Phyre2

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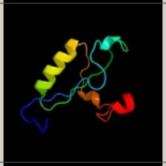
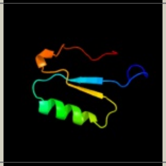
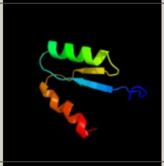
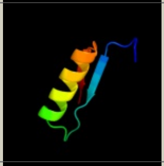
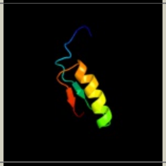
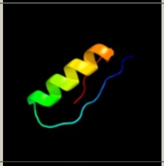
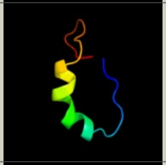
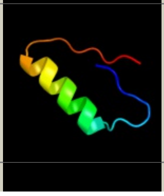
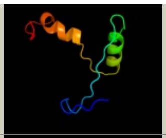
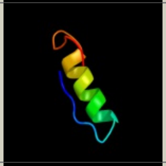
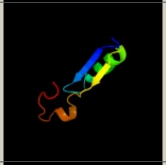
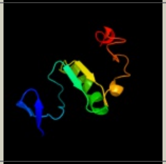
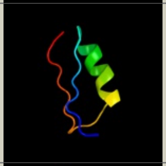
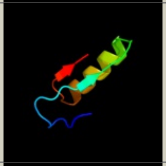
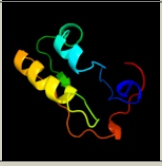
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2vq3B_	Alignment		98.2	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**metalloreductase steap3; **PDBTitle:** crystal structure of the membrane proximal oxidoreductase2 domain of human steap3, the dominant ferric reductase of3 the erythroid transferrin cycle
2	c3dttA_	Alignment		98.0	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadp oxidoreductase; **PDBTitle:** crystal structure of a putative f420 dependent nadp-reductase2 (arth_0613) from arthrobacter sp. fb24 at 1.70 a resolution
3	c2rafC_	Alignment		97.8	15	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative dinucleotide-binding oxidoreductase; **PDBTitle:** crystal structure of putative dinucleotide-binding2 oxidoreductase (np_786167.1) from lactobacillus plantarum3 at 1.60 a resolution
4	d1jaya_	Alignment		97.8	25	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
5	d1wdka3	Alignment		78.2	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
6	d3cuma2	Alignment		71.9	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
7	c3d1lB_	Alignment		70.3	5	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative nadp oxidoreductase bf3122; **PDBTitle:** crystal structure of putative nadp oxidoreductase bf3122 from2 bacteroides fragilis
8	c3b0vD_	Alignment		69.6	19	**PDB header:**oxidoreductase/rna **Chain:** D: **PDB Molecule:**trna-dihydrouridine synthase; **PDBTitle:** trna-dihydrouridine synthase from thermus thermophilus in complex with2 trna
9	d1pgja2	Alignment		64.4	6	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
10	d1vpda2	Alignment		57.6	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
11	d1f0ya2	Alignment		52.3	10	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain

12	c2f6rA_	Alignment		45.6	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bifunctional coenzyme a synthase; **PDBTitle:** crystal structure of bifunctional coenzyme a synthase (coa synthase):2 (18044849) from mus musculus at 1.70 a resolution
13	d1mv8a2	Alignment		43.2	4	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
14	c3s5pA_	Alignment		40.2	26	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose 5-phosphate isomerase; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase b rpib from giardia2 lamblia
15	c2yv3B_	Alignment		37.0	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aspartate-semialdehyde dehydrogenase; **PDBTitle:** crystal structure of aspartate semialdehyde dehydrogenase from thermus2 thermophilus hb8
16	d2cvza2	Alignment		36.4	25	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
17	d1nn4a_	Alignment		31.8	15	**Fold:**Ribose/Galactose isomerase RpiB/AlsB **Superfamily:**Ribose/Galactose isomerase RpiB/AlsB **Family:**Ribose/Galactose isomerase RpiB/AlsB
18	d1vhna_	Alignment		31.4	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
19	d1i36a2	Alignment		28.2	8	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
20	d1yt8a4	Alignment		27.5	15	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
21	c3he8A_	Alignment	not modelled	26.1	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase; **PDBTitle:** structural study of clostridium thermocellum ribose-5-phosphate2 isomerase b
22	c3i2vA_	Alignment	not modelled	26.0	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenylyltransferase and sulfurtransferase mocs3; **PDBTitle:** crystal structure of human mocs3 rhodanese-like domain
23	d1xrsb2	Alignment	not modelled	25.4	5	**Fold:**Dodecin subunit-like **Superfamily:**D-lysine 5,6-aminomutase beta subunit KamE, N-terminal domain **Family:**D-lysine 5,6-aminomutase beta subunit KamE, N-terminal domain
24	d1b25a1	Alignment	not modelled	22.6	19	**Fold:**Aldehyde ferredoxin oxidoreductase, C-terminal domains **Superfamily:**Aldehyde ferredoxin oxidoreductase, C-terminal domains **Family:**Aldehyde ferredoxin oxidoreductase, C-terminal domains
25	c3aaxB_	Alignment	not modelled	21.6	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative thiosulfate sulfurtransferase; **PDBTitle:** crystal structure of probable thiosulfate sulfurtransferase2 cysa3 (rv3117) from mycobacterium tuberculosis: monoclinic3 form
26	d2vvpa1	Alignment	not modelled	21.6	27	**Fold:**Ribose/Galactose isomerase RpiB/AlsB **Superfamily:**Ribose/Galactose isomerase RpiB/AlsB **Family:**Ribose/Galactose isomerase RpiB/AlsB
27	d1t4aa_	Alignment	not modelled	21.2	8	**Fold:**PurS-like **Superfamily:**PurS-like **Family:**PurS subunit of FGAM synthetase
28	d1umka2	Alignment	not modelled	20.0	12	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases

29	d2i76a2	Alignment	not modelled	19.7	9	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
30	c2zayA_	Alignment	not modelled	19.4	16	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of response regulator from desulfuromonas2 acetoxidans
31	c2yx5A_	Alignment	not modelled	19.1	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0062 protein mj1593; **PDBTitle:** crystal structure of methanocaldococcus jannaschii purs, one of the2 subunits of formylglycinamide ribonucleotide amidotransferase in the3 purine biosynthetic pathway
32	d3bula2	Alignment	not modelled	18.8	10	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
33	d2pgda2	Alignment	not modelled	18.5	11	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
34	d2a9pa1	Alignment	not modelled	17.1	11	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
35	d1aora1	Alignment	not modelled	17.0	15	**Fold:**Aldehyde ferredoxin oxidoreductase, C-terminal domains **Superfamily:**Aldehyde ferredoxin oxidoreductase, C-terminal domains **Family:**Aldehyde ferredoxin oxidoreductase, C-terminal domains
36	d1qx4a2	Alignment	not modelled	16.9	10	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
37	c3kevA_	Alignment	not modelled	16.3	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**galieria sulfuraria dcun1 domain-containing protein; **PDBTitle:** x-ray crystal structure of a dcun1 domain-containing protein from2 galdieria sulfuraria
38	c3dzbA_	Alignment	not modelled	15.9	2	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**prephenate dehydrogenase; **PDBTitle:** crystal structure of prephenate dehydrogenase from streptococcus2 thermophilus
39	c3hpxB_	Alignment	not modelled	15.9	18	**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)
40	c1bmtB_	Alignment	not modelled	15.8	13	**PDB header:**methyltransferase **Chain:** B: **PDB Molecule:**methionine synthase; **PDBTitle:** how a protein binds b12: a 3.o angstrom x-ray structure of2 the b12-binding domains of methionine synthase
41	d1o1xa_	Alignment	not modelled	15.7	20	**Fold:**Ribose/Galactose isomerase RpiB/AlsB **Superfamily:**Ribose/Galactose isomerase RpiB/AlsB **Family:**Ribose/Galactose isomerase RpiB/AlsB
42	c3cumA_	Alignment	not modelled	15.3	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable 3-hydroxyisobutyrate dehydrogenase; **PDBTitle:** crystal structure of a possible 3-hydroxyisobutyrate dehydrogenase2 from pseudomonas aeruginosa pao1
43	c1wsrA_	Alignment	not modelled	15.1	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminomethyltransferase; **PDBTitle:** crystal structure of human t-protein of glycine cleavage2 system
44	c3ch4B_	Alignment	not modelled	15.1	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphomevalonate kinase; **PDBTitle:** the crystal structure of human phosphomavelonate kinase at2 1.8 a resolution
45	c1b4nD_	Alignment	not modelled	14.8	19	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**formaldehyde ferredoxin oxidoreductase; **PDBTitle:** formaldehyde ferredoxin oxidoreductase from pyrococcus furiosus,2 complexed with glutarate
46	c1aorB_	Alignment	not modelled	14.6	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aldehyde ferredoxin oxidoreductase; **PDBTitle:** structure of a hyperthermophilic tungstopterin enzyme,2 aldehyde ferredoxin oxidoreductase
47	d2bjca1	Alignment	not modelled	14.1	6	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
48	c3aerB_	Alignment	not modelled	13.8	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**light-independent protochlorophyllide reductase subunit b; **PDBTitle:** structure of the light-independent protochlorophyllide reductase2 catalyzing a key reduction for greening in the dark
49	d1uf9a_	Alignment	not modelled	13.4	9	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
50	d3ci0k2	Alignment	not modelled	13.4	28	**Fold:**SAM domain-like **Superfamily:**GspK insert domain-like **Family:**GspK insert domain-like
51	c2jrlA_	Alignment	not modelled	13.0	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** solution structure of the beryllofluoride-activated ntrc4 receiver2 domain dimer
52	c3g0oA_	Alignment	not modelled	12.7	7	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-hydroxyisobutyrate dehydrogenase; **PDBTitle:** crystal structure of 3-hydroxyisobutyrate dehydrogenase2 (ygbj) from salmonella typhimurium
53	c3crnA_	Alignment	not modelled	12.5	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator receiver domain protein, chey-like;

						PDBTitle: crystal structure of response regulator receiver domain protein (chey-2 like) from methanospirillum hungatei jf-1
54	c3pefA_	Alignment	not modelled	12.5	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**6-phosphogluconate dehydrogenase, nad-binding; **PDBTitle:** crystal structure of gamma-hydroxybutyrate dehydrogenase from2 geobacter metallireducens in complex with nadp+
55	c1yb4A_	Alignment	not modelled	12.2	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**tartronic semialdehyde reductase; **PDBTitle:** crystal structure of the tartronic semialdehyde reductase from2 salmonella typhimurium lt2
56	c3ckyA_	Alignment	not modelled	12.1	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2-hydroxymethyl glutarate dehydrogenase; **PDBTitle:** structural and kinetic properties of a beta-hydroxyacid dehydrogenase2 involved in nicotinate fermentation
57	c2l8nA_	Alignment	not modelled	11.9	17	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional repressor cytr; **PDBTitle:** nmr structure of the cytidine repressor dna binding domain in presence2 of operator half-site dna
58	d1vhta_	Alignment	not modelled	11.7	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
59	d1jdqa_	Alignment	not modelled	11.5	19	**Fold:**IF3-like **Superfamily:**SirA-like **Family:**SirA-like
60	c2zwmA_	Alignment	not modelled	11.4	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulatory protein yycf; **PDBTitle:** crystal structure of yycf receiver domain from bacillus2 subtilis
61	d2hsga1	Alignment	not modelled	11.3	17	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
62	c3cfyA_	Alignment	not modelled	10.9	15	**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
63	d1uxca_	Alignment	not modelled	10.7	22	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
64	c3pduF_	Alignment	not modelled	10.7	9	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**3-hydroxyisobutyrate dehydrogenase family protein; **PDBTitle:** crystal structure of gamma-hydroxybutyrate dehydrogenase from2 geobacter sulfurreducens in complex with nadp+
65	c2is9A_	Alignment	not modelled	10.6	6	**PDB header:**transcription **Chain:** A: **PDB Molecule:**defective in cullin neddylation protein 1; **PDBTitle:** structure of yeast dcn-1
66	d1qpza1	Alignment	not modelled	10.6	5	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
67	c2gz3D_	Alignment	not modelled	10.6	18	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**aspartate beta-semialdehyde dehydrogenase; **PDBTitle:** structure of aspartate semialdehyde dehydrogenase (asadh) from2 streptococcus pneumoniae complexed with nadp and aspartate-3 semialdehyde
68	c3gl9B_	Alignment	not modelled	10.6	8	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**response regulator; **PDBTitle:** the structure of a histidine kinase-response regulator2 complex sheds light into two-component signaling and3 reveals a novel cis autophosphorylation mechanism
69	d2g5ca2	Alignment	not modelled	10.1	8	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
70	d1lcda_	Alignment	not modelled	10.1	6	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
71	d1efaa1	Alignment	not modelled	10.0	6	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
72	c1vpdA_	Alignment	not modelled	10.0	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**tartronate semialdehyde reductase; **PDBTitle:** x-ray crystal structure of tartronate semialdehyde reductase2 [salmonella typhimurium lt2]
73	d1dcja_	Alignment	not modelled	9.9	14	**Fold:**IF3-like **Superfamily:**SirA-like **Family:**SirA-like
74	c3hdvB_	Alignment	not modelled	9.8	20	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator receiver protein from2 pseudomonas putida
75	c3eodA_	Alignment	not modelled	9.7	8	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**protein hnr; **PDBTitle:** crystal structure of n-terminal domain of e. coli rssb
76	d2hjsa1	Alignment	not modelled	9.5	8	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
77	d1qkka_	Alignment	not modelled	9.4	16	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related

78	c3iwdC_	Alignment	not modelled	9.4	13	**PDB header:**lyase **Chain:** C: **PDB Molecule:**s-adenosylmethionine decarboxylase; **PDBTitle:** t. maritima adometdc complex with 5'-deoxy-5'-dimethyl2 thioadenosine
79	d2cnda2	Alignment	not modelled	9.4	9	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
80	c2rhmD_	Alignment	not modelled	9.4	7	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**putative kinase; **PDBTitle:** crystal structure of a putative kinase (caur_3907) from chloroflexus2 aurantiacus j-10-fl at 1.70 a resolution
81	c3lteH_	Alignment	not modelled	9.3	9	**PDB header:**transcription **Chain:** H: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator (signal receiver domain) from2 bermanella marisrubri
82	c3hzuA_	Alignment	not modelled	9.3	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thiosulfate sulfurtransferase ssea; **PDBTitle:** crystal structure of probable thiosulfate sulfurtransferase ssea2 (rhodanese) from mycobacterium tuberculosis
83	d2f1ka2	Alignment	not modelled	9.3	6	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
84	c2yxbA_	Alignment	not modelled	9.2	34	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**coenzyme b12-dependent mutase; **PDBTitle:** crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
85	d1uxda_	Alignment	not modelled	9.2	22	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
86	d1xhfa1	Alignment	not modelled	9.1	14	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
87	d1m98a1	Alignment	not modelled	9.0	36	**Fold:**Orange carotenoid protein, N-terminal domain **Superfamily:**Orange carotenoid protein, N-terminal domain **Family:**Orange carotenoid protein, N-terminal domain
88	c2k29A_	Alignment	not modelled	9.0	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**antitoxin relb; **PDBTitle:** structure of the dbd domain of e. coli antitoxin relb
89	c1zuiA_	Alignment	not modelled	8.7	5	**PDB header:**transferase **Chain:** A: **PDB Molecule:**shikimate kinase; **PDBTitle:** structural basis for shikimate-binding specificity of helicobacter2 pylori shikimate kinase
90	d1fmfa_	Alignment	not modelled	8.6	21	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
91	c2lcvA_	Alignment	not modelled	8.5	17	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**hth-type transcriptional repressor cytr; **PDBTitle:** structure of the cytidine repressor dna-binding domain; an alternate2 calculation
92	c2nqqA_	Alignment	not modelled	8.3	21	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**molybdopterin biosynthesis protein moea; **PDBTitle:** moea r137q
93	c3nhzA_	Alignment	not modelled	8.2	18	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**two component system transcriptional regulator mtra; **PDBTitle:** structure of n-terminal domain of mtra
94	c1ys4A_	Alignment	not modelled	8.1	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aspartate-semialdehyde dehydrogenase; **PDBTitle:** structure of aspartate-semialdehyde dehydrogenase from2 methanococcus jannaschii
95	c2uyyD_	Alignment	not modelled	8.0	16	**PDB header:**cytokine **Chain:** D: **PDB Molecule:**n-pac protein; **PDBTitle:** structure of the cytokine-like nuclear factor n-pac
96	c3h0kA_	Alignment	not modelled	8.0	6	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0200 protein sso1041; **PDBTitle:** crystal structure of an adenylated kinase related protein from2 sulfolobus solfataricus to 3.25a
97	d1pj5a4	Alignment	not modelled	7.9	15	**Fold:**Folate-binding domain **Superfamily:**Folate-binding domain **Family:**Aminomethyltransferase folate-binding domain
98	c2i76B_	Alignment	not modelled	7.9	3	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of protein tm1727 from thermotoga maritima
99	c2pjuD_	Alignment	not modelled	7.9	15	**PDB header:**transcription **Chain:** D: **PDB Molecule:**propionate catabolism operon regulatory protein; **PDBTitle:** crystal structure of propionate catabolism operon2 regulatory protein prpr