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1	c3fpkB_	 Alignment		100.0	90	PDB header: flavoprotein, oxidoreductase Chain: B: PDB Molecule: ferredoxin-nadp reductase; PDBTitle: crystal structure of ferredoxin-nadp reductase from salmonella2 typhimurium
2	c1a8pA_	 Alignment		100.0	32	PDB header: oxidoreductase Chain: A: PDB Molecule: nadph\;ferredoxin oxidoreductase; PDBTitle: ferredoxin reductase from azotobacter vinelandii
3	c1krhA_	 Alignment		100.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: benzoate 1,2-dioxygenase reductase; PDBTitle: x-ray stucture of benzoate dioxygenase reductase
4	c1gvhA_	 Alignment		100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: flavoheomprotein; PDBTitle: the x-ray structure of ferric escherichia coli2 flavohemoglobin reveals an unsuspected geometry of the3 distal heme pocket
5	c2bgjB_	 Alignment		100.0	29	PDB header: oxidoreductase Chain: B: PDB Molecule: ferredoxin-nadp(h) reductase; PDBTitle: x-ray structure of the ferredoxin-nadp(h) reductase from2 rhodobacter capsulatus at 2.1 angstroms
6	c2eixA_	 Alignment		100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh-cytochrome b5 reductase; PDBTitle: the structure of physarum polycephalum cytochrome b5 reductase
7	c2r6hC_	 Alignment		100.0	19	PDB header: oxidoreductase Chain: C: PDB Molecule: nadh:ubiquinone oxidoreductase, na translocating, f PDBTitle: crystal structure of the domain comprising the nad binding and the fad2 binding regions of the nadh:ubiquinone oxidoreductase, na3 translocating, f subunit from porphyromonas gingivalis
8	c1qfjD_	 Alignment		100.0	17	PDB header: oxidoreductase Chain: D: PDB Molecule: protein (flavin reductase); PDBTitle: crystal structure of nad(p)h:flavin oxidoreductase from escherichia2 coli
9	c2ok8D_	 Alignment		100.0	19	PDB header: oxidoreductase Chain: D: PDB Molecule: putative ferredoxin--nadp reductase; PDBTitle: ferredoxin-nadp+ reductase from plasmodium falciparum
10	c1umkA_	 Alignment		100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh-cytochrome b5 reductase; PDBTitle: the structure of human erythrocyte nadh-cytochrome b52 reductase
11	c1qgyA_	 Alignment		100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: ferredoxin--nadp+ reductase; PDBTitle: ferredoxin:nadp+ reductase mutant with lys 75 replaced by glu (k75e)

12	c1cqxB_	Alignment		100.0	17	PDB header: lipid binding protein Chain: B: PDB Molecule: flavoheomprotein; PDBTitle: crystal structure of the flavohemoglobin from alcaligenes eutrophus at2 1.75 a resolution
13	c1fncA_	Alignment		100.0	21	PDB header: oxidoreductase (nadp+(a), ferredoxin(a)) Chain: A: PDB Molecule: ferredoxin-nadp+ reductase; PDBTitle: refined crystal structure of spinach ferredoxin reductase2 at 1.7 angstroms resolution: oxidized, reduced, and 2'-3 phospho-5'-amp bound states
14	c1tvcA_	Alignment		100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: methane monooxygenase component c; PDBTitle: fad and nadh binding domain of methane monooxygenase2 reductase from methylococcus capsulatus (bath)
15	c2b5oA_	Alignment		100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: ferredoxin--nadp reductase; PDBTitle: ferredoxin-nadp reductase
16	c1jb9A_	Alignment		100.0	22	PDB header: oxidoreductase Chain: A: PDB Molecule: ferredoxin-nadp reductase; PDBTitle: crystal structure of the ferredoxin:nadp+ reductase from maize root at2 1.7 angstroms
17	c2rc5D_	Alignment		100.0	22	PDB header: oxidoreductase Chain: D: PDB Molecule: ferredoxin-nadp reductase; PDBTitle: refined structure of fnr from leptospira interrogans
18	c1ep3B_	Alignment		100.0	13	PDB header: oxidoreductase Chain: B: PDB Molecule: dihydroorotate dehydrogenase b (pyrk subunit); PDBTitle: crystal structure of lactococcus lactis dihydroorotate dehydrogenase2 b. data collected under cryogenic conditions.
19	c1cneA_	Alignment		100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: nitrate reductase; PDBTitle: structural studies on corn nitrate reductase: refined2 structure of the cytochrome b reductase fragment at 2.53 angstroms, its adp complex and an active site mutant and4 modeling of the cytochrome b domain
20	c2piaA_	Alignment		100.0	17	PDB header: reductase Chain: A: PDB Molecule: phthalate dioxygenase reductase; PDBTitle: phthalate dioxygenase reductase: a modular structure for2 electron transfer from pyridine nucleotides to [2fe-2s]
21	c2gpiA_	Alignment	not modelled	100.0	17	PDB header: fad-binding protein Chain: A: PDB Molecule: siderophore-interacting protein; PDBTitle: crystal structure of a siderophore-interacting protein (sputcn32_0076)2 from shewanella putrefaciens cn-32 at 2.20 a resolution
22	d1fdra2	Alignment	not modelled	100.0	99	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Reductases
23	c1f20A_	Alignment	not modelled	100.0	22	PDB header: oxidoreductase Chain: A: PDB Molecule: nitric-oxide synthase; PDBTitle: crystal structure of rat neuronal nitric-oxide synthase fad/nadp+2 domain at 1.9a resolution.
24	c1ddiA_	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: sulfite reductase [nadph] flavoprotein alpha- PDBTitle: crystal structure of sir-fp60
25	c1t1IA_	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: nitric-oxide synthase, brain; PDBTitle: crystal structure of rat neuronal nitric-oxide synthase2 reductase module at 2.3 a resolution.
26	c2qtzA_	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: methionine synthase reductase; PDBTitle: crystal structure of the nadp+-bound fad-containing fnr-like module of2 human methionine synthase reductase
27	d1a8pa2	Alignment	not modelled	100.0	28	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Reductases
28	c1j9zB_	Alignment	not modelled	99.9	21	PDB header: oxidoreductase Chain: B: PDB Molecule: nadph-cytochrome p450 reductase; PDBTitle: cypr-w677g

29	c3qftA	Alignment	not modelled	99.9	19	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh--cytochrome p450 reductase; PDBTitle: crystal structure of nadph-cytochrome p450 reductase (fad/nadph domain2 and r457h mutant)
30	d1qfja2	Alignment	not modelled	99.9	15	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Reductases
31	c2bpoA	Alignment	not modelled	99.9	22	PDB header: reductase Chain: A: PDB Molecule: nadh-cytochrom p450 reductase; PDBTitle: crystal structure of the yeast cpr triple mutant: d74g,2 y75f, k78a.
32	d1gvha3	Alignment	not modelled	99.9	15	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Flavohemoglobin, C-terminal domain
33	d1tvca2	Alignment	not modelled	99.9	13	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Aromatic dioxygenase reductase-like
34	d1krha2	Alignment	not modelled	99.9	25	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Aromatic dioxygenase reductase-like
35	d1umka2	Alignment	not modelled	99.9	19	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Reductases
36	d2cnda2	Alignment	not modelled	99.9	16	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Reductases
37	d1qx4a2	Alignment	not modelled	99.9	18	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Reductases
38	d1cqxa3	Alignment	not modelled	99.9	17	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Flavohemoglobin, C-terminal domain
39	d2bmwa2	Alignment	not modelled	99.9	19	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Reductases
40	d1gawa2	Alignment	not modelled	99.9	22	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Reductases
41	d1fnda2	Alignment	not modelled	99.9	20	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Reductases
42	d1qfza2	Alignment	not modelled	99.9	21	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Reductases
43	d1ndha2	Alignment	not modelled	99.9	21	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Reductases
44	d1sm4a2	Alignment	not modelled	99.9	20	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Reductases
45	d1jb9a2	Alignment	not modelled	99.9	22	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Reductases
46	d2piaa2	Alignment	not modelled	99.8	17	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Aromatic dioxygenase reductase-like
47	d1ddga2	Alignment	not modelled	99.8	19	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: NADPH-cytochrome p450 reductase-like
48	d1f20a2	Alignment	not modelled	99.8	16	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: NADPH-cytochrome p450 reductase-like
49	c3a1fA	Alignment	not modelled	99.8	14	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome b-245 heavy chain; PDBTitle: the crystal structure of nadph binding domain of gp91(phox)
50	d1fdra1	Alignment	not modelled	99.8	100	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
51	d1ja1a3	Alignment	not modelled	99.8	17	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: NADPH-cytochrome p450 reductase-like
52	c3lrxC	Alignment	not modelled	99.8	10	PDB header: oxidoreductase Chain: C: PDB Molecule: putative hydrogenase; PDBTitle: crystal structure of the c-terminal domain (residues 78-226)2 of pf1911 hydrogenase from pyrococcus furiosus, northeast3 structural genomics consortium target pfr246a
53	d1ep3b2	Alignment	not modelled	99.8	11	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Dihydroorotate dehydrogenase B, PyrK subunit
54	d1a8pa1	Alignment	not modelled	99.7	37	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like

					Family: Ferredoxin reductase FAD-binding domain-like
55	d1gvha2	Alignment	not modelled	99.6	22 Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
56	d1ep3b1	Alignment	not modelled	99.6	15 Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
57	d1qx4a1	Alignment	not modelled	99.5	19 Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
58	d1krha1	Alignment	not modelled	99.5	26 Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
59	d2cnda1	Alignment	not modelled	99.5	15 Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
60	d1cqxa2	Alignment	not modelled	99.5	21 Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
61	d1umka1	Alignment	not modelled	99.5	19 Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
62	d2bmwa1	Alignment	not modelled	99.5	19 Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
63	d1ndha1	Alignment	not modelled	99.5	21 Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
64	d1sm4a1	Alignment	not modelled	99.5	19 Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
65	d1qfja1	Alignment	not modelled	99.5	20 Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
66	d2piaa1	Alignment	not modelled	99.4	20 Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
67	d1fnda1	Alignment	not modelled	99.4	22 Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
68	d1qfza1	Alignment	not modelled	99.4	20 Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
69	d1gawa1	Alignment	not modelled	99.3	22 Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
70	d1tvca1	Alignment	not modelled	99.3	23 Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
71	d1jb9a1	Alignment	not modelled	99.1	21 Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
72	d1ddga1	Alignment	not modelled	97.0	24 Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: NADPH-cytochrome p450 reductase FAD-binding domain-like
73	d1f20a1	Alignment	not modelled	96.3	28 Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: NADPH-cytochrome p450 reductase FAD-binding domain-like
74	d1ja1a1	Alignment	not modelled	95.4	27 Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: NADPH-cytochrome p450 reductase FAD-binding domain-like
75	d1f0ka_	Alignment	not modelled	82.8	18 Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Peptidoglycan biosynthesis glycosyltransferase MurG
76	d1o5za1	Alignment	not modelled	78.8	12 Fold: MurD-like peptide ligases, peptide-binding domain Superfamily: MurD-like peptide ligases, peptide-binding domain Family: Folylpolyglutamate synthetase, C-terminal domain
77	c1o5za_	Alignment	not modelled	57.2	12 PDB header: ligase Chain: A: PDB Molecule: folylpolyglutamate synthase/dihydrofolate synthase; PDBTitle: crystal structure of folylpolyglutamate synthase (tm0166) from2 thermotoga maritima at 2.10 a resolution
78	d1pn3a_	Alignment	not modelled	50.7	11 Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Gtf glycosyltransferase
79	c1w78A_	Alignment	not modelled	44.3	11 PDB header: synthase Chain: A: PDB Molecule: folc bifunctional protein; PDBTitle: e.coli folc in complex with dhpp and adp
80	d1liira_	Alignment	not modelled	35.9	15 Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Gtf glycosyltransferase
81	c3pnrB_	Alignment	not modelled	30.8	9 PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: pbcip-c; PDBTitle: structure of pbcip-c in complex with falcipain-2

82	c3sp1B_	Alignment	not modelled	30.6	21	PDB header: ligase Chain: B: PDB Molecule: cysteinyI-trna synthetase; PDBTitle: crystal structure of cysteinyI-trna synthetase (cyss) from borrelia2 burgdorferi
83	c3zq4C_	Alignment	not modelled	25.4	12	PDB header: hydrolase Chain: C: PDB Molecule: ribonuclease j 1; PDBTitle: unusual, dual endo- and exo-nuclease activity in the degradosome2 explained by crystal structure analysis of rnase j1
84	d2hzba1	Alignment	not modelled	25.1	18	Fold: CofD-like Superfamily: CofD-like Family: CofD-like
85	c2p0yA_	Alignment	not modelled	24.8	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein lp_0780; PDBTitle: crystal structure of q88yi3_lacpl from lactobacillus2 plantarum. northeast structural genomics consortium target3 lpr6
86	c2ppvA_	Alignment	not modelled	24.3	14	PDB header: transferase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a protein belonging to the upf0052 (se_0549) from2 staphylococcus epidermidis atcc 12228 at 2.00 a resolution
87	d2bvca2	Alignment	not modelled	23.2	7	Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: Glutamine synthetase catalytic domain
88	c2q7xA_	Alignment	not modelled	22.7	18	PDB header: transferase Chain: A: PDB Molecule: upf0052 protein sp_1565; PDBTitle: crystal structure of a putative phospho transferase (sp_1565) from2 streptococcus pneumoniae tigr4 at 2.00 a resolution
89	d1rrva_	Alignment	not modelled	22.6	13	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Gtf glycosyltransferase
90	c3fkyD_	Alignment	not modelled	21.7	6	PDB header: ligase Chain: D: PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of the glutamine synthetase gln1deltan182 from the yeast saccharomyces cerevisiae
91	c2q41D_	Alignment	not modelled	21.3	9	PDB header: transferase Chain: D: PDB Molecule: spermidine synthase 1; PDBTitle: ensemble refinement of the protein crystal structure of spermidine2 synthase from arabidopsis thaliana gene at1g23820
92	c2d3aj_	Alignment	not modelled	20.2	10	PDB header: ligase Chain: J: PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of the maize glutamine synthetase2 complexed with adp and methionine sulfoximine phosphate
93	c2qc8J_	Alignment	not modelled	19.8	7	PDB header: ligase Chain: J: PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of human glutamine synthetase in complex with adp2 and methionine sulfoximine phosphate
94	d2b2ca1	Alignment	not modelled	19.2	13	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Spermidine synthase
95	c3ng0A_	Alignment	not modelled	18.9	3	PDB header: ligase Chain: A: PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of glutamine synthetase from synechocystis sp. pcc2 6803
96	c3o6xC_	Alignment	not modelled	18.8	7	PDB header: ligase Chain: C: PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of the type iii glutamine synthetase from2 bacteroides fragilis
97	c3adnB_	Alignment	not modelled	18.5	13	PDB header: transferase Chain: B: PDB Molecule: spermidine synthase; PDBTitle: crystal structure of spermidine synthase from e. coli.
98	d1f52a2	Alignment	not modelled	18.3	3	Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: Glutamine synthetase catalytic domain
99	d1uira_	Alignment	not modelled	17.8	16	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Spermidine synthase