Phyre2

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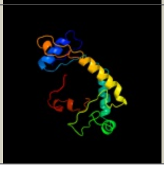
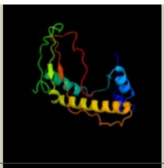
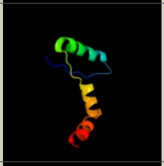
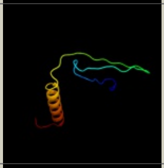
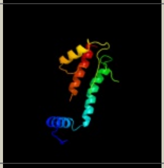
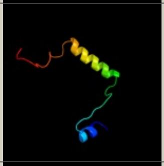
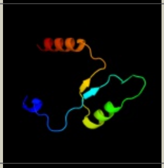
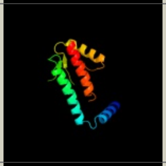
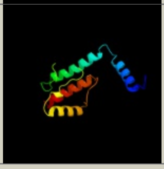
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2csga1	Alignment		100.0	85	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**YbiU-like
2	c2dbiA_	Alignment		100.0	98	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ybiu; **PDBTitle:** crystal structure of a hypothetical protein jw0805 from2 escherichia coli
3	c2opwA_	Alignment		99.3	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**phyhd1 protein; **PDBTitle:** crystal structure of human phytanoyl-coa dioxygenase phyhd1 (apo)
4	d2fcta1	Alignment		99.2	15	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**PhyH-like
5	d2a1xa1	Alignment		99.2	16	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**PhyH-like
6	c3gjbA_	Alignment		99.1	17	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**cytc3; **PDBTitle:** cytc3 with fe(ii) and alpha-ketoglutarate
7	c3emrA_	Alignment		99.0	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ectd; **PDBTitle:** crystal structure analysis of the ectoine hydroxylase ectd from2 salibacillus salexigens
8	c2rdsA_	Alignment		98.7	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**1-deoxypentalenic acid 11-beta hydroxylase; fe(ii)/alpha- **PDBTitle:** crystal structure of ptlh with fe/oxalylglycine and ent-1-2 deoxypentalenic acid bound
9	c3nnlB_	Alignment		98.0	18	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**cura; **PDBTitle:** halogenase domain from cura module (crystal form iii)
10	d1dcsa_	Alignment		96.7	16	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Penicillin synthase-like
11	c3on7C_	Alignment		95.9	18	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**oxidoreductase, iron/ascorbate family; **PDBTitle:** crystal structure of a putative oxygenase (so_2589) from shewanella2 oneidensis at 2.20 a resolution

12	c3ooxA_	Alignment		95.0	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative 2og-fe(ii) oxygenase family protein; **PDBTitle:** crystal structure of a putative 2og-fe(ii) oxygenase family protein2 (cc_0200) from caulobacter crescentus at 1.44 a resolution
13	d1w9ya1	Alignment		90.1	13	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Penicillin synthase-like
14	c3dkqB_	Alignment		89.8	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**pkhd-type hydroxylase sbal_3634; **PDBTitle:** crystal structure of putative oxygenase (yp_001051978.1) from2 shewanella baltica os155 at 2.26 a resolution
15	c3e77A_	Alignment		89.4	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoserine aminotransferase; **PDBTitle:** human phosphoserine aminotransferase in complex with plp
16	c2g19A_	Alignment		87.4	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**egl nine homolog 1; **PDBTitle:** cellular oxygen sensing: crystal structure of hypoxia-2 inducible factor prolyl hydroxylase (phd2)
17	c3ms5A_	Alignment		78.8	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**gamma-butyrobetaine dioxygenase; **PDBTitle:** crystal structure of human gamma-butyrobetaine,2-oxoglutarate2 dioxygenase 1 (bbox1)
18	d1gp6a_	Alignment		77.5	11	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Penicillin synthase-like
19	c3m5uA_	Alignment		76.7	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoserine aminotransferase; **PDBTitle:** crystal structure of phosphoserine aminotransferase from2 campylobacter jejuni
20	d2c0ra1	Alignment		76.1	16	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
21	c3qm2A_	Alignment	not modelled	68.7	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoserine aminotransferase; **PDBTitle:** 2.25 angstrom crystal structure of phosphoserine aminotransferase2 (serc) from salmonella enterica subsp. enterica serovar typhimurium
22	d1odma_	Alignment	not modelled	66.3	7	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Penicillin synthase-like
23	d1w23a_	Alignment	not modelled	65.0	14	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
24	d2z1ca1	Alignment	not modelled	57.1	25	**Fold:**OB-fold **Superfamily:**HupF/HypC-like **Family:**HupF/HypC-like
25	c2jijA_	Alignment	not modelled	51.4	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**prolyl-4 hydroxylase; **PDBTitle:** crystal structure of the apo form of chlamydomonas2 reinhardtii prolyl-4 hydroxylase type i
26	d1v70a_	Alignment	not modelled	49.7	18	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
27	c3ouiA_	Alignment	not modelled	49.7	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**egl nine homolog 1; **PDBTitle:** phd2-r717 with 40787422
28	c3pvjB_	Alignment	not modelled	48.5	3	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**alpha-ketoglutarate-dependent taurine dioxygenase; **PDBTitle:** crystal structure of the fe(ii)/alpha-ketoglutarate dependent taurine2 dioxygenase from pseudomonas putida kt2440

29	d1y9qa2	Alignment	not modelled	44.9	24	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Probable transcriptional regulator VC1968, C-terminal domain
30	d2toda1	Alignment	not modelled	44.8	14	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
31	c3gt2A_	Alignment	not modelled	44.1	18	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of the p60 domain from m. avium2 paratuberculosis antigen map1272c
32	d1bjna_	Alignment	not modelled	44.0	14	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
33	c3pbiA_	Alignment	not modelled	43.5	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**invasion protein; **PDBTitle:** structure of the peptidoglycan hydrolase ripb (rv1478) from2 mycobacterium tuberculosis at 1.6 resolution
34	d2ot2a1	Alignment	not modelled	43.3	26	**Fold:**OB-fold **Superfamily:**HupF/HypC-like **Family:**HupF/HypC-like
35	c3itqB_	Alignment	not modelled	43.2	23	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**prolyl 4-hydroxylase, alpha subunit domain protein; **PDBTitle:** crystal structure of a prolyl 4-hydroxylase from bacillus anthracis
36	d1otja_	Alignment	not modelled	42.8	6	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**TauD/TfdA-like
37	c2a1dH_	Alignment	not modelled	42.5	11	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** H: **PDB Molecule:**staphylocoagulase; **PDBTitle:** staphylocoagulase bound to bovine thrombin
38	c3r1jB_	Alignment	not modelled	42.1	6	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**alpha-ketoglutarate-dependent taurine dioxygenase; **PDBTitle:** crystal structure of alpha-ketoglutarate-dependent taurine dioxygenase2 from mycobacterium avium, native form
39	d2bnma2	Alignment	not modelled	41.8	19	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1459-like
40	c2doqD_	Alignment	not modelled	40.5	43	**PDB header:**cell cycle **Chain:** D: **PDB Molecule:**sfi1p; **PDBTitle:** crystal structure of sfi1p/cdc31p complex
41	d1bw0a_	Alignment	not modelled	40.3	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
42	d1q3qa2	Alignment	not modelled	40.2	13	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**Group II chaperonin (CCT, TRIC), apical domain
43	d1oiha_	Alignment	not modelled	39.6	10	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**TauD/TfdA-like
44	c2hbkA_	Alignment	not modelled	37.1	12	**PDB header:**hydrolase, gene regulation **Chain:** A: **PDB Molecule:**exosome complex exonuclease rrp6; **PDBTitle:** structure of the yeast nuclear exosome component, rrp6p,2 reveals an interplay between the active site and the hrdc3 domain; protein in complex with mn
45	d7odca1	Alignment	not modelled	36.9	27	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
46	c3sahA_	Alignment	not modelled	35.5	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exosome component 10; **PDBTitle:** crystal structure of the human rrp6 catalytic domain with y436a2 mutation in the catalytic site
47	c3cewA_	Alignment	not modelled	35.0	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized cupin protein; **PDBTitle:** crystal structure of a cupin protein (bf4112) from bacteroides2 fragilis. northeast structural genomics consortium target bfr205
48	c3d3rA_	Alignment	not modelled	35.0	21	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**hydrogenase assembly chaperone hypc/hupf; **PDBTitle:** crystal structure of the hydrogenase assembly chaperone hypc/hupf2 family protein from shewanella oneidensis mr-1
49	d1g7oa1	Alignment	not modelled	34.8	12	**Fold:**GST C-terminal domain-like **Superfamily:**GST C-terminal domain-like **Family:**Glutathione S-transferase (GST), C-terminal domain
50	c3h7yA_	Alignment	not modelled	34.6	9	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**bacilysin biosynthesis protein bacb; **PDBTitle:** crystal structure of bacb, an enzyme involved in bacilysin synthesis,2 in tetragonal form
51	d3d3ra1	Alignment	not modelled	34.2	21	**Fold:**OB-fold **Superfamily:**HupF/HypC-like **Family:**HupF/HypC-like
52	c2on3A_	Alignment	not modelled	33.7	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**ornithine decarboxylase; **PDBTitle:** a structural insight into the inhibition of human and2 leishmania donovani ornithine decarboxylases by 3-aminooxy-3 1-aminopropane
53	c3cp8C_	Alignment	not modelled	33.3	15	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**trna uridine 5-carboxymethylaminomethyl **PDBTitle:** crystal structure of gida from chlorobium tepidum
						Fold:PLP-dependent transferase-like

54	d1vp4a_	Alignment	not modelled	33.3	14	**Superfamily:**PLP-dependent transferases **Family:**AAT-like
55	d2hbka2	Alignment	not modelled	31.6	12	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
56	c3kt4A_	Alignment	not modelled	30.9	5	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pkhd-type hydroxylase tpa1; **PDBTitle:** crystal structure of tpa1 from saccharomyces cerevisiae, a2 component of the messenger ribonucleoprotein complex
57	d1f3ta1	Alignment	not modelled	30.7	14	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
58	c2xivA_	Alignment	not modelled	30.4	13	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**hypothetical invasion protein; **PDBTitle:** structure of rv1477, hypothetical invasion protein of2 mycobacterium tuberculosis
59	d2evra2	Alignment	not modelled	30.1	43	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**NlpC/P60
60	c3fcrA_	Alignment	not modelled	27.8	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative aminotransferase; **PDBTitle:** crystal structure of putative aminotransferase (yp_614685.1) from2 silicibacter sp. tm1040 at 1.80 a resolution
61	d1njjb1	Alignment	not modelled	27.7	14	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
62	d1sfna_	Alignment	not modelled	27.6	16	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
63	d1pmma_	Alignment	not modelled	27.2	19	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Pyridoxal-dependent decarboxylase
64	c3lnoA_	Alignment	not modelled	26.8	9	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of domain of unknown function duf59 from2 bacillus anthracis
65	c3bq9A_	Alignment	not modelled	26.6	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**predicted rossmann fold nucleotide-binding domain- **PDBTitle:** crystal structure of predicted nucleotide-binding protein from2 idiomarina baltica os145
66	c3dxvA_	Alignment	not modelled	26.4	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**alpha-amino-epsilon-caprolactam racemase; **PDBTitle:** the crystal structure of alpha-amino-epsilon-caprolactam racemase from2 achromobacter obae
67	c3thtB_	Alignment	not modelled	25.9	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**alkylated dna repair protein alkb homolog 8; **PDBTitle:** crystal structure and rna binding properties of the rrm/alkb domains2 in human abh8, an enzyme catalyzing trna hypermodification, northeast3 structural genomics consortium target hr5601b
68	d1uwda_	Alignment	not modelled	25.6	14	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Fe-S cluster assembly (FSCA) domain-like **Family:**PaaD-like
69	c2fg0B_	Alignment	not modelled	25.4	43	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cog0791: cell wall-associated hydrolases (invasion- **PDBTitle:** crystal structure of a putative gamma-d-glutamyl-l-diamino acid2 endopeptidase (npun_r0659) from nostoc punctiforme pcc 73102 at 1.793 a resolution
70	c1knwA_	Alignment	not modelled	25.3	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**diaminopimelate decarboxylase; **PDBTitle:** crystal structure of diaminopimelate decarboxylase
71	c3ibmB_	Alignment	not modelled	24.4	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**cupin 2, conserved barrel domain protein; **PDBTitle:** crystal structure of cupin 2 domain-containing protein hhal_0468 from2 halorhodospira halophila
72	c2wl2B_	Alignment	not modelled	24.3	15	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**dna gyrase subunit a; **PDBTitle:** crystal structure of n-terminal domain of gyra with the2 antibiotic simocyclinone d8
73	c2ozjB_	Alignment	not modelled	22.8	22	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**cupin 2, conserved barrel; **PDBTitle:** crystal structure of a cupin superfamily protein (dsy2733) from2 desulfitobacterium hafniense dcb-2 at 1.60 a resolution
74	c2xcqA_	Alignment	not modelled	22.8	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**dna gyrase subunit b, dna gyrase subunit a; **PDBTitle:** the 2.98a crystal structure of the catalytic core (b'a'2 region) of staphylococcus aureus dna gyrase
75	c3s6eB_	Alignment	not modelled	22.5	23	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**rna-binding protein 39; **PDBTitle:** crystal structure of a rna binding motif protein 39 (rbm39) from mus2 musculus at 0.95 a resolution
76	c3t18D_	Alignment	not modelled	22.2	14	**PDB header:**transferase **Chain:** D: **PDB Molecule:**aminotransferase class i and ii; **PDBTitle:** crystal structure of aminotransferase from anaerococcus prevotii dsm2 20548.
77	c3h41A_	Alignment	not modelled	22.0	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nlp/p60 family protein; **PDBTitle:** crystal structure of a nlpc/p60 family protein (bce_2878) from2 bacillus cereus atcc 10987 at 1.79 a resolution
						PDB header:structural genomics, unknown function

78	c3h8uA_	Alignment	not modelled	21.5	17	**Chain:** A: **PDB Molecule:**uncharacterized conserved protein with double-stranded **PDBTitle:** crystal structure of uncharacterized conserved protein with double-2 stranded beta-helix domain (yp_001338853.1) from klebsiella3 pneumoniae subsp. pneumoniae mgh 78578 at 1.80 a resolution
79	c3jzvA_	Alignment	not modelled	21.5	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein rru_a2000; **PDBTitle:** crystal structure of rru_a2000 from rhodospirillum rubrum: a cupin-22 domain.
80	d1d7ka1	Alignment	not modelled	20.9	19	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
81	d2mev1_	Alignment	not modelled	20.6	19	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Picornaviridae-like VP (VP1, VP2, VP3 and VP4)
82	d1t0fa2	Alignment	not modelled	20.6	20	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**TnsA endonuclease, N-terminal domain
83	c2pfyA_	Alignment	not modelled	20.5	17	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative exported protein; **PDBTitle:** crystal structure of dctp7, a bordetella pertussis2 extracytoplasmic solute receptor binding pyroglutamic acid
84	d1apaa_	Alignment	not modelled	20.3	11	**Fold:**Ribosome inactivating proteins (RIP) **Superfamily:**Ribosome inactivating proteins (RIP) **Family:**Plant cytotoxins
85	c3dnfB_	Alignment	not modelled	20.3	23	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**4-hydroxy-3-methylbut-2-enyl diphosphate reductase; **PDBTitle:** structure of (e)-4-hydroxy-3-methyl-but-2-enyl diphosphate reductase,2 the terminal enzyme of the non-mevalonate pathway
86	c2xcsD_	Alignment	not modelled	20.1	17	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**dna gyrase subunit b, dna gyrase subunit a; **PDBTitle:** the 2.1a crystal structure of s. aureus gyrase complex with gsk2994232 and dna
87	c2kp6A_	Alignment	not modelled	19.9	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of protein cv0237 from2 chromobacterium violaceum. northeast structural genomics3 consortium (nesg) target cvt1
88	c3dydB_	Alignment	not modelled	19.8	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**tyrosine aminotransferase; **PDBTitle:** human tyrosine aminotransferase
89	c2pb2B_	Alignment	not modelled	19.7	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**acetylornithine/succinyldiaminopimelate aminotransferase; **PDBTitle:** structure of biosynthetic n-acetylornithine aminotransferase from2 salmonella typhimurium: studies on substrate specificity and3 inhibitor binding
90	c2vpvA_	Alignment	not modelled	19.7	3	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**protein mif2; **PDBTitle:** dimerization domain of mif2p
91	d1knwa1	Alignment	not modelled	19.4	22	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
92	c3fjsC_	Alignment	not modelled	18.8	13	**PDB header:**biosynthetic protein **Chain:** C: **PDB Molecule:**uncharacterized protein with rmlc-like cupin fold; **PDBTitle:** crystal structure of a putative biosynthetic protein with rmlc-like2 cupin fold (reut_b4087) from ralstonia eutropha jmp134 at 1.90 a3 resolution
93	d1y0ka1	Alignment	not modelled	18.6	41	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**PA4535-like
94	c3uyjA_	Alignment	not modelled	18.4	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**lysine-specific demethylase 8; **PDBTitle:** crystal structure of jmjd5 catalytic core domain in complex with2 nickle and alpha-kg
95	c1e40A_	Alignment	not modelled	18.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-amylase; **PDBTitle:** tris/maltotriose complex of chimaeric amylase from b.2 amyloliquefaciens and b. licheniformis at 2.2a
96	d1zvpa1	Alignment	not modelled	17.9	60	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**VC0802-like
97	d1bvua2	Alignment	not modelled	17.4	18	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
98	d1gtma2	Alignment	not modelled	16.7	18	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
99	c2p3eA_	Alignment	not modelled	16.4	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**diaminopimelate decarboxylase; **PDBTitle:** crystal structure of aq1208 from aquifex aeolicus