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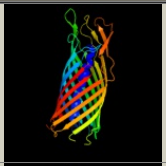
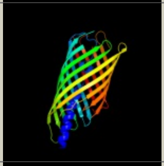
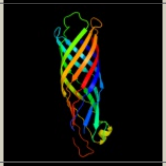
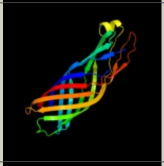
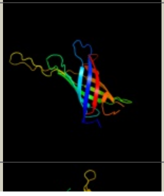
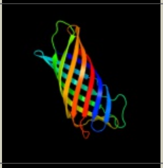
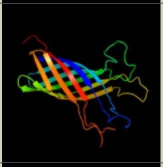
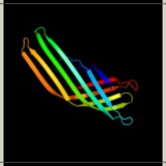
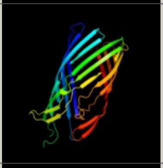
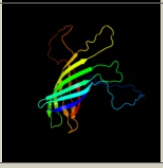
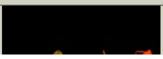
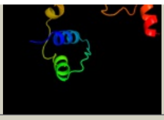
Description	P33666
Date	Wed Jan 25 15:20:50 GMT 2012
Unique Job ID	868320e2b339c08a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3kvnA_	Alignment		100.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**esterase esta; **PDBTitle:** crystal structure of the full-length autotransporter esta from2 pseudomonas aeruginosa
2	c3sljA_	Alignment		100.0	15	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**serine protease espp; **PDBTitle:** pre-cleavage structure of the autotransporter espp - n1023a mutant
3	d1uynx_	Alignment		99.9	13	**Fold:**Transmembrane beta-barrels **Superfamily:**Autotransporter **Family:**Autotransporter
4	c3qq2C_	Alignment		99.9	18	**PDB header:**membrane protein/protein transport **Chain:** C: **PDB Molecule:**brka autotransporter; **PDBTitle:** crystal structure of the beta domain of the bordetella autotransporter2 brka
5	c3aehB_	Alignment		99.9	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hemoglobin-binding protease hbp autotransporter; **PDBTitle:** integral membrane domain of autotransporter hbp
6	c2qomB_	Alignment		99.9	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**serine protease espp; **PDBTitle:** the crystal structure of the e.coli espp autotransporter beta-domain.
7	c2x27X_	Alignment		98.0	13	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**outer membrane protein oprg; **PDBTitle:** crystal structure of the outer membrane protein oprg from2 pseudomonas aeruginosa
8	c3qraA_	Alignment		97.8	17	**PDB header:**cell invasion **Chain:** A: **PDB Molecule:**attachment invasion locus protein; **PDBTitle:** the crystal structure of ail, the attachment invasion locus protein of2 yersinia pestis
9	c2f1tB_	Alignment		97.3	13	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**outer membrane protein w; **PDBTitle:** outer membrane protein ompw
10	d1qjpa_	Alignment		97.2	11	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
11	c2jmmA_	Alignment		97.1	18	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein a; **PDBTitle:** nmr solution structure of a minimal transmembrane beta-2 barrel platform protein

12	c3nb3C_	Alignment		96.7	10	**PDB header:**virus **Chain:** C: **PDB Molecule:**outer membrane protein a; **PDBTitle:** the host outer membrane proteins ompa and ompc are packed at specific2 sites in the shigella phage sf6 virion as structural components
13	d1p4ta_	Alignment		96.5	16	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
14	d1g90a_	Alignment		96.3	13	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
15	d1qj8a_	Alignment		95.4	12	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
16	c2k0lA_	Alignment		94.4	11	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein a; **PDBTitle:** nmr structure of the transmembrane domain of the outer2 membrane protein a from klebsiella pneumoniae in dhpc3 micelles.
17	d2vdfa1	Alignment		92.8	15	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPT-like **Family:**Outer membrane adhesin/invasin OpcA
18	d1t16a_	Alignment		90.7	12	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Outer membrane protein transport protein
19	c3dwoX_	Alignment		90.5	16	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**probable outer membrane protein; **PDBTitle:** crystal structure of a pseudomonas aeruginosa fadl homologue
20	c2lhfA_	Alignment		88.6	12	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein h1; **PDBTitle:** solution structure of outer membrane protein h (oprh) from p.2 aeruginosa in dhpc micelles
21	d2zfga1	Alignment	not modelled	87.5	18	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
22	c2wjqA_	Alignment	not modelled	86.9	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**probable n-acetylneuraminic acid outer membrane channel **PDBTitle:** nanc porin structure in hexagonal crystal form.
23	c2ervA_	Alignment	not modelled	83.2	16	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**hypothetical protein paer03002360; **PDBTitle:** crystal structure of the outer membrane enzyme pagl
24	c3dzmB_	Alignment	not modelled	79.7	15	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hypothetical conserved protein; **PDBTitle:** crystal structure of a major outer membrane protein from thermus2 thermophilus hb27
25	c3nsgA_	Alignment	not modelled	75.0	15	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein f; **PDBTitle:** crystal structure of ompf, an outer membrane protein from salmonella2 typhi
26	c3bryB_	Alignment	not modelled	69.5	11	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**tbux; **PDBTitle:** crystal structure of the ralstonia pickettii toluene2 transporter tbux
27	d2fgqx1	Alignment	not modelled	67.8	9	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
28	c2iwvD_	Alignment	not modelled	65.2	11	**PDB header:**ion channel **Chain:** D: **PDB Molecule:**outer membrane protein g; **PDBTitle:** structure of the monomeric outer membrane porin ompg in the2 open and closed conformation
						

29	d1vp5a_	Alignment		64.2	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
30	d1osma_	Alignment	not modelled	64.1	16	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
31	d1c9wa_	Alignment	not modelled	57.9	26	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
32	d1tlya_	Alignment	not modelled	54.6	13	**Fold:**Transmembrane beta-barrels **Superfamily:**Tsx-like channel **Family:**Tsx-like channel
33	d3eaua1	Alignment	not modelled	53.9	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
34	c2xueB_	Alignment	not modelled	52.3	23	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**lysine-specific demethylase 6b; **PDBTitle:** crystal structure of jmjd3
35	c3flpJ_	Alignment	not modelled	51.6	17	**PDB header:**sugar binding protein **Chain:** J: **PDB Molecule:**sap-like pentraxin; **PDBTitle:** crystal structure of native heptameric sap-like pentraxin2 from limulus polyphemus
36	c3n6qF_	Alignment	not modelled	50.8	12	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**yghz aldo-keto reductase; **PDBTitle:** crystal structure of yghz from e. coli
37	c3n50E_	Alignment	not modelled	48.9	25	**PDB header:**transcription **Chain:** E: **PDB Molecule:**transcription factor coe3; **PDBTitle:** human early b-cell factor 3 (ebf3) ipt/tig and hlhlh domains
38	d1i78a_	Alignment	not modelled	48.8	10	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPT-like **Family:**Outer membrane protease OMPT
39	d1vqoa1	Alignment	not modelled	47.6	23	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**C-terminal domain of ribosomal protein L2
40	c2z4lC_	Alignment	not modelled	46.4	25	**PDB header:**ribosome **Chain:** C: **PDB Molecule:**50s ribosomal protein l2; **PDBTitle:** crystal structure of the bacterial ribosome from escherichia2 coli in complex with paromomycin and ribosome recycling3 factor (rrf). this file contains the 50s subunit of the4 first 70s ribosome, with paromomycin and rrf bound. the5 entire crystal structure contains two 70s ribosomes and is6 described in remark 400.
41	c2k4tA_	Alignment	not modelled	45.0	13	**PDB header:**membrane protein,apoptosis **Chain:** A: **PDB Molecule:**voltage-dependent anion-selective channel **PDBTitle:** solution structure of human vdac-1 in ldao micelles
42	c3lutA_	Alignment	not modelled	43.7	20	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**voltage-gated potassium channel subunit beta-2; **PDBTitle:** a structural model for the full-length shaker potassium channel kv1.2
43	c3erpA_	Alignment	not modelled	41.4	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** structure of idp01002, a putative oxidoreductase from and essential2 gene of salmonella typhimurium
44	c2vqiA_	Alignment	not modelled	41.3	9	**PDB header:**transport **Chain:** A: **PDB Molecule:**outer membrane usher protein papc; **PDBTitle:** structure of the p pilus usher (papc) translocation pore
45	c3up8B_	Alignment	not modelled	41.0	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative 2,5-diketo-d-gluconic acid reductase b; **PDBTitle:** crystal structure of a putative 2,5-diketo-d-gluconic acid reductase b
46	d1lqaa_	Alignment	not modelled	39.6	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
47	c3jsbA_	Alignment	not modelled	38.1	34	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**rna-directed rna polymerase; **PDBTitle:** crystal structure of the n-terminal domain of the lymphocytic2 choriomeningitis virus l protein
48	d1l1fa2	Alignment	not modelled	36.8	27	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
49	c1ynpA_	Alignment	not modelled	36.3	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase; **PDBTitle:** aldo-keto reductase akr11c1 from bacillus halodurans (apo form)
50	d1pz1a_	Alignment	not modelled	36.2	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
51	d1mi3a_	Alignment	not modelled	36.1	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
52	c2ki0A_	Alignment	not modelled	35.9	64	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**ds119; **PDBTitle:** nmr structure of a de novo designed beta alpha beta
53	c2ke4A_	Alignment	not modelled	34.9	25	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**cdc42-interacting protein 4; **PDBTitle:** the nmr structure of the tc10 and cdc42 interacting domain2 of cip4

54	d1iyjb1	Alignment	not modelled	34.1	29	**Fold:**BRCA2 helical domain **Superfamily:**BRCA2 helical domain **Family:**BRCA2 helical domain
55	c3brzA_	Alignment	not modelled	34.0	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**todx; **PDBTitle:** crystal structure of the pseudomonas putida toluene2 transporter todx
56	c2eo2A_	Alignment	not modelled	33.6	36	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**adult male hypothalamus cdna, riken full-length **PDBTitle:** solution structure of the insertion region (510-573) of2 fthfs domain from mouse methylenetetrahydrofolate3 dehydrogenase (nadp+ dependent) 1-like protein
57	d2dlqa1	Alignment	not modelled	32.8	54	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
58	d2j01d1	Alignment	not modelled	31.6	22	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**C-terminal domain of ribosomal protein L2
59	c1kqsA_	Alignment	not modelled	30.2	26	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**ribosomal protein l2; **PDBTitle:** the haloarcula marismortui 50s complexed with a2 pretranslocational intermediate in protein synthesis
60	d1rl2a1	Alignment	not modelled	29.9	22	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**C-terminal domain of ribosomal protein L2
61	c3a8tA_	Alignment	not modelled	29.9	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenylate isopentenyltransferase; **PDBTitle:** plant adenylate isopentenyltransferase in complex with atp
62	c1vliA_	Alignment	not modelled	29.8	23	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**spore coat polysaccharide biosynthesis protein spse; **PDBTitle:** crystal structure of spore coat polysaccharide biosynthesis protein2 spse (bsu37870) from bacillus subtilis at 2.38 a resolution
63	d1tuza_	Alignment	not modelled	29.8	27	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**EF-hand modules in multidomain proteins
64	c2ns2A_	Alignment	not modelled	29.7	30	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**spindlin-1; **PDBTitle:** crystal structure of spindlin1
65	d3proc2	Alignment	not modelled	29.3	55	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Alpha-lytic protease prodomain **Family:**Alpha-lytic protease prodomain
66	c3h7rA_	Alignment	not modelled	29.3	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldo-keto reductase; **PDBTitle:** crystal structure of the plant stress-response enzyme akr4c8
67	c2ftcB_	Alignment	not modelled	29.2	17	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**mitochondrial ribosomal protein l2; **PDBTitle:** structural model for the large subunit of the mammalian mitochondrial2 ribosome
68	d1vlia2	Alignment	not modelled	29.2	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**NeuB-like
69	d1j96a_	Alignment	not modelled	28.9	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
70	d1frba_	Alignment	not modelled	28.8	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
71	d2zjra1	Alignment	not modelled	28.7	29	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**C-terminal domain of ribosomal protein L2
72	c3buvB_	Alignment	not modelled	28.5	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**3-oxo-5-beta-steroid 4-dehydrogenase; **PDBTitle:** crystal structure of human delta(4)-3-ketosteroid 5-beta-reductase in2 complex with nadp and hepes. resolution: 1.35 a.
73	c3njqB_	Alignment	not modelled	28.5	21	**PDB header:**viral protein/inhibitor **Chain:** B: **PDB Molecule:**orf 17; **PDBTitle:** crystal structure of kaposi's sarcoma-associated herpesvirus protease2 in complex with dimer disruptor
74	c3d5bD_	Alignment	not modelled	28.5	18	**PDB header:**ribosome **Chain:** D: **PDB Molecule:**50s ribosomal protein l2; **PDBTitle:** structural basis for translation termination on the 70s ribosome. this2 file contains the 50s subunit of one 70s ribosome. the entire crystal3 structure contains two 70s ribosomes as described in remark 400.
75	c1tkeA_	Alignment	not modelled	28.1	29	**PDB header:**ligase **Chain:** A: **PDB Molecule:**threonyl-trna synthetase; **PDBTitle:** crystal structure of the editing domain of threonyl-trna2 synthetase complexed with serine
76	d1bvua2	Alignment	not modelled	28.0	30	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
77	c1vbjB_	Alignment	not modelled	27.7	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**prostaglandin f synthase; **PDBTitle:** the crystal structure of prostaglandin f synthase from2 trypanosoma brucei
78	d1hqta_	Alignment	not modelled	27.4	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
						PDB header:oxidoreductase

79	c3f7jB_	Alignment	not modelled	27.4	17	**Chain:** B: **PDB Molecule:**yvgn protein; **PDBTitle:** b.subtilis yvgn
80	c3h7uA_	Alignment	not modelled	26.8	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldo-keto reductase; **PDBTitle:** crystal structure of the plant stress-response enzyme akr4c9
81	d1ah4a_	Alignment	not modelled	26.6	30	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
82	d1b65a_	Alignment	not modelled	26.4	23	**Fold:**DmpA/ArgJ-like **Superfamily:**DmpA/ArgJ-like **Family:**DmpA-like
83	c2zkra_	Alignment	not modelled	26.2	23	**PDB header:**ribosomal protein/rna **Chain:** A: **PDB Molecule:**rna expansion segment es3; **PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
84	d1qr0a1	Alignment	not modelled	25.9	10	**Fold:**4'-phosphopantetheinyl transferase **Superfamily:**4'-phosphopantetheinyl transferase **Family:**4'-Phosphopantetheinyl transferase SFP
85	c2ze5A_	Alignment	not modelled	25.7	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**isopentenyl transferase; **PDBTitle:** crystal structure of adenosine phosphate-isopentenyltransferase
86	d1afsa_	Alignment	not modelled	25.6	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
87	c2j9uB_	Alignment	not modelled	25.5	26	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**vacuolar protein sorting-associated protein 36; **PDBTitle:** 2 angstrom x-ray structure of the yeast escrt-i vps28 c-2 terminus in complex with the nzf-n domain from escrt-ii
88	d2j9ub1	Alignment	not modelled	25.5	26	**Fold:**Rubredoxin-like **Superfamily:**Ran binding protein zinc finger-like **Family:**Ran binding protein zinc finger-like
89	c3b3dA_	Alignment	not modelled	25.4	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative morphine dehydrogenase; **PDBTitle:** b.subtilis ytbe
90	d1ur3m_	Alignment	not modelled	25.2	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
91	d2alra_	Alignment	not modelled	25.2	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
92	c1htoB_	Alignment	not modelled	25.0	29	**PDB header:**ligase **Chain:** B: **PDB Molecule:**glutamine synthetase; **PDBTitle:** crystallographic structure of a relaxed glutamine synthetase from2 mycobacterium tuberculosis
93	d1s1pa_	Alignment	not modelled	24.9	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
94	d1miua1	Alignment	not modelled	24.9	26	**Fold:**BRCA2 helical domain **Superfamily:**BRCA2 helical domain **Family:**BRCA2 helical domain
95	d1q5ma_	Alignment	not modelled	24.9	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
96	c2yfqA_	Alignment	not modelled	24.8	40	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nad-specific glutamate dehydrogenase; **PDBTitle:** crystal structure of glutamate dehydrogenase from2 peptoniphilus asaccharolyticus
97	d2zdra2	Alignment	not modelled	24.6	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**NeuB-like
98	c2gyaA_	Alignment	not modelled	24.6	17	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**50s ribosomal protein l2; **PDBTitle:** structure of the 50s subunit of a pre-translocational e.2 coli ribosome obtained by fitting atomic models for rna and3 protein components into cryo-em map emd-1056
99	c3fozB_	Alignment	not modelled	24.4	25	**PDB header:**transferase/rna **Chain:** B: **PDB Molecule:**trna delta(2)-isopentenylpyrophosphate transferase; **PDBTitle:** structure of e. coli isopentenyl-trna transferase in complex with e.2 coli trna(phe)
100	d1gtma2	Alignment	not modelled	24.3	33	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
101	c4a1cA_	Alignment	not modelled	24.1	20	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**rpl8; **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 4.
102	c2j8pA_	Alignment	not modelled	23.4	31	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**cleavage stimulation factor 64 kda subunit; **PDBTitle:** nmr structure of c-terminal domain of human cstf-64
103	c3jyzA_	Alignment	not modelled	23.3	25	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**type iv pilin structural subunit; **PDBTitle:** crystal structure of pseudomonas aeruginosa (strain:2 pa110594) typeiv pilin in space group p41212
104	c1rl2A_	Alignment	not modelled	23.2	22	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**protein (ribosomal protein l2); **PDBTitle:** ribosomal protein l2 rna-binding domain from bacillus2 stearothermophilus

105	d1us0a_	Alignment	not modelled	22.9	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
106	c2b66D_	Alignment	not modelled	22.8	22	**PDB header:**ribosome **Chain:** D: **PDB Molecule:**50s ribosomal protein l2; **PDBTitle:** 50s ribosomal subunit from a crystal structure of release factor rf1,2 trnas and mrna bound to the ribosome. this file contains the 50s3 subunit from a crystal structure of release factor rf1, trnas and4 mrna bound to the ribosome and is described in remark 400
107	c2oz6A_	Alignment	not modelled	22.7	23	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**virulence factor regulator; **PDBTitle:** crystal structure of virulence factor regulator from pseudomonas2 aeruginosa in complex with camp
108	d2pfxa1	Alignment	not modelled	22.5	28	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**Atu0492-like
109	d1qwka_	Alignment	not modelled	22.4	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
110	c3bboE_	Alignment	not modelled	22.4	33	**PDB header:**ribosome **Chain:** E: **PDB Molecule:**ribosomal protein l2; **PDBTitle:** homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
111	c2hb0B_	Alignment	not modelled	21.8	40	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**cfa/i fimbrial subunit e; **PDBTitle:** crystal structure of cfae, the adhesive subunit of cfa/i2 fimbria of enterotoxigenic escherichia coli
112	c2ov3A_	Alignment	not modelled	21.8	8	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**periplasmic binding protein component of an abc **PDBTitle:** crystal structure of 138-173 znua deletion mutant plus zinc2 bound
113	d2slia1	Alignment	not modelled	21.8	36	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Leech intramolecular trans-sialidase, N-terminal domain
114	c1kn7A_	Alignment	not modelled	21.8	42	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**voltage-gated potassium channel protein kv1.4; **PDBTitle:** solution structure of the tandem inactivation domain2 (residues 1-75) of potassium channel rck4 (kv1.4)
115	c3ohnA_	Alignment	not modelled	21.7	7	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane usher protein fimd; **PDBTitle:** crystal structure of the fimd translocation domain
116	d1u04a1	Alignment	not modelled	21.7	42	**Fold:**SH3-like barrel **Superfamily:**PAZ domain **Family:**PAZ domain
117	c1zgdB_	Alignment	not modelled	21.6	10	**PDB header:**plant protein **Chain:** B: **PDB Molecule:**chalcone reductase; **PDBTitle:** chalcone reductase complexed with nadp+ at 1.7 angstrom2 resolution
118	c2drhD_	Alignment	not modelled	21.6	15	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**361aa long hypothetical d-aminopeptidase; **PDBTitle:** crystal structure of the ph0078 protein from pyrococcus horikoshii ot3
119	c2b99A_	Alignment	not modelled	21.5	31	**PDB header:**transferase **Chain:** A: **PDB Molecule:**riboflavin synthase; **PDBTitle:** crystal structure of an archaeal pentameric riboflavin2 synthase complex with a substrate analog inhibitor
120	c2ql8A_	Alignment	not modelled	21.3	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative redox protein; **PDBTitle:** crystal structure of a putative redox protein (lsei_0423) from2 lactobacillus casei atcc 334 at 1.50 a resolution