Phyre2

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Description	P11989
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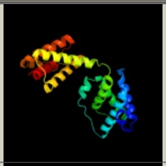
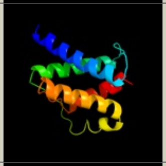
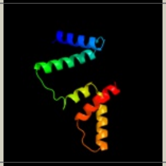
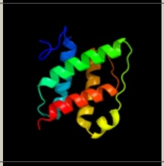
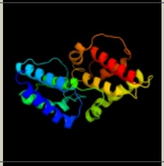
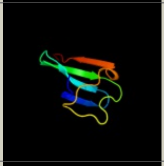
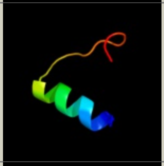
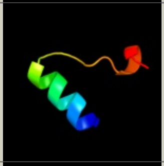
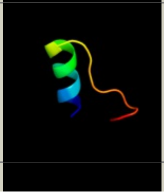
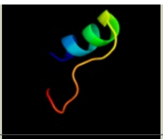
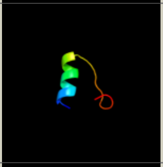
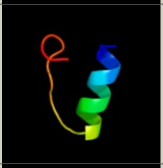
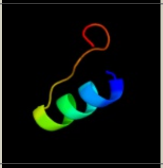
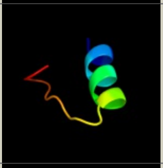
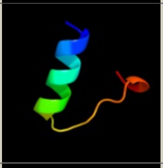
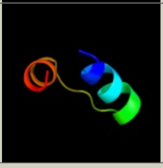
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1h99A_	Alignment		100.0	42	**PDB header:**transcriptional antiterminator **Chain:** A: **PDB Molecule:**transcription antiterminator lict; **PDBTitle:** prd of lict antiterminator from bacillus subtilis
2	d1h99a2	Alignment		99.8	38	**Fold:**PTS-regulatory domain, PRD **Superfamily:**PTS-regulatory domain, PRD **Family:**PTS-regulatory domain, PRD
3	c3gwhB_	Alignment		99.8	23	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional antiterminator (bglg family); **PDBTitle:** crystallographic ab initio protein solution far below atomic2 resolution
4	d1h99a1	Alignment		99.8	49	**Fold:**PTS-regulatory domain, PRD **Superfamily:**PTS-regulatory domain, PRD **Family:**PTS-regulatory domain, PRD
5	c3sqnB_	Alignment		99.7	12	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**conserved domain protein; **PDBTitle:** putative mga family transcriptional regulator from enterococcus2 faecalis
6	d1l1ca_	Alignment		99.6	44	**Fold:**GroES-like **Superfamily:**SacY-like RNA-binding domain **Family:**BglG-like antiterminator proteins
7	d1auua_	Alignment		99.6	39	**Fold:**GroES-like **Superfamily:**SacY-like RNA-binding domain **Family:**BglG-like antiterminator proteins
8	c3nufB_	Alignment		97.2	22	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**prd-containing transcription regulator; **PDBTitle:** crystal structure of a prd-containing transcription regulator2 (lsei_2718) from lactobacillus casei atcc 334 at 1.38 a resolution
9	c2kciA_	Alignment		35.2	5	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative acyl carrier protein; **PDBTitle:** solution nmr structure of gmet_2339 from geobacter2 metallireducens. northeast structural genomics consortium3 target gmr141
10	c3lmoA_	Alignment		33.0	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**specialized acyl carrier protein; **PDBTitle:** crystal structure of specialized acyl carrier protein2 (rpa2022) from rhodopseudomonas palustris, northeast3 structural genomics consortium target rpr324
11	d2jq4a1	Alignment		30.0	10	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**Acyl-carrier protein (ACP)

12	c2jq4A_	Alignment		30.0	10	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**hypothetical protein atu2571; **PDBTitle:** complete resonance assignments and solution structure2 calculation of atc2521 (nesg id: att6) from agrobacterium3 tumefaciens
13	d1f80d_	Alignment		27.9	5	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**Acyl-carrier protein (ACP)
14	c2qnwA_	Alignment		25.5	24	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** toxoplasma gondii apicoplast-targeted acyl carrier protein
15	c2l4bA_	Alignment		25.4	5	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** solution structure of a putative acyl carrier protein from anaplasma2 phagocytophilum. seattle structural genomics center for infectious3 disease target anpha.01018.a
16	c2fvfA_	Alignment		23.9	14	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** structure of 10:0-acp (protein with docked fatty acid)
17	c3ce7A_	Alignment		23.3	14	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**specific mitochodrial acyl carrier protein; **PDBTitle:** crystal structure of toxoplasma specific mitochodrial acyl2 carrier protein, 59.m03510
18	c1x3oA_	Alignment		23.0	14	**PDB header:**lipid transport **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** crystal structure of the acyl carrier protein from thermus2 thermophilus hb8
19	c2ehtA_	Alignment		22.4	14	**PDB header:**lipid transport **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** crystal structure of acyl carrier protein from aquifex aeolicus (form2 2)
20	c3d9wA_	Alignment		21.5	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative acetyltransferase; **PDBTitle:** crystal structure analysis of nocardia farcinica arylamine2 n-acetyltransferase
21	c2cnrA_	Alignment	not modelled	21.3	29	**PDB header:**lipid transport **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** structural studies on the interaction of scfas acp with2 acps
22	d1t3ta1	Alignment	not modelled	20.8	22	**Fold:**RuvA C-terminal domain-like **Superfamily:**FGAM synthase PurL, linker domain **Family:**FGAM synthase PurL, linker domain
23	d1gyta2	Alignment	not modelled	20.3	29	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Leucine aminopeptidase, C-terminal domain
24	c2fq2A_	Alignment	not modelled	19.5	10	**PDB header:**lipid transport **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** solution structure of minor conformation of holo-acyl2 carrier protein from malaria parasite plasmodium falciparum
25	c2vefB_	Alignment	not modelled	18.9	31	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dihydropteroate synthase; **PDBTitle:** dihydropteroate synthase from streptococcus pneumoniae
26	c3ejbC_	Alignment	not modelled	18.3	14	**PDB header:**oxidoreductase/lipid transport **Chain:** C: **PDB Molecule:**acyl carrier protein; **PDBTitle:** crystal structure of p450bioi in complex with tetradecanoic2 acid ligated acyl carrier protein
27	c2dnwA_	Alignment	not modelled	18.0	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** solution structure of rsgi ruh-059, an acp domain of acyl2 carrier protein, mitochondrial [precursor] from human cdna
28	d1vlpa1	Alignment	not modelled	17.6	11	**Fold:**alpha/beta-Hammerhead **Superfamily:**Nicotinate/Quinolinate PRTase N-terminal domain-like **Family:**Monomeric nicotinate phosphoribosyltransferase N-terminal domain-like
						PDB header:protein transport

29	c2cgqA_	Alignment	not modelled	17.4	5	**Chain:** A: **PDB Molecule:**acyl carrier protein acpa; **PDBTitle:** a putative acyl carrier protein(rv0033) from mycobacterium2 tuberculosis
30	c3jruB_	Alignment	not modelled	17.0	38	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable cytosol aminopeptidase; **PDBTitle:** crystal structure of leucyl aminopeptidase (pepa) from xoo0834,2 xanthomonas oryzae pv. oryzae kacc10331
31	d2pnga1	Alignment	not modelled	17.0	32	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**Acyl-carrier protein (ACP)
32	c1gytG_	Alignment	not modelled	16.0	29	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**cytosol aminopeptidase; **PDBTitle:** e. coli aminopeptidase a (pepa)
33	d1d0qa_	Alignment	not modelled	16.0	32	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**DNA primase zinc finger
34	c3kr5E_	Alignment	not modelled	16.0	19	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**m17 leucyl aminopeptidase; **PDBTitle:** structure of a protease 4
35	d1xm8a_	Alignment	not modelled	15.9	17	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Glyoxalase II (hydroxyacylglutathione hydrolase)
36	c2amwA_	Alignment	not modelled	15.5	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ne2163; **PDBTitle:** solution nmr structure of protein ne2163 from nitrosomonas europaea.2 northeast structural genomics consortium target net1.
37	c2lkiA_	Alignment	not modelled	15.5	9	**PDB header:**lipid transport **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** solution nmr structure of holo acyl carrier protein ne2163 from2 nitrosomonas europaea. northeast structural genomics consortium3 target net1.
38	d1k47a1	Alignment	not modelled	15.1	9	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**GHMP Kinase, N-terminal domain
39	c2kwlA_	Alignment	not modelled	14.9	20	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** solution structure of acyl carrier protein from borrelia burgdorferi
40	d1lama1	Alignment	not modelled	14.6	31	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Leucine aminopeptidase, C-terminal domain
41	d1ybea2	Alignment	not modelled	14.0	14	**Fold:**alpha/beta-Hammerhead **Superfamily:**Nicotinate/Quinolinate PRTase N-terminal domain-like **Family:**Monomeric nicotinate phosphoribosyltransferase N-terminal domain-like
42	c2l3vA_	Alignment	not modelled	13.9	26	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** nmr structure of acyl carrier protein from brucella melitensis
43	c3kzwD_	Alignment	not modelled	13.6	25	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**cytosol aminopeptidase; **PDBTitle:** crystal structure of cytosol aminopeptidase from staphylococcus aureus2 col
44	c3peiA_	Alignment	not modelled	13.3	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cytosol aminopeptidase; **PDBTitle:** crystal structure of cytosol aminopeptidase from francisella2 tularensis
45	d1or5a_	Alignment	not modelled	12.9	23	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**Acyl-carrier protein (ACP)
46	d1t8ka_	Alignment	not modelled	12.8	14	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**Acyl-carrier protein (ACP)
47	c2bmbA_	Alignment	not modelled	12.5	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**folic acid synthesis protein fol1; **PDBTitle:** x-ray structure of the bifunctional 6-hydroxymethyl-7,8-2 dihydroxypterin pyrophosphokinase dihydropteroate synthase3 from saccharomyces cerevisiae
48	c1lanA_	Alignment	not modelled	12.5	31	**PDB header:**hydrolase (alpha-aminoacylpeptide) **Chain:** A: **PDB Molecule:**leucine aminopeptidase; **PDBTitle:** leucine aminopeptidase complex with l-leucinal
49	d1dv5a_	Alignment	not modelled	12.3	25	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**apo-D-alanyl carrier protein
50	d3bl9a2	Alignment	not modelled	11.9	14	**Fold:**mRNA decapping enzyme DcpS N-terminal domain **Superfamily:**mRNA decapping enzyme DcpS N-terminal domain **Family:**mRNA decapping enzyme DcpS N-terminal domain
51	c1wd6B_	Alignment	not modelled	11.9	17	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**protein ydhr; **PDBTitle:** crystal structure of jw1657 from escherichia coli
52	c2uv1B_	Alignment	not modelled	11.8	14	**PDB header:**inhibitor **Chain:** B: **PDB Molecule:**host-nuclease inhibitor protein gam; **PDBTitle:** hexagonal crystal form of gams from bacteriophage lambda.
53	c3d5pB_	Alignment	not modelled	11.7	21	**PDB header:**gene regulation **Chain:** B: **PDB Molecule:**putative glucan synthesis regulator of smi1/knr4 family; **PDBTitle:** crystal structure of a putative glucan synthesis regulator of2 smi1/knr4 family (bf1740) from bacteroides fragilis nctc 9343 at 1.453 a resolution
						Fold: Acyl carrier protein-like

54	d1nq4a_	Alignment	not modelled	11.6	30	**Superfamily:**ACP-like **Family:**Acyl-carrier protein (ACP)
55	d1vkua_	Alignment	not modelled	11.5	5	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**Acyl-carrier protein (ACP)
56	d1klpa_	Alignment	not modelled	11.4	18	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**Acyl-carrier protein (ACP)
57	c3ij3A_	Alignment	not modelled	11.4	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cytosol aminopeptidase; **PDBTitle:** 1.8 angstrom resolution crystal structure of cytosol aminopeptidase2 from coxiella burnetii
58	d1s4ea1	Alignment	not modelled	10.8	22	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**GHMP Kinase, N-terminal domain
59	c2y5sA_	Alignment	not modelled	10.8	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydropteroate synthase; **PDBTitle:** crystal structure of burkholderia cenocepacia dihydropteroate2 synthase complexed with 7,8-dihydropteroate.
60	d1j2jb_	Alignment	not modelled	10.5	17	**Fold:**Spectrin repeat-like **Superfamily:**GAT-like domain **Family:**GAT domain
61	d1eyea_	Alignment	not modelled	10.5	31	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
62	d1qh5a_	Alignment	not modelled	10.4	27	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Glyoxalase II (hydroxyacylglutathione hydrolase)
63	c3h8gC_	Alignment	not modelled	10.0	29	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**cytosol aminopeptidase; **PDBTitle:** bestatin complex structure of leucine aminopeptidase from pseudomonas2 putida
64	c3gdfA_	Alignment	not modelled	9.9	38	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable nadp-dependent mannitol dehydrogenase; **PDBTitle:** crystal structure of the nadp-dependent mannitol dehydrogenase from2 cladosporium herbarum.
65	d2d8xa2	Alignment	not modelled	9.7	33	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
66	c3nwsA_	Alignment	not modelled	9.5	10	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division control protein 13; **PDBTitle:** crystal structure of the n-terminal domain of the yeast telomere-2 binding and telomerase regulatory protein cdc13
67	d2py6a1	Alignment	not modelled	9.2	16	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**FkbM-like
68	c3n00B_	Alignment	not modelled	9.2	36	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**nuclear receptor corepressor 1; **PDBTitle:** crystal structure of a deletion mutant of human reverba ligand binding2 domain bound with an ncor id1 peptide determined to 2.60a
69	c3lw9B_	Alignment	not modelled	9.1	12	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**invasion protein inva; **PDBTitle:** structure of a cytoplasmic domain of salmonella inva
70	c2vp8A_	Alignment	not modelled	9.0	38	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydropteroate synthase 2; **PDBTitle:** structure of mycobacterium tuberculosis rv1207
71	d1vlra2	Alignment	not modelled	9.0	14	**Fold:**mRNA decapping enzyme DcpS N-terminal domain **Superfamily:**mRNA decapping enzyme DcpS N-terminal domain **Family:**mRNA decapping enzyme DcpS N-terminal domain
72	d2rk5a1	Alignment	not modelled	8.7	23	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
73	d2icga1	Alignment	not modelled	8.4	23	**Fold:**SMI1/KNR4-like **Superfamily:**SMI1/KNR4-like **Family:**SMI1/KNR4-like
74	d2af8a_	Alignment	not modelled	8.3	30	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**Acyl-carrier protein (ACP)
75	d1w5ra1	Alignment	not modelled	8.0	24	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Arylamine N-acetyltransferase
76	c2k2wA_	Alignment	not modelled	7.9	28	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**recombination and dna repair protein; **PDBTitle:** second brct domain of nbs1
77	c3aicC_	Alignment	not modelled	7.9	14	**PDB header:**transferase **Chain:** C: **PDB Molecule:**glucosyltransferase-si; **PDBTitle:** crystal structure of glucansucrase from streptococcus mutans
78	c3llbA_	Alignment	not modelled	7.8	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** the crystal structure of the protein pa3983 with unknown2 function from pseudomonas aeruginosa pao1
79	d2r2za1	Alignment	not modelled	7.8	15	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
80	c2gcuD_	Alignment	not modelled	7.7	13	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**putative hydroxyacylglutathione hydrolase 3;

						PDBTitle: x-ray structure of gene product from arabidopsis thaliana2 at1g53580
81	c2hc9A_	Alignment	not modelled	7.6	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**leucine aminopeptidase 1; **PDBTitle:** structure of caenorhabditis elegans leucine aminopeptidase-zinc2 complex (lap1)
82	c2dgyA_	Alignment	not modelled	7.4	18	**PDB header:**translation **Chain:** A: **PDB Molecule:**mgc11102 protein; **PDBTitle:** solution structure of the eukaryotic initiation factor 1a2 in mgc11102 protein
83	d2prva1	Alignment	not modelled	7.4	23	**Fold:**SMI1/KNR4-like **Superfamily:**SMI1/KNR4-like **Family:**SMI1/KNR4-like
84	c2ejwB_	Alignment	not modelled	7.3	29	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**homoserine dehydrogenase; **PDBTitle:** homoserine dehydrogenase from thermus thermophilus hb8
85	d2o02a1	Alignment	not modelled	7.2	14	**Fold:**alpha-alpha superhelix **Superfamily:**14-3-3 protein **Family:**14-3-3 protein
86	d1dvka_	Alignment	not modelled	7.0	16	**Fold:**Functional domain of the splicing factor Prp18 **Superfamily:**Functional domain of the splicing factor Prp18 **Family:**Functional domain of the splicing factor Prp18
87	c3pshA_	Alignment	not modelled	7.0	18	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**protein hi_1472; **PDBTitle:** classification of a haemophilus influenzae abc transporter hi1470/712 through its cognate molybdate periplasmic binding protein mola (mola3 bound to molybdate)
88	d2tpta3	Alignment	not modelled	7.0	8	**Fold:**alpha/beta-Hammerhead **Superfamily:**Pyrimidine nucleoside phosphorylase C-terminal domain **Family:**Pyrimidine nucleoside phosphorylase C-terminal domain
89	d1pvhb_	Alignment	not modelled	6.9	16	**Fold:**4-helical cytokines **Superfamily:**4-helical cytokines **Family:**Long-chain cytokines
90	d2ezwa1	Alignment	not modelled	6.8	17	**Fold:**Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit **Superfamily:**Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit **Family:**Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit
91	d2bsza1	Alignment	not modelled	6.7	14	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Arylamine N-acetyltransferase
92	d2plia1	Alignment	not modelled	6.7	15	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
93	c2dzaA_	Alignment	not modelled	6.7	38	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydropteroate synthase; **PDBTitle:** crystal structure of dihydropteroate synthase from thermus2 thermophilus hb8 in complex with 4-aminobenzoate
94	c1vlpA_	Alignment	not modelled	6.6	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate phosphoribosyltransferase; **PDBTitle:** crystal structure of a putative nicotinate phosphoribosyltransferase2 (yor209c, npt1) from saccharomyces cerevisiae at 1.75 a resolution
95	c3gr6A_	Alignment	not modelled	6.6	38	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**enoyl-[acyl-carrier-protein] reductase [nadh]; **PDBTitle:** crystal structure of the staphylococcus aureus enoyl-acyl2 carrier protein reductase (fabi) in complex with nadp and3 triclosan
96	c2p18A_	Alignment	not modelled	6.5	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glyoxalase ii; **PDBTitle:** crystal structure of the leishmania infantum glyoxalase ii
97	c3mixA_	Alignment	not modelled	6.4	16	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**flagellar biosynthesis protein flha; **PDBTitle:** crystal structure of the cytosolic domain of b. subtilis flha
98	d3bzka2	Alignment	not modelled	6.4	27	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Tex HhH-containing domain-like
99	c3s55F_	Alignment	not modelled	6.3	38	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**putative short-chain dehydrogenase/reductase; **PDBTitle:** crystal structure of a putative short-chain dehydrogenase/reductase2 from mycobacterium abscessus bound to nad