Phyre2

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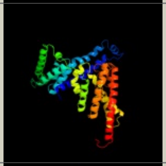
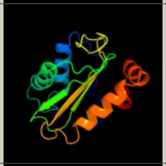
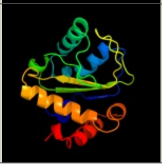
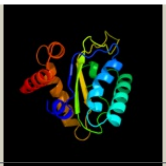
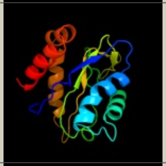
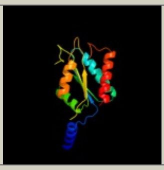
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2r48a1	Alignment		100.0	46	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Fructose specific IIB subunit-like
2	c2kyrA_	Alignment		100.0	35	**PDB header:**transferase **Chain:** A: **PDB Molecule:**fructose-like phosphotransferase enzyme iib component 1; **PDBTitle:** solution structure of enzyme iib subunit of pts system from2 escherichia coli k12. northeast structural genomics consortium target3 er315/ontario center for structural proteomics target ec0544
3	d2r4qa1	Alignment		100.0	42	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Fructose specific IIB subunit-like
4	c3qnqD_	Alignment		100.0	13	**PDB header:**membrane protein, transport protein **Chain:** D: **PDB Molecule:**pts system, cellobiose-specific iic component; **PDBTitle:** crystal structure of the transporter chbc, the iic component from the2 n,n'-diacetylchitobiose-specific phosphotransferase system
5	c3urrB_	Alignment		100.0	27	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pts iia-like nitrogen-regulatory protein ptsn; **PDBTitle:** structure of pts iia-like nitrogen-regulatory protein ptsn (bth_i0484)2 (ptsn)
6	c2a0jA_	Alignment		100.0	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pts system, nitrogen regulatory iia protein; **PDBTitle:** crystal structure of nitrogen regulatory protein iia-ntr from2 neisseria meningitidis
7	d1a6ja_	Alignment		100.0	26	**Fold:**Phoshotransferase/anion transport protein **Superfamily:**Phoshotransferase/anion transport protein **Family:**IIA domain of mannitol-specific and ntr phosphotransferase EII
8	c3oxpB_	Alignment		100.0	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphotransferase enzyme ii, a component; **PDBTitle:** structure of phosphotransferase enzyme ii, a component from yersinia2 pestis co92 at 1.2 a resolution
9	c3oxpA_	Alignment		100.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphotransferase enzyme ii, a component; **PDBTitle:** structure of phosphotransferase enzyme ii, a component from yersinia2 pestis co92 at 1.2 a resolution
10	c2oq3A_	Alignment		99.9	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mannitol-specific cryptic phosphotransferase **PDBTitle:** solution structure of the mannitol- specific cryptic2 phosphotransferase enzyme iia cmtb from escherichia coli
11	c3bjvA_	Alignment		99.9	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rmpa; **PDBTitle:** the crystal structure of a putative pts iia(ptxa) from streptococcus2 mutans

12	c2oqtD_	Alignment		99.9	19	**PDB header:**transferase **Chain:** D: **PDB Molecule:**hypothetical protein spy0176; **PDBTitle:** structural genomics, the crystal structure of a putative2 pts iia domain from streptococcus pyogenes m1 gas
13	d1a3aa_	Alignment		99.9	29	**Fold:**Phoshotransferase/anion transport protein **Superfamily:**Phoshotransferase/anion transport protein **Family:**IIA domain of mannitol-specific and ntr phosphotransferase EII
14	d1xiza_	Alignment		99.9	22	**Fold:**Phoshotransferase/anion transport protein **Superfamily:**Phoshotransferase/anion transport protein **Family:**IIA domain of mannitol-specific and ntr phosphotransferase EII
15	c1hynQ_	Alignment		98.3	18	**PDB header:**membrane protein **Chain:** Q: **PDB Molecule:**band 3 anion transport protein; **PDBTitle:** crystal structure of the cytoplasmic domain of human2 erythrocyte band-3 protein
16	d1hynp_	Alignment		98.3	21	**Fold:**Phoshotransferase/anion transport protein **Superfamily:**Phoshotransferase/anion transport protein **Family:**Anion transport protein, cytoplasmic domain
17	c1tvmA_	Alignment		96.6	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pts system, galactitol-specific iib component; **PDBTitle:** nmr structure of enzyme gatb of the galactitol-specific2 phosphoenolpyruvate-dependent phosphotransferase system
18	d2a5la1	Alignment		96.3	16	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**WrbA-like
19	d1ycga1	Alignment		95.2	12	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
20	d1iiba_	Alignment		94.7	13	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Lactose/Cellobiose specific IIB subunit
21	c3czcA_	Alignment	not modelled	94.7	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rmpb; **PDBTitle:** the crystal structure of a putative pts iib(ptxb) from2 streptococcus mutans
22	c3nbmA_	Alignment	not modelled	94.6	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pts system, lactose-specific iibc components; **PDBTitle:** the lactose-specific iib component domain structure of the2 phosphoenolpyruvate:carbohydrate phosphotransferase system (pts) from3 streptococcus pneumoniae.
23	c3fniA_	Alignment	not modelled	94.4	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative diflavin flavoprotein a 3; **PDBTitle:** crystal structure of a diflavin flavoprotein a3 (all3895) from nostoc2 sp., northeast structural genomics consortium target nsr431a
24	d2arka1	Alignment	not modelled	94.1	17	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**WrbA-like
25	c2l2qA_	Alignment	not modelled	93.9	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pts system, cellobiose-specific iib component (cela); **PDBTitle:** solution structure of cellobiose-specific phosphotransferase iib2 component protein from borrelia burgdorferi
26	d1ydga_	Alignment	not modelled	93.5	28	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**WrbA-like
27	d1vkra_	Alignment	not modelled	93.4	15	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Lactose/Cellobiose specific IIB subunit

28	c1vkrA_	Alignment	not modelled	93.4	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mannitol-specific pts system enzyme iiabc components; **PDBTitle:** structure of iib domain of the mannitol-specific permease enzyme ii
29	d1e5da1	Alignment	not modelled	90.6	18	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
30	c3p0rA_	Alignment	not modelled	88.2	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**azoreductase; **PDBTitle:** crystal structure of azoreductase from bacillus anthracis str. sterne
31	d1vmea1	Alignment	not modelled	85.9	8	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
32	c2zkiH_	Alignment	not modelled	83.4	16	**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)
33	c3snoA_	Alignment	not modelled	83.4	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical aminotransferase; **PDBTitle:** crystal structure of a hypothetical aminotransferase (ncgl2491) from2 corynebacterium glutamicum atcc 13032 kitasato at 1.60 a resolution
34	c3d7nA_	Alignment	not modelled	83.3	27	**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
35	c2ohiB_	Alignment		82.9	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**type a flavoprotein fpra; **PDBTitle:** crystal structure of coenzyme f420h2 oxidase (fpra), a diiron2 flavoprotein, reduced state
36	d1u7ga_	Alignment	not modelled	82.8	20	**Fold:**Ammonium transporter **Superfamily:**Ammonium transporter **Family:**Ammonium transporter
37	c3klbA_	Alignment	not modelled	80.8	16	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**putative flavoprotein; **PDBTitle:** crystal structure of putative flavoprotein in complex with fmn2 (yp_213683.1) from bacteroides fragilis nctc 9343 at 1.75 a3 resolution
38	c3rh0A_	Alignment	not modelled	80.0	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**arsenate reductase; **PDBTitle:** corynebacterium glutamicum mycothiol/mycoredoxin1-dependent arsenate2 reductase cg_arsc2
39	d1sqsa_	Alignment	not modelled	80.0	12	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Hypothetical protein SP1951
40	c3b6iB_	Alignment	not modelled	77.8	23	**PDB header:**flavoprotein **Chain:** B: **PDB Molecule:**flavoprotein wrba; **PDBTitle:** wrba from escherichia coli, native structure
41	c1zggA_	Alignment	not modelled	77.4	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative low molecular weight protein-tyrosine- **PDBTitle:** solution structure of a low molecular weight protein2 tyrosine phosphatase from bacillus subtilis
42	c3f2vA_	Alignment	not modelled	77.2	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**general stress protein 14; **PDBTitle:** crystal structure of the general stress protein 142 (tde0354) in complex with fmn from treponema denticola,3 northeast structural genomics consortium target tdr58.
43	c1ychD_	Alignment	not modelled	77.0	13	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**nitric oxide reductase; **PDBTitle:** x-ray crystal structures of moorella thermoacetica fpra.2 novel diiron site structure and mechanistic insights into3 a scavenging nitric oxide reductase
44	c2q9uB_	Alignment	not modelled	77.0	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**a-type flavoprotein; **PDBTitle:** crystal structure of the flavodiiron protein from giardia2 intestinalis
45	d1t0ba_	Alignment	not modelled	70.3	26	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**ThuA-like
46	c2q62A_	Alignment	not modelled	70.0	12	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**arsh; **PDBTitle:** crystal structure of arsh from sinorhizobium meliloti
47	c1e5dA_	Alignment	not modelled	68.8	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**rubredoxin\:oxygen oxidoreductase; **PDBTitle:** rubredoxin oxygen:oxidoreductase (roo) from anaerobe2 desulfovibrio gigas
48	c1vmeB_	Alignment	not modelled	64.4	11	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**flavoprotein; **PDBTitle:** crystal structure of flavoprotein (tm0755) from thermotoga maritima at2 1.80 a resolution
49	c1y8qD_	Alignment	not modelled	61.3	8	**PDB header:**ligase **Chain:** D: **PDB Molecule:**ubiquitin-like 2 activating enzyme e1b; **PDBTitle:** sumo e1 activating enzyme sae1-sae2-mg-atp complex
50	c3kydB_	Alignment	not modelled	61.3	5	**PDB header:**ligase **Chain:** B: **PDB Molecule:**sumo-activating enzyme subunit 2; **PDBTitle:** human sumo e1~sumo1-amp tetrahedral intermediate mimic
51	d5nula_	Alignment	not modelled	57.6	23	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins

						Family: Flavodoxin-related
52	c3h9gA_	Alignment	not modelled	56.7	13	**PDB header:**transferase/antibiotic **Chain:** A: **PDB Molecule:**mccb protein; **PDBTitle:** crystal structure of e. coli mccb + mcca-n7isoasn
53	d1acoa2	Alignment	not modelled	55.1	8	**Fold:**Aconitase iron-sulfur domain **Superfamily:**Aconitase iron-sulfur domain **Family:**Aconitase iron-sulfur domain
54	d2qwxa1	Alignment	not modelled	53.2	22	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
55	c2v9cA_	Alignment	not modelled	53.0	31	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fmn-dependent nadh-azoreductase 1; **PDBTitle:** x-ray crystallographic structure of a pseudomonas2 aeruginosa azoreductase in complex with methyl red.
56	c3izcs_	Alignment	not modelled	52.5	18	**PDB header:**ribosome **Chain:** S: **PDB Molecule:**60s ribosomal protein rpl20 (l18ae); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
57	d2b3ya2	Alignment	not modelled	51.5	26	**Fold:**Aconitase iron-sulfur domain **Superfamily:**Aconitase iron-sulfur domain **Family:**Aconitase iron-sulfur domain
58	c3k9cA_	Alignment	not modelled	51.2	15	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, laci family protein; **PDBTitle:** crystal structure of laci transcriptional regulator from rhodococcus2 species.
59	c3hlyA_	Alignment	not modelled	50.1	12	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**flavodoxin-like domain; **PDBTitle:** crystal structure of the flavodoxin-like domain from2 synechococcus sp q5mzp6_synp6 protein. northeast structural3 genomics consortium target snr135d.
60	d1qrda_	Alignment	not modelled	50.0	24	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
61	c3cswB_	Alignment	not modelled	49.0	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative branched-chain-amino-acid aminotransferase; **PDBTitle:** crystal structure of a putative branched-chain amino acid2 aminotransferase (tm0831) from thermotoga maritima at 2.15 a3 resolution
62	c2ad5B_	Alignment	not modelled	49.0	27	**PDB header:**ligase **Chain:** B: **PDB Molecule:**ctp synthase; **PDBTitle:** mechanisms of feedback regulation and drug resistance of ctp2 synthetases: structure of the e. coli ctps/ctp complex at 2.8-3 angstrom resolution.
63	d1jw9b_	Alignment	not modelled	48.1	13	**Fold:**Activating enzymes of the ubiquitin-like proteins **Superfamily:**Activating enzymes of the ubiquitin-like proteins **Family:**Molybdenum cofactor biosynthesis protein MoeB
64	c1zj8B_	Alignment	not modelled	47.2	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**probable ferredoxin-dependent nitrite reductase nira; **PDBTitle:** structure of mycobacterium tuberculosis nira protein
65	c3iz5s_	Alignment	not modelled	47.2	14	**PDB header:**ribosome **Chain:** S: **PDB Molecule:**60s ribosomal protein l18a (l18ae); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
66	c5acnA_	Alignment	not modelled	47.0	8	**PDB header:**lyase(carbon-oxygen) **Chain:** A: **PDB Molecule:**aconitase; **PDBTitle:** structure of activated aconitase. formation of the (4fe-4s)2 cluster in the crystal
67	c3c1iA_	Alignment	not modelled	46.8	17	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**ammonia channel; **PDBTitle:** substrate binding, deprotonation and selectivity at the2 periplasmic entrance of the e. coli ammonia channel amtb
68	c3djeA_	Alignment	not modelled	44.5	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fructosyl amine: oxygen oxidoreductase; **PDBTitle:** crystal structure of the deglycating enzyme fructosamine2 oxidase from aspergillus fumigatus (amadoriase ii) in3 complex with fsa
69	c1wrvB_	Alignment	not modelled	44.5	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**branched-chain amino acid aminotransferase; **PDBTitle:** crystal structure of t.th.hb8 branched-chain amino acid2 aminotransferase
70	c1jrxA_	Alignment	not modelled	42.9	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**flavocytochrome c; **PDBTitle:** crystal structure of arg402ala mutant flavocytochrome c32 from shewanella frigidimarina
71	c2b2hA_	Alignment	not modelled	42.2	20	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**ammonium transporter; **PDBTitle:** ammonium transporter amt-1 from a. fulgidus (as)
72	c3fvwA_	Alignment	not modelled	40.9	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative nad(p)h-dependent fmn reductase; **PDBTitle:** crystal structure of the q8dwd8_strmu protein from2 streptococcus mutans. northeast structural genomics3 consortium target smr99.
73	c3o1hB_	Alignment	not modelled	40.0	25	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**periplasmic protein tort; **PDBTitle:** crystal structure of the tors sensor domain - tort complex in the2 presence of tmao
74	c2gi4A_	Alignment	not modelled	39.9	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**possible phosphotyrosine protein phosphatase; **PDBTitle:** solution structure of the low molecular weight protein2 tyrosine phosphatase from campylobacter jejuni.

75	d1rtta_	Alignment	not modelled	39.8	16	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**NADPH-dependent FMN reductase
76	d1t5ba_	Alignment	not modelled	39.8	21	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
77	c3ry3B_	Alignment	not modelled	39.7	22	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**putative solute-binding protein; **PDBTitle:** putative solute-binding protein from yersinia pestis.
78	c1qo8A_	Alignment	not modelled	39.3	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**flavocytochrome c3 fumarate reductase; **PDBTitle:** the structure of the open conformation of a flavocytochrome2 c3 fumarate reductase
79	c3edoA_	Alignment	not modelled	39.0	11	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**putative trp repressor binding protein; **PDBTitle:** crystal structure of flavoprotein in complex with fmn2 (yp_193882.1) from lactobacillus acidophilus ncfm at 1.203 a resolution
80	d1h05a_	Alignment	not modelled	38.8	16	**Fold:**Flavodoxin-like **Superfamily:**Type II 3-dehydroquinate dehydratase **Family:**Type II 3-dehydroquinate dehydratase
81	c1zfnA_	Alignment	not modelled	38.4	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenylyltransferase thif; **PDBTitle:** structural analysis of escherichia coli thif
82	c2b76N_	Alignment	not modelled	38.3	7	**PDB header:**oxidoreductase **Chain:** N: **PDB Molecule:**fumarate reductase iron-sulfur protein; **PDBTitle:** e. coli quinol fumarate reductase frda e49q mutation
83	c2hpvA_	Alignment	not modelled	37.5	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fmn-dependent nadh-azoreductase; **PDBTitle:** crystal structure of fmn-dependent azoreductase from enterococcus2 faecalis
84	c2b3yB_	Alignment	not modelled	37.2	24	**PDB header:**lyase **Chain:** B: **PDB Molecule:**iron-responsive element binding protein 1; **PDBTitle:** structure of a monoclinic crystal form of human cytosolic aconitase2 (irp1)
85	d2gk3a1	Alignment	not modelled	36.9	23	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**STM3548-like
86	d1gtza_	Alignment	not modelled	35.8	18	**Fold:**Flavodoxin-like **Superfamily:**Type II 3-dehydroquinate dehydratase **Family:**Type II 3-dehydroquinate dehydratase
87	d1gqoa_	Alignment	not modelled	35.3	11	**Fold:**Flavodoxin-like **Superfamily:**Type II 3-dehydroquinate dehydratase **Family:**Type II 3-dehydroquinate dehydratase
88	c3lcmB_	Alignment	not modelled	35.3	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of smu.1420 from streptococcus mutans ua159
89	c2hqbA_	Alignment	not modelled	34.9	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional activator of comk gene; **PDBTitle:** crystal structure of a transcriptional activator of comk2 gene from bacillus halodurans
90	d1d1qa_	Alignment	not modelled	34.8	14	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
91	c1y8qA_	Alignment	not modelled	34.3	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**ubiquitin-like 1 activating enzyme e1a; **PDBTitle:** sumo e1 activating enzyme sae1-sae2-mg-atp complex
92	d1iyea_	Alignment	not modelled	34.2	18	**Fold:**D-aminoacid aminotransferase-like PLP-dependent enzymes **Superfamily:**D-aminoacid aminotransferase-like PLP-dependent enzymes **Family:**D-aminoacid aminotransferase-like PLP-dependent enzymes
93	c3rpeA_	Alignment	not modelled	34.0	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**modulator of drug activity b; **PDBTitle:** 1.1 angstrom crystal structure of putative modulator of drug activity2 (mdab) from yersinia pestis co92.
94	c1gx7A_	Alignment	not modelled	34.0	21	**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
95	c1a3wB_	Alignment	not modelled	33.2	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase; **PDBTitle:** pyruvate kinase from saccharomyces cerevisiae complexed with fbp, pg,2 mn2+ and k+
96	c3n8kG_	Alignment	not modelled	32.8	16	**PDB header:**lyase **Chain:** G: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** type ii dehydroquinase from mycobacterium tuberculosis complexed with2 citrazinic acid
97	c3jviA_	Alignment	not modelled	32.6	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein tyrosine phosphatase; **PDBTitle:** product state mimic crystal structure of protein tyrosine phosphatase2 from entamoeba histolytica
98	c2cwdA_	Alignment	not modelled	32.3	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**low molecular weight phosphotyrosine protein phosphatase; **PDBTitle:** crystal structure of tt1001 protein from thermus thermophilus hb8
99	c2rejA_	Alignment	not modelled	32.3	23	**PDB header:**choline-binding protein **Chain:** A: **PDB Molecule:**putative glycine betaine abc transporter protein; **PDBTitle:** abc-transporter choline binding protein in unliganded semi-2 closed conformation

100	d1s1ma1	Alignment	not modelled	32.0	19	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
101	c2akjA_	Alignment	not modelled	31.6	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ferredoxin--nitrite reductase, chloroplast; **PDBTitle:** structure of spinach nitrite reductase
102	c2an1D_	Alignment	not modelled	31.3	24	**PDB header:**transferase **Chain:** D: **PDB Molecule:**putative kinase; **PDBTitle:** structural genomics, the crystal structure of a putative kinase from2 salmonella typhimurim lt2
103	d1pvva2	Alignment	not modelled	31.1	12	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
104	c3lwzC_	Alignment	not modelled	30.9	15	**PDB header:**lyase **Chain:** C: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** 1.65 angstrom resolution crystal structure of type ii 3-2 dehydroquinate dehydratase (aroq) from yersinia pestis
105	c3hd6A_	Alignment	not modelled	30.8	11	**PDB header:**membrane protein, transport protein **Chain:** A: **PDB Molecule:**ammonium transporter rh type c; **PDBTitle:** crystal structure of the human rhesus glycoprotein rhcg
106	d1ekxa2	Alignment	not modelled	30.6	13	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
107	d1liua2	Alignment	not modelled	30.1	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
108	c3dmdA_	Alignment	not modelled	29.8	19	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**signal recognition particle receptor; **PDBTitle:** structures and conformations in solution of the signal recognition2 particle receptor from the archaeon pyrococcus furiosus
109	c2rjoA_	Alignment	not modelled	29.2	9	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**twin-arginine translocation pathway signal protein; **PDBTitle:** crystal structure of twin-arginine translocation pathway signal2 protein from burkholderia phytofirmans
110	d1uqra_	Alignment	not modelled	29.1	16	**Fold:**Flavodoxin-like **Superfamily:**Type II 3-dehydroquinate dehydratase **Family:**Type II 3-dehydroquinate dehydratase
111	c3khdC_	Alignment	not modelled	29.1	18	**PDB header:**transferase **Chain:** C: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of pff1300w.
112	c2eq8C_	Alignment	not modelled	28.8	31	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**pyruvate dehydrogenase complex, dihydrolipoamide **PDBTitle:** crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdp
113	d3c7ba3	Alignment	not modelled	27.7	11	**Fold:**Nitrite and sulphite reductase 4Fe-4S domain-like **Superfamily:**Nitrite and sulphite reductase 4Fe-4S domain-like **Family:**Nitrite and sulphite reductase 4Fe-4S domain-like
114	c1nekB_	Alignment	not modelled	27.6	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
115	c3chgB_	Alignment	not modelled	27.1	22	**PDB header:**ligand binding protein **Chain:** B: **PDB Molecule:**glycine betaine-binding protein; **PDBTitle:** the compatible solute-binding protein opuac from bacillus2 subtilis in complex with dmsa
116	d2bcgg1	Alignment	not modelled	26.8	18	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**GDI-like N domain
117	c3t66A_	Alignment	not modelled	26.8	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**nickel abc transporter (nickel-binding protein); **PDBTitle:** crystal structure of nickel abc transporter from bacillus halodurans
118	d2fz5a1	Alignment	not modelled	26.7	19	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
119	d1c0aa2	Alignment	not modelled	26.5	20	**Fold:**DCoH-like **Superfamily:**GAD domain-like **Family:**GAD domain
120	c2eq9C_	Alignment	not modelled	25.3	24	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**pyruvate dehydrogenase complex, dihydrolipoamide **PDBTitle:** crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdb