Phyre^{2}

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Description	P0AF43
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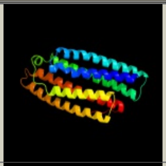
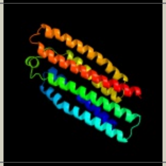
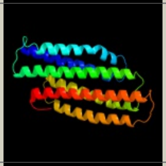
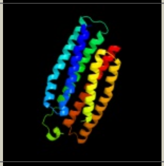
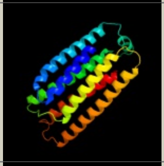
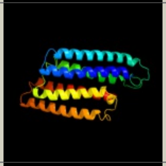
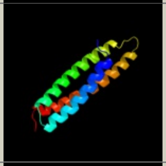
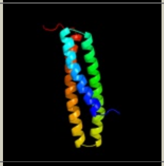
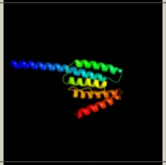
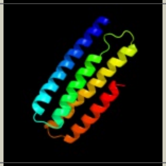
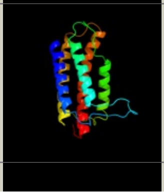
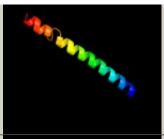
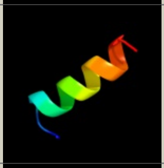
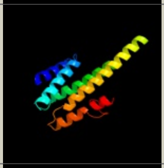
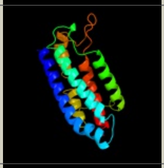
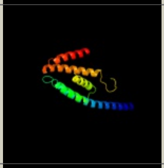
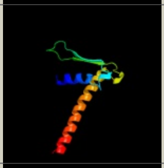
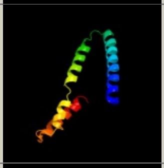
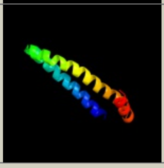
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1sumb_	Alignment		99.9	12	**Fold:**Spectrin repeat-like **Superfamily:**PhoU-like **Family:**PhoU-like
2	d1t72a_	Alignment		99.9	12	**Fold:**Spectrin repeat-like **Superfamily:**PhoU-like **Family:**PhoU-like
3	d1xwma_	Alignment		99.9	11	**Fold:**Spectrin repeat-like **Superfamily:**PhoU-like **Family:**PhoU-like
4	c2i0mA_	Alignment		99.9	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**phosphate transport system protein phou; **PDBTitle:** crystal structure of the phosphate transport system regulatory protein2 phou from streptococcus pneumoniae
5	c3l39A_	Alignment		99.5	13	**PDB header:**phosphate-binding protein **Chain:** A: **PDB Molecule:**putative phou-like phosphate regulatory protein; **PDBTitle:** crystal structure of putative phou-like phosphate regulatory2 protein (bt4638) from bacteroides thetaiotaomicron vpi-54823 at 1.93 a resolution
6	c2oltB_	Alignment		99.3	12	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a phou-like protein (so_3770) from shewanella2 oneidensis mr-1 at 2.00 a resolution
7	d1vcta1	Alignment		98.8	18	**Fold:**Spectrin repeat-like **Superfamily:**PhoU-like **Family:**PhoU-like
8	c2bknA_	Alignment		98.4	17	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**hypothetical protein ph0236; **PDBTitle:** structure analysis of unknown function protein
9	c3pjaK_	Alignment		59.3	12	**PDB header:**hydrolase **Chain:** K: **PDB Molecule:**translin-associated protein x; **PDBTitle:** crystal structure of human c3po complex
10	c2wb7B_	Alignment		59.2	13	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**pt26-6p; **PDBTitle:** pt26-6p
11	c3ke4B_	Alignment		54.9	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**hypothetical cytosolic protein; **PDBTitle:** crystal structure of a pduo-type atp:cob(i)alamin adenosyltransferase2 from bacillus cereus

12	c2z5hB_	Alignment		48.2	20	**PDB header:**contractile protein **Chain:** B: **PDB Molecule:**general control protein gcn4 and tropomyosin **PDBTitle:** crystal structure of the head-to-tail junction of2 tropomyosin complexed with a fragment of tnt
13	d1p1ja1	Alignment		46.2	35	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
14	d2o8pa1	Alignment		44.2	9	**Fold:**alpha-alpha superhelix **Superfamily:**14-3-3 protein **Family:**14-3-3 protein
15	d1vkoa1	Alignment		43.5	24	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
16	d1rtyb_	Alignment		43.2	18	**Fold:**Ferritin-like **Superfamily:**Cobalamin adenosyltransferase-like **Family:**Cobalamin adenosyltransferase
17	d1j1ja_	Alignment		41.0	16	**Fold:**alpha-alpha superhelix **Superfamily:**Translin **Family:**Translin
18	d1xppa_	Alignment		35.3	10	**Fold:**DCoH-like **Superfamily:**RBP11-like subunits of RNA polymerase **Family:**RBP11/RpoL
19	c2hn1A_	Alignment		33.6	10	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**magnesium and cobalt transporter; **PDBTitle:** crystal structure of a cora soluble domain from a. fulgidus in complex2 with co2+
20	c3qd8M_	Alignment		33.5	9	**PDB header:**metal binding protein **Chain:** M: **PDB Molecule:**probable bacterioferritin bfrb; **PDBTitle:** crystal structure of mycobacterium tuberculosis bfrb
21	d1i5na_	Alignment	not modelled	32.4	9	**Fold:**Four-helical up-and-down bundle **Superfamily:**Histidine-containing phosphotransfer domain, HPT domain **Family:**Chemotaxis protein CheA P1 domain
22	c3t6gB_	Alignment	not modelled	32.1	12	**PDB header:**signaling protein, cell adhesion **Chain:** B: **PDB Molecule:**breast cancer anti-estrogen resistance protein 1; **PDBTitle:** structure of the complex between nsp3 (shep1) and p130cas
23	d1s3qa1	Alignment	not modelled	30.9	8	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ferritin
24	c2yu0A_	Alignment	not modelled	30.7	25	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**interferon-activable protein 205; **PDBTitle:** solution structures of the paad_dapin domain of mus2 musculus interferon-activatable protein 205
25	c3p5nA_	Alignment	not modelled	30.0	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**riboflavin uptake protein; **PDBTitle:** structure and mechanism of the s component of a bacterial ecf2 transporter
26	c2jd8C_	Alignment	not modelled	29.8	7	**PDB header:**metal transport **Chain:** C: **PDB Molecule:**ferritin homolog; **PDBTitle:** crystal structure of the zn-soaked ferritin from the2 hyperthermophilic archaeal anaerobe pyrococcus furiosus
27	c1vkoA_	Alignment	not modelled	29.4	24	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**inositol-3-phosphate synthase; **PDBTitle:** crystal structure of inositol-3-phosphate synthase (ce21227) from2 caenorhabditis elegans at 2.30 a resolution
28	c2lchA_	Alignment	not modelled	29.4	11	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**protein or38; **PDBTitle:** solution nmr structure of a protein with a redesigned hydrophobic2 core, northeast structural genomics consortium target or38

29	c1p1hD_	Alignment	not modelled	29.3	35	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**inositol-3-phosphate synthase; **PDBTitle:** crystal structure of the 1l-myo-inositol/nad+ complex
30	d1k6ka_	Alignment	not modelled	29.2	14	**Fold:**Double Clp-N motif **Superfamily:**Double Clp-N motif **Family:**Double Clp-N motif
31	c1kmiZ_	Alignment	not modelled	28.6	6	**PDB header:**signaling protein **Chain:** Z: **PDB Molecule:**chemotaxis protein chez; **PDBTitle:** crystal structure of an e.coli chemotaxis protein, chez
32	d2e74f1	Alignment	not modelled	28.1	29	**Fold:**Single transmembrane helix **Superfamily:**PetM subunit of the cytochrome b6f complex **Family:**PetM subunit of the cytochrome b6f complex
33	d1zwwa1	Alignment	not modelled	27.3	11	**Fold:**BAR/IMD domain-like **Superfamily:**BAR/IMD domain-like **Family:**BAR domain
34	c1p58C_	Alignment	not modelled	27.2	33	**PDB header:**virus **Chain:** C: **PDB Molecule:**major envelope protein e; **PDBTitle:** complex organization of dengue virus membrane proteins as revealed by2 9.5 angstrom cryo-em reconstruction
35	d2o02a1	Alignment	not modelled	27.1	14	**Fold:**alpha-alpha superhelix **Superfamily:**14-3-3 protein **Family:**14-3-3 protein
36	c2gzdC_	Alignment	not modelled	26.8	26	**PDB header:**protein transport **Chain:** C: **PDB Molecule:**rab11 family-interacting protein 2; **PDBTitle:** crystal structure of rab11 in complex with rab11-fip2
37	c2qrxA_	Alignment	not modelled	25.9	9	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**gm27569p; **PDBTitle:** crystal structure of drosophila melanogaster translin2 protein
38	d1eq1a_	Alignment	not modelled	25.8	11	**Fold:**Apolipophorin-III **Superfamily:**Apolipophorin-III **Family:**Apolipophorin-III
39	c2qr4B_	Alignment	not modelled	25.7	5	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**peptidase m3b, oligoendopeptidase f; **PDBTitle:** crystal structure of oligoendopeptidase-f from enterococcus faecium
40	d1vlga_	Alignment	not modelled	25.6	4	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ferritin
41	c1ha0A_	Alignment	not modelled	23.9	10	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**protein (hemagglutinin precursor); **PDBTitle:** hemagglutinin precursor ha0
42	d1u1ia1	Alignment	not modelled	23.8	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
43	d1or4a_	Alignment	not modelled	23.8	13	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
44	c3fb2B_	Alignment	not modelled	23.8	8	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**spectrin alpha chain, brain spectrin; **PDBTitle:** crystal structure of the human brain alpha spectrin repeats2 15 and 16. northeast structural genomics consortium target3 hr5563a.
45	d2elba1	Alignment	not modelled	23.4	11	**Fold:**BAR/IMD domain-like **Superfamily:**BAR/IMD domain-like **Family:**BAR domain
46	c3kp3B_	Alignment	not modelled	22.3	17	**PDB header:**transcription regulator/antibiotic **Chain:** B: **PDB Molecule:**transcriptional regulator tcar; **PDBTitle:** staphylococcus epidermidis in complex with ampicillin
47	c3hnwB_	Alignment	not modelled	22.2	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a basic coiled-coil protein of unknown function2 from eubacterium eligens atcc 27750
48	c2kvcA_	Alignment	not modelled	22.2	10	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** solution structure of the mycobacterium tuberculosis protein rv0543c,2 a member of the duf3349 superfamily. seattle structural genomics3 center for infectious disease target mytud.17112.a
49	c2wr2B_	Alignment	not modelled	22.1	10	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**hemagglutinin; **PDBTitle:** structure of influenza h2 avian hemagglutinin with avian2 receptor
50	d2axti1	Alignment	not modelled	22.0	14	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction center protein I, PsbI **Family:**PsbI-like
51	d1dlca3	Alignment	not modelled	21.9	9	**Fold:**Toxins' membrane translocation domains **Superfamily:**delta-Endotoxin (insectocide), N-terminal domain **Family:**delta-Endotoxin (insectocide), N-terminal domain
52	d2d2sa1	Alignment	not modelled	21.6	10	**Fold:**alpha-alpha superhelix **Superfamily:**Cullin repeat-like **Family:**Exocyst complex component
53	c3lk5A_	Alignment	not modelled	21.6	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**geranylgeranyl pyrophosphate synthase; **PDBTitle:** crystal structure of putative geranylgeranyl pyrophosphate synthase2 from corynebacterium glutamicum
54	c2nt8A_	Alignment	not modelled	19.8	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cobalamin adenosyltransferase; **PDBTitle:** atp bound at the active site of a pduo type atp:co(i)rrinoid2 adenosyltransferase from lactobacillus reuteri
						PDB header:viral protein

55	c1xnlA_	Alignment	not modelled	19.8	44	**Chain:** A: **PDB Molecule:**membrane protein gp37; **PDBTitle:** aslv fusion peptide
56	c3kyiA_	Alignment	not modelled	19.8	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative histidine protein kinase; **PDBTitle:** crystal structure of the phosphorylated p1 domain of chea3 in complex2 with chey6 from r. sphaeroides
57	d1tqga_	Alignment	not modelled	19.7	12	**Fold:**Four-helical up-and-down bundle **Superfamily:**Histidine-containing phosphotransfer domain, HPT domain **Family:**Chemotaxis protein CheA P1 domain
58	c2zhzC_	Alignment	not modelled	19.6	14	**PDB header:**transferase **Chain:** C: **PDB Molecule:**atp:cob(i)alamin adenosyltransferase, putative; **PDBTitle:** crystal structure of a pduo-type atp:cobalamin adenosyltransferase2 from burkholderia thailandensis
59	d1twfk_	Alignment	not modelled	19.5	24	**Fold:**DCoH-like **Superfamily:**RBP11-like subunits of RNA polymerase **Family:**RBP11/RpoL
60	c3nmdA_	Alignment	not modelled	19.4	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cgmp dependent protein kinase; **PDBTitle:** crystal structure of the leucine zipper domain of cgmp dependent2 protein kinase i beta
61	c1b9uA_	Alignment	not modelled	19.2	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein (atp synthase); **PDBTitle:** membrane domain of the subunit b of the e.coli atp synthase
62	d1t01a1	Alignment	not modelled	19.2	14	**Fold:**Four-helical up-and-down bundle **Superfamily:**alpha-catenin/vinculin-like **Family:**alpha-catenin/vinculin
63	c2bbjB_	Alignment	not modelled	18.7	6	**PDB header:**metal transport/membrane protein **Chain:** B: **PDB Molecule:**divalent cation transport-related protein; **PDBTitle:** crystal structure of the cora mg2+ transporter
64	c3axjB_	Alignment	not modelled	18.7	14	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**translin associated factor x, isoform b; **PDBTitle:** high resolution crystal structure of c3po
65	d256ba_	Alignment	not modelled	18.5	17	**Fold:**Four-helical up-and-down bundle **Superfamily:**Cytochromes **Family:**Cytochrome b562
66	c2c5iT_	Alignment	not modelled	18.5	6	**PDB header:**protein transport **Chain:** T: **PDB Molecule:**t-snare affecting a late golgi compartment **PDBTitle:** n-terminal domain of tlg1 complexed with n-terminus of2 vps51 in distorted conformation
67	c2ariA_	Alignment	not modelled	18.4	30	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**envelope polyprotein gp160; **PDBTitle:** solution structure of micelle-bound fusion domain of hiv-12 gp41
68	d1rkea1	Alignment	not modelled	18.3	13	**Fold:**Four-helical up-and-down bundle **Superfamily:**alpha-catenin/vinculin-like **Family:**alpha-catenin/vinculin
69	c1j1dF_	Alignment	not modelled	18.3	20	**PDB header:**contractile protein **Chain:** F: **PDB Molecule:**troponin i; **PDBTitle:** crystal structure of the 46kda domain of human cardiac2 troponin in the ca2+ saturated form
70	c3mp7B_	Alignment	not modelled	18.3	33	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**preprotein translocase subunit sece; **PDBTitle:** lateral opening of a translocon upon entry of protein suggests the2 mechanism of insertion into membranes
71	d1io1a_	Alignment	not modelled	18.2	19	**Fold:**Phase 1 flagellin **Superfamily:**Phase 1 flagellin **Family:**Phase 1 flagellin
72	c2k6sB_	Alignment	not modelled	18.2	26	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**rab11fip2 protein; **PDBTitle:** structure of rab11-fip2 c-terminal coiled-coil domain
73	c2p90B_	Alignment	not modelled	18.1	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein cgl1923; **PDBTitle:** the crystal structure of a protein of unknown function from2 corynebacterium glutamicum atcc 13032
74	c1ykuB_	Alignment	not modelled	18.1	13	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hypothetical protein pxo2-61; **PDBTitle:** crystal structure of a sensor domain homolog
75	c3hjlA_	Alignment	not modelled	18.0	12	**PDB header:**proton transport **Chain:** A: **PDB Molecule:**flagellar motor switch protein flig; **PDBTitle:** the structure of full-length flig from aquifex aeolicus
76	c1ytzI_	Alignment	not modelled	18.0	11	**PDB header:**contractile protein **Chain:** I: **PDB Molecule:**troponin i; **PDBTitle:** crystal structure of skeletal muscle troponin in the ca2+-2 activated state
77	c3sogA_	Alignment	not modelled	18.0	7	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**amphiphysin; **PDBTitle:** crystal structure of the bar domain of human amphiphysin, isoform 1
78	d1xata_	Alignment	not modelled	17.7	20	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**Galactoside acetyltransferase-like
79	c3bt6B_	Alignment	not modelled	17.5	14	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**influenza b hemagglutinin (ha); **PDBTitle:** crystal structure of influenza b virus hemagglutinin
80	c3a0bX_	Alignment	not modelled	17.5	19	**PDB header:**electron transport **Chain:** X: **PDB Molecule:**photosystem ii reaction center protein x; **PDBTitle:** crystal structure of br-substituted photosystem ii complex
81	c3a0bx_	Alignment	not modelled	17.5	19	**PDB header:**electron transport **Chain:** X: **PDB Molecule:**photosystem ii reaction center protein x;

						PDBTitle: crystal structure of br-substituted photosystem ii complex
82	c3a0hX_	Alignment	not modelled	17.5	19	**PDB header:**electron transport **Chain:** X: **PDB Molecule:**photosystem ii reaction center protein x; **PDBTitle:** crystal structure of i-substituted photosystem ii complex
83	c3a0hx_	Alignment	not modelled	17.5	19	**PDB header:**electron transport **Chain:** X: **PDB Molecule:**photosystem ii reaction center protein x; **PDBTitle:** crystal structure of i-substituted photosystem ii complex
84	d1ciia1	Alignment	not modelled	17.5	15	**Fold:**Toxins' membrane translocation domains **Superfamily:**Colicin **Family:**Colicin
85	d1s35a2	Alignment	not modelled	17.5	7	**Fold:**Spectrin repeat-like **Superfamily:**Spectrin repeat **Family:**Spectrin repeat
86	d1t6ua_	Alignment	not modelled	17.5	13	**Fold:**Four-helical up-and-down bundle **Superfamily:**Nickel-containing superoxide dismutase, NiSOD **Family:**Nickel-containing superoxide dismutase, NiSOD
87	d2iuba1	Alignment	not modelled	17.3	10	**Fold:**CorA soluble domain-like **Superfamily:**CorA soluble domain-like **Family:**CorA soluble domain-like
88	c3ci9B_	Alignment	not modelled	17.3	14	**PDB header:**transcription **Chain:** B: **PDB Molecule:**heat shock factor-binding protein 1; **PDBTitle:** crystal structure of the human hsbp1
89	c1yv0I_	Alignment	not modelled	17.3	11	**PDB header:**contractile protein **Chain:** I: **PDB Molecule:**troponin i, fast skeletal muscle; **PDBTitle:** crystal structure of skeletal muscle troponin in the ca2+-2 free state
90	c1hf9B_	Alignment	not modelled	17.3	23	**PDB header:**atpase inhibitor **Chain:** B: **PDB Molecule:**atpase inhibitor (mitochondrial); **PDBTitle:** c-terminal coiled-coil domain from bovine if1
91	c1dlcA_	Alignment	not modelled	17.2	9	**PDB header:**toxin **Chain:** A: **PDB Molecule:**delta-endotoxin cryiiia; **PDBTitle:** crystal structure of insecticidal delta-endotoxin from2 bacillus thuringiensis at 2.5 angstroms resolution
92	c1zxjB_	Alignment	not modelled	17.2	10	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein mg377 homolog; **PDBTitle:** crystal structure of the hypthetical mycoplasma protein,2 mpn555
93	c1t6fA_	Alignment	not modelled	17.1	19	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**geminin; **PDBTitle:** crystal structure of the coiled-coil dimerization motif of2 geminin
94	c3o3nA_	Alignment	not modelled	16.9	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**alpha-subunit 2-hydroxyisocaproyl-coa dehydratase; **PDBTitle:** (r)-2-hydroxyisocaproyl-coa dehydratase in complex with its substrate2 (r)-2-hydroxyisocaproyl-coa
95	c3pl4A_	Alignment	not modelled	16.9	13	**PDB header:**motor protein **Chain:** A: **PDB Molecule:**flagellar motor switch protein; **PDBTitle:** crystal structure of flig (residue 116-343) from h. pylori
96	c3l8jA_	Alignment	not modelled	16.8	12	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**programmed cell death protein 10; **PDBTitle:** crystal structure of ccm3, a cerebral cavernous malformation protein2 critical for vascular integrity
97	d2etsa1	Alignment	not modelled	16.8	5	**Fold:**Four-helical up-and-down bundle **Superfamily:**YppE-like **Family:**YppE-like
98	c1s5lx_	Alignment	not modelled	16.6	19	**PDB header:**photosynthesis **Chain:** X: **PDB Molecule:**photosystem ii psbx protein; **PDBTitle:** architecture of the photosynthetic oxygen evolving center
99	c2ah6B_	Alignment	not modelled	16.5	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**bh1595, unknown conserved protein; **PDBTitle:** crystal structure of a putative cobalamin adenosyltransferase (bh1595)2 from bacillus halodurans c-125 at 1.60 a resolution