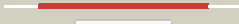



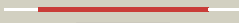



















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1485_(hemH)_1675023_1676057
Date	Fri Aug 2 13:30:06 BST 2019
Unique Job ID	649bc5d889c43d04

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2hrca1</a>	 Alignment		100.0	28	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> Chelatase <b>Family:</b> Ferrochelatase
2	<a href="#">d1lbqa_</a>	 Alignment		100.0	22	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> Chelatase <b>Family:</b> Ferrochelatase
3	<a href="#">d2hk6a1</a>	 Alignment		100.0	30	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> Chelatase <b>Family:</b> Ferrochelatase
4	<a href="#">c5zt7A_</a>	 Alignment		100.0	14	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> sirohhydrochlorin ferrochelatase; <b>PDBTitle:</b> sirb from bacillus subtilis with co2+
5	<a href="#">c2xvzA_</a>	 Alignment		100.0	18	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> chelataase, putative; <b>PDBTitle:</b> cobalt chelatase cbik (periplasmatic) from desulvobrio2 vulgaris hildenborough (co-crystallized with cobalt)
6	<a href="#">d1qgoa_</a>	 Alignment		99.9	17	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> Chelatase <b>Family:</b> Cobalt chelatase CbiK
7	<a href="#">c2jh3C_</a>	 Alignment		99.6	17	<b>PDB header:</b> ribosomal protein <b>Chain:</b> C: <b>PDB Molecule:</b> ribosomal protein s2-related protein; <b>PDBTitle:</b> the crystal structure of dr2241 from deinococcus2 radiodurans at 1.9 a resolution reveals a multi-domain3 protein with structural similarity to chelatases but also4 with two additional novel domains
8	<a href="#">c4ccsA_</a>	 Alignment		99.5	19	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> cbix; <b>PDBTitle:</b> the structure of cbix, the terminal enzyme for biosynthesis2 of siroheme in denitrifying bacteria
9	<a href="#">c3lyhB_</a>	 Alignment		99.2	15	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> cobalamin (vitamin b12) biosynthesis cbix protein; <b>PDBTitle:</b> crystal structure of putative cobalamin (vitamin b12) biosynthesis2 cbix protein (yp_958415.1) from marinobacter aquaeolei vt8 at 1.60 a3 resolution
10	<a href="#">c1tjnA_</a>	 Alignment		98.5	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> sirohhydrochlorin cobaltochelataase; <b>PDBTitle:</b> crystal structure of hypothetical protein af0721 from archaeoglobus2 fulgidus
11	<a href="#">d1tjna_</a>	 Alignment		98.5	14	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> Chelatase <b>Family:</b> CbiX-like

12	<a href="#">c5tchG</a>	Alignment		92.6	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
13	<a href="#">c2ekcA</a>	Alignment		91.7	12	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> structural study of project id aq_1548 from aquifex aeolicus vf5
14	<a href="#">c3vndD</a>	Alignment		89.6	22	<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
15	<a href="#">d1ujpa</a>	Alignment		88.4	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phoshate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
16	<a href="#">c3navB</a>	Alignment		87.3	20	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> crystal structure of an alpha subunit of tryptophan synthase from2 vibrio cholerae o1 biovar el tor str. n16961
17	<a href="#">d1qopa</a>	Alignment		85.7	23	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phoshate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
18	<a href="#">d2csua1</a>	Alignment		85.7	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
19	<a href="#">d2dlad2</a>	Alignment		85.5	20	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Formate/glycerate dehydrogenase catalytic domain-like <b>Family:</b> Formate/glycerate dehydrogenases, substrate-binding domain
20	<a href="#">c2i6oa</a>	Alignment		85.2	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> sulfolobus solfataricus protein tyrosine <b>PDBTitle:</b> crystal structure of the complex of the archaeal sulfolobus2 ptp-fold phosphatase with phosphopeptides n-g-(p)y-k-n
21	<a href="#">c2csuB</a>	Alignment	not modelled	84.4	21	<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
22	<a href="#">c5ey5A</a>	Alignment	not modelled	81.7	21	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> lbcats-a; <b>PDBTitle:</b> lbcats
23	<a href="#">c4n7bA</a>	Alignment	not modelled	80.5	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> lytb; <b>PDBTitle:</b> structure of the e-1-hydroxy-2-methyl-but-2-enyl-4-diphosphate2 reductase from plasmodium falciparum
24	<a href="#">c4u0pB</a>	Alignment	not modelled	79.9	15	<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
25	<a href="#">c5kzmA</a>	Alignment	not modelled	78.9	18	<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
26	<a href="#">c5exkG</a>	Alignment	not modelled	78.9	17	<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
27	<a href="#">c5k9xA</a>	Alignment	not modelled	78.2	15	<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
28	<a href="#">c3ke8A</a>	Alignment	not modelled	78.1	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-hydroxy-3-methylbut-2-enyl diphosphate reductase; <b>PDBTitle:</b> crystal structure of isph:hmbpp-complex <b>PDB header:</b> ligase

29	<a href="#">c4yajA</a>	Alignment	not modelled	76.9	23	<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)
30	<a href="#">d2d59a1</a>	Alignment	not modelled	76.3	14	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> CoA-binding domain
31	<a href="#">c3urkA</a>	Alignment	not modelled	75.8	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> 4-hydroxy-3-methylbut-2-enyl diphosphate reductase; <b>PDBTitle:</b> isph in complex with propynyl diphosphate (1061)
32	<a href="#">d1vj5a1</a>	Alignment	not modelled	73.7	17	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> phosphatase domain of polynucleotide kinase
33	<a href="#">c3dnfB</a>	Alignment	not modelled	71.2	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> 4-hydroxy-3-methylbut-2-enyl diphosphate reductase; <b>PDBTitle:</b> structure of (e)-4-hydroxy-3-methyl-but-2-enyl diphosphate reductase,2 the terminal enzyme of the non-mevalonate pathway
34	<a href="#">c3ff4A</a>	Alignment	not modelled	69.4	19	<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
35	<a href="#">c4eacC</a>	Alignment	not modelled	67.6	14	<b>PDB header:</b> lyase <b>Chain:</b> C; <b>PDB Molecule:</b> mannonate dehydratase; <b>PDBTitle:</b> crystal structure of mannonate dehydratase from escherichia coli2 strain k12
36	<a href="#">c5ak1A</a>	Alignment	not modelled	66.4	12	<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
37	<a href="#">d1xima</a>	Alignment	not modelled	65.9	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> Xylose isomerase
38	<a href="#">d2pt0a1</a>	Alignment	not modelled	65.8	24	<b>Fold:</b> (Phosphotyrosine protein) phosphatases II <b>Superfamily:</b> (Phosphotyrosine protein) phosphatases II <b>Family:</b> Myo-inositol hexaphosphate phosphohydrolase (phytase) PhyA
39	<a href="#">d1euca1</a>	Alignment	not modelled	65.2	12	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> CoA-binding domain
40	<a href="#">c2yv2A</a>	Alignment	not modelled	65.0	25	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> succinyl-coa synthetase alpha chain; <b>PDBTitle:</b> crystal structure of succinyl-coa synthetase alpha chain from2 aeropyrum pernix k1
41	<a href="#">c2nu8D</a>	Alignment	not modelled	64.7	24	<b>PDB header:</b> ligase <b>Chain:</b> D; <b>PDB Molecule:</b> succinyl-coa ligase [adp-forming] subunit alpha; <b>PDBTitle:</b> c123at mutant of e. coli succinyl-coa synthetase
42	<a href="#">c2fpgA</a>	Alignment	not modelled	61.5	10	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> succinyl-coa ligase [gdp-forming] alpha-chain, <b>PDBTitle:</b> crystal structure of pig gtp-specific succinyl-coa synthetase in2 complex with gdp
43	<a href="#">d1fpza</a>	Alignment	not modelled	60.6	17	<b>Fold:</b> (Phosphotyrosine protein) phosphatases II <b>Superfamily:</b> (Phosphotyrosine protein) phosphatases II <b>Family:</b> Dual specificity phosphatase-like
44	<a href="#">c6dkeA</a>	Alignment	not modelled	60.5	11	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> fatty acid kinase (fak) b1 protein; <b>PDBTitle:</b> the x-ray crystal structure of streptococcus pneumoniae fatty acid2 kinase (fak) b1 protein loaded with palmitic acid (c16:0) to 1.763 angstrom resolution
45	<a href="#">c6me1A</a>	Alignment	not modelled	60.3	24	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> succinate--coa ligase subunit alpha; <b>PDBTitle:</b> succinyl-coa synthase from campylobacter jejuni
46	<a href="#">d1iuka</a>	Alignment	not modelled	60.2	18	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> CoA-binding domain
47	<a href="#">c1u24A</a>	Alignment	not modelled	60.2	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> myo-inositol hexaphosphate phosphohydrolase; <b>PDBTitle:</b> crystal structure of selenomonas ruminantium phytase
48	<a href="#">d1y81a1</a>	Alignment	not modelled	56.4	23	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> CoA-binding domain
49	<a href="#">d1j4aa2</a>	Alignment	not modelled	56.0	23	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Formate/glycerate dehydrogenase catalytic domain-like <b>Family:</b> Formate/glycerate dehydrogenases, substrate-binding domain
50	<a href="#">c3zvmA</a>	Alignment	not modelled	55.3	17	<b>PDB header:</b> hydrolase/transferase/dna phosphatase/kinase; <b>Chain:</b> A; <b>PDB Molecule:</b> bifunctional polynucleotide phosphatase/kinase; <b>PDBTitle:</b> the structural basis for substrate recognition by mammalian2 polynucleotide kinase 3' phosphatase
51	<a href="#">c5kinC</a>	Alignment	not modelled	55.3	15	<b>PDB header:</b> lyase <b>Chain:</b> C; <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> crystal structure of tryptophan synthase alpha beta complex from2 streptococcus pneumoniae
52	<a href="#">c3mwdB</a>	Alignment	not modelled	54.9	20	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> atp-citrate synthase; <b>PDBTitle:</b> truncated human atp-citrate lyase with citrate bound
53	<a href="#">c5e09A</a>	Alignment	not modelled	52.4	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> cellulase; <b>PDBTitle:</b> structural insight of a trimodular halophilic cellulase with a family2 46 carbohydrate-binding module

54	<a href="#">c4u5iB_</a>	Alignment	not modelled	52.2	9	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> endoglucanase h; <b>PDBTitle:</b> complex structure of mutant ctcel5e (e314a) with xylobiose
55	<a href="#">c2hk1D_</a>	Alignment	not modelled	49.7	10	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> d-psicose 3-epimerase; <b>PDBTitle:</b> crystal structure of d-psicose 3-epimerase (dpease) in the presence of 2 d-fructose
56	<a href="#">d2p10a1</a>	Alignment	not modelled	49.6	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> MI19387-like
57	<a href="#">d1nh8a2</a>	Alignment	not modelled	48.0	32	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GlnB-like <b>Family:</b> ATP phosphoribosyltransferase (ATP-PRTase, HisG), regulatory C-terminal domain
58	<a href="#">c1yj5B_</a>	Alignment	not modelled	47.7	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 5' polynucleotide kinase-3' phosphatase catalytic domain; <b>PDBTitle:</b> molecular architecture of mammalian polynucleotide kinase, a dna2 repair enzyme
59	<a href="#">c4rrfD_</a>	Alignment	not modelled	46.9	15	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> threonine--trna ligase; <b>PDBTitle:</b> editing domain of threonyl-trna synthetase from methanococcus2 jannaschii with l-ser3aa
60	<a href="#">c1qzuB_</a>	Alignment	not modelled	46.0	32	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein mds018; <b>PDBTitle:</b> crystal structure of human phosphopantothenoylcysteine decarboxylase
61	<a href="#">c3icgD_</a>	Alignment	not modelled	46.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> endoglucanase d; <b>PDBTitle:</b> crystal structure of the catalytic and carbohydrate binding domain of 2 endoglucanase d from clostridium cellulovorans
62	<a href="#">c5v1tA_</a>	Alignment	not modelled	45.7	10	<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 suia
63	<a href="#">d1qzua_</a>	Alignment	not modelled	45.6	29	<b>Fold:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD <b>Superfamily:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD <b>Family:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
64	<a href="#">d1rd5a_</a>	Alignment	not modelled	45.6	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
65	<a href="#">c2yv1A_</a>	Alignment	not modelled	45.2	27	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> succinyl-coa ligase [adp-forming] subunit alpha; <b>PDBTitle:</b> crystal structure of succinyl-coa synthetase alpha chain from 2 methanocaldococcus jannaschii dsm 2661
66	<a href="#">c2p10D_</a>	Alignment	not modelled	44.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> ml19387 protein; <b>PDBTitle:</b> crystal structure of a putative phosphonopyruvate hydrolase (ml19387)2 from mesorhizobium loti maff303099 at 2.15 a resolution
67	<a href="#">c3wqoB_</a>	Alignment	not modelled	44.7	9	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein mj1311; <b>PDBTitle:</b> crystal structure of d-tagatose 3-epimerase-like protein
68	<a href="#">c6hxqA_</a>	Alignment	not modelled	44.5	20	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> citryl-coa synthetase small subunit; <b>PDBTitle:</b> structure of citryl-coa synthetase from hydrogenobacter thermophilus
69	<a href="#">c2jepB_</a>	Alignment	not modelled	44.5	11	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> xyloglucanase; <b>PDBTitle:</b> native family 5 xyloglucanase from paenibacillus pabuli
70	<a href="#">c4amuB_</a>	Alignment	not modelled	44.5	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> ornithine carbamoyltransferase, catabolic; <b>PDBTitle:</b> structure of ornithine carbamoyltransferase from mycoplasma2 penetrans with a p321 space group
71	<a href="#">c2duwA_</a>	Alignment	not modelled	41.7	13	<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 of 2 klebsiella pneumoniae
72	<a href="#">c3bdkB_</a>	Alignment	not modelled	40.4	14	<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
73	<a href="#">d1l6sa_</a>	Alignment	not modelled	40.3	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> 5-aminolaevalinate dehydratase, ALAD (porphobilinogen synthase)
74	<a href="#">c1fvoB_</a>	Alignment	not modelled	39.5	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> ornithine transcarbamylase; <b>PDBTitle:</b> crystal structure of human ornithine transcarbamylase complexed with 2 carbamoyl phosphate
75	<a href="#">c4ky3A_</a>	Alignment	not modelled	38.7	14	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> designed protein or327; <b>PDBTitle:</b> three-dimensional structure of the orthorhombic crystal of 2 computationally designed insertion domain , northeast structural3 genomics consortium (nesg) target or327
76	<a href="#">c2ov3A_</a>	Alignment	not modelled	38.6	9	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic binding protein component of an abc type zinc <b>PDBTitle:</b> crystal structure of 138-173 znua deletion mutant plus zinc bound
77	<a href="#">c3d4iD_</a>	Alignment	not modelled	37.2	8	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> sts-2 protein; <b>PDBTitle:</b> crystal structure of the 2h-phosphatase domain of sts-2
78	<a href="#">d2cfua2</a>	Alignment	not modelled	36.6	15	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase

						<b>Family:</b> Alkylsulfatase-like
79	<a href="#">c2hl2A_</a>	Alignment	not modelled	36.5	13	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> threonyl-trna synthetase; <b>PDBTitle:</b> crystal structure of the editing domain of threonyl-trna2 synthetase from pyrococcus abyssi in complex with an3 analog of seryladenylate
80	<a href="#">d1geqa_</a>	Alignment	not modelled	36.5	12	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
81	<a href="#">c3lupA_</a>	Alignment	not modelled	35.7	12	<b>PDB header:</b> structure genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> degv family protein; <b>PDBTitle:</b> crystal structure of fatty acid binding degv family protein sag13422 from streptococcus agalactiae
82	<a href="#">c4rkka_</a>	Alignment	not modelled	34.9	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> laforin; <b>PDBTitle:</b> structure of a product bound phosphatase
83	<a href="#">c1fpzF_</a>	Alignment	not modelled	34.8	17	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> cyclin-dependent kinase inhibitor 3; <b>PDBTitle:</b> crystal structure analysis of kinase associated phosphatase (kap) with2 a substitution of the catalytic site cysteine (cys140) to a serine
84	<a href="#">c3sdsA_</a>	Alignment	not modelled	34.8	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ornithine carbamoyltransferase, mitochondrial; <b>PDBTitle:</b> crystal structure of a mitochondrial ornithine carbamoyltransferase2 from coccidioides immitis
85	<a href="#">d1h3da2</a>	Alignment	not modelled	34.8	25	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GlnB-like <b>Family:</b> ATP phosphoribosyltransferase (ATP-PRTase, HisG), regulatory C-terminal domain
86	<a href="#">c5ow0B_</a>	Alignment	not modelled	33.6	9	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> electron transfer flavoprotein, beta subunit; <b>PDBTitle:</b> crystal structure of an electron transfer flavoprotein from2 geobacillus metallireducens
87	<a href="#">c1oi7A_</a>	Alignment	not modelled	33.1	18	<b>PDB header:</b> synthetase <b>Chain:</b> A: <b>PDB Molecule:</b> succinyl-coa synthetase alpha chain; <b>PDBTitle:</b> the crystal structure of succinyl-coa synthetase alpha2 subunit from thermus thermophilus
88	<a href="#">d1dxya2</a>	Alignment	not modelled	31.7	18	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Formate/glycerate dehydrogenase catalytic domain-like <b>Family:</b> Formate/glycerate dehydrogenases, substrate-binding domain
89	<a href="#">c2zunB_</a>	Alignment	not modelled	31.4	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 458aa long hypothetical endo-1,4-beta-glucanase; <b>PDBTitle:</b> functional analysis of hyperthermophilic endocellulase from2 the archaeon pyrococcus horikoshii
90	<a href="#">c6ndiB_</a>	Alignment	not modelled	31.1	19	<b>PDB header:</b> sugar binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> 2.60 angstrom resolution crystal structure of periplasmic binding and2 sugar binding domain of lacI family protein from klebsiella3 pneumoniae.
91	<a href="#">c4yztA_</a>	Alignment	not modelled	30.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cellulose hydrolase; <b>PDBTitle:</b> crystal structure of a tri-modular gh5 (subfamily 4) endo-beta-1, 4-2 glucanase from bacillus licheniformis complexed with cellotetraose
92	<a href="#">c3guwB_</a>	Alignment	not modelled	30.5	7	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein af_1765; <b>PDBTitle:</b> crystal structure of the tatd-like protein (af1765) from archaeoglobus2 fulgidus, northeast structural genomics consortium target gr121
93	<a href="#">c5g1oF_</a>	Alignment	not modelled	30.4	12	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> cad protein; <b>PDBTitle:</b> aspartate transcarbamoylase domain of human cad in apo form
94	<a href="#">c5ol2E_</a>	Alignment	not modelled	30.2	14	<b>PDB header:</b> flavoprotein <b>Chain:</b> E: <b>PDB Molecule:</b> electron transfer flavoprotein small subunit; <b>PDBTitle:</b> the electron transferring flavoprotein/butyryl-coa dehydrogenase2 complex from clostridium difficile
95	<a href="#">d2c1ha1</a>	Alignment	not modelled	30.0	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> 5-aminolaevulinic acid dehydratase, ALAD (porphobilinogen synthase)
96	<a href="#">c3wh9A_</a>	Alignment	not modelled	29.9	9	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endo-beta-1,4-mannanase; <b>PDBTitle:</b> the ligand-free structure of manbk from aspergillus niger bk01
97	<a href="#">c6q5zA_</a>	Alignment	not modelled	29.7	18	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> conotoxin vc7.2; <b>PDBTitle:</b> h-vc7.2, h-superfamily conotoxin
98	<a href="#">c3up8B_</a>	Alignment	not modelled	29.7	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative 2,5-diketo-d-gluconic acid reductase b; <b>PDBTitle:</b> crystal structure of a putative 2,5-diketo-d-gluconic acid reductase b
99	<a href="#">c3wflA_</a>	Alignment	not modelled	29.5	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-mannanase; <b>PDBTitle:</b> crystal structure of glycoside hydrolase family 5 beta-mannanase from2 talaromyces trachyspermus
100	<a href="#">d1fzta_</a>	Alignment	not modelled	29.4	6	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Cofactor-dependent phosphoglycerate mutase
101	<a href="#">c2yn2A_</a>	Alignment	not modelled	29.1	9	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein ynl108c; <b>PDBTitle:</b> huf protein - paralogue of the tau55 histidine phosphatase domain



102	<a href="#">c5hm8C_</a>	 Alignment	not modelled	29.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> adenosylhomocysteinase; <b>PDBTitle:</b> 2.85 angstrom crystal structure of s-adenosylhomocysteinase from <i>2 cryptosporidium parvum</i> in complex with adenosine and nad.
103	<a href="#">c2hm4A_</a>	 Alignment	not modelled	28.7	21	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> nematocyst outer wall antigen; <b>PDBTitle:</b> nematocyst outer wall antigen, nw1 k21p
104	<a href="#">c3rgiA_</a>	 Alignment	not modelled	28.7	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> disd protein; <b>PDBTitle:</b> trans-acting transferase from disorazole synthase
105	<a href="#">d1oi7a1</a>	 Alignment	not modelled	28.5	23	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> CoA-binding domain
106	<a href="#">c3hjtB_</a>	 Alignment	not modelled	28.5	13	<b>PDB header:</b> cell adhesion, transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> lmb; <b>PDBTitle:</b> structure of laminin binding protein (lmb) of streptococcus agalactiae2 a bifunctional protein with adhesin and metal transporting activity
107	<a href="#">c6au1B_</a>	 Alignment	not modelled	28.1	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative hemin storage protein; <b>PDBTitle:</b> structure of the pgab (bpsb) glycoside hydrolase domain from <i>2 bordetella bronchiseptica</i>
108	<a href="#">d1wkya2</a>	 Alignment	not modelled	27.7	9	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
109	<a href="#">c3d64A_</a>	 Alignment	not modelled	27.7	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> adenosylhomocysteinase; <b>PDBTitle:</b> crystal structure of s-adenosyl-l-homocysteine hydrolase from <i>2 burkholderia pseudomallei</i>
110	<a href="#">d1ppq4a_</a>	 Alignment	not modelled	27.6	9	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> "Helical backbone" metal receptor <b>Family:</b> TroA-like
111	<a href="#">c4kpuB_</a>	 Alignment	not modelled	27.5	13	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> electron transfer flavoprotein alpha/beta-subunit; <b>PDBTitle:</b> electron transferring flavoprotein of acidaminococcus fermentans:2 towards a mechanism of flavin-based electron bifurcation
112	<a href="#">c3dmyA_</a>	 Alignment	not modelled	27.2	14	<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 <i>e.coli</i>
113	<a href="#">c4rrcA_</a>	 Alignment	not modelled	27.1	15	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> probable threonine--trna ligase 2; <b>PDBTitle:</b> n-terminal editing domain of threonyl-trna synthetase from <i>aeropyrum2 pernix</i> with l-thr3aa (snapshot 3)
114	<a href="#">d1tz9a_</a>	 Alignment	not modelled	27.1	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> UxuA-like
115	<a href="#">c3gxgA_</a>	 Alignment	not modelled	26.6	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative phosphatase (duf442); <b>PDBTitle:</b> crystal structure of putative phosphatase (duf442) (yp_001181608.1)2 from <i>shewanella putrefaciens</i> cn-32 at 1.60 a resolution
116	<a href="#">d1gp6a_</a>	 Alignment	not modelled	26.4	14	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> Clavaminatase synthase-like <b>Family:</b> Penicillin synthase-like
117	<a href="#">c4uxdC_</a>	 Alignment	not modelled	25.8	11	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> 2-dehydro-3-deoxy-d-gluconate/2-dehydro-3-deoxy- <b>PDBTitle:</b> 2-keto 3-deoxygluconate aldolase from <i>picrophilus torridus</i>
118	<a href="#">c5xtuA_</a>	 Alignment	not modelled	25.5	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> gdsl-family esterase; <b>PDBTitle:</b> crystal structure of gdsl esterase of <i>photobacterium</i> sp. j15
119	<a href="#">d1pv8a_</a>	 Alignment	not modelled	25.5	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> 5-aminolaevulinatase dehydratase, ALAD (porphobilinogen synthase)
120	<a href="#">c3jugA_</a>	 Alignment	not modelled	25.4	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-mannanase; <b>PDBTitle:</b> crystal structure of endo-beta-1,4-mannanase from the alkaliphilic <i>2 bacillus</i> sp. n16-5