

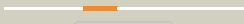
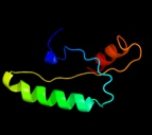




















#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2isba1</a>	 Alignment		100.0	29	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> FumA C-terminal domain-like <b>Family:</b> FumA C-terminal domain-like
2	<a href="#">c2qv6D_</a>	 Alignment		87.6	15	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> gtp cyclohydrolase iii; <b>PDBTitle:</b> gtp cyclohydrolase iii from m. jannaschii (mj0145)2 complexed with gtp and metal ions
3	<a href="#">c4a1oB_</a>	 Alignment		63.6	26	<b>PDB header:</b> transferase-hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional purine biosynthesis protein purh; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis purh complexed with 2 aicar and a novel nucleotide cfair, at 2.48 a resolution.
4	<a href="#">d1pkxa2</a>	 Alignment		61.2	23	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> AlCAR transformylase domain of bifunctional purine biosynthesis enzyme ATIC
5	<a href="#">c3p2oA_</a>	 Alignment		59.8	20	<b>PDB header:</b> oxidoreductase, hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional protein fold; <b>PDBTitle:</b> crystal structure of fold bifunctional protein from campylobacter2 jejuni
6	<a href="#">d1ed7a_</a>	 Alignment		58.6	18	<b>Fold:</b> WW domain-like <b>Superfamily:</b> Carbohydrate binding domain <b>Family:</b> Carbohydrate binding domain
7	<a href="#">c1zcza_</a>	 Alignment		57.7	21	<b>PDB header:</b> transferase/hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional purine biosynthesis protein purh; <b>PDBTitle:</b> crystal structure of phosphoribosylaminoimidazolecarboxamide2 formyltransferase / imp cyclohydrolase (tm1249) from thermotoga3 maritima at 1.88 a resolution
8	<a href="#">c3l07B_</a>	 Alignment		51.7	20	<b>PDB header:</b> oxidoreductase,hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional protein fold; <b>PDBTitle:</b> methylenetetrahydrofolate dehydrogenase/methylenetetrahydrofolate2 cyclohydrolase, putative bifunctional protein fold from francisella3 tularensis.
9	<a href="#">c3fpnA_</a>	 Alignment		51.7	20	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> geobacillus stearothermophilus uvra interaction <b>PDBTitle:</b> crystal structure of uvra-uvrb interaction domains
10	<a href="#">c3p2oB_</a>	 Alignment		45.7	21	<b>PDB header:</b> oxidoreductase, hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional protein fold; <b>PDBTitle:</b> crystal structure of fold bifunctional protein from campylobacter2 jejuni
11	<a href="#">d1g8ma2</a>	 Alignment		45.3	18	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> AlCAR transformylase domain of bifunctional purine biosynthesis enzyme ATIC

12	<a href="#">d12asa_</a>	Alignment		43.5	23	<b>Fold:</b> Class II aaRS and biotin synthetases <b>Superfamily:</b> Class II aaRS and biotin synthetases <b>Family:</b> Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
13	<a href="#">c1thzA_</a>	Alignment		43.3	18	<b>PDB header:</b> transferase, hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional purine biosynthesis protein purh; <b>PDBTitle:</b> crystal structure of avian aicar transformylase in complex2 with a novel inhibitor identified by virtual ligand3 screening
14	<a href="#">c1k98A_</a>	Alignment		40.0	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methionine synthase; <b>PDBTitle:</b> adomet complex of meth c-terminal fragment
15	<a href="#">d1yqea1</a>	Alignment		39.8	8	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> AF0625-like <b>Family:</b> AF0625-like
16	<a href="#">c3p9zA_</a>	Alignment		39.6	24	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> uroporphyrinogen iii cosynthase (hemd); <b>PDBTitle:</b> crystal structure of uroporphyrinogen-iii synthetase from helicobacter2 pylori 26695
17	<a href="#">d1zcza2</a>	Alignment		38.5	21	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> AlCAR transformylase domain of bifunctional purine biosynthesis enzyme ATIC
18	<a href="#">d1ei5a2</a>	Alignment		36.8	25	<b>Fold:</b> Streptavidin-like <b>Superfamily:</b> D-aminopeptidase, middle and C-terminal domains <b>Family:</b> D-aminopeptidase, middle and C-terminal domains
19	<a href="#">c2vdc1_</a>	Alignment		36.8	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> I: <b>PDB Molecule:</b> glutamate synthase [nadph] small chain; <b>PDBTitle:</b> the 9.5 a resolution structure of glutamate synthase from2 cryo-electron microscopy and its oligomerization behavior3 in solution: functional implications.
20	<a href="#">c2xmoB_</a>	Alignment		36.8	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> lmo2642 protein; <b>PDBTitle:</b> the crystal structure of lmo2642
21	<a href="#">c2c2xB_</a>	Alignment	not modelled	34.8	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> methylenetetrahydrofolate dehydrogenase- <b>PDBTitle:</b> three dimensional structure of bifunctional2 methylenetetrahydrofolate dehydrogenase-cyclohydrolase3 from mycobacterium tuberculosis
22	<a href="#">d1a4ia2</a>	Alignment	not modelled	34.8	16	<b>Fold:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Superfamily:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Family:</b> Tetrahydrofolate dehydrogenase/cyclohydrolase
23	<a href="#">d3bula2</a>	Alignment	not modelled	31.8	25	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Cobalamin (vitamin B12)-binding domain <b>Family:</b> Cobalamin (vitamin B12)-binding domain
24	<a href="#">c2gfgC_</a>	Alignment	not modelled	30.4	9	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> upf0204 protein ph0006; <b>PDBTitle:</b> structure of protein of unknown function ph0006 from pyrococcus2 horikoshii
25	<a href="#">c1jr2A_</a>	Alignment	not modelled	30.0	24	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> uroporphyrinogen-iii synthase; <b>PDBTitle:</b> structure of uroporphyrinogen iii synthase
26	<a href="#">d1jr2a_</a>	Alignment	not modelled	30.0	24	<b>Fold:</b> HemD-like <b>Superfamily:</b> HemD-like <b>Family:</b> HemD-like
27	<a href="#">c1a4iB_</a>	Alignment	not modelled	29.2	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> methylenetetrahydrofolate dehydrogenase / <b>PDBTitle:</b> human tetrahydrofolate dehydrogenase / cyclohydrolase
28	<a href="#">c2d49A_</a>	Alignment	not modelled	29.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> chitinase c; <b>PDBTitle:</b> solution structure of the chitin-binding domain of2 streptomyces griseus chitinase c

29	<a href="#">d1edza2</a>	Alignment	not modelled	28.5	8	<b>Fold:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Superfamily:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Family:</b> Tetrahydrofolate dehydrogenase/cyclohydrolase
30	<a href="#">c3q3vA</a>	Alignment	not modelled	27.6	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoglycerate kinase; <b>PDBTitle:</b> crystal structure of phosphoglycerate kinase from campylobacter2 jejuni.
31	<a href="#">c3ibgF</a>	Alignment	not modelled	27.5	17	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> atpase, subunit of the get complex; <b>PDBTitle:</b> crystal structure of aspergillus fumigatus get3 with bound2 adp
32	<a href="#">d2qqba1</a>	Alignment	not modelled	26.9	35	<b>Fold:</b> RPA2825-like <b>Superfamily:</b> RPA2825-like <b>Family:</b> RPA2825-like
33	<a href="#">d1sf8a</a>	Alignment	not modelled	26.0	23	<b>Fold:</b> HSP90 C-terminal domain <b>Superfamily:</b> HSP90 C-terminal domain <b>Family:</b> HSP90 C-terminal domain
34	<a href="#">d1b8aa1</a>	Alignment	not modelled	25.9	6	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Anticodon-binding domain
35	<a href="#">d1aiwa</a>	Alignment	not modelled	25.8	7	<b>Fold:</b> WW domain-like <b>Superfamily:</b> Carbohydrate binding domain <b>Family:</b> Carbohydrate binding domain
36	<a href="#">d1o6aa</a>	Alignment	not modelled	25.8	15	<b>Fold:</b> Surface presentation of antigens (SPOA) <b>Superfamily:</b> Surface presentation of antigens (SPOA) <b>Family:</b> Surface presentation of antigens (SPOA)
37	<a href="#">d2gfqa1</a>	Alignment	not modelled	23.8	9	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> AF0625-like <b>Family:</b> AF0625-like
38	<a href="#">d1xmpa</a>	Alignment	not modelled	23.5	10	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) <b>Family:</b> N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
39	<a href="#">d2piaa1</a>	Alignment	not modelled	23.2	0	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> Ferredoxin reductase FAD-binding domain-like
40	<a href="#">c3trhl</a>	Alignment	not modelled	22.6	14	<b>PDB header:</b> lyase <b>Chain:</b> I: <b>PDB Molecule:</b> phosphoribosylaminoimidazole carboxylase <b>PDBTitle:</b> structure of a phosphoribosylaminoimidazole carboxylase catalytic2 subunit (pure) from coxiella burnetii
41	<a href="#">c3cr8C</a>	Alignment	not modelled	22.5	30	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> sulfate adenylyltransferase, adenylylsulfate <b>PDBTitle:</b> hexameric aps kinase from thiobacillus denitrificans
42	<a href="#">d1goia1</a>	Alignment	not modelled	22.0	18	<b>Fold:</b> WW domain-like <b>Superfamily:</b> Carbohydrate binding domain <b>Family:</b> Carbohydrate binding domain
43	<a href="#">d1stza2</a>	Alignment	not modelled	21.5	6	<b>Fold:</b> Profilin-like <b>Superfamily:</b> GAF domain-like <b>Family:</b> HrcA C-terminal domain-like
44	<a href="#">c2iheA</a>	Alignment	not modelled	21.3	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> single-stranded dna-binding protein; <b>PDBTitle:</b> crystal structure of wild-type single-stranded dna binding protein2 from thermus aquaticus
45	<a href="#">d1fnda1</a>	Alignment	not modelled	21.2	21	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> Ferredoxin reductase FAD-binding domain-like
46	<a href="#">c4a5oB</a>	Alignment	not modelled	20.5	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional protein fold; <b>PDBTitle:</b> crystal structure of pseudomonas aeruginosa n5, n10-2 methylenetetrahydrofolate dehydrogenase-cyclohydrolase (fold)
47	<a href="#">d1ni9a</a>	Alignment	not modelled	20.4	25	<b>Fold:</b> Carbohydrate phosphatase <b>Superfamily:</b> Carbohydrate phosphatase <b>Family:</b> GlpX-like bacterial fructose-1,6-bisphosphatase
48	<a href="#">d1whka</a>	Alignment	not modelled	20.0	17	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Cap-Gly domain <b>Family:</b> Cap-Gly domain
49	<a href="#">c3o59X</a>	Alignment	not modelled	19.9	46	<b>PDB header:</b> transferase <b>Chain:</b> X: <b>PDB Molecule:</b> dna polymerase ii large subunit; <b>PDBTitle:</b> dna polymerase d large subunit dp2(1-300) from pyrococcus horikoshii
50	<a href="#">c3orsD</a>	Alignment	not modelled	19.8	18	<b>PDB header:</b> isomerase,biosynthetic protein <b>Chain:</b> D: <b>PDB Molecule:</b> n5-carboxyaminoimidazole ribonucleotide mutase; <b>PDBTitle:</b> crystal structure of n5-carboxyaminoimidazole ribonucleotide mutase2 from staphylococcus aureus
51	<a href="#">d1v58a1</a>	Alignment	not modelled	19.7	11	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> DsbC/DsbG C-terminal domain-like
52	<a href="#">c3hjbA</a>	Alignment	not modelled	19.6	30	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> glucose-6-phosphate isomerase; <b>PDBTitle:</b> 1.5 angstrom crystal structure of glucose-6-phosphate isomerase from2 vibrio cholerae.
53	<a href="#">d1vkza2</a>	Alignment	not modelled	19.3	23	<b>Fold:</b> PreATP-grasp domain <b>Superfamily:</b> PreATP-grasp domain <b>Family:</b> BC N-terminal domain-like
54	<a href="#">d2cp6a1</a>	Alignment	not modelled	19.3	15	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Cap-Gly domain <b>Family:</b> Cap-Gly domain

55	<a href="#">d2oz4a1</a>	Alignment	not modelled	19.2	29	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C2 set domains
56	<a href="#">d2eyqa1</a>	Alignment	not modelled	18.9	6	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> CarD-like <b>Family:</b> CarD-like
57	<a href="#">d2coza1</a>	Alignment	not modelled	18.8	16	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Cap-Gly domain <b>Family:</b> Cap-Gly domain
58	<a href="#">d1fyba1</a>	Alignment	not modelled	18.5	13	<b>Fold:</b> Plant proteinase inhibitors <b>Superfamily:</b> Plant proteinase inhibitors <b>Family:</b> Plant proteinase inhibitors
59	<a href="#">c2o2cB</a>	Alignment	not modelled	17.9	25	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> glucose-6-phosphate isomerase, glycosomal; <b>PDBTitle:</b> crystal structure of phosphoglucose isomerase from t. brucei2 containing glucose-6-phosphate in the active site
60	<a href="#">d1q50a</a>	Alignment	not modelled	17.9	30	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> Phosphoglucose isomerase, PGI
61	<a href="#">c3c00B</a>	Alignment	not modelled	17.9	12	<b>PDB header:</b> membrane protein, protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> escu; <b>PDBTitle:</b> crystal structural of the mutated g247t escu/spas c-terminal domain
62	<a href="#">c3tliC</a>	Alignment	not modelled	17.8	26	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> double-strand break repair protein mre11a; <b>PDBTitle:</b> crystal structure of human mre11: understanding tumorigenic mutations
63	<a href="#">c1t10A</a>	Alignment	not modelled	17.8	30	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> glucose-6-phosphate isomerase; <b>PDBTitle:</b> phosphoglucose isomerase from leishmania mexicana in complex with2 substrate d-fructose-6-phosphate
64	<a href="#">c3pr3B</a>	Alignment	not modelled	17.7	35	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> glucose-6-phosphate isomerase; <b>PDBTitle:</b> crystal structure of plasmodium falciparum glucose-6-phosphate2 isomerase (pf14_0341) in complex with fructose-6-phosphate
65	<a href="#">c3nbuC</a>	Alignment	not modelled	17.6	30	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> glucose-6-phosphate isomerase; <b>PDBTitle:</b> crystal structure of pgi glucosephosphate isomerase
66	<a href="#">c3lerA</a>	Alignment	not modelled	17.6	8	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from2 campylobacter jejuni subsp. jejuni nctc 11168
67	<a href="#">d2gc6a1</a>	Alignment	not modelled	17.4	15	<b>Fold:</b> MurD-like peptide ligases, peptide-binding domain <b>Superfamily:</b> MurD-like peptide ligases, peptide-binding domain <b>Family:</b> Folylpolyglutamate synthetase, C-terminal domain
68	<a href="#">d2buna1</a>	Alignment	not modelled	17.2	18	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Acylphosphatase/BLUF domain-like <b>Family:</b> BLUF domain
69	<a href="#">d4sgbi</a>	Alignment	not modelled	17.2	19	<b>Fold:</b> Plant proteinase inhibitors <b>Superfamily:</b> Plant proteinase inhibitors <b>Family:</b> Plant proteinase inhibitors
70	<a href="#">d1yrxa1</a>	Alignment	not modelled	17.1	18	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Acylphosphatase/BLUF domain-like <b>Family:</b> BLUF domain
71	<a href="#">c3en2A</a>	Alignment	not modelled	17.1	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> probable primosomal replication protein n; <b>PDBTitle:</b> three-dimensional structure of the protein prib from2 ralstonia solanacearum at the resolution 2.3a. northeast3 structural genomics consortium target rsr213c.
72	<a href="#">c2crvA</a>	Alignment	not modelled	16.9	14	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> translation initiation factor if-2; <b>PDBTitle:</b> solution structure of c-terminal domain of mitochondrial2 translational initiationfactor 2
73	<a href="#">c2jmbA</a>	Alignment	not modelled	16.8	24	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein atu4866; <b>PDBTitle:</b> solution structure of the protein atu4866 from agrobacterium2 tumefaciens
74	<a href="#">d1wlfa2</a>	Alignment	not modelled	16.8	15	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Cdc48 N-terminal domain-like
75	<a href="#">d1y1la</a>	Alignment	not modelled	16.8	31	<b>Fold:</b> Phosphotyrosine protein phosphatases I-like <b>Superfamily:</b> Phosphotyrosine protein phosphatases I <b>Family:</b> Low-molecular-weight phosphotyrosine protein phosphatases
76	<a href="#">c3fmxX</a>	Alignment	not modelled	16.6	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> X: <b>PDB Molecule:</b> tartrate dehydrogenase/decarboxylase; <b>PDBTitle:</b> crystal structure of tartrate dehydrogenase from pseudomonas2 putida complexed with nadh
77	<a href="#">d2cnda1</a>	Alignment	not modelled	16.6	25	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> Ferredoxin reductase FAD-binding domain-like
78	<a href="#">d2byca1</a>	Alignment	not modelled	16.4	8	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Acylphosphatase/BLUF domain-like <b>Family:</b> BLUF domain
79	<a href="#">d1hm5a</a>	Alignment	not modelled	16.2	35	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> Phosphoglucose isomerase, PGI
						<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative c-1-tetrahydrofolate synthase,

80	<a href="#">c4a26B_</a>	Alignment	not modelled	16.2	15	cytoplasmic; <b>PDBTitle:</b> the crystal structure of leishmania major n5,n10-2 methylenetetrahydrofolate dehydrogenase/cyclohydrolase
81	<a href="#">d1whha_</a>	Alignment	not modelled	15.9	30	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Cap-Gly domain <b>Family:</b> Cap-Gly domain
82	<a href="#">d2al3a1</a>	Alignment	not modelled	15.9	13	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> UBX domain
83	<a href="#">d1iata_</a>	Alignment	not modelled	15.8	35	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> Phosphoglucose isomerase, PGI
84	<a href="#">d1pjua1</a>	Alignment	not modelled	15.8	20	<b>Fold:</b> Plant proteinase inhibitors <b>Superfamily:</b> Plant proteinase inhibitors <b>Family:</b> Plant proteinase inhibitors
85	<a href="#">d1gzda_</a>	Alignment	not modelled	15.7	35	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> Phosphoglucose isomerase, PGI
86	<a href="#">c1fybA_</a>	Alignment	not modelled	15.6	17	<b>PDB header:</b> hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> proteinase inhibitor; <b>PDBTitle:</b> solution structure of c1-t1, a two-domain proteinase2 inhibitor derived from the circular precursor protein na-3 propi from nicotiana glauca
87	<a href="#">c3k1rA_</a>	Alignment	not modelled	15.4	17	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> harmonin; <b>PDBTitle:</b> structure of harmonin npdz1 in complex with the sample of 2 sans
88	<a href="#">d1u0fa_</a>	Alignment	not modelled	15.4	35	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> Phosphoglucose isomerase, PGI
89	<a href="#">c3cyyA_</a>	Alignment	not modelled	15.1	19	<b>PDB header:</b> peptide binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> tight junction protein zo-1; <b>PDBTitle:</b> the crystal structure of zo-1 pdz2 in complex with the cx43 peptide
90	<a href="#">d1qx4a1</a>	Alignment	not modelled	15.1	14	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> Ferredoxin reductase FAD-binding domain-like
91	<a href="#">c2e4hA_</a>	Alignment	not modelled	15.0	24	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> restin; <b>PDBTitle:</b> solution structure of cytoskeletal protein in complex with 2 tubulin tail
92	<a href="#">d1n0ua3</a>	Alignment	not modelled	15.0	10	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> Translational machinery components
93	<a href="#">c2wu8A_</a>	Alignment	not modelled	14.8	30	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> glucose-6-phosphate isomerase; <b>PDBTitle:</b> structural studies of phosphoglucose isomerase from mycobacterium tuberculosis h37rv
94	<a href="#">d1u11a_</a>	Alignment	not modelled	14.7	19	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) <b>Family:</b> N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
95	<a href="#">c2jlhA_</a>	Alignment	not modelled	14.7	15	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> yop proteins translocation protein u; <b>PDBTitle:</b> crystal structure of the cytoplasmic domain of yersinia2 pestis yscu n263a mutant
96	<a href="#">d2ix0a3</a>	Alignment	not modelled	14.5	13	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
97	<a href="#">c3ijfX_</a>	Alignment	not modelled	14.3	22	<b>PDB header:</b> hydrolase <b>Chain:</b> X: <b>PDB Molecule:</b> cytidine deaminase; <b>PDBTitle:</b> crystal structure of cytidine deaminase from mycobacterium2 tuberculosis
98	<a href="#">d1sm4a1</a>	Alignment	not modelled	14.2	14	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> Ferredoxin reductase FAD-binding domain-like
99	<a href="#">d1krha1</a>	Alignment	not modelled	14.1	21	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> Ferredoxin reductase FAD-binding domain-like