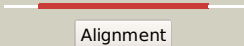

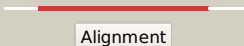

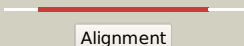







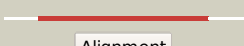




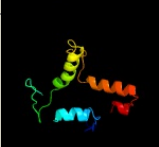






# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1054 (- )_1176933_1177247
Date	Wed Jul 31 22:05:13 BST 2019
Unique Job ID	6fba87eb50d374e0

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3nkhB_</a>	 Alignment		99.2	19	<b>PDB header:</b> recombination <b>Chain:</b> B: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> crystal structure of integrase from mrsa strain staphylococcus aureus
2	<a href="#">c1z1bA_</a>	 Alignment		99.1	13	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> crystal structure of a lambda integrase dimer bound to a2 coc' core site
3	<a href="#">c5dcfA_</a>	 Alignment		99.1	19	<b>PDB header:</b> recombination <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine recombinase xerd,dna translocase ftsk; <b>PDBTitle:</b> c-terminal domain of xerd recombinase in complex with gamma domain of ftsk
4	<a href="#">c5jivA_</a>	 Alignment		99.1	18	<b>PDB header:</b> recombination <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine recombinase xerh; <b>PDBTitle:</b> crystal structure of xerh site-specific recombinase bound to 2 palindromic difh substrate: post-cleavage complex
5	<a href="#">c2a3vA_</a>	 Alignment		98.8	15	<b>PDB header:</b> recombination <b>Chain:</b> A: <b>PDB Molecule:</b> site-specific recombinase inti4; <b>PDBTitle:</b> structural basis for broad dna-specificity in integron recombination
6	<a href="#">c6en2A_</a>	 Alignment		98.6	17	<b>PDB header:</b> recombination <b>Chain:</b> A: <b>PDB Molecule:</b> int protein; <b>PDBTitle:</b> structure of the tn1549 transposon integrase (aa 82-397, r225k) in 2 complex with a circular intermediate dna (ci6b-dna)
7	<a href="#">c5vzfA_</a>	 Alignment		98.5	18	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> gp33; <b>PDBTitle:</b> integrase from mycobacterium phage brujita
8	<a href="#">d1p7da_</a>	 Alignment		98.4	13	<b>Fold:</b> DNA breaking-rejoining enzymes <b>Superfamily:</b> DNA breaking-rejoining enzymes <b>Family:</b> Lambda integrase-like, catalytic core
9	<a href="#">c1ma7A_</a>	 Alignment		98.3	9	<b>PDB header:</b> hydrolase, ligase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> cre recombinase; <b>PDBTitle:</b> crystal structure of cre site-specific recombinase 2 complexed with a mutant dna substrate, loxp-a8/t27
10	<a href="#">c5hxyE_</a>	 Alignment		98.2	19	<b>PDB header:</b> recombination <b>Chain:</b> E: <b>PDB Molecule:</b> tyrosine recombinase xera; <b>PDBTitle:</b> crystal structure of xera recombinase
11	<a href="#">c1crxA_</a>	 Alignment		98.0	11	<b>PDB header:</b> replication/dna <b>Chain:</b> A: <b>PDB Molecule:</b> cre recombinase; <b>PDBTitle:</b> cre recombinase/dna complex reaction intermediate i

12	<a href="#">d1aiha_</a>	Alignment		98.0	19	<b>Fold:</b> DNA breaking-rejoining enzymes <b>Superfamily:</b> DNA breaking-rejoining enzymes <b>Family:</b> Lambda integrase-like, catalytic core
13	<a href="#">d1ae9a_</a>	Alignment		97.8	13	<b>Fold:</b> DNA breaking-rejoining enzymes <b>Superfamily:</b> DNA breaking-rejoining enzymes <b>Family:</b> Lambda integrase-like, catalytic core
14	<a href="#">d5crxb2</a>	Alignment		97.7	11	<b>Fold:</b> DNA breaking-rejoining enzymes <b>Superfamily:</b> DNA breaking-rejoining enzymes <b>Family:</b> Lambda integrase-like, catalytic core
15	<a href="#">c4a8eA_</a>	Alignment		97.6	19	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> probable tyrosine recombinase xerc-like; <b>PDBTitle:</b> the structure of a dimeric xer recombinase from archaea
16	<a href="#">c5c6kB_</a>	Alignment		97.4	24	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> bacteriophage p2 integrase catalytic domain
17	<a href="#">c1a0pA_</a>	Alignment		97.2	19	<b>PDB header:</b> dna recombination <b>Chain:</b> A: <b>PDB Molecule:</b> site-specific recombinase xerd; <b>PDBTitle:</b> site-specific recombinase, xerd
18	<a href="#">d1a0pa2</a>	Alignment		96.6	19	<b>Fold:</b> DNA breaking-rejoining enzymes <b>Superfamily:</b> DNA breaking-rejoining enzymes <b>Family:</b> Lambda integrase-like, catalytic core
19	<a href="#">d1f44a2</a>	Alignment		95.9	9	<b>Fold:</b> DNA breaking-rejoining enzymes <b>Superfamily:</b> DNA breaking-rejoining enzymes <b>Family:</b> Lambda integrase-like, catalytic core
20	<a href="#">c3uxuA_</a>	Alignment		95.4	13	<b>PDB header:</b> recombination <b>Chain:</b> A: <b>PDB Molecule:</b> probable integrase; <b>PDBTitle:</b> the structure of the catalytic domain of the sulfobolus spindle-shaped2 viral integrase reveals an evolutionarily conserved catalytic core3 and supports a mechanism of dna cleavage in trans
21	<a href="#">c5ks8F_</a>	Alignment	not modelled	58.4	4	<b>PDB header:</b> ligase <b>Chain:</b> F: <b>PDB Molecule:</b> pyruvate carboxylase subunit beta; <b>PDBTitle:</b> crystal structure of two-subunit pyruvate carboxylase from2 methylobacillus flagellatus
22	<a href="#">c5ks8D_</a>	Alignment	not modelled	47.5	4	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> pyruvate carboxylase subunit beta; <b>PDBTitle:</b> crystal structure of two-subunit pyruvate carboxylase from2 methylobacillus flagellatus
23	<a href="#">c3bleA_</a>	Alignment	not modelled	45.4	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> citramalate synthase from leptospira interrogans; <b>PDBTitle:</b> crystal structure of the catalytic domain of licms in complexed with2 malonate
24	<a href="#">c3ivuB_</a>	Alignment	not modelled	43.4	8	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> homocitrate synthase, mitochondrial; <b>PDBTitle:</b> homocitrate synthase lys4 bound to 2-og
25	<a href="#">c2nx9B_</a>	Alignment	not modelled	39.8	10	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> oxaloacetate decarboxylase 2, subunit alpha; <b>PDBTitle:</b> crystal structure of the carboxyltransferase domain of the2 oxaloacetate decarboxylase na+ pump from vibrio cholerae
26	<a href="#">c1ydnA_</a>	Alignment	not modelled	38.1	8	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> hydroxymethylglutaryl-coa lyase; <b>PDBTitle:</b> crystal structure of the hmg-coa lyase from brucella melitensis,2 northeast structural genomics target lr35.
27	<a href="#">d1rqba2</a>	Alignment	not modelled	36.5	10	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> HMGL-like
						<b>PDB header:</b> lyase/oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> 4-hydroxy-2-oxoalate aldolase; <b>PDBTitle:</b> crystal and solution structures of the bifunctional

28	<a href="#">c4lrtC_</a>	Alignment	not modelled	35.5	15	enzyme2 (aldolase/aldehyde dehydrogenase) from thermomonospora curvata,3 reveal a cofactor-binding domain motion during nad+ and coa4 accommodation within the shared cofactor-binding site
29	<a href="#">c4jn6C_</a>	Alignment	not modelled	35.4	13	<b>PDB header:</b> lyase/oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> 4-hydroxy-2-oxovalerate aldolase; <b>PDBTitle:</b> crystal structure of the aldolase-dehydrogenase complex from2 mycobacterium tuberculosis hrv37
30	<a href="#">c3dxiB_</a>	Alignment	not modelled	32.9	8	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative aldolase; <b>PDBTitle:</b> crystal structure of the n-terminal domain of a putative2 aldolase (bvj_2661) from bacteroides vulgatus
31	<a href="#">c3ewbX_</a>	Alignment	not modelled	30.2	9	<b>PDB header:</b> transferase <b>Chain:</b> X: <b>PDB Molecule:</b> 2-isopropylmalate synthase; <b>PDBTitle:</b> crystal structure of n-terminal domain of putative 2-isopropylmalate2 synthase from listeria monocytogenes
32	<a href="#">c3rmjB_</a>	Alignment	not modelled	27.1	8	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-isopropylmalate synthase; <b>PDBTitle:</b> crystal structure of truncated alpha-isopropylmalate synthase from2 neisseria meningitidis
33	<a href="#">c2qqdG_</a>	Alignment	not modelled	27.0	25	<b>PDB header:</b> lyase <b>Chain:</b> G: <b>PDB Molecule:</b> pyruvoyl-dependent arginine decarboxylase (ec <b>PDBTitle:</b> n47a mutant of pyruvoyl-dependent arginine decarboxylase2 from methanococcus jannashii
34	<a href="#">c6e1jB_</a>	Alignment	not modelled	26.2	9	<b>PDB header:</b> plant protein <b>Chain:</b> B: <b>PDB Molecule:</b> 2-isopropylmalate synthase, a genome specific 1; <b>PDBTitle:</b> crystal structure of methylthioalkylmalate synthase (bjmam1.1) from2 brassica juncea
35	<a href="#">c3eegB_</a>	Alignment	not modelled	25.2	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-isopropylmalate synthase; <b>PDBTitle:</b> crystal structure of a 2-isopropylmalate synthase from2 cytophaga hutchinsonii
36	<a href="#">c2hjnA_</a>	Alignment	not modelled	24.8	14	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> maintenance of ploidy protein mob1; <b>PDBTitle:</b> structural and functional analysis of saccharomyces2 cerevisiae mob1
37	<a href="#">c2xfiB_</a>	Alignment	not modelled	24.8	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> dyne7; <b>PDBTitle:</b> induced-fit and allosteric effects upon polyene binding2 revealed by crystal structures of the dynemicin3 thioesterase
38	<a href="#">c2b9sA_</a>	Alignment	not modelled	23.6	18	<b>PDB header:</b> isomerase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> topoisomerase i-like protein; <b>PDBTitle:</b> crystal structure of heterodimeric l. donovani topoisomerase i-2 vanadate-dna complex
39	<a href="#">c3hzpA_</a>	Alignment	not modelled	21.4	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> ntf2-like protein of unknown function; <b>PDBTitle:</b> crystal structure of ntf2-like protein of unknown function mn2a_05052 from prochlorococcus marinus (yp_291699.1) from prochlorococcus sp.3 natl2a at 1.40 a resolution
40	<a href="#">c5eo4A_</a>	Alignment	not modelled	20.8	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> thioesterase; <b>PDBTitle:</b> structural and biochemical characterization of the hypothetical2 protein sav2348 from staphylococcus aureus.
41	<a href="#">c1nmvG_</a>	Alignment	not modelled	18.3	8	<b>PDB header:</b> lyase/oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> 4-hydroxy-2-oxovalerate aldolase; <b>PDBTitle:</b> crystal structure of a bifunctional aldolase-dehydrogenase :2 sequestering a reactive and volatile intermediate
42	<a href="#">c1ydoC_</a>	Alignment	not modelled	17.8	12	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> hmg-coa lyase; <b>PDBTitle:</b> crystal structure of the bacillis subtilis hmg-coa lyase, northeast2 structural genomics target sr181.
43	<a href="#">c2w3xE_</a>	Alignment	not modelled	17.7	20	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> cale7; <b>PDBTitle:</b> crystal structure of a bifunctional hotdog fold2 thioesterase in enediyne biosynthesis, cale7
44	<a href="#">c4ov9A_</a>	Alignment	not modelled	17.1	8	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> isopropylmalate synthase; <b>PDBTitle:</b> structure of isopropylmalate synthase binding with alpha-2 isopropylmalate
45	<a href="#">d1k4ta2</a>	Alignment	not modelled	17.0	16	<b>Fold:</b> DNA breaking-rejoining enzymes <b>Superfamily:</b> DNA breaking-rejoining enzymes <b>Family:</b> Eukaryotic DNA topoisomerase I, catalytic core
46	<a href="#">d1rr8c1</a>	Alignment	not modelled	16.4	15	<b>Fold:</b> DNA breaking-rejoining enzymes <b>Superfamily:</b> DNA breaking-rejoining enzymes <b>Family:</b> Eukaryotic DNA topoisomerase I, catalytic core
47	<a href="#">c3m0zD_</a>	Alignment	not modelled	14.9	13	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> putative aldolase; <b>PDBTitle:</b> crystal structure of putative aldolase from klebsiella pneumoniae.
48	<a href="#">c1rr2A_</a>	Alignment	not modelled	13.5	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> transcarboxylase 5s subunit; <b>PDBTitle:</b> propionibacterium shermanii transcarboxylase 5s subunit bound to 2-2 ketobutyric acid
49	<a href="#">c4lqqB_</a>	Alignment	not modelled	13.0	16	<b>PDB header:</b> transferase/transferase activator <b>Chain:</b> B: <b>PDB Molecule:</b> cbk1 kinase activator protein mob2; <b>PDBTitle:</b> crystal structure of the cbk1(t743e)-mob2 kinase-coactivator complex2 in crystal form b
50	<a href="#">c2bcwC_</a>	Alignment	not modelled	12.4	14	<b>PDB header:</b> ribosome <b>Chain:</b> C: <b>PDB Molecule:</b> elongation factor g; <b>PDBTitle:</b> coordinates of the n-terminal domain of ribosomal protein l11,c-2 terminal domain of ribosomal protein l7/l12 and a portion of the g3 domain of elongation factor g, as fitted into cryo-em map of an4 escherichia coli 70s*ef-g*gdp*fusidic acid complex
51	<a href="#">c1a31A_</a>	Alignment	not modelled	11.6	19	<b>PDB header:</b> isomerase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> protein (topoisomerase i); <b>PDBTitle:</b> human reconstituted dna topoisomerase i in covalent complex2 with a 22 base pair dna duplex
52	<a href="#">d2hlja1</a>	Alignment	not modelled	10.5	18	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase

						<b>Family:</b> 4HBT-like
53	<a href="#">d2oiwa1</a>	Alignment	not modelled	10.3	18	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
54	<a href="#">d2oafa1</a>	Alignment	not modelled	10.2	14	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
55	<a href="#">c2cw6B</a>	Alignment	not modelled	10.0	11	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> hydroxymethylglutaryl-coa lyase, mitochondrial; <b>PDBTitle:</b> crystal structure of human hmg-coa lyase: insights into2 catalysis and the molecular basis for3 hydroxymethylglutaric aciduria
56	<a href="#">c2ftpA</a>	Alignment	not modelled	9.8	12	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> hydroxymethylglutaryl-coa lyase; <b>PDBTitle:</b> crystal structure of hydroxymethylglutaryl-coa lyase from pseudomonas2 aeruginosa
57	<a href="#">d1x9ya2</a>	Alignment	not modelled	9.7	16	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> Cystatin/monellin <b>Family:</b> Staphopain B, prodomain
58	<a href="#">c3ck1B</a>	Alignment	not modelled	9.3	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative thioesterase; <b>PDBTitle:</b> crystal structure of a putative thioesterase (reut_a2179) from2 ralstonia eutropha jmp134 at 1.74 a resolution
59	<a href="#">c1p6gE</a>	Alignment	not modelled	9.3	13	<b>PDB header:</b> ribosome <b>Chain:</b> E: <b>PDB Molecule:</b> 30s ribosomal protein s5; <b>PDBTitle:</b> real space refined coordinates of the 30s subunit fitted into the low2 resolution cryo-em map of the ef-g.gtp state of e. coli 70s ribosome
60	<a href="#">d1hjra</a>	Alignment	not modelled	8.9	15	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> RuvC resolvase
61	<a href="#">d2uube1</a>	Alignment	not modelled	8.6	11	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> Translational machinery components
62	<a href="#">c6a4cA</a>	Alignment	not modelled	8.5	22	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein mxan_0049; <b>PDBTitle:</b> solution structure of mxan_0049
63	<a href="#">d1w26a2</a>	Alignment	not modelled	8.4	19	<b>Fold:</b> Ribosome binding domain-like <b>Superfamily:</b> Trigger factor ribosome-binding domain <b>Family:</b> Trigger factor ribosome-binding domain
64	<a href="#">d1ka8a</a>	Alignment	not modelled	7.8	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> P4 origin-binding domain-like
65	<a href="#">d2qale1</a>	Alignment	not modelled	7.6	11	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> Translational machinery components
66	<a href="#">d1h3oa</a>	Alignment	not modelled	7.5	19	<b>Fold:</b> Histone-fold <b>Superfamily:</b> Histone-fold <b>Family:</b> TBP-associated factors, TAFs
67	<a href="#">c1h3oA</a>	Alignment	not modelled	7.5	19	<b>PDB header:</b> transcription/tdbp-associated factors <b>Chain:</b> A: <b>PDB Molecule:</b> transcription initiation factor tfiid 135 kda subunit; <b>PDBTitle:</b> crystal structure of the human taf4-taf12 (tafi135-tafii20) complex
68	<a href="#">c4qj1A</a>	Alignment	not modelled	7.5	11	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino) phosphoribosylamino] <b>PDBTitle:</b> crystal structure of 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)2 methylideneamino] imidazole-4-carboxamide isomerase (hisa).
69	<a href="#">d1nvma2</a>	Alignment	not modelled	7.2	8	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> HMGL-like
70	<a href="#">c4y9iA</a>	Alignment	not modelled	7.1	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> mycobacterium tuberculosis paralogous family 11; <b>PDBTitle:</b> structure of f420-h2 dependent reductase (fdr-a) msmeg_2027
71	<a href="#">d1p9ya</a>	Alignment	not modelled	7.1	19	<b>Fold:</b> Ribosome binding domain-like <b>Superfamily:</b> Trigger factor ribosome-binding domain <b>Family:</b> Trigger factor ribosome-binding domain
72	<a href="#">c3bg3B</a>	Alignment	not modelled	6.9	8	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> pyruvate carboxylase, mitochondrial; <b>PDBTitle:</b> crystal structure of human pyruvate carboxylase (missing the biotin2 carboxylase domain at the n-terminus)
73	<a href="#">d1t11a2</a>	Alignment	not modelled	6.8	10	<b>Fold:</b> Ribosome binding domain-like <b>Superfamily:</b> Trigger factor ribosome-binding domain <b>Family:</b> Trigger factor ribosome-binding domain
74	<a href="#">d1hlva2</a>	Alignment	not modelled	6.5	11	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Centromere-binding
75	<a href="#">d1p4wa</a>	Alignment	not modelled	6.4	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> C-terminal effector domain of the bipartite response regulators <b>Family:</b> GerE-like (LuxR/UhpA family of transcriptional regulators)
76	<a href="#">c2d3o1</a>	Alignment	not modelled	6.4	14	<b>PDB header:</b> ribosome <b>Chain:</b> 1: <b>PDB Molecule:</b> trigger factor; <b>PDBTitle:</b> structure of ribosome binding domain of the trigger factor on the 50s2 ribosomal subunit from d. radiodurans
77	<a href="#">c3a9iA</a>	Alignment	not modelled	6.2	6	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> homocitrate synthase; <b>PDBTitle:</b> crystal structure of homocitrate synthase from thermus

						thermophilus2 complexed with lys
78	<a href="#">d2ia9a1</a>	Alignment	not modelled	5.8	12	<b>Fold:</b> SpoVG-like <b>Superfamily:</b> SpoVG-like <b>Family:</b> SpoVG-like
79	<a href="#">c2zyfA</a>	Alignment	not modelled	5.6	8	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> homocitrate synthase; <b>PDBTitle:</b> crystal structure of homocitrate synthase from thermophilus2 complexed with magnesium ion and alpha-ketoglutarate
80	<a href="#">c4lifuA</a>	Alignment	not modelled	5.6	5	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> regulatory protein sdia; <b>PDBTitle:</b> crystal structure of escherichia coli sdia in the space group c2
81	<a href="#">d1hywa</a>	Alignment	not modelled	5.5	23	<b>Fold:</b> gpW/XkdW-like <b>Superfamily:</b> Head-to-tail joining protein W, gpW <b>Family:</b> Head-to-tail joining protein W, gpW
82	<a href="#">c2jwIB</a>	Alignment	not modelled	5.5	22	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> protein tolR; <b>PDBTitle:</b> solution structure of periplasmic domain of tolR from h.2 influenzae with saxes data
83	<a href="#">c4exqA</a>	Alignment	not modelled	5.3	22	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> uroporphyrinogen decarboxylase; <b>PDBTitle:</b> crystal structure of uroporphyrinogen decarboxylase (upd) from2 burkholderia thailandensis e264
84	<a href="#">c2nscA</a>	Alignment	not modelled	5.3	19	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> trigger factor; <b>PDBTitle:</b> structures of and interactions between domains of trigger factor from2 themotoga maritima
85	<a href="#">c3r5wO</a>	Alignment	not modelled	5.3	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> O: <b>PDB Molecule:</b> deazaflavin-dependent nitroreductase; <b>PDBTitle:</b> structure of ddn, the deazaflavin-dependent nitroreductase from2 mycobacterium tuberculosis involved in bioreductive activation of pa-3 824, with co-factor f420
86	<a href="#">d1r3ba</a>	Alignment	not modelled	5.2	9	<b>Fold:</b> Bromodomain-like <b>Superfamily:</b> Mob1/phocein <b>Family:</b> Mob1/phocein
87	<a href="#">c3r5yC</a>	Alignment	not modelled	5.2	25	<b>PDB header:</b> unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> structure of a deazaflavin-dependent nitroreductase from nocardia2 farcinica, with co-factor f420
88	<a href="#">c2i9zB</a>	Alignment	not modelled	5.1	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative septation protein spovg; <b>PDBTitle:</b> structural genomics, the crystal structure of full-length spovg from2 staphylococcus epidermidis atcc 12228
89	<a href="#">d2i9xa1</a>	Alignment	not modelled	5.1	15	<b>Fold:</b> SpoVG-like <b>Superfamily:</b> SpoVG-like <b>Family:</b> SpoVG-like
90	<a href="#">c2ra4B</a>	Alignment	not modelled	5.1	17	<b>PDB header:</b> cytokine <b>Chain:</b> B: <b>PDB Molecule:</b> small-inducible cytokine a13; <b>PDBTitle:</b> crystal structure of human monocyte chemoattractant protein 4 (mcp-2 4/cc113)