Phyre2

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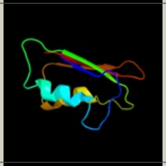
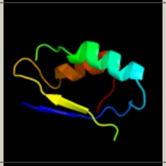
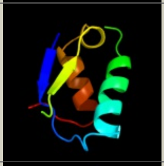
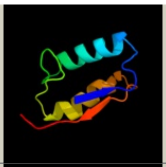
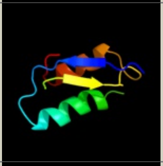
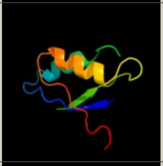
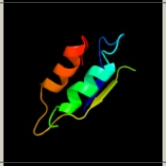
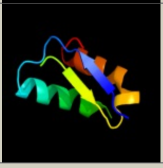
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1jdqa_	Alignment		99.9	34	**Fold:**IF3-like **Superfamily:**SirA-like **Family:**SirA-like
2	d1je3a_	Alignment		99.8	31	**Fold:**IF3-like **Superfamily:**SirA-like **Family:**SirA-like
3	d1dcja_	Alignment		99.8	23	**Fold:**IF3-like **Superfamily:**SirA-like **Family:**SirA-like
4	c3hz7A_	Alignment		99.8	27	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the sira-like protein (dsy4693) from2 desulfitobacterium hafniense, northeast structural genomics3 consortium target dhr2a
5	d1pava_	Alignment		99.8	19	**Fold:**IF3-like **Superfamily:**SirA-like **Family:**SirA-like
6	c1yg0A_	Alignment		94.8	19	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**cop associated protein; **PDBTitle:** solution structure of apo-copp from helicobacter pylori
7	d1cc8a_	Alignment		92.8	13	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
8	d1p6ta1	Alignment		89.4	16	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
9	d2qifa1	Alignment		89.4	19	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
10	c2ofhX_	Alignment		88.9	16	**PDB header:**hydrolase, membrane protein **Chain:** X: **PDB Molecule:**zinc-transporting atpase; **PDBTitle:** solution structure of the n-terminal domain of the zinc(ii) atpase2 ziaa in its apo form
11	c2kt2A_	Alignment		88.4	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**mercuric reductase; **PDBTitle:** structure of nmera, the n-terminal hma domain of tn501 mercuric2 reductase

12	c1y3kA_	Alignment		88.0	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 1; **PDBTitle:** solution structure of the apo form of the fifth domain of2 menkes protein
13	c2ldiA_	Alignment		87.8	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**zinc-transporting atpase; **PDBTitle:** nmr solution structure of ziaan sub mutant
14	c2l3mA_	Alignment		87.8	14	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**copper-ion-binding protein; **PDBTitle:** solution structure of the putative copper-ion-binding protein from2 bacillus anthracis str. ames
15	d1kvja_	Alignment		87.6	10	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
16	d2d9ia1	Alignment		85.2	14	**Fold:**IF3-like **Superfamily:**SMR domain-like **Family:**Smr domain
17	d1p6ta2	Alignment		84.3	10	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
18	c2kyzA_	Alignment		83.9	19	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**heavy metal binding protein; **PDBTitle:** nmr structure of heavy metal binding protein tm0320 from thermotoga2 maritima
19	c2gcfA_	Alignment		81.9	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cation-transporting atpase pacs; **PDBTitle:** solution structure of the n-terminal domain of the coppper(i) atpase2 pacs in its apo form
20	d1mwza_	Alignment		81.0	11	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
21	c1yjrA_	Alignment	not modelled	80.2	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 1; **PDBTitle:** solution structure of the apo form of the sixth soluble2 domain a69p mutant of menkes protein
22	d1sb6a_	Alignment	not modelled	80.0	18	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
23	d1q8la_	Alignment	not modelled	79.1	14	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
24	d2ggpb1	Alignment	not modelled	78.2	15	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
25	d2aw0a_	Alignment	not modelled	77.0	8	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
26	c3dxsX_	Alignment	not modelled	76.5	18	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**copper-transporting atpase ran1; **PDBTitle:** crystal structure of a copper binding domain from hma7, a p-2 type atpase
27	d1cpza_	Alignment	not modelled	75.0	18	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
28	c2vkcA_	Alignment	not modelled	73.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nedd4-binding protein 2; **PDBTitle:** solution structure of the b3bp smr domain
29	d1s6ua_	Alignment	not modelled	69.9	15	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain

						Family:HMA, heavy metal-associated domain
30	d1osda_	Alignment	not modelled	68.6	20	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
31	c2kkhA_	Alignment	not modelled	68.5	17	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**putative heavy metal transporter; **PDBTitle:** structure of the zinc binding domain of the atpase hma4
32	c3qwuA_	Alignment	not modelled	68.2	12	**PDB header:**ligase **Chain:** A: **PDB Molecule:**dna ligase; **PDBTitle:** putative atp-dependent dna ligase from aquifex aeolicus.
33	d1afia_	Alignment	not modelled	67.3	28	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
34	c2k2pA_	Alignment	not modelled	63.0	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu1203; **PDBTitle:** solution nmr structure of protein atu1203 from agrobacterium2 tumefaciens. northeast structural genomics consortium (nesg) target3 att10, ontario center for structural proteomics target atc1183
35	c2zqeA_	Alignment	not modelled	62.2	16	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**muts2 protein; **PDBTitle:** crystal structure of the smr domain of thermus thermophilus muts2
36	c2rogA_	Alignment	not modelled	61.5	22	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**heavy metal binding protein; **PDBTitle:** solution structure of thermus thermophilus hb8 ttha17182 protein in living e. coli cells
37	c3q87B_	Alignment	not modelled	51.0	7	**PDB header:**transferase activator/transferase **Chain:** B: **PDB Molecule:**n6 adenine specific dna methylase; **PDBTitle:** structure of eukaryotic translation termination complex2 methyltransferase mtq2-trm112
38	c3grzA_	Alignment	not modelled	46.9	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribosomal protein l11 methyltransferase; **PDBTitle:** crystal structure of ribosomal protein l11 methylase from2 lactobacillus delbrueckii subsp. bulgaricus
39	c2aivA_	Alignment	not modelled	41.8	9	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**fragment of nucleoporin nup116/nsp116; **PDBTitle:** multiple conformations in the ligand-binding site of the2 yeast nuclear pore targeting domain of nup116p
40	c3ntaA_	Alignment	not modelled	41.4	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fad-dependent pyridine nucleotide-disulphide **PDBTitle:** structure of the shewanella loihica pv-4 nadh-dependent persulfide2 reductase
41	c3dlcA_	Alignment	not modelled	38.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative s-adenosyl-l-methionine-dependent **PDBTitle:** crystal structure of a putative s-adenosyl-l-methionine-dependent2 methyltransferase (mmp1179) from methanococcus maripaludis at 1.15 a3 resolution
42	c2ga7A_	Alignment	not modelled	36.0	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 1; **PDBTitle:** solution structure of the copper(i) form of the third metal-2 binding domain of atp7a protein (menkes disease protein)
43	c3nf5A_	Alignment	not modelled	34.4	9	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**nucleoporin nup116; **PDBTitle:** crystal structure of the c-terminal domain of nuclear pore complex2 component nup116 from candida glabrata
44	c1ko6A_	Alignment	not modelled	33.6	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nuclear pore complex protein nup98; **PDBTitle:** crystal structure of c-terminal autoproteolytic domain of2 nucleoporin nup98
45	d1jvaa3	Alignment	not modelled	31.0	13	**Fold:**Homing endonuclease-like **Superfamily:**Homing endonucleases **Family:**Intein endonuclease
46	c3fryB_	Alignment	not modelled	30.8	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable copper-exporting p-type atpase a; **PDBTitle:** crystal structure of the copa c-terminal metal binding domain
47	c2q5xA_	Alignment	not modelled	30.0	14	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**nuclear pore complex protein nup98; **PDBTitle:** crystal structure of the c-terminal domain of hnup98
48	c3icrA_	Alignment	not modelled	28.0	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**coenzyme a-disulfide reductase; **PDBTitle:** crystal structure of oxidized bacillus anthracis coadr-rhd
49	c2kngA_	Alignment	not modelled	27.2	32	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**protein lsr2; **PDBTitle:** solution structure of c-domain of lsr2
50	c3dh0B_	Alignment	not modelled	26.9	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sam dependent methyltransferase; **PDBTitle:** crystal structure of a sam dependent methyltransferase from2 aquifex aeolicus
51	c2rmlA_	Alignment	not modelled	26.3	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting p-type atpase copa; **PDBTitle:** solution structure of the n-terminal soluble domains of2 bacillus subtilis copa
52	d2nxca1	Alignment	not modelled	26.1	11	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Ribosomal protein L11 methyltransferase PrmA
53	c2ropA_	Alignment	not modelled	25.6	5	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 2; **PDBTitle:** solution structure of domains 3 and 4 of human atp7b
54	c2ip2B_	Alignment	not modelled	24.4	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**probable phenazine-specific

		Alignment				methyltransferase; **PDBTitle:** structure of the pyocyanin biosynthetic protein phzm
55	c3kepA_	Alignment	not modelled	24.3	12	**PDB header:**protein transport, rna binding protein **Chain:** A: **PDB Molecule:**nucleoporin nup145; **PDBTitle:** crystal structure of the autoproteolytic domain from the2 nuclear pore complex component nup145 from saccharomyces3 cerevisiae
56	c2ziuA_	Alignment	not modelled	23.8	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mus81 protein; **PDBTitle:** crystal structure of the mus81-eme1 complex
57	d1fe0a_	Alignment	not modelled	22.2	9	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
58	c3e05B_	Alignment	not modelled	20.0	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**precorrin-6y c5,15-methyltransferase (decarboxylating); **PDBTitle:** crystal structure of precorrin-6y c5,15-methyltransferase from2 geobacter metallireducens gs-15
59	d2cc0a1	Alignment	not modelled	19.9	18	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**NodB-like polysaccharide deacetylase
60	c2c1iA_	Alignment	not modelled	18.6	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidoglycan glcnac deacetylase; **PDBTitle:** structure of streptococcus pnemoniae peptidoglycan2 deacetylase (sppgda) d 275 n mutant.
61	d1l3ia_	Alignment	not modelled	18.3	5	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Precorrin-6Y methyltransferase (CbiT)
62	d2obba1	Alignment	not modelled	18.1	9	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**BT0820-like
63	c3c5yD_	Alignment	not modelled	18.0	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
64	c2pwyB_	Alignment	not modelled	17.6	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**trna (adenine-n(1)-)-methyltransferase; **PDBTitle:** crystal structure of a m1a58 trna methyltransferase
65	c3cg6A_	Alignment	not modelled	17.5	16	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**growth arrest and dna-damage-inducible 45 gamma; **PDBTitle:** crystal structure of gadd45 gamma
66	d1qupa2	Alignment	not modelled	17.3	17	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
67	c3gwzB_	Alignment	not modelled	16.4	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**mmcr; **PDBTitle:** structure of the mitomycin 7-o-methyltransferase mmcr
68	c2ew9A_	Alignment	not modelled	16.4	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 2; **PDBTitle:** solution structure of apowln5-6
69	c2aj1A_	Alignment	not modelled	16.3	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable cadmium-transporting atpase; **PDBTitle:** solution structure of apocada
70	d1wj4a_	Alignment	not modelled	15.0	14	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**UBX domain
71	c3d00A_	Alignment	not modelled	14.7	14	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**tungsten formylmethanofuran dehydrogenase subunit e; **PDBTitle:** crystal structure of a tungsten formylmethanofuran dehydrogenase2 subunit e (fmde)-like protein (syn_00638) from syntrophus3 aciditrophicus at 1.90 a resolution
72	d1a8pa2	Alignment	not modelled	14.7	9	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
73	d1j23a_	Alignment	not modelled	14.4	8	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**XPF/Rad1/Mus81 nuclease
74	c3p9kD_	Alignment	not modelled	14.3	21	**PDB header:**transferase **Chain:** D: **PDB Molecule:**caffeic acid o-methyltransferase; **PDBTitle:** crystal structure of perennial ryegrass lpomt1 complexed with s-2 adenosyl-l-homocysteine and coniferaldehyde
75	d2b3ta1	Alignment	not modelled	13.9	19	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**N5-glutamine methyltransferase, HemK
76	c1kyzC_	Alignment	not modelled	13.9	9	**PDB header:**transferase **Chain:** C: **PDB Molecule:**caffeic acid 3-o-methyltransferase; **PDBTitle:** crystal structure analysis of caffeic acid/5-hydroxyferulic2 acid 3/5-o-methyltransferase ferulic acid complex
77	c3e8sA_	Alignment	not modelled	13.6	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative sam dependent methyltransferase; **PDBTitle:** crystal structure of putative sam dependent methyltransferase in2 complex with sah (np_744700.1) from pseudomonas putida kt2440 at 2.103 a resolution
78	d1h8ca_	Alignment	not modelled	13.6	21	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**UBX domain
						PDB header:protein/rna complex

79	c2eseA_	Alignment	not modelled	13.5	16	**Chain:** A: **PDB Molecule:**vts1p; **PDBTitle:** structure of the sam domain of vts1p in complex with rna
80	d2c1ia1	Alignment	not modelled	13.1	8	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**NodB-like polysaccharide deacetylase
81	c3lteH_	Alignment	not modelled	13.0	9	**PDB header:**transcription **Chain:** H: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator (signal receiver domain) from2 bermanella marisrubri
82	d1ny1a_	Alignment	not modelled	12.9	8	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**NodB-like polysaccharide deacetylase
83	c3njrB_	Alignment	not modelled	12.5	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**precorrin-6y methylase; **PDBTitle:** crystal structure of c-terminal domain of precorrin-6y c5,15-2 methyltransferase from rhodobacter capsulatus
84	c3fpnB_	Alignment	not modelled	12.4	5	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**geobacillus stearothermophilus uvrb interaction **PDBTitle:** crystal structure of uvra-uvrb interaction domains
85	d2j13a1	Alignment	not modelled	12.0	17	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**NodB-like polysaccharide deacetylase
86	c2b6gA_	Alignment	not modelled	11.8	17	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**vts1p; **PDBTitle:** rna recognition by the vts1 sam domain
87	d1dusa_	Alignment	not modelled	11.4	8	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Hypothetical protein MJ0882
88	d1o54a_	Alignment	not modelled	11.1	9	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**tRNA(1-methyladenosine) methyltransferase-like
89	d2naca2	Alignment	not modelled	11.1	15	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**Formate/glycerate dehydrogenases, substrate-binding domain
90	d2bgwa2	Alignment	not modelled	10.9	12	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**XPF/Rad1/Mus81 nuclease
91	c3onoA_	Alignment	not modelled	10.5	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose/galactose isomerase; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase lacab_rpib from2 vibrio parahaemolyticus
92	c2ppwA_	Alignment	not modelled	10.5	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**conserved domain protein; **PDBTitle:** the crystal structure of uncharacterized ribose 5-phosphate isomerase2 rpib from streptococcus pneumoniae
93	d1jg5a_	Alignment	not modelled	10.4	8	**Fold:**GTP cyclohydrolase I feedback regulatory protein, GFRP **Superfamily:**GTP cyclohydrolase I feedback regulatory protein, GFRP **Family:**GTP cyclohydrolase I feedback regulatory protein, GFRP
94	c3mtiA_	Alignment	not modelled	10.2	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rrna methylase; **PDBTitle:** the crystal structure of a rrna methylase from streptococcus2 thermophilus to 1.95a
95	d2cr5a1	Alignment	not modelled	10.1	17	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**UBX domain
96	d2b2na1	Alignment	not modelled	9.6	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
97	c3hm2G_	Alignment	not modelled	9.6	20	**PDB header:**transferase **Chain:** G: **PDB Molecule:**precorrin-6y c5,15-methyltransferase; **PDBTitle:** crystal structure of putative precorrin-6y c5,15-2 methyltransferase targeted domain from corynebacterium3 diphtheriae
98	c3id5F_	Alignment	not modelled	9.5	7	**PDB header:**transferase/ribosomal protein/rna **Chain:** F: **PDB Molecule:**fibrillarin-like rrna/trna 2'-o-methyltransferase; **PDBTitle:** crystal structure of sulfolobus solfataricus c/d rnp assembled with2 nop5, fibrillarin, l7ae and a split half c/d rna
99	c2kyrA_	Alignment	not modelled	9.5	25	**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