Phyre^2

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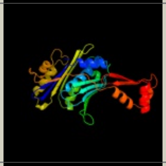
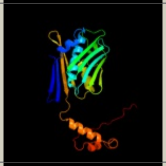
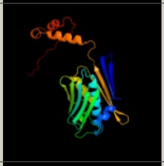
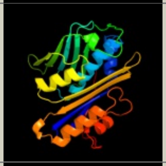
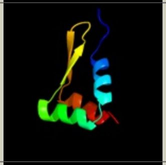
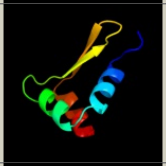
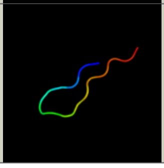
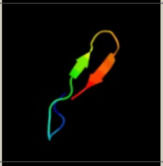
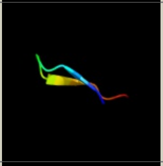
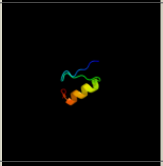
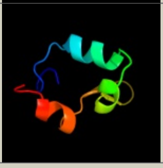
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1vzyA_	Alignment		100.0	24	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**33 kda chaperonin; **PDBTitle:** crystal structure of the bacillus subtilis hsp33
2	c1vq0A_	Alignment		100.0	24	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**33 kda chaperonin; **PDBTitle:** crystal structure of 33 kda chaperonin (heat shock protein 33 homolog)2 (hsp33) (tm1394) from thermotoga maritima at 2.20 a resolution
3	c1hw7A_	Alignment		100.0	100	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**heat shock protein hsp33; **PDBTitle:** hsp33, heat shock protein with redox-regulated chaperone activity
4	d1hw7a_	Alignment		100.0	100	**Fold:**Hsp33 domain **Superfamily:**Hsp33 domain **Family:**Hsp33 domain
5	c1i7fA_	Alignment		100.0	97	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**heat shock protein 33; **PDBTitle:** crystal structure of the hsp33 domain with constitutive chaperone2 activity
6	d1vzya1	Alignment		100.0	24	**Fold:**Hsp33 domain **Superfamily:**Hsp33 domain **Family:**Hsp33 domain
7	d1vq0a1	Alignment		100.0	23	**Fold:**Hsp33 domain **Superfamily:**Hsp33 domain **Family:**Hsp33 domain
8	d1xjha_	Alignment		99.8	100	**Fold:**HSP33 redox switch-like **Superfamily:**HSP33 redox switch-like **Family:**HSP33 redox switch-like
9	d1vzya2	Alignment		99.7	30	**Fold:**HSP33 redox switch-like **Superfamily:**HSP33 redox switch-like **Family:**HSP33 redox switch-like
10	d1vq0a2	Alignment		99.6	28	**Fold:**HSP33 redox switch-like **Superfamily:**HSP33 redox switch-like **Family:**HSP33 redox switch-like
11	c2jz8A_	Alignment		67.4	27	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein bh09830; **PDBTitle:** solution nmr structure of bh09830 from bartonella henselae2 modeled with one zn+2 bound. northeast structural genomics3 consortium target bnr55

12	c2h3eB_	Alignment		59.3	24	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aspartate carbamoyltransferase regulatory chain; **PDBTitle:** structure of wild-type e. coli aspartate transcarbamoylase in the2 presence of n-phosphonacetyl-l-isoasparagine at 2.3a resolution
13	d2fzcb2	Alignment		54.2	21	**Fold:**Rubredoxin-like **Superfamily:**Aspartate carbamoyltransferase, Regulatory-chain, C-terminal domain **Family:**Aspartate carbamoyltransferase, Regulatory-chain, C-terminal domain
14	d1ywsa1	Alignment		50.4	24	**Fold:**Rubredoxin-like **Superfamily:**CSL zinc finger **Family:**CSL zinc finger
15	c1pg5B_	Alignment		48.2	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aspartate carbamoyltransferase regulatory chain; **PDBTitle:** crystal structure of the unligated (t-state) aspartate2 transcarbamoylase from the extremely thermophilic archaeon sulfolobus3 acidocaldarius
16	c2jrrA_	Alignment		47.8	29	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of q5lls5 from silicibacter2 pomeroyi. northeast structural genomics consortium target3 sir90
17	d1pg5b2	Alignment		44.6	19	**Fold:**Rubredoxin-like **Superfamily:**Aspartate carbamoyltransferase, Regulatory-chain, C-terminal domain **Family:**Aspartate carbamoyltransferase, Regulatory-chain, C-terminal domain
18	c2eluA_	Alignment		40.8	32	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein 406; **PDBTitle:** solution structure of the 5th c2h2 zinc finger of human2 zinc finger protein 406
19	c2zaeB_	Alignment		38.8	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ribonuclease p protein component 4; **PDBTitle:** crystal structure of protein ph1601p in complex with protein ph1771p2 of archaeal ribonuclease p from pyrococcus horikoshii ot3
20	c1y6uA_	Alignment		37.3	11	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**excisionase from transposon tn916; **PDBTitle:** the structure of the excisionase (xis) protein from2 conjugative transposon tn916 provides insights into the3 regulation of heterobivalent tyrosine recombinases
21	c2jvmA_	Alignment	not modelled	36.3	31	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of rhodobacter sphaeroides protein2 rhos4_26430. northeast structural genomics consortium3 target rhr95
22	d1zu1a1	Alignment	not modelled	34.4	21	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**HkH motif-containing C2H2 finger
23	d1nzja_	Alignment	not modelled	31.9	32	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
24	d1gtra2	Alignment	not modelled	30.7	5	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
25	d2atcb2	Alignment	not modelled	27.9	25	**Fold:**Rubredoxin-like **Superfamily:**Aspartate carbamoyltransferase, Regulatory-chain, C-terminal domain **Family:**Aspartate carbamoyltransferase, Regulatory-chain, C-terminal domain
26	c2eodA_	Alignment	not modelled	27.9	24	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**tnf receptor-associated factor 4; **PDBTitle:** solution structure of traf-type zinc finger domains (190-248) from human tnf receptor-associated factor 4
27	c2be7E_	Alignment	not modelled	27.5	25	**PDB header:**transferase **Chain:** E: **PDB Molecule:**aspartate carbamoyltransferase regulatory chain; **PDBTitle:** crystal structure of the unliganded (t-state) aspartate2 transcarbamoylase of the psychrophilic bacterium moritella profunda
						Fold: Rubredoxin-like

28	d1wiia_	Alignment	not modelled	27.0	10	**Superfamily:**Zinc beta-ribbon **Family:**Putative zinc binding domain
29	c2l8eA_	Alignment	not modelled	26.6	44	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**polyhomeotic-like protein 1; **PDBTitle:** solution nmr structure of fcs domain of human polyhomeotic homolog 12 (hph1)
30	c3mv2A_	Alignment	not modelled	26.0	13	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**coatomer subunit alpha; **PDBTitle:** crystal structure of a-cop in complex with e-cop
31	c3q9qB_	Alignment	not modelled	26.0	16	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**heat shock protein beta-1; **PDBTitle:** hspb1 fragment second crystal form
32	c3t7vA_	Alignment	not modelled	25.2	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methylornithine synthase pylb; **PDBTitle:** crystal structure of methylornithine synthase (pylb)
33	c2xvcA_	Alignment	not modelled	23.8	8	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**escrt-iii; **PDBTitle:** molecular and structural basis of escrt-iii recruitment to2 membranes during archaeal cell division
34	d1j09a2	Alignment	not modelled	23.2	10	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
35	c2elpA_	Alignment	not modelled	22.1	29	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein 406; **PDBTitle:** solution structure of the 13th c2h2 zinc finger of human2 zinc finger protein 406
36	d1wgea1	Alignment	not modelled	21.2	16	**Fold:**Rubredoxin-like **Superfamily:**CSL zinc finger **Family:**CSL zinc finger
37	c3mkrB_	Alignment	not modelled	20.8	27	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**coatomer subunit alpha; **PDBTitle:** crystal structure of yeast alpha/epsilon-cop subcomplex of the copi2 vesicular coat
38	c2wulB_	Alignment	not modelled	20.8	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glutaredoxin related protein 5; **PDBTitle:** crystal structure of the human glutaredoxin 5 with bound2 glutathione in an fes cluster
39	c2ywwA_	Alignment	not modelled	20.8	19	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**aspartate carbamoyltransferase regulatory chain; **PDBTitle:** crystal structure of aspartate carbamoyltransferase2 regulatory chain from methanocaldococcus jannaschii
40	c2d0oA_	Alignment	not modelled	20.8	15	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**diol dehydratase-reactivating factor large **PDBTitle:** strcuture of diol dehydratase-reactivating factor complexed2 with adp and mg2+
41	c1wysA_	Alignment	not modelled	20.8	30	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**riken cdna 2310008m20 protein; **PDBTitle:** solution structure of the first zf-an1 domain of mouse2 riken cdna 2310008m20 protein
42	d2yrka1	Alignment	not modelled	20.7	36	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**HkH motif-containing C2H2 finger
43	c2k5rA_	Alignment	not modelled	20.6	0	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein xf2673; **PDBTitle:** solution nmr structure of xf2673 from xylella fastidiosa.2 northeast structural genomics consortium target xfr39
44	c1pqvS_	Alignment	not modelled	20.1	30	**PDB header:**transferase/transcription **Chain:** S: **PDB Molecule:**transcription elongation factor s-ii; **PDBTitle:** rna polymerase ii-tfiis complex
45	c1y1yS_	Alignment	not modelled	20.1	30	**PDB header:**transferase/transcription/dna-rna hybrid **Chain:** S: **PDB Molecule:**transcription elongation factor s-ii; **PDBTitle:** rna polymerase ii-tfiis-dna/rna complex
46	d1gx5a_	Alignment	not modelled	19.4	17	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**RNA-dependent RNA-polymerase
47	c2xigA_	Alignment	not modelled	18.9	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**ferric uptake regulation protein; **PDBTitle:** the structure of the helicobacter pylori ferric uptake2 regulator fur reveals three functional metal binding sites
48	c2w0tA_	Alignment	not modelled	18.9	29	**PDB header:**transcription **Chain:** A: **PDB Molecule:**lethal(3)malignant brain tumor-like 2 protein; **PDBTitle:** solution structure of the fcs zinc finger domain of human2 lmbl2
49	d1vd4a_	Alignment	not modelled	18.1	11	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
50	c2l6lA_	Alignment	not modelled	17.7	24	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**dnaj homolog subfamily c member 24; **PDBTitle:** solution structure of human j-protein co-chaperone, dph4
51	c3iufA_	Alignment	not modelled	17.5	41	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**zinc finger protein ubi-d4; **PDBTitle:** crystal structure of the c2h2-type zinc finger domain of2 human ubi-d4
52	d1hxra_	Alignment	not modelled	17.3	33	**Fold:**Mss4-like **Superfamily:**Mss4-like **Family:**RabGEF Mss4
53	d1wfea_	Alignment	not modelled	17.3	30	**Fold:**AN1-like Zinc finger **Superfamily:**AN1-like Zinc finger **Family:**AN1-like Zinc finger
						Fold:DNA/RNA polymerases

54	d1nb4a_	Alignment	not modelled	16.9	17	**Superfamily:**DNA/RNA polymerases **Family:**RNA-dependent RNA-polymerase
55	c3cixA_	Alignment	not modelled	16.5	45	**PDB header:**adomet binding protein **Chain:** A: **PDB Molecule:**fefe-hydrogenase maturase; **PDBTitle:** x-ray structure of the [fefe]-hydrogenase maturase hyde from2 thermotoga maritima in complex with thiocyanate
56	d2jnya1	Alignment	not modelled	16.3	8	**Fold:**Trm112p-like **Superfamily:**Trm112p-like **Family:**Trm112p-like
57	c1zu1A_	Alignment	not modelled	16.3	27	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**rna binding protein zfa; **PDBTitle:** solution structure of the n-terminal zinc fingers of the2 xenopus laevis double stranded rna binding protein zfa
58	c2j6aA_	Alignment	not modelled	16.2	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein trm112; **PDBTitle:** crystal structure of s. cerevisiae ynr046w, a zinc finger2 protein from the erf1 methyltransferase complex.
59	d2dkta1	Alignment	not modelled	15.7	14	**Fold:**CHY zinc finger-like **Superfamily:**CHY zinc finger-like **Family:**CHY zinc finger
60	c1xf7A_	Alignment	not modelled	15.4	22	**PDB header:**transcription **Chain:** A: **PDB Molecule:**wilms' tumor protein; **PDBTitle:** high resolution nmr structure of the wilms' tumor2 suppressor protein (wt1) finger 3
61	d1xf7a_	Alignment	not modelled	15.4	22	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
62	d2fu5a1	Alignment	not modelled	15.3	33	**Fold:**Mss4-like **Superfamily:**Mss4-like **Family:**RabGEF Mss4
63	d2pk7a1	Alignment	not modelled	15.3	15	**Fold:**Trm112p-like **Superfamily:**Trm112p-like **Family:**Trm112p-like
64	c1rikA_	Alignment	not modelled	15.0	22	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**e6apc1 peptide; **PDBTitle:** e6-binding zinc finger (e6apc1)
65	c1arfA_	Alignment	not modelled	14.5	22	**PDB header:**transcription regulation **Chain:** A: **PDB Molecule:**yeast transcription factor adr1; **PDBTitle:** structures of dna-binding mutant zinc finger domains:2 implications for dna binding
66	d1llmc2	Alignment	not modelled	14.5	44	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
67	d1tkea2	Alignment	not modelled	14.4	7	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**ThrRS/AlaRS common domain **Family:**Threonyl-tRNA synthetase (ThrRS), second 'additional' domain
68	c3py7A_	Alignment	not modelled	14.4	23	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**maltose-binding periplasmic protein,paxillin ld1,protein e6 **PDBTitle:** crystal structure of full-length bovine papillomavirus oncoprotein e62 in complex with ld1 motif of paxillin at 2.3a resolution
69	d1wima_	Alignment	not modelled	14.3	14	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**RING finger domain, C3HC4
70	d1wpba_	Alignment	not modelled	14.2	33	**Fold:**YfbU-like **Superfamily:**YfbU-like **Family:**YfbU-like
71	d2dmda2	Alignment	not modelled	13.9	50	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
72	c2js4A_	Alignment	not modelled	13.9	8	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0434 protein bb2007; **PDBTitle:** solution nmr structure of bordetella bronchiseptica protein2 bb2007. northeast structural genomics consortium target3 bor54
73	c2hz7A_	Alignment	not modelled	13.5	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutaminyl-trna synthetase; **PDBTitle:** crystal structure of the glutaminyl-trna synthetase from2 deinococcus radiodurans
74	c2jr7A_	Alignment	not modelled	13.4	16	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**dph3 homolog; **PDBTitle:** solution structure of human desr1
75	d2hf1a1	Alignment	not modelled	13.2	8	**Fold:**Trm112p-like **Superfamily:**Trm112p-like **Family:**Trm112p-like
76	d1k81a_	Alignment	not modelled	12.8	23	**Fold:**Zinc-binding domain of translation initiation factor 2 beta **Superfamily:**Zinc-binding domain of translation initiation factor 2 beta **Family:**Zinc-binding domain of translation initiation factor 2 beta
77	d1a1ia3	Alignment	not modelled	12.8	44	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
78	d2yt9a2	Alignment	not modelled	12.8	27	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
79	c3ol0C_	Alignment	not modelled	12.8	23	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**de novo designed monomer trefoil-fold sub-domain which **PDBTitle:** crystal structure of monofoil-4p homo-trimer: de novo designed monomer2 trefoil-fold sub-domain which forms homo-trimer assembly

80	d1njqa_	Alignment	not modelled	12.7	22	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Plant C2H2 finger (QALGGH zinc finger)
81	c3iraA_	Alignment	not modelled	12.7	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved protein; **PDBTitle:** the crystal structure of one domain of the conserved protein from2 methanosarcina mazei go1
82	d1vbka2	Alignment	not modelled	12.6	8	**Fold:**THUMP domain **Superfamily:**THUMP domain-like **Family:**THUMP domain
83	c2d9kA_	Alignment	not modelled	12.6	13	**PDB header:**immune system **Chain:** A: **PDB Molecule:**fln29 gene product; **PDBTitle:** solution structure of the zf-traf domain of fln29 gene2 product
84	c3h5jA_	Alignment	not modelled	12.5	32	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3-isopropylmalate dehydratase small subunit; **PDBTitle:** leud_1-168 small subunit of isopropylmalate isomerase (rv2987c) from2 mycobacterium tuberculosis
85	d2ds5a1	Alignment	not modelled	12.5	38	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**ClpX chaperone zinc binding domain
86	c2pjhA_	Alignment	not modelled	12.3	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**nuclear protein localization protein 4 homolog; **PDBTitle:** strctural model of the p97 n domain- npl4 ubd complex
87	d1k3sa_	Alignment	not modelled	12.2	15	**Fold:**Secretion chaperone-like **Superfamily:**Type III secretory system chaperone-like **Family:**Type III secretory system chaperone
88	c1ovxB_	Alignment	not modelled	12.1	38	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**atp-dependent clp protease atp-binding subunit clpx; **PDBTitle:** nmr structure of the e. coli clpx chaperone zinc binding domain dimer
89	c3e2iA_	Alignment	not modelled	12.1	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thymidine kinase; **PDBTitle:** crystal structure of thymidine kinase from s. aureus
90	c2hlgA_	Alignment	not modelled	12.0	29	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**fruit-specific protein; **PDBTitle:** nmr solution structure of a new tomato peptide
91	c4a17Y_	Alignment	not modelled	11.9	30	**PDB header:**ribosome **Chain:** Y: **PDB Molecule:**rpl37a; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 2.
92	d2ct1a2	Alignment	not modelled	11.9	22	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
93	c1x4vA_	Alignment	not modelled	11.9	20	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**hypothetical protein loc130617; **PDBTitle:** solution structure of the zf-an1 domain from human2 hypothetical protein loc130617
94	d1kjwa2	Alignment	not modelled	11.8	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
95	d1e4ft2	Alignment	not modelled	11.6	8	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
96	c3aiiA_	Alignment	not modelled	11.5	27	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamyl-trna synthetase; **PDBTitle:** archaeal non-discriminating glutamyl-trna synthetase from2 methanothermobacter thermautotrophicus
97	d1nj1a2	Alignment	not modelled	11.5	33	**Fold:**IF3-like **Superfamily:**C-terminal domain of ProRS **Family:**C-terminal domain of ProRS
98	c1tr8A_	Alignment	not modelled	11.4	23	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**conserved protein (mth177); **PDBTitle:** crystal structure of archaeal nascent polypeptide-associated complex2 (aenac)
99	c2hcuA_	Alignment	not modelled	11.3	37	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3-isopropylmalate dehydratase small subunit; **PDBTitle:** crystal structure of smu.1381 (or leud) from streptococcus2 mutans