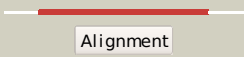

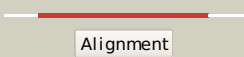

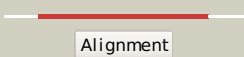

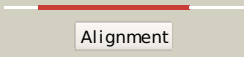

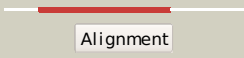

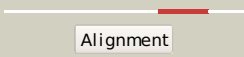
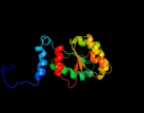
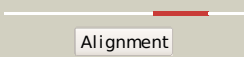

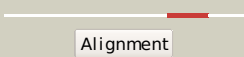

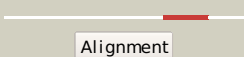

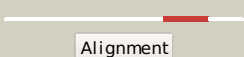



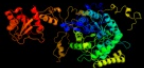










# Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P27253
Date	Thu Jan 5 11:43:33 GMT 2012
Unique Job ID	e9a796d14d3bb0a9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">cle1cA_</a>	 Alignment		100.0	58	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> methylmalonyl-coa mutase alpha chain; <b>PDBTitle:</b> methylmalonyl-coa mutase h244a mutant
2	<a href="#">c3bicA_</a>	 Alignment		100.0	58	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> methylmalonyl-coa mutase, mitochondrial precursor; <b>PDBTitle:</b> crystal structure of human methylmalonyl-coa mutase
3	<a href="#">c6reqB_</a>	 Alignment		100.0	27	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> protein (methylmalonyl-coa mutase); <b>PDBTitle:</b> methylmalonyl-coa mutase, 3-carboxypropyl-coa inhibitor complex
4	<a href="#">d7reqa1</a>	 Alignment		100.0	62	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Cobalamin (vitamin B12)-dependent enzymes <b>Family:</b> Methylmalonyl-CoA mutase, N-terminal (CoA-binding) domain
5	<a href="#">d7reqb1</a>	 Alignment		100.0	26	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Cobalamin (vitamin B12)-dependent enzymes <b>Family:</b> Methylmalonyl-CoA mutase, N-terminal (CoA-binding) domain
6	<a href="#">d7reqb2</a>	 Alignment		100.0	16	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Cobalamin (vitamin B12)-binding domain <b>Family:</b> Cobalamin (vitamin B12)-binding domain
7	<a href="#">d7reqa2</a>	 Alignment		100.0	53	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Cobalamin (vitamin B12)-binding domain <b>Family:</b> Cobalamin (vitamin B12)-binding domain
8	<a href="#">dlccwa_</a>	 Alignment		99.6	25	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Cobalamin (vitamin B12)-binding domain <b>Family:</b> Cobalamin (vitamin B12)-binding domain
9	<a href="#">dlxrsb1</a>	 Alignment		99.5	24	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Cobalamin (vitamin B12)-binding domain <b>Family:</b> Cobalamin (vitamin B12)-binding domain
10	<a href="#">clxrsB_</a>	 Alignment		99.5	24	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> d-lysine 5,6-aminomutase beta subunit; <b>PDBTitle:</b> crystal structure of lysine 5,6-aminomutase in complex with plp, 2 cobalamin, and 5'-deoxyadenosine
11	<a href="#">c2yxbA_</a>	 Alignment		99.4	42	<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 from <i>M. aeropyrum pernix</i>

12	<a href="#">c3koxA_</a>	Alignment		99.4	17	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> d-ornithine aminomutase e component; <b>PDBTitle:</b> crystal structure of ornithine 4,5 aminomutase in complex with 2,4-2 diaminobutyrate (anaerobic)
13	<a href="#">d1fmfa_</a>	Alignment		99.1	24	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Cobalamin (vitamin B12)-binding domain <b>Family:</b> Cobalamin (vitamin B12)-binding domain
14	<a href="#">c1y80A_</a>	Alignment		99.1	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> predicted cobalamin binding protein; <b>PDBTitle:</b> structure of a corrinoid (factor iim)-binding protein from2 moorella thermoacetica
15	<a href="#">c1bmtB_</a>	Alignment		99.0	18	<b>PDB header:</b> methyltransferase <b>Chain:</b> B: <b>PDB Molecule:</b> methionine synthase; <b>PDBTitle:</b> how a protein binds b12: a 3.0 angstrom x-ray structure of2 the b12-binding domains of methionine synthase
16	<a href="#">c2i2xD_</a>	Alignment		98.9	16	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> methyltransferase 1; <b>PDBTitle:</b> crystal structure of methanol:cobalamin methyltransferase complex2 mtabc from methanosarcina barkeri
17	<a href="#">d1ccwb_</a>	Alignment		98.9	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Cobalamin (vitamin B12)-dependent enzymes <b>Family:</b> Glutamate mutase, large subunit
18	<a href="#">c3ezxA_</a>	Alignment		98.8	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> monomethylamine corrinoid protein 1; <b>PDBTitle:</b> structure of methanosarcina barkeri monomethylamine2 corrinoid protein
19	<a href="#">d3bula2</a>	Alignment		98.7	17	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Cobalamin (vitamin B12)-binding domain <b>Family:</b> Cobalamin (vitamin B12)-binding domain
20	<a href="#">c1k98A_</a>	Alignment		98.5	19	<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
21	<a href="#">c1zfjA_</a>	Alignment	not modelled	95.6	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> inosine monophosphate dehydrogenase; <b>PDBTitle:</b> inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
22	<a href="#">d1krwa_</a>	Alignment	not modelled	95.6	13	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
23	<a href="#">c1ys7B_</a>	Alignment	not modelled	95.6	18	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulatory protein prra; <b>PDBTitle:</b> crystal structure of the response regulator protein prra complexed with2 mg2 +
24	<a href="#">d1o4ua1</a>	Alignment	not modelled	95.5	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Nicotinate/Quinolinate PRTase C-terminal domain-like <b>Family:</b> NadC C-terminal domain-like
25	<a href="#">c2b7pA_</a>	Alignment	not modelled	95.5	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable nicotinate-nucleotide pyrophosphorylase; <b>PDBTitle:</b> crystal structure of quinolinic acid phosphoribosyltransferase from2 helicobacter pylori
26	<a href="#">d1yioa2</a>	Alignment	not modelled	95.0	11	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
27	<a href="#">d1qpoa1</a>	Alignment	not modelled	95.0	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Nicotinate/Quinolinate PRTase C-terminal domain-like <b>Family:</b> NadC C-terminal domain-like
28	<a href="#">c2jbmA_</a>	Alignment	not modelled	95.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nicotinate-nucleotide pyrophosphorylase; <b>PDBTitle:</b> qprtase structure from human

29	<a href="#">c1o4uA_</a>	Alignment	not modelled	94.9	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> type ii quinolic acid phosphoribosyltransferase; <b>PDBTitle:</b> crystal structure of a nicotinate nucleotide pyrophosphorylase2 (tm1645) from thermotoga maritima at 2.50 a resolution
30	<a href="#">d1j5ta_</a>	Alignment	not modelled	94.6	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
31	<a href="#">d1wa3a1</a>	Alignment	not modelled	94.5	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
32	<a href="#">d1ys7a2</a>	Alignment	not modelled	94.5	17	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
33	<a href="#">c3qjaA_</a>	Alignment	not modelled	94.1	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> indole-3-glycerol phosphate synthase; <b>PDBTitle:</b> crystal structure of the mycobacterium tuberculosis indole-3-glycerol2 phosphate synthase (trpc) in apo form
34	<a href="#">d1mvoa_</a>	Alignment	not modelled	93.8	13	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
35	<a href="#">d1zesal</a>	Alignment	not modelled	93.7	10	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
36	<a href="#">c2c3zA_</a>	Alignment	not modelled	93.6	19	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> indole-3-glycerol phosphate synthase; <b>PDBTitle:</b> crystal structure of a truncated variant of indole-3-2 glycerol phosphate synthase from sulfobolus solfataricus
37	<a href="#">c3hdgE_</a>	Alignment	not modelled	93.2	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> E: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of the n-terminal domain of an2 uncharacterized protein (ws1339) from wolinnella3 succinogenes
38	<a href="#">d1u0sy_</a>	Alignment	not modelled	93.1	11	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
39	<a href="#">c1qpoA_</a>	Alignment	not modelled	92.6	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> quinolinate acid phosphoribosyl transferase; <b>PDBTitle:</b> quinolinate phosphoribosyl transferase (qaprtase) apo-enzyme from2 mycobacterium tuberculosis
40	<a href="#">d1muma_</a>	Alignment	not modelled	92.5	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Phosphoenolpyruvate mutase/isocitrate lyase-like
41	<a href="#">d2ayxa1</a>	Alignment	not modelled	92.5	11	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
42	<a href="#">d1a53a_</a>	Alignment	not modelled	92.1	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
43	<a href="#">c3ktoA_</a>	Alignment	not modelled	92.0	18	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator receiver protein; <b>PDBTitle:</b> crystal structure of response regulator receiver protein2 from pseudoalteromonas atlantica
44	<a href="#">c2yv1A_</a>	Alignment	not modelled	91.9	27	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> succinyl-coa ligase [adp-forming] subunit alpha; <b>PDBTitle:</b> crystal structure of succinyl-coa synthetase alpha chain from2 methanocaldococcus jannaschii dsm 2661
45	<a href="#">d1qapa1</a>	Alignment	not modelled	91.7	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Nicotinate/Quinolinate PRTase C-terminal domain-like <b>Family:</b> NadC C-terminal domain-like
46	<a href="#">c3b8fF_</a>	Alignment	not modelled	91.7	13	<b>PDB header:</b> lyase <b>Chain:</b> F: <b>PDB Molecule:</b> pa4872 oxaloacetate decarboxylase; <b>PDBTitle:</b> crystal structure of oxaloacetate decarboxylase from pseudomonas2 aeruginosa (pa4872) in complex with oxalate and mg2+.
47	<a href="#">c1x1oC_</a>	Alignment	not modelled	91.6	16	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> nicotinate-nucleotide pyrophosphorylase; <b>PDBTitle:</b> crystal structure of project id tt0268 from thermus thermophilus hb8
48	<a href="#">c3eool_</a>	Alignment	not modelled	91.6	16	<b>PDB header:</b> lyase <b>Chain:</b> L: <b>PDB Molecule:</b> methylisocitrate lyase; <b>PDBTitle:</b> 2.9a crystal structure of methyl-isocitrate lyase from2 burkholderia pseudomallei
49	<a href="#">c2qr3A_</a>	Alignment	not modelled	91.4	13	<b>PDB header:</b> transcription regulator; <b>Chain:</b> A: <b>PDB Molecule:</b> two-component system response regulator; <b>PDBTitle:</b> crystal structure of the n-terminal signal receiver domain of two-2 component system response regulator from bacteroides fragilis
50	<a href="#">c3ih1A_</a>	Alignment	not modelled	91.3	11	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> methylisocitrate lyase; <b>PDBTitle:</b> crystal structure of carboxyvinyl-carboxyphosphonate phosphorylmutase2 from bacillus anthracis
51	<a href="#">d1zh2a1</a>	Alignment	not modelled	91.2	11	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
52	<a href="#">d1dbwa_</a>	Alignment	not modelled	91.2	16	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
53	<a href="#">d1peya_</a>	Alignment	not modelled	90.9	8	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like

					<b>Family:</b> CheY-related
54	<a href="#">dli4na_</a>	Alignment	not modelled	90.8	17 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
55	<a href="#">c3jteA_</a>	Alignment	not modelled	90.5	15 <b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator receiver protein; <b>PDBTitle:</b> crystal structure of response regulator receiver domain2 protein from clostridium thermocellum
56	<a href="#">d2nu7b1_</a>	Alignment	not modelled	90.4	15 <b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Succinyl-CoA synthetase domains <b>Family:</b> Succinyl-CoA synthetase domains
57	<a href="#">c3tdmD_</a>	Alignment	not modelled	90.3	9 <b>PDB header:</b> de novo protein <b>Chain:</b> D: <b>PDB Molecule:</b> computationally designed two-fold symmetric tim-barrel <b>PDBTitle:</b> computationally designed tim-barrel protein, halflfr
58	<a href="#">c2ayxA_</a>	Alignment	not modelled	90.3	8 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sensor kinase protein rcsc; <b>PDBTitle:</b> solution structure of the e.coli rcsc c-terminus (residues2 700-949) containing linker region and phosphoreceiver3 domain
59	<a href="#">c1gv1D_</a>	Alignment	not modelled	90.1	18 <b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> malate dehydrogenase; <b>PDBTitle:</b> structural basis for thermophilic protein stability:2 structures of thermophilic and mesophilic malate3 dehydrogenases
60	<a href="#">c1ldbA_</a>	Alignment	not modelled	89.9	27 <b>PDB header:</b> oxidoreductase(choh(d)-nad(a)) <b>Chain:</b> A: <b>PDB Molecule:</b> apo-l-lactate dehydrogenase; <b>PDBTitle:</b> structure determination and refinement of bacillus2 stearothermophilus lactate dehydrogenase
61	<a href="#">c3eywA_</a>	Alignment	not modelled	89.8	15 <b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> c-terminal domain of glutathione-regulated potassium-efflux <b>PDBTitle:</b> crystal structure of the c-terminal domain of e. coli kefc in complex2 with keff
62	<a href="#">c1ytkA_</a>	Alignment	not modelled	89.7	23 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nicotinate phosphoribosyltransferase from thermoplasma <b>PDBTitle:</b> crystal structure of a nicotinate phosphoribosyltransferase from2 thermoplasma acidophilum with nicotinate mononucleotide
63	<a href="#">c3l0gD_</a>	Alignment	not modelled	89.7	16 <b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> nicotinate-nucleotide pyrophosphorylase; <b>PDBTitle:</b> crystal structure of nicotinate-nucleotide pyrophosphorylase from2 ehrlichia chaffeensis at 2.05a resolution
64	<a href="#">d1zfja1_</a>	Alignment	not modelled	89.6	16 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Inosine monophosphate dehydrogenase (IMPDH) <b>Family:</b> Inosine monophosphate dehydrogenase (IMPDH)
65	<a href="#">d2d59a1_</a>	Alignment	not modelled	89.5	17 <b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> CoA-binding domain
66	<a href="#">c3lyeA_</a>	Alignment	not modelled	89.3	20 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> oxaloacetate acetyl hydrolase; <b>PDBTitle:</b> crystal structure of oxaloacetate acetylhydrolase
67	<a href="#">c2yv2A_</a>	Alignment	not modelled	89.3	22 <b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> succinyl-coa synthetase alpha chain; <b>PDBTitle:</b> crystal structure of succinyl-coa synthetase alpha chain from2 aeropyrum pernix k1
68	<a href="#">c1zlpA_</a>	Alignment	not modelled	89.1	19 <b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> petal death protein; <b>PDBTitle:</b> petal death protein psr132 with cysteine-linked glutaraldehyde forming2 a thiohemiacetal adduct
69	<a href="#">d1y81a1_</a>	Alignment	not modelled	89.0	13 <b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> CoA-binding domain
70	<a href="#">c3nhzA_</a>	Alignment	not modelled	88.3	14 <b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> two component system transcriptional regulator mtra; <b>PDBTitle:</b> structure of n-terminal domain of mtra
71	<a href="#">d1y0ea_</a>	Alignment	not modelled	88.3	19 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> NanE-like
72	<a href="#">d1jr1a1_</a>	Alignment	not modelled	88.1	16 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Inosine monophosphate dehydrogenase (IMPDH) <b>Family:</b> Inosine monophosphate dehydrogenase (IMPDH)
73	<a href="#">c2jk1A_</a>	Alignment	not modelled	88.0	16 <b>PDB header:</b> dna-binding <b>Chain:</b> A: <b>PDB Molecule:</b> hydrogenase transcriptional regulatory protein hupr1; <b>PDBTitle:</b> crystal structure of the wild-type hupr receiver domain
74	<a href="#">d1piia2_</a>	Alignment	not modelled	87.9	13 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
75	<a href="#">d1s2wa_</a>	Alignment	not modelled	87.9	15 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Phosphoenolpyruvate mutase/isocitrate lyase-like
76	<a href="#">c1me9A_</a>	Alignment	not modelled	87.8	18 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> inosine-5'-monophosphate dehydrogenase; <b>PDBTitle:</b> inosine monophosphate dehydrogenase (impdh) from2 tritrichomonas foetus with imp bound
77	<a href="#">c3crnA_</a>	Alignment	not modelled	87.7	12 <b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator receiver domain protein, chey-like; <b>PDBTitle:</b> crystal structure of response regulator receiver domain protein (chey-2 like) from methanospirillum hungatei jf-1
					<b>PDB header:</b> oxidoreductase

78	<a href="#">c1ur5C_</a>	Alignment	not modelled	87.6	16	<b>Chain:</b> C: <b>PDB Molecule:</b> malate dehydrogenase; <b>PDBTitle:</b> stabilization of a tetrameric malate dehydrogenase by2 introduction of a disulfide bridge at the dimer/dimer3 interface
79	<a href="#">c3pajA_</a>	Alignment	not modelled	87.3	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nicotinate-nucleotide pyrophosphorylase, carboxylating; <b>PDBTitle:</b> 2.00 angstrom resolution crystal structure of a quinolinate2 phosphoribosyltransferase from vibrio cholerae o1 biovar eltor str.3 n16961
80	<a href="#">c1e8cB_</a>	Alignment	not modelled	87.2	15	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-n-acetylmuramoylalanyl-d-glutamate--2,6- <b>PDBTitle:</b> structure of mure the udp-n-acetylmuramyl tripeptide2 synthetase from e. coli
81	<a href="#">d1ny5a1</a>	Alignment	not modelled	87.1	15	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
82	<a href="#">c1qapA_</a>	Alignment	not modelled	86.9	19	<b>PDB header:</b> glycosyltransferase <b>Chain:</b> A: <b>PDB Molecule:</b> quinolinic acid phosphoribosyltransferase; <b>PDBTitle:</b> quinolinic acid phosphoribosyltransferase with bound2 quinolinic acid
83	<a href="#">d1qkka_</a>	Alignment	not modelled	86.7	13	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
84	<a href="#">d1jbea_</a>	Alignment	not modelled	86.6	7	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
85	<a href="#">c2fpgA_</a>	Alignment	not modelled	86.5	10	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> succinyl-coa ligase [gdp-forming] alpha-chain, <b>PDBTitle:</b> crystal structure of pig gtp-specific succinyl-coa2 synthetase in complex with gdp
86	<a href="#">c2jrlA_</a>	Alignment	not modelled	86.3	10	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator (ntrc family); <b>PDBTitle:</b> solution structure of the beryllofluoride-activated ntrc4 receiver2 domain dimer
87	<a href="#">c2v6bB_</a>	Alignment	not modelled	86.2	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> l-lactate dehydrogenase; <b>PDBTitle:</b> crystal structure of lactate dehydrogenase from deinococcus2 radiodurans (apo form)
88	<a href="#">c3fa4D_</a>	Alignment	not modelled	86.1	17	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> 2,3-dimethylmalate lyase; <b>PDBTitle:</b> crystal structure of 2,3-dimethylmalate lyase, a pep mutase/isocitrate2 lyase superfamily member, triclinic crystal form
89	<a href="#">d1iuka_</a>	Alignment	not modelled	86.0	9	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> CoA-binding domain
90	<a href="#">d1ujqa_</a>	Alignment	not modelled	86.0	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Phosphoenolpyruvate mutase/isocitrate lyase-like
91	<a href="#">d1thfd_</a>	Alignment	not modelled	85.9	8	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Histidine biosynthesis enzymes
92	<a href="#">d1xcfa_</a>	Alignment	not modelled	85.7	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
93	<a href="#">c3dl2A_</a>	Alignment	not modelled	85.4	24	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin-conjugating enzyme e2 variant 3; <b>PDBTitle:</b> hexagonal structure of the Idh domain of human ubiquitin-2 conjugating enzyme e2-like isoform a
94	<a href="#">c3rqia_</a>	Alignment	not modelled	85.3	14	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator protein; <b>PDBTitle:</b> crystal structure of a response regulator protein from burkholderia2 pseudomallei with a phosphorylated aspartic acid, calcium ion and3 citrate
95	<a href="#">c2v82A_</a>	Alignment	not modelled	85.3	21	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-dehydro-3-deoxy-6-phosphogalactonate aldolase; <b>PDBTitle:</b> kdpgal complexed to kdpgal
96	<a href="#">d2pl1a1</a>	Alignment	not modelled	84.9	11	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
97	<a href="#">c8ldhA_</a>	Alignment	not modelled	84.7	20	<b>PDB header:</b> oxidoreductase(choh(d)-nad(a)) <b>Chain:</b> A: <b>PDB Molecule:</b> m4 apo-lactate dehydrogenase; <b>PDBTitle:</b> refined crystal structure of dogfish m4 apo-lactate2 dehydrogenase
98	<a href="#">d1rd5a_</a>	Alignment	not modelled	84.7	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
99	<a href="#">c3cu5B_</a>	Alignment	not modelled	84.7	10	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> two component transcriptional regulator, arac family; <b>PDBTitle:</b> crystal structure of a two component transcriptional regulator arac2 from clostridium phytofermentans isdg
100	<a href="#">c1yadD_</a>	Alignment	not modelled	84.5	15	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> regulatory protein teni; <b>PDBTitle:</b> structure of teni from bacillus subtilis
101	<a href="#">c2nu8D_</a>	Alignment	not modelled	84.1	23	<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
102	<a href="#">d1vc4a_</a>	Alignment	not modelled	84.1	22	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes



103	<a href="#">c2zwmA_</a>	Alignment	not modelled	83.8	11	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein yycf; <b>PDBTitle:</b> crystal structure of yycf receiver domain from bacillus2 subtilis
104	<a href="#">c3a0rB_</a>	Alignment	not modelled	83.8	8	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> response regulator; <b>PDBTitle:</b> crystal structure of histidine kinase thka (tm1359) in complex with2 response regulator protein trra (tm1360)
105	<a href="#">c2x41A_</a>	Alignment	not modelled	83.7	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-glucosidase; <b>PDBTitle:</b> structure of beta-glucosidase 3b from thermotoga neapolitana2 in complex with glucose
106	<a href="#">c2p10D_</a>	Alignment	not modelled	83.5	21	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> ml19387 protein; <b>PDBTitle:</b> crystal structure of a putative phosphonopyruvate hydrolase (ml19387)2 from mesorhizobium loti maff303099 at 2.15 a resolution
107	<a href="#">c2d4aC_</a>	Alignment	not modelled	83.4	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> malate dehydrogenase; <b>PDBTitle:</b> structure of the malate dehydrogenase from aeropyrum pernix
108	<a href="#">c1hyhA_</a>	Alignment	not modelled	83.3	27	<b>PDB header:</b> oxidoreductase (choh(d)-nad+(a)) <b>Chain:</b> A: <b>PDB Molecule:</b> l-2-hydroxyisocaproate dehydrogenase; <b>PDBTitle:</b> crystal structure of l-2-hydroxyisocaproate dehydrogenase from2 lactobacillus confusus at 2.2 angstroms resolution-an example of3 strong asymmetry between subunits
109	<a href="#">c3b2nA_</a>	Alignment	not modelled	83.2	10	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein q99uf4; <b>PDBTitle:</b> crystal structure of dna-binding response regulator, luxr family, from2 staphylococcus aureus
110	<a href="#">c2gjlA_</a>	Alignment	not modelled	83.1	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein pa1024; <b>PDBTitle:</b> crystal structure of 2-nitropropane dioxygenase
111	<a href="#">c3tqvA_</a>	Alignment	not modelled	82.9	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nicotinate-nucleotide pyrophosphorylase; <b>PDBTitle:</b> structure of the nicotinate-nucleotide pyrophosphorylase from2 francisella tularensis.
112	<a href="#">c1zn2A_</a>	Alignment	not modelled	82.9	10	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> response regulatory protein; <b>PDBTitle:</b> low resolution structure of response regulator styr
113	<a href="#">c3cfyA_</a>	Alignment	not modelled	82.8	8	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative luxo repressor protein; <b>PDBTitle:</b> crystal structure of signal receiver domain of putative luxo2 repressor protein from vibrio parahaemolyticus
114	<a href="#">c3d0oA_</a>	Alignment	not modelled	82.8	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-lactate dehydrogenase 1; <b>PDBTitle:</b> crystal structure of lactate dehydrogenase from2 staphylococcus aureus
115	<a href="#">c3inpA_</a>	Alignment	not modelled	82.7	14	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> d-ribulose-phosphate 3-epimerase; <b>PDBTitle:</b> 2.05 angstrom resolution crystal structure of d-ribulose-phosphate 3-2 epimerase from francisella tularensis.
116	<a href="#">d2a9pa1</a>	Alignment	not modelled	82.6	11	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
117	<a href="#">d1znnal</a>	Alignment	not modelled	82.5	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> PdxS-like
118	<a href="#">d1ytda1</a>	Alignment	not modelled	82.4	23	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Nicotinate/Quinolinate PRTase C-terminal domain-like <b>Family:</b> NadC C-terminal domain-like
119	<a href="#">c3nepX_</a>	Alignment	not modelled	82.2	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> X: <b>PDB Molecule:</b> malate dehydrogenase; <b>PDBTitle:</b> 1.55a resolution structure of malate dehydrogenase from salinibacter2 ruber
120	<a href="#">c3ilmD_</a>	Alignment	not modelled	82.2	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> alr3790 protein; <b>PDBTitle:</b> crystal structure of the alr3790 protein from anabaena sp. northeast2 structural genomics consortium target nsr437h