























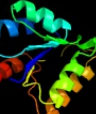








# Phyre2

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Description	RVBD0957_(purH)_1068209_1069780
Date	Fri Jul 26 01:50:55 BST 2019
Unique Job ID	53c18c42ad9129b6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4a1oB_</a>	 Alignment		100.0	100	<b>PDB header:</b> transferase-hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional purine biosynthesis protein purh; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis purh complexed with2 aicar and a novel nucleotide cfair, at 2.48 a resolution.
2	<a href="#">c1thzA_</a>	 Alignment		100.0	38	<b>PDB header:</b> transferase, hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional purine biosynthesis protein purh; <b>PDBTitle:</b> crystal structure of avian aicar transformylase in complex2 with a novel inhibitor identified by virtual ligand3 screening
3	<a href="#">c4ehiB_</a>	 Alignment		100.0	39	<b>PDB header:</b> hydrolase,transferase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional purine biosynthesis protein purh; <b>PDBTitle:</b> an x-ray crystal structure of a putative bifunctional2 phosphoribosylaminoimidazolecarboxamide formyltransferase/imp3 cyclohydrolase
4	<a href="#">c1zczA_</a>	 Alignment		100.0	40	<b>PDB header:</b> transferase/hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional purine biosynthesis protein purh; <b>PDBTitle:</b> crystal structure of phosphoribosylaminoimidazolecarboxamide2 formyltransferase / imp cyclohydrolase (tm1249) from thermotoga3 maritima at 1.88 a resolution
5	<a href="#">d1zcza2</a>	 Alignment		100.0	43	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> AICAR transformylase domain of bifunctional purine biosynthesis enzyme ATIC
6	<a href="#">d1g8ma2</a>	 Alignment		100.0	32	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> AICAR transformylase domain of bifunctional purine biosynthesis enzyme ATIC
7	<a href="#">d1pkxa2</a>	 Alignment		100.0	33	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> AICAR transformylase domain of bifunctional purine biosynthesis enzyme ATIC
8	<a href="#">d1pkxa1</a>	 Alignment		100.0	45	<b>Fold:</b> Methylglyoxal synthase-like <b>Superfamily:</b> Methylglyoxal synthase-like <b>Family:</b> Inosicase
9	<a href="#">d1g8ma1</a>	 Alignment		100.0	45	<b>Fold:</b> Methylglyoxal synthase-like <b>Superfamily:</b> Methylglyoxal synthase-like <b>Family:</b> Inosicase
10	<a href="#">c6nkoA_</a>	 Alignment		100.0	35	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> forh; <b>PDBTitle:</b> crystal structure of forh
11	<a href="#">d1zczal</a>	 Alignment		100.0	36	<b>Fold:</b> Methylglyoxal synthase-like <b>Superfamily:</b> Methylglyoxal synthase-like <b>Family:</b> Inosicase

12	<a href="#">d1a9xa2</a>	Alignment		99.4	22	<b>Fold:</b> Methylglyoxal synthase-like <b>Superfamily:</b> Methylglyoxal synthase-like <b>Family:</b> Carbamoyl phosphate synthetase, large subunit allosteric, C-terminal domain
13	<a href="#">c2yvqA_</a>	Alignment		99.3	17	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> carbamoyl-phosphate synthase; <b>PDBTitle:</b> crystal structure of mgs domain of carbamoyl-phosphate2 synthetase from homo sapiens
14	<a href="#">d1wo8a1</a>	Alignment		98.6	25	<b>Fold:</b> Methylglyoxal synthase-like <b>Superfamily:</b> Methylglyoxal synthase-like <b>Family:</b> Methylglyoxal synthase, MgsA
15	<a href="#">c5dotA_</a>	Alignment		98.5	18	<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
16	<a href="#">c5douC_</a>	Alignment		98.4	19	<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
17	<a href="#">c1m6vE_</a>	Alignment		98.2	29	<b>PDB header:</b> ligase <b>Chain:</b> E: <b>PDB Molecule:</b> carbamoyl phosphate synthetase large chain; <b>PDBTitle:</b> crystal structure of the g359f (small subunit) point mutant of2 carbamoyl phosphate synthetase
18	<a href="#">c6f2cK_</a>	Alignment		98.0	23	<b>PDB header:</b> lyase <b>Chain:</b> K: <b>PDB Molecule:</b> methylglyoxal synthase; <b>PDBTitle:</b> methylglyoxal synthase mgsa from bacillus subtilis
19	<a href="#">d1vmda_</a>	Alignment		97.1	22	<b>Fold:</b> Methylglyoxal synthase-like <b>Superfamily:</b> Methylglyoxal synthase-like <b>Family:</b> Methylglyoxal synthase, MgsA
20	<a href="#">c4ggmX_</a>	Alignment		97.1	24	<b>PDB header:</b> hydrolase <b>Chain:</b> X: <b>PDB Molecule:</b> udp-2,3-diacetylglucosamine pyrophosphatase lpxi; <b>PDBTitle:</b> structure of lpxi
21	<a href="#">c2piuD_</a>	Alignment	not modelled	89.3	19	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> propionate catabolism operon regulatory protein; <b>PDBTitle:</b> crystal structure of propionate catabolism operon regulatory protein2 prpr
22	<a href="#">c3ff4A_</a>	Alignment	not modelled	88.2	16	<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
23	<a href="#">d1iuKa_</a>	Alignment	not modelled	86.8	30	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> CoA-binding domain
24	<a href="#">c2o7pA_</a>	Alignment	not modelled	84.6	37	<b>PDB header:</b> hydrolase, oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> riboflavin biosynthesis protein ribd; <b>PDBTitle:</b> the crystal structure of ribd from escherichia coli in complex with2 the oxidised nadp+ cofactor in the active site of the reductase3 domain
25	<a href="#">d1b93a_</a>	Alignment	not modelled	84.0	21	<b>Fold:</b> Methylglyoxal synthase-like <b>Superfamily:</b> Methylglyoxal synthase-like <b>Family:</b> Methylglyoxal synthase, MgsA
26	<a href="#">d2pjua1</a>	Alignment	not modelled	84.0	19	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> PrpR receptor domain-like <b>Family:</b> PrpR receptor domain-like
27	<a href="#">d2d59a1</a>	Alignment	not modelled	83.8	16	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> CoA-binding domain
28	<a href="#">c2q5cA_</a>	Alignment	not modelled	81.9	28	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> ntrc family transcriptional regulator; <b>PDBTitle:</b> crystal structure of ntrc family transcriptional regulator from2 clostridium acetobutylicum

29	<a href="#">c4e38A</a>	 Alignment	not modelled	81.5	24	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> keto-hydroxyglutarate-aldolase/keto-deoxy-phosphogluconate <b>PDBTitle:</b> crystal structure of probable keto-hydroxyglutarate-aldolase from2 vibionales bacterium swat-3 (target efi-502156)
30	<a href="#">d2isba1</a>	 Alignment	not modelled	81.3	28	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> FumA C-terminal domain-like <b>Family:</b> FumA C-terminal domain-like
31	<a href="#">d2ioja1</a>	 Alignment	not modelled	79.7	27	<b>Fold:</b> MurF and HprK N-domain-like <b>Superfamily:</b> HprK N-terminal domain-like <b>Family:</b> DRTGG domain
32	<a href="#">d1wbha1</a>	 Alignment	not modelled	78.5	24	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
33	<a href="#">d2b3za2</a>	 Alignment	not modelled	78.2	25	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> Deoxycytidylate deaminase-like
34	<a href="#">c3ia7A</a>	 Alignment	not modelled	77.4	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> calg4; <b>PDBTitle:</b> crystal structure of calg4, the calicheamicin glycosyltransferase
35	<a href="#">c4nmIA</a>	 Alignment	not modelled	76.9	16	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ribulose 5-phosphate isomerase; <b>PDBTitle:</b> 2.60 angstrom resolution crystal structure of putative ribose 5-2 phosphate isomerase from toxoplasma gondii me49 in complex with dl-3 malic acid
36	<a href="#">d2vzsa5</a>	 Alignment	not modelled	76.1	23	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
37	<a href="#">c2duwA</a>	 Alignment	not modelled	74.4	21	<b>PDB header:</b> ligand binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative coa-binding protein; <b>PDBTitle:</b> solution structure of putative coa-binding protein of2 klebsiella pneumoniae
38	<a href="#">d1y81a1</a>	 Alignment	not modelled	73.5	24	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> CoA-binding domain
39	<a href="#">c4yajA</a>	 Alignment	not modelled	73.5	14	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha subunit of acetyl-coenzyme a synthetase <b>PDBTitle:</b> ca. korarchaeum cryptofilum dinucleotide forming acetyl-coenzyme a2 synthetase 1 (apo form)
40	<a href="#">c6oviA</a>	 Alignment	not modelled	73.4	23	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> keto-deoxy-phosphogluconate aldolase; <b>PDBTitle:</b> crystal structure of kdpg aldolase from legionella pneumophila with2 pyruvate captured at low ph as a covalent carbinolamine intermediate
41	<a href="#">d1mkza</a>	 Alignment	not modelled	71.9	21	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MogA-like
42	<a href="#">c3p9zA</a>	 Alignment	not modelled	71.6	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> uroporphyrinogen iii cosynthase (hemd); <b>PDBTitle:</b> crystal structure of uroporphyrinogen-iii synthetase from helicobacter2 pylori 26695
43	<a href="#">c1xtzA</a>	 Alignment	not modelled	71.1	13	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ribose-5-phosphate isomerase; <b>PDBTitle:</b> crystal structure of the s. cerevisiae d-ribose-5-phosphate isomerase:2 comparison with the archeal and bacterial enzymes
44	<a href="#">c4qccA</a>	 Alignment	not modelled	71.1	31	<b>PDB header:</b> structural protein, lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-dehydro-3-deoxy-6-phosphogalactonate aldolase, peptidyl- <b>PDBTitle:</b> structure of a cube-shaped, highly porous protein cage designed by2 fusing symmetric oligomeric domains
45	<a href="#">d1ko7a1</a>	 Alignment	not modelled	69.2	17	<b>Fold:</b> MurF and HprK N-domain-like <b>Superfamily:</b> HprK N-terminal domain-like <b>Family:</b> HPr kinase/phoshatase HprK N-terminal domain
46	<a href="#">c2yw3E</a>	 Alignment	not modelled	69.0	34	<b>PDB header:</b> lyase <b>Chain:</b> E: <b>PDB Molecule:</b> 4-hydroxy-2-oxoglutarate aldolase/2-deydro-3- <b>PDBTitle:</b> crystal structure analysis of the 4-hydroxy-2-oxoglutarate aldolase/2-2 deydro-3-deoxyphosphogluconate aldolase from tthb1
47	<a href="#">c3u7jA</a>	 Alignment	not modelled	68.1	24	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ribose-5-phosphate isomerase a; <b>PDBTitle:</b> crystal structure of ribose-5-phosphate isomerase a from burkholderia2 thailandensis
48	<a href="#">d1mxsa</a>	 Alignment	not modelled	67.4	27	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
49	<a href="#">c3ouzA</a>	 Alignment	not modelled	67.3	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> biotin carboxylase; <b>PDBTitle:</b> crystal structure of biotin carboxylase-adp complex from campylobacter2 jejuni
50	<a href="#">c4x84C</a>	 Alignment	not modelled	65.4	19	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> ribose-5-phosphate isomerase a; <b>PDBTitle:</b> crystal structure of ribose-5-phosphate isomerase a from pseudomonas2 aeruginosa
51	<a href="#">c5dniB</a>	 Alignment	not modelled	65.2	23	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> putative l(+)-tartrate dehydratase subunit beta; <b>PDBTitle:</b> crystal structure of methanocaldococcus jannaschii fumarate hydratase2 beta subunit
52	<a href="#">c4bk9B</a>	 Alignment	not modelled	63.8	25	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-dehydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxo <b>PDBTitle:</b> crystal structure of 2-keto-3-deoxy-6-phospho-gluconate aldolase from2 zymomonas mobilis atcc 29191
53	<a href="#">c6mcaD</a>	 Alignment	not modelled	63.5	28	<b>PDB header:</b> lyase/lyase inhibitor <b>Chain:</b> D: <b>PDB Molecule:</b> fumarate hydratase;

53	<a href="#">c0msu0_</a>	Alignment	not modelled	63.3	20	<b>PDBTitle:</b> crystal structure of mitochondrial fumarate hydratase from leishmania2 major in a complex with inhibitor thiomalate <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> 457aa long hypothetical protein; <b>PDBTitle:</b> crystal structure of ph0766 from pyrococcus horikoshii ot3
54	<a href="#">c2csuB_</a>	Alignment	not modelled	62.6	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ribd; <b>PDBTitle:</b> acinetobacter baumannii ribd, form 2
55	<a href="#">c3zpgA_</a>	Alignment	not modelled	62.3	30	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> Xylose isomerase
56	<a href="#">d1qt1a_</a>	Alignment	not modelled	60.1	18	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> ACDE2-like
57	<a href="#">d1ytl1_</a>	Alignment	not modelled	56.8	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-mannosidase; <b>PDBTitle:</b> structure of fungal beta-mannosidase from glycoside hydrolase family 22 of trichoderma harzianum
58	<a href="#">c4cvuA_</a>	Alignment	not modelled	56.4	18	<b>PDB header:</b> transferase,hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> hpr kinase/phosphatase; <b>PDBTitle:</b> x-ray structure of the hpr kinase/phosphatase from staphylococcus2 xylosus at 1.95 a resolution
59	<a href="#">c1ko7B_</a>	Alignment	not modelled	56.0	17	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> BT0820-like
60	<a href="#">d2obba1</a>	Alignment	not modelled	55.5	10	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Renal dipeptidase
61	<a href="#">d1itua_</a>	Alignment	not modelled	55.1	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-glucosidase; <b>PDBTitle:</b> crystal structure of intracellular family 1 beta-2 glucosidase bgl1a from the basidiomycete phanerochaete3 chrysosporium in substrate-free form
62	<a href="#">c2e3zB_</a>	Alignment	not modelled	54.9	27	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> crystal structure of tryptophan synthase alpha chain from legionella2 pneumophila subsp. pneumophila
63	<a href="#">c5k9xA_</a>	Alignment	not modelled	53.6	16	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> ribose 5-phosphate isomerase; <b>PDBTitle:</b> ribose 5-phosphate isomerase from plasmodium falciparum
64	<a href="#">c2f8mB_</a>	Alignment	not modelled	53.3	17	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> CoA-binding domain
65	<a href="#">d2csua1</a>	Alignment	not modelled	52.8	28	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein mj0159; <b>PDBTitle:</b> crystal structure of uncharacterized protein mj0159 from2 methanocaldococcus jannaschii
66	<a href="#">c2qyxB_</a>	Alignment	not modelled	52.6	15	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Peptidoglycan biosynthesis glycosyltransferase MurG
67	<a href="#">d1f0ka_</a>	Alignment	not modelled	52.6	23	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Gtf glycosyltransferase
68	<a href="#">d1pn3a_</a>	Alignment	not modelled	52.5	23	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MogA-like
69	<a href="#">d1y5ea1</a>	Alignment	not modelled	51.6	24	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
70	<a href="#">d1ujpa_</a>	Alignment	not modelled	50.8	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 3'-5'-exonuclease; <b>PDBTitle:</b> crystal structure of an uncharacterized amidohydrolase from2 saccharomyces cerevisiae
71	<a href="#">c3e2vA_</a>	Alignment	not modelled	49.3	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ditrans,polycis-undecaprenyl-diphosphate synthase ((2e,6e)- <b>PDBTitle:</b> poly-cis-prenyltransferase
72	<a href="#">c6acsA_</a>	Alignment	not modelled	48.0	12	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ribose 5-phosphate isomerase; <b>PDBTitle:</b> crystal structure of thermophilus ribose-5-phosphate isomerase2 complexed with arabinose-5-phosphate
73	<a href="#">c1uj6A_</a>	Alignment	not modelled	47.6	29	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> beta-glucosidase; <b>PDBTitle:</b> crystal structure of beta-glucosidase bglm-g1 from marine metagenome
74	<a href="#">c5ns6C_</a>	Alignment	not modelled	47.2	29	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> espg2 glycosyltransferase; <b>PDBTitle:</b> structural analysis of espg2 glycosyltransferase
75	<a href="#">c5du2B_</a>	Alignment	not modelled	46.8	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-glucosidase; <b>PDBTitle:</b> trichoderma harzianum gh1 beta-glucosidase thbg12
76	<a href="#">c5jboA_</a>	Alignment	not modelled	45.8	27	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> protein fdra; <b>PDBTitle:</b> crystal structure of a predicated acyl-coa synthetase from e.coli
77	<a href="#">c3dmyA_</a>	Alignment	not modelled	45.6	10	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Family 1 of glycosyl hydrolase
78	<a href="#">d1cbga_</a>	Alignment	not modelled	44.2	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> putative integron gene cassette protein; <b>PDBTitle:</b> structure from the mobile metagenome of cole harbour salt marsh:2 integron cassette protein hfx_cass1
79	<a href="#">c3fuyC_</a>	Alignment	not modelled	44.0	39	

80	<a href="#">c1lkzB_</a>	Alignment	not modelled	43.5	24	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> ribose 5-phosphate isomerase a; <b>PDBTitle:</b> crystal structure of d-ribose-5-phosphate isomerase (rpiA) from2 escherichia coli.
81	<a href="#">c3iv4A_</a>	Alignment	not modelled	42.8	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> a putative oxidoreductase with a thioredoxin fold
82	<a href="#">d1o8bb1</a>	Alignment	not modelled	42.6	21	<b>Fold:</b> NagB/RpiA/CoA transferase-like <b>Superfamily:</b> NagB/RpiA/CoA transferase-like <b>Family:</b> D-ribose-5-phosphate isomerase (RpiA), catalytic domain
83	<a href="#">c5xgzA_</a>	Alignment	not modelled	41.9	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-glycosidase; <b>PDBTitle:</b> metagenomic glucose-tolerant glycosidase
84	<a href="#">c3labA_</a>	Alignment	not modelled	41.4	30	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative kdpg (2-keto-3-deoxy-6-phosphogluconate) aldolase; <b>PDBTitle:</b> crystal structure of a putative kdpg (2-keto-3-deoxy-6-2 phosphogluconate) aldolase from oleispira antarctica
85	<a href="#">c3d8tB_</a>	Alignment	not modelled	40.3	17	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> uroporphyrinogen-iii synthase; <b>PDBTitle:</b> thermus thermophilus uroporphyrinogen iii synthase
86	<a href="#">c2v82A_</a>	Alignment	not modelled	40.3	26	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-dehydro-3-deoxy-6-phosphogalactonate aldolase; <b>PDBTitle:</b> kdpgal complexed to kdpgal
87	<a href="#">c3tsaA_</a>	Alignment	not modelled	40.0	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ndp-rhamnosyltransferase; <b>PDBTitle:</b> spinosyn rhamnosyltransferase spng
88	<a href="#">c2xdqA_</a>	Alignment	not modelled	39.7	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> light-independent protochlorophyllide reductase subunit n; <b>PDBTitle:</b> dark operative protochlorophyllide oxidoreductase (chl-chlb)2 complex
89	<a href="#">c1x7fA_</a>	Alignment	not modelled	39.2	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> outer surface protein; <b>PDBTitle:</b> crystal structure of an uncharacterized b. cereus protein
90	<a href="#">c1nh7A_</a>	Alignment	not modelled	39.1	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> atp phosphoribosyltransferase; <b>PDBTitle:</b> atp phosphoribosyltransferase (atp-prtase) from mycobacterium2 tuberculosis
91	<a href="#">c5cdjA_</a>	Alignment	not modelled	39.1	16	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> rubisco large subunit-binding protein subunit alpha, <b>PDBTitle:</b> apical domain of chloroplast chaperonin 60a
92	<a href="#">d1zpva1</a>	Alignment	not modelled	38.8	29	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> SP0238-like
93	<a href="#">c5tchG_</a>	Alignment	not modelled	38.5	19	<b>PDB header:</b> lyase <b>Chain:</b> G: <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> crystal structure of tryptophan synthase from m. tuberculosis -2 ligand-free form, trpa-g66v mutant
94	<a href="#">d1rd5a_</a>	Alignment	not modelled	37.2	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
95	<a href="#">c5uf2A_</a>	Alignment	not modelled	37.1	20	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ribose 5-phosphate isomerase a; <b>PDBTitle:</b> crystal structure of ribose 5 phosphate isomerase a from neisseria2 gonorrhoeae
96	<a href="#">d1yrra2</a>	Alignment	not modelled	35.9	23	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> N-acetylglucosamine-6-phosphate deacetylase, NagA, catalytic domain
97	<a href="#">c4mwaA_</a>	Alignment	not modelled	35.7	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; <b>PDBTitle:</b> 1.85 angstrom crystal structure of gcpe protein from bacillus2 anthracis
98	<a href="#">c3ta9B_</a>	Alignment	not modelled	35.6	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> glycoside hydrolase family 1; <b>PDBTitle:</b> beta-glycosidase a from the halothermophile h. orenii
99	<a href="#">c3ahxC_</a>	Alignment	not modelled	35.3	16	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> beta-glucosidase a; <b>PDBTitle:</b> crystal structure of beta-glucosidase a from bacterium clostridium2 cellulovorans
100	<a href="#">d1rrva_</a>	Alignment	not modelled	35.3	24	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Gtf glycosyltransferase
101	<a href="#">c1lk5C_</a>	Alignment	not modelled	35.0	11	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> d-ribose-5-phosphate isomerase; <b>PDBTitle:</b> structure of the d-ribose-5-phosphate isomerase from2 pyrococcus horikoshii
102	<a href="#">d1tz9a_</a>	Alignment	not modelled	34.9	24	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> UxuA-like
103	<a href="#">c2yyaB_</a>	Alignment	not modelled	34.0	20	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoribosylamine--glycine ligase; <b>PDBTitle:</b> crystal structure of gar synthetase from aquifex aeolicus
104	<a href="#">c2pjmA_</a>	Alignment	not modelled	33.7	31	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ribose-5-phosphate isomerase a; <b>PDBTitle:</b> structure of ribose 5-phosphate isomerase a from2 methanocaldococcus jannaschii
105	<a href="#">d1bqca_</a>	Alignment	not modelled	33.5	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases

106	<a href="#">d1k77a_</a>	Alignment	not modelled	33.0	22	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> Hypothetical protein YgbM (EC1530)
107	<a href="#">c3wh5A_</a>	Alignment	not modelled	32.1	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-glucosidase; <b>PDBTitle:</b> crystal structure of gh1 beta-glucosidase td2f2
108	<a href="#">d1xima_</a>	Alignment	not modelled	31.9	22	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> Xylose isomerase
109	<a href="#">c2z1sA_</a>	Alignment	not modelled	31.8	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-glucosidase b; <b>PDBTitle:</b> beta-glucosidase b from paenibacillus polymyxa complexed with2 cellotetraose
110	<a href="#">c2f00A_</a>	Alignment	not modelled	31.6	17	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramate--l-alanine ligase; <b>PDBTitle:</b> escherichia coli murc
111	<a href="#">d1un7a2</a>	Alignment	not modelled	31.4	24	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> N-acetylglucosamine-6-phosphate deacetylase, NagA, catalytic domain
112	<a href="#">c3ahyD_</a>	Alignment	not modelled	31.4	25	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> beta-glucosidase; <b>PDBTitle:</b> crystal structure of beta-glucosidase 2 from fungus trichoderma reesei2 in complex with tris
113	<a href="#">c5n6uC_</a>	Alignment	not modelled	31.2	22	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> beta-mannosidase; <b>PDBTitle:</b> crystal structure of beta-d-mannosidase from dictyoglomus2 thermophilum.
114	<a href="#">c5ogzB_</a>	Alignment	not modelled	31.1	19	<b>PDB header:</b> sugar binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> beta-glucosidase a; <b>PDBTitle:</b> crystal structure of ruminiclostridium thermocellum beta-glucosidase a
115	<a href="#">c2ppvA_</a>	Alignment	not modelled	30.8	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a protein belonging to the upf0052 (se_0549) from2 staphylococcus epidermidis atcc 12228 at 2.00 a resolution
116	<a href="#">d1xsza2</a>	Alignment	not modelled	30.2	33	<b>Fold:</b> TBP-like <b>Superfamily:</b> RalF, C-terminal domain <b>Family:</b> RalF, C-terminal domain
117	<a href="#">c1i8tB_</a>	Alignment	not modelled	29.7	17	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-galactopyranose mutase; <b>PDBTitle:</b> strcuture of udp-galactopyranose mutase from e.coli
118	<a href="#">c4gmkB_</a>	Alignment	not modelled	29.5	21	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> ribose-5-phosphate isomerase a; <b>PDBTitle:</b> crystal structure of ribose 5-phosphate isomerase from the probiotic2 bacterium lactobacillus salivarius ucc118
119	<a href="#">d1vffa1</a>	Alignment	not modelled	29.4	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Family 1 of glycosyl hydrolase
120	<a href="#">d1ve4a1</a>	Alignment	not modelled	29.4	32	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like