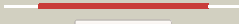
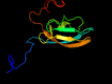


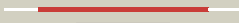
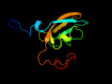

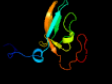







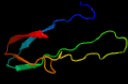



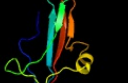

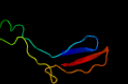
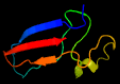






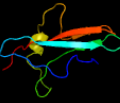
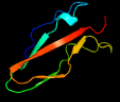


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1849_(ureB)_2097654_2097968
Date	Fri Aug 2 13:30:46 BST 2019
Unique Job ID	e1b76811d8d669c9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d4ubpb_</a>	 Alignment		100.0	48	<b>Fold:</b> beta-clip <b>Superfamily:</b> Urease, beta-subunit <b>Family:</b> Urease, beta-subunit
2	<a href="#">d1e9ya1</a>	 Alignment		100.0	44	<b>Fold:</b> beta-clip <b>Superfamily:</b> Urease, beta-subunit <b>Family:</b> Urease, beta-subunit
3	<a href="#">c1e9za_</a>	 Alignment		100.0	44	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> urease subunit alpha; <b>PDBTitle:</b> crystal structure of helicobacter pylori urease
4	<a href="#">d1ejxb_</a>	 Alignment		100.0	50	<b>Fold:</b> beta-clip <b>Superfamily:</b> Urease, beta-subunit <b>Family:</b> Urease, beta-subunit
5	<a href="#">c4z42B_</a>	 Alignment		100.0	40	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> urease subunit beta; <b>PDBTitle:</b> crystal structure of urease from yersinia enterocolitica
6	<a href="#">c3qgaD_</a>	 Alignment		100.0	40	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> fusion of urease beta and gamma subunits; <b>PDBTitle:</b> 3.0 a model of iron containing urease urea2b2 from helicobacter2 mustelae
7	<a href="#">c3la4A_</a>	 Alignment		100.0	41	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> urease; <b>PDBTitle:</b> crystal structure of the first plant urease from jack bean (canavalia2 ensiformis)
8	<a href="#">c5z87B_</a>	 Alignment		88.5	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> emgh1; <b>PDBTitle:</b> structural of a novel b-glucosidase emgh1 at 2.3 angstrom from2 erythrobacter marinus
9	<a href="#">c5wabD_</a>	 Alignment		86.3	11	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> putative beta-glucosidase; <b>PDBTitle:</b> crystal structure of bifidobacterium adolescentis gh3 beta-glucosidase
10	<a href="#">d2co7b1</a>	 Alignment		83.6	18	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> PapD-like <b>Family:</b> Pilus chaperone
11	<a href="#">c3ac0B_</a>	 Alignment		83.5	30	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-glucosidase i; <b>PDBTitle:</b> crystal structure of beta-glucosidase from kluyveromyces marxianus in2 complex with glucose

12	<a href="#">c1yewl_</a>	Alignment		83.4	23	<b>PDB header:</b> oxidoreductase, membrane protein <b>Chain:</b> I: <b>PDB Molecule:</b> particulate methane monooxygenase, b subunit; <b>PDBTitle:</b> crystal structure of particulate methane monooxygenase
13	<a href="#">c3zz1A_</a>	Alignment		83.3	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-d-glucoside glucohydrolase; <b>PDBTitle:</b> crystal structure of a glycoside hydrolase family 3 beta-glucosidase,2 bgl1 from hypocrea jecorina at 2.1a resolution.
14	<a href="#">c3rgbA_</a>	Alignment		83.1	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> methane monooxygenase subunit b2; <b>PDBTitle:</b> crystal structure of particulate methane monooxygenase from2 methylococcus capsulatus (bath)
15	<a href="#">c3zk0A_</a>	Alignment		81.6	16	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> sco3965; <b>PDBTitle:</b> the crystal structure of a cu(i) metallochaperone from2 streptomyces lividans in its apo form
16	<a href="#">c4i3gB_</a>	Alignment		81.2	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-glucosidase; <b>PDBTitle:</b> crystal structure of desr, a beta-glucosidase from streptomyces2 venezuelae in complex with d-glucose.
17	<a href="#">c3u48A_</a>	Alignment		80.5	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> jmb19063; <b>PDBTitle:</b> from soil to structure: a novel dimeric family 3-beta-glucosidase2 isolated from compost using metagenomic analysis
18	<a href="#">c2co7B_</a>	Alignment		79.6	18	<b>PDB header:</b> fibril protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative fimbriae assembly chaperone; <b>PDBTitle:</b> salmonella enterica safai pilin in complex with the safb2 chaperone (type ii)
19	<a href="#">c4djmA_</a>	Alignment		79.3	21	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> drab; <b>PDBTitle:</b> crystal structure of the e. coli chaperone drab
20	<a href="#">c1z9sA_</a>	Alignment		79.1	19	<b>PDB header:</b> chaperone/immune system <b>Chain:</b> A: <b>PDB Molecule:</b> chaperone protein caf1m; <b>PDBTitle:</b> crystal structure of the native chaperone:subunit:subunit2 caf1m:caf1:caf1 complex
21	<a href="#">c5z9sB_</a>	Alignment	not modelled	79.1	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> glycosyl hydrolase family 3 protein; <b>PDBTitle:</b> functional and structural characterization of a beta-glucosidase2 involved in saponin metabolism from intestinal bacteria
22	<a href="#">c5d6hA_</a>	Alignment	not modelled	78.8	13	<b>PDB header:</b> chaperone/protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> csuc; <b>PDBTitle:</b> crystal structure of csuc-csua/b chaperone-major subunit pre-assembly2 complex from csu biofilm-mediating pili of acinetobacter baumannii
23	<a href="#">c2x41A_</a>	Alignment	not modelled	78.4	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-glucosidase; <b>PDBTitle:</b> structure of beta-glucosidase 3b from thermotoga neapolitana in2 complex with glucose
24	<a href="#">c4zo9B_</a>	Alignment	not modelled	77.6	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> lin1840 protein; <b>PDBTitle:</b> crystal structure of mutant (d270a) beta-glucosidase from listeria2 innocua in complex with laminaribiose
25	<a href="#">c5yotB_</a>	Alignment	not modelled	77.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> isoprimeverose-producing enzyme; <b>PDBTitle:</b> isoprimeverose-producing enzyme from aspergillus oryzae in complex2 with isoprimeverose
26	<a href="#">c5jp0A_</a>	Alignment	not modelled	75.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-glucosidase bogh3b; <b>PDBTitle:</b> bacteroides ovatus xyloglucan pul gh3b with bound glucose
27	<a href="#">c5ghuA_</a>	Alignment	not modelled	73.5	19	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> probable fimbrial chaperone yadv; <b>PDBTitle:</b> crystal structure of ecpd chaperone at 1.63 angstrom
28	<a href="#">d1w8oa1</a>	Alignment	not modelled	72.9	14	<b>Fold:</b> immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> E-set domains of sugar-utilizing enzymes

29	<a href="#">c3k25B_</a>	Alignment	not modelled	72.8	25	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> slr1438 protein; <b>PDBTitle:</b> crystal structure of slr1438 protein from synechocystis sp. pcc 6803,2 northeast structural genomics consortium target sgr112
30	<a href="#">c5tf0B_</a>	Alignment	not modelled	72.7	10	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> glycosyl hydrolase family 3 n-terminal domain protein; <b>PDBTitle:</b> crystal structure of glycosyl hydrolase family 3 n-terminal domain2 protein from bacteroides intestinalis
31	<a href="#">d1p5va1</a>	Alignment	not modelled	72.5	18	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> PapD-like <b>Family:</b> Pilus chaperone
32	<a href="#">c1so9A_</a>	Alignment	not modelled	72.3	17	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome c oxidase assembly protein ctag; <b>PDBTitle:</b> solution structure of apocox11, 30 structures
33	<a href="#">d1so9a_</a>	Alignment	not modelled	72.3	17	<b>Fold:</b> Ctag/Cox11 <b>Superfamily:</b> Ctag/Cox11 <b>Family:</b> Ctag/Cox11
34	<a href="#">c4d0jD_</a>	Alignment	not modelled	72.3	19	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> beta-glucosidase; <b>PDBTitle:</b> crystal structure of glycoside hydrolase family 3 beta-2 glucosidase cel3a from the moderately thermophilic fungus3 rasamsonia emersonii
35	<a href="#">c2zooA_</a>	Alignment	not modelled	70.8	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> probable nitrite reductase; <b>PDBTitle:</b> crystal structure of nitrite reductase from pseudoalteromonas2 haloplanktis tac125
36	<a href="#">c5wabC_</a>	Alignment	not modelled	70.4	11	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> putative beta-glucosidase; <b>PDBTitle:</b> crystal structure of bifidobacterium adolescentis gh3 beta-glucosidase
37	<a href="#">c5zl1A_</a>	Alignment	not modelled	70.2	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative copper-type nitrite reductase; <b>PDBTitle:</b> hexameric structure of copper-containing nitrite reductase of an2 anammox organism ksu-1
38	<a href="#">c4iidB_</a>	Alignment	not modelled	69.1	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-glucosidase 1; <b>PDBTitle:</b> crystal structure of beta-glucosidase 1 from aspergillus aculeatus in2 complex with 1-deoxynojirimycin
39	<a href="#">c5k6lA_</a>	Alignment	not modelled	65.0	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> b-glucosidase; <b>PDBTitle:</b> structure of a gh3 b-glucosidase from cow rumen metagenome
40	<a href="#">c4lesA_</a>	Alignment	not modelled	64.8	10	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> protein - conserved hypothetical; <b>PDBTitle:</b> 2.2 angstrom crystal structure of conserved hypothetical protein from2 bacillus anthracis.
41	<a href="#">c3kw8A_</a>	Alignment	not modelled	64.7	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative copper oxidase; <b>PDBTitle:</b> two-domain laccase from streptomyces coelicolor at 2.3 a resolution
42	<a href="#">c3g5wC_</a>	Alignment	not modelled	64.6	19	<b>PDB header:</b> metal binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> multicopper oxidase type 1; <b>PDBTitle:</b> crystal structure of blue copper oxidase from nitrosomonas europaea
43	<a href="#">c6q7jB_</a>	Alignment	not modelled	64.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> exo-1,4-beta-xylosidase xlnD; <b>PDBTitle:</b> gh3 exo-beta-xylosidase (xlnD) in complex with xylobiose aziridine2 activity based probe
44	<a href="#">d1oe1a1</a>	Alignment	not modelled	57.7	15	<b>Fold:</b> Cupredoxin-like <b>Superfamily:</b> Cupredoxins <b>Family:</b> Multidomain cupredoxins
45	<a href="#">c2aanA_</a>	Alignment	not modelled	52.7	12	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> auracyanin a; <b>PDBTitle:</b> auracyanin a: a "blue" copper protein from the green thermophilic2 photosynthetic bacterium,chloroflexus aurantiacus
46	<a href="#">c5wvpA_</a>	Alignment	not modelled	50.6	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-glucosidase; <b>PDBTitle:</b> expression, characterization and crystal structure of a novel beta-2 glucosidase from paenibacillus barengoltzii
47	<a href="#">d1ndsA1</a>	Alignment	not modelled	50.2	11	<b>Fold:</b> Cupredoxin-like <b>Superfamily:</b> Cupredoxins <b>Family:</b> Multidomain cupredoxins
48	<a href="#">c5a7mA_</a>	Alignment	not modelled	49.2	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-xylosidase; <b>PDBTitle:</b> the structure of hypocrea jecorina beta-xylosidase xyl3a (bxl1)
49	<a href="#">c2qsvA_</a>	Alignment	not modelled	48.8	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of protein of unknown function from porphyromonas2 gingivalis w83
50	<a href="#">c3rfrl_</a>	Alignment	not modelled	47.4	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> I: <b>PDB Molecule:</b> pmob; <b>PDBTitle:</b> crystal structure of particulate methane monooxygenase (pmmo) from2 methylocystis sp. strain m
51	<a href="#">c2k6zA_</a>	Alignment	not modelled	47.2	33	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein ttha1943; <b>PDBTitle:</b> solution structures of copper loaded form pcua (trans2 conformation of the peptide bond involving the nitrogen of3 p14)
52	<a href="#">c3qbtH_</a>	Alignment	not modelled	45.0	18	<b>PDB header:</b> protein transport/hydrolase <b>Chain:</b> H: <b>PDB Molecule:</b> inositol polyphosphate 5-phosphatase ocr1-1; <b>PDBTitle:</b> crystal structure of ocr1 540-678 in complex with rab8a:gppnhp
53	<a href="#">c6hbeA_</a>	Alignment	not modelled	44.9	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> copper-containing nitrite reductase; <b>PDBTitle:</b> cu-containing nitrite reductase (nirk) from thermus scotoductus sa-01

54	<a href="#">d14ia1</a>	Alignment	not modelled	44.7	8	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> PapD-like <b>Family:</b> Pilus chaperone
55	<a href="#">c5n76C</a>	Alignment	not modelled	44.4	33	<b>PDB header:</b> nickel-binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> coot; <b>PDBTitle:</b> crystal structure of the apo-form of the co dehydrogenase accessory2 protein coot from rhodospirillum rubrum
56	<a href="#">c2i8F</a>	Alignment	not modelled	42.6	31	<b>PDB header:</b> signaling protein <b>Chain:</b> F: <b>PDB Molecule:</b> anabaena sensory rhodopsin transducer protein; <b>PDBTitle:</b> anabaena sensory rhodopsin transducer
57	<a href="#">d3bwuc1</a>	Alignment	not modelled	41.3	11	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> PapD-like <b>Family:</b> Pilus chaperone
58	<a href="#">d1jova</a>	Alignment	not modelled	38.6	14	<b>Fold:</b> Supersandwich <b>Superfamily:</b> Galactose mutarotase-like <b>Family:</b> Hypothetical protein HI1317
59	<a href="#">c4ncdA</a>	Alignment	not modelled	38.3	10	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> gram-negative pili assembly chaperone, n-terminal domain <b>PDBTitle:</b> crystal structure of class 5 fimbriae chaperone cfaa
60	<a href="#">d1cuoa</a>	Alignment	not modelled	38.1	14	<b>Fold:</b> Cupredoxin-like <b>Superfamily:</b> Cupredoxins <b>Family:</b> Plastocyanin/azurin-like
61	<a href="#">c14ia</a>	Alignment	not modelled	37.3	8	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> sfae protein; <b>PDBTitle:</b> crystal structure of the periplasmic chaperone sfae
62	<a href="#">d1libya</a>	Alignment	not modelled	36.9	7	<b>Fold:</b> Cupredoxin-like <b>Superfamily:</b> Cupredoxins <b>Family:</b> Nitrosocyanin
63	<a href="#">c3q48B</a>	Alignment	not modelled	36.7	16	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> chaperone cupb2; <b>PDBTitle:</b> crystal structure of pseudomonas aeruginosa cupb2 chaperone
64	<a href="#">c3q1nA</a>	Alignment	not modelled	36.4	15	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> galactose mutarotase related enzyme; <b>PDBTitle:</b> crystal structure of a galactose mutarotase-like protein (Isej_2598)2 from lactobacillus casei atcc 334 at 1.61 a resolution
65	<a href="#">c2x3bB</a>	Alignment	not modelled	36.3	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> toxic extracellular endopeptidase; <b>PDBTitle:</b> asap1 inactive mutant e294a, an extracellular toxic zinc2 metalloendopeptidase
66	<a href="#">c4bq3A</a>	Alignment	not modelled	35.7	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> b-agarase; <b>PDBTitle:</b> structural analysis of an exo-beta-agarase
67	<a href="#">c5dfkA</a>	Alignment	not modelled	34.6	14	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable fimbrial chaperone ecpb; <b>PDBTitle:</b> crystal structure of the escherichia coli common pilus chaperone, ecpb
68	<a href="#">c3nreB</a>	Alignment	not modelled	33.7	21	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> aldose 1-epimerase; <b>PDBTitle:</b> crystal structure of a putative aldose 1-epimerase (b2544) from2 escherichia coli k12 at 1.59 a resolution
69	<a href="#">c5nbsA</a>	Alignment	not modelled	33.5	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-glucosidase; <b>PDBTitle:</b> structural studies of a glycoside hydrolase family 3 beta-glucosidase2 from the model fungus neurospora crassa
70	<a href="#">c3mwxA</a>	Alignment	not modelled	33.2	13	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> aldose 1-epimerase; <b>PDBTitle:</b> crystal structure of a putative galactose mutarotase (bsu18360) from2 bacillus subtilis at 1.45 a resolution
71	<a href="#">c2f1eA</a>	Alignment	not modelled	32.5	33	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> protein apag; <b>PDBTitle:</b> solution structure of apag protein
72	<a href="#">d1qhqa</a>	Alignment	not modelled	32.5	11	<b>Fold:</b> Cupredoxin-like <b>Superfamily:</b> Cupredoxins <b>Family:</b> Plastocyanin/azurin-like
73	<a href="#">d1x9la</a>	Alignment	not modelled	32.4	27	<b>Fold:</b> Common fold of diphtheria toxin/transcription factors/cytochrome f <b>Superfamily:</b> DR1885-like metal-binding protein <b>Family:</b> DR1885-like metal-binding protein
74	<a href="#">d1xvsa</a>	Alignment	not modelled	32.1	28	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> ApaG-like <b>Family:</b> ApaG-like
75	<a href="#">c4r4gA</a>	Alignment	not modelled	31.1	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative lipoprotein ycda; <b>PDBTitle:</b> crystal structure of a putative lipoprotein (ycda) from bacillus2 subtilis subsp. subtilis str. 168 at 2.62 a resolution
76	<a href="#">c4f7kA</a>	Alignment	not modelled	30.1	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> laccase; <b>PDBTitle:</b> crystal structure of lac15 from a marine microbial metagenome
77	<a href="#">c4bifC</a>	Alignment	not modelled	29.8	21	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> cupin 2 conserved barrel domain protein; <b>PDBTitle:</b> biochemical and structural characterisation of a novel2 manganese-dependent hydroxynitrile lyase from bacteria
78	<a href="#">d1mzya1</a>	Alignment	not modelled	28.6	11	<b>Fold:</b> Cupredoxin-like <b>Superfamily:</b> Cupredoxins <b>Family:</b> Multidomain cupredoxins
79	<a href="#">c3dcdA</a>	Alignment	not modelled	28.5	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> galactose mutarotase related enzyme; <b>PDBTitle:</b> x-ray structure of the galactose mutarotase related enzyme q5fkd7 from2 lactobacillus acidophilus at the resolution 1.9a. northeast3 structural genomics consortium target lar33.
						<b>Fold:</b> Hypothetical protein TM1070

80	<a href="#">d1nc7a_</a>	Alignment	not modelled	27.3	14	<b>Superfamily:</b> Hypothetical protein TM1070 <b>Family:</b> Hypothetical protein TM1070
81	<a href="#">c4knuB_</a>	Alignment	not modelled	27.2	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> multicopper oxidase type 1; <b>PDBTitle:</b> copper nitrite reductase from nitrosomonas europaea at ph 6.5
82	<a href="#">c3jt0B_</a>	Alignment	not modelled	27.2	13	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> lamin-b1; <b>PDBTitle:</b> crystal structure of the c-terminal fragment (426-558) lamin-b1 from2 homo sapiens, northeast structural genomics consortium target hr5546a
83	<a href="#">d1snra2</a>	Alignment	not modelled	26.3	15	<b>Fold:</b> Cupredoxin-like <b>Superfamily:</b> Cupredoxins <b>Family:</b> Multidomain cupredoxins
84	<a href="#">c2l0dA_</a>	Alignment	not modelled	25.7	16	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> cell surface protein; <b>PDBTitle:</b> solution nmr structure of putative cell surface protein ma_4588 (272-2 376 domain) from methanosarcina acetivorans, northeast structural3 genomics consortium target mvr254a
85	<a href="#">d1tzaa_</a>	Alignment	not modelled	25.3	22	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> ApaG-like <b>Family:</b> ApaG-like
86	<a href="#">c3t9wA_</a>	Alignment	not modelled	24.5	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> small laccase, multi-copper oxidase; <b>PDBTitle:</b> small laccase from amycolatopsis sp. atcc 39116
87	<a href="#">c2lw6A_</a>	Alignment	not modelled	23.6	44	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> avrpiz-t protein; <b>PDBTitle:</b> solution structure of an avirulence protein avrpiz-t from pathogen2 magnaportheorzyae
88	<a href="#">d1hfua1</a>	Alignment	not modelled	23.5	19	<b>Fold:</b> Cupredoxin-like <b>Superfamily:</b> Cupredoxins <b>Family:</b> Multidomain cupredoxins
89	<a href="#">c3wkoA_</a>	Alignment	not modelled	23.2	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nitrite reductase; <b>PDBTitle:</b> copper-containing nitrite reductase from thermophilic bacterium2 geobacillus thermodenitrificans
90	<a href="#">d1mspa_</a>	Alignment	not modelled	22.4	36	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> PapD-like <b>Family:</b> MSP-like
91	<a href="#">c5z6pB_</a>	Alignment	not modelled	21.5	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> b-agarase; <b>PDBTitle:</b> the crystal structure of an agarase, agwh50c
92	<a href="#">d1xq4a_</a>	Alignment	not modelled	20.9	44	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> ApaG-like <b>Family:</b> ApaG-like
93	<a href="#">c1qniE_</a>	Alignment	not modelled	20.4	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> nitrous-oxide reductase; <b>PDBTitle:</b> crystal structure of nitrous oxide reductase from pseudomonas nautica,2 at 2.4a resolution
94	<a href="#">c2llIA_</a>	Alignment	not modelled	20.4	20	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> lamin-b2; <b>PDBTitle:</b> solution nmr structure of c-terminal globular domain of human lamin-2 b2, northeast structural genomics consortium target hr8546a
95	<a href="#">c3tasC_</a>	Alignment	not modelled	20.3	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> small laccase, multi-copper oxidase; <b>PDBTitle:</b> small laccase from streptomyces viridosporus t7a
96	<a href="#">c3mpbA_</a>	Alignment	not modelled	19.8	26	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> sugar isomerase; <b>PDBTitle:</b> z5688 from e. coli o157:h7 bound to fructose
97	<a href="#">c3ay2A_</a>	Alignment	not modelled	19.5	16	<b>PDB header:</b> antitumor protein, antiviral protein <b>Chain:</b> A: <b>PDB Molecule:</b> lipid modified azurin protein; <b>PDBTitle:</b> crystal structure of neisserial azurin
98	<a href="#">d1cc3a_</a>	Alignment	not modelled	18.6	13	<b>Fold:</b> Cupredoxin-like <b>Superfamily:</b> Cupredoxins <b>Family:</b> Plastocyanin/azurin-like
99	<a href="#">c1qunA_</a>	Alignment	not modelled	18.6	11	<b>PDB header:</b> chaperone/structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> papd-like chaperone fimc; <b>PDBTitle:</b> x-ray structure of the fimc-fimh chaperone adhesin complex2 from uropathogenic e.coli