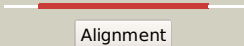

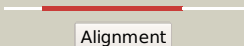

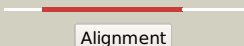







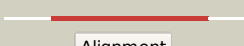













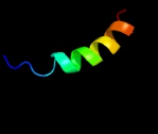






# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2525c_(- )_2849862_2850584
Date	Wed Aug 7 12:50:15 BST 2019
Unique Job ID	265b96c5e65809f3

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4pmnB_</a>	 Alignment		100.0	99	<b>PDB header:</b> unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> tat-secreted protein rv2525c; <b>PDBTitle:</b> crystal structure of the mycobacterium tuberculosis tat-secreted2 protein rv2525c in complex with mes (monoclinic crystal form i)
2	<a href="#">c1sfsA_</a>	 Alignment		100.0	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> 1.07 a crystal structure of an uncharacterized b. stearothermophilus2 protein
3	<a href="#">d1sfsa_</a>	 Alignment		100.0	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> 1,4-beta-N-acetylMuraminidase
4	<a href="#">d1jfxa_</a>	 Alignment		97.8	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> 1,4-beta-N-acetylMuraminidase
5	<a href="#">c2nw0B_</a>	 Alignment		97.7	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> plyb; <b>PDBTitle:</b> crystal structure of a lysin
6	<a href="#">c4krtA_</a>	 Alignment		97.7	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> autolytic lysozyme; <b>PDBTitle:</b> x-ray structure of endolysin from clostridium perfringens phage2 phism101
7	<a href="#">c2wagA_</a>	 Alignment		97.5	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> lysozyme, putative; <b>PDBTitle:</b> the structure of a family 25 glycosyl hydrolase from2 bacillus anthracis.
8	<a href="#">c5a6sA_</a>	 Alignment		97.5	17	<b>PDB header:</b> structural protein <b>Chain:</b> A; <b>PDB Molecule:</b> endolysin; <b>PDBTitle:</b> crystal structure of the ctp11 endolysin reveals how its2 activity is regulated by a secondary translation product
9	<a href="#">c4jz5A_</a>	 Alignment		97.3	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> gp26; <b>PDBTitle:</b> high-resolution structure of catalytic domain of endolysin ply40 from2 bacteriophage p40 of listeria monocytogenes
10	<a href="#">c2x8rE_</a>	 Alignment		97.2	18	<b>PDB header:</b> hydrolase <b>Chain:</b> E; <b>PDB Molecule:</b> glycosyl hydrolase; <b>PDBTitle:</b> the structure of a family gh25 lysozyme from aspergillus2 fumigatus
11	<a href="#">c4ff5A_</a>	 Alignment		96.7	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> glycosyl hydrolase 25; <b>PDBTitle:</b> structure basis of a novel virulence factor gh1p a glycosyl hydrolase2 25 of streptococcus pneumoniae participating in host cell invasion

12	<a href="#">c2wwcA</a>	Alignment		96.4	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 1,4-beta-n-acetylmuramidase; <b>PDBTitle:</b> 3d-structure of the modular autolysin lytc from2 streptococcus pneumoniae in complex with synthetic3 peptidoglycan ligand
13	<a href="#">c5jipB</a>	Alignment		95.2	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> cortical-lytic enzyme; <b>PDBTitle:</b> crystal structure of the clostridium perfringens spore cortex lytic2 enzyme slem
14	<a href="#">d2j8ga2</a>	Alignment		86.7	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> 1,4-beta-N-acetylmuraminidase
15	<a href="#">c2j8fA</a>	Alignment		72.5	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lysozyme; <b>PDBTitle:</b> crystal structure of the modular cpl-1 endolysin complexed with a2 peptidoglycan analogue (e94q mutant in complex with a disaccharide-3 pentapeptide)
16	<a href="#">c2pq4B</a>	Alignment		57.7	32	<b>PDB header:</b> chaperone/oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> periplasmic nitrate reductase precursor; <b>PDBTitle:</b> nmr solution structure of napd in complex with napa1-352 signal peptide
17	<a href="#">d1i60a</a>	Alignment		56.7	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> loll-like
18	<a href="#">c5tnvA</a>	Alignment		48.7	17	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ap endonuclease, family protein 2; <b>PDBTitle:</b> crystal structure of a xylose isomerase-like tim barrel protein from2 mycobacterium smegmatis in complex with magnesium
19	<a href="#">c1p84E</a>	Alignment		47.5	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> ubiquinol-cytochrome c reductase iron-sulfur subunit; <b>PDBTitle:</b> hdbt inhibited yeast cytochrome bc1 complex
20	<a href="#">c2fynO</a>	Alignment		46.3	36	<b>PDB header:</b> oxidoreductase <b>Chain:</b> O: <b>PDB Molecule:</b> ubiquinol-cytochrome c reductase iron-sulfur <b>PDBTitle:</b> crystal structure analysis of the double mutant rhodobacter2 sphaeroides bc1 complex
21	<a href="#">c3dx5A</a>	Alignment	not modelled	43.7	11	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein asbf; <b>PDBTitle:</b> crystal structure of the probable 3-dhs dehydratase asbf involved in2 the petrobactin synthesis from bacillus anthracis
22	<a href="#">d1bxca</a>	Alignment	not modelled	42.3	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> Xylose isomerase
23	<a href="#">d1k77a</a>	Alignment	not modelled	42.1	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> Hypothetical protein YgbM (EC1530)
24	<a href="#">c2e76D</a>	Alignment	not modelled	41.3	12	<b>PDB header:</b> photosynthesis <b>Chain:</b> D: <b>PDB Molecule:</b> cytochrome b6-f complex iron-sulfur subunit; <b>PDBTitle:</b> crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus
25	<a href="#">c3s6dA</a>	Alignment	not modelled	37.0	16	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative triosephosphate isomerase; <b>PDBTitle:</b> crystal structure of a putative triosephosphate isomerase from2 coccidioides immitis
26	<a href="#">d2q02a1</a>	Alignment	not modelled	37.0	7	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> loll-like
27	<a href="#">d2j85a1</a>	Alignment	not modelled	36.9	21	<b>Fold:</b> STIV B116-like <b>Superfamily:</b> STIV B116-like <b>Family:</b> STIV B116-like
28	<a href="#">c6cwhB</a>	Alignment	not modelled	35.9	21	<b>PDB header:</b> sugar binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> surface (s-) layer glycoprotein; <b>PDBTitle:</b> crystal structure of spaa-slh in complex with 4,6-pyr-beta-d-mannacome2 (p1)
						<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> ubiquinol-cytochrome c reductase iron-

29	<a href="#">c2fyuE</a>	Alignment	not modelled	33.2	18	sulfur subunit, <b>PDBTitle:</b> crystal structure of bovine heart mitochondrial bc1 with jg1442 inhibitor
30	<a href="#">c1vioA</a>	Alignment	not modelled	32.7	20	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> ribosomal small subunit pseudouridine synthase a; <b>PDBTitle:</b> crystal structure of pseudouridylate synthase
31	<a href="#">c3ju2A</a>	Alignment	not modelled	31.7	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein smc04130; <b>PDBTitle:</b> crystal structure of protein smc04130 from sinorhizobium meliloti 1021
32	<a href="#">d1tz9a</a>	Alignment	not modelled	31.3	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> UxuA-like
33	<a href="#">c6fo2R</a>	Alignment	not modelled	29.9	16	<b>PDB header:</b> membrane protein <b>Chain:</b> R: <b>PDB Molecule:</b> cytochrome b-c1 complex subunit rieske, mitochondrial; <b>PDBTitle:</b> cryoem structure of bovine cytochrome bc1 with no ligand bound
34	<a href="#">c3ogrA</a>	Alignment	not modelled	28.2	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> complex structure of beta-galactosidase from trichoderma reesei with2 galactose
35	<a href="#">c2qw5B</a>	Alignment	not modelled	25.9	15	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> xylose isomerase-like tim barrel; <b>PDBTitle:</b> crystal structure of a putative sugar phosphate isomerase/epimerase2 (ava4194) from anabaena variabilis atcc 29413 at 1.78 a resolution
36	<a href="#">d2g0wa1</a>	Alignment	not modelled	25.4	10	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> loll-like
37	<a href="#">c3c85D</a>	Alignment	not modelled	25.4	15	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> putative glutathione-regulated potassium-efflux system <b>PDBTitle:</b> crystal structure of trka domain of putative glutathione-regulated2 potassium-efflux kefb from vibrio parahaemolyticus
38	<a href="#">c1xc6A</a>	Alignment	not modelled	25.2	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> native structure of beta-galactosidase from penicillium sp. in complex2 with galactose
39	<a href="#">d1ltqa1</a>	Alignment	not modelled	25.1	17	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> phosphatase domain of polynucleotide kinase
40	<a href="#">d1bxba</a>	Alignment	not modelled	23.7	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> Xylose isomerase
41	<a href="#">c5ak1A</a>	Alignment	not modelled	23.1	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> carbohydrate binding family 6; <b>PDBTitle:</b> the penta-modular cellulosomal arabinoxylanase ctxyl5a2 structure as revealed by x-ray crystallography
42	<a href="#">c3cqkB</a>	Alignment	not modelled	23.1	8	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> l-ribulose-5-phosphate 3-epimerase ulae; <b>PDBTitle:</b> crystal structure of l-xylulose-5-phosphate 3-epimerase ulae (form b)2 complex with zn2+ and sulfate
43	<a href="#">c6daoB</a>	Alignment	not modelled	21.5	17	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> trans-o-hydroxybenzylidenepyruvate hydratase-aldolase; <b>PDBTitle:</b> nahe wt selenomethionine
44	<a href="#">c4wcxC</a>	Alignment	not modelled	20.5	11	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> biotin and thiamin synthesis associated; <b>PDBTitle:</b> crystal structure of hydg: a maturase of the [fef]-hydrogenase
45	<a href="#">d1xima</a>	Alignment	not modelled	19.8	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> Xylose isomerase
46	<a href="#">c2ogfD</a>	Alignment	not modelled	19.0	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> hypothetical protein mj0408; <b>PDBTitle:</b> crystal structure of protein mj0408 from methanococcus jannaschii,2 pfam duf372
47	<a href="#">c4kqxB</a>	Alignment	not modelled	18.8	15	<b>PDB header:</b> oxidoreductase/oxidoreductase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> ketol-acid reductoisomerase; <b>PDBTitle:</b> mutant slackia exigua kari ddv in complex with nad and an inhibitor
48	<a href="#">c5jp6A</a>	Alignment	not modelled	18.6	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative polysaccharide deacetylase; <b>PDBTitle:</b> bdellovibrio bacteriovorus peptidoglycan deacetylase bd3279
49	<a href="#">d1qt1a</a>	Alignment	not modelled	18.5	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> Xylose isomerase
50	<a href="#">d1xlma</a>	Alignment	not modelled	17.3	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> Xylose isomerase
51	<a href="#">c3t7vA</a>	Alignment	not modelled	16.9	8	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methylornithine synthase pylb; <b>PDBTitle:</b> crystal structure of methylornithine synthase (pylb)
52	<a href="#">c5hmqE</a>	Alignment	not modelled	14.9	13	<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
53	<a href="#">d2obpa1</a>	Alignment	not modelled	14.3	27	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ReutB4095-like
54	<a href="#">c2fhoA</a>	Alignment	not modelled	14.2	18	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> spliceosomal protein sf3b155; <b>PDBTitle:</b> nmr solution structure of the human spliceosomal protein2 complex p14-sf3b155

55	<a href="#">c4nz3A</a>	Alignment	not modelled	13.6	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> deacetylase da1; <b>PDBTitle:</b> structure of vibrio cholerae chitin de-n-acetylase in complex with2 di(n-acetyl-d-glucosamine) (cbs) in p 21 21 21
56	<a href="#">d2ceva</a>	Alignment	not modelled	13.5	16	<b>Fold:</b> Arginase/deacetylase <b>Superfamily:</b> Arginase/deacetylase <b>Family:</b> Arginase-like amidino hydrolases
57	<a href="#">c3kwsB</a>	Alignment	not modelled	13.5	12	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> putative sugar isomerase; <b>PDBTitle:</b> crystal structure of putative sugar isomerase (yp_001305149.1) from2 parabacteroides distazonis atcc 8503 at 1.68 a resolution
58	<a href="#">c3vylB</a>	Alignment	not modelled	12.9	13	<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
59	<a href="#">c3cnyA</a>	Alignment	not modelled	12.4	18	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> inositol catabolism protein iole; <b>PDBTitle:</b> crystal structure of a putative inositol catabolism protein iole2 (iole, lp_3607) from lactobacillus plantarum wcf51 at 1.85 a3 resolution
60	<a href="#">c1uytC</a>	Alignment	not modelled	12.1	10	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> acetyl-coa carboxylase; <b>PDBTitle:</b> acetyl-coa carboxylase carboxyltransferase domain
61	<a href="#">d1mhhe</a>	Alignment	not modelled	11.9	27	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Immunoglobulin-binding domains <b>Family:</b> Immunoglobulin-binding domains
62	<a href="#">c5zeeA</a>	Alignment	not modelled	11.6	12	<b>PDB header:</b> hydrolase/inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> arginase; <b>PDBTitle:</b> crystal structure of entamoeba histolytica arginase in complex with2 n(omega)-hydroxy-l-arginine (noha) at 1.74 a
63	<a href="#">c5l0lB</a>	Alignment	not modelled	11.4	26	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of uncharacterized protein lpg0439
64	<a href="#">c4rtbA</a>	Alignment	not modelled	10.8	15	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> hydrg protein; <b>PDBTitle:</b> x-ray structure of the fefe-hydrogenase maturase hydrg from2 carboxydotherrmus hydrogenoformans
65	<a href="#">d2aeba1</a>	Alignment	not modelled	10.5	19	<b>Fold:</b> Arginase/deacetylase <b>Superfamily:</b> Arginase/deacetylase <b>Family:</b> Arginase-like amidino hydrolases
66	<a href="#">d1jmla</a>	Alignment	not modelled	10.5	20	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Immunoglobulin-binding domains <b>Family:</b> Immunoglobulin-binding domains
67	<a href="#">c2f9jP</a>	Alignment	not modelled	9.7	18	<b>PDB header:</b> rna binding protein <b>Chain:</b> P: <b>PDB Molecule:</b> splicing factor 3b subunit 1; <b>PDBTitle:</b> 3.0 angstrom resolution structure of a y22m mutant of the spliceosomal2 protein p14 bound to a region of sf3b155
68	<a href="#">d1yx1a1</a>	Alignment	not modelled	9.5	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> KguE-like
69	<a href="#">c4rl4B</a>	Alignment	not modelled	9.3	23	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> gtp cyclohydrolase-2; <b>PDBTitle:</b> crystal structure of gtp cyclohydrolase ii from helicobacter pylori2 26695
70	<a href="#">c1gthD</a>	Alignment	not modelled	9.3	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> dihydropyrimidine dehydrogenase; <b>PDBTitle:</b> dihydropyrimidine dehydrogenase (dpg) from pig, ternary complex with2 nadph and 5-iodouracil
71	<a href="#">c3nipB</a>	Alignment	not modelled	9.3	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-guanidinopropionase; <b>PDBTitle:</b> crystal structure of pseudomonas aeruginosa guanidinopropionase2 complexed with 1,6-diaminohexane
72	<a href="#">d1vioa1</a>	Alignment	not modelled	9.3	20	<b>Fold:</b> Pseudouridine synthase <b>Superfamily:</b> Pseudouridine synthase <b>Family:</b> Pseudouridine synthase RsuA/RluD
73	<a href="#">c2qx2A</a>	Alignment	not modelled	9.2	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> sex pheromone staph-cam373; <b>PDBTitle:</b> structure of the c-terminal domain of sex pheromone staph-cam3732 precursor from staphylococcus aureus
74	<a href="#">d2glka1</a>	Alignment	not modelled	9.1	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> Xylose isomerase
75	<a href="#">d1b25a2</a>	Alignment	not modelled	8.9	21	<b>Fold:</b> Aldehyde ferredoxin oxidoreductase, N-terminal domain <b>Superfamily:</b> Aldehyde ferredoxin oxidoreductase, N-terminal domain <b>Family:</b> Aldehyde ferredoxin oxidoreductase, N-terminal domain
76	<a href="#">d2gp4a1</a>	Alignment	not modelled	8.9	12	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> LeuD/IlvD-like <b>Family:</b> IlvD/EDD C-terminal domain-like
77	<a href="#">d2ptla</a>	Alignment	not modelled	8.8	20	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Immunoglobulin-binding domains <b>Family:</b> Immunoglobulin-binding domains
78	<a href="#">c1mk2B</a>	Alignment	not modelled	8.8	29	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> madh-interacting protein; <b>PDBTitle:</b> smad3 sbd complex
79	<a href="#">d1hz6a</a>	Alignment	not modelled	8.7	20	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Immunoglobulin-binding domains <b>Family:</b> Immunoglobulin-binding domains
80	<a href="#">d1k52a</a>	Alignment	not modelled	8.6	20	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Immunoglobulin-binding domains <b>Family:</b> Immunoglobulin-binding domains
						<b>PDB header:</b> structural protein

81	<a href="#">c3pywA_</a>	Alignment	not modelled	8.5	8	<b>Chain:</b> A: <b>PDB Molecule:</b> s-layer protein sap; <b>PDBTitle:</b> the structure of the slh domain from b. anthracis surface array2 protein at 1.8a
82	<a href="#">d1mo0a_</a>	Alignment	not modelled	8.4	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Triosephosphate isomerase (TIM) <b>Family:</b> Triosephosphate isomerase (TIM)
83	<a href="#">c2htfA_</a>	Alignment	not modelled	8.3	50	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase mu; <b>PDBTitle:</b> the solution structure of the brct domain from human2 polymerase reveals homology with the tdt brct domain
84	<a href="#">c4nvtD_</a>	Alignment	not modelled	8.2	19	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> crystal structure of triosephosphate isomerase from brucella2 melitensis
85	<a href="#">c3bdkB_</a>	Alignment	not modelled	8.0	23	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> d-mannonate dehydratase; <b>PDBTitle:</b> crystal structure of streptococcus suis mannonate2 dehydratase complexed with substrate analogue
86	<a href="#">c4hn3C_</a>	Alignment	not modelled	7.9	18	<b>PDB header:</b> signaling protein <b>Chain:</b> C: <b>PDB Molecule:</b> lmo1757 protein; <b>PDBTitle:</b> the crystal structure of a sex pheromone precursor (lmo1757) from2 listeria monocytogenes egd-e
87	<a href="#">c3obeB_</a>	Alignment	not modelled	7.6	11	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> sugar phosphate isomerase/epimerase; <b>PDBTitle:</b> crystal structure of a sugar phosphate isomerase/epimerase (bdi_3400)2 from parabacteroides distasonis atcc 8503 at 1.70 a resolution
88	<a href="#">d7reqb2</a>	Alignment	not modelled	7.6	29	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Cobalamin (vitamin B12)-binding domain <b>Family:</b> Cobalamin (vitamin B12)-binding domain
89	<a href="#">d2cyga1</a>	Alignment	not modelled	7.5	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
90	<a href="#">d1n55a_</a>	Alignment	not modelled	7.5	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Triosephosphate isomerase (TIM) <b>Family:</b> Triosephosphate isomerase (TIM)
91	<a href="#">c4b8nC_</a>	Alignment	not modelled	7.3	6	<b>PDB header:</b> electron transport <b>Chain:</b> C: <b>PDB Molecule:</b> cytochrome b5-host origin; <b>PDBTitle:</b> cytochrome b5 of ostreococcus tauri virus 2
92	<a href="#">d1oqya2</a>	Alignment	not modelled	7.2	33	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
93	<a href="#">c2eivH_</a>	Alignment	not modelled	7.1	17	<b>PDB header:</b> hydrolase <b>Chain:</b> H: <b>PDB Molecule:</b> arginase; <b>PDBTitle:</b> crystal structure of the arginase from thermus thermophilus
94	<a href="#">d2a0ma1</a>	Alignment	not modelled	6.9	19	<b>Fold:</b> Arginase/deacetylase <b>Superfamily:</b> Arginase/deacetylase <b>Family:</b> Arginase-like amidino hydrolases
95	<a href="#">c2dp3A_</a>	Alignment	not modelled	6.9	17	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> crystal structure of a double mutant (c202a/a198v) of triosephosphate2 isomerase from giardia lamblia
96	<a href="#">c3krsB_</a>	Alignment	not modelled	6.8	23	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> structure of triosephosphate isomerase from cryptosporidium parvum at2 1.55a resolution
97	<a href="#">d1suxa_</a>	Alignment	not modelled	6.7	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Triosephosphate isomerase (TIM) <b>Family:</b> Triosephosphate isomerase (TIM)
98	<a href="#">c4z3wB_</a>	Alignment	not modelled	6.7	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> benzoyl-coa reductase, putative; <b>PDBTitle:</b> active site complex bambc of benzoyl coenzyme a reductase in complex2 with 1,5 dienoyl-coa
99	<a href="#">d1xp3a1</a>	Alignment	not modelled	6.6	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> Endonuclease IV