Phyre2

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Description	P71311
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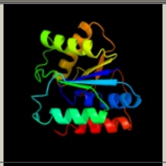
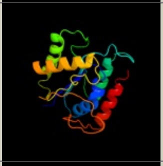
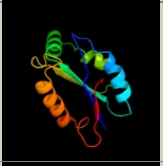
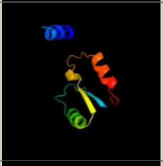
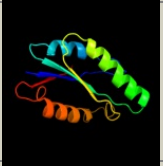
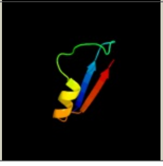
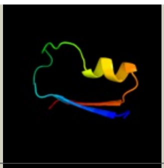
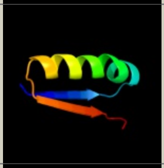
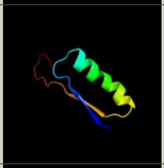
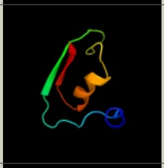
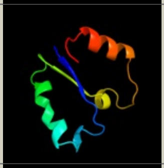
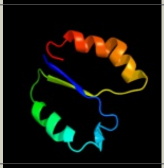
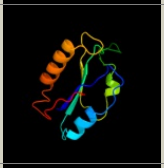
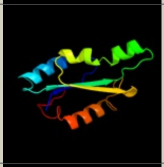
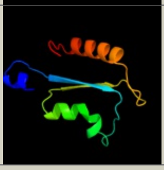
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2ixdB_	Alignment		100.0	26	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**lmbe-related protein; **PDBTitle:** crystal structure of the putative deacetylase bc1534 from2 bacilus cereus
2	d1uana_	Alignment		100.0	27	**Fold:**LmbE-like **Superfamily:**LmbE-like **Family:**LmbE-like
3	c3dfiA_	Alignment		100.0	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pseudoaglycone deacetylase dbv21; **PDBTitle:** the crystal structure of antimicrobial reagent a40926 pseudoaglycone2 deacetylase dbv21
4	c1q7tA_	Alignment		100.0	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hypothetical protein rv1170; **PDBTitle:** rv1170 (mshb) from mycobacterium tuberculosis
5	c3dfmA_	Alignment		100.0	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**teicoplanin pseudoaglycone deacetylase orf2; **PDBTitle:** the crystal structure of the zinc inhibited form of2 teicoplanin deacetylase orf2
6	d1q74a_	Alignment		100.0	27	**Fold:**LmbE-like **Superfamily:**LmbE-like **Family:**LmbE-like
7	c1t9gR_	Alignment		91.6	13	**PDB header:**oxidoreductase, electron transport **Chain:** R: **PDB Molecule:**electron transfer flavoprotein alpha-subunit, **PDBTitle:** structure of the human mcad:etf complex
8	c3eywA_	Alignment		91.0	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**c-terminal domain of glutathione-regulated potassium-efflux **PDBTitle:** crystal structure of the c-terminal domain of e. coli kefc in complex2 with keff
9	d1efva1	Alignment		90.9	13	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
10	d1qrda_	Alignment		84.6	19	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
11	d1dxqa_	Alignment		84.4	16	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase

12	d1d4aa_	Alignment		81.5	22	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
13	d2qwxa1	Alignment		81.4	16	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
14	c2r60A_	Alignment		80.7	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycosyl transferase, group 1; **PDBTitle:** structure of apo sucrose phosphate synthase (sps) of2 halothermothrix orenii
15	c1f8sA_	Alignment		75.0	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-amino acid oxidase; **PDBTitle:** crystal structure of l-amino acid oxidase from calloselasma2 rhodostoma, complexed with three molecules of o-aminobenzoate.
16	c3f2vA_	Alignment		72.2	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**general stress protein 14; **PDBTitle:** crystal structure of the general stress protein 142 (tde0354) in complex with fmn from treponema denticola,3 northeast structural genomics consortium target tdr58.
17	c3ha2B_	Alignment		71.9	11	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nadph-quinone reductase; **PDBTitle:** crystal structure of protein (nadph-quinone reductase) from2 p.pentosaceus, northeast structural genomics consortium target ptr24a
18	c1o94D_	Alignment		71.9	19	**PDB header:**electron transport **Chain:** D: **PDB Molecule:**electron transfer flavoprotein alpha-subunit; **PDBTitle:** ternary complex between trimethylamine dehydrogenase and2 electron transferring flavoprotein
19	c3ih5A_	Alignment		70.4	19	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**electron transfer flavoprotein alpha-subunit; **PDBTitle:** crystal structure of electron transfer flavoprotein alpha-2 subunit from bacteroides thetaiotaomicron
20	d1efpb_	Alignment		70.4	19	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
21	c2e1mA_	Alignment	not modelled	64.5	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-glutamate oxidase; **PDBTitle:** crystal structure of l-glutamate oxidase from streptomyces sp. x-119-6
22	d1v4va_	Alignment	not modelled	58.8	16	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDP-N-acetylglucosamine 2-epimerase
23	c3dzcA_	Alignment	not modelled	58.2	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine 2-epimerase; **PDBTitle:** 2.35 angstrom resolution structure of wecb (vc0917), a udp-n-2 acetylglucosamine 2-epimerase from vibrio cholerae.
24	d3clsc1	Alignment	not modelled	58.0	23	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
25	c3ot5D_	Alignment	not modelled	56.2	15	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**udp-n-acetylglucosamine 2-epimerase; **PDBTitle:** 2.2 angstrom resolution crystal structure of putative udp-n-2 acetylglucosamine 2-epimerase from listeria monocytogenes
26	d1f0ka_	Alignment	not modelled	55.8	25	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Peptidoglycan biosynthesis glycosyltransferase MurG
27	d3clsd1	Alignment	not modelled	54.1	18	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
28	d1reoa1	Alignment	not modelled	42.8	24	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
						Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes

29	d1vb3a1	Alignment	not modelled	40.6	16	**Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
30	c3jx9B_	Alignment	not modelled	40.1	14	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative phosphoheptose isomerase; **PDBTitle:** crystal structure of putative phosphoheptose isomerase2 (yp_001815198.1) from exiguobacterium sp. 255-15 at 1.95 a resolution
31	c3iuuA_	Alignment	not modelled	39.5	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative metallopeptidase; **PDBTitle:** crystal structure of putative metallopeptidase (yp_676511.1) from2 mesorhizobium sp. bnc1 at 2.13 a resolution
32	d1o94c_	Alignment	not modelled	38.3	22	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
33	c2b9yA_	Alignment	not modelled	35.3	34	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative aminooxidase; **PDBTitle:** crystal structure of cla-producing fatty acid isomerase2 from p. acnes
34	c2cmgA_	Alignment	not modelled	34.9	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**spermidine synthase; **PDBTitle:** crystal structure of spermidine synthase from helicobacter2 pylori
35	c3lteH_	Alignment	not modelled	32.9	23	**PDB header:**transcription **Chain:** H: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator (signal receiver domain) from2 bermanella marisrubri
36	d1gph11	Alignment	not modelled	31.8	14	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
37	d1ecfa1	Alignment	not modelled	31.4	16	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
38	c3qi7A_	Alignment	not modelled	30.9	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of a putative transcriptional regulator2 (yp_001089212.1) from clostridium difficile 630 at 1.86 a resolution
39	c2iyaB_	Alignment	not modelled	29.4	8	**PDB header:**transferase **Chain:** B: **PDB Molecule:**oleandomycin glycosyltransferase; **PDBTitle:** the crystal structure of macrolide glycosyltransferases: a2 blueprint for antibiotic engineering
40	d2d59a1	Alignment	not modelled	28.0	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
41	c3dezA_	Alignment	not modelled	27.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**orotate phosphoribosyltransferase; **PDBTitle:** crystal structure of orotate phosphoribosyltransferase from2 streptococcus mutans
42	c3c4vB_	Alignment	not modelled	27.0	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**predicted glycosyltransferases; **PDBTitle:** structure of the retaining glycosyltransferase msha:the2 first step in mycothiol biosynthesis. organism:3 corynebacterium glutamicum : complex with udp and 1l-ins-1-4 p.
43	d2acva1	Alignment	not modelled	26.0	12	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDPGT-like
44	c1ps9A_	Alignment	not modelled	25.5	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2,4-dienoyl-coa reductase; **PDBTitle:** the crystal structure and reaction mechanism of e. coli 2,4-2 dienoyl coa reductase
45	c3ia7A_	Alignment	not modelled	25.3	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**calg4; **PDBTitle:** crystal structure of calg4, the calicheamicin glycosyltransferase
46	d1fmfa_	Alignment	not modelled	24.6	14	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
47	c2jb1B_	Alignment	not modelled	23.8	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**l-amino acid oxidase; **PDBTitle:** the l-amino acid oxidase from rhodococcus opacus in complex2 with l-alanine
48	d1k68a_	Alignment	not modelled	22.9	19	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
49	c2xagA_	Alignment	not modelled	22.4	27	**PDB header:**transcription **Chain:** A: **PDB Molecule:**lysine-specific histone demethylase 1; **PDBTitle:** crystal structure of lsd1-corest in complex with para-bromo-2 (-)-trans-2-phenylcyclopropyl-1-amine
50	c2v1dA_	Alignment	not modelled	22.4	27	**PDB header:**oxidoreductase/repressor **Chain:** A: **PDB Molecule:**lysine-specific histone demethylase 1; **PDBTitle:** structural basis of lsd1-corest selectivity in histone h32 recognition
51	c3rpeA_	Alignment	not modelled	22.3	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**modulator of drug activity b; **PDBTitle:** 1.1 angstrom crystal structure of putative modulator of drug activity2 (mdab) from yersinia pestis co92.
52	c2hkoA_	Alignment	not modelled	22.2	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**lysine-specific histone demethylase 1; **PDBTitle:** crystal structure of lsd1
53	c3d0qB_	Alignment	not modelled	22.1	8	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein calg3; **PDBTitle:** crystal structure of calg3 from micromonospora echinospora determined2 in space group i222
						PDB header:transferase **Chain:** A: **PDB Molecule:**probable trna (5-methylaminomethyl-2-

54	c2hmaA_	Alignment	not modelled	21.5	8	thiouridylate)- **PDBTitle:** the crystal structure of trna (5-methylaminomethyl-2-thiouridylate)-2 methyltransferase trmu from streptococcus pneumoniae
55	c3q9cF_	Alignment	not modelled	21.5	8	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**acetylpolyamine amidohydrolase; **PDBTitle:** crystal structure of h159a apah complexed with n8-acetylspermidine
56	d1a9xa3	Alignment	not modelled	21.4	24	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
57	d2aeea1	Alignment	not modelled	21.2	24	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
58	c3menC_	Alignment	not modelled	20.9	8	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**acetylpolyamine aminohydrolase; **PDBTitle:** crystal structure of acetylpolyamine aminohydrolase from burkholderia2 pseudomallei, iodide soak
59	c1k97A_	Alignment	not modelled	20.8	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**argininosuccinate synthase; **PDBTitle:** crystal structure of e. coli argininosuccinate synthetase in complex2 with aspartate and citrulline
60	d1k66a_	Alignment	not modelled	19.4	18	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
61	c3devB_	Alignment	not modelled	19.1	12	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**sh1221; **PDBTitle:** crystal structure of sh1221 protein from staphylococcus haemolyticus,2 northeast structural genomics consortium target shr87
62	c2yxbA_	Alignment	not modelled	19.0	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**coenzyme b12-dependent mutase; **PDBTitle:** crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
63	c2bi8A_	Alignment	not modelled	18.9	38	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**udp-galactopyranose mutase; **PDBTitle:** udp-galactopyranose mutase from klebsiella pneumoniae with2 reduced fad
64	c3m3hA_	Alignment	not modelled	17.4	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**orotate phosphoribosyltransferase; **PDBTitle:** 1.75 angstrom resolution crystal structure of an orotate2 phosphoribosyltransferase from bacillus anthracis str. 'ames3 ancestor'
65	d2iida1	Alignment	not modelled	17.4	30	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
66	d1ir6a_	Alignment	not modelled	17.3	21	**Fold:**DHH phosphoesterases **Superfamily:**DHH phosphoesterases **Family:**Exonuclease RecJ
67	c1ir6A_	Alignment	not modelled	17.3	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exonuclease recj; **PDBTitle:** crystal structure of exonuclease recj bound to manganese
68	d1ybha3	Alignment	not modelled	17.2	14	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase PP module
69	d1p3da1	Alignment	not modelled	17.2	23	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain **Family:**MurCD N-terminal domain
70	c2gwrA_	Alignment	not modelled	16.8	24	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**dna-binding response regulator mtra; **PDBTitle:** crystal structure of the response regulator protein mtra from2 mycobacterium tuberculosis
71	d2ji7a3	Alignment	not modelled	16.8	19	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase PP module
72	d2c1ha1	Alignment	not modelled	16.7	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
73	d1y0ba1	Alignment	not modelled	16.7	26	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
74	c3enkB_	Alignment	not modelled	16.6	15	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**udp-glucose 4-epimerase; **PDBTitle:** 1.9a crystal structure of udp-glucose 4-epimerase from2 burkholderia pseudomallei
75	c3q9sA_	Alignment	not modelled	16.2	19	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna-binding response regulator; **PDBTitle:** crystal structure of rra(1-215) from deinococcus radiodurans
76	c2xhyD_	Alignment	not modelled	16.2	8	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**6-phospho-beta-glucosidase bgla; **PDBTitle:** crystal structure of e.coli bgla
77	d2pw6a1	Alignment	not modelled	16.1	20	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**LigB-like **Family:**LigB-like
78	c3iaaB_	Alignment	not modelled	15.8	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**calg2; **PDBTitle:** crystal structure of calg2, calicheamicin glycosyltransferase, tdp2 bound form
79	d1k92a1	Alignment	not modelled	15.6	16	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
						PDB header:hydrolase

80	c3qomA_	Alignment	not modelled	15.4	8	**Chain:** A: **PDB Molecule:**6-phospho-beta-glucosidase; **PDBTitle:** crystal structure of 6-phospho-beta-glucosidase from lactobacillus2 plantarum
81	d1mzva_	Alignment	not modelled	15.4	24	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
82	c2dy0A_	Alignment	not modelled	14.8	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenine phosphoribosyltransferase; **PDBTitle:** crystal structure of project jw0458 from escherichia coli
83	d2afwa1	Alignment	not modelled	14.6	21	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Glutaminyl-peptide cyclotransferase-like
84	d1seza1	Alignment	not modelled	14.3	33	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
85	c3ai0A_	Alignment	not modelled	14.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-glucosidase; **PDBTitle:** crystal structure of beta-glucosidase from termite neotermes2 koshunensis in complex with para-nitrophenyl-beta-d-glucopyranoside
86	d1o57a2	Alignment	not modelled	13.9	18	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
87	d1xlma_	Alignment	not modelled	13.8	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
88	c1jscA_	Alignment	not modelled	13.7	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**acetohydroxy-acid synthase; **PDBTitle:** crystal structure of the catalytic subunit of yeast2 acetohydroxyacid synthase: a target for herbicidal3 inhibitors
89	c2p6pB_	Alignment	not modelled	13.6	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycosyl transferase; **PDBTitle:** x-ray crystal structure of c-c bond-forming dtdp-d-olivose-transferase2 urdgt2
90	c1ecjB_	Alignment	not modelled	13.6	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glutamine phosphoribosylpyrophosphate **PDBTitle:** escherichia coli glutamine phosphoribosylpyrophosphate2 (prpp) amidotransferase complexed with 2 amp per tetramer
91	d1efpa1	Alignment	not modelled	13.4	15	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
92	d1e4mm_	Alignment	not modelled	13.3	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Family 1 of glycosyl hydrolase
93	c3khtA_	Alignment	not modelled	12.8	20	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator from hahella chejuensis
94	d1c0pa1	Alignment	not modelled	12.7	24	**Fold:**Nucleotide-binding domain **Superfamily:**Nucleotide-binding domain **Family:**D-aminoacid oxidase, N-terminal domain
95	c2c4kD_	Alignment	not modelled	12.5	30	**PDB header:**regulatory protein **Chain:** D: **PDB Molecule:**phosphoribosyl pyrophosphate synthetase- **PDBTitle:** crystal structure of human phosphoribosylpyrophosphate2 synthetase-associated protein 39 (pap39)
96	c2jf7B_	Alignment	not modelled	12.4	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**strictosidine-o-beta-d-glucosidase; **PDBTitle:** structure of strictosidine glucosidase
97	c1c0iA_	Alignment	not modelled	12.3	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-amino acid oxidase; **PDBTitle:** crystal structure of d-amino acid oxidase in complex with2 two anthranylate molecules
98	d1bxca_	Alignment	not modelled	12.1	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
99	d1dkua2	Alignment	not modelled	12.0	24	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like