Phyre²

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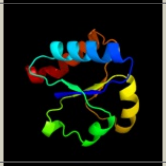
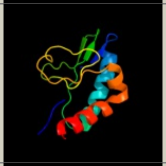
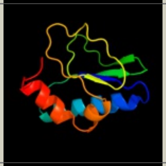
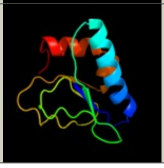
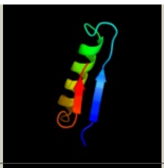
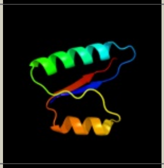
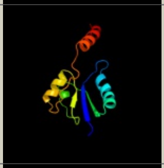
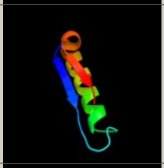
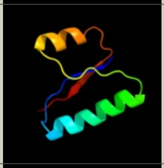
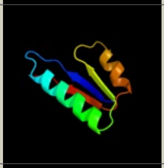
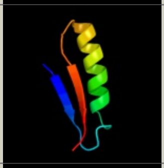
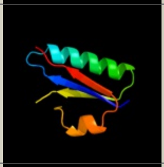
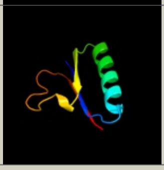
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3czcA_	Alignment		99.9	38	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rmpb; **PDBTitle:** the crystal structure of a putative pts iib(ptxb) from2 streptococcus mutans
2	c1tvmA_	Alignment		99.8	14	**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
3	d1vkra_	Alignment		99.7	13	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Lactose/Cellobiose specific IIB subunit
4	c1vkrA_	Alignment		99.7	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
5	d1iiba_	Alignment		99.2	16	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Lactose/Cellobiose specific IIB subunit
6	c2l2qA_	Alignment		99.2	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
7	c3sqnB_	Alignment		99.1	12	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**conserved domain protein; **PDBTitle:** putative mga family transcriptional regulator from enterococcus2 faecalis
8	c3nbmA_	Alignment		99.1	19	**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.
9	c2kyrA_	Alignment		97.9	15	**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
10	d2r48a1	Alignment		97.2	13	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Fructose specific IIB subunit-like
11	d2r4qa1	Alignment		95.8	15	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Fructose specific IIB subunit-like

12	d1dg9a_	Alignment		94.4	23	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
13	d1ycga1	Alignment		94.4	9	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
14	c2q5cA_	Alignment		93.7	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**ntrc family transcriptional regulator; **PDBTitle:** crystal structure of ntrc family transcriptional regulator from2 clostridium acetobutylicum
15	c3jviA_	Alignment		93.5	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein tyrosine phosphatase; **PDBTitle:** product state mimic crystal structure of protein tyrosine phosphatase2 from entamoeba histolytica
16	d1vmea1	Alignment		93.3	14	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
17	d1e5da1	Alignment		92.9	16	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
18	c1zggA_	Alignment		92.8	18	**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
19	d1ydga_	Alignment		92.4	21	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**WrbA-like
20	d1f4pa_	Alignment		92.2	16	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
21	c3f6sI_	Alignment	not modelled	92.0	16	**PDB header:**electron transport **Chain:** I: **PDB Molecule:**flavodoxin; **PDBTitle:** desulfovibrio desulfuricans (atcc 29577) oxidized flavodoxin2 alternate conformers
22	c1u2pA_	Alignment	not modelled	91.5	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**low molecular weight protein-tyrosine- **PDBTitle:** crystal structure of mycobacterium tuberculosis low2 molecular protein tyrosine phosphatase (mptpa) at 1.9a3 resolution
23	c3nhzA_	Alignment	not modelled	91.2	14	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**two component system transcriptional regulator mtra; **PDBTitle:** structure of n-terminal domain of mtra
24	c3rofA_	Alignment	not modelled	91.1	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**low molecular weight protein-tyrosine-phosphatase ptpa; **PDBTitle:** crystal structure of the s. aureus protein tyrosine phosphatase ptpa
25	d1tlla2	Alignment	not modelled	90.7	11	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Cytochrome p450 reductase N-terminal domain-like
26	c2cwdA_	Alignment	not modelled	90.6	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**low molecular weight phosphotyrosine protein phosphatase; **PDBTitle:** crystal structure of tt1001 protein from thermus thermophilus hb8
27	d1d1qa_	Alignment	not modelled	90.2	8	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
28	d2arka1	Alignment	not modelled	89.8	11	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins

						Family: WrbA-like
29	c1vmeB_	Alignment	not modelled	89.4	13	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**flavoprotein; **PDBTitle:** crystal structure of flavoprotein (tm0755) from thermotoga maritima at2 1.80 a resolution
30	d5pnta_	Alignment	not modelled	88.8	23	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
31	c3hlyA_	Alignment	not modelled	88.4	16	**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.
32	c2gi4A_	Alignment	not modelled	88.3	21	**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.
33	c2ohiB_	Alignment	not modelled	88.1	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
34	c1bvyF_	Alignment	not modelled	86.7	9	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**protein (cytochrome p450 bm-3); **PDBTitle:** complex of the heme and fmn-binding domains of the2 cytochrome p450(bm-3)
35	d1bvyf_	Alignment	not modelled	86.7	9	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
36	c2hnbA_	Alignment	not modelled	86.7	13	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**protein mioc; **PDBTitle:** solution structure of a bacterial holo-flavodoxin
37	c3fniA_	Alignment	not modelled	86.6	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
38	d2a5la1	Alignment	not modelled	85.9	14	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**WrbA-like
39	c3d7nA_	Alignment	not modelled	85.2	18	**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
40	d5nula_	Alignment	not modelled	83.7	20	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
41	c3he8A_	Alignment	not modelled	83.4	45	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase; **PDBTitle:** structural study of clostridium thermocellum ribose-5-phosphate2 isomerase b
42	d1b1ca_	Alignment	not modelled	83.3	8	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Cytochrome p450 reductase N-terminal domain-like
43	c3m1pA_	Alignment	not modelled	82.8	35	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose 5-phosphate isomerase; **PDBTitle:** structure of ribose 5-phosphate isomerase type b from trypanosoma2 cruzi, soaked with allose-6-phosphate
44	c3k7pA_	Alignment	not modelled	82.8	35	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose 5-phosphate isomerase; **PDBTitle:** structure of mutant of ribose 5-phosphate isomerase type b from2 trypanosoma cruzi.
45	d1ykga1	Alignment	not modelled	82.8	11	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Cytochrome p450 reductase N-terminal domain-like
46	d2vvpa1	Alignment	not modelled	82.5	30	**Fold:**Ribose/Galactose isomerase RpiB/AlsB **Superfamily:**Ribose/Galactose isomerase RpiB/AlsB **Family:**Ribose/Galactose isomerase RpiB/AlsB
47	c2wmyH_	Alignment	not modelled	82.2	24	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**putative acid phosphatase wzb; **PDBTitle:** crystal structure of the tyrosine phosphatase wzb from2 escherichia coli k30 in complex with sulphate.
48	d1ja1a2	Alignment	not modelled	82.1	7	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Cytochrome p450 reductase N-terminal domain-like
49	d1nn4a_	Alignment	not modelled	81.8	35	**Fold:**Ribose/Galactose isomerase RpiB/AlsB **Superfamily:**Ribose/Galactose isomerase RpiB/AlsB **Family:**Ribose/Galactose isomerase RpiB/AlsB
50	c3s5pA_	Alignment	not modelled	81.7	40	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose 5-phosphate isomerase; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase b rpib from giardia2 lamblia
51	c3edoA_	Alignment	not modelled	81.6	12	**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
52	c2fekA_	Alignment	not modelled	81.3	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**low molecular weight protein-tyrosine- **PDBTitle:** structure of a protein tyrosine phosphatase
53	d1iowa1	Alignment	not modelled	80.7	20	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**D-Alanine ligase N-terminal domain
						PDB header:flavoprotein

54	c3klbA_	Alignment	not modelled	78.0	15	**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
55	c2an1D_	Alignment	not modelled	77.7	16	**PDB header:**transferase **Chain:** D: **PDB Molecule:**putative kinase; **PDBTitle:** structural genomics, the crystal structure of a putative kinase from2 salmonella typhimurim lt2
56	c3hr4C_	Alignment	not modelled	77.2	9	**PDB header:**oxidoreductase/metal binding protein **Chain:** C: **PDB Molecule:**nitric oxide synthase, inducible; **PDBTitle:** human inos reductase and calmodulin complex
57	d1zh2a1	Alignment	not modelled	77.1	10	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
58	c3b6iB_	Alignment	not modelled	76.2	21	**PDB header:**flavoprotein **Chain:** B: **PDB Molecule:**flavoprotein wrba; **PDBTitle:** wrba from escherichia coli, native structure
59	c3orsD_	Alignment	not modelled	75.8	21	**PDB header:**isomerase,biosynthetic protein **Chain:** D: **PDB Molecule:**n5-carboxyaminoimidazole ribonucleotide mutase; **PDBTitle:** crystal structure of n5-carboxyaminoimidazole ribonucleotide mutase2 from staphylococcus aureus
60	c2ppwA_	Alignment	not modelled	75.0	25	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**conserved domain protein; **PDBTitle:** the crystal structure of uncharacterized ribose 5-phosphate isomerase2 rpib from streptococcus pneumoniae
61	d1s8na_	Alignment	not modelled	75.0	15	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
62	c3qd5B_	Alignment	not modelled	74.2	42	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative ribose-5-phosphate isomerase; **PDBTitle:** crystal structure of a putative ribose-5-phosphate isomerase from2 coccidioides immitis solved by combined iodide ion sad and mr
63	d2fcra_	Alignment	not modelled	74.0	11	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
64	d1czna_	Alignment	not modelled	73.8	15	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
65	c3onoA_	Alignment	not modelled	73.0	31	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose/galactose isomerase; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase lacab_rpib from2 vibrio parahaemolyticus
66	c1e5dA_	Alignment	not modelled	69.6	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**rubredoxin\:oxygen oxidoreductase; **PDBTitle:** rubredoxin oxygen:oxidoreductase (roo) from anaerobe2 desulfovibrio gigas
67	c2l18A_	Alignment	not modelled	69.3	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**arsenate reductase; **PDBTitle:** an arsenate reductase in the phosphate binding state
68	c2q9uB_	Alignment	not modelled	69.0	7	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**a-type flavoprotein; **PDBTitle:** crystal structure of the flavodiiron protein from giardia2 intestinalis
69	c2jjmH_	Alignment	not modelled	68.3	18	**PDB header:**transferase **Chain:** H: **PDB Molecule:**glycosyl transferase, group 1 family protein; **PDBTitle:** crystal structure of a family gt4 glycosyltransferase from2 bacillus anthracis orf ba1558.
70	c2wc1A_	Alignment	not modelled	68.1	14	**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
71	c1kh2D_	Alignment	not modelled	67.7	17	**PDB header:**ligase **Chain:** D: **PDB Molecule:**argininosuccinate synthetase; **PDBTitle:** crystal structure of thermus thermophilus hb82 argininosuccinate synthetase in complex with atp
72	d2fz5a1	Alignment	not modelled	67.5	13	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
73	d1jf8a_	Alignment	not modelled	67.2	11	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
74	d1yoba1	Alignment	not modelled	65.8	13	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
75	d1otha2	Alignment	not modelled	65.3	13	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
76	c3c5yD_	Alignment	not modelled	64.4	29	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**ribose/galactose isomerase; **PDBTitle:** crystal structure of a putative ribose 5-phosphate isomerase2 (saro_3514) from novosphingobium aromaticivorans dsm at 1.81 a3 resolution
77	c3tl6B_	Alignment	not modelled	64.3	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**purine nucleoside phosphorylase; **PDBTitle:** crystal structure of purine nucleoside phosphorylase from entamoeba2 histolytica
78	c1ychD_	Alignment	not modelled	64.1	9	**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
						Fold: Phosphorylase/hydrolase-like

79	d1vhwa_	Alignment	not modelled	63.8	16	**Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
80	d1y1la_	Alignment	not modelled	63.8	14	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
81	d1duvg2	Alignment	not modelled	61.8	15	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
82	d1mvoa_	Alignment	not modelled	61.5	16	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
83	d1o4va_	Alignment	not modelled	59.9	23	**Fold:**Flavodoxin-like **Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) **Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
84	d2eyqa5	Alignment	not modelled	59.6	8	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
85	c3lcmB_	Alignment	not modelled	59.6	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of smu.1420 from streptococcus mutans ua159
86	d1vlva2	Alignment	not modelled	58.8	15	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
87	d1dxha2	Alignment	not modelled	58.2	11	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
88	c3f6cB_	Alignment	not modelled	58.2	8	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**positive transcription regulator evga; **PDBTitle:** crystal structure of n-terminal domain of positive transcription2 regulator evga from escherichia coli
89	d1k9sa_	Alignment	not modelled	57.0	16	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
90	d2ac7a1	Alignment	not modelled	56.9	12	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
91	c2zkiH_	Alignment	not modelled	56.6	14	**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)
92	c3lp6D_	Alignment	not modelled	56.4	26	**PDB header:**lyase **Chain:** D: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase catalytic subunit; **PDBTitle:** crystal structure of rv3275c-e60a from mycobacterium tuberculosis at2 1.7a resolution
93	c1k97A_	Alignment	not modelled	56.3	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**argininosuccinate synthase; **PDBTitle:** crystal structure of e. coli argininosuccinate synthetase in complex2 with aspartate and citrulline
94	d1qcza_	Alignment	not modelled	55.8	26	**Fold:**Flavodoxin-like **Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) **Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
95	d1jl3a_	Alignment	not modelled	54.9	18	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
96	c3t38B_	Alignment	not modelled	54.8	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**arsenate reductase; **PDBTitle:** corynebacterium glutamicum thioredoxin-dependent arsenate reductase2 cg_arsc1'
97	d1rlia_	Alignment	not modelled	54.6	22	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Hypothetical protein YwqN
98	d1xhfa1	Alignment	not modelled	54.5	13	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
99	d1o1xa_	Alignment	not modelled	54.0	27	**Fold:**Ribose/Galactose isomerase RpiB/AlsB **Superfamily:**Ribose/Galactose isomerase RpiB/AlsB **Family:**Ribose/Galactose isomerase RpiB/AlsB
100	c2fw9A_	Alignment	not modelled	52.2	28	**PDB header:**lyase **Chain:** A: **PDB Molecule:**n5-carboxyaminoimidazole ribonucleotide mutase; **PDBTitle:** structure of pure (n5-carboxyaminoimidazole ribonucleotide mutase)2 h59f from the acidophilic bacterium acetobacter aceti, at ph 8
101	d1u11a_	Alignment	not modelled	52.1	28	**Fold:**Flavodoxin-like **Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) **Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
102	c1nvtA_	Alignment	not modelled	51.3	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**shikimate 5'-dehydrogenase; **PDBTitle:** crystal structure of shikimate dehydrogenase (aroe or2 mj1084) in complex with nadp+
103	d1odka_	Alignment	not modelled	51.2	16	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
						PDB header:structural genomics, unknown function

104	c1wv9B_	Alignment	not modelled	50.6	24	**Chain:** B: **PDB Molecule:**rhodanese homolog tt1651; **PDBTitle:** crystal structure of rhodanese homolog tt1651 from an2 extremely thermophilic bacterium thermus thermophilus hb8
105	c3cfyA_	Alignment	not modelled	50.5	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative luxo repressor protein; **PDBTitle:** crystal structure of signal receiver domain of putative luxo2 repressor protein from vibrio parahaemolyticus
106	c3eywA_	Alignment	not modelled	47.4	18	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**c-terminal domain of glutathione-regulated potassium-efflux **PDBTitle:** crystal structure of the c-terminal domain of e. coli kefc in complex2 with keff
107	c2w37A_	Alignment	not modelled	47.3	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase, catabolic; **PDBTitle:** crystal structure of the hexameric catabolic ornithine2 transcarbamylase from lactobacillus hilgardii
108	c1z34A_	Alignment	not modelled	46.9	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**purine nucleoside phosphorylase; **PDBTitle:** crystal structure of trichomonas vaginalis purine nucleoside2 phosphorylase complexed with 2-fluoro-2'-deoxyadenosine
109	d1a4ia1	Alignment	not modelled	45.1	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
110	d1nksa_	Alignment	not modelled	43.8	29	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
111	c1kgsA_	Alignment	not modelled	43.6	14	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna binding response regulator d; **PDBTitle:** crystal structure at 1.50 a of an ompr/phob homolog from thermotoga2 maritima
112	c3qpbB_	Alignment	not modelled	42.8	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**uridine phosphorylase; **PDBTitle:** crystal structure of streptococcus pyogenes uridine phosphorylase2 reveals a subclass of the np-i superfamily
113	c3updA_	Alignment	not modelled	42.6	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** 2.9 angstrom crystal structure of ornithine carbamoyltransferase2 (argf) from vibrio vulnificus
114	d1oboa_	Alignment	not modelled	42.5	11	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
115	c3rggD_	Alignment	not modelled	42.4	13	**PDB header:**lyase **Chain:** D: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase, pure protein; **PDBTitle:** crystal structure of treponema denticola pure bound to air
116	d1p8aa_	Alignment	not modelled	42.3	14	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
117	d1dl5a1	Alignment	not modelled	42.1	16	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Protein-L-isoaspartyl O-methyltransferase
118	d1kgsa2	Alignment	not modelled	42.1	14	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
119	d1rtta_	Alignment	not modelled	42.0	14	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**NADPH-dependent FMN reductase
120	c2otcA_	Alignment	not modelled	41.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** ornithine transcarbamoylase complexed with n-2 (phosphonacetyl)-l-ornithine