Phyre2

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Description	P32676
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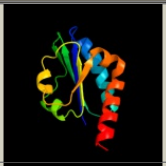
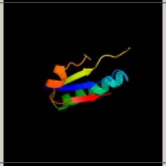
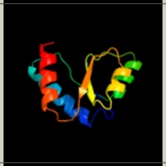
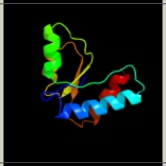
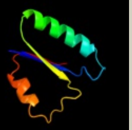
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2kyrA_	Alignment		100.0	31	**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	33	**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	29	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Fructose specific IIB subunit-like
4	c1tvmA_	Alignment		97.3	16	**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	d2a5la1	Alignment		96.5	16	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**WrbA-like
6	c3czcA_	Alignment		96.3	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rmpb; **PDBTitle:** the crystal structure of a putative pts iib(ptxb) from2 streptococcus mutans
7	d1iiba_	Alignment		96.3	14	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Lactose/Cellobiose specific IIB subunit
8	c2l2qA_	Alignment		96.1	17	**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
9	d1vkra_	Alignment		95.6	13	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Lactose/Cellobiose specific IIB subunit
10	c1vkrA_	Alignment		95.6	13	**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
11	c3nbmA_	Alignment		95.3	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pts system, lactose-specific iiabc components; **PDBTitle:** the lactose-specific iib component domain structure of the2 phosphoenolpyruvate:carbohydrate phosphotransferase system (pts) from3 streptococcus pneumoniae.

12	d2arka1	Alignment		94.8	20	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**WrbA-like
13	d1ydga_	Alignment		94.7	13	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**WrbA-like
14	d1ycga1	Alignment		93.2	15	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
15	d1qrda_	Alignment		91.4	19	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
16	c3p0rA_	Alignment		90.7	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**azoreductase; **PDBTitle:** crystal structure of azoreductase from bacillus anthracis str. sterne
17	d1vmea1	Alignment		89.3	5	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
18	c3d7nA_	Alignment		87.9	21	**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	c3fniA_	Alignment		87.5	13	**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
20	d1t5ba_	Alignment		86.7	14	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
21	c3b6iB_	Alignment	not modelled	85.7	11	**PDB header:**flavoprotein **Chain:** B: **PDB Molecule:**flavoprotein wrba; **PDBTitle:** wrba from escherichia coli, native structure
22	c2gi4A_	Alignment	not modelled	84.1	22	**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.
23	c3rpeA_	Alignment	not modelled	82.7	16	**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.
24	c1zggA_	Alignment	not modelled	79.7	23	**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
25	c2zkiH_	Alignment	not modelled	79.2	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)
26	d1e5da1	Alignment	not modelled	77.2	15	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
27	c3f2vA_	Alignment	not modelled	75.8	8	**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.
						PDB header:oxidoreductase

28	c3rh0A_	Alignment	not modelled	71.1	14	**Chain:** A: **PDB Molecule:**arsenate reductase; **PDBTitle:** corynebacterium glutamicum mycothiol/mycoredoxin1-dependent arsenate2 reductase cg_arsc2
29	c2ohiB_	Alignment	not modelled	64.8	13	**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	64.8	19	**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	d1t0ba_	Alignment	not modelled	63.3	27	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**ThuA-like
32	d2qwxa1	Alignment	not modelled	61.8	21	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
33	c3klbA_	Alignment	not modelled	61.6	17	**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
34	c2hpvA_	Alignment	not modelled	58.4	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fmn-dependent nadh-azoreductase; **PDBTitle:** crystal structure of fmn-dependent azoreductase from enterococcus2 faecalis
35	c2q62A_	Alignment	not modelled	57.8	11	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**arsh; **PDBTitle:** crystal structure of arsh from sinorhizobium meliloti
36	c3jviA_	Alignment	not modelled	57.1	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein tyrosine phosphatase; **PDBTitle:** product state mimic crystal structure of protein tyrosine phosphatase2 from entamoeba histolytica
37	c2wc1A_	Alignment	not modelled	51.4	20	**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
38	c3snoA_	Alignment	not modelled	50.0	15	**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
39	d2z98a1	Alignment	not modelled	49.4	8	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
40	d1sqsa_	Alignment	not modelled	49.0	13	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Hypothetical protein SP1951
41	c3fvwA_	Alignment	not modelled	48.2	15	**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.
42	c1vmeB_	Alignment	not modelled	43.8	5	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**flavoprotein; **PDBTitle:** crystal structure of flavoprotein (tm0755) from thermotoga maritima at2 1.80 a resolution
43	c3lcmB_	Alignment	not modelled	42.7	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of smu.1420 from streptococcus mutans ua159
44	d1acoa2	Alignment	not modelled	37.8	8	**Fold:**Aconitase iron-sulfur domain **Superfamily:**Aconitase iron-sulfur domain **Family:**Aconitase iron-sulfur domain
45	d1dxqa_	Alignment	not modelled	36.1	19	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
46	c2cwdA_	Alignment	not modelled	35.8	31	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**low molecular weight phosphotyrosine protein phosphatase; **PDBTitle:** crystal structure of tt1001 protein from thermus thermophilus hb8
47	d1rtta_	Alignment	not modelled	33.2	16	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**NADPH-dependent FMN reductase
48	d1k4ma_	Alignment	not modelled	31.6	19	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Adenylyltransferase
49	c5acnA_	Alignment	not modelled	30.2	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
50	d5nula_	Alignment	not modelled	27.7	16	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
51	d1d1qa_	Alignment	not modelled	27.5	10	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
52	c3chgB_	Alignment	not modelled	27.0	31	**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
53	d1h05a_	Alignment	not modelled	25.8	11	**Fold:**Flavodoxin-like **Superfamily:**Type II 3-dehydroquinate dehydratase

						Family: Type II 3-dehydroquinate dehydratase
54	c3cgiD_	Alignment	not modelled	25.6	14	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**propanediol utilization protein pduu; **PDBTitle:** crystal structure of the pduu shell protein from the pdu2 microcompartment
55	c3k9cA_	Alignment	not modelled	23.0	13	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, laci family protein; **PDBTitle:** crystal structure of laci transcriptional regulator from rhodococcus2 species.
56	d1gqoa_	Alignment	not modelled	22.7	11	**Fold:**Flavodoxin-like **Superfamily:**Type II 3-dehydroquinate dehydratase **Family:**Type II 3-dehydroquinate dehydratase
57	d2b3ya2	Alignment	not modelled	22.6	24	**Fold:**Aconitase iron-sulfur domain **Superfamily:**Aconitase iron-sulfur domain **Family:**Aconitase iron-sulfur domain
58	c3h9gA_	Alignment	not modelled	22.4	15	**PDB header:**transferase/antibiotic **Chain:** A: **PDB Molecule:**mccb protein; **PDBTitle:** crystal structure of e. coli mccb + mcca-n7isoasn
59	d1g3qa_	Alignment	not modelled	21.9	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
60	c1ychD_	Alignment	not modelled	21.7	15	**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
61	d2fz5a1	Alignment	not modelled	21.6	21	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
62	c3kydB_	Alignment	not modelled	20.9	9	**PDB header:**ligase **Chain:** B: **PDB Molecule:**sumo-activating enzyme subunit 2; **PDBTitle:** human sumo e1~sumo1-amp tetrahedral intermediate mimic
63	c3f6sI_	Alignment	not modelled	19.8	25	**PDB header:**electron transport **Chain:** I: **PDB Molecule:**flavodoxin; **PDBTitle:** desulfovibrio desulfuricans (atcc 29577) oxidized flavodoxin2 alternate conformers
64	d1jw9b_	Alignment	not modelled	19.7	16	**Fold:**Activating enzymes of the ubiquitin-like proteins **Superfamily:**Activating enzymes of the ubiquitin-like proteins **Family:**Molybdenum cofactor biosynthesis protein MoeB
65	d1gsaa1	Alignment	not modelled	19.5	12	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**Prokaryotic glutathione synthetase, N-terminal domain
66	d1jf8a_	Alignment	not modelled	19.5	7	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
67	c3o1hB_	Alignment	not modelled	19.4	14	**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
68	c2b3yB_	Alignment	not modelled	19.3	21	**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)
69	c3n8kG_	Alignment	not modelled	19.2	11	**PDB header:**lyase **Chain:** G: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** type ii dehydroquinase from mycobacterium tuberculosis complexed with2 citrazinic acid
70	c1y8qD_	Alignment	not modelled	19.0	9	**PDB header:**ligase **Chain:** D: **PDB Molecule:**ubiquitin-like 2 activating enzyme e1b; **PDBTitle:** sumo e1 activating enzyme sae1-sae2-mg-atp complex
71	c3t38B_	Alignment	not modelled	19.0	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**arsenate reductase; **PDBTitle:** corynebacterium glutamicum thioredoxin-dependent arsenate reductase2 cg_arsc1'
72	c3lwzC_	Alignment	not modelled	18.8	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
73	d1uqra_	Alignment	not modelled	18.8	7	**Fold:**Flavodoxin-like **Superfamily:**Type II 3-dehydroquinate dehydratase **Family:**Type II 3-dehydroquinate dehydratase
74	c3rsbB_	Alignment	not modelled	18.7	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**adenosylcobinamide-phosphate guanylyltransferase; **PDBTitle:** structure of the archaeal gtp:adocbi-p guanylyltransferase (coby) from2 methanocaldococcus jannaschii
75	c3cswB_	Alignment	not modelled	18.6	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
76	c2fzvC_	Alignment	not modelled	18.2	11	**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
77	c2l18A_	Alignment	not modelled	18.1	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**arsenate reductase; **PDBTitle:** an arsenate reductase in the phosphate binding state
78	c2b76N_	Alignment	not modelled	18.1	8	**PDB header:**oxidoreductase **Chain:** N: **PDB Molecule:**fumarate reductase iron-sulfur protein;

						PDBTitle: e. coli quinol fumarate reductase frda e49q mutation
79	d1q6za1	Alignment	not modelled	17.5	22	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
80	c2ad5B_	Alignment	not modelled	17.5	25	**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.
81	d1vkna1	Alignment	not modelled	17.3	9	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
82	c3hrlA_	Alignment	not modelled	17.3	12	**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
83	c2q9uB_	Alignment	not modelled	17.0	8	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**a-type flavoprotein; **PDBTitle:** crystal structure of the flavodiiron protein from giardia2 intestinalis
84	c3hlyA_	Alignment	not modelled	17.0	15	**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.
85	c3djeA_	Alignment	not modelled	16.5	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
86	d1rlia_	Alignment	not modelled	16.5	13	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Hypothetical protein YwqN
87	d1d4aa_	Alignment	not modelled	16.4	20	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
88	c3ia0c_	Alignment	not modelled	14.9	20	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**ethanolamine utilization protein euts; **PDBTitle:** ethanolamine utilization microcompartment shell subunit,2 euts-g39v mutant
89	c2opiB_	Alignment	not modelled	14.8	23	**PDB header:**lyase **Chain:** B: **PDB Molecule:**l-fuculose-1-phosphate aldolase; **PDBTitle:** crystal structure of l-fuculose-1-phosphate aldolase from bacteroides2 thetaiotaomicron
90	d1s1ma1	Alignment	not modelled	14.7	19	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
91	c2eq8C_	Alignment	not modelled	14.2	24	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**pyruvate dehydrogenase complex, dihydrolipoamide **PDBTitle:** crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdp
92	d2fzva1	Alignment	not modelled	13.6	11	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**NADPH-dependent FMN reductase
93	d2f1da1	Alignment	not modelled	13.5	22	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Imidazole glycerol phosphate dehydratase
94	c1zfnA_	Alignment	not modelled	13.3	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenylyltransferase thif; **PDBTitle:** structural analysis of escherichia coli thif
95	d1oboa_	Alignment	not modelled	13.3	9	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
96	c2rjoA_	Alignment	not modelled	13.0	7	**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
97	d1e4cp_	Alignment	not modelled	12.4	24	**Fold:**AraD/HMP-PK domain-like **Superfamily:**AraD/HMP-PK domain-like **Family:**AraD-like aldolase/epimerase
98	d5pnta_	Alignment	not modelled	11.9	21	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
99	c2eq9C_	Alignment	not modelled	11.5	24	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**pyruvate dehydrogenase complex, dihydrolipoamide **PDBTitle:** crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdb