Phyre2

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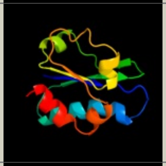
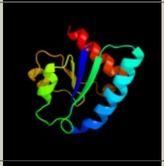
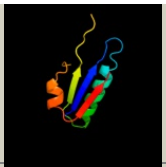
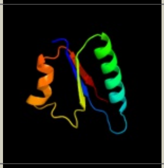
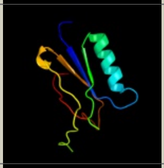
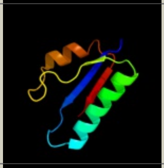
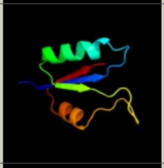
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2kyrA_	Alignment		100.0	100	**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
2	d2r48a1	Alignment		100.0	36	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Fructose specific IIB subunit-like
3	d2r4qa1	Alignment		100.0	40	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Fructose specific IIB subunit-like
4	c1tvmA_	Alignment		97.6	15	**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
5	c3czcA_	Alignment		96.6	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rmpb; **PDBTitle:** the crystal structure of a putative pts iib(ptxb) from2 streptococcus mutans
6	c2l2qA_	Alignment		96.5	13	**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
7	d2a5la1	Alignment		96.5	18	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**WrbA-like
8	d1iiba_	Alignment		96.4	15	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Lactose/Cellobiose specific IIB subunit
9	c1vkrA_	Alignment		96.0	16	**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
10	d1vkra_	Alignment		96.0	16	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Lactose/Cellobiose specific IIB subunit
11	c3nbmA_	Alignment		95.8	16	**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.

12	d1ydga_	Alignment		94.9	30	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**WrbA-like
13	d1ycga1	Alignment		94.3	21	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
14	d2arka1	Alignment		93.8	22	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**WrbA-like
15	c3fniA_	Alignment		90.5	15	**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
16	c3klbA_	Alignment		89.7	19	**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
17	d1vmea1	Alignment		89.2	11	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
18	c3d7nA_	Alignment		88.9	23	**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
19	d1e5da1	Alignment		88.6	20	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
20	d1d4aa_	Alignment		86.7	15	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
21	c3p0rA_	Alignment	not modelled	86.1	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**azoreductase; **PDBTitle:** crystal structure of azoreductase from bacillus anthracis str. sterne
22	c3b6iB_	Alignment	not modelled	82.5	27	**PDB header:**flavoprotein **Chain:** B: **PDB Molecule:**flavoprotein wrba; **PDBTitle:** wrba from escherichia coli, native structure
23	d1qrda_	Alignment	not modelled	82.2	21	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
24	d2qwxa1	Alignment	not modelled	80.3	22	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
25	c1zggA_	Alignment	not modelled	75.9	21	**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
26	c3f2vA_	Alignment	not modelled	72.2	13	**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.
27	c3rh0A_	Alignment	not modelled	71.6	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**arsenate reductase; **PDBTitle:** corynebacterium glutamicum mycothiol/mycoredoxin1-dependent arsenate2 reductase cg_arsc2
28	d1t5ba_	Alignment	not modelled	67.8	21	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase

29	c2ohiB_	Alignment	not modelled	67.7	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**type a flavoprotein fpra; **PDBTitle:** crystal structure of coenzyme f420h2 oxidase (fpra), a diiron2 flavoprotein, reduced state
30	c2v9cA_	Alignment	not modelled	67.6	27	**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.
31	c2zkiH_	Alignment	not modelled	67.1	23	**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)
32	c1woyA_	Alignment	not modelled	66.3	25	**PDB header:**ligase **Chain:** A: **PDB Molecule:**methionyl-trna synthetase; **PDBTitle:** crystal structure of methionyl trna synthetase y225f mutant2 from thermus thermophilus
33	c3fvwA_	Alignment	not modelled	65.8	16	**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.
34	d1dg9a_	Alignment	not modelled	61.2	13	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
35	d1dxqa_	Alignment	not modelled	60.8	20	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
36	c1vmeB_	Alignment	not modelled	56.8	13	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**flavoprotein; **PDBTitle:** crystal structure of flavoprotein (tm0755) from thermotoga maritima at2 1.80 a resolution
37	c2q62A_	Alignment	not modelled	55.8	10	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**arsh; **PDBTitle:** crystal structure of arsh from sinorhizobium meliloti
38	c2gi4A_	Alignment	not modelled	52.5	29	**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.
39	c3jviA_	Alignment	not modelled	51.0	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein tyrosine phosphatase; **PDBTitle:** product state mimic crystal structure of protein tyrosine phosphatase2 from entamoeba histolytica
40	d1t0ba_	Alignment	not modelled	47.9	22	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**ThuA-like
41	c3snoA_	Alignment	not modelled	46.9	23	**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
42	d1oboa_	Alignment	not modelled	43.7	13	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
43	d1sqsa_	Alignment	not modelled	43.2	15	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Hypothetical protein SP1951
44	c3rpeA_	Alignment	not modelled	41.8	22	**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.
45	c3lcmB_	Alignment	not modelled	40.9	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of smu.1420 from streptococcus mutans ua159
46	d1acoa2	Alignment	not modelled	37.3	14	**Fold:**Aconitase iron-sulfur domain **Superfamily:**Aconitase iron-sulfur domain **Family:**Aconitase iron-sulfur domain
47	d1qzua_	Alignment	not modelled	36.3	19	**Fold:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Superfamily:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Family:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
48	c3edoA_	Alignment	not modelled	36.2	19	**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
49	c3k9cA_	Alignment	not modelled	35.6	13	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, laci family protein; **PDBTitle:** crystal structure of laci transcriptional regulator from rhodococcus2 species.
50	d1ja1a2	Alignment	not modelled	34.4	11	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Cytochrome p450 reductase N-terminal domain-like
51	c3cgiD_	Alignment	not modelled	33.5	18	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**propanediol utilization protein pduu; **PDBTitle:** crystal structure of the pduu shell protein from the pdu2 microcompartment
52	c2wc1A_	Alignment	not modelled	32.2	18	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**flavodoxin; **PDBTitle:** three-dimensional structure of the nitrogen fixation2 flavodoxin (niff) from rhodobacter capsulatus at 2.2 a

53	d2z98a1	Alignment	not modelled	31.6	16	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
54	d1rtta_	Alignment	not modelled	31.3	15	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**NADPH-dependent FMN reductase
55	c5acnA_	Alignment	not modelled	31.2	14	**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
56	d1s1ma1	Alignment	not modelled	31.1	15	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
57	c2q9uB_	Alignment	not modelled	30.6	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**a-type flavoprotein; **PDBTitle:** crystal structure of the flavodiiron protein from giardia2 intestinalis
58	c2hpvA_	Alignment	not modelled	29.6	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fmn-dependent nadh-azoreductase; **PDBTitle:** crystal structure of fmn-dependent azoreductase from enterococcus2 faecalis
59	d1iloa_	Alignment	not modelled	27.5	24	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
60	d1t9ba1	Alignment	not modelled	27.2	19	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
61	c3hrlA_	Alignment	not modelled	26.2	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**endonuclease-like protein; **PDBTitle:** crystal structure of a putative endonuclease-like protein (ngo0050)2 from neisseria gonorrhoeae
62	d1tjya_	Alignment	not modelled	25.7	14	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
63	d1rlia_	Alignment	not modelled	22.9	13	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Hypothetical protein YwqN
64	c3h9gA_	Alignment	not modelled	22.2	11	**PDB header:**transferase/antibiotic **Chain:** A: **PDB Molecule:**mccb protein; **PDBTitle:** crystal structure of e. coli mccb + mcca-n7isoasn
65	c3f6sI_	Alignment	not modelled	22.2	24	**PDB header:**electron transport **Chain:** I: **PDB Molecule:**flavodoxin; **PDBTitle:** desulfovibrio desulfuricans (atcc 29577) oxidized flavodoxin2 alternate conformers
66	c3ia0c_	Alignment	not modelled	22.1	8	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**ethanolamine utilization protein euts; **PDBTitle:** ethanolamine utilization microcompartment shell subunit,2 euts-g39v mutant
67	d1b1ca_	Alignment	not modelled	21.7	13	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Cytochrome p450 reductase N-terminal domain-like
68	c2fzvC_	Alignment	not modelled	21.2	10	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**putative arsenical resistance protein; **PDBTitle:** crystal structure of an apo form of a flavin-binding protein from2 shigella flexneri
69	d1d1qa_	Alignment	not modelled	21.2	19	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
70	d1gsaa1	Alignment	not modelled	20.8	28	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**Prokaryotic glutathione synthetase, N-terminal domain
71	c3cswB_	Alignment	not modelled	20.8	9	**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
72	c2hjrK_	Alignment	not modelled	20.3	22	**PDB header:**oxidoreductase **Chain:** K: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** crystal structure of cryptosporidium parvum malate2 dehydrogenase
73	d2b3ya2	Alignment	not modelled	20.3	30	**Fold:**Aconitase iron-sulfur domain **Superfamily:**Aconitase iron-sulfur domain **Family:**Aconitase iron-sulfur domain
74	d5nula_	Alignment	not modelled	20.2	16	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
75	c3djeA_	Alignment	not modelled	20.2	17	**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
76	d1h05a_	Alignment	not modelled	20.0	18	**Fold:**Flavodoxin-like **Superfamily:**Type II 3-dehydroquinate dehydratase **Family:**Type II 3-dehydroquinate dehydratase
77	d1gqoa_	Alignment	not modelled	19.3	13	**Fold:**Flavodoxin-like **Superfamily:**Type II 3-dehydroquinate dehydratase **Family:**Type II 3-dehydroquinate dehydratase
78	c3chgB_	Alignment	not modelled	19.1	36	**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
						Fold:NAD(P)-binding Rossmann-fold domains

79	d1vkna1	Alignment	not modelled	18.9	0	**Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
80	c3t38B_	Alignment	not modelled	18.4	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**arsenate reductase; **PDBTitle:** corynebacterium glutamicum thioredoxin-dependent arsenate reductase2 cg_arsc1'
81	c3kydB_	Alignment	not modelled	18.3	8	**PDB header:**ligase **Chain:** B: **PDB Molecule:**sumo-activating enzyme subunit 2; **PDBTitle:** human sumo e1~sumo1-amp tetrahedral intermediate mimic
82	c2b3yB_	Alignment	not modelled	17.9	27	**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)
83	d1jw9b_	Alignment	not modelled	17.9	14	**Fold:**Activating enzymes of the ubiquitin-like proteins **Superfamily:**Activating enzymes of the ubiquitin-like proteins **Family:**Molybdenum cofactor biosynthesis protein MoeB
84	d1gtza_	Alignment	not modelled	17.8	16	**Fold:**Flavodoxin-like **Superfamily:**Type II 3-dehydroquinate dehydratase **Family:**Type II 3-dehydroquinate dehydratase
85	d1jf8a_	Alignment	not modelled	17.6	8	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
86	c1ychD_	Alignment	not modelled	17.5	20	**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
87	d2f1da1	Alignment	not modelled	17.5	28	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Imidazole glycerol phosphate dehydratase
88	c3k1yE_	Alignment	not modelled	17.1	19	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**oxidoreductase; **PDBTitle:** x-ray structure of oxidoreductase from corynebacterium2 diphtheriae. orthorombic crystal form, northeast structural3 genomics consortium target cdr100d
89	d1rqga2	Alignment	not modelled	17.0	18	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
90	c1y8qD_	Alignment	not modelled	16.5	8	**PDB header:**ligase **Chain:** D: **PDB Molecule:**ubiquitin-like 2 activating enzyme e1b; **PDBTitle:** sumo e1 activating enzyme sae1-sae2-mg-atp complex
91	d2fz5a1	Alignment	not modelled	16.2	21	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
92	c3lwzC_	Alignment	not modelled	16.1	16	**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
93	c1zj8B_	Alignment	not modelled	15.7	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**probable ferredoxin-dependent nitrite reductase nira; **PDBTitle:** structure of mycobacterium tuberculosis nira protein
94	c3kzqE_	Alignment	not modelled	15.6	17	**PDB header:**structural genomics, unknown function **Chain:** E: **PDB Molecule:**putative uncharacterized protein vp2116; **PDBTitle:** the crystal structure of the protein with unknown function from vibrio2 parahaemolyticus rimd 2210633
95	d2fzva1	Alignment	not modelled	15.4	10	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**NADPH-dependent FMN reductase
96	d1uqra_	Alignment	not modelled	15.1	21	**Fold:**Flavodoxin-like **Superfamily:**Type II 3-dehydroquinate dehydratase **Family:**Type II 3-dehydroquinate dehydratase
97	c3n8kG_	Alignment	not modelled	15.1	18	**PDB header:**lyase **Chain:** G: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** type ii dehydroquinase from mycobacterium tuberculosis complexed with2 citrazinic acid
98	c3sp1B_	Alignment	not modelled	14.9	27	**PDB header:**ligase **Chain:** B: **PDB Molecule:**cysteinyl-trna synthetase; **PDBTitle:** crystal structure of cysteinyl-trna synthetase (cyss) from borrelia2 burgdorferi
99	d5pnta_	Alignment	not modelled	14.8	15	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases