Phyre^2

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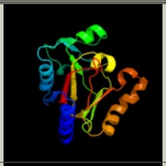
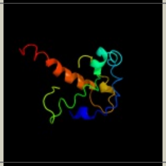
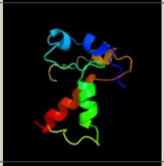
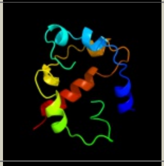
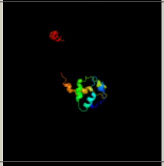
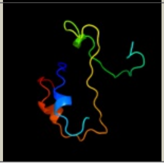
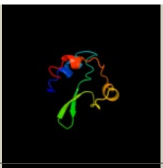
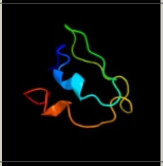
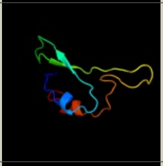
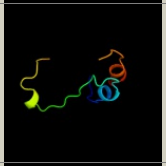
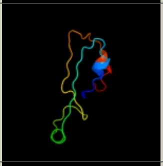
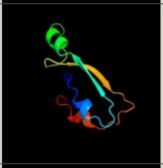
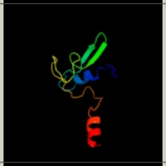
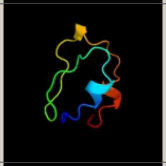
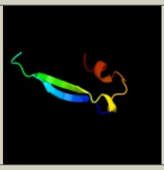
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2g40A_	Alignment		100.0	25	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of a duf162 family protein (dr_1909) from2 deinococcus radiodurans at 1.70 a resolution
2	d2g40a1	Alignment		100.0	25	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**YkgG-like
3	c2b76N_	Alignment		99.4	20	**PDB header:**oxidoreductase **Chain:** N: **PDB Molecule:**fumarate reductase iron-sulfur protein; **PDBTitle:** e. coli quinol fumarate reductase frda e49q mutation
4	c2h89B_	Alignment		99.3	26	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**succinate dehydrogenase ip subunit; **PDBTitle:** avian respiratory complex ii with malonate bound
5	d1nekb1	Alignment		99.3	24	**Fold:**Globin-like **Superfamily:**alpha-helical ferredoxin **Family:**Fumarate reductase/Succinate dehydogenase iron-sulfur protein, C-terminal domain
6	c1nekB_	Alignment		99.3	22	**PDB header:**oxidoreductase/electron transport **Chain:** B: **PDB Molecule:**succinate dehydrogenase iron-sulfur protein; **PDBTitle:** complex ii (succinate dehydrogenase) from e. coli with2 ubiquinone bound
7	d2bs2b1	Alignment		99.2	24	**Fold:**Globin-like **Superfamily:**alpha-helical ferredoxin **Family:**Fumarate reductase/Succinate dehydogenase iron-sulfur protein, C-terminal domain
8	c2bs2E_	Alignment		99.2	24	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**quinol-fumarate reductase iron-sulfur subunit b; **PDBTitle:** quinol:fumarate reductase from wolinella succinogenes
9	d1kf6b1	Alignment		99.2	19	**Fold:**Globin-like **Superfamily:**alpha-helical ferredoxin **Family:**Fumarate reductase/Succinate dehydogenase iron-sulfur protein, C-terminal domain
10	c3cf4A_	Alignment		99.1	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**acetyl-coa decarboxylase/synthase alpha subunit; **PDBTitle:** structure of the codh component of the m. barkeri acds complex
11	d2c42a5	Alignment		98.0	22	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins

12	d3c8ya3	Alignment		97.8	26	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
13	c1gx7A_	Alignment		97.6	36	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**periplasmic [fe] hydrogenase large subunit; **PDBTitle:** best model of the electron transfer complex between2 cytochrome c3 and [fe]-hydrogenase
14	d1xera_	Alignment		97.6	34	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Archaeal ferredoxins
15	c2c3yA_	Alignment		97.5	40	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pyruvate-ferredoxin oxidoreductase; **PDBTitle:** crystal structure of the radical form of2 pyruvate:ferredoxin oxidoreductase from desulfovibrio3 africanus
16	d2fug91	Alignment		97.5	25	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
17	c2fugG_	Alignment		97.5	25	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**nadh-quinone oxidoreductase chain 9; **PDBTitle:** crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus
18	c1c4cA_	Alignment		97.4	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein (fe-only hydrogenase); **PDBTitle:** binding of exogenously added carbon monoxide at the active2 site of the fe-only hydrogenase (cpi) from clostridium3 pasteurianum
19	c1hfeL_	Alignment		97.4	37	**PDB header:**hydrogenase **Chain:** L: **PDB Molecule:**protein (fe-only hydrogenase (e.c.1.18.99.1) **PDBTitle:** 1.6 a resolution structure of the fe-only hydrogenase from2 desulfovibrio desulfuricans
20	c1gthD_	Alignment		97.4	41	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**dihydropyrimidine dehydrogenase; **PDBTitle:** dihydropyrimidine dehydrogenase (dpd) from pig, ternary2 complex with nadph and 5-iodouracil
21	d1gtea5	Alignment	not modelled	97.3	29	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
22	d1jb0c_	Alignment	not modelled	97.2	26	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**7-Fe ferredoxin
23	c2gmhA_	Alignment	not modelled	97.2	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**electron transfer flavoprotein-ubiquinone **PDBTitle:** structure of porcine electron transfer flavoprotein-2 ubiquinone oxidoreductase in complexed with ubiquinone
24	d2fug34	Alignment	not modelled	97.1	22	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
25	d7fd1a_	Alignment	not modelled	97.0	39	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**7-Fe ferredoxin
26	d1hfel2	Alignment	not modelled	97.0	37	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
27	c2fugC_	Alignment	not modelled	97.0	26	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nadh-quinone oxidoreductase chain 3; **PDBTitle:** crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus
28	d1clfa_	Alignment	not modelled	96.9	41	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
29	c1kqfB	Alignment	not modelled	96.9	29	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**formate dehydrogenase, nitrate-

29	c1kqfB_	Alignment	not modelled	96.9	29	inducible, iron-sulfur **PDBTitle:** formate dehydrogenase n from e. coli
30	d1rgva_	Alignment	not modelled	96.8	30	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
31	d1y5ib1	Alignment	not modelled	96.8	30	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
32	c2ivfB_	Alignment	not modelled	96.7	27	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ethylbenzene dehydrogenase beta-subunit; **PDBTitle:** ethylbenzene dehydrogenase from aromatoleum aromaticum
33	c2fgoA_	Alignment	not modelled	96.7	28	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**ferredoxin; **PDBTitle:** structure of the 2[4fe-4s] ferredoxin from pseudomonas2 aeruginosa
34	d1bc6a_	Alignment	not modelled	96.7	36	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**7-Fe ferredoxin
35	c2zvsB_	Alignment	not modelled	96.6	30	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**uncharacterized ferredoxin-like protein yfhl; **PDBTitle:** crystal structure of the 2[4fe-4s] ferredoxin from escherichia coli
36	d2fdna_	Alignment	not modelled	96.6	45	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
37	d1dura_	Alignment	not modelled	96.4	37	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
38	d1blua_	Alignment	not modelled	96.4	24	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
39	d1kqfb1	Alignment	not modelled	96.3	31	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
40	d1h98a_	Alignment	not modelled	96.2	41	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**7-Fe ferredoxin
41	d1fcaa_	Alignment	not modelled	96.1	45	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
42	c3gyxJ_	Alignment	not modelled	96.1	38	**PDB header:**oxidoreductase **Chain:** J: **PDB Molecule:**adenylylsulfate reductase; **PDBTitle:** crystal structure of adenylylsulfate reductase from2 desulfovibrio gigas
43	c2v2kB_	Alignment	not modelled	96.1	40	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**ferredoxin; **PDBTitle:** the crystal structure of fdxa, a 7fe ferredoxin from2 mycobacterium smegmatis
44	d1jnrb_	Alignment	not modelled	96.0	28	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
45	c1ti2F_	Alignment	not modelled	95.9	20	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**pyrogallol hydroxytransferase small subunit; **PDBTitle:** crystal structure of pyrogallol-phloroglucinol2 transhydroxylase from pelobacter acidigallici
46	d1h0hb_	Alignment	not modelled	95.5	21	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
47	d2gmha3	Alignment	not modelled	95.3	24	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**ETF-QO domain-like
48	c2vdcI_	Alignment	not modelled	95.3	18	**PDB header:**oxidoreductase **Chain:** I: **PDB Molecule:**glutamate synthase [nadph] small chain; **PDBTitle:** the 9.5 a resolution structure of glutamate synthase from2 cryo-electron microscopy and its oligomerization behavior3 in solution: functional implications.
49	c1dwlA_	Alignment	not modelled	95.3	26	**PDB header:**electron transfer **Chain:** A: **PDB Molecule:**ferredoxin i; **PDBTitle:** the ferredoxin-cytochrome complex using heteronuclear nmr2 and docking simulation
50	c3c7bE_	Alignment	not modelled	94.8	19	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**sulfite reductase, dissimilatory-type subunit beta; **PDBTitle:** structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
51	c2vpyB_	Alignment	not modelled	94.5	46	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nrfc protein; **PDBTitle:** polysulfide reductase with bound quinone inhibitor,2 pentachlorophenol (pcp)
52	d1iqza_	Alignment	not modelled	94.5	20	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Single 4Fe-4S cluster ferredoxin
53	c2v4jE_	Alignment	not modelled	94.2	17	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**sulfite reductase, dissimilatory-type subunit **PDBTitle:** the crystal structure of desulfovibrio vulgaris2 dissimilatory sulfite reductase bound to dsrc provides3 novel insights into the mechanism of sulfate respiration
						Fold: Ferredoxin-like

54	d1vjwa_	Alignment	not modelled	93.9	30	**Superfamily:**4Fe-4S ferredoxins **Family:**Single 4Fe-4S cluster ferredoxin
55	d1vlfn2	Alignment	not modelled	93.6	23	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
56	d1sj1a_	Alignment	not modelled	93.2	22	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Single 4Fe-4S cluster ferredoxin
57	d1fxra_	Alignment	not modelled	92.8	21	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Single 4Fe-4S cluster ferredoxin
58	d3c7bb1	Alignment	not modelled	92.3	22	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
59	d1gtea1	Alignment	not modelled	92.3	21	**Fold:**Globin-like **Superfamily:**alpha-helical ferredoxin **Family:**Dihydropyrimidine dehydrogenase, N-terminal domain
60	c2fugA_	Alignment	not modelled	91.7	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadh-quinone oxidoreductase chain 1; **PDBTitle:** crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus
61	c2v4jA_	Alignment	not modelled	91.6	43	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sulfite reductase, dissimilatory-type subunit **PDBTitle:** the crystal structure of desulfovibrio vulgaris2 dissimilatory sulfite reductase bound to dsrc provides3 novel insights into the mechanism of sulfate respiration
62	c3c7bA_	Alignment	not modelled	89.8	30	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sulfite reductase, dissimilatory-type subunit alpha; **PDBTitle:** structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
63	d1u3da2	Alignment	not modelled	86.2	21	**Fold:**Cryptochrome/photolyase, N-terminal domain **Superfamily:**Cryptochrome/photolyase, N-terminal domain **Family:**Cryptochrome/photolyase, N-terminal domain
64	c2lciA_	Alignment	not modelled	81.9	19	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**protein or36; **PDBTitle:** solution nmr structure of de novo designed protein, p-loop ntpase2 fold, northeast structural genomics consortium target or36 (casd3 target)
65	d2v4jb1	Alignment		81.5	33	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
66	d1np7a2	Alignment	not modelled	72.2	21	**Fold:**Cryptochrome/photolyase, N-terminal domain **Superfamily:**Cryptochrome/photolyase, N-terminal domain **Family:**Cryptochrome/photolyase, N-terminal domain
67	d1owla2	Alignment	not modelled	72.1	24	**Fold:**Cryptochrome/photolyase, N-terminal domain **Superfamily:**Cryptochrome/photolyase, N-terminal domain **Family:**Cryptochrome/photolyase, N-terminal domain
68	c3bk7A_	Alignment	not modelled	60.8	33	**PDB header:**hydrolyase/translation **Chain:** A: **PDB Molecule:**abc transporter atp-binding protein; **PDBTitle:** structure of the complete abce1/rnaase-l inhibitor protein2 from pyrococcus abysii
69	c1u3cA_	Alignment	not modelled	59.1	21	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**cryptochrome 1 apoprotein; **PDBTitle:** crystal structure of the phr domain of cryptochrome 1 from2 arabidopsis thaliana
70	c1np7A_	Alignment	not modelled	57.8	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dna photolyase; **PDBTitle:** crystal structure analysis of synechocystis sp. pcc6803 cryptochrome
71	c2l69A_	Alignment	not modelled	54.5	25	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**rossmann 2x3 fold protein; **PDBTitle:** solution nmr structure of de novo designed protein, p-loop ntpase2 fold, northeast structural genomics consortium target or28
72	c2vdcF_	Alignment	not modelled	52.9	38	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**glutamate synthase [nadph] large chain; **PDBTitle:** the 9.5 a resolution structure of glutamate synthase from2 cryo-electron microscopy and its oligomerization behavior3 in solution: functional implications.
73	c1llm1A_	Alignment	not modelled	51.1	38	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ferredoxin-dependent glutamate synthase; **PDBTitle:** structural studies on the synchronization of catalytic centers in2 glutamate synthase: native enzyme
74	c2xrzA_	Alignment	not modelled	50.4	26	**PDB header:**lyase/dna **Chain:** A: **PDB Molecule:**deoxyribodipyrimidine photolyase; **PDBTitle:** x-ray structure of archaeal class ii cpd photolyase from2 methanosarcina mazei in complex with intact cpd-lesion
75	c1tezB_	Alignment	not modelled	50.3	24	**PDB header:**lyase/dna **Chain:** B: **PDB Molecule:**deoxyribodipyrimidine photolyase; **PDBTitle:** complex between dna and the dna photolyase from anacystis nidulans
76	c1g8jC_	Alignment	not modelled	50.2	20	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**arsenite oxidase; **PDBTitle:** crystal structure analysis of arsenite oxidase from2 alcaligenes faecalis
77	c3cvyA_	Alignment	not modelled	49.2	10	**PDB header:**lyase/dna **Chain:** A: **PDB Molecule:**re11660p; **PDBTitle:** drosophila melanogaster (6-4) photolyase bound to repaired2 ds dna

78	d1ofda2	Alignment	not modelled	47.6	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
79	d2gm3a1	Alignment	not modelled	43.9	15	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
80	d2j07a2	Alignment	not modelled	42.8	15	**Fold:**Cryptochrome/photolyase, N-terminal domain **Superfamily:**Cryptochrome/photolyase, N-terminal domain **Family:**Cryptochrome/photolyase, N-terminal domain
81	d1zgza1	Alignment	not modelled	40.2	12	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
82	d1vdha_	Alignment	not modelled	40.0	15	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Chlorite dismutase-like
83	d1t0tv_	Alignment	not modelled	36.4	18	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Chlorite dismutase-like
84	c3cvjB_	Alignment	not modelled	36.3	13	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative phosphoheptose isomerase; **PDBTitle:** crystal structure of a putative phosphoheptose isomerase (bh3325) from2 bacillus halodurans c-125 at 2.00 a resolution
85	d2abka_	Alignment	not modelled	36.1	30	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Endonuclease III
86	c3fy4C_	Alignment	not modelled	35.3	11	**PDB header:**lyase **Chain:** C: **PDB Molecule:**6-4 photolyase; **PDBTitle:** (6-4) photolyase crystal structure
87	d1a77a1	Alignment	not modelled	33.9	20	**Fold:**SAM domain-like **Superfamily:**5' to 3' exonuclease, C-terminal subdomain **Family:**5' to 3' exonuclease, C-terminal subdomain
88	c3cg4A_	Alignment	not modelled	33.0	8	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**response regulator receiver domain protein (chey-like); **PDBTitle:** crystal structure of response regulator receiver domain protein (chey-2 like) from methanospirillum hungatei jf-1
89	d1mc8a1	Alignment	not modelled	31.3	15	**Fold:**SAM domain-like **Superfamily:**5' to 3' exonuclease, C-terminal subdomain **Family:**5' to 3' exonuclease, C-terminal subdomain
90	d1xhfa1	Alignment	not modelled	30.0	12	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
91	d1ul1x1	Alignment	not modelled	29.4	26	**Fold:**SAM domain-like **Superfamily:**5' to 3' exonuclease, C-terminal subdomain **Family:**5' to 3' exonuclease, C-terminal subdomain
92	d1ea0a2	Alignment	not modelled	28.9	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
93	d2fcja1	Alignment	not modelled	28.6	20	**Fold:**Toprim domain **Superfamily:**Toprim domain **Family:**Toprim domain
94	c3c3mA_	Alignment	not modelled	27.5	8	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of the n-terminal domain of response regulator2 receiver protein from methanoculleus marisnigri jr1
95	d1dnpa2	Alignment	not modelled	26.8	14	**Fold:**Cryptochrome/photolyase, N-terminal domain **Superfamily:**Cryptochrome/photolyase, N-terminal domain **Family:**Cryptochrome/photolyase, N-terminal domain
96	d1b43a1	Alignment	not modelled	26.6	20	**Fold:**SAM domain-like **Superfamily:**5' to 3' exonuclease, C-terminal subdomain **Family:**5' to 3' exonuclease, C-terminal subdomain
97	c1m6vE_	Alignment	not modelled	25.7	20	**PDB header:**ligase **Chain:** E: **PDB Molecule:**carbamoyl phosphate synthetase large chain; **PDBTitle:** crystal structure of the g359f (small subunit) point mutant of2 carbamoyl phosphate synthetase
98	c1yisA_	Alignment	not modelled	24.8	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**adenylosuccinate lyase; **PDBTitle:** structural genomics of caenorhabditis elegans: adenylosuccinate lyase
99	c2kvgA_	Alignment	not modelled	24.2	32	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger and btb domain-containing protein 32; **PDBTitle:** structure of the three-cys2his2 domain of mouse testis zinc2 finger protein
100	d2nu7b1	Alignment	not modelled	24.0	13	**Fold:**Flavodoxin-like **Superfamily:**Succinyl-CoA synthetase domains **Family:**Succinyl-CoA synthetase domains
101	c3qq5A_	Alignment	not modelled	23.4	57	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**small gtp-binding protein; **PDBTitle:** crystal structure of the [fefe]-hydrogenase maturation protein hydf
102	c2rdmB_	Alignment	not modelled	21.9	14	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of response regulator receiver protein from2 sinorhizobium medicae wsm419
103	d2naca2	Alignment	not modelled	21.9	21	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**Formate/glycerate dehydrogenases, substrate-binding domain

104	d1zh2a1	Alignment	not modelled	21.7	16	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
105	c3hdgE_	Alignment	not modelled	21.5	11	**PDB header:**structural genomics, unknown function **Chain:** E: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the n-terminal domain of an2 uncharacterized protein (ws1339) from wolinella3 succinogenes
106	c3hbrD_	Alignment	not modelled	21.2	19	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**oxa-48; **PDBTitle:** crystal structure of oxa-48 beta-lactamase