Phyre^2

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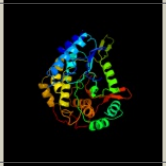
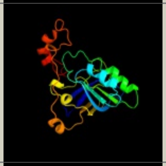
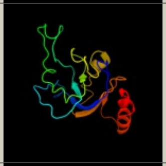
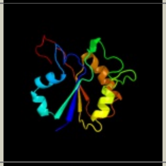
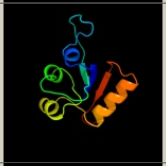
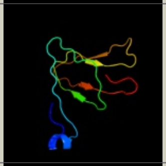
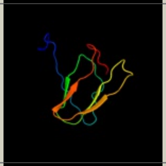
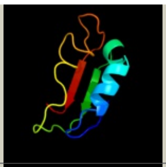
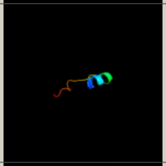
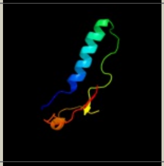
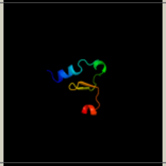
Description	P05791
Date	Thu Jan 5 10:58:53 GMT 2012
Unique Job ID	e21c08d3f378458b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2gp4A_	Alignment		100.0	31	**PDB header:**lyase **Chain:** A: **PDB Molecule:**6-phosphogluconate dehydratase; **PDBTitle:** structure of [fes]cluster-free apo form of 6-phosphogluconate2 dehydratase from shewanella oneidensis
2	d2gp4a2	Alignment		100.0	29	**Fold:**IlvD/EDD N-terminal domain-like **Superfamily:**IlvD/EDD N-terminal domain-like **Family:**IvD/EDD N-terminal domain-like
3	d2gp4a1	Alignment		100.0	31	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**IlvD/EDD C-terminal domain-like
4	d1zyma2	Alignment		92.0	22	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Phosphohistidine domain **Family:**N-terminal domain of enzyme I of the PEP:sugar phosphotransferase system
5	c3fijD_	Alignment		86.0	21	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**lin1909 protein; **PDBTitle:** crystal structure of a uncharacterized protein lin1909
6	d1vbga2	Alignment		81.1	14	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Phosphohistidine domain **Family:**Pyruvate phosphate dikinase, central domain
7	c3nxkE_	Alignment		75.7	14	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**cytoplasmic l-asparaginase; **PDBTitle:** crystal structure of probable cytoplasmic l-asparaginase from2 campylobacter jejuni
8	d1h6za2	Alignment		67.3	19	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Phosphohistidine domain **Family:**Pyruvate phosphate dikinase, central domain
9	d1od5a1	Alignment		65.9	23	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
10	d2et1a1	Alignment		57.9	20	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
11	c2jv2A_	Alignment		56.8	30	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein ph1500; **PDBTitle:** solution structure of the n-terminal domain of ph1500

12	c2pcnA_	Alignment		56.7	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**s-adenosylmethionine:2-demethylmenaquinone **PDBTitle:** crystal structure of s-adenosylmethionine: 2-dimethylmenaquinone2 methyltransferase (gk_1813) from geobacillus kaustophilus hta426
13	c2zkiH_	Alignment		53.1	20	**PDB header:**transcription **Chain:** H: **PDB Molecule:**199aa long hypothetical trp repressor binding **PDBTitle:** crystal structure of hypothetical trp repressor binding2 protein from sul folobus tokodaii (st0872)
14	d1fuia2	Alignment		52.4	8	**Fold:**FucI/AraA N-terminal and middle domains **Superfamily:**FucI/AraA N-terminal and middle domains **Family:**L-fucose isomerase, N-terminal and second domains
15	d1pl8a1	Alignment		50.4	25	**Fold:**GroES-like **Superfamily:**GroES-like **Family:**Alcohol dehydrogenase-like, N-terminal domain
16	c2q8kA_	Alignment		48.7	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**proliferation-associated protein 2g4; **PDBTitle:** the crystal structure of ebp1
17	c2hwgA_	Alignment		48.4	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoenolpyruvate-protein phosphotransferase; **PDBTitle:** structure of phosphorylated enzyme i of the2 phosphoenolpyruvate:sugar phosphotransferase system
18	c3ehkC_	Alignment		46.7	20	**PDB header:**plant protein **Chain:** C: **PDB Molecule:**prunin; **PDBTitle:** crystal structure of pru du amandin, an allergenic protein2 from prunus dulcis
19	d1wsaa_	Alignment		46.6	15	**Fold:**Glutaminase/Asparaginase **Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase
20	d2hi6a1	Alignment		44.3	16	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**AF0055-like
21	d1rk8a_	Alignment	not modelled	44.3	31	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
22	c2v6cA_	Alignment	not modelled	44.1	23	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**proliferation-associated protein 2g4; **PDBTitle:** crystal structure of erbb3 binding protein 1 (ebp1)
23	c3d54D_	Alignment	not modelled	43.9	11	**PDB header:**ligase **Chain:** D: **PDB Molecule:**phosphoribosylformylglycinamidine synthase 1; **PDBTitle:** stucture of purlqs from thermotoga maritima
24	d1gtta1	Alignment	not modelled	42.3	17	**Fold:**FAH **Superfamily:**FAH **Family:**FAH
25	c1nxjA_	Alignment	not modelled	42.1	19	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**probable s-adenosylmethionine:2- **PDBTitle:** structure of rv3853 from mycobacterium tuberculosis
26	d1nxja_	Alignment	not modelled	42.1	19	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**RraA-like **Family:**RraA-like
27	d1fxza2	Alignment	not modelled	41.7	19	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
28	c3kglB_	Alignment	not modelled	41.3	21	**PDB header:**plant protein **Chain:** B: **PDB Molecule:**cruciferin; **PDBTitle:** crystal structure of procruciferin, 11s globulin from2 brassica napus
29	d1wl8a1	Alignment	not modelled	40.5	24	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like

						Family: Class I glutamine amidotransferases (GAT)
30	d1u1ha1	Alignment	not modelled	40.2	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**UROD/MetE-like **Family:**Cobalamin-independent methionine synthase
31	d1agxa_	Alignment	not modelled	40.1	17	**Fold:**Glutaminase/Asparaginase **Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase
32	d1od5a2	Alignment	not modelled	40.0	20	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
33	d1vi4a_	Alignment	not modelled	39.6	17	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**RraA-like **Family:**RraA-like
34	c2d5fB_	Alignment	not modelled	39.4	22	**PDB header:**plant protein **Chain:** B: **PDB Molecule:**glycinin a3b4 subunit; **PDBTitle:** crystal structure of recombinant soybean proglycinin a3b4 subunit, its2 comparison with mature glycinin a3b4 subunit, responsible for hexamer3 assembly
35	d1cnt1_	Alignment	not modelled	39.3	22	**Fold:**4-helical cytokines **Superfamily:**4-helical cytokines **Family:**Long-chain cytokines
36	c1l9xA_	Alignment	not modelled	39.1	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**gamma-glutamyl hydrolase; **PDBTitle:** structure of gamma-glutamyl hydrolase
37	d1l9xa_	Alignment	not modelled	39.1	13	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
38	c1ezaA_	Alignment	not modelled	39.0	16	**PDB header:**phosphotransferase **Chain:** A: **PDB Molecule:**enzyme i; **PDBTitle:** amino terminal domain of enzyme i from escherichia coli nmr,2 restrained regularized mean structure
39	d2a5la1	Alignment	not modelled	38.7	19	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**WrbA-like
40	d1uika2	Alignment	not modelled	38.5	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
41	d1fjca_	Alignment	not modelled	38.5	31	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
42	c2e9qA_	Alignment	not modelled	37.6	18	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**11s globulin subunit beta; **PDBTitle:** recombinant pro-11s globulin of pumpkin
43	c1rkjA_	Alignment	not modelled	36.3	30	**PDB header:**transcription/rna **Chain:** A: **PDB Molecule:**nucleolin; **PDBTitle:** solution structure of the complex formed by the two n-2 terminal rna-binding domains of nucleolin and a pre-rrna3 target
44	c2vriA_	Alignment	not modelled	35.9	22	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**non-structural protein 3; **PDBTitle:** structure of the nsp3 x-domain of human coronavirus nl63
45	c2eaaB_	Alignment	not modelled	35.3	19	**PDB header:**plant protein **Chain:** B: **PDB Molecule:**7s globulin-3; **PDBTitle:** crystal structure of adzuki bean 7s globulin-3
46	d1j3la_	Alignment	not modelled	35.2	16	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**RraA-like **Family:**RraA-like
47	d1uija2	Alignment	not modelled	34.4	15	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
48	c3ksmA_	Alignment	not modelled	33.9	19	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**abc-type sugar transport system, periplasmic component; **PDBTitle:** crystal structure of abc-type sugar transport system, periplasmic2 component from hahella chejuensis
49	d1r31a1	Alignment	not modelled	33.4	35	**Fold:**Ferredoxin-like **Superfamily:**NAD-binding domain of HMG-CoA reductase **Family:**NAD-binding domain of HMG-CoA reductase
50	d1kola2	Alignment	not modelled	33.2	24	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
51	d1o1ya_	Alignment	not modelled	32.7	18	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
52	c3kscD_	Alignment	not modelled	32.3	20	**PDB header:**plant protein **Chain:** D: **PDB Molecule:**lega class; **PDBTitle:** crystal structure of pea prolegumin, an 11s seed globulin2 from pisum sativum l.
53	d1kbla2	Alignment	not modelled	32.1	29	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Phosphohistidine domain **Family:**Pyruvate phosphate dikinase, central domain
54	d1vkma_	Alignment	not modelled	31.7	17	**Fold:**Indigoidine synthase A-like **Superfamily:**Indigoidine synthase A-like **Family:**Indigoidine synthase A-like
55	d1v7la_	Alignment	not modelled	31.2	22	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**LeuD-like
						Fold: Alpha-L RNA-binding motif

56	d1dm9a_	Alignment	not modelled	31.1	15	**Superfamily:**Alpha-L RNA-binding motif **Family:**Heat shock protein 15 kD
57	c1dm9A_	Alignment	not modelled	31.1	15	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**hypothetical 15.5 kd protein in mrca-pcka **PDBTitle:** heat shock protein 15 kd
58	c3qacA_	Alignment	not modelled	30.4	14	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**11s globulin seed storage protein; **PDBTitle:** structure of amaranth 11s proglobulin seed storage protein from2 amaranthus hypochondriacus l.
59	d1qdlb_	Alignment	not modelled	30.2	25	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
60	c3ex7B_	Alignment	not modelled	29.5	26	**PDB header:**hydrolase/rna binding protein/rna **Chain:** B: **PDB Molecule:**rna-binding protein 8a; **PDBTitle:** the crystal structure of ejc in its transition state
61	c1sddA_	Alignment	not modelled	29.3	26	**PDB header:**blood clotting **Chain:** A: **PDB Molecule:**coagulation factor v; **PDBTitle:** crystal structure of bovine factor vai
62	c1gph1_	Alignment	not modelled	29.3	22	**PDB header:**transferase(glutamine amidotransferase) **Chain:** 1: **PDB Molecule:**glutamine phosphoribosyl-pyrophosphate amidotransferase; **PDBTitle:** structure of the allosteric regulatory enzyme of purine biosynthesis
63	d1a8ya3	Alignment	not modelled	29.3	50	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Calsequestrin
64	c1fxzC_	Alignment	not modelled	27.9	17	**PDB header:**plant protein **Chain:** C: **PDB Molecule:**glycinin g1; **PDBTitle:** crystal structure of soybean proglycinin a1ab1b homotrimer
65	c3gmiA_	Alignment	not modelled	27.7	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0348 protein mj0951; **PDBTitle:** crystal structure of a protein of unknown function from2 methanocaldococcus jannaschii
66	d1q5xa_	Alignment	not modelled	27.6	19	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**RraA-like **Family:**RraA-like
67	c2jz7A_	Alignment	not modelled	27.2	19	**PDB header:**selenium-binding protein **Chain:** A: **PDB Molecule:**selenium binding protein; **PDBTitle:** solution nmr structure of selenium-binding protein from2 methanococcus vannielii
68	d1nqua_	Alignment	not modelled	26.9	23	**Fold:**Lumazine synthase **Superfamily:**Lumazine synthase **Family:**Lumazine synthase
69	d1lcya1	Alignment	not modelled	26.1	29	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**HtrA-like serine proteases
70	c2eeyA_	Alignment	not modelled	25.8	20	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**molybdopterin biosynthesis; **PDBTitle:** structure of gk0241 protein from geobacillus kaustophilus
71	c2f3jA_	Alignment	not modelled	25.7	27	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**rna and export factor binding protein 2; **PDBTitle:** the solution structure of the ref2-i mrna export factor2 (residues 1-155).
72	c2ideE_	Alignment	not modelled	25.6	25	**PDB header:**biosynthetic protein **Chain:** E: **PDB Molecule:**molybdenum cofactor biosynthesis protein c; **PDBTitle:** crystal structure of the molybdenum cofactor biosynthesis protein c2 (ttha1789) from thermus theromophilus hb8
73	d1r61a_	Alignment	not modelled	25.6	24	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Putative cyclase **Family:**Putative cyclase
74	c3nojA_	Alignment	not modelled	25.6	29	**PDB header:**lyase **Chain:** A: **PDB Molecule:**4-carboxy-4-hydroxy-2-oxoadipate aldolase/oxaloacetate **PDBTitle:** the structure of hmg/cha aldolase from the protocatechuate degradation2 pathway of pseudomonas putida
75	c1cauB_	Alignment	not modelled	25.5	18	**PDB header:**seed storage protein **Chain:** B: **PDB Molecule:**canavalin; **PDBTitle:** determination of three crystal structures of canavalin by molecular2 replacement
76	c1uz5A_	Alignment	not modelled	25.3	25	**PDB header:**molybdopterin biosynthesis **Chain:** A: **PDB Molecule:**402aa long hypothetical molybdopterin **PDBTitle:** the crystal structure of molybdopterin biosynthesis moea2 protein from pyrococcus horikosii
77	c3fs2A_	Alignment	not modelled	25.1	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-dehydro-3-deoxyphosphooctonate aldolase; **PDBTitle:** crystal structure of 2-dehydro-3-deoxyphosphooctonate2 aldolase from bruciella melitensis at 1.85a resolution
78	d1ekra_	Alignment	not modelled	25.0	20	**Fold:**Ferredoxin-like **Superfamily:**Molybdenum cofactor biosynthesis protein C, MoaC **Family:**Molybdenum cofactor biosynthesis protein C, MoaC
79	d2npta1	Alignment	not modelled	24.7	63	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**PB1 domain
80	c2qv5A_	Alignment	not modelled	24.6	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu2773; **PDBTitle:** crystal structure of uncharacterized protein atu2773 from2 agrobacterium tumefaciens c58
81	c2nq5A_	Alignment	not modelled	24.1	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**5-methyltetrahydropteroyltriglutamate-- **PDBTitle:** crystal structure of methyltransferase from streptococcus2 mutans

82	c1u22A_	Alignment	not modelled	23.7	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**5-methyltetrahydropteroyltriglutamate-- **PDBTitle:** a. thaliana cobalamine independent methionine synthase
83	d2cqaa1	Alignment	not modelled	23.6	35	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**TIP49 domain
84	c2nqqA_	Alignment	not modelled	23.4	14	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**molybdopterin biosynthesis protein moea; **PDBTitle:** moea r137q
85	c3ln3A_	Alignment	not modelled	23.3	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydrodiol dehydrogenase; **PDBTitle:** crystal structure of putative reductase (np_038806.2) from2 mus musculus at 1.18 a resolution
86	c3l7sA_	Alignment	not modelled	22.9	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**5-methyltetrahydropteroyltriglutamate--homocysteine **PDBTitle:** crystal structure of mete coordinated with zinc from streptococcus2 mutans
87	c3fm3B_	Alignment	not modelled	22.6	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**methionine aminopeptidase 2; **PDBTitle:** crystal structure of an encephalitozoon cuniculi methionine2 aminopeptidase type 2
88	c2e5hA_	Alignment	not modelled	22.6	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**zinc finger cchc-type and rna-binding motif- **PDBTitle:** solution structure of rna binding domain in zinc finger2 cchc-type and rna binding motif 1
89	c1t7lA_	Alignment	not modelled	22.6	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**5-methyltetrahydropteroyltriglutamate-- **PDBTitle:** crystal structure of cobalamin-independent methionine2 synthase from t. maritima
90	c3kw8A_	Alignment	not modelled	22.4	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative copper oxidase; **PDBTitle:** two-domain laccase from streptomyces coelicolor at 2.3 a resolution
91	c2dhgA_	Alignment	not modelled	22.4	19	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**trna selenocysteine associated protein (secp43); **PDBTitle:** solution structure of the c-terminal rna recognition motif2 in trna selenocysteine associated protein
92	c3l83A_	Alignment	not modelled	22.1	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutamine amido transferase; **PDBTitle:** crystal structure of glutamine amido transferase from methylobacillus2 flagellatus
93	d2etna2	Alignment	not modelled	22.0	19	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**GreA transcript cleavage factor, C-terminal domain
94	d1a9xb2	Alignment	not modelled	21.8	27	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
95	c3t07D_	Alignment	not modelled	21.5	22	**PDB header:**transferase/transferase inhibitor **Chain:** D: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of s. aureus pyruvate kinase in complex with a2 naturally occurring bis-indole alkaloid
96	c3f56F_	Alignment	not modelled	21.4	17	**PDB header:**structural protein **Chain:** F: **PDB Molecule:**csos1d; **PDBTitle:** the structure of a previously undetected carboxysome shell2 protein: csos1d from prochlorococcus marinus med4
97	d1jlja_	Alignment	not modelled	21.4	10	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
98	c3c3vA_	Alignment	not modelled	21.2	22	**PDB header:**allergen **Chain:** A: **PDB Molecule:**arachin arah3 isoform; **PDBTitle:** crystal structure of peanut major allergen ara h 3
99	c2y0fD_	Alignment	not modelled	21.2	40	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; **PDBTitle:** structure of gcpe (ispg) from thermus thermophilus hb27
100	d1wi0a_	Alignment	not modelled	21.1	63	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**PB1 domain
101	d1ueba3	Alignment	not modelled	21.0	25	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
102	c1yw7A_	Alignment	not modelled	20.9	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**methionine aminopeptidase 2; **PDBTitle:** h-metap2 complexed with a444148
103	c3mvnA_	Alignment	not modelled	20.8	26	**PDB header:**ligase **Chain:** A: **PDB Molecule:**udp-n-acetylmuramate:l-alanyl-gamma-d-glutamayl-medo- **PDBTitle:** crystal structure of a domain from a putative udp-n-acetylmuramate:l-2 alanyl-gamma-d-glutamayl-medo-diaminopimelate ligase from haemophilus3 ducreyi 35000hp
104	c3d7nA_	Alignment	not modelled	20.5	13	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**flavodoxin, wrba-like protein; **PDBTitle:** the crystal structure of the flavodoxin, wrba-like protein from2 agrobacterium tumefaciens
105	c2pkpA_	Alignment	not modelled	20.5	31	**PDB header:**lyase **Chain:** A: **PDB Molecule:**homoaconitase small subunit; **PDBTitle:** crystal structure of 3-isopropylmalate dehydratase (leud)2 from methhanocaldococcus jannaschii dsm2661 (mj1271)
106	c1uijA_	Alignment	not modelled	20.2	14	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**beta subunit of beta conglycinin; **PDBTitle:** crystal structure of soybean beta-conglycinin beta2 homotrimer (i122m/k124w)