Phyre2

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Description	P77596
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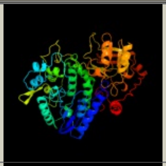
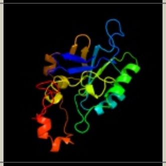
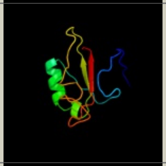
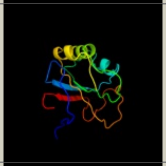
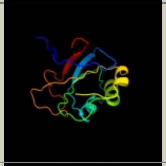
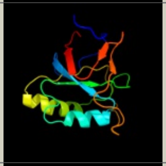
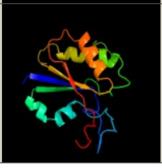
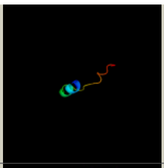
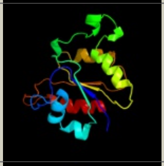
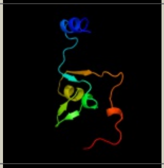
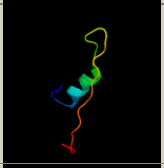
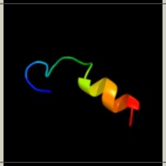
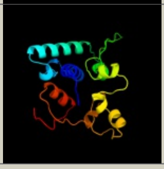
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2gp4A_	Alignment		100.0	28	**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	27	**Fold:**IlvD/EDD N-terminal domain-like **Superfamily:**IlvD/EDD N-terminal domain-like **Family:**lvD/EDD N-terminal domain-like
3	d2gp4a1	Alignment		100.0	26	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**IlvD/EDD C-terminal domain-like
4	c2pcnA_	Alignment		79.3	17	**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
5	c2jv2A_	Alignment		69.3	25	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein ph1500; **PDBTitle:** solution structure of the n-terminal domain of ph1500
6	d1nxja_	Alignment		66.5	15	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**RraA-like **Family:**RraA-like
7	c1nxjA_	Alignment		66.5	15	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**probable s-adenosylmethionine:2- **PDBTitle:** structure of rv3853 from mycobacterium tuberculosis
8	c3c8oB_	Alignment		64.9	18	**PDB header:**hydrolase regulator **Chain:** B: **PDB Molecule:**regulator of ribonuclease activity a; **PDBTitle:** the crystal structure of rraa from pao1
9	d1vi4a_	Alignment		62.5	13	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**RraA-like **Family:**RraA-like
10	d1q5xa_	Alignment		52.4	15	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**RraA-like **Family:**RraA-like
11	d1agxa_	Alignment		51.7	15	**Fold:**Glutaminase/Asparaginase **Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase

12	d1pl8a1	Alignment		50.0	21	**Fold:**GroES-like **Superfamily:**GroES-like **Family:**Alcohol dehydrogenase-like, N-terminal domain
13	d1wsaa_	Alignment		45.6	21	**Fold:**Glutaminase/Asparaginase **Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase
14	d1y0pa2	Alignment		42.7	23	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
15	d2hi6a1	Alignment		40.6	11	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**AF0055-like
16	d1ydga_	Alignment		37.2	13	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**WrbA-like
17	d1fjca_	Alignment		35.2	34	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
18	d1wl8a1	Alignment		35.1	23	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
19	d1r31a1	Alignment		35.0	35	**Fold:**Ferredoxin-like **Superfamily:**NAD-binding domain of HMG-CoA reductase **Family:**NAD-binding domain of HMG-CoA reductase
20	d1j33a_	Alignment		34.4	19	**Fold:**Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) **Superfamily:**Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) **Family:**Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT)
21	d1od5a1	Alignment	not modelled	34.0	18	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
22	d1v7la_	Alignment	not modelled	32.1	17	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**LeuD-like
23	d1zyma2	Alignment	not modelled	32.0	9	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Phosphohistidine domain **Family:**N-terminal domain of enzyme I of the PEP:sugar phosphotransferase system
24	c1dm9A_	Alignment	not modelled	32.0	15	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**hypothetical 15.5 kd protein in mrca-pcka **PDBTitle:** heat shock protein 15 kd
25	d1dm9a_	Alignment	not modelled	32.0	15	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Heat shock protein 15 kD
26	d1kola2	Alignment	not modelled	31.9	24	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
27	d1j3la_	Alignment	not modelled	31.8	26	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**RraA-like **Family:**RraA-like
28	c1sddA_	Alignment	not modelled	31.5	21	**PDB header:**blood clotting **Chain:** A: **PDB Molecule:**coagulation factor v; **PDBTitle:** crystal structure of bovine factor vai
29	d1ujva_	Alignment	not modelled	31.4	32	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like

						Family:PDZ domain
30	d1o7ja_	Alignment	not modelled	31.0	12	**Fold:**Glutaminase/Asparaginase **Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase
31	d1r61a_	Alignment	not modelled	28.7	15	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Putative cyclase **Family:**Putative cyclase
32	d1rk8a_	Alignment	not modelled	28.4	21	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
33	c1rkjA_	Alignment	not modelled	26.9	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
34	c3l83A_	Alignment	not modelled	25.9	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutamine amido transferase; **PDBTitle:** crystal structure of glutamine amido transferase from methylobacillus2 flagellatus
35	d1a9xb2	Alignment	not modelled	25.3	22	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
36	d1lcya1	Alignment	not modelled	25.0	34	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**HtrA-like serine proteases
37	d2etna2	Alignment	not modelled	24.4	14	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**GreA transcript cleavage factor, C-terminal domain
38	c2qv5A_	Alignment	not modelled	24.3	26	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu2773; **PDBTitle:** crystal structure of uncharacterized protein atu2773 from2 agrobacterium tumefaciens c58
39	c3nojA_	Alignment	not modelled	24.2	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
40	c3t6oA_	Alignment	not modelled	24.1	18	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sulfate transporter/antisigma-factor antagonist stas; **PDBTitle:** the structure of an anti-sigma-factor antagonist (stas) domain protein2 from planctomyces limnophilus.
41	c3f43A_	Alignment	not modelled	24.0	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative anti-sigma factor antagonist tm1081; **PDBTitle:** crystal structure of a putative anti-sigma factor antagonist (tm1081)2 from thermotoga maritima at 1.59 a resolution
42	c3kw8A_	Alignment	not modelled	23.6	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative copper oxidase; **PDBTitle:** two-domain laccase from streptomyces coelicolor at 2.3 a resolution
43	d2et1a1	Alignment	not modelled	23.3	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
44	d1k78a1	Alignment	not modelled	22.9	31	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
45	c3fm3B_	Alignment	not modelled	22.9	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**methionine aminopeptidase 2; **PDBTitle:** crystal structure of an encephalitozoon cuniculi methionine2 aminopeptidase type 2
46	d2bs2a2	Alignment	not modelled	22.8	26	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
47	c1yw7A_	Alignment	not modelled	22.4	32	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**methionine aminopeptidase 2; **PDBTitle:** h-metap2 complexed with a444148
48	d6paxa1	Alignment	not modelled	21.5	31	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
49	d1kbla2	Alignment	not modelled	21.5	12	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Phosphohistidine domain **Family:**Pyruvate phosphate dikinase, central domain
50	d2f23a2	Alignment	not modelled	21.5	14	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**GreA transcript cleavage factor, C-terminal domain
51	c2pkpA_	Alignment	not modelled	21.3	24	**PDB header:**lyase **Chain:** A: **PDB Molecule:**homoaconitase small subunit; **PDBTitle:** crystal structure of 3-isopropylmalate dehydratase (leud)2 from methhanocaldococcus jannaschii dsm2661 (mj1271)
52	d1qdlb_	Alignment	not modelled	21.1	18	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
53	d1sdda1	Alignment	not modelled	20.7	21	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
54	c3ln3A_	Alignment	not modelled	20.3	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
55	c3mvnA	Alignment	not modelled	19.9	10	**PDB header:**ligase **Chain:** A: **PDB Molecule:**udp-n-acetylmuramate:l-alanyl-gamma-d-glutamayl-medo-

55	c3mvhA_	Alignment	not modelled	19.9	10	**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
56	d1jb0k_	Alignment	not modelled	18.8	44	**Fold:**Photosystem I reaction center subunit X, PsaK **Superfamily:**Photosystem I reaction center subunit X, PsaK **Family:**Photosystem I reaction center subunit X, PsaK
57	c1jb0K_	Alignment	not modelled	18.8	44	**PDB header:**photosynthesis **Chain:** K: **PDB Molecule:**photosystem 1 reaction centre subunit x; **PDBTitle:** crystal structure of photosystem i: a photosynthetic reaction center2 and core antenna system from cyanobacteria
58	c1ezaA_	Alignment	not modelled	18.8	14	**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
59	c2cdqB_	Alignment	not modelled	18.0	26	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aspartokinase; **PDBTitle:** crystal structure of arabidopsis thaliana aspartate kinase2 complexed with lysine and s-adenosylmethionine
60	d1vbga2	Alignment	not modelled	17.8	12	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Phosphohistidine domain **Family:**Pyruvate phosphate dikinase, central domain
61	d1ueba3	Alignment	not modelled	17.8	6	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
62	c1wa1X_	Alignment	not modelled	17.7	16	**PDB header:**reductase **Chain:** X: **PDB Molecule:**dissimilatory copper-containing nitrite **PDBTitle:** crystal structure of h313q mutant of alcaligenes2 xylosoxidans nitrite reductase
63	c2hcuA_	Alignment	not modelled	17.6	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3-isopropylmalate dehydratase small subunit; **PDBTitle:** crystal structure of smu.1381 (or leud) from streptococcus2 mutans
64	c3cdzA_	Alignment	not modelled	17.2	21	**PDB header:**blood clotting **Chain:** A: **PDB Molecule:**coagulation factor viii heavy chain; **PDBTitle:** crystal structure of human factor viii
65	c2y0fD_	Alignment	not modelled	17.1	20	**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
66	d2cqaa1	Alignment	not modelled	17.1	18	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**TIP49 domain
67	c3soeA_	Alignment	not modelled	17.1	22	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**membrane-associated guanylate kinase, ww and pdz domain- **PDBTitle:** crystal structure of the 3rd pdz domain of the human membrane-2 associated guanylate kinase, ww and pdz domain-containing protein 33 (magi3)
68	c1gph1_	Alignment	not modelled	17.0	22	**PDB header:**transferase(glutamine amidotransferase) **Chain:** 1: **PDB Molecule:**glutamine phosphoribosyl-pyrophosphate amidotransferase; **PDBTitle:** structure of the allosteric regulatory enzyme of purine biosynthesis
69	d1l5oa_	Alignment	not modelled	16.6	18	**Fold:**Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) **Superfamily:**Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) **Family:**Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT)
70	c2p4vA_	Alignment	not modelled	16.4	10	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor greb; **PDBTitle:** crystal structure of the transcript cleavage factor, greb2 at 2.6a resolution
71	c2e5hA_	Alignment	not modelled	16.2	11	**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
72	c2c5qE_	Alignment	not modelled	16.0	8	**PDB header:**structural genomics,unknown function **Chain:** E: **PDB Molecule:**rraa-like protein yer010c; **PDBTitle:** crystal structure of yeast yer010cp
73	d1p3da2	Alignment	not modelled	16.0	19	**Fold:**MurD-like peptide ligases, peptide-binding domain **Superfamily:**MurD-like peptide ligases, peptide-binding domain **Family:**MurCDEF C-terminal domain
74	c1ecjB_	Alignment	not modelled	15.7	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glutamine phosphoribosylpyrophosphate **PDBTitle:** escherichia coli glutamine phosphoribosylpyrophosphate2 (prpp) amidotransferase complexed with 2 amp per tetramer
75	d2j5wa4	Alignment	not modelled	15.7	21	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
76	c3lzkC_	Alignment	not modelled	15.4	25	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**fumarylacetoacetate hydrolase family protein; **PDBTitle:** the crystal structure of a probably aromatic amino acid2 degradation protein from sinorhizobium meliloti 1021
77	c3nyeA_	Alignment	not modelled	15.2	30	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-arginine dehydrogenase; **PDBTitle:** crystal structure of pseudomonas aeruginosa d-arginine dehydrogenase2 in complex with imino-arginine
78	d1kv7a1	Alignment	not modelled	15.2	21	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
						Fold: Cupredoxin-like

79	d1oe1a1	Alignment	not modelled	15.1	16	**Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
80	d2a9va1	Alignment	not modelled	15.0	23	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
81	c1kzlA_	Alignment	not modelled	15.0	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**riboflavin synthase; **PDBTitle:** riboflavin synthase from s.pombe bound to2 carboxyethyllumazine
82	d1lvla1	Alignment	not modelled	14.9	32	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
83	d1l5ja2	Alignment	not modelled	14.7	18	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**LeuD-like
84	c2zooA_	Alignment	not modelled	14.5	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable nitrite reductase; **PDBTitle:** crystal structure of nitrite reductase from pseudoalteromonas2 haloplanktis tac125
85	d2j5wa3	Alignment	not modelled	14.5	21	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
86	d1e3ja2	Alignment	not modelled	14.1	36	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
87	c3u7jA_	Alignment	not modelled	13.9	20	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase a from burkholderia2 thailandensis
88	d1h6za2	Alignment	not modelled	13.9	24	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Phosphohistidine domain **Family:**Pyruvate phosphate dikinase, central domain
89	c3g5wC_	Alignment	not modelled	13.7	16	**PDB header:**metal binding protein **Chain:** C: **PDB Molecule:**multicopper oxidase type 1; **PDBTitle:** crystal structure of blue copper oxidase from nitrosomonas europaea
90	d1e8ca2	Alignment	not modelled	13.7	24	**Fold:**MurD-like peptide ligases, peptide-binding domain **Superfamily:**MurD-like peptide ligases, peptide-binding domain **Family:**MurCDEF C-terminal domain
91	d1o1ya_	Alignment	not modelled	13.6	25	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
92	d1fxza2	Alignment	not modelled	13.4	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
93	c2e28A_	Alignment	not modelled	13.4	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure analysis of pyruvate kinase from bacillus2 stearothermophilus
94	d1pl8a2	Alignment	not modelled	13.2	35	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
95	d1aoza1	Alignment	not modelled	13.1	16	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
96	d1ykfa2	Alignment	not modelled	13.1	27	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
97	c3cgnA_	Alignment	not modelled	13.0	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase; **PDBTitle:** crystal structure of thermophilic slyd
98	c1yq4A_	Alignment	not modelled	13.0	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**succinate dehydrogenase flavoprotein subunit; **PDBTitle:** avian respiratory complex ii with 3-nitropropionate and ubiquinone
99	c3fijD_	Alignment	not modelled	12.9	18	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**lin1909 protein; **PDBTitle:** crystal structure of a uncharacterized protein lin1909