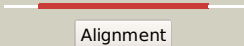

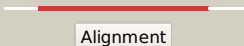

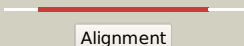







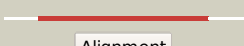











# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0869c_(moaA)_966268_967350
Date	Fri Jul 26 01:50:46 BST 2019
Unique Job ID	d46d98abd10cf494

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1tv8a_</a>	 Alignment		100.0	33	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Radical SAM enzymes <b>Family:</b> MoCo biosynthesis proteins
2	<a href="#">c6efnA_</a>	 Alignment		100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> sporulation killing factor maturation protein skfb; <b>PDBTitle:</b> structure of a ripp maturase, skfb
3	<a href="#">c5v1tA_</a>	 Alignment		100.0	16	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> radical sam; <b>PDBTitle:</b> crystal structure of streptococcus suis suib bound to precursor2 peptide sua
4	<a href="#">c4k39A_</a>	 Alignment		100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> anaerobic sulfatase-maturing enzyme; <b>PDBTitle:</b> native ansmece with bound adomet and cp18cys peptide
5	<a href="#">c5wggA_</a>	 Alignment		100.0	13	<b>PDB header:</b> peptide binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> radical sam domain protein; <b>PDBTitle:</b> structural insights into thioether bond formation in the biosynthesis2 of sactipeptides
6	<a href="#">c6c8vA_</a>	 Alignment		100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> coenzyme pqq synthesis protein e; <b>PDBTitle:</b> x-ray structure of pqqe from methylobacterium extorquens
7	<a href="#">c6b4cH_</a>	 Alignment		100.0	15	<b>PDB header:</b> antiviral protein <b>Chain:</b> H: <b>PDB Molecule:</b> viperin; <b>PDBTitle:</b> structure of viperin from trichoderma virens
8	<a href="#">c4wxcC_</a>	 Alignment		100.0	15	<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 [fefe]-hydrogenase
9	<a href="#">c5vslB_</a>	 Alignment		100.0	20	<b>PDB header:</b> antiviral protein <b>Chain:</b> B: <b>PDB Molecule:</b> radical s-adenosyl methionine domain-containing protein 2; <b>PDBTitle:</b> crystal structure of viperin with bound [4fe-4s] cluster and s-2 adenosylhomocysteine (sah)
10	<a href="#">c2yx0A_</a>	 Alignment		99.9	14	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> radical sam enzyme; <b>PDBTitle:</b> crystal structure of p. horikoshii tyw1
11	<a href="#">c4m7tA_</a>	 Alignment		99.9	21	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> btrn; <b>PDBTitle:</b> crystal structure of btrn in complex with adomet and 2-doia

12	<a href="#">c3c8fA_</a>	Alignment		99.9	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate formate-lyase 1-activating enzyme; <b>PDBTitle:</b> 4fe-4s-pyruvate formate-lyase activating enzyme with partially2 disordered adomet
13	<a href="#">c5th5C_</a>	Alignment		99.9	14	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> 7-carboxy-7-deazaguanine synthase; <b>PDBTitle:</b> crystal structure of quee from bacillus subtilis with 6-carboxypterin-2 5'-deoxyadenosyl ester bound
14	<a href="#">c3t7vA_</a>	Alignment		99.8	16	<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)
15	<a href="#">c3rfaB_</a>	Alignment		99.8	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ribosomal rna large subunit methyltransferase n; <b>PDBTitle:</b> x-ray structure of rlmn from escherichia coli in complex with s-2 adenosylmethionine
16	<a href="#">d1r30a_</a>	Alignment		99.8	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Radical SAM enzymes <b>Family:</b> Biotin synthase
17	<a href="#">c1r30A_</a>	Alignment		99.8	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> biotin synthase; <b>PDBTitle:</b> the crystal structure of biotin synthase, an s-adenosylmethionine-2 dependent radical enzyme
18	<a href="#">c2a5hC_</a>	Alignment		99.8	19	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> l-lysine 2,3-aminomutase; <b>PDBTitle:</b> 2.1 angstrom x-ray crystal structure of lysine-2,3-aminomutase from2 clostridium subterminale sb4, with michaelis analog (l-alpha-lysine3 external aldimine form of pyridoxal-5'-phosphate).
19	<a href="#">c5exkG_</a>	Alignment		99.8	21	<b>PDB header:</b> transferase <b>Chain:</b> G: <b>PDB Molecule:</b> lipoyl synthase; <b>PDBTitle:</b> crystal structure of m. tuberculosis lipoyl synthase with 6-2 thiooctanoyl peptide intermediate
20	<a href="#">c3cixA_</a>	Alignment		99.8	17	<b>PDB header:</b> adomet binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> fefe-hydrogenase maturase; <b>PDBTitle:</b> x-ray structure of the [fefe]-hydrogenase maturase hyde from2 thermotoga maritima in complex with thiocyanate
21	<a href="#">c6fz6B_</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> probable dual-specificity rna methyltransferase rlmn; <b>PDBTitle:</b> crystal structure of a radical sam methyltransferase from2 sphaerobacter thermophilus
22	<a href="#">c3rfaA_</a>	Alignment	not modelled	99.8	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ribosomal rna large subunit methyltransferase n; <b>PDBTitle:</b> x-ray structure of rlmn from escherichia coli in complex with s-2 adenosylmethionine
23	<a href="#">c4rtbA_</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> hydg protein; <b>PDBTitle:</b> x-ray structure of the fefe-hydrogenase maturase hydg from2 carboxythermus hydrogenoformans
24	<a href="#">c4jc0B_</a>	Alignment	not modelled	99.8	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> ribosomal protein s12 methylthiotransferase rimo; <b>PDBTitle:</b> crystal structure of thermotoga maritima holo rimo in complex with2 pentasulfide, northeast structural genomics consortium target vr77
25	<a href="#">c4u0pB_</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> lipoyl synthase 2; <b>PDBTitle:</b> the crystal structure of lipoyl synthase in complex with s-adenosyl2 homocysteine
26	<a href="#">c2z2uA_</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> upf0026 protein mj0257; <b>PDBTitle:</b> crystal structure of archaeal tyw1
27	<a href="#">c3canA_</a>	Alignment	not modelled	99.7	14	<b>PDB header:</b> lyase activator <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate-formate lyase-activating enzyme; <b>PDBTitle:</b> crystal structure of a domain of pyruvate-formate lyase-activating2 enzyme from bacteroides vulgatus atcc 8482 <b>PDB header:</b> lyase

28	<a href="#">c4njkA_</a>	Alignment	not modelled	99.7	23	<b>Chain:</b> A: <b>PDB Molecule:</b> 7-carboxy-7-deazaguanine synthase; <b>PDBTitle:</b> crystal structure of quee from burkholderia multivorans in complex2 with adomet, 7-carboxy-7-deazaguanine, and mg2+
29	<a href="#">c6nhbB_</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 7-carboxy-7-deazaguanine synthase; <b>PDBTitle:</b> crystal structure of quee from escherichia coli
30	<a href="#">d1olta_</a>	Alignment	not modelled	99.7	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Radical SAM enzymes <b>Family:</b> Oxygen-independent coproporphyrinogen III oxidase HemN
31	<a href="#">c6fd2B_</a>	Alignment	not modelled	99.6	19	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative apramycin biosynthetic oxidoreductase 4; <b>PDBTitle:</b> radical sam 1,2-diol dehydratase aprd4 in complex with its substrate2 paromamine
32	<a href="#">c4r33A_</a>	Alignment	not modelled	99.6	18	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> nosl; <b>PDBTitle:</b> x-ray structure of the tryptophan lyase nosl with tryptophan and s-2 adenosyl-l-homocysteine bound
33	<a href="#">c5ul4A_</a>	Alignment	not modelled	99.5	15	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> oxsb protein; <b>PDBTitle:</b> structure of cobalamin-dependent s-adenosylmethionine radical enzyme2 oxsb with aqua-cobalamin and s-adenosylmethionine bound
34	<a href="#">c5l7jA_</a>	Alignment	not modelled	99.3	15	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> elp3 family; <b>PDBTitle:</b> crystal structure of elp3 from dehalococcoides mccartyi
35	<a href="#">c2qgqF_</a>	Alignment	not modelled	99.3	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> F: <b>PDB Molecule:</b> protein tm_1862; <b>PDBTitle:</b> crystal structure of tm_1862 from thermotoga maritima. northeast2 structural genomics consortium target vr77
36	<a href="#">c6qk7C_</a>	Alignment	not modelled	99.1	16	<b>PDB header:</b> translation <b>Chain:</b> C: <b>PDB Molecule:</b> elongator complex protein 3; <b>PDBTitle:</b> elongator catalytic subcomplex elp123 lobe
37	<a href="#">c4fheA_</a>	Alignment	not modelled	99.1	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> spore photoproduct lyase; <b>PDBTitle:</b> spore photoproduct lyase c140a mutant
38	<a href="#">c6iazA_</a>	Alignment	not modelled	98.9	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> histone acetyltransferase, elp3 family; <b>PDBTitle:</b> the archaeal methanocaldococcus infernus elp3 with n-terminus deletion2 (1-46)
39	<a href="#">c3ivuB_</a>	Alignment	not modelled	97.8	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> homocitrate synthase, mitochondrial; <b>PDBTitle:</b> homocitrate synthase lys4 bound to 2-og
40	<a href="#">c3rmjB_</a>	Alignment	not modelled	96.9	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-isopropylmalate synthase; <b>PDBTitle:</b> crystal structure of truncated alpha-isopropylmalate synthase from2 neisseria meningitidis
41	<a href="#">c3bleA_</a>	Alignment	not modelled	96.8	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> citramalate synthase from leptospira interrogans; <b>PDBTitle:</b> crystal structure of the catalytic domain of licms in complexed with2 malonate
42	<a href="#">c3ewbX_</a>	Alignment	not modelled	96.7	14	<b>PDB header:</b> transferase <b>Chain:</b> X: <b>PDB Molecule:</b> 2-isopropylmalate synthase; <b>PDBTitle:</b> crystal structure of n-terminal domain of putative 2-isopropylmalate2 synthase from listeria monocytogenes
43	<a href="#">c6e1jB_</a>	Alignment	not modelled	96.6	12	<b>PDB header:</b> plant protein <b>Chain:</b> B: <b>PDB Molecule:</b> 2-isopropylmalate synthase, a genome specific 1; <b>PDBTitle:</b> crystal structure of methylthioalkylmalate synthase (bjumam1.1) from2 brassica juncea
44	<a href="#">c2ftpA_</a>	Alignment	not modelled	96.5	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> hydroxymethylglutaryl-coa lyase; <b>PDBTitle:</b> crystal structure of hydroxymethylglutaryl-coa lyase from pseudomonas2 aeruginosa
45	<a href="#">c3eegB_</a>	Alignment	not modelled	96.2	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-isopropylmalate synthase; <b>PDBTitle:</b> crystal structure of a 2-isopropylmalate synthase from2 cytophaga hutchinsonii
46	<a href="#">c2cw6B_</a>	Alignment	not modelled	95.0	14	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> hydroxymethylglutaryl-coa lyase, mitochondrial; <b>PDBTitle:</b> crystal structure of human hmg-coa lyase: insights into2 catalysis and the molecular basis for3 hydroxymethylglutaric aciduria
47	<a href="#">c1ydoC_</a>	Alignment	not modelled	94.7	16	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> hmg-coa lyase; <b>PDBTitle:</b> crystal structure of the bacillis subtilis hmg-coa lyase, northeast2 structural genomics target sr181.
48	<a href="#">c1ydnA_</a>	Alignment	not modelled	92.4	17	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> hydroxymethylglutaryl-coa lyase; <b>PDBTitle:</b> crystal structure of the hmg-coa lyase from brucella melitensis,2 northeast structural genomics target lr35.
49	<a href="#">c1nvmG_</a>	Alignment	not modelled	92.1	17	<b>PDB header:</b> lyase/oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> 4-hydroxy-2-oxovalerate aldolase; <b>PDBTitle:</b> crystal structure of a bifunctional aldolase-dehydrogenase :2 sequestering a reactive and volatile intermediate
50	<a href="#">c4jn6C_</a>	Alignment	not modelled	91.9	19	<b>PDB header:</b> lyase/oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> 4-hydroxy-2-oxovalerate aldolase; <b>PDBTitle:</b> crystal structure of the aldolase-dehydrogenase complex from2 mycobacterium tuberculosis hrv37
51	<a href="#">d1nvma2</a>	Alignment	not modelled	91.6	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> HMGL-like
52	<a href="#">c5zmyF_</a>	Alignment	not modelled	90.1	14	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> cis-epoxysuccinate hydrolase; <b>PDBTitle:</b> crystal structure of a cis-epoxysuccinate hydrolase producing d(-)-2 tartaric acids

53	<a href="#">c4ov9A_</a>	Alignment	not modelled	90.1	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> isopropylmalate synthase; <b>PDBTitle:</b> structure of isopropylmalate synthase binding with alpha-2 isopropylmalate
54	<a href="#">c1rr2A_</a>	Alignment	not modelled	82.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> transcarboxylase 5s subunit; <b>PDBTitle:</b> propionibacterium shermanii transcarboxylase 5s subunit bound to 2-2 ketobutyric acid
55	<a href="#">c3hpxB_</a>	Alignment	not modelled	80.2	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-isopropylmalate synthase; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis leuA active site2 domain 1-425 (truncation mutant delta:426-644)
56	<a href="#">c4lrtC_</a>	Alignment	not modelled	79.6	23	<b>PDB header:</b> lyase/oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> 4-hydroxy-2-oxovalerate aldolase; <b>PDBTitle:</b> crystal and solution structures of the bifunctional enzyme2 (aldolase/aldehyde dehydrogenase) from thermomonospora curvata,3 reveal a cofactor-binding domain motion during nad+ and coa4 accommodation within the shared cofactor-binding site
57	<a href="#">c3khdC_</a>	Alignment	not modelled	78.5	12	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> pyruvate kinase; <b>PDBTitle:</b> crystal structure of pff1300w.
58	<a href="#">c1sr9A_</a>	Alignment	not modelled	77.9	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-isopropylmalate synthase; <b>PDBTitle:</b> crystal structure of leuA from mycobacterium tuberculosis
59	<a href="#">c2zyfA_</a>	Alignment	not modelled	75.4	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> homocitrate synthase; <b>PDBTitle:</b> crystal structure of homocitrate synthase from thermus thermophilus2 complexed with magnesium ion and alpha-ketoglutarate
60	<a href="#">c5xfmD_</a>	Alignment	not modelled	72.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> alpha-glucosidase; <b>PDBTitle:</b> crystal structure of beta-arabinopyranosidase
61	<a href="#">d1u7pa_</a>	Alignment	not modelled	72.3	11	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Magnesium-dependent phosphatase-1, Mdp1
62	<a href="#">c5ks8D_</a>	Alignment	not modelled	71.1	12	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> pyruvate carboxylase subunit beta; <b>PDBTitle:</b> crystal structure of two-subunit pyruvate carboxylase from2 methylobacillus flagellatus
63	<a href="#">c2iswB_</a>	Alignment	not modelled	70.9	21	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> putative fructose-1,6-bisphosphate aldolase; <b>PDBTitle:</b> structure of giardia fructose-1,6-biphosphate aldolase in2 complex with phosphoglycolohydroxamate
64	<a href="#">c3a9iA_</a>	Alignment	not modelled	64.1	13	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> homocitrate synthase; <b>PDBTitle:</b> crystal structure of homocitrate synthase from thermus thermophilus2 complexed with lys
65	<a href="#">c3chvA_</a>	Alignment	not modelled	63.3	13	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> prokaryotic domain of unknown function (duf849) with a tim <b>PDBTitle:</b> crystal structure of a prokaryotic domain of unknown function (duf849)2 member (spoa0042) from silicibacter pomeroyi dss-3 at 1.45 a3 resolution
66	<a href="#">c2zq0B_</a>	Alignment	not modelled	62.4	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> alpha-glucosidase (alpha-glucosidase subb); <b>PDBTitle:</b> crystal structure of subb complexed with acarbose
67	<a href="#">c1qhoA_</a>	Alignment	not modelled	61.5	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-amylase; <b>PDBTitle:</b> five-domain alpha-amylase from bacillus stearothermophilus,2 maltose/acarbose complex
68	<a href="#">c5m99A_</a>	Alignment	not modelled	61.1	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-amylase; <b>PDBTitle:</b> functional characterization and crystal structure of thermostable2 amylase from thermotoga petrophila, reveals high thermostability and3 an archaic form of dimerization
69	<a href="#">c2nx9B_</a>	Alignment	not modelled	59.6	15	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> oxaloacetate decarboxylase 2, subunit alpha; <b>PDBTitle:</b> crystal structure of the carboxyltransferase domain of the2 oxaloacetate decarboxylase na+ pump from vibrio cholerae
70	<a href="#">c3pm6B_</a>	Alignment	not modelled	59.2	13	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> putative fructose-bisphosphate aldolase; <b>PDBTitle:</b> crystal structure of a putative fructose-1,6-biphosphate aldolase from2 coccidioides immitis solved by combined sad mr
71	<a href="#">c6irtA_</a>	Alignment	not modelled	59.0	13	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> 4f2 cell-surface antigen heavy chain; <b>PDBTitle:</b> human lat1-4f2hc complex bound with bch
72	<a href="#">c5kzmA_</a>	Alignment	not modelled	58.7	14	<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-beta chain complex from2 francisella tularensis
73	<a href="#">c2wcsA_</a>	Alignment	not modelled	57.2	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha amylase, catalytic region; <b>PDBTitle:</b> crystal structure of debranching enzyme from nostoc2 punctiforme (npde)
74	<a href="#">c3c6cA_</a>	Alignment	not modelled	56.3	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-keto-5-aminohexanoate cleavage enzyme; <b>PDBTitle:</b> crystal structure of a putative 3-keto-5-aminohexanoate cleavage2 enzyme (reut_c6226) from ralstonia eutropha jmp134 at 1.72 a3 resolution
75	<a href="#">c2aaaA_</a>	Alignment	not modelled	55.4	15	<b>PDB header:</b> glycosidase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-amylase; <b>PDBTitle:</b> calcium binding in alpha-amylases: an x-ray diffraction study at 2.12 angstroms resolution of two enzymes from aspergillus
						<b>Fold:</b> TIM beta/alpha-barrel

76	<a href="#">d1bf2a3</a>	Alignment	not modelled	55.3	16	<b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
77	<a href="#">c2p0oA</a>	Alignment	not modelled	54.2	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein duf871; <b>PDBTitle:</b> crystal structure of a conserved protein from locus ef_2437 in2 enterococcus faecalis with an unknown function
78	<a href="#">d2nlya1</a>	Alignment	not modelled	53.9	11	<b>Fold:</b> 7-stranded beta/alpha barrel <b>Superfamily:</b> Glycoside hydrolase/deacetylase <b>Family:</b> Divergent polysaccharide deacetylase
79	<a href="#">c2lqoA</a>	Alignment	not modelled	52.6	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative glutaredoxin rv3198.1/mt3292; <b>PDBTitle:</b> mrx1 reduced
80	<a href="#">c3dxiB</a>	Alignment	not modelled	52.5	10	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative aldolase; <b>PDBTitle:</b> crystal structure of the n-terminal domain of a putative2 aldolase (bvu_2661) from bacteroides vulgatus
81	<a href="#">d1pama4</a>	Alignment	not modelled	52.1	10	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
82	<a href="#">c5h06C</a>	Alignment	not modelled	51.2	18	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> amyp; <b>PDBTitle:</b> crystal structure of amyp in complex with maltose
83	<a href="#">d2obba1</a>	Alignment	not modelled	50.9	11	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> BT0820-like
84	<a href="#">c6arhA</a>	Alignment	not modelled	50.2	17	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetylneuraminate lyase; <b>PDBTitle:</b> crystal structure of human nal at a resolution of 1.6 angstrom
85	<a href="#">d1ea9c3</a>	Alignment	not modelled	48.8	24	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
86	<a href="#">c5hqca</a>	Alignment	not modelled	48.6	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glycoside hydrolase family 97 enzyme; <b>PDBTitle:</b> a glycoside hydrolase family 97 enzyme r171k variant from2 pseudoalteromonas sp. strain k8
87	<a href="#">d1qhoa4</a>	Alignment	not modelled	47.8	25	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
88	<a href="#">d3bmva4</a>	Alignment	not modelled	47.8	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
89	<a href="#">c5d88A</a>	Alignment	not modelled	47.5	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> predicted protease of the collagenase family; <b>PDBTitle:</b> the structure of the u32 peptidase mk0906
90	<a href="#">c5zxbB</a>	Alignment	not modelled	46.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> cyclic maltosyl-maltose hydrolase; <b>PDBTitle:</b> cyclic alpha-maltosyl-(1-->6)-maltose hydrolase from arthrobacter2 globiformis, ligand-free form
91	<a href="#">c3a47A</a>	Alignment	not modelled	45.5	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> oligo-1,6-glucosidase; <b>PDBTitle:</b> crystal structure of isomaltase from saccharomyces cerevisiae
92	<a href="#">c5zcbA</a>	Alignment	not modelled	45.5	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-glucosidase; <b>PDBTitle:</b> crystal structure of alpha-glucosidase
93	<a href="#">d1cgta4</a>	Alignment	not modelled	44.1	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
94	<a href="#">c3vndD</a>	Alignment	not modelled	43.9	11	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> crystal structure of tryptophan synthase alpha-subunit from the2 psychrophile shewanella frigidimarina k14-2
95	<a href="#">c4as2D</a>	Alignment	not modelled	43.6	14	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> phosphorylcholine phosphatase; <b>PDBTitle:</b> pseudomonas aeruginosa phosphorylcholine phosphatase. monoclinic form
96	<a href="#">d1yhta1</a>	Alignment	not modelled	43.3	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-N-acetylhexosaminidase catalytic domain
97	<a href="#">d1qvia3</a>	Alignment	not modelled	43.0	22	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
98	<a href="#">c1cygA</a>	Alignment	not modelled	42.9	17	<b>PDB header:</b> glycosyltransferase <b>Chain:</b> A: <b>PDB Molecule:</b> cyclodextrin glucanotransferase; <b>PDBTitle:</b> cyclodextrin glucanotransferase (e.c.2.4.1.19) (cgtase)
99	<a href="#">c3no5C</a>	Alignment	not modelled	42.4	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a pfam duf849 domain containing protein2 (reut_a1631) from ralstonia eutropha jmp134 at 1.90 a resolution
100	<a href="#">d1ua7a2</a>	Alignment	not modelled	41.9	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
101	<a href="#">c1bagA</a>	Alignment	not modelled	41.2	17	<b>PDB header:</b> alpha-amylase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-1,4-glucan-4-glucanohydrolase; <b>PDBTitle:</b> alpha-amylase from bacillus subtilis complexed with2 maltopentaose
102	<a href="#">d1n7ka</a>	Alignment	not modelled	41.1	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase

103	<a href="#">c3wy3A_</a>	Alignment	not modelled	40.6	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-glucosidase; <b>PDBTitle:</b> crystal structure of alpha-glucosidase mutant d202n in complex with2 glucose and glycerol
104	<a href="#">c1m53A_</a>	Alignment	not modelled	40.4	20	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> isomaltulose synthase; <b>PDBTitle:</b> crystal structure of isomaltulose synthase (pali) from2 klebsiella sp. lx3
105	<a href="#">d1h3ga3</a>	Alignment	not modelled	40.4	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
106	<a href="#">c1lwhA_</a>	Alignment	not modelled	40.1	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-alpha-glucanotransferase; <b>PDBTitle:</b> crystal structure of t. maritima 4-alpha-glucanotransferase
107	<a href="#">c2y7eA_</a>	Alignment	not modelled	39.4	18	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-keto-5-aminohexanoate cleavage enzyme; <b>PDBTitle:</b> crystal structure of the 3-keto-5-aminohexanoate cleavage enzyme2 (kce) from candidatus cloacamonas acidaminovorans (tetragonal form)
108	<a href="#">d1uoka2</a>	Alignment	not modelled	39.0	26	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
109	<a href="#">c4jclA_</a>	Alignment	not modelled	38.1	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cyclomaltodextrin glucanotransferase; <b>PDBTitle:</b> crystal structure of alpha-cgt from paenibacillus macerans at 1.72 angstrom resolution
110	<a href="#">c4j7rA_</a>	Alignment	not modelled	37.6	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> isoamylase; <b>PDBTitle:</b> crystal structure of chlamydomonas reinhardtii isoamylase 1 (isa1)
111	<a href="#">c4e2oA_</a>	Alignment	not modelled	37.6	22	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-amylase; <b>PDBTitle:</b> crystal structure of alpha-amylase from geobacillus thermoleovorans,2 gta, complexed with acarbose
112	<a href="#">d2gjpa2</a>	Alignment	not modelled	37.4	22	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
113	<a href="#">c5ey5A_</a>	Alignment	not modelled	37.3	19	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> lbcats-a; <b>PDBTitle:</b> lbcats
114	<a href="#">c3bmwA_</a>	Alignment	not modelled	37.2	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cyclomaltodextrin glucanotransferase; <b>PDBTitle:</b> cyclodextrin glycosyl transferase from thermoanaerobacterium2 thermosulfurigenes em1 mutant s77p complexed with a maltoheptaose3 inhibitor
115	<a href="#">d1m53a2</a>	Alignment	not modelled	37.0	22	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
116	<a href="#">d2aaaa2</a>	Alignment	not modelled	36.7	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
117	<a href="#">c6daoB_</a>	Alignment	not modelled	36.0	22	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> trans-o-hydroxybenzylidenepyruvate hydratase-aldolase; <b>PDBTitle:</b> nahe wt selenomethionine
118	<a href="#">d1e43a2</a>	Alignment	not modelled	36.0	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
119	<a href="#">c4n4qD_</a>	Alignment	not modelled	35.9	14	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> acylneuraminate lyase; <b>PDBTitle:</b> crystal structure of n-acetylneuraminate lyase from mycoplasma2 synoviae, crystal form ii
120	<a href="#">c5x7uA_</a>	Alignment	not modelled	35.5	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> trehalose synthase; <b>PDBTitle:</b> trehalose synthase from thermobaculum terrenum