








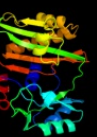









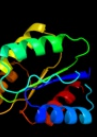




# Phyre2

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Description	P0A836
Date	Thu Jan 5 11:06:47 GMT 2012
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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2nu9E_</a>	 Alignment		100.0	100	<b>PDB header:</b> ligase <b>Chain:</b> E: <b>PDB Molecule:</b> succinyl-coa synthetase beta chain; <b>PDBTitle:</b> c123at mutant of e. coli succinyl-coa synthetase2 orthorhombic crystal form
2	<a href="#">c1eucB_</a>	 Alignment		100.0	45	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> succinyl-coa synthetase, beta chain; <b>PDBTitle:</b> crystal structure of dephosphorylated pig heart, gtp-2 specific succinyl-coa synthetase
3	<a href="#">c3mwdA_</a>	 Alignment		100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-citrate synthase; <b>PDBTitle:</b> truncated human atp-citrate lyase with citrate bound
4	<a href="#">d1eucb2</a>	 Alignment		100.0	36	<b>Fold:</b> ATP-grasp <b>Superfamily:</b> Glutathione synthetase ATP-binding domain-like <b>Family:</b> Succinyl-CoA synthetase, beta-chain, N-terminal domain
5	<a href="#">d2nu7b2</a>	 Alignment		100.0	100	<b>Fold:</b> ATP-grasp <b>Superfamily:</b> Glutathione synthetase ATP-binding domain-like <b>Family:</b> Succinyl-CoA synthetase, beta-chain, N-terminal domain
6	<a href="#">c1wr2A_</a>	 Alignment		100.0	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ph1789; <b>PDBTitle:</b> crystal structure of ph1788 from pyrococcus horikoshii ot3
7	<a href="#">d2nu7b1</a>	 Alignment		100.0	100	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Succinyl-CoA synthetase domains <b>Family:</b> Succinyl-CoA synthetase domains
8	<a href="#">d1eucb1</a>	 Alignment		100.0	55	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Succinyl-CoA synthetase domains <b>Family:</b> Succinyl-CoA synthetase domains
9	<a href="#">c2csuB_</a>	 Alignment		99.7	26	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> 457aa long hypothetical protein; <b>PDBTitle:</b> crystal structure of ph0766 from pyrococcus horikoshii ot3
10	<a href="#">d2csua3</a>	 Alignment		99.7	26	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Succinyl-CoA synthetase domains <b>Family:</b> Succinyl-CoA synthetase domains
11	<a href="#">c3bg5C_</a>	 Alignment		99.2	18	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> pyruvate carboxylase; <b>PDBTitle:</b> crystal structure of staphylococcus aureus pyruvate2 carboxylase

12	<a href="#">c1m6vE_</a>	Alignment		99.1	15	<b>PDB header:</b> ligase <b>Chain:</b> E: <b>PDB Molecule:</b> carbamoyl phosphate synthetase large chain; <b>PDBTitle:</b> crystal structure of the g359f (small subunit) point mutant of2 carbamoyl phosphate synthetase
13	<a href="#">d1a9xa5</a>	Alignment		99.1	15	<b>Fold:</b> ATP-grasp <b>Superfamily:</b> Glutathione synthetase ATP-binding domain-like <b>Family:</b> BC ATP-binding domain-like
14	<a href="#">c3g8cB_</a>	Alignment		99.0	18	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> biotin carboxylase; <b>PDBTitle:</b> crystal stucture of biotin carboxylase in complex with2 biotin, bicarbonate, adp and mg ion
15	<a href="#">c1w96B_</a>	Alignment		99.0	18	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> acetyl-coenzyme a carboxylase; <b>PDBTitle:</b> crystal structure of biotin carboxylase domain of acetyl-2 coenzyme a carboxylase from saccharomyces cerevisiae in3 complex with soraphen a
16	<a href="#">c1ulzA_</a>	Alignment		99.0	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate carboxylase n-terminal domain; <b>PDBTitle:</b> crystal structure of the biotin carboxylase subunit of pyruvate2 carboxylase
17	<a href="#">c2dzdB_</a>	Alignment		99.0	21	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> pyruvate carboxylase; <b>PDBTitle:</b> crystal structure of the biotin carboxylase domain of2 pyruvate carboxylase
18	<a href="#">c1vkzA_</a>	Alignment		99.0	25	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylamine--glycine ligase; <b>PDBTitle:</b> crystal structure of phosphoribosylamine--glycine ligase (tm1250) from2 thermotoga maritima at 2.30 a resolution
19	<a href="#">c2yyaB_</a>	Alignment		99.0	25	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoribosylamine--glycine ligase; <b>PDBTitle:</b> crystal structure of gar synthetase from aquifex aeolicus
20	<a href="#">c3lp8A_</a>	Alignment		98.9	26	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylamine-glycine ligase; <b>PDBTitle:</b> crystal structure of phosphoribosylamine-glycine ligase from2 ehrlichia chaffeensis
21	<a href="#">c2xd4A_</a>	Alignment	not modelled	98.9	29	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylamine--glycine ligase; <b>PDBTitle:</b> nucleotide-bound structures of bacillus subtilis glycylamide2 ribonucleotide synthetase
22	<a href="#">c2ip4A_</a>	Alignment	not modelled	98.9	32	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylamine--glycine ligase; <b>PDBTitle:</b> crystal structure of glycylamide ribonucleotide synthetase from2 thermus thermophilus hb8
23	<a href="#">c2hjwA_</a>	Alignment	not modelled	98.9	20	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> acetyl-coa carboxylase 2; <b>PDBTitle:</b> crystal structure of the bc domain of acc2
24	<a href="#">c3dmyA_</a>	Alignment	not modelled	98.9	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> protein fdra; <b>PDBTitle:</b> crystal structure of a predicated acyl-coa synthetase from e.coli
25	<a href="#">d1a9xa6</a>	Alignment	not modelled	98.9	28	<b>Fold:</b> ATP-grasp <b>Superfamily:</b> Glutathione synthetase ATP-binding domain-like <b>Family:</b> BC ATP-binding domain-like
26	<a href="#">c1kjjA_</a>	Alignment	not modelled	98.9	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylglycylamide formyltransferase 2; <b>PDBTitle:</b> crystal structure of glycylamide ribonucleotide2 transformylase in complex with mg-atp-gamma-s
27	<a href="#">d1w96a3</a>	Alignment	not modelled	98.9	19	<b>Fold:</b> ATP-grasp <b>Superfamily:</b> Glutathione synthetase ATP-binding domain-like <b>Family:</b> BC ATP-binding domain-like
28	<a href="#">d2j9ga3</a>	Alignment	not modelled	98.9	17	<b>Fold:</b> ATP-grasp <b>Superfamily:</b> Glutathione synthetase ATP-binding domain-like <b>Family:</b> BC ATP-binding domain-like
29	<a href="#">c2vnaA_</a>	Alignment	not modelled	98.9	21	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> acetyl-coa carboxylase;

29	<a href="#">c2vpvA_</a>	Alignment	not modelled	98.8	21	<b>PDBTitle:</b> crystal structure of biotin carboxylase from s. aureus2 <b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> d-alanine:d-lactate ligase; <b>PDBTitle:</b> d-alanine:d-lactate ligase (lmdl2) of vancomycin-resistant2 leuconostoc mesenteroides
30	<a href="#">c1ehiB_</a>	Alignment	not modelled	98.8	15	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> biotin carboxylase; <b>PDBTitle:</b> crystal structure of biotin carboxylase-adp complex from campylobacter2 jejuni
31	<a href="#">c3ouzA_</a>	Alignment	not modelled	98.7	22	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione biosynthesis bifunctional protein gshab; <b>PDBTitle:</b> crystal structure of a bifunctional glutathione synthetase from2 streptococcus agalactiae
32	<a href="#">c3ln6A_</a>	Alignment	not modelled	98.7	23	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylglycinamide synthetase; <b>PDBTitle:</b> crystal structure of gar synthetase from geobacillus kaustophilus
33	<a href="#">c2ys6A_</a>	Alignment	not modelled	98.7	32	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione biosynthesis bifunctional protein gshab; <b>PDBTitle:</b> crystal structure of a bifunctional glutathione synthetase from2 pasteurella multocida
34	<a href="#">c3ln7A_</a>	Alignment	not modelled	98.7	19	<b>Fold:</b> ATP-grasp <b>Superfamily:</b> Glutathione synthetase ATP-binding domain-like <b>Family:</b> BC ATP-binding domain-like
35	<a href="#">d1ulza3</a>	Alignment	not modelled	98.7	15	<b>Fold:</b> ATP-grasp <b>Superfamily:</b> Glutathione synthetase ATP-binding domain-like <b>Family:</b> BC ATP-binding domain-like
36	<a href="#">d1vkza3</a>	Alignment	not modelled	98.7	26	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoribosylaminoimidazole carboxylase, atpase subunit; <b>PDBTitle:</b> crystal structure of purk: n5-carboxyaminoimidazole ribonucleotide2 synthetase
37	<a href="#">c3q2oB_</a>	Alignment	not modelled	98.6	18	<b>PDB header:</b> ligase <b>Chain:</b> K: <b>PDB Molecule:</b> propionyl-coa carboxylase, alpha subunit; <b>PDBTitle:</b> crystal structure of the holoenzyme of propionyl-coa carboxylase (pcc)
38	<a href="#">c3n6rK_</a>	Alignment	not modelled	98.6	18	<b>PDB header:</b> ligase <b>Chain:</b> E: <b>PDB Molecule:</b> methylcrotonyl-coa carboxylase, alpha-subunit; <b>PDBTitle:</b> crystal structure of p. aeruginosa 3-methylcrotonyl-coa carboxylase2 (mcc) 750 kd holoenzyme, coa complex
39	<a href="#">c3u9sE_</a>	Alignment	not modelled	98.6	21	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> d-alanine-d-alanine ligase a; <b>PDBTitle:</b> the crystal structure of the d-alanyl-alanine synthetase a from2 salmonella enterica subsp. enterica serovar typhimurium str. lt2
40	<a href="#">c3i12A_</a>	Alignment	not modelled	98.6	16	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> propionyl-coa carboxylase alpha chain, <b>PDBTitle:</b> solution structure of b domain from human propionyl-coa2 carboxylase alpha subunit
41	<a href="#">c2cqyA_</a>	Alignment	not modelled	98.6	21	<b>Fold:</b> ATP-grasp <b>Superfamily:</b> Glutathione synthetase ATP-binding domain-like <b>Family:</b> ATP-binding domain of peptide synthetases
42	<a href="#">d1iowa2</a>	Alignment	not modelled	98.6	17	<b>PDB header:</b> ligase(peptidoglycan synthesis) <b>Chain:</b> A: <b>PDB Molecule:</b> d-alanine--d-alanine ligase; <b>PDBTitle:</b> vancomycin resistance: structure of d-alanine:d-alanine2 ligase at 2.3 angstroms resolution
43	<a href="#">c2dlnA_</a>	Alignment	not modelled	98.6	17	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> acetyl-coa carboxylase 2; <b>PDBTitle:</b> the biotin carboxylase (bc) domain of human acetyl-coa2 carboxylase 2 (acc2) in complex with soraphen a
44	<a href="#">c3gidB_</a>	Alignment	not modelled	98.6	20	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> d-alanine-d-alanine ligase; <b>PDBTitle:</b> crystal structure of d-alanine-d-alanine ligase from helicobacter2 pylori
45	<a href="#">c2pvpB_</a>	Alignment	not modelled	98.5	17	<b>PDB header:</b> ligase,biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> n5-carboxyaminoimidazole ribonucleotide synthetase; <b>PDBTitle:</b> crystal structure of n5-carboxyaminoimidazole synthetase from2 staphylococcus aureus complexed with adp
46	<a href="#">c3orqA_</a>	Alignment	not modelled	98.5	16	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> trifunctional purine biosynthetic protein adenosine-3; <b>PDBTitle:</b> human glycinamide ribonucleotide synthetase
47	<a href="#">c2qk4A_</a>	Alignment	not modelled	98.5	26	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Succinyl-CoA synthetase domains <b>Family:</b> Succinyl-CoA synthetase domains
48	<a href="#">d1oi7a2</a>	Alignment	not modelled	98.5	15	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> biotin carboxylase; <b>PDBTitle:</b> crystal structure of the biotin carboxylase subunit, f363a2 mutant, of acetyl-coa carboxylase from escherichia coli.
49	<a href="#">c2gpwC_</a>	Alignment	not modelled	98.5	17	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> d-alanine-d-alanine ligase; <b>PDBTitle:</b> allosteric inhibition of staphylococcus aureus d-alanine:d-alanine2 ligase revealed by crystallographic studies
50	<a href="#">c2i80B_</a>	Alignment	not modelled	98.5	16	<b>Fold:</b> ATP-grasp <b>Superfamily:</b> Glutathione synthetase ATP-binding domain-like <b>Family:</b> BC ATP-binding domain-like
51	<a href="#">d1kjqaz</a>	Alignment	not modelled	98.4	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 433aa long hypothetical phosphoribosylglycinamide formyl <b>PDBTitle:</b> crystal structure of probable phosphoribosylglycinamide formyl2 transferase from pyrococcus horikoshii ot3 complexed with adp
52	<a href="#">c2dwcB_</a>	Alignment	not modelled	98.4	19	<b>PDB header:</b> ligase



78	<a href="#">c2zdqA</a>	Alignment	not modelled	97.7	21	<b>Chain:</b> A: <b>PDB Molecule:</b> d-alanine--d-alanine ligase; <b>PDBTitle:</b> crystal structure of d-alanine:d-alanine ligase with atp2 and d-alanine:d-alanine from thermus thermophilus hb8
79	<a href="#">c3uvzB</a>	Alignment	not modelled	97.7	13	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoribosylaminoimidazole carboxylase, atpase subunit; <b>PDBTitle:</b> crystal structure of phosphoribosylaminoimidazole carboxylase, atpase2 subunit from burkholderia ambifaria
80	<a href="#">c2r85B</a>	Alignment	not modelled	97.6	17	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> purp protein pf1517; <b>PDBTitle:</b> crystal structure of purp from pyrococcus furiosus complexed with amp
81	<a href="#">d1uc8a2</a>	Alignment	not modelled	97.6	24	<b>Fold:</b> ATP-grasp <b>Superfamily:</b> Glutathione synthetase ATP-binding domain-like <b>Family:</b> Lysine biosynthesis enzyme LysX ATP-binding domain
82	<a href="#">c2p0aA</a>	Alignment	not modelled	97.6	12	<b>PDB header:</b> neuropeptide <b>Chain:</b> A: <b>PDB Molecule:</b> synapsin-3; <b>PDBTitle:</b> the crystal structure of human synapsin iii (syn3) in complex with2 amppnp
83	<a href="#">c2pn1A</a>	Alignment	not modelled	97.5	26	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> carbamoylphosphate synthase large subunit; <b>PDBTitle:</b> crystal structure of carbamoylphosphate synthase large subunit (split2 gene in mj) (zp_00538348.1) from exiguobacterium sp. 255-15 at 2.00 a3 resolution
84	<a href="#">c1z2pX</a>	Alignment	not modelled	97.5	17	<b>PDB header:</b> transferase <b>Chain:</b> X: <b>PDB Molecule:</b> inositol 1,3,4-trisphosphate 5/6-kinase; <b>PDBTitle:</b> inositol 1,3,4-trisphosphate 5/6-kinase in complex with mg2+/-amp-2 pcp/ins(1,3,4)p3
85	<a href="#">c2nu8D</a>	Alignment	not modelled	97.5	21	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> succinyl-coa ligase [adp-forming] subunit alpha; <b>PDBTitle:</b> c123at mutant of e. coli succinyl-coa synthetase
86	<a href="#">c1uc8B</a>	Alignment	not modelled	97.3	24	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> lysine biosynthesis enzyme; <b>PDBTitle:</b> crystal structure of a lysine biosynthesis enzyme, lysx,2 from thermus thermophilus hb8
87	<a href="#">c1pk8D</a>	Alignment	not modelled	97.3	15	<b>PDB header:</b> membrane protein <b>Chain:</b> D: <b>PDB Molecule:</b> rat synapsin i; <b>PDBTitle:</b> crystal structure of rat synapsin i c domain complexed to2 ca.atp
88	<a href="#">d1i7na2</a>	Alignment	not modelled	97.0	17	<b>Fold:</b> ATP-grasp <b>Superfamily:</b> Glutathione synthetase ATP-binding domain-like <b>Family:</b> Synapsin C-terminal domain
89	<a href="#">d1gsaa2</a>	Alignment	not modelled	96.5	14	<b>Fold:</b> ATP-grasp <b>Superfamily:</b> Glutathione synthetase ATP-binding domain-like <b>Family:</b> ATP-binding domain of peptide synthetases
90	<a href="#">d1pk8a2</a>	Alignment	not modelled	96.2	18	<b>Fold:</b> ATP-grasp <b>Superfamily:</b> Glutathione synthetase ATP-binding domain-like <b>Family:</b> Synapsin C-terminal domain
91	<a href="#">c2r7mA</a>	Alignment	not modelled	95.9	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> 5-formaminoimidazole-4-carboxamide-1-(beta)-d- <b>PDBTitle:</b> crystal structure of faicar synthetase (purp) from m.2 jannaschii complexed with amp
92	<a href="#">c2qb5B</a>	Alignment	not modelled	95.7	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> inositol-tetrakisphosphate 1-kinase; <b>PDBTitle:</b> crystal structure of human inositol 1,3,4-trisphosphate 5/6-kinase2 (itpk1) in complex with adp and mn2+
93	<a href="#">c1gshA</a>	Alignment	not modelled	95.7	10	<b>PDB header:</b> glutathione biosynthesis ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione biosynthetic ligase; <b>PDBTitle:</b> structure of escherichia coli glutathione synthetase at ph 7.5
94	<a href="#">c3df7A</a>	Alignment	not modelled	95.5	10	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative atp-grasp superfamily protein; <b>PDBTitle:</b> crystal structure of a putative atp-grasp superfamily2 protein from archaeoglobus fulgidus
95	<a href="#">c3bezC</a>	Alignment	not modelled	94.6	34	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> protease 4; <b>PDBTitle:</b> crystal structure of escherichia coli signal peptide peptidase (sppa),2 semet crystals
96	<a href="#">c3t9aA</a>	Alignment	not modelled	94.4	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> inositol pyrophosphate kinase; <b>PDBTitle:</b> crystal structure of the catalytic domain of human diphosphoinositol 2 pentakisphosphate kinase 2 (ppip5k2) in complex with amppnp at ph 7.0
97	<a href="#">c2z04A</a>	Alignment	not modelled	91.7	35	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylaminoimidazole carboxylase atpase <b>PDBTitle:</b> crystal structure of phosphoribosylaminoimidazole2 carboxylase atpase subunit from aquifex aeolicus
98	<a href="#">c3l6uA</a>	Alignment	not modelled	91.4	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc-type sugar transport system periplasmic <b>PDBTitle:</b> crystal structure of abc-type sugar transport system,2 periplasmic component from exiguobacterium sibiricum
99	<a href="#">c3kuxA</a>	Alignment	not modelled	86.2	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> structure of the ypo2259 putative oxidoreductase from yersinia pestis
100	<a href="#">c3clkB</a>	Alignment	not modelled	85.3	13	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcription regulator; <b>PDBTitle:</b> crystal structure of a transcription regulator from lactobacillus2 plantarum
101	<a href="#">c3c3kA</a>	Alignment	not modelled	85.2	19	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> alanine racemase; <b>PDBTitle:</b> crystal structure of an uncharacterized protein from actinobacillus2 succinogenes
102	<a href="#">c3ezvA</a>	Alignment	not modelled	81.4	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> monomethylamine corrinoid protein 1;



102	<a href="#">c3e2AA</a>	Alignment	not modelled	81.4	19	<b>PDBTitle:</b> structure of methanosarcina barkeri monomethylamine2 corrinoid protein
103	<a href="#">d1t35a</a>	Alignment	not modelled	79.7	17	<b>Fold:</b> MCP/YpsA-like <b>Superfamily:</b> MCP/YpsA-like <b>Family:</b> MoCo carrier protein-like
104	<a href="#">d2nvwa1</a>	Alignment	not modelled	78.3	8	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
105	<a href="#">c3qk7C</a>	Alignment	not modelled	77.8	17	<b>PDB header:</b> transcription regulator <b>Chain:</b> C: <b>PDB Molecule:</b> transcriptional regulators; <b>PDBTitle:</b> crystal structure of putative transcriptional regulator from yersinia2 pestis biovar microtus str. 91001
106	<a href="#">c3bolB</a>	Alignment	not modelled	76.8	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 5-methyltetrahydrofolate s-homocysteine <b>PDBTitle:</b> cobalamin-dependent methionine synthase (1-566) from2 thermotoga maritima complexed with zn2+
107	<a href="#">c2x7xA</a>	Alignment	not modelled	75.5	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sensor protein; <b>PDBTitle:</b> fructose binding periplasmic domain of hybrid two component2 system bt1754
108	<a href="#">d1yqea1</a>	Alignment	not modelled	75.0	17	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> AF0625-like <b>Family:</b> AF0625-like
109	<a href="#">c3k9cA</a>	Alignment	not modelled	73.7	18	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, laci family protein; <b>PDBTitle:</b> crystal structure of laci transcriptional regulator from rhodococcus2 species.
110	<a href="#">c2a5hC</a>	Alignment	not modelled	73.5	18	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> l-lysine 2,3-aminomutase; <b>PDBTitle:</b> 2.1 angstrom x-ray crystal structure of lysine-2,3-aminomutase from2 clostridium subterminale sb4, with michaelis analog (l-alpha-lysine3 external aldimine form of pyridoxal-5'-phosphate).
111	<a href="#">c3oqbF</a>	Alignment	not modelled	73.2	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> oxidoreductase; <b>PDBTitle:</b> crystal structure of putative oxidoreductase from bradyrhizobium2 japonicum usda 110
112	<a href="#">c3evnA</a>	Alignment	not modelled	73.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase, gfo/ldh/moca family; <b>PDBTitle:</b> crystal structure of putative oxidoreductase from streptococcus2 agalactiae 2603v/r
113	<a href="#">c3f4lF</a>	Alignment	not modelled	72.7	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> putative oxidoreductase yhhx; <b>PDBTitle:</b> crystal structure of a probable oxidoreductase yhhx in2 triclinic form. northeast structural genomics target er647
114	<a href="#">c3d02A</a>	Alignment	not modelled	72.7	13	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative laci-type transcriptional regulator; <b>PDBTitle:</b> crystal structure of periplasmic sugar-binding protein2 (yp_001338366.1) from klebsiella pneumoniae subsp. pneumoniae mgh3 78578 at 1.30 a resolution
115	<a href="#">c3lrxC</a>	Alignment	not modelled	72.5	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> putative hydrogenase; <b>PDBTitle:</b> crystal structure of the c-terminal domain (residues 78-226)2 of pf1911 hydrogenase from pyrococcus furiosus, northeast3 structural genomics consortium target pfr246a
116	<a href="#">d3bofa2</a>	Alignment	not modelled	71.6	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Homocysteine S-methyltransferase <b>Family:</b> Homocysteine S-methyltransferase
117	<a href="#">d1vhxa</a>	Alignment	not modelled	71.4	15	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Putative Holliday junction resolvase RuvX
118	<a href="#">d1jxha</a>	Alignment	not modelled	71.3	15	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Thiamin biosynthesis kinases
119	<a href="#">c2yxbA</a>	Alignment	not modelled	70.9	21	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> coenzyme b12-dependent mutase; <b>PDBTitle:</b> crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
120	<a href="#">c3oa0B</a>	Alignment	not modelled	70.1	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> lipopolysaccharide biosynthesis protein wbpB; <b>PDBTitle:</b> crystal structure of the wlbA (wbpB) dehydrogenase from thermus2 thermophilus in complex with nad and udp-glcnac