Phyre^2

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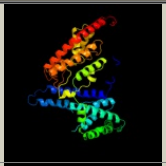
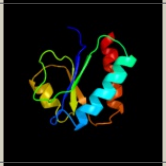
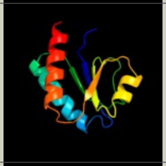
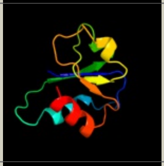
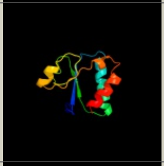
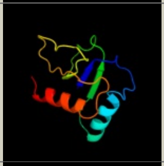
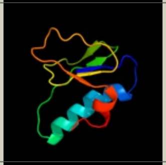
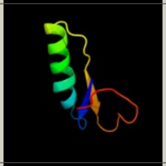
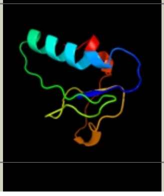
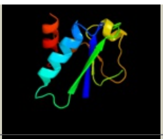
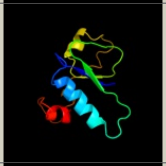
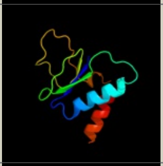
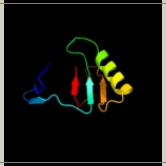
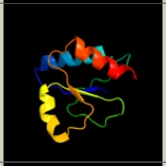
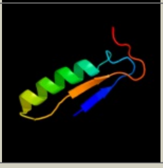
Description	P69826
Date	Thu Jan 5 12:12:09 GMT 2012
Unique Job ID	686b397af55d4a6d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3qnqD_	Alignment		100.0	12	**PDB header:**membrane protein, transport protein **Chain:** D: **PDB Molecule:**pts system, cellobiose-specific iic component; **PDBTitle:** crystal structure of the transporter chbc, the iic component from the2 n,n'-diacetylchitobiose-specific phosphotransferase system
2	d1vkra_	Alignment		99.8	42	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Lactose/Cellobiose specific IIB subunit
3	c1vkrA_	Alignment		99.8	42	**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
4	c3czcA_	Alignment		99.5	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rmpb; **PDBTitle:** the crystal structure of a putative pts iib(ptxb) from2 streptococcus mutans
5	c1tvmA_	Alignment		98.9	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
6	d1iiba_	Alignment		98.0	20	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Lactose/Cellobiose specific IIB subunit
7	c2kyrA_	Alignment		97.9	14	**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
8	c2l2qA_	Alignment		97.4	22	**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	d2r48a1	Alignment		97.2	21	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Fructose specific IIB subunit-like
10	c3nbmA_	Alignment		97.1	10	**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.
11	d2r4qa1	Alignment		96.8	19	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Fructose specific IIB subunit-like

12	c3rofA_	Alignment		96.5	24	**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
13	c2gi4A_	Alignment		96.4	24	**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.
14	c3jviA_	Alignment		96.2	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein tyrosine phosphatase; **PDBTitle:** product state mimic crystal structure of protein tyrosine phosphatase2 from entamoeba histolytica
15	c2cwdA_	Alignment		96.0	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**low molecular weight phosphotyrosine protein phosphatase; **PDBTitle:** crystal structure of tt1001 protein from thermus thermophilus hb8
16	d1d1qa_	Alignment		95.1	24	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
17	c1u2pA_	Alignment		94.6	30	**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
18	d1x9ia_	Alignment		94.5	15	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**double-SIS domain
19	c3sqnB_	Alignment		94.5	13	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**conserved domain protein; **PDBTitle:** putative mga family transcriptional regulator from enterococcus2 faecalis
20	c1zggA_	Alignment		94.5	27	**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
21	d5pnta_	Alignment	not modelled	92.4	24	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
22	d1y1la_	Alignment	not modelled	91.4	23	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
23	d1dg9a_	Alignment	not modelled	91.4	23	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
24	c2l18A_	Alignment	not modelled	90.4	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**arsenate reductase; **PDBTitle:** an arsenate reductase in the phosphate binding state
25	c3b9yA_	Alignment	not modelled	89.3	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**ammonium transporter family rh-like protein; **PDBTitle:** crystal structure of the nitrosomonas europaea rh protein
26	c1y80A_	Alignment	not modelled	88.9	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**predicted cobalamin binding protein; **PDBTitle:** structure of a corrinoid (factor iiim)-binding protein from2 moorella thermoacetica
27	c2wmyH_	Alignment	not modelled	88.6	17	**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.
28	c3c3jA_	Alignment	not modelled	88.4	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative tagatose-6-phosphate ketose/aldose isomerase; **PDBTitle:** crystal structure of tagatose-6-phosphate ketose/aldose isomerase from2 escherichia coli
						PDB header:sugar binding protein

29	c2a3nA_	Alignment	not modelled	88.1	15	**Chain:** A: **PDB Molecule:**putative glucosamine-fructose-6-phosphate aminotransferase; **PDBTitle:** crystal structure of a putative glucosamine-fructose-6-phosphate2 aminotransferase (stm4540.s) from salmonella typhimurium lt2 at 1.353 a resolution
30	d1jf8a_	Alignment	not modelled	87.7	15	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
31	c3g68A_	Alignment	not modelled	87.4	10	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative phosphosugar isomerase; **PDBTitle:** crystal structure of a putative phosphosugar isomerase (cd3275) from2 clostridium difficile 630 at 1.80 a resolution
32	c3tbfA_	Alignment	not modelled	86.9	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glucosamine--fructose-6-phosphate aminotransferase **PDBTitle:** c-terminal domain of glucosamine-fructose-6-phosphate aminotransferase2 from francisella tularensis.
33	c3i0zB_	Alignment	not modelled	85.9	16	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative tagatose-6-phosphate ketose/aldose isomerase; **PDBTitle:** crystal structure of putative putative tagatose-6-phosphate2 ketose/aldose isomerase (np_344614.1) from streptococcus pneumoniae3 tigr4 at 1.70 a resolution
34	c2amlB_	Alignment	not modelled	83.7	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sis domain protein; **PDBTitle:** crystal structure of lmo0035 protein (46906266) from listeria2 monocytogenes 4b f2365 at 1.50 a resolution
35	d1jl3a_	Alignment	not modelled	82.6	17	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
36	c3odpA_	Alignment	not modelled	82.0	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative tagatose-6-phosphate ketose/aldose isomerase; **PDBTitle:** crystal structure of a putative tagatose-6-phosphate ketose/aldose2 isomerase (nt01cx_0292) from clostridium novyi nt at 2.35 a3 resolution
37	c1jxaA_	Alignment	not modelled	77.5	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glucosamine 6-phosphate synthase; **PDBTitle:** glucosamine 6-phosphate synthase with glucose 6-phosphate
38	d1moqa_	Alignment	not modelled	77.5	16	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**double-SIS domain
39	d1r9ja3	Alignment	not modelled	76.9	16	**Fold:**TK C-terminal domain-like **Superfamily:**TK C-terminal domain-like **Family:**Transketolase C-terminal domain-like
40	d1vima_	Alignment	not modelled	74.4	19	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
41	c3b3jA_	Alignment	not modelled	73.3	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histone-arginine methyltransferase carm1; **PDBTitle:** the 2.55 a crystal structure of the apo catalytic domain of2 coactivator-associated arginine methyl transferase i(carm1:28-507,3 residues 28-146 and 479-507 not ordered)
42	c3fj1A_	Alignment	not modelled	73.1	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative phosphosugar isomerase; **PDBTitle:** crystal structure of putative phosphosugar isomerase (yp_167080.1)2 from silicibacter pomeroyi dss-3 at 1.75 a resolution
43	c2zj3A_	Alignment	not modelled	72.4	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glucosamine--fructose-6-phosphate **PDBTitle:** isomerase domain of human glucose:fructose-6-phosphate2 amidotransferase
44	c3euaD_	Alignment	not modelled	71.8	12	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**putative fructose-aminoacid-6-phosphate deglycase; **PDBTitle:** crystal structure of a putative phosphosugar isomerase (bsu32610) from2 bacillus subtilis at 1.90 a resolution
45	c2decA_	Alignment	not modelled	71.7	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**325aa long hypothetical protein; **PDBTitle:** crystal structure of the ph0510 protein from pyrococcus horikoshii ot3
46	d1gpra_	Alignment	not modelled	70.5	12	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Glucose permease-like
47	d1glaf_	Alignment	not modelled	68.9	18	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Glucose permease-like
48	d1ccwa_	Alignment	not modelled	65.0	14	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
49	d1p8aa_	Alignment	not modelled	65.0	20	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
50	c3knzA_	Alignment	not modelled	61.9	20	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**putative sugar binding protein; **PDBTitle:** crystal structure of putative sugar binding protein (np_459565.1) from2 salmonella typhimurium lt2 at 2.50 a resolution
51	d2gpra_	Alignment	not modelled	60.9	19	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Glucose permease-like
52	c3fkjA_	Alignment	not modelled	60.4	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative phosphosugar isomerases;

52	c3fkjA_	Alignment	not modelled	60.4	18	**PDBTitle:** crystal structure of a putative phosphosugar isomerase (stm_0572) from2 salmonella typhimurium lt2 at 2.12 a resolution
53	c2fekA_	Alignment	not modelled	60.3	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**low molecular weight protein-tyrosine- **PDBTitle:** structure of a protein tyrosine phosphatase
54	c2xhzC_	Alignment	not modelled	57.8	16	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**arabinose 5-phosphate isomerase; **PDBTitle:** probing the active site of the sugar isomerase domain from e. coli2 arabinose-5-phosphate isomerase via x-ray crystallography
55	c2e6kB_	Alignment	not modelled	57.8	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**transketolase; **PDBTitle:** x-ray structure of thermus thermopilus hb8 tt0505
56	d2f3ga_	Alignment	not modelled	57.2	17	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Glucose permease-like
57	d1ycga1	Alignment	not modelled	56.6	16	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
58	c3etnD_	Alignment	not modelled	54.9	15	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**putative phosphosugar isomerase involved in capsule **PDBTitle:** crystal structure of putative phosphosugar isomerase involved in2 capsule formation (yp_209877.1) from bacteroides fragilis nctc 93433 at 1.70 a resolution
59	c2an1D_	Alignment	not modelled	53.6	18	**PDB header:**transferase **Chain:** D: **PDB Molecule:**putative kinase; **PDBTitle:** structural genomics, the crystal structure of a putative kinase from2 salmonella typhimurim lt2
60	d1otha2	Alignment	not modelled	49.0	8	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
61	c2otcA_	Alignment	not modelled	48.9	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** ornithine transcarbamoylase complexed with n-2 (phosphonacetyl)-l-ornithine
62	c2v7eB_	Alignment	not modelled	48.6	24	**PDB header:**transferase **Chain:** B: **PDB Molecule:**histone-arginine methyltransferase carm1; **PDBTitle:** crystal structure of coactivator-associated arginine2 methyltransferase 1 (carm1), unliganded
63	d1pvva2	Alignment	not modelled	47.1	16	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
64	d1jkea_	Alignment	not modelled	46.4	9	**Fold:**DTD-like **Superfamily:**DTD-like **Family:**DTD-like
65	c2kncA_	Alignment	not modelled	45.9	18	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
66	d3bula2	Alignment	not modelled	45.7	11	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
67	d1g6q1_	Alignment	not modelled	44.3	22	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Arginine methyltransferase
68	c2puwA_	Alignment	not modelled	44.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**isomerase domain of glutamine-fructose-6-phosphate **PDBTitle:** the crystal structure of isomerase domain of glucosamine-6-phosphate2 synthase from candida albicans
69	d1j5xa_	Alignment	not modelled	43.8	13	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**double-SIS domain
70	d1yb3a1	Alignment	not modelled	43.8	12	**Fold:**YktB/PF0168-like **Superfamily:**YktB/PF0168-like **Family:**PF0168-like
71	c1wv9B_	Alignment	not modelled	43.0	22	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**rhodanese homolog tt1651; **PDBTitle:** crystal structure of rhodanese homolog tt1651 from an2 extremely thermophilic bacterium thermus thermophilus hb8
72	d1m3sa_	Alignment	not modelled	42.7	19	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
73	c2w37A_	Alignment	not modelled	42.2	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase, catabolic; **PDBTitle:** crystal structure of the hexameric catabolic ornithine2 transcarbamylase from lactobacillus hilgardii
74	d1vlva2	Alignment	not modelled	40.5	12	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
75	d2naca2	Alignment	not modelled	40.3	31	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**Formate/glycerate dehydrogenases, substrate-binding domain
76	d1duvg2	Alignment	not modelled	39.5	18	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
77	c3ko7E_	Alignment	not modelled	39.1	8	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**d-tyrosyl-trna(tyr) deacylase;

77	c3k07E_	Alignment	not modelled	39.1	8	**PDBTitle:** dtd from plasmodium falciparum in complex with d-lysine
78	c1fvoB_	Alignment	not modelled	38.9	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ornithine transcarbamylase; **PDBTitle:** crystal structure of human ornithine transcarbamylase complexed with2 carbamoyl phosphate
79	c3q98A_	Alignment	not modelled	38.5	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transcarbamylase; **PDBTitle:** structure of ygew encoded protein from e. coli
80	c3shoA_	Alignment	not modelled	38.0	18	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, rpir family; **PDBTitle:** crystal structure of rpir transcription factor from sphaerobacter2 thermophilus (sugar isomerase domain)
81	c3hd6A_	Alignment	not modelled	38.0	14	**PDB header:**membrane protein, transport protein **Chain:** A: **PDB Molecule:**ammonium transporter rh type c; **PDBTitle:** crystal structure of the human rhesus glycoprotein rhcg
82	d1dxha2	Alignment	not modelled	36.6	12	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
83	d1yt8a4	Alignment	not modelled	36.6	22	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
84	c2kncB_	Alignment	not modelled	35.1	17	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**integrin beta-3; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
85	c1vlvA_	Alignment	not modelled	34.9	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of ornithine carbamoyltransferase (tm1097) from2 thermotoga maritima at 2.25 a resolution
86	c1ortD_	Alignment	not modelled	33.5	12	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ornithine transcarbamoylase; **PDBTitle:** ornithine transcarbamoylase from pseudomonas aeruginosa
87	c2pv7B_	Alignment	not modelled	32.5	27	**PDB header:**isomerase, oxidoreductase **Chain:** B: **PDB Molecule:**t-protein [includes: chorismate mutase (ec 5.4.99.5) (cm) **PDBTitle:** crystal structure of chorismate mutase / prephenate dehydrogenase2 (tyra) (1574749) from haemophilus influenzae rd at 2.00 a resolution
88	c3fxaA_	Alignment	not modelled	32.2	15	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**sis domain protein; **PDBTitle:** crystal structure of a putative sugar-phosphate isomerase2 (lmof2365_0531) from listeria monocytogenes str. 4b f2365 at 1.60 a3 resolution
89	c3updA_	Alignment	not modelled	31.0	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** 2.9 angstrom crystal structure of ornithine carbamoyltransferase2 (argf) from vibrio vulnificus
90	c2okvC_	Alignment	not modelled	30.8	9	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**probable d-tyrosyl-trna(tyr) deacylase 1; **PDBTitle:** c-myc dna unwinding element binding protein
91	d1jeoa_	Alignment	not modelled	30.8	21	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
92	c2dboA_	Alignment	not modelled	30.0	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**d-tyrosyl-trna(tyr) deacylase; **PDBTitle:** crystal structure of d-tyr-trna(tyr) deacylase from aquifex aeolicus
93	c2yybA_	Alignment	not modelled	28.8	41	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ttha1606; **PDBTitle:** crystal structure of ttha1606 from thermus thermophilus hb8
94	c2hnbA_	Alignment	not modelled	27.9	26	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**protein mioc; **PDBTitle:** solution structure of a bacterial holo-flavodoxin
95	d1gpua3	Alignment	not modelled	27.5	14	**Fold:**TK C-terminal domain-like **Superfamily:**TK C-terminal domain-like **Family:**Transketolase C-terminal domain-like
96	d1j7ga_	Alignment	not modelled	26.7	4	**Fold:**DTD-like **Superfamily:**DTD-like **Family:**DTD-like
97	d1okga2	Alignment	not modelled	26.3	5	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
98	d2fyta1	Alignment	not modelled	26.2	18	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Arginine methyltransferase
99	c2o7jA_	Alignment	not modelled	26.0	7	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**oligopeptide abc transporter, periplasmic **PDBTitle:** the x-ray crystal structure of a thermophilic cellobiose2 binding protein bound with cellopentaose
100	d1vmea1	Alignment	not modelled	25.5	16	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
101	d1ml4a2	Alignment	not modelled	25.2	8	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
102	d2gk3a1	Alignment	not modelled	25.0	38	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**STM3548-like
						PDB header:transport protein

103	c3lvuB_	Alignment	not modelled	24.9	14	**Chain:** B: **PDB Molecule:**abc transporter, periplasmic substrate-binding protein; **PDBTitle:** crystal structure of abc transporter, periplasmic substrate-binding2 protein spo2066 from silicibacter pomeroyi
104	c3t38B_	Alignment	not modelled	24.5	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**arsenate reductase; **PDBTitle:** corynebacterium glutamicum thioredoxin-dependent arsenate reductase2 cg_arsc1'
105	d1wy7a1	Alignment	not modelled	24.1	12	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Ta1320-like
106	c2ohiB_	Alignment	not modelled	24.1	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
107	d1e5da1	Alignment	not modelled	23.7	13	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
108	c1ml4A_	Alignment	not modelled	23.5	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aspartate transcarbamoylase; **PDBTitle:** the pala-liganded aspartate transcarbamoylase catalytic subunit from2 pyrococcus abyssi
109	d1f3la_	Alignment	not modelled	22.7	18	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Arginine methyltransferase
110	c3eshB_	Alignment	not modelled	22.2	32	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein similar to metal-dependent hydrolase; **PDBTitle:** crystal structure of a probable metal-dependent hydrolase2 from staphylococcus aureus. northeast structural genomics3 target zr314
111	d2oara1	Alignment	not modelled	22.2	12	**Fold:**Gated mechanosensitive channel **Superfamily:**Gated mechanosensitive channel **Family:**Gated mechanosensitive channel
112	c3s3lB_	Alignment	not modelled	22.0	24	**PDB header:**transferase **Chain:** B: **PDB Molecule:**cerj; **PDBTitle:** crystal structure of cerj from streptomyces tendae
113	d7reqa2	Alignment	not modelled	21.9	13	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
114	d1ekxa2	Alignment	not modelled	20.7	19	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase