Phyre^2

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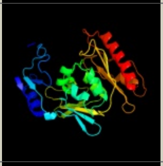
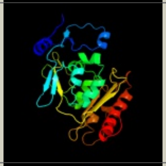
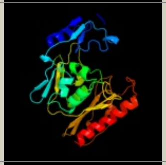
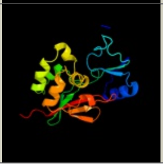
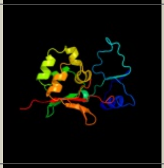
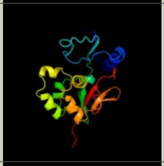
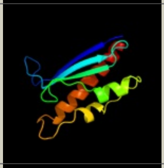
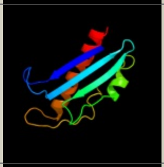
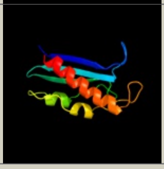
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1t3qF_	Alignment		100.0	20	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**quinoline 2-oxidoreductase medium subunit; **PDBTitle:** crystal structure of quinoline 2-oxidoreductase from pseudomonas2 putida 86
2	c1n62C_	Alignment		100.0	24	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**carbon monoxide dehydrogenase medium chain; **PDBTitle:** crystal structure of the mo,cu-co dehydrogenase (codh), n-2 butylisocyanide-bound state
3	c3hrdC_	Alignment		100.0	24	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nicotinate dehydrogenase fad-subunit; **PDBTitle:** crystal structure of nicotinate dehydrogenase
4	c1ffuF_	Alignment		100.0	28	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**cutm, flavoprotein of carbon monoxide **PDBTitle:** carbon monoxide dehydrogenase from hydrogenophaga2 pseudoflava which lacks the mo-pyranopterin moiety of the3 molybdenum cofactor
5	c2w3rG_	Alignment		100.0	23	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**xanthine dehydrogenase; **PDBTitle:** crystal structure of xanthine dehydrogenase (desulfo form)2 from rhodobacter capsulatus in complex with hypoxanthine
6	c1wygA_	Alignment		100.0	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**xanthine dehydrogenase/oxidase; **PDBTitle:** crystal structure of a rat xanthine dehydrogenase triple mutant2 (c535a, c992r and c1324s)
7	c3etrM_	Alignment		100.0	19	**PDB header:**oxidoreductase **Chain:** M: **PDB Molecule:**xanthine dehydrogenase/oxidase; **PDBTitle:** crystal structure of xanthine oxidase in complex with2 lumazine
8	c3b9jJ_	Alignment		100.0	19	**PDB header:**oxidoreductase **Chain:** J: **PDB Molecule:**xanthine oxidase; **PDBTitle:** structure of xanthine oxidase with 2-hydroxy-6-methylpurine
9	c1rm6E_	Alignment		100.0	22	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**4-hydroxybenzoyl-coa reductase beta subunit; **PDBTitle:** structure of 4-hydroxybenzoyl-coa reductase from thauera2 aromatica
10	d1n62c2	Alignment		100.0	25	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CO dehydrogenase flavoprotein N-terminal domain-like
11	d1ffvc2	Alignment		100.0	25	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CO dehydrogenase flavoprotein N-terminal domain-like

12	d1t3qc2	Alignment		100.0	22	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CO dehydrogenase flavoprotein N-terminal domain-like
13	d1v97a6	Alignment		100.0	21	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CO dehydrogenase flavoprotein N-terminal domain-like
14	d1rm6b2	Alignment		100.0	23	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CO dehydrogenase flavoprotein N-terminal domain-like
15	d1jroa4	Alignment		100.0	25	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CO dehydrogenase flavoprotein N-terminal domain-like
16	d3b9jb2	Alignment		100.0	21	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CO dehydrogenase flavoprotein N-terminal domain-like
17	d1v97a4	Alignment		99.9	16	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**CO dehydrogenase flavoprotein C-terminal domain-like **Family:**CO dehydrogenase flavoprotein C-terminal domain-like
18	d1jroa3	Alignment		99.9	21	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**CO dehydrogenase flavoprotein C-terminal domain-like **Family:**CO dehydrogenase flavoprotein C-terminal domain-like
19	d1t3qc1	Alignment		99.8	18	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**CO dehydrogenase flavoprotein C-terminal domain-like **Family:**CO dehydrogenase flavoprotein C-terminal domain-like
20	d1n62c1	Alignment		99.8	22	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**CO dehydrogenase flavoprotein C-terminal domain-like **Family:**CO dehydrogenase flavoprotein C-terminal domain-like
21	d1ffvc1	Alignment	not modelled	99.8	30	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**CO dehydrogenase flavoprotein C-terminal domain-like **Family:**CO dehydrogenase flavoprotein C-terminal domain-like
22	d1rm6b1	Alignment	not modelled	99.8	22	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**CO dehydrogenase flavoprotein C-terminal domain-like **Family:**CO dehydrogenase flavoprotein C-terminal domain-like
23	c2wdwB_	Alignment	not modelled	97.8	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative hexose oxidase; **PDBTitle:** the native crystal structure of the primary hexose oxidase (2 dbv29) in antibiotic a40926 biosynthesis
24	c2uuvC_	Alignment	not modelled	97.7	18	**PDB header:**transferase **Chain:** C: **PDB Molecule:**alkyldihydroxyacetonephosphate synthase; **PDBTitle:** alkyldihydroxyacetonephosphate synthase in p1
25	c3fwaA_	Alignment	not modelled	97.7	20	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**reticuline oxidase; **PDBTitle:** structure of berberine bridge enzyme, c166a variant in complex with2 (s)-reticuline
26	c2vfvA_	Alignment	not modelled	97.6	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**xylitol oxidase; **PDBTitle:** alditol oxidase from streptomyces coelicolor a3(2): complex2 with sulphite
27	c2ipiD_	Alignment	not modelled	97.3	14	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**aclacinomycin oxidoreductase (aknox); **PDBTitle:** crystal structure of aclacinomycin oxidoreductase
28	d1hska1	Alignment	not modelled	97.3	16	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase (MurB), N-terminal domain
						PDB header:oxidoreductase

29	c3popD_	Alignment	not modelled	97.1	15	**Chain:** D: **PDB Molecule:**gilr oxidase; **PDBTitle:** the crystal structure of gilr, an oxidoreductase that catalyzes the2 terminal step of gilvocarcin biosynthesis
30	c1zr6A_	Alignment	not modelled	97.1	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glucooligosaccharide oxidase; **PDBTitle:** the crystal structure of an acremonium strictum glucooligosaccharide2 oxidase reveals a novel flavinylation
31	c2y3rC_	Alignment	not modelled	97.0	15	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**taml; **PDBTitle:** structure of the tirandamycin-bound fad-dependent2 tirandamycin oxidase taml in p21 space group
32	c3bw7A_	Alignment	not modelled	97.0	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytokinin dehydrogenase 1; **PDBTitle:** maize cytokinin oxidase/dehydrogenase complexed with the allenic2 cytokinin analog ha-1
33	c1f0xA_	Alignment	not modelled	97.0	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-lactate dehydrogenase; **PDBTitle:** crystal structure of d-lactate dehydrogenase, a peripheral2 membrane respiratory enzyme.
34	c3d2hA_	Alignment	not modelled	97.0	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**berberine bridge-forming enzyme; **PDBTitle:** structure of berberine bridge enzyme from eschscholzia californica,2 monoclinic crystal form
35	d1f0xa2	Alignment	not modelled	96.8	16	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**FAD-linked oxidases, N-terminal domain
36	c2bvfA_	Alignment	not modelled	96.7	21	**PDB header:**oxidase **Chain:** A: **PDB Molecule:**6-hydroxy-d-nicotine oxidase; **PDBTitle:** crystal structure of 6-hydoxy-d-nicotine oxidase from2 arthrobacter nicotinovorans. crystal form 3 (p1)
37	c1hskA_	Alignment	not modelled	96.7	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**udp-n-acetylenolpyruvoylglucosamine reductase; **PDBTitle:** crystal structure of s. aureus murb
38	c1mbbA_	Alignment	not modelled	96.6	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**uridine diphospho-n-acetylenolpyruvylglucosamine **PDBTitle:** oxidoreductase
39	c2exrA_	Alignment	not modelled	96.6	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytokinin dehydrogenase 7; **PDBTitle:** x-ray structure of cytokinin oxidase/dehydrogenase (ckx)2 from arabidopsis thaliana at5g21482
40	c3pm9A_	Alignment	not modelled	96.3	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of a putative dehydrogenase (rpa1076) from2 rhodopseudomonas palustris cga009 at 2.57 a resolution
41	d2i0ka2	Alignment	not modelled	96.3	13	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**FAD-linked oxidases, N-terminal domain
42	c3js8A_	Alignment	not modelled	96.1	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cholesterol oxidase; **PDBTitle:** solvent-stable cholesterol oxidase
43	c3i99A_	Alignment	not modelled	95.7	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**udp-n-acetylenolpyruvoylglucosamine reductase; **PDBTitle:** the crystal structure of the udp-n-acetylenolpyruvoylglucosamine2 reductase from the vibrio cholerae o1 biovar tor
44	c1i19B_	Alignment	not modelled	95.6	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**cholesterol oxidase; **PDBTitle:** crystal structure of cholesterol oxidase from b.sterolicum
45	d1wvfa2	Alignment	not modelled	95.3	10	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**FAD-linked oxidases, N-terminal domain
46	c1wveB_	Alignment	not modelled	95.1	10	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**4-cresol dehydrogenase [hydroxylating] **PDBTitle:** p-cresol methylhydroxylase: alteration of the structure of2 the flavoprotein subunit upon its binding to the3 cytochrome subunit
47	d1uxya1	Alignment	not modelled	94.1	14	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase (MurB), N-terminal domain
48	c1ahuB_	Alignment	not modelled	92.8	8	**PDB header:**flavoenzyme **Chain:** B: **PDB Molecule:**vanillyl-alcohol oxidase; **PDBTitle:** structure of the octameric flavoenzyme vanillyl-alcohol2 oxidase in complex with p-cresol
49	d1e8ga2	Alignment	not modelled	91.0	8	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**FAD-linked oxidases, N-terminal domain
50	c2gquA_	Alignment	not modelled	86.6	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**udp-n-acetylenolpyruvylglucosamine reductase; **PDBTitle:** crystal structure of udp-n-acetylenolpyruvylglucosamine2 reductase (murb) from thermus caldophilus
51	d1w1oa2	Alignment	not modelled	85.3	13	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**FAD-linked oxidases, N-terminal domain
52	c2yvsA_	Alignment	not modelled	83.2	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glycolate oxidase subunit glce; **PDBTitle:** crystal structure of glycolate oxidase subunit glce from thermus2 thermophilus hb8
53	d1j3ka_	Alignment	not modelled	38.8	22	**Fold:**Dihydrofolate reductase-like **Superfamily:**Dihydrofolate reductase-like **Family:**Dihydrofolate reductases
						PDB header:oxidoreductase

54	c2blcA_	Alignment	not modelled	38.8	25	**Chain:** A: **PDB Molecule:**dihydrofolate reductase-thymidylate synthase; **PDBTitle:** sp21 double mutant p. vivax dihydrofolate reductase in2 complex with des-chloropyrimethamine
55	d3dfra_	Alignment	not modelled	26.0	19	**Fold:**Dihydrofolate reductase-like **Superfamily:**Dihydrofolate reductase-like **Family:**Dihydrofolate reductases
56	d1a9xa3	Alignment	not modelled	24.1	17	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
57	c3dg8B_	Alignment	not modelled	20.4	22	**PDB header:**oxidoreductase, transferase **Chain:** B: **PDB Molecule:**bifunctional dihydrofolate reductase-thymidylate **PDBTitle:** quadruple mutant (n51i+c59r+s108n+i164l) plasmodium2 falciparum dihydrofolate reductase-thymidylate synthase3 (pfdhfr-ts) complexed with rjf670, nadph, and dump
58	c3jsuA_	Alignment	not modelled	12.3	22	**PDB header:**oxidoreductase, transferase **Chain:** A: **PDB Molecule:**dihydrofolate reductase-thymidylate synthase; **PDBTitle:** quadruple mutant(n51i+c59r+s108n+i164l) plasmodium falciparum2 dihydrofolate reductase-thymidylate synthase(pfdhfr-ts) complexed3 with qn254, nadph, and dump
59	d1i1ga2	Alignment	not modelled	11.9	16	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Lrp/AsnC-like transcriptional regulator C-terminal domain
60	d1qwga_	Alignment	not modelled	11.6	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**(2r)-phospho-3-sulfolactate synthase ComA **Family:**(2r)-phospho-3-sulfolactate synthase ComA
61	d1u83a_	Alignment	not modelled	11.4	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**(2r)-phospho-3-sulfolactate synthase ComA **Family:**(2r)-phospho-3-sulfolactate synthase ComA
62	c1u83A_	Alignment	not modelled	11.4	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**phosphosulfolactate synthase; **PDBTitle:** psl synthase from bacillus subtilis
63	c2kr1A_	Alignment	not modelled	10.4	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**ubiquitin protein ligase e3a; **PDBTitle:** solution nmr structure of zinc binding n-terminal domain of ubiquitin-2 protein ligase e3a from homo sapiens. northeast structural genomics3 consortium (nesg) target hr3662
64	d1vdra_	Alignment	not modelled	10.0	25	**Fold:**Dihydrofolate reductase-like **Superfamily:**Dihydrofolate reductase-like **Family:**Dihydrofolate reductases
65	c2e1aD_	Alignment	not modelled	9.4	12	**PDB header:**transcription **Chain:** D: **PDB Molecule:**75aa long hypothetical regulatory protein asnc; **PDBTitle:** crystal structure of ffrp-dm1
66	d1jr1a4	Alignment	not modelled	9.4	21	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
67	c3q94B_	Alignment	not modelled	9.4	9	**PDB header:**lyase **Chain:** B: **PDB Molecule:**fructose-bisphosphate aldolase, class ii; **PDBTitle:** the crystal structure of fructose 1,6-bisphosphate aldolase from2 bacillus anthracis str. 'ames ancestor'
68	d1mo1a_	Alignment	not modelled	9.2	7	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
69	d1gvfa_	Alignment	not modelled	9.1	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class II FBP aldolase
70	c2zxkB_	Alignment	not modelled	9.0	4	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**red chlorophyll catabolite reductase, **PDBTitle:** crystal structure of semet-red chlorophyll catabolite2 reductase
71	c3e0bA_	Alignment	not modelled	8.9	33	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydrofolate reductase; **PDBTitle:** bacillus anthracis dihydrofolate reductase complexed with2 nadph and 2,4-diamino-5-(3-(2,5-dimethoxyphenyl)prop-1-3 ynyl)-6-ethylpyrimidine (ucp120b)
72	c2dyoB_	Alignment	not modelled	8.8	56	**PDB header:**protein turnover/protein turnover **Chain:** B: **PDB Molecule:**autophagy protein 16; **PDBTitle:** the crystal structure of saccharomyces cerevisiae atg5-2 atg16(1-57) complex
73	d1li4a2	Alignment	not modelled	8.7	20	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**S-adenosylhomocystein hydrolase
74	d1ou0a_	Alignment	not modelled	8.4	20	**Fold:**Flavodoxin-like **Superfamily:**Precorrin-8X methylmutase CbiC/CobH **Family:**Precorrin-8X methylmutase CbiC/CobH
75	c1zdrB_	Alignment	not modelled	8.2	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**dihydrofolate reductase; **PDBTitle:** dhfr from bacillus stearothermophilus
76	d1v8ba2	Alignment	not modelled	7.2	13	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**S-adenosylhomocystein hydrolase
77	c3ihsB_	Alignment	not modelled	7.0	9	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**phosphocarrier protein hpr; **PDBTitle:** crystal structure of a phosphocarrier protein hpr from2 bacillus anthracis str. ames
78	c3dhyC_	Alignment	not modelled	6.6	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

79	c2djwF_	Alignment	not modelled	6.6	25	**PDB header:**unknown function **Chain:** F: **PDB Molecule:**probable transcriptional regulator, asnc family; **PDBTitle:** crystal structure of ttha0845 from thermus thermophilus hb8
80	d1aoea_	Alignment	not modelled	6.5	23	**Fold:**Dihydrofolate reductase-like **Superfamily:**Dihydrofolate reductase-like **Family:**Dihydrofolate reductases
81	d1t6t1_	Alignment	not modelled	6.3	21	**Fold:**Toprim domain **Superfamily:**Toprim domain **Family:**Toprim domain
82	d1a9xa4	Alignment	not modelled	6.1	30	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
83	c2zbcH_	Alignment	not modelled	6.0	11	**PDB header:**transcription **Chain:** H: **PDB Molecule:**83aa long hypothetical transcriptional regulator asnc; **PDBTitle:** crystal structure of sts042, a stand-alone ram module protein, from2 hyperthermophilic archaeon sulfolobus tokodaii strain7.
84	d1cm3a_	Alignment	not modelled	5.9	13	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
85	c3gxxB_	Alignment	not modelled	5.9	17	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcription elongation factor spt6; **PDBTitle:** structure of the sh2 domain of the candida glabrata2 transcription elongation factor spt6, crystal form b
86	d1ou5a2	Alignment	not modelled	5.8	17	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Poly A polymerase head domain-like
87	c3d64A_	Alignment	not modelled	5.8	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adenosylhomocysteinase; **PDBTitle:** crystal structure of s-adenosyl-l-homocysteine hydrolase from2 burkholderia pseudomallei
88	c3oneA_	Alignment	not modelled	5.7	18	**PDB header:**hydrolase/hydrolase substrate **Chain:** A: **PDB Molecule:**adenosylhomocysteinase; **PDBTitle:** crystal structure of lupinus luteus s-adenosyl-l-homocysteine2 hydrolase in complex with adenine
89	c1v8bA_	Alignment	not modelled	5.6	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adenosylhomocysteinase; **PDBTitle:** crystal structure of a hydrolase
90	d2cg4a2	Alignment	not modelled	5.2	12	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Lrp/AsnC-like transcriptional regulator C-terminal domain
91	c3e56A_	Alignment	not modelled	5.2	10	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** the 2.0 angstrom resolution crystal structure of npr1517, a putative2 heterocyst differentiation inhibitor from nostoc punctiforme
92	c3n58D_	Alignment	not modelled	5.2	20	**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