **Family:**Aspartate/glutamate racemase
47	c3h5dD_	Alignment	not modelled	64.8	15	**PDB header:**lyase **Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** dihydrodipicolinate synthase from drug-resistant streptococcus2 pneumoniae
48	c3zu0A_	Alignment	not modelled	64.2	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nad nucleotidase; **PDBTitle:** structure of haemophilus influenzae nad nucleotidase (nadn)
49	c3navB_	Alignment	not modelled	64.0	15	**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
50	c2z1aA_	Alignment	not modelled	63.4	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**5'-nucleotidase; **PDBTitle:** crystal structure of 5'-nucleotidase precursor from thermus2 thermophilus hb8
51	c3eooL_	Alignment	not modelled	63.0	18	**PDB header:**lyase **Chain:** L: **PDB Molecule:**methylisocitrate lyase; **PDBTitle:** 2.9a crystal structure of methyl-isocitrate lyase from2 burkholderia pseudomallei
52	c3dmdA_	Alignment	not modelled	62.6	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**signal recognition particle receptor; **PDBTitle:** structures and conformations in solution of the signal recognition2 particle receptor from the archaeon pyrococcus furiosus
53	d1o66a_	Alignment	not modelled	61.4	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Ketopantoate hydroxymethyltransferase PanB
						PDB header:lyase

54	c3dz1A_	Alignment	not modelled	61.1	11	**Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 rhodopseudomonas palustris at 1.87a resolution
55	c3e96B_	Alignment	not modelled	60.1	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 bacillus clausii
56	c3ivuB_	Alignment	not modelled	60.0	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**homocitrate synthase, mitochondrial; **PDBTitle:** homocitrate synthase lys4 bound to 2-og
57	c2p10D_	Alignment	not modelled	58.8	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
58	c1zlpA_	Alignment	not modelled	58.6	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**petal death protein; **PDBTitle:** petal death protein psr132 with cysteine-linked glutaraldehyde forming2 a thiohemiacetal adduct
59	c1zfjA_	Alignment	not modelled	57.8	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**inosine monophosphate dehydrogenase; **PDBTitle:** inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
60	c3o1hB_	Alignment	not modelled	56.3	13	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**periplasmic protein tort; **PDBTitle:** crystal structure of the tors sensor domain - tort complex in the2 presence of tmao
61	c2cnwF_	Alignment	not modelled	56.0	19	**PDB header:**signal recognition **Chain:** F: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** gdpalf4 complex of the srp gtpases ffh and ftsy
62	d1g2oa_	Alignment	not modelled	55.5	16	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
63	c2vsnB_	Alignment	not modelled	54.9	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**xcogt; **PDBTitle:** structure and topological arrangement of an o-glcnac2 transferase homolog: insight into molecular control of3 intracellular glycosylation
64	c2j7pA_	Alignment	not modelled	54.5	16	**PDB header:**signal recognition **Chain:** A: **PDB Molecule:**signal recognition particle protein; **PDBTitle:** gmppnp-stabilized ng domain complex of the srp gtpases ffh2 and ftsy
65	c3hcwB_	Alignment	not modelled	54.4	13	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**maltose operon transcriptional repressor; **PDBTitle:** crystal structure of probable maltose operon transcriptional repressor2 malr from staphylococcus areus
66	c3bg5C_	Alignment	not modelled	53.9	11	**PDB header:**ligase **Chain:** C: **PDB Molecule:**pyruvate carboxylase; **PDBTitle:** crystal structure of staphylococcus aureus pyruvate2 carboxylase
67	d1chma1	Alignment	not modelled	53.7	8	**Fold:**Ribonuclease H-like motif **Superfamily:**Creatinase/prolidase N-terminal domain **Family:**Creatinase/prolidase N-terminal domain
68	c3lrmB_	Alignment	not modelled	52.7	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-galactosidase 1; **PDBTitle:** structure of alfa-galactosidase from saccharomyces cerevisiae with2 raffinose
69	c2qygC_	Alignment	not modelled	52.6	16	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**ribulose bisphosphate carboxylase-like protein 2; **PDBTitle:** crystal structure of a rubisco-like protein rlp2 from rhodopseudomonas2 palustris
70	c1yb2A_	Alignment	not modelled	51.8	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ta0852; **PDBTitle:** structure of a putative methyltransferase from thermoplasma2 acidophilum.
71	d1yb2a1	Alignment	not modelled	51.8	10	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**tRNA(1-methyladenosine) methyltransferase-like
72	c3daqB_	Alignment	not modelled	51.3	25	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from methicillin-2 resistant staphylococcus aureus
73	d1ykwa1	Alignment	not modelled	50.9	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**RuBisCo, C-terminal domain **Family:**RuBisCo, large subunit, C-terminal domain
74	c3gndC_	Alignment	not modelled	50.5	14	**PDB header:**lyase **Chain:** C: **PDB Molecule:**aldolase lsrf; **PDBTitle:** crystal structure of e. coli lsrf in complex with ribulose-5-phosphate
75	c3lyeA_	Alignment	not modelled	50.1	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**oxaloacetate acetyl hydrolase; **PDBTitle:** crystal structure of oxaloacetate acetylhydrolase
76	c3lciA_	Alignment	not modelled	49.8	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**n-acetylneuraminate lyase; **PDBTitle:** the d-sialic acid aldolase mutant v251w
77	d1li4a2	Alignment	not modelled	48.1	13	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**S-adenosylhomocystein hydrolase
78	c3pe3D_	Alignment	not modelled	47.9	12	**PDB header:**transferase **Chain:** D: **PDB Molecule:**udp-n-acetylglucosamine--peptide n- **PDBTitle:** structure of human o-glcnac transferase and its complex with a peptide2 substrate
						Fold: Flavodoxin-like **Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole

79	d1o4va_	Alignment	not modelled	47.5	20	carboxylase, PurE) **Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
80	c3n58D_	Alignment	not modelled	47.4	18	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**adenosylhomocysteinase; **PDBTitle:** crystal structure of s-adenosyl-l-homocysteine hydrolase from brucella2 melitensis in ternary complex with nad and adenosine, orthorhombic3 form
81	c1xuzA_	Alignment	not modelled	47.2	19	**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
82	d1fuia2	Alignment	not modelled	47.0	3	**Fold:**FucI/AraA N-terminal and middle domains **Superfamily:**FucI/AraA N-terminal and middle domains **Family:**L-fucose isomerase, N-terminal and second domains
83	c3s99A_	Alignment	not modelled	46.9	14	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**basic membrane lipoprotein; **PDBTitle:** crystal structure of a basic membrane lipoprotein from brucella2 melitensis, iodide soak
84	d1dbqa_	Alignment	not modelled	45.9	11	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
85	d2zdra2	Alignment	not modelled	45.5	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**NeuB-like
86	d1meoa_	Alignment	not modelled	44.6	9	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
87	d1b74a1	Alignment	not modelled	44.5	22	**Fold:**ATC-like **Superfamily:**Aspartate/glutamate racemase **Family:**Aspartate/glutamate racemase
88	c2qiwA_	Alignment	not modelled	44.3	20	**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
89	c3gv0A_	Alignment	not modelled	43.8	11	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, laci family; **PDBTitle:** crystal structure of laci family transcription regulator from2 agrobacterium tumefaciens
90	c3fluD_	Alignment	not modelled	43.3	13	**PDB header:**lyase **Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from the pathogen2 neisseria meningitidis
91	c2ehhE_	Alignment	not modelled	43.1	10	**PDB header:**lyase **Chain:** E: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 aquifex aeolicus
92	c3raoB_	Alignment	not modelled	43.1	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative luciferase-like monooxygenase; **PDBTitle:** crystal structure of the luciferase-like monooxygenase from bacillus2 cereus atcc 10987.
93	c3fkkA_	Alignment	not modelled	42.5	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**l-2-keto-3-deoxyarabonate dehydratase; **PDBTitle:** structure of l-2-keto-3-deoxyarabonate dehydratase
94	c2qmoA_	Alignment	not modelled	41.5	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**dethiobiotin synthetase; **PDBTitle:** crystal structure of dethiobiotin synthetase (biod) from helicobacter2 pylori
95	c3g8rA_	Alignment	not modelled	41.1	19	**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
96	c1telA_	Alignment	not modelled	41.0	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ribulose bisphosphate carboxylase, large subunit; **PDBTitle:** crystal structure of a rubisco-like protein from chlorobium2 tepidum
97	c2yv4A_	Alignment	not modelled	40.9	14	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**hypothetical protein ph0435; **PDBTitle:** crystal structure of c-terminal sua5 domain from pyrococcus horikoshii2 hypothetical sua5 protein ph0435
98	d2z1aa2	Alignment	not modelled	40.8	24	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain
99	d1tlfa_	Alignment	not modelled	40.5	18	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
100	c3eegB_	Alignment	not modelled	40.3	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**2-isopropylmalate synthase; **PDBTitle:** crystal structure of a 2-isopropylmalate synthase from2 cytophaga hutchinsonii
101	d1ps9a1	Alignment	not modelled	39.8	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
102	d1hl2a_	Alignment	not modelled	37.8	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
103	c3h14A_	Alignment	not modelled	37.6	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminotransferase, classes i and ii; **PDBTitle:** crystal structure of a putative aminotransferase from silicibacter2 pomeroyi

104	d1h1ya_	Alignment	not modelled	36.7	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
105	c3fa4D_	Alignment	not modelled	36.4	23	**PDB header:**lyase **Chain:** D: **PDB Molecule:**2,3-dimethylmalate lyase; **PDBTitle:** crystal structure of 2,3-dimethylmalate lyase, a pep mutase/isocitrate2 lyase superfamily member, triclinic crystal form
106	c3si9B_	Alignment	not modelled	36.2	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from bartonella2 henselae
107	c3gveB_	Alignment	not modelled	36.1	27	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**yfkn protein; **PDBTitle:** crystal structure of calcineurin-like phosphoesterase yfkn from2 bacillus subtilis
108	c3gkaB_	Alignment	not modelled	35.7	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**n-ethylmaleimide reductase; **PDBTitle:** crystal structure of n-ethylmaleimidine reductase from2 burkholderia pseudomallei
109	d1ujqa_	Alignment	not modelled	35.5	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like
110	c3b9qA_	Alignment	not modelled	35.2	18	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**chloroplast srp receptor homolog, alpha subunit **PDBTitle:** the crystal structure of cpftsy from arabidopsis thaliana
111	c2h31A_	Alignment	not modelled	35.0	11	**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
112	c3d64A_	Alignment	not modelled	34.8	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adenosylhomocysteinase; **PDBTitle:** crystal structure of s-adenosyl-l-homocysteine hydrolase from2 burkholderia pseudomallei
113	c3eb2A_	Alignment	not modelled	34.7	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative dihydrodipicolinate synthetase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 rhodopseudomonas palustris at 2.0a resolution
114	d1nqka_	Alignment	not modelled	34.5	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Bacterial luciferase-like **Family:**Ssud-like monoxygenases
115	d1v8ba2	Alignment	not modelled	34.3	6	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**S-adenosylhomocystein hydrolase
116	d1qcza_	Alignment	not modelled	34.0	12	**Fold:**Flavodoxin-like **Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) **Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
117	c1j8yF_	Alignment	not modelled	33.2	18	**PDB header:**signaling protein **Chain:** F: **PDB Molecule:**signal recognition 54 kda protein; **PDBTitle:** signal recognition particle conserved gtpase domain from a.2 ambivalens t112a mutant
118	c3d0cB_	Alignment	not modelled	33.1	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 oceanobacillus iheyensis at 1.9 a resolution
119	c2rfgB_	Alignment	not modelled	32.4	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from hahella2 chejuensis at 1.5a resolution
120	c3noeA_	Alignment	not modelled	32.1	8	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from pseudomonas2 aeruginosa