























Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2583c_(relA)_2907836_2910208
Date	Wed Aug 7 12:50:22 BST 2019
Unique Job ID	239210fc3ba4cad9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xnxB_	 Alignment		100.0	97	PDB header: hydrolase, transferase Chain: B: PDB Molecule: bifunctional (p)ppgpp synthase/hydrolase rela; PDBTitle: crystallographic structure of the enzymatically active n-terminal2 domain of the rel protein from mycobacterium tuberculosis
2	c1vj7B_	 Alignment		100.0	48	PDB header: hydrolase, transferase Chain: B: PDB Molecule: bifunctional rela/spot; PDBTitle: crystal structure of the bifunctional catalytic fragment of relseq,2 the rela/spot homolog from streptococcus equisimilis.
3	d1vj7a1	 Alignment		100.0	51	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: HD domain
4	c3nr1A_	 Alignment		100.0	33	PDB header: hydrolase Chain: A: PDB Molecule: hd domain-containing protein 3; PDBTitle: a metazoan ortholog of spot hydrolyzes ppppp and plays a role in2 starvation responses
5	d1vj7a2	 Alignment		100.0	45	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: RelA/SpoT domain
6	c3nqwB_	 Alignment		100.0	30	PDB header: hydrolase Chain: B: PDB Molecule: cg11900; PDBTitle: a metazoan ortholog of spot hydrolyzes ppppp and plays a role in2 starvation responses
7	c4yf1D_	 Alignment		100.0	26	PDB header: hydrolase Chain: D: PDB Molecule: lmo0812 protein; PDBTitle: 1.85 angstrom crystal structure of lmo0812 from listeria monocytogenes2 egd-e
8	d2be3a1	 Alignment		100.0	21	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: RelA/SpoT domain
9	c6ex0B_	 Alignment		100.0	25	PDB header: transferase Chain: B: PDB Molecule: gtp pyrophosphokinase; PDBTitle: crystal structure of relp (sas2) from staphylococcus aureus bound to2 pppppp in the post-catalytic state
10	c5dedA_	 Alignment		100.0	25	PDB header: transferase Chain: A: PDB Molecule: gtp pyrophosphokinase yjbm; PDBTitle: crystal structure of the small alarmone synthetase 1 from bacillus2 subtilis bound to its product pppppp
11	c6fgkA_	 Alignment		99.9	26	PDB header: transferase Chain: A: PDB Molecule: gtp pyrophosphokinase ywac; PDBTitle: crystal structure of the small alarmone synthetase 2 from bacillus2 subtilis

12	c3l9dA_	Alignment		99.9	24	PDB header: transferase Chain: A: PDB Molecule: putative gtp pyrophosphokinase; PDBTitle: the crystal structure of smu.1046c from streptococcus mutans ua159
13	c3hvezB_	Alignment		99.9	59	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the tgs domain of the cleop_03100 protein from2 clostridium leptum, northeast structural genomics consortium target3 qlr13a
14	c2kmmA_	Alignment		99.9	49	PDB header: hydrolase Chain: A: PDB Molecule: guanosine-3',5'-bis(diphosphate) 3'- PDBTitle: solution nmr structure of the tgs domain of pg1808 from2 porphyromonas gingivalis. northeast structural genomics3 consortium target pgr122a (418-481)
15	c2ekiA_	Alignment		99.8	27	PDB header: signaling protein Chain: A: PDB Molecule: developmentally-regulated gtp-binding protein 1; PDBTitle: solution structures of the tgs domain of human2 developmentally-regulated gtp-binding protein 1
16	d1tkeal	Alignment		99.7	26	Fold: beta-Grasp (ubiquitin-like) Superfamily: TGS-like Family: TGS domain
17	d1wxqa2	Alignment		99.7	31	Fold: beta-Grasp (ubiquitin-like) Superfamily: TGS-like Family: G domain-linked domain
18	d1nyra2	Alignment		99.7	25	Fold: beta-Grasp (ubiquitin-like) Superfamily: TGS-like Family: TGS domain
19	c3ibwA_	Alignment		99.6	20	PDB header: transferase Chain: A: PDB Molecule: gtp pyrophosphokinase; PDBTitle: crystal structure of the act domain from gtp pyrophosphokinase of2 chlorobium tepidum. northeast structural genomics consortium target3 ctr148a
20	c1wwtA_	Alignment		99.5	23	PDB header: ligase Chain: A: PDB Molecule: threonyl-trna synthetase, cytoplasmic; PDBTitle: solution structure of the tgs domain from human threonyl-2 trna synthetase
21	d1u8sa2	Alignment	not modelled	98.6	18	Fold: Ferredoxin-like Superfamily: ACT-like Family: Glycine cleavage system transcriptional repressor
22	c1tkeA_	Alignment	not modelled	98.6	26	PDB header: ligase Chain: A: PDB Molecule: threonyl-trna synthetase; PDBTitle: crystal structure of the editing domain of threonyl-trna2 synthetase complexed with serine
23	c4a9aB_	Alignment	not modelled	98.5	25	PDB header: translation Chain: B: PDB Molecule: ribosome-interacting gtpase 1; PDBTitle: structure of rbg1 in complex with tma46 dfrp domain
24	c4v1ac_	Alignment	not modelled	98.5	18	PDB header: ribosome Chain: C: PDB Molecule: PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 22 of 2
25	c2lvwA_	Alignment	not modelled	98.4	15	PDB header: transferase Chain: A: PDB Molecule: acetolactate synthase isozyme 1 small subunit; PDBTitle: solution nmr studies of the dimeric regulatory subunit ilvn of the2 e.coli acetohydroxyacid synthase i (ahas i)
26	c2dwqB_	Alignment	not modelled	98.4	30	PDB header: hydrolase Chain: B: PDB Molecule: gtp-binding protein; PDBTitle: thermus thermophilus ychf gtp-binding protein
27	c2ohfA_	Alignment	not modelled	98.4	22	PDB header: hydrolase Chain: A: PDB Molecule: gtp-binding protein 9; PDBTitle: crystal structure of human ola1 in complex with amppcp
28	d1sc6a3	Alignment	not modelled	98.3	17	Fold: Ferredoxin-like Superfamily: ACT-like Family: Phosphoglycerate dehydrogenase, regulatory (C-terminal) domain

29	c1wxqA	Alignment	not modelled	98.3	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: gtp-binding protein; PDBTitle: crystal structure of gtp binding protein from pyrococcus horikoshii2 ot3
30	c5ee1A	Alignment	not modelled	98.2	17	PDB header: hydrolase Chain: A: PDB Molecule: obg-like atpase 1; PDBTitle: crystal structure of osychf1 at ph 7.85
31	d2f1fa1	Alignment	not modelled	98.2	19	Fold: Ferredoxin-like Superfamily: ACT-like Family: IlvH-like
32	d2pc6a2	Alignment	not modelled	98.1	15	Fold: Ferredoxin-like Superfamily: ACT-like Family: IlvH-like
33	c1jalA	Alignment	not modelled	98.1	29	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: yichf protein; PDBTitle: yichf protein (hi0393)
34	d2fgca2	Alignment	not modelled	98.1	15	Fold: Ferredoxin-like Superfamily: ACT-like Family: IlvH-like
35	c2pc6C	Alignment	not modelled	98.0	16	PDB header: lyase Chain: C: PDB Molecule: probable acetolactate synthase isozyme iii (small subunit); PDBTitle: crystal structure of putative acetolactate synthase- small subunit2 from nitrosomonas europaea
36	d1ygya3	Alignment	not modelled	98.0	18	Fold: Ferredoxin-like Superfamily: ACT-like Family: Phosphoglycerate dehydrogenase, regulatory (C-terminal) domain
37	c2fgcA	Alignment	not modelled	98.0	15	PDB header: transferase Chain: A: PDB Molecule: acetolactate synthase, small subunit; PDBTitle: crystal structure of acetolactate synthase- small subunit from2 thermotoga maritima
38	c1ni3A	Alignment	not modelled	98.0	22	PDB header: hydrolase Chain: A: PDB Molecule: yichf gtp-binding protein; PDBTitle: structure of the schizosaccharomyces pombe yichf gtpase
39	c2f1fA	Alignment	not modelled	97.9	19	PDB header: transferase Chain: A: PDB Molecule: acetolactate synthase isozyme iii small subunit; PDBTitle: crystal structure of the regulatory subunit of acetoxyacid2 synthase isozyme iii from e. coli
40	c1qf6A	Alignment	not modelled	97.9	29	PDB header: ligase/rna Chain: A: PDB Molecule: threonyl-trna synthetase; PDBTitle: structure of e. coli threonyl-trna synthetase complexed with its2 cognate trna
41	c1nyqA	Alignment	not modelled	97.9	25	PDB header: ligase Chain: A: PDB Molecule: threonyl-trna synthetase 1; PDBTitle: structure of staphylococcus aureus threonyl-trna synthetase2 complexed with an analogue of threonyl adenylate
42	c1u8sB	Alignment	not modelled	97.8	19	PDB header: transcription Chain: B: PDB Molecule: glycine cleavage system transcriptional PDBTitle: crystal structure of putative glycine cleavage system2 transcriptional repressor
43	d1zpa1	Alignment	not modelled	97.6	18	Fold: Ferredoxin-like Superfamily: ACT-like Family: SP0238-like
44	c2nyiB	Alignment	not modelled	97.4	19	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: unknown protein; PDBTitle: crystal structure of an unknown protein from galdieria sulphuraria
45	d1u8sa1	Alignment	not modelled	97.3	13	Fold: Ferredoxin-like Superfamily: ACT-like Family: Glycine cleavage system transcriptional repressor
46	c1y7pB	Alignment	not modelled	97.2	21	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein af1403; PDBTitle: 1.9 a crystal structure of a protein of unknown function2 af1403 from archaeoglobus fulgidus, probable metabolic3 regulator
47	c3n0vD	Alignment	not modelled	97.1	14	PDB header: hydrolase Chain: D: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (pp_0327)2 from pseudomonas putida kt2440 at 2.25 a resolution
48	c1ybaC	Alignment	not modelled	96.8	17	PDB header: oxidoreductase Chain: C: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: the active form of phosphoglycerate dehydrogenase
49	c1ygyA	Alignment	not modelled	96.7	18	PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: crystal structure of d-3-phosphoglycerate dehydrogenase from2 mycobacterium tuberculosis
50	c3k5pA	Alignment	not modelled	96.7	16	PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: crystal structure of amino acid-binding act: d-isomer specific 2-2 hydroxyacid dehydrogenase catalytic domain from brucella melitensis
51	c3nrB	Alignment	not modelled	96.7	17	PDB header: hydrolase Chain: D: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (puru_2 pp_1943) from pseudomonas putida kt2440 at 2.05 a resolution
52	d2f06a2	Alignment	not modelled	96.5	21	Fold: Ferredoxin-like Superfamily: ACT-like Family: BT0572-like
53	c3o1lB	Alignment	not modelled	96.5	18	PDB header: hydrolase Chain: B: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (pspto_4314)2 from pseudomonas syringae pv. tomato str. dc3000 at 2.20 a resolution
						PDB header: ribosome

54	c4ce4c_	Alignment	not modelled	96.5	22	Chain: C: PDB Molecule: PDBTitle: 39s large subunit of the porcine mitochondrial ribosome
55	c2qmxB_	Alignment	not modelled	96.2	13	PDB header: ligase Chain: B: PDB Molecule: prephenate dehydratase; PDBTitle: the crystal structure of l-phe inhibited prephenate dehydratase from2 chlorobium tepidum t1s
56	c3w7bB_	Alignment	not modelled	96.1	18	PDB header: hydrolase Chain: B: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of formyltetrahydrofolate deformylase from thermus2 thermophilus hb8
57	c3obiC_	Alignment	not modelled	96.1	19	PDB header: hydrolase Chain: C: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (np_949368)2 from rhodopseudomonas palustris cga009 at 1.95 a resolution
58	c6dzsD_	Alignment	not modelled	96.1	16	PDB header: oxidoreductase Chain: D: PDB Molecule: homoserine dehydrogenase; PDBTitle: mycobacterial homoserine dehydrogenase thra in complex with nadp
59	c3louB_	Alignment	not modelled	96.0	10	PDB header: hydrolase Chain: B: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of formyltetrahydrofolate deformylase (yp_105254.1)2 from burkholderia mallei atcc 23344 at 1.90 a resolution
60	c3mwbA_	Alignment	not modelled	95.9	15	PDB header: lyase Chain: A: PDB Molecule: prephenate dehydratase; PDBTitle: the crystal structure of prephenate dehydratase in complex with l-phe2 from arthrobacter aureus at 2.0a
61	d1zud21	Alignment	not modelled	95.9	12	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: ThiS
62	c6npaD_	Alignment	not modelled	95.9	22	PDB header: oxidoreductase Chain: D: PDB Molecule: tmbp, (r)-1-hydroxy-2-trimethylaminoethylphosphonate PDBTitle: x-ray crystal structure of tmbp, (r)-1-hydroxy-2-2 trimethylaminoethylphosphonate oxygenase, with (r)-1-hydroxy-2-3 trimethylaminoethylphosphonate
63	c2f06B_	Alignment	not modelled	95.8	19	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of protein bt0572 from bacteroides thetaiotaomicron
64	d1phza1	Alignment	not modelled	95.8	15	Fold: Ferredoxin-like Superfamily: ACT-like Family: Phenylalanine metabolism regulatory domain
65	d2qmwa2	Alignment	not modelled	95.7	11	Fold: Ferredoxin-like Superfamily: ACT-like Family: Phenylalanine metabolism regulatory domain
66	c4n71A_	Alignment	not modelled	95.5	24	PDB header: oxidoreductase Chain: A: PDB Molecule: predicted hd phosphohydrolase phnz; PDBTitle: x-ray crystal structure of 2-amino-1-hydroxyethylphosphonate-bound2 phnz
67	c4lubA_	Alignment	not modelled	95.5	13	PDB header: lyase Chain: A: PDB Molecule: putative prephenate dehydratase; PDBTitle: x-ray structure of prephenate dehydratase from streptococcus mutans
68	c2p mA_	Alignment	not modelled	95.1	13	PDB header: oxidoreductase Chain: A: PDB Molecule: protein (phenylalanine-4-hydroxylase); PDBTitle: structure of phenylalanine hydroxylase dephosphorylated
69	c1rwuA_	Alignment	not modelled	95.0	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical upf0250 protein ybed; PDBTitle: solution structure of conserved protein ybed from e. coli
70	d1rwua_	Alignment	not modelled	95.0	13	Fold: Ferredoxin-like Superfamily: YbeD/HP0495-like Family: YbeD-like
71	c2qmWA_	Alignment	not modelled	95.0	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: prephenate dehydratase; PDBTitle: the crystal structure of the prephenate dehydratase (pdt) from2 staphylococcus aureus subsp. aureus mu50
72	c3mtjA_	Alignment	not modelled	94.9	17	PDB header: oxidoreductase Chain: A: PDB Molecule: homoserine dehydrogenase; PDBTitle: the crystal structure of a homoserine dehydrogenase from thiobacillus2 denitrificans to 2.15a
73	c5uscB_	Alignment	not modelled	94.8	18	PDB header: hydrolase Chain: B: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase tyra from bacillus2 anthracis in complex with nad and l-tyrosine
74	c2hj1A_	Alignment	not modelled	94.8	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a 3d domain-swapped dimer of protein hi0395 from2 haemophilus influenzae
75	d2hj1a1	Alignment	not modelled	94.8	17	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: HI0395-like
76	c3luyA_	Alignment	not modelled	94.7	10	PDB header: isomerase Chain: A: PDB Molecule: probable chorismate mutase; PDBTitle: putative chorismate mutase from bifidobacterium adolescentis
77	c3cwiA_	Alignment	not modelled	94.5	17	PDB header: biosynthetic protein Chain: A: PDB Molecule: thiamine-biosynthesis protein this; PDBTitle: crystal structure of thiamine biosynthesis protein (this)2 from geobacter metallireducens. northeast structural3 genomics consortium target gmr137
78	d1tygb_	Alignment	not modelled	94.3	15	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: ThiS
79	c5il5A_	Alignment	not modelled	94.1	12	PDB header: oxidoreductase Chain: A: PDB Molecule: phenylalanine-4-hydroxylase;

79	c3ksA	Alignment	not modelled	94.1	12	PDBTitle: phenylalanine hydroxylase from dictyostelium - bh2 complex PDB header: oxidoreductase
80	c5denA	Alignment	not modelled	93.6	13	Chain: A; PDB Molecule: phenylalanine-4-hydroxylase; PDBTitle: the first structure of a full-length mammalian phenylalanine2 hydroxylase reveals the architecture of an auto-inhibited tetramer
81	d1vjka	Alignment	not modelled	93.3	31	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: MoaD
82	c2qieB	Alignment	not modelled	93.2	16	PDB header: transferase Chain: B; PDB Molecule: molybdopterin synthase small subunit; PDBTitle: staphylococcus aureus molybdopterin synthase in complex with precursor2 z
83	d2f06a1	Alignment	not modelled	93.2	13	Fold: Ferredoxin-like Superfamily: ACT-like Family: BT0572-like
84	c2mdaB	Alignment	not modelled	92.7	16	PDB header: oxidoreductase Chain: B; PDB Molecule: tyrosine 3-monooxygenase; PDBTitle: the solution structure of the regulatory domain of tyrosine2 hydroxylase
85	c1tdjA	Alignment	not modelled	92.7	6	PDB header: allostery Chain: A; PDB Molecule: biosynthetic threonine deaminase; PDBTitle: threonine deaminase (biosynthetic) from e. coli
86	c3po0A	Alignment	not modelled	92.5	24	PDB header: protein binding Chain: A; PDB Molecule: small archaeal modifier protein 1; PDBTitle: crystal structure of samp1 from haloferax volcanii
87	c1tygG	Alignment	not modelled	92.4	15	PDB header: biosynthetic protein Chain: G; PDB Molecule: yjbs; PDBTitle: structure of the thiazole synthase/this complex
88	c2kl0A	Alignment	not modelled	92.2	12	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: putative thiamin biosynthesis this; PDBTitle: solution nmr structure of rhodopseudomonas palustris rpa3574,2 northeast structural genomics consortium (nesg) target rpr325
89	d2cu3a1	Alignment	not modelled	92.1	27	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: ThiS
90	d2qgsa1	Alignment	not modelled	91.2	18	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: HD domain
91	c5yeiF	Alignment	not modelled	91.0	13	PDB header: transferase Chain: F; PDB Molecule: aspartokinase; PDBTitle: mechanistic insight into the regulation of pseudomonas aeruginosa2 aspartate kinase
92	c4n6eB	Alignment	not modelled	89.9	25	PDB header: lyase/biosynthetic protein Chain: B; PDB Molecule: this/moad family protein; PDBTitle: crystal structure of amycolatopsis orientalis bexx/cyso complex
93	c6jzbD	Alignment	not modelled	89.7	18	PDB header: transferase Chain: D; PDB Molecule: moad/this family protein; PDBTitle: structural analysis of molybdopterin synthases from two mycobacteria2 pathogens
94	c2dqB	Alignment	not modelled	89.3	41	PDB header: hydrolase, dna binding protein Chain: B; PDB Molecule: deoxyguanosinetriphosphate triphosphohydrolase, putative; PDBTitle: crystal structure of dntp triphosphohydrolase from thermus2 thermophilus hb8, which is homologous to dgtp triphosphohydrolase
95	c5ihyB	Alignment	not modelled	88.7	25	PDB header: hydrolase Chain: B; PDB Molecule: uncharacterized protein; PDBTitle: the crystal structure of bacillus subtilis semet-ypgq
96	d1y7pa2	Alignment	not modelled	88.6	18	Fold: Ferredoxin-like Superfamily: ACT-like Family: AF1403 N-terminal domain-like
97	c5mpoA	Alignment	not modelled	88.4	20	PDB header: transferase Chain: A; PDB Molecule: molybdopterin synthase sulfur carrier subunit; PDBTitle: crystal structure of human molybdopterin synthase complex
98	c2lqjA	Alignment	not modelled	87.8	12	PDB header: hydrolase Chain: A; PDB Molecule: mg2+ transport protein; PDBTitle: solution structure of the c-terminal domain of the mgtc protein from2 mycobacterium tuberculosis
99	d1jala2	Alignment	not modelled	87.7	24	Fold: beta-Grasp (ubiquitin-like) Superfamily: TGS-like Family: G domain-linked domain
100	c4s1cA	Alignment	not modelled	87.4	31	PDB header: hydrolase Chain: A; PDB Molecule: lmo1466 protein; PDBTitle: crystal structure of l. monocytogenes phosphodiesterase pgph hd domain
101	d2joqa1	Alignment	not modelled	87.2	4	Fold: Ferredoxin-like Superfamily: YbeD/HP0495-like Family: HP0495-like
102	c5z81A	Alignment	not modelled	87.1	18	PDB header: chaperone Chain: A; PDB Molecule: heat shock protein 15; PDBTitle: trimeric structure of vibrio cholerae heat shock protein 15 at 2.32 angstrom resolution
103	c1dm9A	Alignment	not modelled	87.1	12	PDB header: structural genomics Chain: A; PDB Molecule: hypothetical 15.5 kd protein in mrca-pcka intergenic PDBTitle: heat shock protein 15 kd
104	d1dm9a	Alignment	not modelled	87.1	12	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Heat shock protein 15 kd

105	c5xf9F_	Alignment	not modelled	87.0	26	PDB header: oxidoreductase Chain: F; PDB Molecule: nad-reducing hydrogenase; PDBTitle: crystal structure of nad+-reducing [nife]-hydrogenase in the air-2 oxidized state
106	c2ogiA_	Alignment	not modelled	85.8	45	PDB header: hydrolase Chain: A; PDB Molecule: hypothetical protein sag1661; PDBTitle: crystal structure of a putative metal dependent phosphohydrolase2 (sag1661) from streptococcus agalactiae serogroup v at 1.85 a3 resolution
107	c3dwmA_	Alignment	not modelled	85.7	20	PDB header: transferase Chain: A; PDB Molecule: 9.5 kda culture filtrate antigen cfp10a; PDBTitle: crystal structure of mycobacterium tuberculosis cyso, an antigen
108	c2m19A_	Alignment	not modelled	85.6	25	PDB header: protein binding Chain: A; PDB Molecule: molybdopterin converting factor subunit 1; PDBTitle: solution structure of the haloferax volcanii hvo 2177 protein
109	c2dtjA_	Alignment	not modelled	84.6	22	PDB header: transferase Chain: A; PDB Molecule: aspartokinase; PDBTitle: crystal structure of regulatory subunit of aspartate kinase2 from corynebacterium glutamicum
110	c6jc0A_	Alignment	not modelled	84.0	12	PDB header: transferase Chain: A; PDB Molecule: putative molybdenum cofactor biosynthesis protein d2 PDBTitle: structural analysis of molybdopterin synthases from two mycobacteria2 pathogens
111	d1ni3a2	Alignment	not modelled	83.9	19	Fold: beta-Grasp (ubiquitin-like) Superfamily: TGS-like Family: G domain-linked domain
112	c2k6pA_	Alignment	not modelled	83.4	14	PDB header: unknown function Chain: A; PDB Molecule: uncharacterized protein hp_1423; PDBTitle: solution structure of hypothetical protein, hp1423
113	c1v8cA_	Alignment	not modelled	83.0	22	PDB header: protein binding Chain: A; PDB Molecule: moad related protein; PDBTitle: crystal structure of moad related protein from thermus2 thermophilus hb8
114	c2g1eA_	Alignment	not modelled	82.8	20	PDB header: transferase Chain: A; PDB Molecule: hypothetical protein ta0895; PDBTitle: solution structure of ta0895
115	c3s1tB_	Alignment	not modelled	82.8	24	PDB header: transferase Chain: B; PDB Molecule: aspartokinase; PDBTitle: structure of the regulatory domain of aspartokinase (rv3709c; ak-beta)2 in complex with threonine from mycobacterium tuberculosis
116	c3p96A_	Alignment	not modelled	82.6	13	PDB header: hydrolase Chain: A; PDB Molecule: phosphoserine phosphatase serb; PDBTitle: crystal structure of phosphoserine phosphatase serb from mycobacterium2 avium, native form
117	d1fm0d_	Alignment	not modelled	81.5	38	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: MoaD
118	c2bs2E_	Alignment	not modelled	80.9	20	PDB header: oxidoreductase Chain: E; PDB Molecule: quinol-fumarate reductase iron-sulfur subunit b; PDBTitle: quinol:fumarate reductase from wolinnella succinogenes
119	d1rwsa_	Alignment	not modelled	80.7	39	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: ThiS
120	c3gqsB_	Alignment	not modelled	79.9	24	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: adenylate cyclase-like protein; PDBTitle: crystal structure of the fha domain of ct664 protein from chlamydia2 trachomatis