Phyre^2

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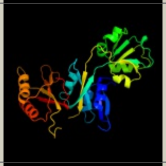
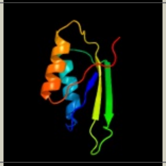
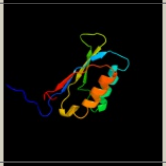
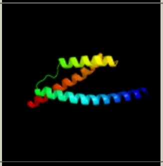
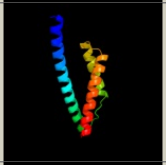
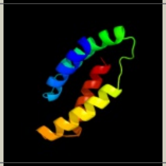
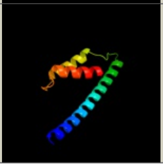
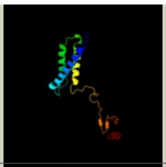
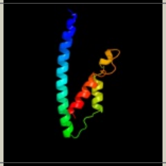
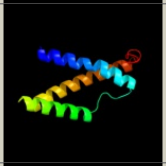
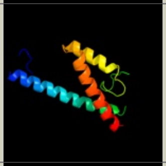
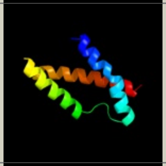
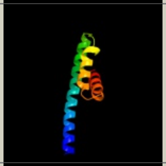
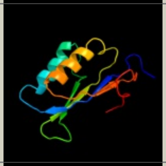
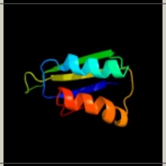
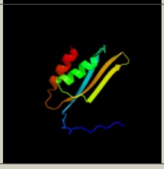
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3mwbA_	Alignment		100.0	25	**PDB header:**lyase **Chain:** A: **PDB Molecule:**prephenate dehydratase; **PDBTitle:** the crystal structure of prephenate dehydratase in complex with l-phe2 from arthrobacter aurescens to 2.0a
2	c2qmxB_	Alignment		100.0	33	**PDB header:**ligase **Chain:** B: **PDB Molecule:**prephenate dehydratase; **PDBTitle:** the crystal structure of l-phe inhibited prephenate dehydratase from2 chlorobium tepidum tls
3	c3luyA_	Alignment		100.0	23	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**probable chorismate mutase; **PDBTitle:** putative chorismate mutase from bifidobacterium adolescentis
4	c2qmwA_	Alignment		100.0	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**prephenate dehydratase; **PDBTitle:** the crystal structure of the prephenate dehydratase (pdt) from2 staphylococcus aureus subsp. aureus mu50
5	d2qmwa1	Alignment		100.0	28	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
6	d2qmwa2	Alignment		99.9	17	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Phenylalanine metabolism regulatory domain
7	d1phza1	Alignment		99.9	20	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Phenylalanine metabolism regulatory domain
8	c3rmiA_	Alignment		99.8	26	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**chorismate mutase protein; **PDBTitle:** crystal structure of chorismate mutase from bartonella henselae str.2 houston-1 in complex with malate
9	d1ecma_	Alignment		99.8	100	**Fold:**Chorismate mutase II **Superfamily:**Chorismate mutase II **Family:**Dimeric chorismate mutase
10	d2gtvx1	Alignment		99.8	34	**Fold:**Chorismate mutase II **Superfamily:**Chorismate mutase II **Family:**monomeric chorismate mutase
11	d2d8da1	Alignment		99.8	28	**Fold:**Chorismate mutase II **Superfamily:**Chorismate mutase II **Family:**Dimeric chorismate mutase

12	c3nvtA_	Alignment		99.7	25	**PDB header:**transferase/isomerase **Chain:** A: **PDB Molecule:**3-deoxy-d-arabino-heptulosonate 7-phosphate synthase; **PDBTitle:** 1.95 angstrom crystal structure of a bifunctional 3-deoxy-7-2 phosphoheptulonate synthase/chorismate mutase (aroa) from listeria3 monocytogenes egd-e
13	d1ybza1	Alignment		99.7	33	**Fold:**Chorismate mutase II **Superfamily:**Chorismate mutase II **Family:**Dimeric chorismate mutase
14	d2fp1a1	Alignment		99.6	23	**Fold:**Chorismate mutase II **Superfamily:**Chorismate mutase II **Family:**Secreted chorismate mutase-like
15	d2h9da1	Alignment		99.6	22	**Fold:**Chorismate mutase II **Superfamily:**Chorismate mutase II **Family:**Dimeric chorismate mutase
16	c2gbbA_	Alignment		99.6	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative chorismate mutase; **PDBTitle:** crystal structure of secreted chorismate mutase from2 yersinia pestis
17	c2qbvA_	Alignment		99.5	33	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**chorismate mutase; **PDBTitle:** crystal structure of intracellular chorismate mutase from2 mycobacterium tuberculosis
18	c2phmA_	Alignment		99.3	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein (phenylalanine-4-hydroxylase); **PDBTitle:** structure of phenylalanine hydroxylase dephosphorylated
19	d1ygya3	Alignment		97.4	13	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Phosphoglycerate dehydrogenase, regulatory (C-terminal) domain
20	c1u8sB_	Alignment		97.4	9	**PDB header:**transcription **Chain:** B: **PDB Molecule:**glycine cleavage system transcriptional **PDBTitle:** crystal structure of putative glycine cleavage system2 transcriptional repressor
21	c2nyiB_	Alignment	not modelled	97.2	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**unknown protein; **PDBTitle:** crystal structure of an unknown protein from galdieria2 sulphuraria
22	c3ibwA_	Alignment	not modelled	97.1	6	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gtp pyrophosphokinase; **PDBTitle:** crystal structure of the act domain from gtp2 pyrophosphokinase of chlorobium tepidum. northeast3 structural genomics consortium target ctr148a
23	d2f1fa1	Alignment	not modelled	97.0	14	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**IlvH-like
24	d1u8sa2	Alignment	not modelled	96.9	9	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Glycine cleavage system transcriptional repressor
25	d2pc6a2	Alignment	not modelled	96.9	15	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**IlvH-like
26	c2f1fA_	Alignment	not modelled	96.8	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetolactate synthase isozyme iii small subunit; **PDBTitle:** crystal structure of the regulatory subunit of2 acetohydroxyacid synthase isozyme iii from e. coli
27	d2f06a1	Alignment	not modelled	96.6	18	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**BT0572-like
28	d2fgca2	Alignment	not modelled	96.5	7	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**IlvH-like

29	d5csma_	Alignment	not modelled	96.5	22	**Fold:**Chorismate mutase II **Superfamily:**Chorismate mutase II **Family:**Allosteric chorismate mutase
30	c2pc6C_	Alignment	not modelled	96.4	15	**PDB header:**lyase **Chain:** C: **PDB Molecule:**probable acetolactate synthase isozyme iii (small subunit); **PDBTitle:** crystal structure of putative acetolactate synthase- small subunit2 from nitrosomonas europaea
31	d1zpva1	Alignment	not modelled	96.4	4	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**SP0238-like
32	d2f06a2	Alignment	not modelled	96.0	21	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**BT0572-like
33	d1sc6a3	Alignment	not modelled	96.0	15	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Phosphoglycerate dehydrogenase, regulatory (C-terminal) domain
34	c2fgcA_	Alignment	not modelled	96.0	7	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetolactate synthase, small subunit; **PDBTitle:** crystal structure of acetolactate synthase- small subunit from2 thermotoga maritima
35	c1ygyA_	Alignment	not modelled	95.9	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** crystal structure of d-3-phosphoglycerate dehydrogenase from2 mycobacterium tuberculosis
36	c2f06B_	Alignment	not modelled	95.3	20	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of protein bt0572 from bacteroides thetaiotaomicron
37	d1u8sa1	Alignment	not modelled	94.9	9	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Glycine cleavage system transcriptional repressor
38	c3n0vD_	Alignment	not modelled	94.7	13	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (pp_0327)2 from pseudomonas putida kt2440 at 2.25 a resolution
39	c1y7pB_	Alignment	not modelled	94.5	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein af1403; **PDBTitle:** 1.9 a crystal structure of a protein of unknown function2 af1403 from archaeoglobus fulgidus, probable metabolic3 regulator
40	c3l6gA_	Alignment	not modelled	94.1	17	**PDB header:**glycine betaine-binding protein **Chain:** A: **PDB Molecule:**betaine abc transporter permease and substrate binding **PDBTitle:** crystal structure of lactococcal opuac in its open conformation
41	c1tdjA_	Alignment	not modelled	94.0	14	**PDB header:**allostery **Chain:** A: **PDB Molecule:**biosynthetic threonine deaminase; **PDBTitle:** threonine deaminase (biosynthetic) from e. coli
42	c3o1lB_	Alignment	not modelled	93.8	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (pspto_4314)2 from pseudomonas syringae pv. tomato str. dc3000 at 2.20 a resolution
43	c3louB_	Alignment	not modelled	93.1	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of formyltetrahydrofolate deformylase (yp_105254.1)2 from burkholderia mallei atcc 23344 at 1.90 a resolution
44	c3mtjA_	Alignment	not modelled	92.8	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**homoserine dehydrogenase; **PDBTitle:** the crystal structure of a homoserine dehydrogenase from thiobacillus2 denitrificans to 2.15a
45	d1xs5a_	Alignment	not modelled	92.5	7	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
46	c3gxaA_	Alignment	not modelled	92.2	11	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**outer membrane lipoprotein gna1946; **PDBTitle:** crystal structure of gna1946
47	c3tmgA_	Alignment	not modelled	91.9	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**glycine betaine, l-proline abc transporter, **PDBTitle:** crystal structure of glycine betaine, l-proline abc transporter,2 glycine/betaine/l-proline-binding protein (prox) from borrelia3 burgdorferi
48	c3l76B_	Alignment	not modelled	91.7	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aspartokinase; **PDBTitle:** crystal structure of aspartate kinase from synechocystis
49	c2f5xC_	Alignment	not modelled	91.5	16	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**bugd; **PDBTitle:** structure of periplasmic binding protein bugd
50	c3tqwA_	Alignment	not modelled	89.8	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**methionine-binding protein; **PDBTitle:** structure of a abc transporter, periplasmic substrate-binding protein2 from coxiella burnetii
51	c3nrbD_	Alignment	not modelled	89.7	13	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (puru,2 pp_1943) from pseudomonas putida kt2440 at 2.05 a resolution
52	c3ir1F_	Alignment	not modelled	89.0	11	**PDB header:**protein binding **Chain:** F: **PDB Molecule:**outer membrane lipoprotein gna1946; **PDBTitle:** crystal structure of lipoprotein gna1946 from neisseria2 meningitidis
						PDB header:immune system **Chain:** A: **PDB Molecule:**abc-type metal ion transport system,

53	c3k2dA_	Alignment	not modelled	88.4	5	periplasmic component; **PDBTitle:** crystal structure of immunogenic lipoprotein a from vibrio vulnificus
54	c1p99A_	Alignment	not modelled	88.0	8	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein pg110; **PDBTitle:** 1.7a crystal structure of protein pg110 from staphylococcus2 aureus
55	d1p99a_	Alignment	not modelled	88.0	8	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
56	c3e4rA_	Alignment	not modelled	87.8	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**nitrate transport protein; **PDBTitle:** crystal structure of the alkanesulfonate binding protein2 (ssua) from the phytopathogenic bacteria xanthomonas3 axonopodis pv. citri bound to hepes
57	c2dvzA_	Alignment	not modelled	86.9	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative exported protein; **PDBTitle:** structure of a periplasmic transporter
58	c2x26A_	Alignment	not modelled	84.8	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**periplasmic aliphatic sulphonates-binding protein; **PDBTitle:** crystal structure of the periplasmic aliphatic sulphonate2 binding protein ssua from escherichia coli
59	c2qpqC_	Alignment	not modelled	84.5	17	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**protein bug27; **PDBTitle:** structure of bug27 from bordetella pertussis
60	c3obiC_	Alignment	not modelled	84.2	11	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (np_949368)2 from rhodopseudomonas palustris cga009 at 1.95 a resolution
61	d1tdja2	Alignment	not modelled	83.7	13	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Allosteric threonine deaminase C-terminal domain
62	c1r48A_	Alignment	not modelled	83.1	26	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**proline/betaine transporter; **PDBTitle:** solution structure of the c-terminal cytoplasmic domain2 residues 468-497 of escherichia coli protein prop
63	c1u8cB_	Alignment	not modelled	83.1	16	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**integrin beta-3; **PDBTitle:** a novel adaptation of the integrin psi domain revealed from its2 crystal structure
64	c2dtjA_	Alignment	not modelled	81.8	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aspartokinase; **PDBTitle:** crystal structure of regulatory subunit of aspartate kinase2 from corynebacterium glutamicum
65	c3un6A_	Alignment	not modelled	80.9	10	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical protein saouhsc_00137; **PDBTitle:** 2.0 angstrom crystal structure of ligand binding component of abc-type2 import system from staphylococcus aureus with zinc bound
66	c3n5lA_	Alignment	not modelled	79.8	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**binding protein component of abc phosphonate transporter; **PDBTitle:** crystal structure of a binding protein component of abc phosphonate2 transporter (pa3383) from pseudomonas aeruginosa at 1.97 a resolution
67	c1ybaC_	Alignment	not modelled	77.6	15	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** the active form of phosphoglycerate dehydrogenase
68	c3k6sB_	Alignment	not modelled	76.7	23	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**integrin beta-2; **PDBTitle:** structure of integrin alphaxbeta2 ectodomain
69	c2de4B_	Alignment	not modelled	74.1	8	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dibenzothiophene desulfurization enzyme b; **PDBTitle:** crystal structure of dszb c27s mutant in complex with biphenyl-2-2 sulfinic acid
70	c3fcuB_	Alignment	not modelled	73.8	16	**PDB header:**cell adhesion/blood clotting **Chain:** B: **PDB Molecule:**integrin beta-3; **PDBTitle:** structure of headpiece of integrin aiibb3 in open conformation
71	c3uifA_	Alignment	not modelled	72.7	19	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sulfonate abc transporter, periplasmic sulfonate-binding **PDBTitle:** crystal structure of putative sulfonate abc transporter, periplasmic2 sulfonate-binding protein ssua from methylobacillus flagellatus kt
72	c3hn0A_	Alignment	not modelled	72.6	9	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**nitrate transport protein; **PDBTitle:** crystal structure of an abc transporter (bdi_1369) from2 parabacteroides distasonis at 1.75 a resolution
73	c2zhoB_	Alignment	not modelled	69.1	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aspartokinase; **PDBTitle:** crystal structure of the regulatory subunit of aspartate2 kinase from thermus thermophilus (ligand free form)
74	c3qslA_	Alignment	not modelled	69.0	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative exported protein; **PDBTitle:** structure of cae31940 from bordetella bronchiseptica rb50
75	c2j0wA_	Alignment	not modelled	66.5	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lysine-sensitive aspartokinase 3; **PDBTitle:** crystal structure of e. coli aspartokinase iii in complex2 with aspartate and adp (r-state)
76	c3ix1A_	Alignment	not modelled	66.0	10	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding **PDBTitle:** periplasmic n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding2 protein from bacillus halodurans

77	c3ix1B_	Alignment	not modelled	66.0	10	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding **PDBTitle:** periplasmic n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding2 protein from bacillus halodurans
78	c3ab4K_	Alignment	not modelled	65.5	10	**PDB header:**transferase **Chain:** K: **PDB Molecule:**aspartokinase; **PDBTitle:** crystal structure of feedback inhibition resistant mutant of aspartate2 kinase from corynebacterium glutamicum in complex with lysine and3 threonine
79	c3p96A_	Alignment	not modelled	65.5	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphoserine phosphatase serb; **PDBTitle:** crystal structure of phosphoserine phosphatase serb from mycobacterium2 avium, native form
80	d1tdja3	Alignment	not modelled	65.1	11	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Allosteric threonine deaminase C-terminal domain
81	d2hmfa3	Alignment	not modelled	64.9	19	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Aspartokinase allosteric domain-like
82	c3c1nA_	Alignment	not modelled	64.5	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable aspartokinase; **PDBTitle:** crystal structure of allosteric inhibition threonine-sensitive2 aspartokinase from methanococcus jannaschii with l-threonine
83	c2re1A_	Alignment	not modelled	63.7	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aspartokinase, alpha and beta subunits; **PDBTitle:** crystal structure of aspartokinase alpha and beta subunits
84	c2v25B_	Alignment	not modelled	61.7	11	**PDB header:**receptor **Chain:** B: **PDB Molecule:**major cell-binding factor; **PDBTitle:** structure of the campylobacter jejuni antigen peb1a, an2 aspartate and glutamate receptor with bound aspartate
85	c3m05A_	Alignment	not modelled	57.9	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein pepe_1480; **PDBTitle:** the crystal structure of a functionally unknown protein2 pepe_1480 from pediococcus pentosaceus atcc 25745
86	d2cdqa2	Alignment	not modelled	56.7	18	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Aspartokinase allosteric domain-like
87	c2x7pA_	Alignment	not modelled	54.4	14	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**possible thiamine biosynthesis enzyme; **PDBTitle:** the conserved candida albicans ca3427 gene product defines a new2 family of proteins exhibiting the generic periplasmic binding3 protein structural fold
88	c2cdqB_	Alignment	not modelled	52.1	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aspartokinase; **PDBTitle:** crystal structure of arabidopsis thaliana aspartate kinase2 complexed with lysine and s-adenosylmethionine
89	c1j8yF_	Alignment	not modelled	45.4	12	**PDB header:**signaling protein **Chain:** F: **PDB Molecule:**signal recognition 54 kda protein; **PDBTitle:** signal recognition particle conserved gtpase domain from a.2 ambivalens t112a mutant
90	d2hmfa2	Alignment	not modelled	45.2	9	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Aspartokinase allosteric domain-like
91	c2xu6B_	Alignment	not modelled	43.8	10	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**mdv1 coiled coil; **PDBTitle:** mdv1 coiled coil domain
92	c3mahA_	Alignment	not modelled	42.4	6	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aspartokinase; **PDBTitle:** a putative c-terminal regulatory domain of aspartate kinase from2 porphyromonas gingivalis w83.
93	c3kzgB_	Alignment	not modelled	42.4	13	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**arginine 3rd transport system periplasmic binding **PDBTitle:** crystal structure of an arginine 3rd transport system2 periplasmic binding protein from legionella pneumophila
94	c2yhsA_	Alignment	not modelled	41.0	16	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** structure of the e. coli srp receptor ftsy
95	d2a5sa1	Alignment	not modelled	38.8	11	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
96	d2j0wa2	Alignment	not modelled	38.7	23	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Aspartokinase allosteric domain-like
97	c2og2A_	Alignment	not modelled	38.5	15	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**putative signal recognition particle receptor; **PDBTitle:** crystal structure of chloroplast ftsy from arabidopsis2 thaliana
98	c2i4cA_	Alignment	not modelled	36.9	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**bicarbonate transporter; **PDBTitle:** crystal structure of bicarbonate transport protein cmpa from2 synechocystis sp. pcc 6803 in complex with bicarbonate and calcium
99	c2ke4A_	Alignment	not modelled	35.4	10	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**cdc42-interacting protein 4; **PDBTitle:** the nmr structure of the tc10 and cdc42 interacting domain2 of cip4
100	c3h1gA_	Alignment	not modelled	34.2	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**chemotaxis protein chey homolog; **PDBTitle:** crystal structure of chey mutant t84a of helicobacter pylori
101	c3r84O_	Alignment	not modelled	33.7	16	**PDB header:**transcription **Chain:** O: **PDB Molecule:**mediator of rna polymerase ii

101	c3r84O_	Alignment	not modelled	33.7	10	transcription subunit 11; **PDBTitle:** structure of the mediator head subcomplex med11/22
102	c2rc9A_	Alignment	not modelled	30.8	11	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**glutamate [nmda] receptor subunit 3a; **PDBTitle:** crystal structure of the nr3a ligand binding core complex with acpc at2 1.96 angstrom resolution
103	d2czla1	Alignment	not modelled	27.4	9	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
104	c3k5pA_	Alignment	not modelled	25.4	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** crystal structure of amino acid-binding act: d-isomer specific 2-2 hydroxyacid dehydrogenase catalytic domain from brucella melitensis
105	d1ozja_	Alignment	not modelled	25.4	10	**Fold:**SMAD MH1 domain **Superfamily:**SMAD MH1 domain **Family:**SMAD MH1 domain
106	c2cnwF_	Alignment	not modelled	25.4	11	**PDB header:**signal recognition **Chain:** F: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** gdpalf4 complex of the srp gtpases ffh and ftsy
107	c3i42A_	Alignment	not modelled	24.9	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**response regulator receiver domain protein (chey- **PDBTitle:** structure of response regulator receiver domain (chey-like)2 from methylobacillus flagellatus
108	d3dhxa1	Alignment	not modelled	23.9	23	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**NIL domain-like
109	c2rejA_	Alignment	not modelled	23.6	11	**PDB header:**choline-binding protein **Chain:** A: **PDB Molecule:**putative glycine betaine abc transporter protein; **PDBTitle:** abc-transporter choline binding protein in unliganded semi-2 closed conformation
110	c2wmyH_	Alignment	not modelled	23.4	16	**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.
111	d1qnta2	Alignment	not modelled	22.6	50	**Fold:**Ribonuclease H-like motif **Superfamily:**Methylated DNA-protein cysteine methyltransferase domain **Family:**Methylated DNA-protein cysteine methyltransferase domain
112	d1w36d1	Alignment	not modelled	21.9	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
113	d1nwpa_	Alignment	not modelled	21.5	6	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
114	d2qswa1	Alignment	not modelled	21.3	16	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**NIL domain-like
115	c1gk4A_	Alignment	not modelled	21.3	14	**PDB header:**vimentin **Chain:** A: **PDB Molecule:**vimentin; **PDBTitle:** human vimentin coil 2b fragment (cys2)
116	c2ia0A_	Alignment	not modelled	21.2	33	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator pf0864; **PDBTitle:** transcriptional regulatory protein pf0864 from pyrococcus furiosus a2 member of the asnc family (pf0864)
117	d1us5a_	Alignment	not modelled	21.0	15	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
118	c3hv1A_	Alignment	not modelled	20.6	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**polar amino acid abc uptake transporter substrate **PDBTitle:** crystal structure of a polar amino acid abc uptake2 transporter substrate binding protein from streptococcus3 thermophilus