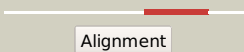

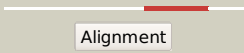

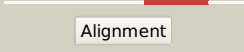

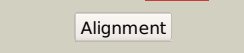



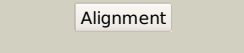

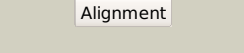


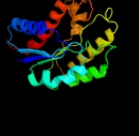
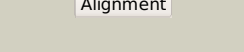
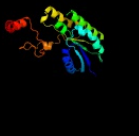
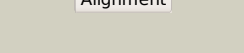

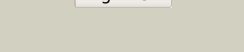
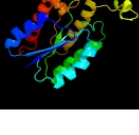


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1565c_(-)_1771646_1773835
Date	Fri Aug 2 13:30:15 BST 2019
Unique Job ID	ecc50c3da4ba68d0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4h08A_</a>	 Alignment		99.1	8	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative hydrolase; <b>PDBTitle:</b> crystal structure of a putative hydrolase (bt3161) from bacteroides2 thetaiotaomicron vpi-5482 at 1.80 a resolution
2	<a href="#">c4iyjA_</a>	 Alignment		99.1	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> gdsl-like protein; <b>PDBTitle:</b> crystal structure of a putative acylhydrolase (bacuni_03406) from2 bacteroides uniformis atcc 8492 at 1.37 a resolution
3	<a href="#">c3p94A_</a>	 Alignment		99.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> gdsl-like lipase; <b>PDBTitle:</b> crystal structure of a gdsl-like lipase (bdi_0976) from2 parabacteroides distasonis atcc 8503 at 1.93 a resolution
4	<a href="#">c4rshB_</a>	 Alignment		99.0	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> lipolytic protein g-d-s-l family; <b>PDBTitle:</b> structure of a putative lipolytic protein of g-d-s-l family from2 desulfitobacterium hafniense dcb-2
5	<a href="#">d1es9a_</a>	 Alignment		99.0	15	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> SGNH hydrolase <b>Family:</b> Acetylhydrolase
6	<a href="#">c2o14A_</a>	 Alignment		98.9	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein yxim; <b>PDBTitle:</b> x-ray crystal structure of protein yxim_bacsu from bacillus subtilis.2 northeast structural genomics consortium target sr595
7	<a href="#">c4jggB_</a>	 Alignment		98.9	12	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> esterase tesa; <b>PDBTitle:</b> crystal structure of tesa
8	<a href="#">d1yzfa1</a>	 Alignment		98.9	16	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> SGNH hydrolase <b>Family:</b> TAP-like
9	<a href="#">c6iqbA_</a>	 Alignment		98.8	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> sgnh-hydrolase family esterase; <b>PDBTitle:</b> esterase aline4 mutant-s13a
10	<a href="#">d1fxwf_</a>	 Alignment		98.8	14	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> SGNH hydrolase <b>Family:</b> Acetylhydrolase
11	<a href="#">c3milA_</a>	 Alignment		98.8	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> isoamyl acetate-hydrolyzing esterase; <b>PDBTitle:</b> crystal structure of isoamyl acetate-hydrolyzing esterase from2 saccharomyces cerevisiae

12	<a href="#">c5ufyA_</a>	Alignment		98.8	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acyltransferase; <b>PDBTitle:</b> structure of streptococcus pneumoniae peptidoglycan o-2 acetyltransferase a (oata) c-terminal catalytic domain
13	<a href="#">c4s1pA_</a>	Alignment		98.8	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> shel_16390 protein, a putative sgnh hydrolase from slackia2 heliotrinireducens
14	<a href="#">d1jr1a_</a>	Alignment		98.8	17	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> SGNH hydrolase <b>Family:</b> TAP-like
15	<a href="#">c5jd3A_</a>	Alignment		98.7	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lae5; <b>PDBTitle:</b> crystal structure of lae5, an alpha/beta hydrolase enzyme from the2 metagenome of lake arreo, spain
16	<a href="#">c6njcB_</a>	Alignment		98.7	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> sialate o-acylesterase; <b>PDBTitle:</b> crystal structure of the sialate o-acylesterase from bacteroides2 vulgatus
17	<a href="#">c6iq8B_</a>	Alignment		98.7	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> carboxylesterase; <b>PDBTitle:</b> esterase crme10 mutant-d178a
18	<a href="#">c3hp4A_</a>	Alignment		98.7	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> gdsl-esterase; <b>PDBTitle:</b> crystal structure of psychrotrophic esterase esta from2 pseudoalteromonas sp. 643a inhibited by monoethylphosphonate
19	<a href="#">c2vptA_</a>	Alignment		98.6	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lipolytic enzyme; <b>PDBTitle:</b> clostridium thermocellum family 3 carbohydrate esterase
20	<a href="#">c3rjtA_</a>	Alignment		98.6	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lipolytic protein g-d-s-l family; <b>PDBTitle:</b> crystal structure of lipolytic protein g-d-s-l family from2 alicyclobacillus acidocaldarius subsp. acidocaldarius dsm 446
21	<a href="#">c4jhiA_</a>	Alignment	not modelled	98.6	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> acetyl xylan esterase; <b>PDBTitle:</b> crystal structure of of axe2, an acetyl xylan esterase from geobacillus2 stearothermophilus
22	<a href="#">c4lhsA_</a>	Alignment	not modelled	98.6	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a putative gdsl-like lipase (bacova_00914) from2 bacteroides ovatus atcc 8483 at 1.40 a resolution
23	<a href="#">c2waoA_</a>	Alignment	not modelled	98.6	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endoglucanase e; <b>PDBTitle:</b> structure of a family two carbohydrate esterase from clostridium2 thermocellum in complex with cellohexaose
24	<a href="#">d2hsja1</a>	Alignment	not modelled	98.6	14	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> SGNH hydrolase <b>Family:</b> Acetylhydrolase
25	<a href="#">c4rw0B_</a>	Alignment	not modelled	98.6	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> lipolytic protein g-d-s-l family; <b>PDBTitle:</b> crystal structure of a member of the lipolytic protein g-d-s-l family2 from veillonella parvula dsm 2008
26	<a href="#">d3bzwa1</a>	Alignment	not modelled	98.6	11	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> SGNH hydrolase <b>Family:</b> BT2961-like
27	<a href="#">c3bzwa_</a>	Alignment	not modelled	98.6	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative lipase; <b>PDBTitle:</b> crystal structure of a putative lipase from bacteroides2 thetaiotaomicron
28	<a href="#">c4hf7A_</a>	Alignment	not modelled	98.5	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative acylhydrolase; <b>PDBTitle:</b> crystal structure of a gdsl-like lipase (bt0569) from bacteroides2 thetaiotaomicron vpi-5482 at 1.77 a resolution

29	<a href="#">c4c1bC</a>	Alignment	not modelled	98.5	14	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> orf1-encoded protein; <b>PDBTitle:</b> esterase domain of the zfl2-1 orf1 protein from the zebrafish zfl2-12 retrotransposon
30	<a href="#">c5hoeB</a>	Alignment	not modelled	98.4	11	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> hydrolase; <b>PDBTitle:</b> crystal structure of est24, a carbohydrate acetyltransferase from <i>Sinorhizobium meliloti</i>
31	<a href="#">c2waaA</a>	Alignment	not modelled	98.4	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> xylan esterase, putative, axe2c; <b>PDBTitle:</b> structure of a family two carbohydrate esterase from <i>Cellvibrio japonicus</i>
32	<a href="#">c4k40B</a>	Alignment	not modelled	98.4	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> gdsI-like lipase/acylhydrolase family protein; <b>PDBTitle:</b> peptidoglycan o-acetyltransferase in action, 0 min
33	<a href="#">d1vjga</a>	Alignment	not modelled	98.4	12	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> SGNH hydrolase <b>Family:</b> Hypothetical protein alr1529
34	<a href="#">d2o14a2</a>	Alignment	not modelled	98.4	14	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> SGNH hydrolase <b>Family:</b> YxiM C-terminal domain-like
35	<a href="#">d1esca</a>	Alignment	not modelled	98.3	13	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> SGNH hydrolase <b>Family:</b> Esterase
36	<a href="#">c4devE</a>	Alignment	not modelled	98.3	12	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> acetyl-xylan esterase est2a; <b>PDBTitle:</b> an acetyl xylan esterase (est2a) from the rumen bacterium <i>Butyrivibrio proteoclasticus</i> .
37	<a href="#">c4q9aA</a>	Alignment	not modelled	98.3	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> tat pathway signal sequence domain protein; <b>PDBTitle:</b> crystal structure of a putative gdsI-like lipase (parmer_00689) from <i>Parabacteroides merdae</i> ATCC 43184 at 2.86 Å resolution
38	<a href="#">c4xvhA</a>	Alignment	not modelled	98.3	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> carbohydrate esterase family 2 (ce2); <b>PDBTitle:</b> crystal structure of a <i>Corynebacterium thermopiles</i> ( <i>myceliophthora2 fergusonii</i> ) carbohydrate esterase family 2 (ce2) enzyme plus3 carbohydrate binding domain (cbd)
39	<a href="#">c4tx1C</a>	Alignment	not modelled	98.3	11	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> esterase; <b>PDBTitle:</b> the crystal structure of carbohydrate acetyltransferase family member2 from <i>Sinorhizobium meliloti</i>
40	<a href="#">d1k7ca</a>	Alignment	not modelled	98.3	15	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> SGNH hydrolase <b>Family:</b> Rhamnogalacturonan acetyltransferase
41	<a href="#">c3dciB</a>	Alignment	not modelled	98.2	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> arylesterase; <b>PDBTitle:</b> the structure of a putative arylesterase from <i>Agrobacterium tumefaciens</i> str. c58
42	<a href="#">c2q0qC</a>	Alignment	not modelled	98.2	16	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> aryl esterase; <b>PDBTitle:</b> structure of the native <i>M. smegmatis</i> aryl esterase
43	<a href="#">c4q7qA</a>	Alignment	not modelled	98.2	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> lipolytic protein g-d-s-l family; <b>PDBTitle:</b> the crystal structure of a possible lipase from <i>Chitinophaga pinensis</i> DSM 2588
44	<a href="#">c3x0hA</a>	Alignment	not modelled	98.1	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> carbohydrate esterase 1; <b>PDBTitle:</b> crystal structure of a carbohydrate esterase family 1 from <i>Talaromyces cellulolyticus</i>
45	<a href="#">c3dc7B</a>	Alignment	not modelled	98.0	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein lp_3323; <b>PDBTitle:</b> crystal structure of the protein q88s8 from <i>Lactobacillus plantarum</i> .2 northeast structural genomics consortium target lpr109.
46	<a href="#">c5ma1A</a>	Alignment	not modelled	97.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lipase; <b>PDBTitle:</b> crystal structure of extracellular lipase from <i>Streptomyces rimosus</i> at 2.17 Å resolution
47	<a href="#">d3dc7a1</a>	Alignment	not modelled	97.9	14	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> SGNH hydrolase <b>Family:</b> BT2961-like
48	<a href="#">c2w9xA</a>	Alignment	not modelled	97.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative acetyl xylan esterase; <b>PDBTitle:</b> the active site of a carbohydrate esterase displays 2 divergent catalytic and non-catalytic binding functions
49	<a href="#">c4m8kA</a>	Alignment	not modelled	97.8	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein, gdsI-like lipase/acylhydrolase family <b>PDBTitle:</b> crystal structure of a putative gdsI-like lipase (bacuni_00748) from <i>Bacteroides uniformis</i> ATCC 8492 at 1.90 Å resolution
50	<a href="#">c4hyqA</a>	Alignment	not modelled	97.8	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phospholipase a1; <b>PDBTitle:</b> crystal structure of phospholipase a1 from <i>Streptomyces albidoflavus</i> na297
51	<a href="#">c6j11A</a>	Alignment	not modelled	97.4	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> thermolabile hemolysin; <b>PDBTitle:</b> crystal structure of vvp1pA g389d from <i>Vibrio vulnificus</i>
52	<a href="#">c4nrDA</a>	Alignment	not modelled	97.3	10	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a putative gdsI-like lipase (bacova_04955) from <i>Bacteroides ovatus</i> ATCC 8483 at 2.10 Å resolution
53	<a href="#">c4i8iA</a>	Alignment	not modelled	97.3	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a duf4886 family protein

						(bacuni_01406) from2 bacteroides uniformis atcc 8492 at 1.50 a resolution
54	<a href="#">c4kncA</a>	Alignment	not modelled	97.0	13	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> alginate biosynthesis protein algx; <b>PDBTitle:</b> structural and functional characterization of pseudomonas aeruginosa2 algx
55	<a href="#">c5xtuA</a>	Alignment	not modelled	96.3	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> gdsl-family esterase; <b>PDBTitle:</b> crystal structure of gdsl esterase of photobacterium sp. j15
56	<a href="#">c4o8vA</a>	Alignment	not modelled	95.5	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> alginate biosynthesis protein algj; <b>PDBTitle:</b> o-acetyltransferase domain of pseudomonas putida algj
57	<a href="#">c3nvbA</a>	Alignment	not modelled	95.5	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of n-terminal part of the protein bf1531 from2 bacteroides fragilis containing phosphatase domain complexed with mg3 and tungstate
58	<a href="#">c3auzA</a>	Alignment	not modelled	93.2	16	<b>PDB header:</b> recombination <b>Chain:</b> A: <b>PDB Molecule:</b> dna double-strand break repair protein mre11; <b>PDBTitle:</b> crystal structure of mre11 with manganese
59	<a href="#">c4nzka</a>	Alignment	not modelled	92.8	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a dhwh family protein (eubsir_00411) from2 eubacterium siraeum dsm 15702 at 1.49 a resolution
60	<a href="#">c5v8eB</a>	Alignment	not modelled	89.9	10	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> bacillus cereus patb1; <b>PDBTitle:</b> structure of bacillus cereus patb1
61	<a href="#">d1ii7a</a>	Alignment	not modelled	89.0	16	<b>Fold:</b> Metallo-dependent phosphatases <b>Superfamily:</b> Metallo-dependent phosphatases <b>Family:</b> DNA double-strand break repair nuclease
62	<a href="#">c3av0A</a>	Alignment	not modelled	88.8	14	<b>PDB header:</b> recombination <b>Chain:</b> A: <b>PDB Molecule:</b> dna double-strand break repair protein mre11; <b>PDBTitle:</b> crystal structure of mre11-rad50 bound to atp s
63	<a href="#">c6o93A</a>	Alignment	not modelled	82.6	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> d-alanyl transferase dltD; <b>PDBTitle:</b> d-alanyl transferase dltD from enterococcus faecalis
64	<a href="#">d1zmba1</a>	Alignment	not modelled	82.0	13	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> SGNH hydrolase <b>Family:</b> Putative acetylxyylan esterase-like
65	<a href="#">c4ltyD</a>	Alignment	not modelled	81.6	5	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> exonuclease subunit sbcd; <b>PDBTitle:</b> crystal structure of e.coli sbcd at 1.8 a resolution
66	<a href="#">d1a9xa3</a>	Alignment	not modelled	79.8	7	<b>Fold:</b> PreATP-grasp domain <b>Superfamily:</b> PreATP-grasp domain <b>Family:</b> BC N-terminal domain-like
67	<a href="#">c3kvnA</a>	Alignment	not modelled	77.5	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> esterase esta; <b>PDBTitle:</b> crystal structure of the full-length autotransporter esta from2 pseudomonas aeruginosa
68	<a href="#">c3bmaC</a>	Alignment	not modelled	76.6	12	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> d-alanyl-lipoteichoic acid synthetase; <b>PDBTitle:</b> crystal structure of d-alanyl-lipoteichoic acid synthetase from2 streptococcus pneumoniae r6
69	<a href="#">c6pfxB</a>	Alignment	not modelled	76.0	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> d-alanyl transferase dltD; <b>PDBTitle:</b> d-alanyl transferase dltD from enterococcus faecium
70	<a href="#">c2xmoB</a>	Alignment	not modelled	70.7	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> lmo2642 protein; <b>PDBTitle:</b> the crystal structure of lmo2642
71	<a href="#">d1qvwa</a>	Alignment	not modelled	70.2	13	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> DJ-1/Pfpl
72	<a href="#">c5ulbA</a>	Alignment	not modelled	69.9	14	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative sugar abc transporter; <b>PDBTitle:</b> crystal structure of sugar abc transporter from yersinia2 enterocolitica subsp. enterocolitica 8081
73	<a href="#">c3t1iC</a>	Alignment	not modelled	68.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> double-strand break repair protein mre11a; <b>PDBTitle:</b> crystal structure of human mre11: understanding tumorigenic mutations
74	<a href="#">d2hrca1</a>	Alignment	not modelled	67.3	14	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> Chelatase <b>Family:</b> Ferrochelatase
75	<a href="#">c3ff4A</a>	Alignment	not modelled	66.5	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of uncharacterized protein chu_1412
76	<a href="#">c3tzzA</a>	Alignment	not modelled	65.7	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> polyketide synthase pks13; <b>PDBTitle:</b> crystal structure of a fragment containing the acyltransferase domain2 of pks13 from mycobacterium tuberculosis in the carboxypalmitoylated3 form at 2.5 a
77	<a href="#">d3bula2</a>	Alignment	not modelled	63.5	13	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Cobalamin (vitamin B12)-binding domain <b>Family:</b> Cobalamin (vitamin B12)-binding domain
78	<a href="#">d1fmfa</a>	Alignment	not modelled	62.3	19	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Cobalamin (vitamin B12)-binding domain <b>Family:</b> Cobalamin (vitamin B12)-binding domain
79	<a href="#">c3u7vA</a>	Alignment	not modelled	62.0	6	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-galactosidase;

79	<a href="#">c3u7vA</a>	Alignment	not modelled	62.0	0	<b>PDBTitle:</b> the structure of a putative beta-galactosidase from caulobacter2 crescentus cb15.
80	<a href="#">c4o5aA</a>	Alignment	not modelled	61.8	10	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> laci family transcription regulator; <b>PDBTitle:</b> the crystal structure of a laci family transcriptional regulator from2 bifidobacterium animalis subsp. lactis dsm 10140
81	<a href="#">c2oblA</a>	Alignment	not modelled	59.2	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> escn; <b>PDBTitle:</b> structural and biochemical analysis of a prototypical atpase from the2 type iii secretion system of pathogenic bacteria
82	<a href="#">d1kja2</a>	Alignment	not modelled	59.2	13	<b>Fold:</b> PreATP-grasp domain <b>Superfamily:</b> PreATP-grasp domain <b>Family:</b> BC N-terminal domain-like
83	<a href="#">d2yvta1</a>	Alignment	not modelled	58.5	11	<b>Fold:</b> Metallo-dependent phosphatases <b>Superfamily:</b> Metallo-dependent phosphatases <b>Family:</b> TT1561-like
84	<a href="#">c4fcxB</a>	Alignment	not modelled	58.2	11	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> dna repair protein rad32; <b>PDBTitle:</b> s.pombe mre11 apoenzym
85	<a href="#">d2nxfA1</a>	Alignment	not modelled	58.0	9	<b>Fold:</b> Metallo-dependent phosphatases <b>Superfamily:</b> Metallo-dependent phosphatases <b>Family:</b> ADPRibase-Mn-like
86	<a href="#">c6npjC</a>	Alignment	not modelled	56.2	16	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> translocator escn; <b>PDBTitle:</b> structure of the assembled atpase escn in complex with its central2 stalk esco from the enteropathogenic e. coli (epec) type iii3 secretion system
87	<a href="#">d1ccwa</a>	Alignment	not modelled	55.4	20	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Cobalamin (vitamin B12)-binding domain <b>Family:</b> Cobalamin (vitamin B12)-binding domain
88	<a href="#">c4irxA</a>	Alignment	not modelled	55.3	8	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sugar abc transporter, periplasmic sugar-binding protein; <b>PDBTitle:</b> crystal structure of caulobacter myo-inositol binding protein bound to2 myo-inositol
89	<a href="#">c4pz0A</a>	Alignment	not modelled	54.8	11	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> sugar abc transporter, sugar-binding protein; <b>PDBTitle:</b> the crystal structure of a solute binding protein from bacillus2 anthracis str. ames in complex with quorum-sensing signal3 autoinducer-2 (ai-2)
90	<a href="#">c4ivnB</a>	Alignment	not modelled	54.4	10	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> the vibrio vulnificus nanr protein complexed with mannac-6p
91	<a href="#">d1wraa1</a>	Alignment	not modelled	54.1	13	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> Pce catalytic domain-like
92	<a href="#">d1u9ca</a>	Alignment	not modelled	53.4	13	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> DJ-1/Pfp1
93	<a href="#">d1xrsb1</a>	Alignment	not modelled	52.6	14	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Cobalamin (vitamin B12)-binding domain <b>Family:</b> Cobalamin (vitamin B12)-binding domain
94	<a href="#">c4fbkB</a>	Alignment	not modelled	51.9	11	<b>PDB header:</b> hydrolase, protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> dna repair and telomere maintenance protein nbs1,dna repair <b>PDBTitle:</b> crystal structure of a covalently fused nbs1-mre11 complex with one2 manganese ion per active site
95	<a href="#">c2yxbA</a>	Alignment	not modelled	51.6	12	<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
96	<a href="#">c4lrUA</a>	Alignment	not modelled	50.0	12	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> glyoxalase iii (glutathione-independent); <b>PDBTitle:</b> crystal structure of glyoxalase iii (orf 19.251) from candida albicans
97	<a href="#">c4yleA</a>	Alignment	not modelled	48.9	7	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic binding protein/laci transcriptional regulator; <b>PDBTitle:</b> crystal structure of an abc transporter solute binding protein2 (ipr025997) from burkholderia multivorans (bmul_1631, target efi-3 511115) with an unknown ligand modelled as alpha-d-erythrofuranoose
98	<a href="#">c6dspB</a>	Alignment	not modelled	46.4	18	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> autoinducer 2-binding protein lsrB; <b>PDBTitle:</b> lsrB from clostridium saccharobutylicum in complex with ai-2
99	<a href="#">c2xhzC</a>	Alignment	not modelled	46.4	13	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> arabinose 5-phosphate isomerase; <b>PDBTitle:</b> probing the active site of the sugar isomerase domain from e. coli2 arabinose-5-phosphate isomerase via x-ray crystallography
100	<a href="#">c5uqiA</a>	Alignment	not modelled	45.9	10	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphosugar isomerase; <b>PDBTitle:</b> e. coli cft073 c3406 in complex with a5p
101	<a href="#">c3lvtA</a>	Alignment	not modelled	43.9	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glycosyl hydrolase, family 38; <b>PDBTitle:</b> the crystal structure of a protein in the glycosyl hydrolase family 382 from enterococcus faecalis to 2.55a
102	<a href="#">c2q8uA</a>	Alignment	not modelled	43.5	8	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> exonuclease, putative; <b>PDBTitle:</b> crystal structure of mre11 from thermotoga maritima msb8 (tm1635) at2 2.20 a resolution
103	<a href="#">c6ccia</a>	Alignment	not modelled	42.3	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein eskimo 1;



						<b>PDBTitle:</b> the crystal structure of xoat1
104	<a href="#">c5b4bB_</a>	Alignment	not modelled	42.2	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-2,3-diacetylglucosamine hydrolase; <b>PDBTitle:</b> crystal structure of lpxh with lipid x in spacegroup c2
105	<a href="#">c3fxaA_</a>	Alignment	not modelled	42.0	14	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> sis domain protein; <b>PDBTitle:</b> crystal structure of a putative sugar-phosphate isomerase2 (lmof2365_0531) from listeria monocytogenes str. 4b f2365 at 1.60 a3 resolution
106	<a href="#">c3h10B_</a>	Alignment	not modelled	41.8	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> maleylacetate reductase; <b>PDBTitle:</b> crystal structure of maleylacetate reductase from agrobacterium2 tumefaciens
107	<a href="#">c3qg5D_</a>	Alignment	not modelled	41.2	8	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> mre11; <b>PDBTitle:</b> the mre11:rad50 complex forms an atp dependent molecular clamp in dna2 double-strand break repair
108	<a href="#">c2wwbB_</a>	Alignment	not modelled	40.9	22	<b>PDB header:</b> ribosome <b>Chain:</b> B: <b>PDB Molecule:</b> protein transport protein sec61 subunit gamma; <b>PDBTitle:</b> cryo-em structure of the mammalian sec61 complex bound to the actively2 translating wheat germ 80s ribosome
109	<a href="#">c2i2xD_</a>	Alignment	not modelled	40.3	14	<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
110	<a href="#">c5douC_</a>	Alignment	not modelled	39.5	9	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> carbamoyl-phosphate synthase [ammonia], mitochondrial; <b>PDBTitle:</b> crystal structure of human carbamoyl phosphate synthetase i (cps1),2 ligand-bound form
111	<a href="#">c5dotA_</a>	Alignment	not modelled	39.5	7	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> carbamoyl-phosphate synthase [ammonia], mitochondrial; <b>PDBTitle:</b> crystal structure of human carbamoyl phosphate synthetase i (cps1),2 apo form
112	<a href="#">c5ydmA_</a>	Alignment	not modelled	39.4	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pkcs; <b>PDBTitle:</b> the crystal structure of the acyl transferase domain of spnd complex2 with benzylmalonyl
113	<a href="#">d1n57a_</a>	Alignment	not modelled	39.1	13	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> DJ-1/Pfpl
114	<a href="#">d1duvg2</a>	Alignment	not modelled	39.0	8	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
115	<a href="#">c4g97A_</a>	Alignment	not modelled	38.9	16	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator receiver; <b>PDBTitle:</b> crystal structure of the response regulator phyr from brucella abortus
116	<a href="#">c5syrA_</a>	Alignment	not modelled	38.8	7	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable atp synthase spa1/mxib; <b>PDBTitle:</b> crystal structure of atpase delta1-79 spa47 r350a
117	<a href="#">c3im9A_</a>	Alignment	not modelled	38.6	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> malonyl coa-acyl carrier protein transacylase; <b>PDBTitle:</b> crystal structure of mcat from staphylococcus aureus
118	<a href="#">c1y80A_</a>	Alignment	not modelled	38.3	13	<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 from moorella2 thermoacetica
119	<a href="#">d2gc6a1</a>	Alignment	not modelled	37.1	15	<b>Fold:</b> MurD-like peptide ligases, peptide-binding domain <b>Superfamily:</b> MurD-like peptide ligases, peptide-binding domain <b>Family:</b> Folypolyglutamate synthetase, C-terminal domain
120	<a href="#">c3cvjB_</a>	Alignment	not modelled	36.6	8	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> putative phosphoheptose isomerase; <b>PDBTitle:</b> crystal structure of a putative phosphoheptose isomerase (bh3325) from2 bacillus halodurans c-125 at 2.00 a resolution