Phyre^2

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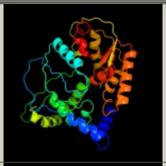
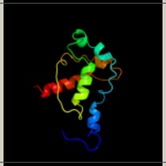
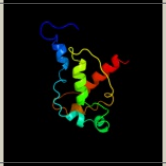
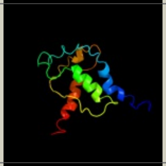
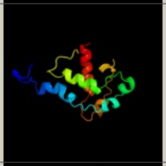
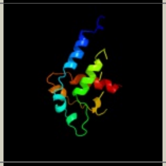
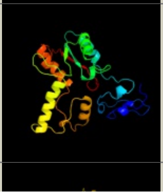
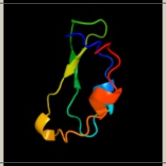
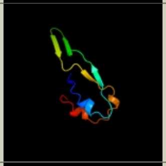
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3kwlA_	Alignment		99.7	10	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a hypothetical protein from helicobacter pylori
2	c2h89B_	Alignment		99.6	23	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**succinate dehydrogenase ip subunit; **PDBTitle:** avian respiratory complex ii with malonate bound
3	c1nekB_	Alignment		99.5	21	**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
4	d1nekb1	Alignment		99.5	21	**Fold:**Globin-like **Superfamily:**alpha-helical ferredoxin **Family:**Fumarate reductase/Succinate dehydogenase iron-sulfur protein, C-terminal domain
5	c2b76N_	Alignment		99.5	19	**PDB header:**oxidoreductase **Chain:** N: **PDB Molecule:**fumarate reductase iron-sulfur protein; **PDBTitle:** e. coli quinol fumarate reductase frda e49q mutation
6	d1kf6b1	Alignment		99.5	20	**Fold:**Globin-like **Superfamily:**alpha-helical ferredoxin **Family:**Fumarate reductase/Succinate dehydogenase iron-sulfur protein, C-terminal domain
7	c2bs2E_	Alignment		99.4	18	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**quinol-fumarate reductase iron-sulfur subunit b; **PDBTitle:** quinol:fumarate reductase from wolinella succinogenes
8	d2bs2b1	Alignment		99.4	19	**Fold:**Globin-like **Superfamily:**alpha-helical ferredoxin **Family:**Fumarate reductase/Succinate dehydogenase iron-sulfur protein, C-terminal domain
9	c3cf4A_	Alignment		99.1	17	**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
10	c1gx7A_	Alignment		98.2	17	**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
11	c1hfeL_	Alignment		98.1	17	**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

12	c1c4cA_	Alignment		98.0	14	**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
13	d2c42a5	Alignment		97.6	22	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
14	d1jb0c_	Alignment		97.4	31	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**7-Fe ferredoxin
15	d2fug91	Alignment		97.4	28	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
16	c2fugG_	Alignment		97.4	28	**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
17	d3c8ya3	Alignment		97.3	19	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
18	c2c3yA_	Alignment		97.3	38	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pyruvate-ferredoxin oxidoreductase; **PDBTitle:** crystal structure of the radical form of2 pyruvate:ferredoxin oxidoreductase from desulfovibrio3 africanus
19	d1xera_	Alignment		97.1	20	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Archaeal ferredoxins
20	c2vdcI_	Alignment		97.0	15	**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.
21	d1gtea5	Alignment	not modelled	97.0	29	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
22	c1gthD_	Alignment	not modelled	97.0	35	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**dihydropyrimidine dehydrogenase; **PDBTitle:** dihydropyrimidine dehydrogenase (dpd) from pig, ternary2 complex with nadph and 5-iodouracil
23	c2gmhA_	Alignment	not modelled	96.9	23	**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	d1hfel2	Alignment	not modelled	96.8	30	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
25	d2fug34	Alignment	not modelled	96.8	22	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
26	d1rgva_	Alignment	not modelled	96.8	18	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
27	c1kqfB_	Alignment	not modelled	96.8	32	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**formate dehydrogenase, nitrate-inducible, iron-sulfur **PDBTitle:** formate dehydrogenase n from e. coli
28	d1blua_	Alignment	not modelled	96.7	18	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
29	d2fdna_	Alignment	not modelled	96.7	33	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins

30	c2fgoA_	Alignment	not modelled	96.6	20	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**ferredoxin; **PDBTitle:** structure of the 2[4fe-4s] ferredoxin from pseudomonas2 aeruginosa
31	d7fd1a_	Alignment	not modelled	96.5	36	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**7-Fe ferredoxin
32	d1bc6a_	Alignment	not modelled	96.5	31	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**7-Fe ferredoxin
33	d1dura_	Alignment	not modelled	96.5	32	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
34	d1clfa_	Alignment	not modelled	96.4	40	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
35	c2zvsB_	Alignment	not modelled	96.3	31	**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	d1fcaa_	Alignment	not modelled	96.3	31	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
37	c2ivfB_	Alignment	not modelled	96.3	43	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ethylbenzene dehydrogenase beta-subunit; **PDBTitle:** ethylbenzene dehydrogenase from aromatoleum aromaticum
38	d1y5ib1	Alignment	not modelled	96.3	43	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
39	c2fugC_	Alignment	not modelled	96.1	24	**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
40	d1h98a_	Alignment	not modelled	96.0	29	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**7-Fe ferredoxin
41	c3gyxJ_	Alignment	not modelled	95.9	33	**PDB header:**oxidoreductase **Chain:** J: **PDB Molecule:**adenylylsulfate reductase; **PDBTitle:** crystal structure of adenylylsulfate reductase from2 desulfovibrio gigas
42	d1kqfb1	Alignment	not modelled	95.8	32	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
43	d1h0hb_	Alignment	not modelled	95.8	16	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
44	d2gmha3	Alignment	not modelled	95.8	22	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**ETF-QO domain-like
45	d1jnrb_	Alignment	not modelled	95.7	29	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
46	c1ti2F_	Alignment	not modelled	95.5	27	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**pyrogallol hydroxytransferase small subunit; **PDBTitle:** crystal structure of pyrogallol-phloroglucinol2 transhydroxylase from pelobacter acidigallici
47	d1vlfn2	Alignment	not modelled	95.4	27	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
48	c3c7bE_	Alignment	not modelled	95.1	31	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**sulfite reductase, dissimilatory-type subunit beta; **PDBTitle:** structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
49	c2vpyB_	Alignment	not modelled	95.0	30	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nrfc protein; **PDBTitle:** polysulfide reductase with bound quinone inhibitor,2 pentachlorophenol (pcp)
50	d1vjwa_	Alignment	not modelled	94.7	30	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Single 4Fe-4S cluster ferredoxin
51	c2v2kB_	Alignment	not modelled	94.7	34	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**ferredoxin; **PDBTitle:** the crystal structure of fdxa, a 7fe ferredoxin from2 mycobacterium smegmatis
52	c1dwlA_	Alignment	not modelled	94.5	21	**PDB header:**electron transfer **Chain:** A: **PDB Molecule:**ferredoxin i; **PDBTitle:** the ferredoxin-cytochrome complex using heteronuclear nmr2 and docking simulation
53	c2v4jE_	Alignment	not modelled	94.1	26	**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
54	d1iqza_	Alignment	not modelled	94.0	18	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Single 4Fe-4S cluster ferredoxin
						Fold: Ferredoxin-like

55	d1sj1a_	Alignment	not modelled	93.4	18	**Superfamily:**4Fe-4S ferredoxins **Family:**Single 4Fe-4S cluster ferredoxin
56	c2fugA_	Alignment	not modelled	92.8	14	**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
57	d3c7bb1	Alignment	not modelled	92.5	32	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
58	d1gtea1	Alignment	not modelled	91.0	20	**Fold:**Globin-like **Superfamily:**alpha-helical ferredoxin **Family:**Dihydropyrimidine dehydrogenase, N-terminal domain
59	c3c7bA_	Alignment	not modelled	90.0	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sulfite reductase, dissimilatory-type subunit alpha; **PDBTitle:** structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
60	d1fxra_	Alignment	not modelled	89.4	17	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Single 4Fe-4S cluster ferredoxin
61	d1jfla1	Alignment	not modelled	85.2	14	**Fold:**ATC-like **Superfamily:**Aspartate/glutamate racemase **Family:**Aspartate/glutamate racemase
62	c3bk7A_	Alignment	not modelled	83.5	28	**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
63	c2v4jA_	Alignment	not modelled	83.2	23	**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
64	c2zskA_	Alignment	not modelled	79.7	18	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**226aa long hypothetical aspartate racemase; **PDBTitle:** crystal structure of ph1733, an aspartate racemase2 homologue, from pyrococcus horikoshii ot3
65	c2jfzB_	Alignment	not modelled	79.2	15	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of helicobacter pylori glutamate racemase2 in complex with d-glutamate and an inhibitor
66	c3hfrA_	Alignment	not modelled	78.9	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of glutamate racemase from listeria monocytogenes
67	c2ohoA_	Alignment	not modelled	76.3	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase; **PDBTitle:** structural basis for glutamate racemase inhibitor
68	d2v4jb1	Alignment	not modelled	73.7	32	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
69	c2jfoB_	Alignment	not modelled	73.0	16	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of enterococcus faecalis glutamate2 racemase in complex with d- and l-glutamate
70	c1zuwA_	Alignment	not modelled	72.8	7	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase 1; **PDBTitle:** crystal structure of b.subtilis glutamate racemase (race) with d-glu
71	c3outC_	Alignment	not modelled	70.9	10	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of glutamate racemase from francisella tularensis2 subsp. tularensis schu s4 in complex with d-glutamate.
72	c3ojcD_	Alignment	not modelled	70.9	18	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**putative aspartate/glutamate racemase; **PDBTitle:** crystal structure of a putative asp/glu racemase from yersinia pestis
73	c2dwuA_	Alignment	not modelled	70.7	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of glutamate racemase isoform race1 from bacillus2 anthracis
74	c2jfqA_	Alignment	not modelled	68.7	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of staphylococcus aureus glutamate2 racemase in complex with d-glutamate
75	c2jfnA_	Alignment	not modelled	67.6	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of escherichia coli glutamate racemase2 in complex with l-glutamate and activator udp-murnac-ala
76	c1b74A_	Alignment	not modelled	66.8	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase; **PDBTitle:** glutamate racemase from aquifex pyrophilus
77	c3gjzB_	Alignment	not modelled	66.3	13	**PDB header:**immune system **Chain:** B: **PDB Molecule:**microcin immunity protein mccf; **PDBTitle:** crystal structure of microcin immunity protein mccf from bacillus2 anthracis str. ames
78	c2yv4A_	Alignment	not modelled	62.3	16	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**hypothetical protein ph0435; **PDBTitle:** crystal structure of c-terminal sua5 domain from pyrococcus horikoshii2 hypothetical sua5 protein ph0435
79	c2vdcF_	Alignment	not modelled	57.6	53	**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.
						PDB header:isomerase

80	c2gzmB_	Alignment	not modelled	56.0	12	**Chain:** B: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of the glutamate racemase from bacillus2 anthracis
81	c1lm1A_	Alignment	not modelled	55.2	53	**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
82	c2dx7B_	Alignment	not modelled	55.2	16	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**aspartate racemase; **PDBTitle:** crystal structure of pyrococcus horikoshii ot3 aspartate racemase2 complex with citric acid
83	c1zrsB_	Alignment	not modelled	54.0	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hypothetical protein; **PDBTitle:** wild-type ld-carboxypeptidase
84	d2auna2	Alignment	not modelled	52.4	15	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**LD-carboxypeptidase A N-terminal domain-like
85	d1ofda2	Alignment	not modelled	50.2	53	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
86	c2vlbC_	Alignment	not modelled	45.6	11	**PDB header:**lyase **Chain:** C: **PDB Molecule:**arylmalonate decarboxylase; **PDBTitle:** structure of unliganded arylmalonate decarboxylase
87	d2fzva1	Alignment	not modelled	42.4	13	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**NADPH-dependent FMN reductase
88	c1g8jC_	Alignment	not modelled	41.0	33	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**arsenite oxidase; **PDBTitle:** crystal structure analysis of arsenite oxidase from2 alcaligenes faecalis
89	c3l4eA_	Alignment	not modelled	40.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized peptidase lmo0363; **PDBTitle:** 1.5a crystal structure of a putative peptidase e protein from listeria2 monocytogenes egd-e
90	d2dx7a1	Alignment	not modelled	39.6	14	**Fold:**ATC-like **Superfamily:**Aspartate/glutamate racemase **Family:**Aspartate/glutamate racemase
91	c3lrmB_	Alignment	not modelled	36.5	8	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-galactosidase 1; **PDBTitle:** structure of alfa-galactosidase from saccharomyces cerevisiae with2 raffinose
92	d1zl0a2	Alignment	not modelled	36.1	14	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**LD-carboxypeptidase A N-terminal domain-like
93	d1ea0a2	Alignment	not modelled	35.3	53	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
94	d2c4ka2	Alignment	not modelled	31.3	11	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
95	c3s81A_	Alignment	not modelled	25.7	11	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative aspartate racemase; **PDBTitle:** crystal structure of putative aspartate racemase from salmonella2 typhimurium
96	d1b74a2	Alignment	not modelled	25.2	16	**Fold:**ATC-like **Superfamily:**Aspartate/glutamate racemase **Family:**Aspartate/glutamate racemase
97	d1i60a_	Alignment	not modelled	24.8	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**IolI-like
98	d1lxja_	Alignment	not modelled	23.9	4	**Fold:**Ferredoxin-like **Superfamily:**MTH1187/YkoF-like **Family:**MTH1187-like
99	c3rotA_	Alignment	not modelled	22.7	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**abc sugar transporter, periplasmic sugar binding protein; **PDBTitle:** crystal structure of abc sugar transporter (periplasmic sugar binding2 protein) from legionella pneumophila
100	d1ei9a_	Alignment	not modelled	21.6	13	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Thioesterases
101	c2kvgA_	Alignment	not modelled	20.8	42	**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