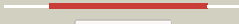



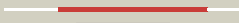



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1075c_(-)_1199431_1200375
Date	Wed Jul 31 22:05:15 BST 2019
Unique Job ID	1044e852f7b520a7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2o14A_	 Alignment		100.0	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein yxim; PDBTitle: x-ray crystal structure of protein yxim_bacsu from bacillus subtilis.2 northeast structural genomics consortium target sr595
2	c3milA_	 Alignment		100.0	13	PDB header: hydrolase Chain: A: PDB Molecule: isoamyl acetate-hydrolyzing esterase; PDBTitle: crystal structure of isoamyl acetate-hydrolyzing esterase from2 saccharomyces cerevisiae
3	c3hp4A_	 Alignment		100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: gdsI-esterase; PDBTitle: crystal structure of psychrotrophic esterase esta from2 pseudoalteromonas sp. 643a inhibited by monoethylphosphonate
4	c6iqbA_	 Alignment		100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: sgnh-hydrolase family esterase; PDBTitle: esterase aline4 mutant-s13a
5	c4iyjA_	 Alignment		100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: gdsI-like protein; PDBTitle: crystal structure of a putative acylhydrolase (bacuni_03406) from2 bacteroides uniformis atcc 8492 at 1.37 a resolution
6	d1jrlA_	 Alignment		100.0	18	Fold: Flavodoxin-like Superfamily: SGNH hydrolase Family: TAP-like
7	c4rshB_	 Alignment		100.0	16	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: lipolytic protein g-d-s-l family; PDBTitle: structure of a putative lipolytic protein of g-d-s-l family from2 desulfotobacterium hafniense dcb-2
8	c3p94A_	 Alignment		100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: gdsI-like lipase; PDBTitle: crystal structure of a gdsI-like lipase (bdi_0976) from2 parabacteroides distasonis atcc 8503 at 1.93 a resolution
9	c6njcB_	 Alignment		100.0	15	PDB header: hydrolase Chain: B: PDB Molecule: sialate o-acetylerase; PDBTitle: crystal structure of the sialate o-acetylerase from bacteroides2 vulgatus
10	c4q7qA_	 Alignment		100.0	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lipolytic protein g-d-s-l family; PDBTitle: the crystal structure of a possible lipase from chitinophaga pinensis2 dsm 2588
11	c4jggB_	 Alignment		100.0	23	PDB header: hydrolase Chain: B: PDB Molecule: esterase tesa; PDBTitle: crystal structure of tesa

12	c6iq8B_	Alignment		100.0	17	PDB header: hydrolase Chain: B: PDB Molecule: carboxylesterase; PDBTitle: esterase crme10 mutant-d178a
13	c3rjtA_	Alignment		100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: lipolytic protein g-d-s-l family; PDBTitle: crystal structure of lipolytic protein g-d-s-l family from2 alicyclobacillus acidocaldarius subsp. acidocaldarius dsm 446
14	c4lhsA_	Alignment		100.0	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative gds-like lipase (bacova_00914) from2 bacteroides ovatus atcc 8483 at 1.40 a resolution
15	d1k7ca_	Alignment		100.0	19	Fold: Flavodoxin-like Superfamily: SGNH hydrolase Family: Rhamnogalacturonan acetyesterase
16	c5jd3A_	Alignment		100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: lae5; PDBTitle: crystal structure of lae5, an alpha/beta hydrolase enzyme from the2 metagenome of lake arreo, spain
17	d1yzfa1	Alignment		100.0	21	Fold: Flavodoxin-like Superfamily: SGNH hydrolase Family: TAP-like
18	c5ma1A_	Alignment		100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: crystal structure of extracelular lipase from streptomyces rimosus at2 1.7a resolution
19	c4jhlA_	Alignment		100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: acetyl xylan esterase; PDBTitle: crystal structure of of axe2, an acetylxylan esterase from geobacillus2 stearothermophilus
20	c4h08A_	Alignment		100.0	13	PDB header: hydrolase Chain: A: PDB Molecule: putative hydrolase; PDBTitle: crystal structure of a putative hydrolase (bt3161) from bacteroides2 thetaiotaomicron vpi-5482 at 1.80 a resolution
21	c4hyqA_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: phospholipase a1; PDBTitle: crystal structure of phospholipase a1 from streptomyces albidoflavus2 na297
22	c3bzwA_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: putative lipase; PDBTitle: crystal structure of a putative lipase from bacteroides2 thetaiotaomicron
23	d3bzwa1	Alignment	not modelled	100.0	15	Fold: Flavodoxin-like Superfamily: SGNH hydrolase Family: BT2961-like
24	d1vjga_	Alignment	not modelled	100.0	16	Fold: Flavodoxin-like Superfamily: SGNH hydrolase Family: Hypothetical protein alr1529
25	c4rw0B_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: B: PDB Molecule: lipolytic protein g-d-s-l family; PDBTitle: crystal structure of a member of the lipolytic protein g-d-s-l family2 from veillonella parvula dsm 2008
26	d2o14a2	Alignment	not modelled	100.0	18	Fold: Flavodoxin-like Superfamily: SGNH hydrolase Family: Yxim C-terminal domain-like
27	c4q9aA_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: tat pathway signal sequence domain protein; PDBTitle: crystal structure of a putative gds-like lipase (parmer_00689) from2 parabacteroides merdae atcc 43184 at 2.86 a resolution
28	c4hf7A_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: putative acylhydrolase; PDBTitle: crystal structure of a gds-like lipase (bt0569) from

					bacteroides2 thetaiotaomicron vpi-5482 at 1.77 a resolution
29	d1esca_	Alignment	not modelled	100.0	21 Fold: Flavodoxin-like Superfamily: SGNH hydrolase Family: Esterase
30	d1es9a_	Alignment	not modelled	100.0	13 Fold: Flavodoxin-like Superfamily: SGNH hydrolase Family: Acetylhydrolase
31	c2waoA_	Alignment	not modelled	99.9	19 PDB header: hydrolase Chain: A: PDB Molecule: endoglucanase e; PDBTitle: structure of a family two carbohydrate esterase from clostridium2 thermocellum in complex with cellohexaose
32	d2hsja1	Alignment	not modelled	99.9	17 Fold: Flavodoxin-like Superfamily: SGNH hydrolase Family: Acetylhydrolase
33	c2vptA_	Alignment	not modelled	99.9	17 PDB header: hydrolase Chain: A: PDB Molecule: lipolytic enzyme; PDBTitle: clostridium thermocellum family 3 carbohydrate esterase
34	d1fxwf_	Alignment	not modelled	99.9	13 Fold: Flavodoxin-like Superfamily: SGNH hydrolase Family: Acetylhydrolase
35	c2w9xA_	Alignment	not modelled	99.9	21 PDB header: hydrolase Chain: A: PDB Molecule: putative acetyl xylan esterase; PDBTitle: the active site of a carbohydrate esterase displays2 divergent3 catalytic and non-catalytic binding functions
36	c3x0hA_	Alignment	not modelled	99.9	16 PDB header: hydrolase Chain: A: PDB Molecule: carbohydrate esterase 1; PDBTitle: crystal structure of a carbohydrate esterase family 1 from talaromyces2 cellulolyticus
37	d3dc7a1	Alignment	not modelled	99.9	16 Fold: Flavodoxin-like Superfamily: SGNH hydrolase Family: BT2961-like
38	c5hoeB_	Alignment	not modelled	99.9	15 PDB header: hydrolase Chain: B: PDB Molecule: hydrolase; PDBTitle: crystal structure of est24, a carbohydrate acylesterase from2 sinorhizobium meliloti
39	c3dc7B_	Alignment	not modelled	99.9	16 PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative uncharacterized protein lp_3323; PDBTitle: crystal structure of the protein q88s8 from lactobacillus plantarum.2 northeast structural genomics consortium target lpr109.
40	c2waaA_	Alignment	not modelled	99.9	18 PDB header: hydrolase Chain: A: PDB Molecule: xylan esterase, putative, axe2c; PDBTitle: structure of a family two carbohydrate esterase from2 cellvibrio japonicus
41	c4c1bC_	Alignment	not modelled	99.9	22 PDB header: hydrolase Chain: C: PDB Molecule: orf1-encoded protein; PDBTitle: esterase domain of the zfl2-1 orf1 protein from the zebrafish zfl2-12 retrotransposon
42	c3dcib_	Alignment	not modelled	99.9	20 PDB header: hydrolase Chain: B: PDB Molecule: arylesterase; PDBTitle: the structure of a putative arylesterase from agrobacterium2 tumefaciens str. c58
43	c4xvhA_	Alignment	not modelled	99.9	23 PDB header: hydrolase Chain: A: PDB Molecule: carbohydrate esterase family 2 (ce2); PDBTitle: crystal structure of a corynascus thermopiles (myceliophthora2 fergusii) carbohydrate esterase family 2 (ce2) enzyme plus3 carbohydrate binding domain (cbd)
44	c4s1pA_	Alignment	not modelled	99.9	17 PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: shel_16390 protein, a putative sgnh hydrolase from slackia2 heliotrinireducens
45	c4devE_	Alignment	not modelled	99.9	20 PDB header: hydrolase Chain: E: PDB Molecule: acetyl-xylan esterase est2a; PDBTitle: an acetyl xylan esterase (est2a) from the rumen bacterium butyrivibrio2 proteoclasticus.
46	c2q0qC_	Alignment	not modelled	99.9	21 PDB header: hydrolase Chain: C: PDB Molecule: aryl esterase; PDBTitle: structure of the native m. smegmatis aryl esterase
47	c4tx1C_	Alignment	not modelled	99.9	19 PDB header: hydrolase Chain: C: PDB Molecule: esterase; PDBTitle: the crystal structure of carbohydrate acylesterase family member2 from sinorhizobium meliloti
48	c4m8kA_	Alignment	not modelled	99.9	18 PDB header: hydrolase Chain: A: PDB Molecule: hypothetical protein, gdsI-like lipase/acylhydrolase family PDBTitle: crystal structure of a putative gdsI-like lipase (bacuni_00748) from2 bacteroides uniformis atcc 8492 at 1.90 a resolution
49	c4k40B_	Alignment	not modelled	99.9	19 PDB header: hydrolase Chain: B: PDB Molecule: gdsI-like lipase/acylhydrolase family protein; PDBTitle: peptidoglycan o-acylesterase in action, 0 min
50	c4nrdA_	Alignment	not modelled	99.9	17 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative gdsI-like lipase (bacova_04955) from2 bacteroides ovatus atcc 8483 at 2.10 a resolution
51	c5ufyA_	Alignment	not modelled	99.9	18 PDB header: transferase Chain: A: PDB Molecule: acyltransferase; PDBTitle: structure of streptococcus pneumoniae peptidoglycan o-2 acetyltransferase a (oata) c-terminal catalytic domain
52	c5w78B_	Alignment	not modelled	99.7	18 PDB header: hydrolase Chain: B: PDB Molecule: acyloxyacyl hydrolase; PDBTitle: human acyloxyacyl hydrolase (aoah), proteolytically processed
53	c6jl1A_	Alignment	not modelled	99.7	22 PDB header: hydrolase Chain: A: PDB Molecule: thermolabile hemolysin; PDBTitle: crystal structure of vvpIpa g389d from vibrio vulnificus

54	c5w7dA	Alignment	not modelled	99.7	16	PDB header: hydrolase Chain: A: PDB Molecule: acyloxyacyl hydrolase; PDBTitle: murine acyloxyacyl hydrolase (aoah), s262a mutant
55	c5xtuA	Alignment	not modelled	99.6	19	PDB header: hydrolase Chain: A: PDB Molecule: gdsl-family esterase; PDBTitle: crystal structure of gdsl esterase of photobacterium sp. j15
56	c3kvnA	Alignment	not modelled	99.5	28	PDB header: hydrolase Chain: A: PDB Molecule: esterase esta; PDBTitle: crystal structure of the full-length autotransporter esta from2 pseudomonas aeruginosa
57	c4i8iA	Alignment	not modelled	98.5	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a duf4886 family protein (bacuni_01406) from2 bacteroides uniformis atcc 8492 at 1.50 a resolution
58	d2apia1	Alignment	not modelled	98.2	18	Fold: Flavodoxin-like Superfamily: SGNH hydrolase Family: Putative acetylxyylan esterase-like
59	c4qn1A	Alignment	not modelled	98.1	19	PDB header: hydrolase Chain: A: PDB Molecule: tail fiber protein; PDBTitle: crystal structure of tail fiber protein gp63.1 from e. coli phage g7c
60	c5a4aA	Alignment	not modelled	98.0	14	PDB header: rna binding protein Chain: A: PDB Molecule: maternal effect protein oskar; PDBTitle: crystal structure of the osk domain of drosophila oskar
61	c3pt5A	Alignment	not modelled	97.1	25	PDB header: hydrolase Chain: A: PDB Molecule: nans (vjhs), a 9-o-acetyl n-acetylneuraminic acid esterase; PDBTitle: crystal structure of nans
62	c3nvbA	Alignment	not modelled	96.5	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of n-terminal part of the protein bf1531 from2 bacteroides fragilis containing phosphatase domain complexed with mg3 and tungstate
63	d1zmba1	Alignment	not modelled	96.2	14	Fold: Flavodoxin-like Superfamily: SGNH hydrolase Family: Putative acetylxyylan esterase-like
64	c4kncA	Alignment	not modelled	94.0	10	PDB header: sugar binding protein Chain: A: PDB Molecule: alginate biosynthesis protein algx; PDBTitle: structural and functional characterization of pseudomonas aeruginosa2 algx
65	c4o8vA	Alignment	not modelled	92.7	13	PDB header: transferase Chain: A: PDB Molecule: alginate biosynthesis protein algj; PDBTitle: o-acetyltransferase domain of pseudomonas putida algj
66	d1uuuya	Alignment	not modelled	92.3	14	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
67	c2is8A	Alignment	not modelled	85.3	13	PDB header: structural protein Chain: A: PDB Molecule: molybdopterin biosynthesis enzyme, moab; PDBTitle: crystal structure of the molybdopterin biosynthesis enzyme moab2 (ttha0341) from thermus thermophilus hb8
68	c6pfxB	Alignment	not modelled	83.9	10	PDB header: transferase Chain: B: PDB Molecule: d-alanyl transferase dltD; PDBTitle: d-alanyl transferase dltD from enterococcus faecium
69	d1jjja	Alignment	not modelled	83.0	14	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
70	c6o93A	Alignment	not modelled	79.9	12	PDB header: transferase Chain: A: PDB Molecule: d-alanyl transferase dltD; PDBTitle: d-alanyl transferase dltD from enterococcus faecalis
71	c2g4rB	Alignment	not modelled	74.1	10	PDB header: biosynthetic protein Chain: B: PDB Molecule: molybdopterin biosynthesis mog protein; PDBTitle: anomalous substructure of moga
72	c3bmaC	Alignment	not modelled	72.3	9	PDB header: ligase Chain: C: PDB Molecule: d-alanyl-lipoteichoic acid synthetase; PDBTitle: crystal structure of d-alanyl-lipoteichoic acid synthetase from2 streptococcus pneumoniae r6
73	c3kbqA	Alignment	not modelled	70.2	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein ta0487; PDBTitle: the crystal structure of the protein cina with unknown function from2 thermoplasma acidophilum
74	c2qq1A	Alignment	not modelled	69.7	4	PDB header: structural protein Chain: A: PDB Molecule: molybdenum cofactor biosynthesis mog; PDBTitle: crystal structure of molybdenum cofactor biosynthesis2 (aq_061) other form from aquifex aeolicus vf5
75	d2f7wa1	Alignment	not modelled	68.3	6	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
76	d1d4oa	Alignment	not modelled	65.1	23	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Transhydrogenase domain III (dIII)
77	c1pt9B	Alignment	not modelled	65.1	23	PDB header: oxidoreductase Chain: B: PDB Molecule: nad(p) transhydrogenase, mitochondrial; PDBTitle: crystal structure analysis of the dii component of transhydrogenase2 with a thio-nicotinamide nucleotide analogue
78	d2g2ca1	Alignment	not modelled	65.1	14	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
79	c4ky3A	Alignment	not modelled	64.7	21	PDB header: de novo protein Chain: A: PDB Molecule: designed protein or327; PDBTitle: three-dimensional structure of the orthorhombic crystal of2 computationally designed insertion domain , northeast

						structural3 genomics consortium (nesg) target or327
80	c4o9uB_	Alignment	not modelled	62.1	24	PDB header: membrane protein Chain: B: PDB Molecule: nad(p) transhydrogenase subunit beta; PDBTitle: mechanism of transhydrogenase coupling proton translocation and2 hydride transfer
81	d1pnoa_	Alignment	not modelled	62.0	21	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Transhydrogenase domain III (dIII)
82	c3rfqC_	Alignment	not modelled	61.6	24	PDB header: biosynthetic protein Chain: C: PDB Molecule: pterin-4-alpha-carbinolamine dehydratase moab2; PDBTitle: crystal structure of pterin-4-alpha-carbinolamine dehydratase moab22 from mycobacterium marinum
83	c5a7mA_	Alignment	not modelled	60.1	14	PDB header: hydrolase Chain: A: PDB Molecule: beta-xylosidase; PDBTitle: the structure of hypocrea jecorina beta-xylosidase xyl3a (bx1)
84	d1mkza_	Alignment	not modelled	58.5	17	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
85	c5hosA_	Alignment	not modelled	56.4	13	PDB header: hydrolase Chain: A: PDB Molecule: cellulase; PDBTitle: crystal structure of the endo-beta-1,4-glucanase xac0029 from2 xanthomonas axonopodis pv. citri
86	c3lp6D_	Alignment	not modelled	56.3	23	PDB header: lyase Chain: D: PDB Molecule: phosphoribosylaminoimidazole carboxylase catalytic subunit; PDBTitle: crystal structure of rv3275c-e60a from mycobacterium tuberculosis at2 1.7a resolution
87	c2pjka_	Alignment	not modelled	55.9	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: 178aa long hypothetical molybdenum cofactor PDBTitle: structure of hypothetical molybdenum cofactor biosynthesis2 protein b from sulfolobus tokodaii
88	c2cg8B_	Alignment	not modelled	55.3	20	PDB header: lyase/transferase Chain: B: PDB Molecule: dihydroneopterin aldolase 6-hydroxymethyl-7,8- PDBTitle: the bifunctional dihydroneopterin aldolase 6-hydroxymethyl-2 7,8-dihydropterin synthase from streptococcus pneumoniae
89	d1h6za1	Alignment	not modelled	54.0	23	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate phosphate dikinase, C-terminal domain
90	c5v8eB_	Alignment	not modelled	52.9	15	PDB header: unknown function Chain: B: PDB Molecule: bacillus cereus patb1; PDBTitle: structure of bacillus cereus patb1
91	c4grdA_	Alignment	not modelled	52.7	20	PDB header: lyase,isomerase Chain: A: PDB Molecule: phosphoribosylaminoimidazole carboxylase catalytic subunit; PDBTitle: crystal structure of phosphoribosylaminoimidazole carboxylase2 catalytic subunit from burkholderia cenocepacia j2315
92	c4wb1B_	Alignment	not modelled	52.6	20	PDB header: oxidoreductase Chain: B: PDB Molecule: cals8; PDBTitle: crystal structure of cals8 from micromonospora echinospora (p294s2 mutant)
93	d1y5ea1	Alignment	not modelled	52.2	15	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
94	c6r62A_	Alignment	not modelled	52.0	16	PDB header: lyase Chain: A: PDB Molecule: hpch/hpai aldolase; PDBTitle: crystal structure of a class ii pyruvate aldolase from sphingomonas2 wittichii rw1 in complex with hydroxypyruvate
95	c5f56A_	Alignment	not modelled	48.8	17	PDB header: dna binding protein/dna Chain: A: PDB Molecule: single-stranded-dna-specific exonuclease; PDBTitle: structure of recj complexed with dna and ssb-ct
96	c2bg5C_	Alignment	not modelled	47.3	13	PDB header: transferase Chain: C: PDB Molecule: phosphoenolpyruvate-protein kinase; PDBTitle: crystal structure of the phosphoenolpyruvate-binding enzyme i-domain2 from the thermoanaerobacter tengcongensis pep: sugar3 phosphotransferase system (pts)
97	c3qz6A_	Alignment	not modelled	44.9	15	PDB header: lyase Chain: A: PDB Molecule: hpch/hpai aldolase; PDBTitle: the crystal structure of hpch/hpai aldolase from desulfibacterium2 hafniense dcb-2
98	c4mf4F_	Alignment	not modelled	43.7	18	PDB header: lyase Chain: F: PDB Molecule: hpch/hpai aldolase/citrate lyase family protein; PDBTitle: crystal structure of a hpch/hpai aldolase/citrate lyase family protein2 from burkholderia cenocepacia j2315
99	c4b4kK_	Alignment	not modelled	42.0	23	PDB header: isomerase Chain: K: PDB Molecule: n5-carboxyaminoimidazole ribonucleotide mutase; PDBTitle: crystal structure of bacillus anthracis pure
100	d1xmpa_	Alignment	not modelled	41.6	23	Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
101	c2fw9A_	Alignment	not modelled	41.6	31	PDB header: lyase Chain: A: PDB Molecule: n5-carboxyaminoimidazole ribonucleotide mutase; PDBTitle: structure of pure (n5-carboxyaminoimidazole ribonucleotide mutase)2 h59f from the acidophilic bacterium acetobacter aceti, at ph 8
102	d1u11a_	Alignment	not modelled	41.3	31	Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)

103	c2ohoA_	Alignment	not modelled	38.6	17	PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase; PDBTitle: structural basis for glutamate racemase inhibitor
104	c3q9cF_	Alignment	not modelled	38.6	14	PDB header: hydrolase Chain: F: PDB Molecule: acetylpolyamine amidohydrolase; PDBTitle: crystal structure of h159a apah complexed with n8-acetylspermidine
105	c4uuwA_	Alignment	not modelled	37.2	11	PDB header: biosynthetic protein Chain: A: PDB Molecule: cina-like protein; PDBTitle: competence or damage-inducible protein cina from thermus thermophilus
106	d1o4va_	Alignment	not modelled	35.1	23	Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
107	c5yotB_	Alignment	not modelled	35.1	15	PDB header: hydrolase Chain: B: PDB Molecule: isoprimeverose-producing enzyme; PDBTitle: isoprimeverose-producing enzyme from aspergillus oryzae in complex2 with isoprimeverose
108	c4b5sB_	Alignment	not modelled	34.4	11	PDB header: lyase Chain: B: PDB Molecule: 4-hydroxy-2-oxo-heptane-1,7-dioate aldolase; PDBTitle: crystal structures of divalent metal dependent pyruvate aldolase,2 hpa1, in complex with pyruvate
109	c2hwgA_	Alignment	not modelled	34.3	15	PDB header: transferase Chain: A: PDB Molecule: phosphoenolpyruvate-protein phosphotransferase; PDBTitle: structure of phosphorylated enzyme i of the phosphoenolpyruvate:sugar2 phosphotransferase system
110	c2vwtA_	Alignment	not modelled	33.9	18	PDB header: lyase Chain: A: PDB Molecule: yfau, 2-keto-3-deoxy sugar aldolase; PDBTitle: crystal structure of yfau, a metal ion dependent class ii2 aldolase from escherichia coli k12 - mg-pyruvate product3 complex
111	c4w7wA_	Alignment	not modelled	33.2	12	PDB header: hydrolase Chain: A: PDB Molecule: cellulase; PDBTitle: high-resolution structure of xaccl5a in complex with cellopentaose
112	d1iuka_	Alignment	not modelled	31.8	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
113	d1dxea_	Alignment	not modelled	31.7	15	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: HpcH/Hpal aldolase
114	c2hroA_	Alignment	not modelled	31.5	15	PDB header: transferase Chain: A: PDB Molecule: phosphoenolpyruvate-protein phosphotransferase; PDBTitle: structure of the full-lenght enzyme i of the pts system from2 staphylococcus carnosus
115	c3menC_	Alignment	not modelled	31.0	16	PDB header: hydrolase Chain: C: PDB Molecule: acetylpolyamine aminohydrolase; PDBTitle: crystal structure of acetylpolyamine aminohydrolase from burkholderia2 pseudomallei, iodide soak
116	c2v5jB_	Alignment	not modelled	29.9	9	PDB header: lyase Chain: B: PDB Molecule: 2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase; PDBTitle: apo class ii aldolase hpcH
117	c1h6zA_	Alignment	not modelled	29.6	23	PDB header: transferase Chain: A: PDB Molecule: pyruvate phosphate dikinase; PDBTitle: 3.0 a resolution crystal structure of glycosomal pyruvate2 phosphate dikinase from trypanosoma brucei
118	d2jdia3	Alignment	not modelled	29.6	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
119	d1vbqa1	Alignment	not modelled	29.2	24	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate phosphate dikinase, C-terminal domain
120	c3g23A_	Alignment	not modelled	28.7	7	PDB header: hydrolase Chain: A: PDB Molecule: ld-carboxypeptidase a; PDBTitle: crystal structure of a ld-carboxypeptidase a (saro_1426) from2 novosphingobium aromaticivorans dsm at 1.89 a resolution