Phyre2

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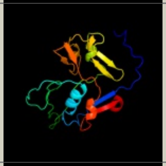
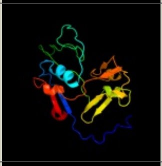
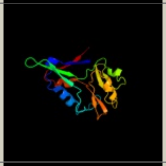
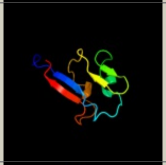
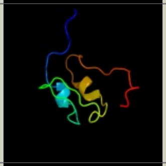
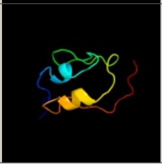
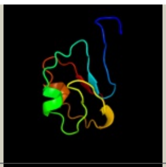
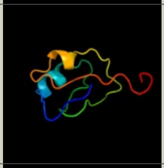
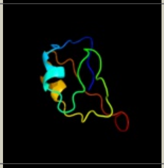
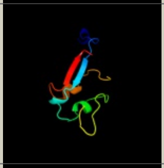
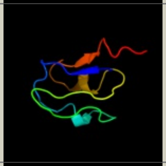
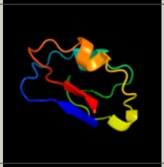
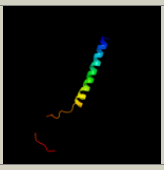
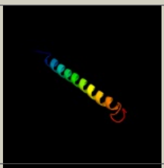
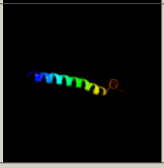
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2ivfB_	Alignment		100.0	39	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ethylbenzene dehydrogenase beta-subunit; **PDBTitle:** ethylbenzene dehydrogenase from aromatoleum aromaticum
2	c1ti2F_	Alignment		100.0	18	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**pyrogallol hydroxytransferase small subunit; **PDBTitle:** crystal structure of pyrogallol-phloroglucinol2 transhydroxylase from pelobacter acidigallici
3	c1kqfB_	Alignment		100.0	24	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**formate dehydrogenase, nitrate-inducible, iron-sulfur **PDBTitle:** formate dehydrogenase n from e. coli
4	d1kqfb1	Alignment		100.0	23	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
5	d1h0hb_	Alignment		100.0	23	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
6	c2vpyB_	Alignment		100.0	30	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nrfc protein; **PDBTitle:** polysulfide reductase with bound quinone inhibitor,2 pentachlorophenol (pcp)
7	d1vlfn2	Alignment		100.0	19	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
8	d1y5ib1	Alignment		100.0	30	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
9	c1gthD_	Alignment		99.5	19	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**dihydropyrimidine dehydrogenase; **PDBTitle:** dihydropyrimidine dehydrogenase (dpd) from pig, ternary2 complex with nadph and 5-iodouracil
10	d2fug91	Alignment		99.5	36	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
11	c2fugG_	Alignment		99.5	36	**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

12	d1xera_	Alignment		99.5	25	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Archaeal ferredoxins
13	c3gyxJ_	Alignment		99.5	30	**PDB header:**oxidoreductase **Chain:** J: **PDB Molecule:**adenylylsulfate reductase; **PDBTitle:** crystal structure of adenylylsulfate reductase from2 desulfovibrio gigas
14	d1jnrb_	Alignment		99.4	30	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
15	d1hfel2	Alignment		99.4	28	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
16	c2c3yA_	Alignment		99.4	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pyruvate-ferredoxin oxidoreductase; **PDBTitle:** crystal structure of the radical form of2 pyruvate:ferredoxin oxidoreductase from desulfovibrio3 africanus
17	d1gtea5	Alignment		99.3	18	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
18	c2zvsB_	Alignment		99.3	24	**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
19	d1jb0c_	Alignment		99.3	35	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**7-Fe ferredoxin
20	c2gmhA_	Alignment		99.3	17	**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
21	d1rgva_	Alignment	not modelled	99.3	20	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
22	d7fd1a_	Alignment	not modelled	99.3	25	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**7-Fe ferredoxin
23	d2c42a5	Alignment	not modelled	99.3	21	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
24	d1blua_	Alignment	not modelled	99.3	20	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
25	d1dura_	Alignment	not modelled	99.2	31	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
26	d1h98a_	Alignment	not modelled	99.2	29	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**7-Fe ferredoxin
27	d3c8ya3	Alignment	not modelled	99.2	24	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
28	d1bc6a_	Alignment	not modelled	99.2	27	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**7-Fe ferredoxin
29	d2fdna_	Alignment	not modelled	99.2	31	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins

						Family: Short-chain ferredoxins
30	c1hfeL_	Alignment	not modelled	99.2	30	**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
31	c2fgoA_	Alignment	not modelled	99.2	21	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**ferredoxin; **PDBTitle:** structure of the 2[4fe-4s] ferredoxin from pseudomonas2 aeruginosa
32	c1gx7A_	Alignment	not modelled	99.1	31	**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
33	d1fcaa_	Alignment	not modelled	99.1	31	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
34	d1clfa_	Alignment	not modelled	99.1	32	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
35	d2fug34	Alignment	not modelled	99.0	22	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
36	d1vjwa_	Alignment	not modelled	99.0	29	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Single 4Fe-4S cluster ferredoxin
37	d2gmha3	Alignment	not modelled	99.0	17	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**ETF-QO domain-like
38	c2v2kB_	Alignment	not modelled	99.0	25	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**ferredoxin; **PDBTitle:** the crystal structure of fdxa, a 7fe ferredoxin from2 mycobacterium smegmatis
39	d3c7bb1	Alignment	not modelled	98.9	28	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
40	d1iqza_	Alignment	not modelled	98.9	24	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Single 4Fe-4S cluster ferredoxin
41	d1sj1a_	Alignment	not modelled	98.9	28	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Single 4Fe-4S cluster ferredoxin
42	c1c4cA_	Alignment	not modelled	98.8	30	**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
43	c3c7bE_	Alignment	not modelled	98.8	22	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**sulfite reductase, dissimilatory-type subunit beta; **PDBTitle:** structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
44	c1dwlA_	Alignment	not modelled	98.8	31	**PDB header:**electron transfer **Chain:** A: **PDB Molecule:**ferredoxin i; **PDBTitle:** the ferredoxin-cytochrome complex using heteronuclear nmr2 and docking simulation
45	c2v4jE_	Alignment	not modelled	98.7	23	**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
46	c3bk7A_	Alignment	not modelled	98.7	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
47	d1fxra_	Alignment	not modelled	98.7	22	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Single 4Fe-4S cluster ferredoxin
48	c2v4jA_	Alignment	not modelled	98.5	15	**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
49	c3c7bA_	Alignment	not modelled	98.4	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sulfite reductase, dissimilatory-type subunit alpha; **PDBTitle:** structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
50	c2fugC_	Alignment	not modelled	98.4	22	**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
51	d2bs2b1	Alignment	not modelled	97.9	30	**Fold:**Globin-like **Superfamily:**alpha-helical ferredoxin **Family:**Fumarate reductase/Succinate dehydogenase iron-sulfur protein, C-terminal domain
52	d1kf6b1	Alignment	not modelled	97.8	28	**Fold:**Globin-like **Superfamily:**alpha-helical ferredoxin **Family:**Fumarate reductase/Succinate dehydogenase iron-sulfur protein, C-terminal domain
53	d1nekb1	Alignment	not modelled	97.7	27	**Fold:**Globin-like **Superfamily:**alpha-helical ferredoxin **Family:**Fumarate reductase/Succinate dehydogenase iron-sulfur

						protein, C-terminal domain
54	c1nekB_	Alignment	not modelled	97.7	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
55	c3cf4A_	Alignment	not modelled	97.6	26	**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
56	c2bs2E_	Alignment	not modelled	97.6	23	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**quinol-fumarate reductase iron-sulfur subunit b; **PDBTitle:** quinol:fumarate reductase from wolinella succinogenes
57	c2b76N_	Alignment	not modelled	97.3	25	**PDB header:**oxidoreductase **Chain:** N: **PDB Molecule:**fumarate reductase iron-sulfur protein; **PDBTitle:** e. coli quinol fumarate reductase frda e49q mutation
58	d2v4jb1	Alignment	not modelled	96.8	33	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
59	c2h89B_	Alignment	not modelled	96.6	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**succinate dehydrogenase ip subunit; **PDBTitle:** avian respiratory complex ii with malonate bound
60	c2e76D_	Alignment		95.4	13	**PDB header:**photosynthesis **Chain:** D: **PDB Molecule:**cytochrome b6-f complex iron-sulfur subunit; **PDBTitle:** crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus
61	d2v4ja1	Alignment	not modelled	94.3	28	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
62	d3c7ba1	Alignment	not modelled	94.1	28	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
63	c1p84E_	Alignment		92.8	9	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur **PDBTitle:** hdbt inhibited yeast cytochrome bc1 complex
64	c2fynO_	Alignment		91.4	21	**PDB header:**oxidoreductase **Chain:** O: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur **PDBTitle:** crystal structure analysis of the double mutant rhodobacter2 sphaeroides bc1 complex
65	c2vdcI_	Alignment	not modelled	88.2	25	**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.
66	c2pq4B_	Alignment	not modelled	87.7	17	**PDB header:**chaperone/oxidoreductase **Chain:** B: **PDB Molecule:**periplasmic nitrate reductase precursor; **PDBTitle:** nmr solution structure of napd in complex with napa1-352 signal peptide
67	c2fyuE_	Alignment	not modelled	86.1	10	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur subunit, **PDBTitle:** crystal structure of bovine heart mitochondrial bc1 with jg1442 inhibitor
68	d2e74d2	Alignment	not modelled	56.5	21	**Fold:**Single transmembrane helix **Superfamily:**ISP transmembrane anchor **Family:**ISP transmembrane anchor
69	d1gtea1	Alignment	not modelled	37.8	31	**Fold:**Globin-like **Superfamily:**alpha-helical ferredoxin **Family:**Dihydropyrimidine dehydrogenase, N-terminal domain
70	c2ww9B_	Alignment	not modelled	33.4	11	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**protein transport protein sss1; **PDBTitle:** cryo-em structure of the active yeast ssh1 complex bound to the2 yeast 80s ribosome
71	c3o0rC_	Alignment	not modelled	32.7	14	**PDB header:**immune system/oxidoreductase **Chain:** C: **PDB Molecule:**nitric oxide reductase subunit c; **PDBTitle:** crystal structure of nitric oxide reductase from pseudomonas2 aeruginosa in complex with antibody fragment
72	c2htfA_	Alignment	not modelled	28.0	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna polymerase mu; **PDBTitle:** the solution structure of the brct domain from human2 polymerase reveals homology with the tdt brct domain
73	d1rhzb_	Alignment	not modelled	27.2	14	**Fold:**Single transmembrane helix **Superfamily:**Preprotein translocase SecE subunit **Family:**Preprotein translocase SecE subunit
74	c2wwbB_	Alignment	not modelled	20.0	21	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**protein transport protein sec61 subunit gamma; **PDBTitle:** cryo-em structure of the mammalian sec61 complex bound to the2 actively translating wheat germ 80s ribosome
75	d1djqa3	Alignment	not modelled	18.6	27	**Fold:**Nucleotide-binding domain **Superfamily:**Nucleotide-binding domain **Family:**N-terminal domain of adrenodoxin reductase-like

76	c1q90R_	Alignment	not modelled	18.6	20	**PDB header:**photosynthesis **Chain:** R: **PDB Molecule:**cytochrome b6-f complex iron-sulfur subunit; **PDBTitle:** structure of the cytochrome b6f (plastohydroquinone : plastocyanin2 oxidoreductase) from chlamydomonas reinhardtii
77	d1q90r_	Alignment	not modelled	18.6	20	**Fold:**Single transmembrane helix **Superfamily:**ISP transmembrane anchor **Family:**ISP transmembrane anchor
78	d1fxda_	Alignment	not modelled	16.6	14	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Single 4Fe-4S cluster ferredoxin
79	c1g8jC_	Alignment	not modelled	14.5	11	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**arsenite oxidase; **PDBTitle:** crystal structure analysis of arsenite oxidase from2 alcaligenes faecalis
80	c2oo4B_	Alignment	not modelled	14.4	22	**PDB header:**cell cycle,signaling protein **Chain:** B: **PDB Molecule:**neurogenic locus notch homolog protein 2; **PDBTitle:** structure of lnr-hd (negative regulatory region) from human notch 2
81	d2alea1	Alignment	not modelled	11.4	35	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**L30e/L7ae ribosomal proteins
82	c2eqpA_	Alignment	not modelled	10.3	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**tumor necrosis factor receptor superfamily **PDBTitle:** solution structure of the stn_tnfrsf12a_tnfr domain of2 tumor necrosis factor receptor superfamily member 12a3 precursor
83	c1moxB_	Alignment	not modelled	9.2	18	**PDB header:**transferase/growth factor **Chain:** B: **PDB Molecule:**epidermal growth factor receptor; **PDBTitle:** crystal structure of human epidermal growth factor receptor (residues2 1-501) in complex with tgf-alpha
84	c2kn0A_	Alignment	not modelled	7.2	27	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**fn14; **PDBTitle:** solution nmr structure of xenopus fn14
85	d2dmda2	Alignment	not modelled	7.2	50	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
86	c2hr7B_	Alignment	not modelled	7.1	27	**PDB header:**transferase **Chain:** B: **PDB Molecule:**insulin receptor; **PDBTitle:** insulin receptor (domains 1-3)
87	c3lpeF_	Alignment	not modelled	7.0	21	**PDB header:**transferase **Chain:** F: **PDB Molecule:**dna-directed rna polymerase subunit e''; **PDBTitle:** crystal structure of spt4/5ngn heterodimer complex from methanococcus2 jannaschii
88	c3lw5H_	Alignment	not modelled	6.8	23	**PDB header:**photosynthesis **Chain:** H: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** improved model of plant photosystem i
89	c1m5iA_	Alignment	not modelled	6.6	27	**PDB header:**antitumor protein **Chain:** A: **PDB Molecule:**apc protein; **PDBTitle:** crystal structure of the coiled coil region 129-250 of the2 tumor suppressor gene product apc
90	c3mk7B_	Alignment	not modelled	6.4	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**cytochrome c oxidase, cbb3-type, subunit o; **PDBTitle:** the structure of cbb3 cytochrome oxidase
91	d1rutx1	Alignment	not modelled	6.4	38	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
92	c2a91A_	Alignment	not modelled	6.3	20	**PDB header:**signaling protein,transferase,membrane p **Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-2; **PDBTitle:** crystal structure of erbb2 domains 1-3
93	d1rh5b_	Alignment	not modelled	6.1	16	**Fold:**Single transmembrane helix **Superfamily:**Preprotein translocase SecE subunit **Family:**Preprotein translocase SecE subunit
94	c3k30B_	Alignment	not modelled	5.4	31	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**histamine dehydrogenase; **PDBTitle:** histamine dehydrogenase from nocardiodes simplex
95	c3na7A_	Alignment	not modelled	5.3	23	**PDB header:**gene regulation, chaperone **Chain:** A: **PDB Molecule:**hp0958; **PDBTitle:** 2.2 angstrom structure of the hp0958 protein from helicobacter pylori2 ccug 17874
96	c2o01H_	Alignment	not modelled	5.0	11	**PDB header:**photosynthesis **Chain:** H: **PDB Molecule:**photosystem i reaction center subunit vi, **PDBTitle:** the structure of a plant photosystem i supercomplex at 3.42 angstrom resolution