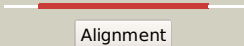

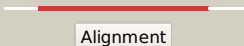

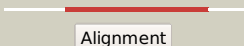







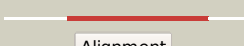










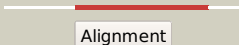

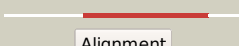
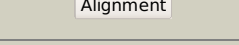
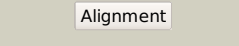


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3856c_(-)_4328579_4329586
Date	Sat Aug 10 22:05:03 BST 2019
Unique Job ID	7ff92ceb48680bc6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3auoB_</a>	 Alignment		100.0	31	<b>PDB header:</b> transferase/dna <b>Chain:</b> B; <b>PDB Molecule:</b> dna polymerase beta family (x family); <b>PDBTitle:</b> dna polymerase x from thermus thermophilus hb8 ternary complex with 1-2 nt gapped dna and ddgtp
2	<a href="#">c2w9mB_</a>	 Alignment		100.0	36	<b>PDB header:</b> dna replication <b>Chain:</b> B; <b>PDB Molecule:</b> polymerase x; <b>PDBTitle:</b> structure of family x dna polymerase from deinococcus2 radiourans
3	<a href="#">d1m65a_</a>	 Alignment		100.0	27	<b>Fold:</b> 7-stranded beta/alpha barrel <b>Superfamily:</b> PHP domain-like <b>Family:</b> PHP domain
4	<a href="#">c2yz5B_</a>	 Alignment		100.0	26	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> histidinol phosphatase; <b>PDBTitle:</b> histidinol phosphate phosphatase complexed with phosphate
5	<a href="#">c3umuA_</a>	 Alignment		100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> histidinol-phosphatase; <b>PDBTitle:</b> crystal structure of l-histidinol phosphate phosphatase (hisk) from2 lactococcus lactis subsp. lactis il1403 complexed with zn, phosphate3 and l-histidinol
6	<a href="#">c3dcpB_</a>	 Alignment		100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> histidinol-phosphatase; <b>PDBTitle:</b> crystal structure of the putative histidinol phosphatase (hisk) from2 listeria monocytogenes. northeast structural genomics consortium3 target lmr141.
7	<a href="#">c3qy6A_</a>	 Alignment		100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> tyrosine-protein phosphatase ywqe; <b>PDBTitle:</b> crystal structures of ywqe from bacillus subtilis and cpsb from2 streptococcus pneumoniae, unique metal-dependent tyrosine3 phosphatases
8	<a href="#">c2wjeA_</a>	 Alignment		100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> tyrosine-protein phosphatase cpsb; <b>PDBTitle:</b> crystal structure of the tyrosine phosphatase cps4b from2 streptococcus pneumoniae tigr4.
9	<a href="#">c2yb1A_</a>	 Alignment		100.0	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> amidohydrolase; <b>PDBTitle:</b> structure of an amidohydrolase from chromobacterium violaceum (efi2 target efi-500202) with bound mn, amp and phosphate.
10	<a href="#">c3f2cA_</a>	 Alignment		99.9	18	<b>PDB header:</b> transferase/dna <b>Chain:</b> A; <b>PDB Molecule:</b> geobacillus kaustophilus dna polc; <b>PDBTitle:</b> dna polymerase polc from geobacillus kaustophilus complex with dna,2 dgtp and mn
11	<a href="#">c4gx9A_</a>	 Alignment		99.9	16	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> dna polymerase iii subunit epsilon,dna polymerase iii <b>PDBTitle:</b> crystal structure of a dna polymerase iii alpha-epsilon chimera

12	<a href="#">c3e0fA_</a>	 Alignment		99.9	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative metal-dependent phosphoesterase; <b>PDBTitle:</b> crystal structure of a putative metal-dependent phosphoesterase2 (bad_1165) from bifidobacterium adolescentis atcc 15703 at 2.40 a3 resolution
13	<a href="#">c3e38A_</a>	 Alignment		99.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> two-domain protein containing predicted php-like metal- <b>PDBTitle:</b> crystal structure of a two-domain protein containing predicted php-2 like metal-dependent phosphoesterase (bvu_3505) from bacteroides3 vulgatus atcc 8482 at 2.20 a resolution
14	<a href="#">c2anuA_</a>	 Alignment		99.9	19	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein tm0559; <b>PDBTitle:</b> crystal structure of predicted metal-dependent phosphoesterase (php2 family) (tm0559) from thermotoga maritima at 2.40 a resolution
15	<a href="#">d2anuA1</a>	 Alignment		99.9	19	<b>Fold:</b> 7-stranded beta/alpha barrel <b>Superfamily:</b> PHP domain-like <b>Family:</b> PHP domain
16	<a href="#">c6k0aC_</a>	 Alignment		99.9	14	<b>PDB header:</b> rna binding protein/rna <b>Chain:</b> C: <b>PDB Molecule:</b> ribonuclease p protein component 3; <b>PDBTitle:</b> cryo-em structure of an archaeal ribonuclease p
17	<a href="#">c3e0dA_</a>	 Alignment		99.9	16	<b>PDB header:</b> transferase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase iii subunit alpha; <b>PDBTitle:</b> insights into the replisome from the crystral structure of2 the ternary complex of the eubacterial dna polymerase iii3 alpha-subunit
18	<a href="#">c2hnhA_</a>	 Alignment		99.9	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase iii alpha subunit; <b>PDBTitle:</b> crystal structure of the catalytic alpha subunit of e. coli2 replicative dna polymerase iii
19	<a href="#">c5fkvA_</a>	 Alignment		99.9	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase iii subunit alpha; <b>PDBTitle:</b> cryo-em structure of the e. coli replicative dna polymerase complex2 bound to dna (dna polymerase iii alpha, beta, epsilon, tau complex)
20	<a href="#">c5lewA_</a>	 Alignment		99.9	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase iii subunit alpha; <b>PDBTitle:</b> dna polymerase
21	<a href="#">c5zb8B_</a>	 Alignment	not modelled	99.8	16	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> pfuendoq; <b>PDBTitle:</b> crystal structure of the novel lesion-specific endonuclease pfuendoq2 from pyrococcus furiosus
22	<a href="#">c6ahuj_</a>	 Alignment	not modelled	99.5	17	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> J: <b>PDB Molecule:</b> ribonuclease p protein subunit p30; <b>PDBTitle:</b> cryo-em structure of human ribonuclease p with mature trna
23	<a href="#">c3wyzA_</a>	 Alignment	not modelled	98.7	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ribonuclease p protein component 3; <b>PDBTitle:</b> on archaeal homologs of the human rnase p protein rpp30 in the2 hyperthermophilic archaeon thermococcus kodakarensis
24	<a href="#">c6agbj_</a>	 Alignment	not modelled	98.4	17	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> J: <b>PDB Molecule:</b> ribonuclease p/mrp protein subunit rpp1; <b>PDBTitle:</b> cryo-em structure of yeast ribonuclease p
25	<a href="#">d2amxA1</a>	 Alignment	not modelled	97.3	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Adenosine/AMP deaminase
26	<a href="#">c4p4oA_</a>	 Alignment	not modelled	97.3	14	<b>PDB header:</b> transferase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase beta; <b>PDBTitle:</b> crystal structure of leishmania infantum polymerase beta: ternary gap2 complex
27	<a href="#">d2bcqa3</a>	 Alignment	not modelled	97.1	11	<b>Fold:</b> Nucleotidyltransferase <b>Superfamily:</b> Nucleotidyltransferase <b>Family:</b> DNA polymerase beta-like
28	<a href="#">c2bcuA_</a>	 Alignment	not modelled	97.1	10	<b>PDB header:</b> transferase, lyase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase lambda; <b>PDBTitle:</b> dna polymerase lambda in complex with a dna duplex2 containing an unpaired damp and a t:t mismatch

29	<a href="#">d1v77a_</a>	Alignment	not modelled	97.0	10	<b>Fold:</b> 7-stranded beta/alpha barrel <b>Superfamily:</b> PHP domain-like <b>Family:</b> RNase P subunit p30
30	<a href="#">d2fmpa3</a>	Alignment	not modelled	97.0	12	<b>Fold:</b> Nucleotidyltransferase <b>Superfamily:</b> Nucleotidyltransferase <b>Family:</b> DNA polymerase beta-like
31	<a href="#">c8icza_</a>	Alignment	not modelled	97.0	11	<b>PDB header:</b> transferase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> protein (dna polymerase beta (e.c.2.7.7.7)); <b>PDBTitle:</b> dna polymerase beta (pol b) (e.c.2.7.7.7) complexed with 2 seven base pairs of dna; soaked in the presence of datp3 (1 millimolar), mncl2 (5 millimolar), and lithium sulfate4 (75 millimolar)
32	<a href="#">c2ihmA_</a>	Alignment	not modelled	96.9	3	<b>PDB header:</b> transferase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase mu; <b>PDBTitle:</b> polymerase mu in ternary complex with gapped 11mer dna duplex and 2 bound incoming nucleotide
33	<a href="#">d1xrta2</a>	Alignment	not modelled	96.9	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Hydantoinase (dihydropyrimidinase), catalytic domain
34	<a href="#">d1jqra_</a>	Alignment	not modelled	96.9	10	<b>Fold:</b> Nucleotidyltransferase <b>Superfamily:</b> Nucleotidyltransferase <b>Family:</b> DNA polymerase beta-like
35	<a href="#">d1jmsa4</a>	Alignment	not modelled	96.8	6	<b>Fold:</b> Nucleotidyltransferase <b>Superfamily:</b> Nucleotidyltransferase <b>Family:</b> DNA polymerase beta-like
36	<a href="#">d2vana2</a>	Alignment	not modelled	96.8	11	<b>Fold:</b> Nucleotidyltransferase <b>Superfamily:</b> Nucleotidyltransferase <b>Family:</b> DNA polymerase beta-like
37	<a href="#">c6ii7A_</a>	Alignment	not modelled	96.8	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> adenosine deaminase; <b>PDBTitle:</b> crystal structure of plasmodium falciparum adenosine deaminase2 c27q+l227i mutant co-complexed with zn ion, hypoxanthine and inosine
38	<a href="#">c1nomA_</a>	Alignment	not modelled	96.7	11	<b>PDB header:</b> nucleotidyltransferase <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase beta; <b>PDBTitle:</b> dna polymerase beta (pol b) (e.c.2.7.7.7), 31-kd domain; soaked in the presence of mncl2 (5 millimolar)
39	<a href="#">c1kdhA_</a>	Alignment	not modelled	96.6	6	<b>PDB header:</b> transferase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> terminal deoxynucleotidyltransferase short <b>PDBTitle:</b> binary complex of murine terminal deoxynucleotidyl 2 transferase with a primer single stranded dna
40	<a href="#">c4rdzA_</a>	Alignment	not modelled	96.3	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> parathion hydrolase; <b>PDBTitle:</b> crystal structure of vmolac in p64 space group
41	<a href="#">d1bf6a_</a>	Alignment	not modelled	96.2	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Phosphotriesterase-like
42	<a href="#">c4gxwA_</a>	Alignment	not modelled	96.2	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> adenosine deaminase; <b>PDBTitle:</b> crystal structure of a cog1816 amidohydrolase (target efi-505188) from 2 burkholderia ambifaria, with bound zn
43	<a href="#">d1vfla1</a>	Alignment	not modelled	96.1	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Adenosine/AMP deaminase
44	<a href="#">c3rcmA_</a>	Alignment	not modelled	96.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> tatd family hydrolase; <b>PDBTitle:</b> crystal structure of efi target 500140:tatd family hydrolase from 2 pseudomonas putida
45	<a href="#">c3ou8B_</a>	Alignment	not modelled	95.9	10	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> adenosine deaminase; <b>PDBTitle:</b> the crystal structure of adenosine deaminase from pseudomonas2 aeruginosa
46	<a href="#">c3ij6A_</a>	Alignment	not modelled	95.5	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized metal-dependent hydrolase; <b>PDBTitle:</b> crystal structure of an uncharacterized metal-dependent hydrolase from 2 lactobacillus acidophilus
47	<a href="#">c6n91A_</a>	Alignment	not modelled	95.5	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> adenosine deaminase; <b>PDBTitle:</b> crystal structure of adenosine deaminase from vibrio cholerae2 complexed with pentostatin (deoxycoformycin)
48	<a href="#">c2y1hA_</a>	Alignment	not modelled	95.5	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative deoxyribonuclease tatdn3; <b>PDBTitle:</b> crystal structure of the human tatd-domain protein 3 (tatdn3)
49	<a href="#">c3rysa_</a>	Alignment	not modelled	95.2	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> adenosine deaminase 1; <b>PDBTitle:</b> the crystal structure of adenine deaminase (aaur1117) from 2 arthrobacter aurescens
50	<a href="#">d1xwya1</a>	Alignment	not modelled	95.0	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> TatD Mg-dependent DNase-like
51	<a href="#">c3k2gA_</a>	Alignment	not modelled	94.4	13	<b>PDB header:</b> resiniferatoxin binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> resiniferatoxin-binding, phosphotriesterase- <b>PDBTitle:</b> crystal structure of a resiniferatoxin-binding protein from 2 rhodobacter sphaeroides
52	<a href="#">d1j6oa_</a>	Alignment	not modelled	94.1	12	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> TatD Mg-dependent DNase-like
53	<a href="#">d2fmpa1</a>	Alignment	not modelled	94.1	22	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> DNA polymerase beta, N-terminal domain-like <b>Family:</b> DNA polymerase beta, N-terminal domain-like
						<b>PDB header:</b> hydrolase

54	<a href="#">c6ijpA_</a>	Alignment	not modelled	93.3	11	<b>Chain:</b> A: <b>PDB Molecule:</b> adenosine/amp deaminase family protein; <b>PDBTitle:</b> the structure of the adal-imp complex
55	<a href="#">d1i0da_</a>	Alignment	not modelled	93.0	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Phosphotriesterase-like
56	<a href="#">d1ad1a_</a>	Alignment	not modelled	92.4	23	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Dihydropteroate synthetase-like <b>Family:</b> Dihydropteroate synthetase
57	<a href="#">c1tx2A_</a>	Alignment	not modelled	92.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dhps, dihydropteroate synthase; <b>PDBTitle:</b> dihydropteroate synthetase, with bound inhibitor manic, from bacillus2 anthracis
58	<a href="#">d1tx2a_</a>	Alignment	not modelled	92.0	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Dihydropteroate synthetase-like <b>Family:</b> Dihydropteroate synthetase
59	<a href="#">d1zzma1</a>	Alignment	not modelled	90.9	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> TatD Mg-dependent DNase-like
60	<a href="#">c3ou8A_</a>	Alignment	not modelled	90.9	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> adenosine deaminase; <b>PDBTitle:</b> the crystal structure of adenosine deaminase from pseudomonas2 aeruginosa
61	<a href="#">c6cluC_</a>	Alignment	not modelled	90.8	20	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> C: <b>PDB Molecule:</b> dihydropteroate synthase; <b>PDBTitle:</b> staphylococcus aureus dihydropteroate synthase (sadhps) f17l e208k2 double mutant structure
62	<a href="#">d1dk2a_</a>	Alignment	not modelled	90.3	21	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> DNA polymerase beta, N-terminal domain-like <b>Family:</b> DNA polymerase beta, N-terminal domain-like
63	<a href="#">c5visB_</a>	Alignment	not modelled	89.6	28	<b>PDB header:</b> hydrolase,oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydropteroate synthase; <b>PDBTitle:</b> 1.73 angstrom resolution crystal structure of dihydropteroate synthase2 (folp-smz_b27) from soil uncultured bacterium.
64	<a href="#">c4o1fB_</a>	Alignment	not modelled	89.6	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydropteroate synthase dhps; <b>PDBTitle:</b> structure of a methyltransferase component in complex with thf2 involved in o-demethylation
65	<a href="#">c5uswD_</a>	Alignment	not modelled	89.6	20	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> dihydropteroate synthase; <b>PDBTitle:</b> the crystal structure of 7,8-dihydropteroate synthase from vibrio2 fischeri es114
66	<a href="#">d2f6ka1</a>	Alignment	not modelled	89.5	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> PP1699/LP2961-like
67	<a href="#">c6omzA_</a>	Alignment	not modelled	89.3	17	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydropteroate synthase; <b>PDBTitle:</b> crystal structure of dihydropteroate synthase from mycobacterium2 smegmatis with bound 6-hydroxymethylpterin-monophosphate
68	<a href="#">d1eyea_</a>	Alignment	not modelled	89.3	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Dihydropteroate synthetase-like <b>Family:</b> Dihydropteroate synthetase
69	<a href="#">c3rhgA_</a>	Alignment	not modelled	89.3	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative phosphotriesterase; <b>PDBTitle:</b> crystal structure of amidohydrolase pmi1525 (target efi-500319) from2 proteus mirabilis hi4320
70	<a href="#">d1ajza_</a>	Alignment	not modelled	89.1	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Dihydropteroate synthetase-like <b>Family:</b> Dihydropteroate synthetase
71	<a href="#">c3nqbB_</a>	Alignment	not modelled	89.1	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> adenine deaminase 2; <b>PDBTitle:</b> crystal structure of adenine deaminase from agrobacterium tumefaciens2 (str. c 58)
72	<a href="#">c2xioA_</a>	Alignment	not modelled	88.5	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative deoxyribonuclease tatdn1; <b>PDBTitle:</b> structure of putative deoxyribonuclease tatdn1 isoform a
73	<a href="#">c3vylB_</a>	Alignment	not modelled	88.3	19	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> l-ribulose 3-epimerase; <b>PDBTitle:</b> structure of l-ribulose 3-epimerase
74	<a href="#">c4djdD_</a>	Alignment	not modelled	87.9	15	<b>PDB header:</b> transferase/vitamin-binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> corrinoid/iron-sulfur protein small subunit; <b>PDBTitle:</b> crystal structure of folate-free corrinoid iron-sulfur protein (cfesp)2 in complex with its methyltransferase (metr)
75	<a href="#">c5uurA_</a>	Alignment	not modelled	87.7	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydropteroate synthase; <b>PDBTitle:</b> xanthomonas albilineans dihydropteroate synthase with 4-aminobenzoic acid
76	<a href="#">d1p1ma2</a>	Alignment	not modelled	87.6	12	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> SAH/MTA deaminase-like
77	<a href="#">d2ffia1</a>	Alignment	not modelled	87.4	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> PP1699/LP2961-like
78	<a href="#">d2paja2</a>	Alignment	not modelled	87.4	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> SAH/MTA deaminase-like
79	<a href="#">d1jmsa1</a>	Alignment	not modelled	87.3	14	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> DNA polymerase beta, N-terminal domain-like <b>Family:</b> DNA polymerase beta, N-terminal domain-like
80	<a href="#">d2d2ja1</a>	Alignment	not modelled	86.6	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases

						<b>Family:</b> Phosphotriesterase-like
81	<a href="#">d1a4ma_</a>	Alignment	not modelled	85.6	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Adenosine/AMP deaminase
82	<a href="#">c2vp8A_</a>	Alignment	not modelled	85.3	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydropteroate synthase 2; <b>PDBTitle:</b> structure of mycobacterium tuberculosis rv1207
83	<a href="#">c3n6qF_</a>	Alignment	not modelled	85.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> yghz aldo-keto reductase; <b>PDBTitle:</b> crystal structure of yghz from e. coli
84	<a href="#">d2bcqa1</a>	Alignment	not modelled	84.6	17	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> DNA polymerase beta, N-terminal domain-like <b>Family:</b> DNA polymerase beta, N-terminal domain-like
85	<a href="#">c2x7vA_</a>	Alignment	not modelled	83.8	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable endonuclease 4; <b>PDBTitle:</b> crystal structure of thermotoga maritima endonuclease iv in2 the presence of zinc
86	<a href="#">c2y5sA_</a>	Alignment	not modelled	83.6	35	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydropteroate synthase; <b>PDBTitle:</b> crystal structure of burkholderia cenocepacia dihydropteroate2 synthase complexed with 7,8-dihydropteroate.
87	<a href="#">c4mupC_</a>	Alignment	not modelled	83.5	13	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> amidohydrolase; <b>PDBTitle:</b> crystal structure of agrobacterium tumefaciens atu3138 (efi target2 505157), apo structure
88	<a href="#">d1nzipa_</a>	Alignment	not modelled	82.8	18	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> DNA polymerase beta, N-terminal domain-like <b>Family:</b> DNA polymerase beta, N-terminal domain-like
89	<a href="#">c2h9aB_</a>	Alignment	not modelled	82.6	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> co dehydrogenase/acetyl-coa synthase, iron-sulfur protein; <b>PDBTitle:</b> corrinoid iron-sulfur protein
90	<a href="#">c3f4cA_</a>	Alignment	not modelled	82.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> organophosphorus hydrolase; <b>PDBTitle:</b> crystal structure of organophosphorus hydrolase from geobacillus2 stearothermophilus strain 10, with glycerol bound
91	<a href="#">d1f6ya_</a>	Alignment	not modelled	81.3	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Dihydropteroate synthetase-like <b>Family:</b> Methyltetrahydrofolate-utilizing methyltransferases
92	<a href="#">c4do7B_</a>	Alignment	not modelled	79.4	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> amidohydrolase 2; <b>PDBTitle:</b> crystal structure of an amidohydrolase (cog3618) from burkholderia2 multivorans (target efi-500235) with bound zn, space group c2
93	<a href="#">c5hmqE_</a>	Alignment	not modelled	78.0	14	<b>PDB header:</b> lyase <b>Chain:</b> E: <b>PDB Molecule:</b> 4-hydroxyphenylpyruvate dioxygenase; <b>PDBTitle:</b> xylose isomerase-like tim barrel/4-hydroxyphenylpyruvate dioxygenase2 fusion protein
94	<a href="#">c6h5hA_</a>	Alignment	not modelled	77.7	17	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> polb4; <b>PDBTitle:</b> a computationally designed drp lyase domain reconstructed from two2 heterologous fragments
95	<a href="#">d3be7a2</a>	Alignment	not modelled	76.4	9	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Zn-dependent arginine carboxypeptidase-like
96	<a href="#">c1pscA_</a>	Alignment	not modelled	75.7	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphotriesterase; <b>PDBTitle:</b> phosphotriesterase from pseudomonas diminuta
97	<a href="#">c3gg7A_</a>	Alignment	not modelled	75.5	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized metalloprotein; <b>PDBTitle:</b> crystal structure of an uncharacterized metalloprotein from2 deinococcus radiodurans
98	<a href="#">c3irsB_</a>	Alignment	not modelled	75.4	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein bb4693; <b>PDBTitle:</b> crystal structure of uncharacterized tim-barrel protein bb4693 from2 bordetella bronchiseptica
99	<a href="#">c2gzxB_</a>	Alignment	not modelled	75.2	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative tatd related dnase; <b>PDBTitle:</b> crystal structure of the tatd deoxyribonuclease mw0446 from2 staphylococcus aureus. northeast structural genomics consortium3 target zr237.
100	<a href="#">c5zfsA_</a>	Alignment	not modelled	75.0	10	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> d-allulose-3-epimerase; <b>PDBTitle:</b> crystal structure of arthrobacter globiformis m30 sugar epimerase2 which can produce d-allulose from d-fructose
101	<a href="#">c3lggA_</a>	Alignment	not modelled	74.5	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> adenosine deaminase cecr1; <b>PDBTitle:</b> crystal structure of human adenosine deaminase growth factor,2 adenosine deaminase type 2 (ada2) complexed with transition state3 analogue, coformycin
102	<a href="#">c3lu2B_</a>	Alignment	not modelled	74.4	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> lmo2462 protein; <b>PDBTitle:</b> structure of lmo2462, a listeria monocytogenes amidohydrolase family2 putative dipeptidase
103	<a href="#">c3tn6A_</a>	Alignment	not modelled	73.8	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphotriesterase; <b>PDBTitle:</b> crystal structure of gkap mutant r230h from geobacillus kaustophilus2 hta426
104	<a href="#">d1yixa1</a>	Alignment	not modelled	73.3	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> TatD Mg-dependent DNase-like
105	<a href="#">c2ragB_</a>	Alignment	not modelled	73.1	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> dipeptidase; <b>PDBTitle:</b> crystal structure of aminohydrolase from caulobacter crescentus
						<b>PDB header:</b> transferase



106	<a href="#">c2yciX_</a>	Alignment	not modelled	71.2	13	<b>Chain:</b> X: <b>PDB Molecule:</b> 5-methyltetrahydrofolate corrinoid/iron sulfur protein <b>PDBTitle:</b> methyltransferase native
107	<a href="#">d2fvka2</a>	Alignment	not modelled	71.1	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Hydantoinase (dihydropyrimidinase), catalytic domain
108	<a href="#">d3bofa1</a>	Alignment	not modelled	71.1	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Dihydropteroate synthetase-like <b>Family:</b> Methyltetrahydrofolate-utilizing methyltransferases
109	<a href="#">c3itcA_</a>	Alignment	not modelled	70.4	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> renal dipeptidase; <b>PDBTitle:</b> crystal structure of sco3058 with bound citrate and glycerol
110	<a href="#">d2i9ua2</a>	Alignment	not modelled	69.9	10	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> SAH/MTA deaminase-like
111	<a href="#">c3b40A_</a>	Alignment	not modelled	69.8	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable dipeptidase; <b>PDBTitle:</b> crystal structure of the probable dipeptidase pvdm from pseudomonas2 aeruginosa
112	<a href="#">d1i60a_</a>	Alignment	not modelled	69.4	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> loll-like
113	<a href="#">d1k1da2</a>	Alignment	not modelled	68.5	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Hydantoinase (dihydropyrimidinase), catalytic domain
114	<a href="#">d1gkra2</a>	Alignment	not modelled	68.4	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Hydantoinase (dihydropyrimidinase), catalytic domain
115	<a href="#">c3cjpA_</a>	Alignment	not modelled	67.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> predicted amidohydrolase, dihydroorotase family; <b>PDBTitle:</b> crystal structure of an uncharacterized amidohydrolase cac3332 from2 clostridium acetobutylicum
116	<a href="#">c3c52B_</a>	Alignment	not modelled	67.4	20	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> fructose-bisphosphate aldolase; <b>PDBTitle:</b> class ii fructose-1,6-bisphosphate aldolase from helicobacter pylori2 in complex with phosphoglycolohydroxamic acid, a competitive3 inhibitor
117	<a href="#">d2imra2</a>	Alignment	not modelled	66.9	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> DR0824-like
118	<a href="#">d2q09a2</a>	Alignment	not modelled	66.3	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Imidazolonepropionase-like
119	<a href="#">c3khdC_</a>	Alignment	not modelled	65.8	14	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> pyruvate kinase; <b>PDBTitle:</b> crystal structure of pff1300w.
120	<a href="#">d1yx1a1</a>	Alignment	not modelled	62.7	12	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> KguE-like