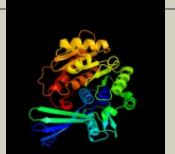
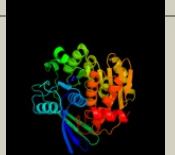
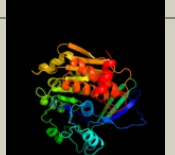
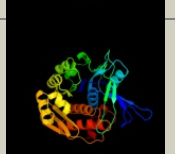
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P0A9J6
Date	Thu Jan 5 11:10:28 GMT 2012
Unique Job ID	4746256fc891f5e5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1rkda_	Alignment		100.0	100	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
2	c3kzhA_	Alignment		100.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable sugar kinase; **PDBTitle:** crystal structure of a putative sugar kinase from2 clostridium perfringens
3	d2fv7a1	Alignment		100.0	36	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
4	c3go6B_	Alignment		100.0	37	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ribokinase rbsk; **PDBTitle:** crystal structure of m. tuberculosis ribokinase (rv2436) in2 complex with ribose and amp-pnp
5	d1vm7a_	Alignment		100.0	39	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
6	c2rbcA_	Alignment		100.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sugar kinase; **PDBTitle:** crystal structure of a putative ribokinase from agrobacterium2 tumefaciens
7	c2c49A_	Alignment		100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sugar kinase mj0406; **PDBTitle:** crystal structure of methanocaldococcus jannaschii2 nucleoside kinase - an archaeal member of the ribokinase3 family
8	c3pl2D_	Alignment		100.0	25	**PDB header:**transferase **Chain:** D: **PDB Molecule:**sugar kinase, ribokinase family; **PDBTitle:** crystal structure of a 5-keto-2-deoxygluconokinase (ncgl0155, cgl0158)2 from corynebacterium glutamicum atcc 13032 kitasato at 1.89 a3 resolution
9	c2nwhA_	Alignment		100.0	26	**PDB header:**signaling protein,transferase **Chain:** A: **PDB Molecule:**carbohydrate kinase; **PDBTitle:** carbohydrate kinase from agrobacterium tumefaciens
10	c3i3yB_	Alignment		100.0	31	**PDB header:**transferase **Chain:** B: **PDB Molecule:**carbohydrate kinase; **PDBTitle:** crystal structure of ribokinase in complex with d-ribose from2 klebsiella pneumoniae
11	c2pkkA_	Alignment		100.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenosine kinase; **PDBTitle:** crystal structure of m tuberculosis adenosine kinase complexed with 2-2 fluro adenosine

12	c3iq0B_	Alignment		100.0	26	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative ribokinase ii; **PDBTitle:** crystal structure of a putative ribokinase ii in complex2 with atp and mg+2 from e.coli
13	c3in1A_	Alignment		100.0	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uncharacterized sugar kinase ydjh; **PDBTitle:** crystal structure of a putative ribokinase in complex with2 adp from e.coli
14	c3cqdB_	Alignment		100.0	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**6-phosphofructokinase isozyme 2; **PDBTitle:** structure of the tetrameric inhibited form of2 phosphofructokinase-2 from escherichia coli
15	c3b1qD_	Alignment		100.0	18	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ribokinase, putative; **PDBTitle:** structure of burkholderia thailandensis nucleoside kinase (bthnk) in2 complex with inosine
16	d1v19a_	Alignment		100.0	26	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
17	c2qcvA_	Alignment		100.0	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative 5-dehydro-2-deoxygluconokinase; **PDBTitle:** crystal structure of a putative 5-dehydro-2-deoxygluconokinase (iolc)2 from bacillus halodurans c-125 at 1.90 a resolution
18	d2abqa1	Alignment		100.0	22	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
19	c2varB_	Alignment		100.0	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**fructokinase; **PDBTitle:** crystal structure of sulfolobus solfataricus 2-keto-3-2 deoxygluconate kinase complexed with 2-keto-3-3 deoxygluconate
20	d2dcna1	Alignment		100.0	22	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
21	c2jg1C_	Alignment	not modelled	100.0	15	**PDB header:**transferase **Chain:** C: **PDB Molecule:**tagatose-6-phosphate kinase; **PDBTitle:** structure of staphylococcus aureus d-tagatose-6-phosphate2 kinase with cofactor and substrate
22	c2jg5B_	Alignment	not modelled	100.0	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**fructose 1-phosphate kinase; **PDBTitle:** crystal structure of a putative phosphofructokinase from2 staphylococcus aureus
23	c2xtbA_	Alignment	not modelled	100.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenosine kinase; **PDBTitle:** crystal structure of trypanosoma brucei rhodesiense2 adenosine kinase complexed with activator
24	d2f02a1	Alignment	not modelled	100.0	19	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
25	d1bx4a_	Alignment	not modelled	100.0	26	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
26	c3looC_	Alignment	not modelled	100.0	22	**PDB header:**transferase **Chain:** C: **PDB Molecule:**anopheles gambiae adenosine kinase; **PDBTitle:** crystal structure of anopheles gambiae adenosine kinase in complex2 with p1,p4-di(adenosine-5) tetraphosphate
27	c3ktnA_	Alignment	not modelled	100.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**carbohydrate kinase, pfkb family; **PDBTitle:** crystal structure of a putative 2-keto-3-deoxygluconate2 kinase from enterococcus faecalis
28	d2afba1	Alignment	not modelled	100.0	24	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
						PDB header:transferase

29	c3gbuD_	Alignment	not modelled	100.0	25	**Chain:** D: **PDB Molecule:**uncharacterized sugar kinase ph1459; **PDBTitle:** crystal structure of an uncharacterized sugar kinase ph1459 from2 pyrococcus horikoshii in complex with atp
30	c3b3lC_	Alignment	not modelled	100.0	19	**PDB header:**transferase **Chain:** C: **PDB Molecule:**ketohexokinase; **PDBTitle:** crystal structures of alternatively-spliced isoforms of human2 ketohexokinase
31	d1tyya_	Alignment	not modelled	100.0	29	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
32	c2absA_	Alignment	not modelled	100.0	21	**PDB header:**signaling protein,transferase **Chain:** A: **PDB Molecule:**adenosine kinase; **PDBTitle:** crystal structure of t. gondii adenosine kinase complexed2 with amp-pcp
33	d2absa1	Alignment	not modelled	100.0	21	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
34	c3julA_	Alignment	not modelled	100.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lin2199 protein; **PDBTitle:** crystal structure of listeria innocua d-tagatose-6-phosphate2 kinase bound with substrate
35	d2ajra1	Alignment	not modelled	100.0	16	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
36	c3lkiA_	Alignment	not modelled	100.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**fructokinase; **PDBTitle:** crystal structure of fructokinase with bound atp from2 xylella fastidiosa
37	c1tz6B_	Alignment	not modelled	100.0	30	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative sugar kinase; **PDBTitle:** crystal structure of aminoimidazole riboside kinase from2 salmonella enterica complexed with aminoimidazole riboside3 and atp analog
38	c3kd6B_	Alignment	not modelled	100.0	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**carbohydrate kinase, pfkb family; **PDBTitle:** crystal structure of nucleoside kinase from chlorobium tepidum in2 complex with amp
39	c3bf5A_	Alignment	not modelled	100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribokinase related protein; **PDBTitle:** crystal structure of putative ribokinase (10640157) from thermoplasma2 acidophilum at 1.91 a resolution
40	c2qhpA_	Alignment	not modelled	100.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**fructokinase; **PDBTitle:** crystal structure of fructokinase (np_810670.1) from bacteroides2 thetaiotaomicron vpi-5482 at 1.80 a resolution
41	c3lhxA_	Alignment	not modelled	100.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ketodeoxygluconokinase; **PDBTitle:** crystal structure of a ketodeoxygluconokinase (kdgk) from2 shigella flexneri
42	c3hj6B_	Alignment	not modelled	100.0	24	**PDB header:**transferase **Chain:** B: **PDB Molecule:**fructokinase; **PDBTitle:** structure of halothermothrix orenii fructokinase (frk)
43	d1vk4a_	Alignment	not modelled	100.0	17	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
44	c2ddmA_	Alignment	not modelled	99.9	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyridoxine kinase; **PDBTitle:** crystal structure of pyridoxal kinase from the escherichia2 coli pdxk gene at 2.1 a resolution
45	d1vi9a_	Alignment	not modelled	99.7	25	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**PfkB-like kinase
46	c2i5bC_	Alignment	not modelled	99.7	21	**PDB header:**transferase **Chain:** C: **PDB Molecule:**phosphomethylpyrimidine kinase; **PDBTitle:** the crystal structure of an adp complex of bacillus2 subtilis pyridoxal kinase provides evidence for the3 parralel emergence of enzyme activity during evolution
47	c3mbjA_	Alignment	not modelled	99.6	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative phosphomethylpyrimidine kinase; **PDBTitle:** crystal structure of a putative phosphomethylpyrimidine kinase2 (bt_4458) from bacteroides thetaiotaomicron vpi-5482 at 2.10 a3 resolution (rhombohedral form)
48	d1ub0a_	Alignment	not modelled	99.6	28	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Thiamin biosynthesis kinases
49	c3ibqA_	Alignment	not modelled	99.6	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyridoxal kinase; **PDBTitle:** crystal structure of pyridoxal kinase from lactobacillus2 plantarum in complex with atp
50	d1lhpa_	Alignment	not modelled	99.6	23	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**PfkB-like kinase
51	d1jxha_	Alignment	not modelled	99.4	23	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Thiamin biosynthesis kinases
52	c3rm5B_	Alignment	not modelled	99.3	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**hydroxymethylpyrimidine/phosphomethylpyrimidine kinase **PDBTitle:** structure of trifunctional thi20 from yeast
53	c3dzvB_	Alignment	not modelled	98.9	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**4-methyl-5-(beta-hydroxyethyl)thiazole kinase; **PDBTitle:** crystal structure of 4-methyl-5-(beta-hydroxyethyl)thiazole2 kinase (np_816404.1) from enterococcus faecalis v583 at3 2.57 a resolution

54	d1kyha_	Alignment	not modelled	98.8	17	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**YjeF C-terminal domain-like
55	d2ax3a1	Alignment	not modelled	98.8	11	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**YjeF C-terminal domain-like
56	d1v8aa_	Alignment	not modelled	98.7	22	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Thiamin biosynthesis kinases
57	c2ax3A_	Alignment	not modelled	98.4	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical protein tm0922; **PDBTitle:** crystal structure of a putative carbohydrate kinase (tm0922) from2 thermotoga maritima msb8 at 2.25 a resolution
58	c2r3bA_	Alignment	not modelled	97.9	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**yjef-related protein; **PDBTitle:** crystal structure of a ribokinase-like superfamily protein (ef1790)2 from enterococcus faecalis v583 at 1.80 a resolution
59	d1ekqa_	Alignment	not modelled	97.9	18	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Thiamin biosynthesis kinases
60	c3k5wA_	Alignment	not modelled	97.9	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**carbohydrate kinase; **PDBTitle:** crystal structure of a carbohydrate kinase (yjef family)from2 helicobacter pylori
61	d1gc5a_	Alignment	not modelled	97.5	19	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**ADP-specific Phosphofructokinase/Glucokinase
62	d1u2xa_	Alignment	not modelled	97.4	16	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**ADP-specific Phosphofructokinase/Glucokinase
63	c3nm3D_	Alignment	not modelled	97.3	19	**PDB header:**transferase **Chain:** D: **PDB Molecule:**thiamine biosynthetic bifunctional enzyme; **PDBTitle:** the crystal structure of candida glabrata thi6, a bifunctional enzyme2 involved in thiamin biosyhthesis of eukaryotes
64	d1l2la_	Alignment	not modelled	97.2	17	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**ADP-specific Phosphofructokinase/Glucokinase
65	c3drwA_	Alignment	not modelled	97.2	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adp-specific phosphofructokinase; **PDBTitle:** crystal structure of a phosphofructokinase from pyrococcus2 horikoshii ot3 with amp
66	d1ua4a_	Alignment	not modelled	97.1	17	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**ADP-specific Phosphofructokinase/Glucokinase
67	c3bgkA_	Alignment	not modelled	96.9	17	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** the crystal structure of hypothetic protein smu.573 from2 streptococcus mutans
68	d2dw4a2	Alignment	not modelled	60.4	24	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
69	c3k5iB_	Alignment	not modelled	44.1	32	**PDB header:**lyase **Chain:** B: **PDB Molecule:**phosphoribosyl-aminoimidazole carboxylase; **PDBTitle:** crystal structure of n5-carboxyaminoimidazole synthase from2 aspergillus clavatus in complex with adp and 5-3 aminoimadazole ribonucleotide
70	c1c0iA_	Alignment	not modelled	43.7	36	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-amino acid oxidase; **PDBTitle:** crystal structure of d-amino acid oxidase in complex with2 two anthranylate molecules
71	c3lzxB_	Alignment	not modelled	38.4	30	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ferredoxin--nadp reductase 2; **PDBTitle:** crystal structure of ferredoxin-nadp+ oxidoreductase from bacillus2 subtilis (form ii)
72	c3d3jA_	Alignment	not modelled	38.2	13	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**enhancer of mrna-decapping protein 3; **PDBTitle:** crystal structure of human edc3p
73	c2hkoA_	Alignment	not modelled	35.4	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**lysine-specific histone demethylase 1; **PDBTitle:** crystal structure of lsd1
74	c2x1lC_	Alignment	not modelled	34.2	11	**PDB header:**ligase **Chain:** C: **PDB Molecule:**methionyl-trna synthetase; **PDBTitle:** crystal structure of mycobacterium smegmatis methionyl-trna2 synthetase in complex with methionine and adenosine
75	c2v1dA_	Alignment	not modelled	34.0	25	**PDB header:**oxidoreductase/repressor **Chain:** A: **PDB Molecule:**lysine-specific histone demethylase 1; **PDBTitle:** structural basis of lsd1-corest selectivity in histone h32 recognition
76	c2xagA_	Alignment	not modelled	34.0	25	**PDB header:**transcription **Chain:** A: **PDB Molecule:**lysine-specific histone demethylase 1; **PDBTitle:** crystal structure of lsd1-corest in complex with para-bromo-2 (-)-trans-2-phenylcyclopropyl-1-amine
77	d1p3da1	Alignment	not modelled	33.5	29	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain **Family:**MurCD N-terminal domain
78	c3kljA_	Alignment	not modelled	28.4	35	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nad(fad)-dependent dehydrogenase, nirb-family (n-terminal **PDBTitle:** crystal structure of nadh:rubredoxin oxidoreductase from clostridium2 acetobutylicum
						Fold: Molybdenum cofactor biosynthesis proteins

79	d1uz5a3	Alignment	not modelled	28.0	21	**Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
80	c3crcB_	Alignment	not modelled	25.7	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein mazg; **PDBTitle:** crystal structure of escherichia coli mazg, the regulator2 of nutritional stress response
81	d1seza1	Alignment	not modelled	24.9	33	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
82	c3d8xB_	Alignment	not modelled	24.4	23	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**thioredoxin reductase 1; **PDBTitle:** crystal structure of saccharomyces cerevisiae nadph dependent2 thioredoxin reductase 1
83	d1rqga2	Alignment	not modelled	23.7	12	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
84	d1c0pa1	Alignment	not modelled	22.9	36	**Fold:**Nucleotide-binding domain **Superfamily:**Nucleotide-binding domain **Family:**D-aminoacid oxidase, N-terminal domain
85	d1wu2a3	Alignment	not modelled	22.7	8	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
86	d1pfva2	Alignment	not modelled	22.1	14	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
87	c3d3kD_	Alignment	not modelled	22.0	11	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**enhancer of mrna-decapping protein 3; **PDBTitle:** crystal structure of human edc3p
88	d2ftsa3	Alignment	not modelled	21.4	13	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
89	c3allA_	Alignment	not modelled	21.3	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2-methyl-3-hydroxypyridine-5-carboxylic acid oxygenase; **PDBTitle:** crystal structure of 2-methyl-3-hydroxypyridine-5-carboxylic acid2 oxygenase, mutant y270a
90	c3djeA_	Alignment	not modelled	20.9	33	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fructosyl amine: oxygen oxidoreductase; **PDBTitle:** crystal structure of the deglycating enzyme fructosamine2 oxidase from aspergillus fumigatus (amadoriase ii) in3 complex with fsa
91	c3kbqA_	Alignment	not modelled	19.4	12	**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
92	c2ct8A_	Alignment	not modelled	19.3	11	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**methionyl-trna synthetase; **PDBTitle:** crystal structure of aquifex aeolicus methionyl-trna2 synthetase complexed with trna(met) and methionyl-adenylate3 anologue
93	d2gtad1	Alignment	not modelled	18.3	22	**Fold:**all-alpha NTP pyrophosphatases **Superfamily:**all-alpha NTP pyrophosphatases **Family:**MazG-like
94	c2bi8A_	Alignment	not modelled	17.7	26	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**udp-galactopyranose mutase; **PDBTitle:** udp-galactopyranose mutase from klebsiella pneumoniae with2 reduced fad
95	d1y5ea1	Alignment	not modelled	17.3	19	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
96	d1d7ya2	Alignment	not modelled	17.2	22	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
97	c2vdcI_	Alignment	not modelled	17.0	29	**PDB header:**oxidoreductase **Chain:** I: **PDB Molecule:**glutamate synthase [nadph] small chain; **PDBTitle:** the 9.5 a resolution structure of glutamate synthase from2 cryo-electron microscopy and its oligomerization behavior3 in solution: functional implications.
98	c3i3lA_	Alignment	not modelled	15.4	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alkylhalidase cmls; **PDBTitle:** crystal structure of cmls, a flavin-dependent halogenase
99	c1apzB_	Alignment	not modelled	15.3	12	**PDB header:**complex (hydrolase/peptide) **Chain:** B: **PDB Molecule:**aspartylglucosaminidase; **PDBTitle:** human aspartylglucosaminidase complex with reaction product