Phyre^2

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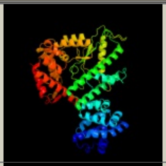
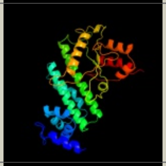
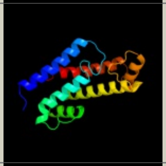
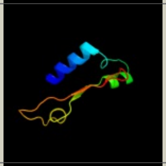
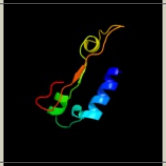
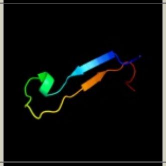
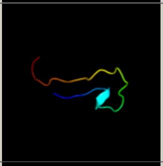
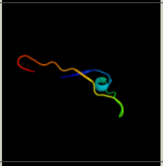
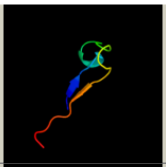
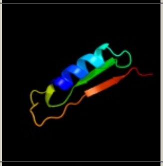
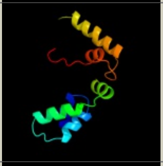
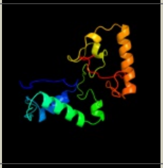
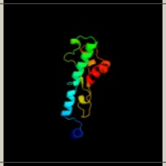
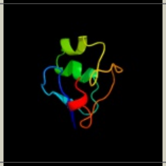
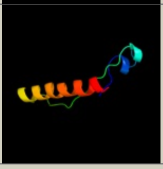
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3k7dA_	Alignment		100.0	100	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutamate-ammonia-ligase adenylyltransferase; **PDBTitle:** c-terminal (adenylylation) domain of e.coli glutamine synthetase2 adenylyltransferase
2	c1v4aA_	Alignment		100.0	97	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutamate-ammonia-ligase adenylyltransferase; **PDBTitle:** structure of the n-terminal domain of escherichia coli2 glutamine synthetase adenylyltransferase
3	d1v4aa2	Alignment		100.0	97	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**GlnE-like domain
4	d1v4aa1	Alignment		100.0	97	**Fold:**Four-helical up-and-down bundle **Superfamily:**Nucleotidyltransferase substrate binding subunit/domain **Family:**Glutamine synthase adenylyltransferase GlnE, domain 2
5	d1knya2	Alignment		95.7	22	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Kanamycin nucleotidyltransferase (KNTase), N-terminal domain
6	c1knyA_	Alignment		95.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**kanamycin nucleotidyltransferase; **PDBTitle:** kanamycin nucleotidyltransferase
7	c2rffA_	Alignment		93.7	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative nucleotidyltransferase; **PDBTitle:** crystal structure of a putative nucleotidyltransferase2 (np_343093.1) from sulfolobus solfataricus at 1.40 a3 resolution
8	d1no5a_	Alignment		91.0	26	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Catalytic subunit of bi-partite nucleotidyltransferase
9	d1wota_	Alignment		89.1	31	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Catalytic subunit of bi-partite nucleotidyltransferase
10	c3c66B_	Alignment		87.3	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**poly(a) polymerase; **PDBTitle:** yeast poly(a) polymerase in complex with fip1 residues 80-105
11	c1q78A_	Alignment		86.5	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly(a) polymerase alpha; **PDBTitle:** crystal structure of poly(a) polymerase in complex with 3'-2 datp and magnesium chloride

12	d1ylqa1	Alignment		85.1	27	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Catalytic subunit of bi-partite nucleotidyltransferase
13	c3jz0B_	Alignment		76.8	20	**PDB header:**transferase/antibiotic **Chain:** B: **PDB Molecule:**lincosamide nucleotidyltransferase; **PDBTitle:** linb complexed with clindamycin and ampcpp
14	c3o7kA_	Alignment		69.4	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**ohcu decarboxylase; **PDBTitle:** crystal structure of 2-oxo-4-hydroxy-4-carboxy-5-ureidoimidazoline2 decarboxylase from klebsiella pneumoniae
15	d1q79a2	Alignment		66.9	14	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Poly(A) polymerase, PAP, N-terminal domain
16	c1kdhA_	Alignment		60.8	13	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**terminal deoxynucleotidyltransferase short **PDBTitle:** binary complex of murine terminal deoxynucleotidyl2 transferase with a primer single stranded dna
17	d2o70a1	Alignment		57.8	18	**Fold:**UraD-like **Superfamily:**UraD-Like **Family:**UraD-like
18	d2q66a2	Alignment		57.2	12	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Poly(A) polymerase, PAP, N-terminal domain
19	c3hvzB_	Alignment		55.9	12	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the tgs domain of the clolep_03100 protein from2 clostridium leptum, northeast structural genomics consortium target3 qlr13a
20	c1sz1A_	Alignment		54.5	20	**PDB header:**transferase/rna **Chain:** A: **PDB Molecule:**trna nucleotidyltransferase; **PDBTitle:** mechanism of cca-adding enzymes specificity revealed by crystal2 structures of ternary complexes
21	d1r89a2	Alignment	not modelled	49.5	18	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Archaeal tRNA CCA-adding enzyme catalytic domain
22	d2fmpa3	Alignment	not modelled	47.1	10	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**DNA polymerase beta-like
23	d1d5ya2	Alignment	not modelled	47.1	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**AraC type transcriptional activator
24	c3r66A_	Alignment	not modelled	44.0	13	**PDB header:**viral protein/antiviral protein **Chain:** A: **PDB Molecule:**non-structural protein 1; **PDBTitle:** crystal structure of human isg15 in complex with ns1 n-terminal region2 from influenza virus b, northeast structural genomics consortium3 target ids hx6481, hr2873, and or2
25	d2bcqa3	Alignment	not modelled	43.9	17	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**DNA polymerase beta-like
26	d2vana2	Alignment	not modelled	42.0	13	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**DNA polymerase beta-like
27	d1xeqa1	Alignment	not modelled	39.7	13	**Fold:**S15/NS1 RNA-binding domain **Superfamily:**S15/NS1 RNA-binding domain **Family:**N-terminal, RNA-binding domain of nonstructural protein NS1
28	d1jqra_	Alignment	not modelled	39.6	33	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**DNA polymerase beta-like
						PDB header:hydrolase

29	c2kmmA_	Alignment	not modelled	36.4	13	**Chain:** A: **PDB Molecule:**guanosine-3',5'-bis(diphosphate) 3'- **PDBTitle:** solution nmr structure of the tgs domain of pg1808 from2 porphyromonas gingivalis. northeast structural genomics3 consortium target pgr122a (418-481)
30	d1bl0a2	Alignment	not modelled	34.8	26	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**AraC type transcriptional activator
31	d1phna_	Alignment	not modelled	33.1	16	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Phycocyanin-like phycobilisome proteins
32	c2q0dA_	Alignment	not modelled	30.9	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rna uridylyl transferase; **PDBTitle:** terminal uridylyl transferase 4 from trypanosoma brucei2 with bound atp
33	d1jmsa4	Alignment	not modelled	29.8	14	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**DNA polymerase beta-like
34	c3ng3A_	Alignment	not modelled	29.5	25	**PDB header:**lyase **Chain:** A: **PDB Molecule:**deoxyribose-phosphate aldolase; **PDBTitle:** crystal structure of deoxyribose phosphate aldolase from mycobacterium2 avium 104 in a schiff base with an unknown aldehyde
35	d1vi7a1	Alignment	not modelled	28.1	35	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**YigZ N-terminal domain-like
36	c2dt5A_	Alignment	not modelled	25.2	28	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**at-rich dna-binding protein; **PDBTitle:** crystal structure of ttha1657 (at-rich dna-binding protein) from2 thermus thermophilus hb8
37	c1nomA_	Alignment	not modelled	24.6	14	**PDB header:**nucleotidyltransferase **Chain:** A: **PDB Molecule:**dna polymerase beta; **PDBTitle:** dna polymerase beta (pol b) (e.c.2.7.7.7), 31-kd domain; soaked in the2 presence of mncl2 (5 millimolar)
38	d2dt5a2	Alignment	not modelled	23.8	28	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Transcriptional repressor Rex, C-terminal domain
39	d2cvea1	Alignment	not modelled	23.6	44	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**YigZ N-terminal domain-like
40	c3f2eA_	Alignment	not modelled	23.3	19	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**sirv coat protein; **PDBTitle:** crystal structure of yellowstone sirv coat protein c-2 terminus
41	d2b8ta1	Alignment	not modelled	22.4	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Type II thymidine kinase
42	d1o0ya_	Alignment	not modelled	22.4	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
43	c3hiyA_	Alignment	not modelled	21.8	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**minor editosome-associated tutase; **PDBTitle:** minor editosome-associated tutase 1 with bound utp and mg
44	d1cpca_	Alignment	not modelled	21.4	14	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Phycocyanin-like phycobilisome proteins
45	d1qmga2	Alignment	not modelled	20.6	23	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
46	c3ngjC_	Alignment	not modelled	20.4	22	**PDB header:**lyase **Chain:** C: **PDB Molecule:**deoxyribose-phosphate aldolase; **PDBTitle:** crystal structure of a putative deoxyribose-phosphate aldolase from2 entamoeba histolytica
47	c3nybA_	Alignment	not modelled	18.2	11	**PDB header:**transferase/rna binding protein **Chain:** A: **PDB Molecule:**poly(a) rna polymerase protein 2; **PDBTitle:** structure and function of the polymerase core of tramp, a rna2 surveillance complex
48	c2ihmA_	Alignment	not modelled	18.1	14	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**dna polymerase mu; **PDBTitle:** polymerase mu in ternary complex with gapped 11mer dna2 duplex and bound incoming nucleotide
49	c2b8tA_	Alignment	not modelled	17.9	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thymidine kinase; **PDBTitle:** crystal structure of thymidine kinase from u.urealyticum in2 complex with thymidine
50	d1pvea_	Alignment	not modelled	17.2	13	**Fold:**XPC-binding domain **Superfamily:**XPC-binding domain **Family:**XPC-binding domain
51	d1r8ka_	Alignment	not modelled	16.6	23	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**PdxA-like
52	d1sfla_	Alignment	not modelled	16.5	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
53	c8iczA_	Alignment	not modelled	16.1	11	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**protein (dna polymerase beta (e.c.2.7.7.7)); **PDBTitle:** dna polymerase beta (pol b) (e.c.2.7.7.7) complexed with2 seven base pairs of dna; soaked in the presence of of datp3 (1 millimolar), mncl2 (5 millimolar), and lithium sulfate4 (75 millimolar)
54	c2bcuA_	Alignment	not modelled	15.7	22	**PDB header:**transferase, lyase/dna **Chain:** A: **PDB Molecule:**dna polymerase lambda;

		Alignment				**PDBTitle:** dna polymerase lambda in complex with a dna duplex2 containing an unpaired damp and a t:t mismatch
55	c2a4aB_	Alignment	not modelled	15.5	18	**PDB header:**lyase **Chain:** B: **PDB Molecule:**deoxyribose-phosphate aldolase; **PDBTitle:** deoxyribose-phosphate aldolase from p. yoelii
56	c1ug9A_	Alignment	not modelled	15.3	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glucodextranase; **PDBTitle:** crystal structure of glucodextranase from arthrobacter globiformis i42
57	c2xvcA_	Alignment	not modelled	15.3	38	**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
58	c2jq5A_	Alignment	not modelled	14.9	17	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**sec-c motif; **PDBTitle:** solution structure of rpa3114, a sec-c motif containing2 protein from rhodopseudomonas palustris; northeast3 structural genomics consortium target rpt5 / ontario4 center for structural proteomics target rp3097
59	c1tltB_	Alignment	not modelled	14.9	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase (virulence factor mvim homolog); **PDBTitle:** crystal structure of a putative oxidoreductase (virulence factor mvim2 homolog)
60	d1ha7a_	Alignment	not modelled	14.8	13	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Phycocyanin-like phycobilisome proteins
61	d1qt1a_	Alignment	not modelled	14.6	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
62	c2j96B_	Alignment	not modelled	14.5	13	**PDB header:**photosynthesis **Chain:** B: **PDB Molecule:**phycoerythrocyanin alpha chain; **PDBTitle:** the e-configuration of alfa-phycoerythrocyanin
63	d1mzha_	Alignment	not modelled	14.4	28	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
64	c1yybA_	Alignment	not modelled	13.3	24	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**programmed cell death protein 5; **PDBTitle:** solution structure of 1-26 fragment of human programmed2 cell death 5 protein
65	c3l9cA_	Alignment	not modelled	13.1	31	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** the crystal structure of smu.777 from streptococcus mutans ua159
66	c3pq1A_	Alignment	not modelled	13.1	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly(a) rna polymerase; **PDBTitle:** crystal structure of human mitochondrial poly(a) polymerase (papd1)
67	c2gf5A_	Alignment	not modelled	13.0	14	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**fadd protein; **PDBTitle:** structure of intact fadd (mort1)
68	c2oczA_	Alignment	not modelled	12.9	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** the structure of a putative 3-dehydroquinate dehydratase from2 streptococcus pyogenes.
69	c1vh6A_	Alignment	not modelled	12.8	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**flagellar protein flis; **PDBTitle:** crystal structure of a flagellar protein
70	d1vh6a_	Alignment	not modelled	12.8	10	**Fold:**Four-helical up-and-down bundle **Superfamily:**Flagellar export chaperone FliS **Family:**Flagellar export chaperone FliS
71	c3oa3A_	Alignment	not modelled	12.7	26	**PDB header:**lyase **Chain:** A: **PDB Molecule:**aldolase; **PDBTitle:** crystal structure of a putative deoxyribose-phosphate aldolase from2 coccidioides immitis
72	d1oqya3	Alignment	not modelled	12.7	17	**Fold:**XPC-binding domain **Superfamily:**XPC-binding domain **Family:**XPC-binding domain
73	c1yveK_	Alignment	not modelled	12.6	23	**PDB header:**oxidoreductase **Chain:** K: **PDB Molecule:**acetohydroxy acid isomeroreductase; **PDBTitle:** acetohydroxy acid isomeroreductase complexed with nadph,2 magnesium and inhibitor ipoha (n-hydroxy-n-3 isopropyloxamate)
74	c2g5xA_	Alignment	not modelled	12.5	3	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ribosome-inactivating protein; **PDBTitle:** crystal structure of lychnin a type 1 ribosome inactivating2 protein (rip)
75	d1sc6a1	Alignment	not modelled	12.5	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
76	c1wr1B_	Alignment	not modelled	12.4	22	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**ubiquitin-like protein dsk2; **PDBTitle:** the complex sturcture of dsk2p uba with ubiquitin
77	c2of5A_	Alignment	not modelled	12.4	17	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**death domain-containing protein cradd; **PDBTitle:** oligomeric death domain complex
78	c1wxpA_	Alignment	not modelled	12.3	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**tho complex subunit 1; **PDBTitle:** solution structure of the death domain of nuclear matrix2 protein p84
79	d1gqna_	Alignment	not modelled	12.1	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
						PDB header:ligase/rna

80	c1f7uA_	Alignment	not modelled	11.8	19	**Chain:** A: **PDB Molecule:**arginyl-trna synthetase; **PDBTitle:** crystal structure of the arginyl-trna synthetase complexed with the2 trna(arg) and l-arg
81	d2fi0a1	Alignment	not modelled	11.8	17	**Fold:**SP0561-like **Superfamily:**SP0561-like **Family:**SP0561-like
82	c3iwfA_	Alignment	not modelled	11.7	15	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcription regulator rpir family; **PDBTitle:** the crystal structure of the n-terminal domain of a rpir2 transcriptional regulator from staphylococcus epidermidis to 1.4a
83	c1hlvA_	Alignment	not modelled	11.7	14	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**major centromere autoantigen b; **PDBTitle:** crystal structure of cenp-b(1-129) complexed with the cenp-2 b box dna
84	d2f4mb1	Alignment	not modelled	11.6	13	**Fold:**XPC-binding domain **Superfamily:**XPC-binding domain **Family:**XPC-binding domain
85	d1qm4a2	Alignment	not modelled	11.6	18	**Fold:**S-adenosylmethionine synthetase **Superfamily:**S-adenosylmethionine synthetase **Family:**S-adenosylmethionine synthetase
86	d1p1xa_	Alignment	not modelled	11.5	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
87	d1hlva2	Alignment	not modelled	11.4	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Centromere-binding
88	d1qp8a1	Alignment	not modelled	11.4	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
89	c1x3wB_	Alignment	not modelled	11.3	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**uv excision repair protein rad23; **PDBTitle:** structure of a peptide:n-glycanase-rad23 complex
90	d1np3a2	Alignment	not modelled	11.2	43	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
91	d1kn1a_	Alignment	not modelled	11.2	5	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Phycocyanin-like phycobilisome proteins
92	c2ytuA_	Alignment	not modelled	11.1	15	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**friend leukemia integration 1 transcription **PDBTitle:** solution structure of the sam_pnt-domain of the human2 friend leukemiaintegration 1 transcription factor
93	d1jboa_	Alignment	not modelled	11.0	17	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Phycocyanin-like phycobilisome proteins
94	d1mxaa2	Alignment	not modelled	10.9	24	**Fold:**S-adenosylmethionine synthetase **Superfamily:**S-adenosylmethionine synthetase **Family:**S-adenosylmethionine synthetase
95	d1dxya1	Alignment	not modelled	10.6	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
96	c2cveA_	Alignment	not modelled	10.6	75	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ttha1053; **PDBTitle:** crystal structure of a conserved hypothetical protein tt1547 from2 thermus thermophilus hb8
97	c2vq3B_	Alignment	not modelled	10.6	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**metalloreductase steap3; **PDBTitle:** crystal structure of the membrane proximal oxidoreductase2 domain of human steap3, the dominant ferric reductase of3 the erythroid transferrin cycle
98	c3d19E_	Alignment	not modelled	10.4	16	**PDB header:**structural genomics, unknown function **Chain:** E: **PDB Molecule:**conserved metalloprotein; **PDBTitle:** crystal structure of a conserved metalloprotein from bacillus cereus
99	c3l2iB_	Alignment	not modelled	10.4	25	**PDB header:**lyase **Chain:** B: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** 1.85 angstrom crystal structure of the 3-dehydroquinate dehydratase2 (arod) from salmonella typhimurium lt2.