

















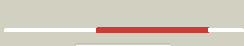








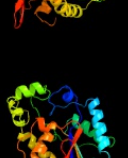


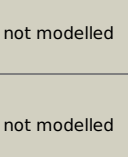


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2228c (-) _2501652_2502746
Date	Mon Aug 5 13:25:36 BST 2019
Unique Job ID	c4592d453b65d944

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4ij5B_	 Alignment		100.0	32	PDB header: hydrolase Chain: B; PDB Molecule: phosphoserine phosphatase 1; PDBTitle: crystal structure of a novel-type phosphoserine phosphatase from <i>hydrogenobacter thermophilus</i> tk-6
2	d1h2ea_	 Alignment		100.0	29	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
3	c4embD_	 Alignment		100.0	24	PDB header: isomerase Chain: D; PDB Molecule: 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase; PDBTitle: crystal structure of a phosphoglycerate mutase gpmA from <i>borrelia burgdorferi</i> b31
4	c4pz9B_	 Alignment		100.0	34	PDB header: hydrolase Chain: B; PDB Molecule: glucosyl-3-phosphoglycerate phosphatase; PDBTitle: the native structure of mycobacterial glucosyl-3-phosphoglycerate 2 phosphatase rv2419c
5	c5zkkA_	 Alignment		100.0	26	PDB header: hydrolase Chain: A; PDB Molecule: phosphoglycerate mutase family protein, putative; PDBTitle: crystal structure of phosphoserine phosphatase from <i>entamoeba histolytica</i>
6	d1e58a_	 Alignment		100.0	25	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
7	c1vjxD_	 Alignment		100.0	24	PDB header: isomerase, hydrolase Chain: D; PDB Molecule: phosphoglycerate mutase 1; PDBTitle: crystal structure of human b type phosphoglycerate mutase
8	d1fzta_	 Alignment		100.0	23	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
9	c6e4bC_	 Alignment		100.0	26	PDB header: hydrolase Chain: C; PDB Molecule: adenosylcobalamin/alpha-ribazole phosphatase; PDBTitle: the crystal structure of a putative alpha-ribazole-5'-p phosphatase2 from <i>escherichia coli</i> str. k-12 substr. mg1655
10	c2a6pA_	 Alignment		100.0	29	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: possible phosphoglycerate mutase gpm2; PDBTitle: structure solution to 2.2 angstrom and functional characterisation of the open reading frame rv3214 from <i>mycobacterium tuberculosis</i>
11	d1xq9a_	 Alignment		100.0	24	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase

12	c5vveA_	Alignment		100.0	25	PDB header: isomerase Chain: A: PDB Molecule: phosphoglycerate mutase; PDBTitle: crystal structure of phosphoglycerate mutase from naegleria fowleri
13	c2yn0A_	Alignment		100.0	19	PDB header: transcription Chain: A: PDB Molecule: transcription factor tau 55 kda subunit; PDBTitle: tau55 histidine phosphatase domain
14	d1qhfa_	Alignment		100.0	24	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
15	c3ll4B_	Alignment		100.0	22	PDB header: hydrolase Chain: B: PDB Molecule: uncharacterized protein ykr043c; PDBTitle: structure of the h13a mutant of ykr043c in complex with fructose-1,6-2 bisphosphate
16	d1riia_	Alignment		100.0	27	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
17	c2yn2A_	Alignment		100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein ynl108c; PDBTitle: huf protein - paralogue of the tau55 histidine phosphatase domain
18	c3r7aA_	Alignment		100.0	23	PDB header: transferase Chain: A: PDB Molecule: phosphoglycerate mutase, putative; PDBTitle: crystal structure of phosphoglycerate mutase from bacillus anthracis2 str. sterne
19	c3f3ka_	Alignment		100.0	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein ykr043c; PDBTitle: the structure of uncharacterized protein ykr043c from saccharomyces2 cerevisiae.
20	c3dcyA_	Alignment		100.0	27	PDB header: apoptosis regulator Chain: A: PDB Molecule: regulator protein; PDBTitle: crystal structure a tp53-induced glycolysis and apoptosis regulator2 protein from homo sapiens.
21	c2ilvB_	Alignment	not modelled	100.0	28	PDB header: transferase, hydrolase Chain: B: PDB Molecule: 6-phosphofructo-2-kinase/fructose-2,6-fructose-2,6-bisphosphate PDBTitle: crystal structure of pfkfb3 in complex with adp and2 fructose-2,6-bisphosphate
22	c5um0A_	Alignment	not modelled	100.0	23	PDB header: isomerase Chain: A: PDB Molecule: 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase; PDBTitle: crystal structure of 2,3-bisphosphoglycerate-dependent2 phosphoglycerate mutase from neisseria gonorrhoeae
23	c3eznB_	Alignment	not modelled	100.0	23	PDB header: isomerase Chain: B: PDB Molecule: 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase; PDBTitle: crystal structure of phosphoglyceromutase from burkholderia2 pseudomallei 1710b
24	c1k6mA_	Alignment	not modelled	100.0	30	PDB header: transferase, hydrolase Chain: A: PDB Molecule: 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2- PDBTitle: crystal structure of human liver 6-phosphofructo-2-kinase/fructose-2,2,6-bisphosphatase
25	c3e9eB_	Alignment	not modelled	100.0	25	PDB header: hydrolase Chain: B: PDB Molecule: zgc:56074; PDBTitle: structure of full-length h11a mutant form of tigar from danio rerio
26	d1bifa2	Alignment	not modelled	100.0	27	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
27	d2hhja1	Alignment	not modelled	100.0	23	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
						PDB header: bifunctional enzyme Chain: A: PDB Molecule: 6-phosphofructo-2-kinase/ fructose-2,6-

28	c1bifA_	Alignment	not modelled	100.0	28	bisphosphatase; PDBTitle: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase bifunctional2 enzyme complexed with atp-g-s and phosphate
29	d3pgma_	Alignment	not modelled	100.0	24	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
30	c3d8hB_	Alignment	not modelled	100.0	25	PDB header: isomerase Chain: B: PDB Molecule: glycolytic phosphoglycerate mutase; PDBTitle: crystal structure of phosphoglycerate mutase from cryptosporidium2 parvum, cgd7_4270
31	c4eo9A_	Alignment	not modelled	100.0	26	PDB header: isomerase Chain: A: PDB Molecule: 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase; PDBTitle: crystal structure of a phosphoglycerate mutase gpm1 from mycobacterium2 leprae
32	d1k6ma2	Alignment	not modelled	100.0	28	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
33	c3h9gB_	Alignment	not modelled	100.0	26	PDB header: hydrolase Chain: B: PDB Molecule: putative alpha-ribazole-5'-phosphate phosphatase cobc; PDBTitle: crystal structure of putative alpha-ribazole-5'-phosphate phosphatase2 cobc from vibrio parahaemolyticus
34	c3mxoB_	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: B: PDB Molecule: serine/threonine-protein phosphatase pgam5, mitochondrial; PDBTitle: crystal structure of human phosphoglycerate mutase family member 52 (pgam5)
35	d1tipa_	Alignment	not modelled	100.0	28	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
36	c3d4iD_	Alignment	not modelled	100.0	25	PDB header: hydrolase Chain: D: PDB Molecule: sts-2 protein; PDBTitle: crystal structure of the 2h-phosphatase domain of sts-2
37	c2ikqA_	Alignment	not modelled	100.0	19	PDB header: signaling protein, immune system Chain: A: PDB Molecule: suppressor of t-cell receptor signaling 1; PDBTitle: crystal structure of mouse sts-1 pgm domain in complex with phosphate
38	c2qniA_	Alignment	not modelled	100.0	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein atu0299; PDBTitle: crystal structure of uncharacterized protein atu0299
39	d1v37a_	Alignment	not modelled	100.0	29	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
40	c3c7tB_	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: B: PDB Molecule: ecdysteroid-phosphate phosphatase; PDBTitle: crystal structure of the ecdysone phosphate phosphatase, eppase, from2 bombix mori in complex with tungstate
41	c3hstD_	Alignment	not modelled	100.0	100	PDB header: hydrolase Chain: D: PDB Molecule: protein rv2228c/mt2287; PDBTitle: n-terminal rnaase h domain of rv2228c from mycobacterium tuberculosis2 as a fusion protein with maltose binding protein
42	c3eozB_	Alignment	not modelled	100.0	20	PDB header: isomerase Chain: B: PDB Molecule: putative phosphoglycerate mutase; PDBTitle: crystal structure of phosphoglycerate mutase from plasmodium2 falciparum, pfd0660w
43	c1ujcA_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: phosphohistidine phosphatase sixa; PDBTitle: structure of the protein histidine phosphatase sixa2 complexed with tungstate
44	c4e19A_	Alignment	not modelled	100.0	44	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease h1; PDBTitle: crystal structure of rnaase h1 from halophilic archaeon halobacterium2 salinarum nrc-1
45	c3u3gA_	Alignment	not modelled	100.0	43	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease h; PDBTitle: structure of lc11-rnaase h1 isolated from compost by metagenomic2 approach: insight into the structural bases for unusual enzymatic3 properties of sto-rnaase h1
46	c2ehgA_	Alignment	not modelled	100.0	33	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease hi; PDBTitle: crystal structure of hyperthermophilic archaeal rnaase hi
47	c4ibnA_	Alignment	not modelled	100.0	26	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease h; PDBTitle: crystal structure of lc9-rnaase h1, a type 1 rnaase h with the type 22 active-site motif
48	c2rfiB_	Alignment	not modelled	100.0	25	PDB header: hydrolase, isomerase Chain: B: PDB Molecule: putative phosphohistidine phosphatase sixa; PDBTitle: crystal structure of the putative phosphohistidine phosphatase sixa2 from agrobacterium tumefaciens
49	c5gg7A_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: hydrolase, nudix family protein; PDBTitle: crystal structure of mycobacterium smegmatis mutt1 in complex with 8-2 oxo-dgtp, 8-oxo-dgmp and pyrophosphate (i)
50	c3f2iD_	Alignment	not modelled	99.9	19	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: alr0221 protein; PDBTitle: crystal structure of the alr0221 protein from nostoc, northeast2 structural genomics consortium target nsr422.
51	c2hb5A_	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: A: PDB Molecule: reverse transcriptase/ribonuclease h; PDBTitle: crystal structure of the moloney murine leukemia virus rnaase h domain
52	c3fjyB_	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: B: PDB Molecule: probable mutt1 protein; PDBTitle: crystal structure of a probable mutt1 protein from

						bifidobacterium2 adolescentis PDB header: hydrolase Chain: B: PDB Molecule: rnh (ribonuclease h); PDBTitle: crystal structure of the ribonuclease h1 from chlorobium2 tepidum
53	c3h08B_	Alignment	not modelled	99.9	30	PDB header: viral protein Chain: A: PDB Molecule: rnase h; PDBTitle: solution structure of pfv rnase h domain
54	c2lsnA_	Alignment	not modelled	99.9	26	PDB header: hydrolase/dna/rna Chain: I: PDB Molecule: ribonuclease h1; PDBTitle: human rnase h catalytic domain mutant d210n in complex with2 14-mer rna/dna hybrid
55	c2qkkI_	Alignment	not modelled	99.9	22	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
56	d1jl2a_	Alignment	not modelled	99.9	31	PDB header: transferase, hydrolase/translation Chain: A: PDB Molecule: reverse transcriptase/ribonuclease h p80; PDBTitle: crystal structure of mouse erf1 in complex with reverse transcriptase2 (rt) of moloney murine leukemia virus
57	c5dmqA_	Alignment	not modelled	99.9	21	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
58	d1jl1a_	Alignment	not modelled	99.9	30	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
59	d1wsib_	Alignment	not modelled	99.9	27	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
60	c4hbzA_	Alignment	not modelled	99.9	22	PDB header: hydrolase, isomerase Chain: A: PDB Molecule: putative phosphohistidine phosphatase, sixa; PDBTitle: the structure of putative phosphohistidine phosphatase sixa from2 nakamurella multipartitia.
61	d1rila_	Alignment	not modelled	99.9	27	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
62	c2e4IA_	Alignment	not modelled	99.9	26	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease hi; PDBTitle: thermodynamic and structural analysis of thermolabile rnase hi from2 shewanella oneidensis mr-1
63	d1eeta1	Alignment	not modelled	99.9	16	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
64	d1mu2a1	Alignment	not modelled	99.9	18	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
65	c2kq2A_	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease h-related protein; PDBTitle: solution nmr structure of the apo form of a ribonuclease h2 domain of protein dsy1790 from desulfitobacterium3 hafniense, northeast structural genomics target dhr1a
66	d1jlaa1	Alignment	not modelled	99.9	18	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
67	d1zbfa1	Alignment	not modelled	99.9	20	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
68	c1mu2A_	Alignment	not modelled	99.9	18	PDB header: transferase Chain: A: PDB Molecule: hiv-2 rt; PDBTitle: crystal structure of hiv-2 reverse transcriptase
69	d1s9ga1	Alignment	not modelled	99.9	16	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
70	d1o1wa_	Alignment	not modelled	99.8	16	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
71	d1s1ta1	Alignment	not modelled	99.8	17	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
72	c2rpiA_	Alignment	not modelled	99.7	32	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease h; PDBTitle: the nmr structure of the submillisecond folding2 intermediate of the thermus thermophilus ribonuclease h
73	c1rthA_	Alignment	not modelled	99.7	18	PDB header: nucleotidyltransferase Chain: A: PDB Molecule: hiv-1 reverse transcriptase; PDBTitle: high resolution structures of hiv-1 rt from four rt-2 inhibitor complexes
74	c5ovnA_	Alignment	not modelled	99.6	22	PDB header: viral protein Chain: A: PDB Molecule: pol protein; PDBTitle: crystal structure of fiv reverse transcriptase
75	c2opqA_	Alignment	not modelled	99.4	22	PDB header: transferase Chain: A: PDB Molecule: reverse transcriptase/ribonuclease h; PDBTitle: crystal structure of I100i mutant hiv-1 reverse transcriptase in2 complex with gw420867x.
76	c4ol8B_	Alignment	not modelled	98.7	10	PDB header: transferase, hydrolase/rna/dna Chain: B: PDB Molecule: reverse transcriptase/ribonuclease h; PDBTitle: ty3 reverse transcriptase bound to dna/rna
77	c4jodA_	Alignment	not modelled	98.0	21	PDB header: hydrolase Chain: A: PDB Molecule: lysophosphatidic acid phosphatase type 6; PDBTitle: crystal structure of human lysophosphatidic acid phosphatase type 62 complexed with tris
78	c2glcA_	Alignment	not modelled	98.0	22	PDB header: hydrolase Chain: A: PDB Molecule: histidine acid phosphatase; PDBTitle: structure of francisella tularensis histidine acid phosphatase bound2 to orthovanadate

79	d1rpaa_	Alignment	not modelled	97.9	29	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Histidine acid phosphatase
80	d1nd6a_	Alignment	not modelled	97.7	26	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Histidine acid phosphatase
81	d1ihpa_	Alignment	not modelled	97.7	18	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Histidine acid phosphatase
82	c5cdhE_	Alignment	not modelled	97.7	22	PDB header: hydrolase/hydrolase inhibitor Chain: E: PDB Molecule: major acid phosphatase; PDBTitle: structure of legionella pneumophila histidine acid phosphatase2 complexed with l(+)-tartrate
83	c4arvB_	Alignment	not modelled	97.7	21	PDB header: hydrolase Chain: B: PDB Molecule: phytase; PDBTitle: yersinia kristensenii phytase apo form
84	d1qwoa_	Alignment	not modelled	97.7	13	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Histidine acid phosphatase
85	c4fdtB_	Alignment	not modelled	97.6	22	PDB header: hydrolase Chain: B: PDB Molecule: putative multiple inositol polyphosphate histidine PDBTitle: crystal structure of a multiple inositol polyphosphate phosphatase
86	c3zhcB_	Alignment	not modelled	97.6	22	PDB header: hydrolase Chain: B: PDB Molecule: phytase; PDBTitle: structure of the phytase from citrobacter braakii at 2.3 angstrom2 resolution.
87	c2wniC_	Alignment	not modelled	97.5	25	PDB header: hydrolase Chain: C: PDB Molecule: 3-phytase; PDBTitle: crystal structure analysis of klebsiella sp asr1 phytase
88	d1dkla_	Alignment	not modelled	97.4	19	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Histidine acid phosphatase
89	d1nt4a_	Alignment	not modelled	97.4	18	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Histidine acid phosphatase
90	c4aruA_	Alignment	not modelled	97.4	19	PDB header: hydrolase Chain: A: PDB Molecule: histidine acid phosphatase; PDBTitle: hafnia alvei phytase in complex with tartrate
91	d1qfxa_	Alignment	not modelled	97.3	14	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Histidine acid phosphatase
92	c2gfiB_	Alignment	not modelled	96.9	21	PDB header: hydrolase Chain: B: PDB Molecule: phytase; PDBTitle: crystal structure of the phytase from d. castellii at 2.3 a
93	c4ol8A_	Alignment	not modelled	93.0	15	PDB header: transferase, hydrolase/rna/dna Chain: A: PDB Molecule: reverse transcriptase/ribonuclease h; PDBTitle: ty3 reverse transcriptase bound to dna/rna
94	c3kk1B_	Alignment	not modelled	72.9	15	PDB header: transferase/dna Chain: B: PDB Molecule: reverse transcriptase p51 subunit; PDBTitle: hiv-1 reverse transcriptase-dna complex with nucleotide inhibitor gs-2 9148-diphosphate bound in nucleotide site
95	c3uuuA_	Alignment	not modelled	72.3	12	PDB header: hydrolase Chain: A: PDB Molecule: lip1, secretory lipase (family 3); PDBTitle: crystal structure of mono- and diacylglycerol lipase from malassezia2 globosa
96	c5gw8A_	Alignment	not modelled	65.4	16	PDB header: hydrolase Chain: A: PDB Molecule: hypothetical secretory lipase (family 3); PDBTitle: crystal structure of a putative dag-like lipase (mgmdl2) from2 malassezia globosa
97	d1rw3a_	Alignment	not modelled	62.9	13	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: Reverse transcriptase
98	c5xk2A_	Alignment	not modelled	58.7	21	PDB header: hydrolase Chain: A: PDB Molecule: diacylglycerol lipase; PDBTitle: crystal structure of mono- and diacylglycerol lipase from aspergillus2 oryzae
99	c4ioxB_	Alignment	not modelled	55.2	21	PDB header: viral protein Chain: B: PDB Molecule: tripartite terminase subunit ul15; PDBTitle: the structure of the herpes simplex virus dna-packaging motor pul15 c-2 terminal nuclease domain provides insights into cleavage of3 concatemeric viral genome precursors
100	c3o0dF_	Alignment	not modelled	54.3	17	PDB header: hydrolase Chain: F: PDB Molecule: triacylglycerol lipase; PDBTitle: crystal structure of lip2 lipase from yarrowia lipolytica at 1.7 a2 resolution
101	d1tiba_	Alignment	not modelled	52.4	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
102	d1tiaa_	Alignment	not modelled	51.9	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
103	c3ngmB_	Alignment	not modelled	49.8	12	PDB header: hydrolase Chain: B: PDB Molecule: extracellular lipase; PDBTitle: crystal structure of lipase from gibberella zeae
104	c3g7nA_	Alignment	not modelled	33.3	20	PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: crystal structure of a triacylglycerol lipase from penicillium2 expansum at 1.3
105	d3tgla_	Alignment	not modelled	32.6	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases

106	dluwca_	Alignment	not modelled	31.1	17	Family: Fungal lipases Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
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