Phyre^2

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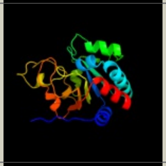
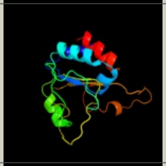
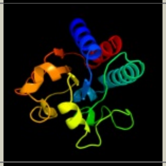
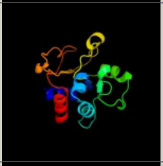
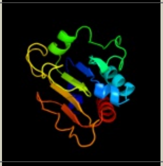
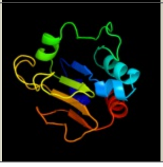
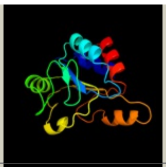
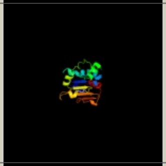
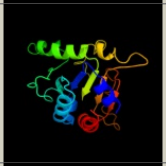
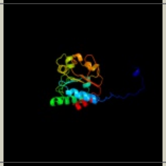
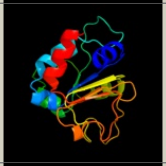
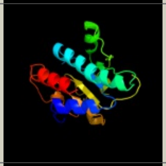
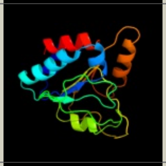
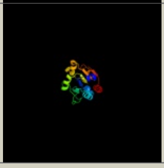
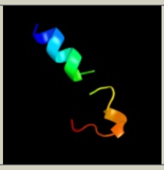
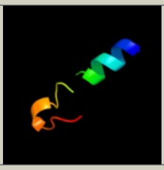
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1pnoa_	Alignment		100.0	56	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Transhydrogenase domain III (dIII)
2	c1pt9B_	Alignment		100.0	63	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nad(p) transhydrogenase, mitochondrial; **PDBTitle:** crystal structure analysis of the diii component of transhydrogenase2 with a thio-nicotinamide nucleotide analogue
3	d1d4oa_	Alignment		100.0	63	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Transhydrogenase domain III (dIII)
4	c2bruC_	Alignment		100.0	100	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nad(p) transhydrogenase subunit beta; **PDBTitle:** complex of the domain i and domain iii of escherichia coli2 transhydrogenase
5	d1q6za1	Alignment		98.1	21	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
6	d2ihta1	Alignment		97.6	20	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
7	d1ozha1	Alignment		97.4	13	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
8	d1ybha1	Alignment		97.3	18	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
9	d2ez9a1	Alignment		97.2	19	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
10	c2ji6B_	Alignment		97.2	20	**PDB header:**lyase **Chain:** B: **PDB Molecule:**oxalyl-coa decarboxylase; **PDBTitle:** x-ray structure of oxalyl-coa decarboxylase in complex with2 3-deaza-thdp and oxalyl-coa
11	d2ji7a1	Alignment		97.2	21	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain

12	d2djia1	Alignment		97.0	24	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
13	c2djiA_	Alignment		96.5	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pyruvate oxidase; **PDBTitle:** crystal structure of pyruvate oxidase from aerococcus2 viridans containing fad
14	d1t9ba1	Alignment		96.5	15	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
15	c1ozhD_	Alignment		96.5	13	**PDB header:**lyase **Chain:** D: **PDB Molecule:**acetolactate synthase, catabolic; **PDBTitle:** the crystal structure of klebsiella pneumoniae acetolactate2 synthase with enzyme-bound cofactor and with an unusual3 intermediate.
16	c2pgnA_	Alignment		96.5	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cyclohexane-1,2-dione hydrolase (cdh); **PDBTitle:** the crystal structure of fad and thdp-dependent cyclohexane-1,2-dione2 hydrolase in complex with cyclohexane-1,2-dione
17	c3cf4G_	Alignment		96.5	22	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**acetyl-coa decarboxylase/synthase epsilon subunit; **PDBTitle:** structure of the codh component of the m. barkeri acds complex
18	c1upaC_	Alignment		96.4	17	**PDB header:**synthase **Chain:** C: **PDB Molecule:**carboxyethylarginine synthase; **PDBTitle:** carboxyethylarginine synthase from streptomyces2 clavuligerus (semet structure)
19	c2v3wC_	Alignment		96.2	17	**PDB header:**lyase **Chain:** C: **PDB Molecule:**benzoylformate decarboxylase; **PDBTitle:** crystal structure of the benzoylformate decarboxylase2 variant l461a from pseudomonas putida
20	c1powA_	Alignment		96.1	17	**PDB header:**oxidoreductase(oxygen as acceptor) **Chain:** A: **PDB Molecule:**pyruvate oxidase; **PDBTitle:** the refined structures of a stabilized mutant and of wild-type2 pyruvate oxidase from lactobacillus plantarum
21	c2ag1A_	Alignment	not modelled	95.9	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**benzaldehyde lyase; **PDBTitle:** crystal structure of benzaldehyde lyase (bal)- semet
22	c2q27B_	Alignment	not modelled	95.8	20	**PDB header:**lyase **Chain:** B: **PDB Molecule:**oxalyl-coa decarboxylase; **PDBTitle:** crystal structure of oxalyl-coa decarboxylase from escherichia coli
23	d1ovma1	Alignment	not modelled	95.7	13	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
24	c2vbgB_	Alignment	not modelled	95.0	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**branched-chain alpha-ketoacid decarboxylase; **PDBTitle:** the complex structure of the branched-chain keto acid2 decarboxylase (kdca) from lactococcus lactis with 2r-1-3 hydroxyethyl-deazathdp
25	c3eyaE_	Alignment	not modelled	94.9	23	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**pyruvate dehydrogenase [cytochrome]; **PDBTitle:** structural basis for membrane binding and catalytic2 activation of the peripheral membrane enzyme pyruvate3 oxidase from escherichia coli
26	c1t9dB_	Alignment	not modelled	94.6	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**acetolactate synthase, mitochondrial; **PDBTitle:** crystal structure of yeast acetohydroxyacid synthase in2 complex with a sulfonylurea herbicide, metsulfuron methyl
27	d1zpda1	Alignment	not modelled	94.4	15	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
28	c1jscA_	Alignment	not modelled	93.8	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**acetohydroxy-acid synthase;

28	c1jscA_	Alignment	not modelled	93.8	16	**PDBTitle:** crystal structure of the catalytic subunit of yeast2 acetohydroxyacid synthase: a target for herbicidal3 inhibitors
29	d1s5pa_	Alignment	not modelled	93.5	26	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
30	c1yi1A_	Alignment	not modelled	93.5	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetolactate synthase; **PDBTitle:** crystal structure of arabidopsis thaliana acetohydroxyacid synthase in2 complex with a sulfonylurea herbicide, tribenuron methyl
31	c3pkiF_	Alignment	not modelled	93.4	10	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**nad-dependent deacetylase sirtuin-6; **PDBTitle:** human sirt6 crystal structure in complex with adp ribose
32	c2w93A_	Alignment	not modelled	93.3	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**pyruvate decarboxylase isozyme 1; **PDBTitle:** crystal structure of the saccharomyces cerevisiae pyruvate2 decarboxylase variant e477q in complex with the surrogate3 pyruvamide
33	c3glsC_	Alignment	not modelled	93.2	19	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**nad-dependent deacetylase sirtuin-3, **PDBTitle:** crystal structure of human sirt3
34	d1pvda1	Alignment	not modelled	93.1	16	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
35	d1yc5a1	Alignment	not modelled	93.0	18	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
36	c2x7jA_	Alignment	not modelled	92.9	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene **PDBTitle:** structure of the menaquinone biosynthesis protein mend from2 bacillus subtilis
37	c3k35D_	Alignment	not modelled	92.7	12	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**nad-dependent deacetylase sirtuin-6; **PDBTitle:** crystal structure of human sirt6
38	d2b4ya1	Alignment	not modelled	92.7	23	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
39	c1ovmC_	Alignment	not modelled	92.7	14	**PDB header:**lyase **Chain:** C: **PDB Molecule:**indole-3-pyruvate decarboxylase; **PDBTitle:** crystal structure of indolepyruvate decarboxylase from2 enterobacter cloacae
40	c2panF_	Alignment	not modelled	92.6	18	**PDB header:**lyase **Chain:** F: **PDB Molecule:**glyoxylate carboligase; **PDBTitle:** crystal structure of e. coli glyoxylate carboligase
41	c2nxwB_	Alignment	not modelled	92.3	23	**PDB header:**lyase **Chain:** B: **PDB Molecule:**phenyl-3-pyruvate decarboxylase; **PDBTitle:** crystal structure of phenylpyruvate decarboxylase of azospirillum2 brasilense
42	d1m2ka_	Alignment	not modelled	91.7	20	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
43	d1ma3a_	Alignment	not modelled	91.4	21	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
44	c1zpdA_	Alignment	not modelled	91.1	12	**PDB header:**alcohol fermentation **Chain:** A: **PDB Molecule:**pyruvate decarboxylase; **PDBTitle:** pyruvate decarboxylase from zymomonas mobilis
45	c2vbiF_	Alignment	not modelled	88.9	16	**PDB header:**lyase **Chain:** F: **PDB Molecule:**pyruvate decarboxylase; **PDBTitle:** holostructure of pyruvate decarboxylase from acetobacter2 pasteurianus
46	d1q1aa_	Alignment	not modelled	88.1	11	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
47	c3jwpA_	Alignment	not modelled	87.0	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulatory protein sir2 homologue; **PDBTitle:** crystal structure of plasmodium falciparum sir2a (pf13_0152) in2 complex with amp
48	c3lq1A_	Alignment	not modelled	86.7	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene- **PDBTitle:** crystal structure of 2-succinyl-6-hydroxy-2,4-cyclohexadiene2 1-carboxylic acid synthase/2-oxoglutarate decarboxylase3 from listeria monocytogenes str. 4b f2365
49	c2jlaD_	Alignment	not modelled	84.1	14	**PDB header:**transferase **Chain:** D: **PDB Molecule:**2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene **PDBTitle:** crystal structure of e.coli mend, 2-succinyl-5-enolpyruvyl-2 6-hydroxy-3-cyclohexadiene-1-carboxylate synthase - semet3 protein
50	d1j8fa_	Alignment	not modelled	83.6	18	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
51	c2hjhB_	Alignment	not modelled	83.0	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**nad-dependent histone deacetylase sir2; **PDBTitle:** crystal structure of the sir2 deacetylase
52	c1q14A_	Alignment	not modelled	74.9	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hst2 protein; **PDBTitle:** structure and autoregulation of the yeast hst2 homolog of sir2
						Fold: Flavodoxin-like

53	d1sqsa_	Alignment	not modelled	74.3	11	**Superfamily:**Flavoproteins **Family:**Hypothetical protein SP1951
54	c8jdwA_	Alignment	not modelled	73.9	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (l-arginine:glycine amidinotransferase); **PDBTitle:** crystal structure of human l-arginine:glycine2 amidinotransferase in complex with l-alanine
55	d1u0ta_	Alignment	not modelled	73.7	29	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**NAD kinase-like
56	d1jdwa_	Alignment	not modelled	72.2	25	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Amidinotransferase
57	c1jdwA_	Alignment	not modelled	72.2	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**l-arginine\:glycine amidinotransferase; **PDBTitle:** crystal structure and mechanism of l-arginine: glycine2 amidinotransferase: a mitochondrial enzyme involved in3 creatine biosynthesis
58	d1z0sa1	Alignment	not modelled	71.1	30	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**NAD kinase-like
59	c1z0zC_	Alignment	not modelled	71.0	30	**PDB header:**transferase **Chain:** C: **PDB Molecule:**probable inorganic polyphosphate/atp-nad kinase; **PDBTitle:** crystal structure of a nad kinase from archaeoglobus2 fulgidus in complex with nad
60	c2eeyA_	Alignment		63.1	41	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**molybdopterin biosynthesis; **PDBTitle:** structure of gk0241 protein from geobacillus kaustophilus
61	c2an1D_	Alignment	not modelled	62.7	21	**PDB header:**transferase **Chain:** D: **PDB Molecule:**putative kinase; **PDBTitle:** structural genomics, the crystal structure of a putative kinase from2 salmonella typhimurim lt2
62	d1ekra_	Alignment		62.4	45	**Fold:**Ferredoxin-like **Superfamily:**Molybdenum cofactor biosynthesis protein C, MoaC **Family:**Molybdenum cofactor biosynthesis protein C, MoaC
63	c2ideE_	Alignment	not modelled	61.7	32	**PDB header:**biosynthetic protein **Chain:** E: **PDB Molecule:**molybdenum cofactor biosynthesis protein c; **PDBTitle:** crystal structure of the molybdenum cofactor biosynthesis protein c2 (ttha1789) from thermus theromophilus hb8
64	d1a9xa4	Alignment	not modelled	59.4	26	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
65	d1jaka1	Alignment	not modelled	58.6	33	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-N-acetylhexosaminidase catalytic domain
66	c2x3yA_	Alignment	not modelled	58.2	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**phosphoheptose isomerase; **PDBTitle:** crystal structure of gmha from burkholderia pseudomallei
67	c3vh3A_	Alignment	not modelled	57.7	10	**PDB header:**metal binding protein/protein transport **Chain:** A: **PDB Molecule:**ubiquitin-like modifier-activating enzyme atg7; **PDBTitle:** crystal structure of atg7ctd-atg8 complex
68	d1bwda_	Alignment	not modelled	56.8	17	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Amidinotransferase
69	d2choa2	Alignment	not modelled	55.4	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**alpha-D-glucuronidase/Hyaluronidase catalytic domain
70	d1yhta1	Alignment	not modelled	55.3	26	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-N-acetylhexosaminidase catalytic domain
71	d1nowa1	Alignment	not modelled	54.5	30	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-N-acetylhexosaminidase catalytic domain
72	d1uxoa_	Alignment	not modelled	52.6	22	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**YdeN-like
73	c3rpmA_	Alignment	not modelled	52.6	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-n-acetyl-hexosaminidase; **PDBTitle:** crystal structure of the first gh20 domain of a novel beta-n-acetyl-2 hexosaminidase strh from streptococcus pneumoniae r6
74	c2ylaA_	Alignment	not modelled	52.2	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-n-acetylhexosaminidase; **PDBTitle:** inhibition of the pneumococcal virulence factor strh and2 molecular insights into n-glycan recognition and3 hydrolysis
75	d2cbia2	Alignment	not modelled	52.1	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**alpha-D-glucuronidase/Hyaluronidase catalytic domain
76	d1dxqa_	Alignment	not modelled	51.5	21	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
						PDB header:oxidoreductase

77	c2axqA_	Alignment	not modelled	50.6	20	**Chain:** A: **PDB Molecule:**saccharopine dehydrogenase; **PDBTitle:** apo histidine-tagged saccharopine dehydrogenase (l-glu2 forming) from saccharomyces cerevisiae
78	c2xsbA_	Alignment	not modelled	50.2	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hyaluronoglucosaminidase; **PDBTitle:** ogoga pugnac complex
79	c3pfnB_	Alignment	not modelled	49.9	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**nad kinase; **PDBTitle:** crystal structure of human nad kinase
80	c3i4aA_	Alignment	not modelled	48.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**n(g),n(g)-dimethylarginine dimethylaminohydrolase **PDBTitle:** crystal structure of dimethylarginine2 dimethylaminohydrolase-1 (ddah-1) in complex with n5-(1-3 iminopropyl)-l-ornithine
81	c1mv8A_	Alignment	not modelled	48.0	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**gdp-mannose 6-dehydrogenase; **PDBTitle:** 1.55 a crystal structure of a ternary complex of gdp-mannose2 dehydrogenase from psuedomonas aeruginosa
82	d1e5qa1	Alignment	not modelled	47.4	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
83	c2eknC_	Alignment	not modelled	46.4	47	**PDB header:**biosynthetic protein **Chain:** C: **PDB Molecule:**probable molybdenum cofactor biosynthesis protein c; **PDBTitle:** structure of ph1811 protein from pyrococcus horikoshii
84	d1ka9f_	Alignment	not modelled	45.8	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
85	d2hc5a1	Alignment	not modelled	44.8	16	**Fold:**FlaG-like **Superfamily:**FlaG-like **Family:**FlaG-like
86	d1thfd_	Alignment	not modelled	44.8	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
87	c3l3bA_	Alignment	not modelled	43.7	18	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**es1 family protein; **PDBTitle:** crystal structure of isoprenoid biosynthesis protein with2 amidotransferase-like domain from ehrlichia chaffeensis at 1.90a3 resolution
88	c2iyaB_	Alignment	not modelled	43.6	31	**PDB header:**transferase **Chain:** B: **PDB Molecule:**oleandomycin glycosyltransferase; **PDBTitle:** the crystal structure of macrolide glycosyltransferases: a2 blueprint for antibiotic engineering
89	c2yl8A_	Alignment	not modelled	43.2	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-n-acetylhexosaminidase; **PDBTitle:** inhibition of the pneumococcal virulence factor strh and2 molecular insights into n-glycan recognition and3 hydrolysis
90	c3gh7A_	Alignment	not modelled	42.9	36	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-hexosaminidase; **PDBTitle:** crystal structure of beta-hexosaminidase from paenibacillus2 sp. ts12 in complex with galnac
91	c3afoB_	Alignment	not modelled	42.7	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**nadh kinase pos5; **PDBTitle:** crystal structure of yeast nadh kinase complexed with nadh
92	c2yzkC_	Alignment	not modelled	41.6	30	**PDB header:**transferase **Chain:** C: **PDB Molecule:**orotate phosphoribosyltransferase; **PDBTitle:** crystal structure of orotate phosphoribosyltransferase from2 aeropyrum pernix
93	c1m04A_	Alignment	not modelled	41.5	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-n-acetylhexosaminidase; **PDBTitle:** mutant streptomyces plicatus beta-hexosaminidase (d313n) in complex2 with product (glcnac)
94	d1j6ua2	Alignment	not modelled	41.1	24	**Fold:**MurD-like peptide ligases, peptide-binding domain **Superfamily:**MurD-like peptide ligases, peptide-binding domain **Family:**MurCDEF C-terminal domain
95	c2g1uA_	Alignment	not modelled	39.9	19	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**hypothetical protein tm1088a; **PDBTitle:** crystal structure of a putative transport protein (tm1088a) from2 thermotoga maritima at 1.50 a resolution
96	d2gjxa1	Alignment	not modelled	39.8	33	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-N-acetylhexosaminidase catalytic domain
97	c1e5lA_	Alignment	not modelled	39.6	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**saccharopine reductase; **PDBTitle:** apo saccharopine reductase from magnaporthe grisea
98	c2cbjA_	Alignment	not modelled	39.6	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hyaluronidase; **PDBTitle:** structure of the clostridium perfringens nagj family 842 glycoside hydrolase, a homologue of human o-glcnacase in3 complex with pugnac
99	d1iira_	Alignment	not modelled	39.4	22	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Gtf glycosyltransferase
100	d1bxca_	Alignment	not modelled	38.9	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
101	d1g5ha1	Alignment	not modelled	38.4	17	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
102	c2qc8J_	Alignment	not modelled	37.7	17	**PDB header:**ligase **Chain:** J: **PDB Molecule:**glutamine synthetase; **PDBTitle:** crystal structure of human glutamine synthetase in

						complex with adp2 and methionine sulfoximine phosphate
103	c2ohdB_	Alignment	not modelled	37.6	33	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**probable molybdenum cofactor biosynthesis protein c; **PDBTitle:** crystal structure of hypothetical molybdenum cofactor biosynthesis2 protein c from sulfolobus tokodaii
104	d1sy7a1	Alignment	not modelled	37.4	13	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Catalase, C-terminal domain
105	c3rcnA_	Alignment	not modelled	37.1	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-n-acetylhexosaminidase; **PDBTitle:** crystal structure of beta-n-acetylhexosaminidase from arthrobacter2 aurescens
106	c2jp3A_	Alignment	not modelled	37.0	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**fxyd domain-containing ion transport regulator 4; **PDBTitle:** solution structure of the human fxyd4 (chif) protein in sds2 micelles
107	d2ahua2	Alignment	not modelled	37.0	16	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
108	c1nouA_	Alignment	not modelled	36.9	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-hexosaminidase beta chain; **PDBTitle:** native human lysosomal beta-hexosaminidase isoform b
109	c2ahvC_	Alignment	not modelled	36.8	14	**PDB header:**transferase **Chain:** C: **PDB Molecule:**putative enzyme ydif; **PDBTitle:** crystal structure of acyl-coa transferase from e. coli o157:h7 (ydif)-2 thioester complex with coa- 1
110	d1ycga1	Alignment	not modelled	36.3	22	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
111	c2jo1A_	Alignment	not modelled	35.6	22	**PDB header:**hydrolase regulator **Chain:** A: **PDB Molecule:**phospholemman; **PDBTitle:** structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
112	d1h5ya_	Alignment	not modelled	34.8	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
113	d1vima_	Alignment	not modelled	34.6	22	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
114	c3canA_	Alignment	not modelled	34.6	17	**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
115	d1s9ra_	Alignment	not modelled	34.5	25	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Arginine deiminase
116	d1ltqa1	Alignment	not modelled	33.8	22	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**phosphatase domain of polynucleotide kinase
117	d2g39a1	Alignment	not modelled	33.4	18	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
118	c2choA_	Alignment	not modelled	33.1	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glucosaminidase; **PDBTitle:** bacteroides thetaiotaomicron hexosaminidase with o-2 glcnacase activity
119	c3othB_	Alignment	not modelled	33.0	19	**PDB header:**transferase/antibiotic **Chain:** B: **PDB Molecule:**calg1; **PDBTitle:** crystal structure of calg1, calicheamicin glycostyltransferase, tdp2 and calicheamicin alpha3i bound form
120	d1qt1a_	Alignment	not modelled	32.1	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase