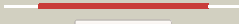



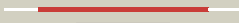


















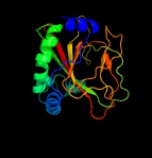

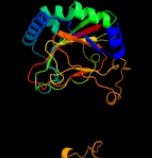
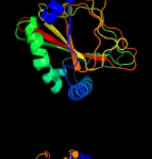



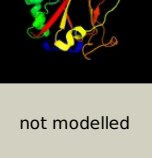


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1501 (-) _1691896_1692717
Date	Fri Aug 2 13:30:08 BST 2019
Unique Job ID	c6ce6db69868b3fb

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4zonB_	 Alignment		100.0	18	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: B: PDB Molecule: verruculogen synthase; PDBTitle: structure of ftmxo1 with fumitremorgen b complex
2	c4naoA_	 Alignment		100.0	13	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxygenase; PDBTitle: crystal structure of eash
3	c5daqA_	 Alignment		100.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: phytanoyl-coa dioxygenase family protein (afu_orthologue PDBTitle: fe(ii)/(alpha)ketoglutarate-dependent dioxygenase asqj in complex with2 4-methoxycycloptin
4	c5m0tA_	 Alignment		100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: alpha-ketoglutarate-dependent non-heme iron oxygenase eash; PDBTitle: alpha-ketoglutarate-dependent non-heme iron oxygenase eash
5	c5zm4B_	 Alignment		100.0	18	PDB header: oxidoreductase Chain: B: PDB Molecule: dioxygenase anda; PDBTitle: fe(ii)/(alpha)ketoglutarate-dependent dioxygenase anda with2 preandiloid c
6	c5yboA_	 Alignment		100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: prha; PDBTitle: fe(ii)/(alpha)ketoglutarate-dependent dioxygenase prha in complex with2 preaustinoid a1
7	c6ec3C_	 Alignment		100.0	20	PDB header: transferase, oxidoreductase Chain: C: PDB Molecule: methyltransferase domain-containing protein; PDBTitle: crystal structure of evdm1
8	c4xbzB_	 Alignment		100.0	14	PDB header: oxidoreductase Chain: B: PDB Molecule: evdo1; PDBTitle: crystal structure of evdo1 from micromonospora carbonacea var.2 aurantiaca
9	c3emrA_	 Alignment		100.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: ectd; PDBTitle: crystal structure analysis of the ectoine hydroxylase ectd from2 salibacillus salexigens
10	d2fcta1	 Alignment		100.0	17	Fold: Double-stranded beta-helix Superfamily: Clavaminate synthase-like Family: PhyH-like
11	c4mhuB_	 Alignment		100.0	13	PDB header: oxidoreductase Chain: B: PDB Molecule: rectoine hydroxylase; PDBTitle: crystal structure of ectd from s. alaskensis with bound fe

12	c5erID	Alignment		100.0	15	PDB header: isomerase Chain: D: PDB Molecule: snon,snon; PDBTitle: crystal structure of the epimerase snon in complex with ni2+,2 succinate and nogalamycin ro
13	c3gjbA	Alignment		100.0	14	PDB header: biosynthetic protein Chain: A: PDB Molecule: cytc3; PDBTitle: cytc3 with fe(ii) and alpha-ketoglutarate
14	c2opwA	Alignment		100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: phyhd1 protein; PDBTitle: crystal structure of human phytanoyl-coa dioxygenase phyhd1 (apo)
15	c5epaE	Alignment		100.0	20	PDB header: lyase Chain: E: PDB Molecule: snok; PDBTitle: crystal structure of non-heme alpha ketoglutarate dependent2 carbocyclase snok from nogalamycin biosynthesis
16	c5ncjB	Alignment		100.0	16	PDB header: oxidoreductase Chain: B: PDB Molecule: leucine hydroxylase; PDBTitle: grie in complex with manganese, succinate and (2s,4r)-5-hydroxyleucine
17	d2a1xa1	Alignment		100.0	21	Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: PhyH-like
18	c4xc9B	Alignment		100.0	17	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidase/hydroxylase; PDBTitle: crystal structure of apo hygx from streptomyces hygroscopicus
19	c4xaaA	Alignment		100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxygenase; PDBTitle: crystal structure of avio1 from streptomyces viridochromogenes tue57
20	c2rdsA	Alignment		100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: 1-deoxypentalenic acid 11-beta hydroxylase; fe(iii)/alpha- PDBTitle: crystal structure of ptlh with fe/oxalylglycine and ent-1-2 deoxypentalenic acid bound
21	c4xabA	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: evdo2; PDBTitle: crystal structure of evdo2 from micromonospora carbonacea var.2 aurantiaca
22	c3nnlB	Alignment	not modelled	100.0	13	PDB header: biosynthetic protein Chain: B: PDB Molecule: cura; PDBTitle: halogenase domain from cura module (crystal form iii)
23	c4iw3J	Alignment	not modelled	99.3	17	PDB header: metal binding protein/translation Chain: J: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a pseudomonas putida prolyl-4-hydroxylase (p4h)2 in complex with elongation factor tu (ef-tu)
24	c6iuqA	Alignment	not modelled	99.3	15	PDB header: oxidoreductase Chain: A: PDB Molecule: prolyl 4-hydroxylase; PDBTitle: crystal structure and expression patterns of prolyl 4-hydroxylases2 from phytophthora capsici
25	c6f0wA	Alignment	not modelled	99.2	12	PDB header: oxidoreductase Chain: A: PDB Molecule: hif prolyl hydroxylase; PDBTitle: prolyl hydroxylase in complex with hypoxia inducible factor oxygen2 degradation domain peptide fragment from trichoplax adhaerens
26	c2g19A	Alignment	not modelled	99.1	14	PDB header: oxidoreductase Chain: A: PDB Molecule: egl nine homolog 1; PDBTitle: cellular oxygen sensing: crystal structure of hypoxia-inducible factor2 prolyl hydroxylase (phd2)
27	c3ouiA	Alignment	not modelled	99.0	13	PDB header: oxidoreductase Chain: A: PDB Molecule: egl nine homolog 1; PDBTitle: phd2-r717 with 40787422
28	c4rgkA	Alignment	not modelled	98.9	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of putative phytanoyl-coa dioxygenase family protein2 ybiu from yersinia pestis

29	c2dbiA_	Alignment	not modelled	98.9	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ybiu; PDBTitle: crystal structure of a hypothetical protein jw0805 from2 escherichia coli
30	d2csga1	Alignment	not modelled	98.8	11	Fold: Double-stranded beta-helix Superfamily: Clavaminatase synthase-like Family: YbiU-like
31	c2jijA_	Alignment	not modelled	98.6	10	PDB header: hydrolase Chain: A: PDB Molecule: prolyl-4 hydroxylase; PDBTitle: crystal structure of the apo form of chlamydomonas2 reinhardtii prolyl-4 hydroxylase type i
32	c5c5tB_	Alignment	not modelled	98.3	11	PDB header: oxidoreductase Chain: B: PDB Molecule: prolyl 4-hydroxylase; PDBTitle: the crystal structure of viral collagen prolyl hydroxylase vcp from2 paramecium bursaria chlorella virus-1 - 2og complex
33	c3dkqB_	Alignment	not modelled	98.1	13	PDB header: oxidoreductase Chain: B: PDB Molecule: pkhd-type hydroxylase sbal_3634; PDBTitle: crystal structure of putative oxygenase (yp_001051978.1) from2 shewanella baltica os155 at 2.26 a resolution
34	c3itqB_	Alignment	not modelled	98.0	15	PDB header: oxidoreductase Chain: B: PDB Molecule: prolyl 4-hydroxylase, alpha subunit domain protein; PDBTitle: crystal structure of a prolyl 4-hydroxylase from bacillus anthracis
35	c3mguA_	Alignment	not modelled	97.9	11	PDB header: oxidoreductase Chain: A: PDB Molecule: pkhd-type hydroxylase tpa1; PDBTitle: structure of s. cerevisiae tpa1 protein, a proline hydroxylase2 modifying ribosomal protein rps23
36	c3kt4A_	Alignment	not modelled	97.9	10	PDB header: oxidoreductase Chain: A: PDB Molecule: pkhd-type hydroxylase tpa1; PDBTitle: crystal structure of tpa1 from saccharomyces cerevisiae, a component2 of the messenger ribonucleoprotein complex
37	d1oiha_	Alignment	not modelled	97.7	19	Fold: Double-stranded beta-helix Superfamily: Clavaminatase synthase-like Family: TauD/TfdA-like
38	c3r1jB_	Alignment	not modelled	97.7	29	PDB header: oxidoreductase Chain: B: PDB Molecule: alpha-ketoglutarate-dependent taurine dioxygenase; PDBTitle: crystal structure of alpha-ketoglutarate-dependent taurine dioxygenase2 from mycobacterium avium, native form
39	c3bvcA_	Alignment	not modelled	97.7	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein ism_01780; PDBTitle: crystal structure of uncharacterized protein ism_01780 from2 roseovarius nubinhibens ism
40	d1otja_	Alignment	not modelled	97.5	20	Fold: Double-stranded beta-helix Superfamily: Clavaminatase synthase-like Family: TauD/TfdA-like
41	c5hsxB_	Alignment	not modelled	97.5	16	PDB header: oxidoreductase Chain: B: PDB Molecule: putative alpha-ketoglutarate-dependent taurine dioxygenase; PDBTitle: crystal structure of a putative alpha-ketoglutarate-dependent taurine2 dioxygenase from burkholderia xenovorans
42	c4j5iH_	Alignment	not modelled	97.4	28	PDB header: oxidoreductase Chain: H: PDB Molecule: alpha-ketoglutarate-dependent taurine dioxygenase; PDBTitle: crystal structure of an alpha-ketoglutarate-dependent taurine2 dioxygenase from mycobacterium smegmatis
43	c3pl0B_	Alignment	not modelled	97.4	13	PDB header: biosynthetic protein Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a bsma homolog (mpe_a2762) from methylobium2 petroleophilum pm1 at 1.91 a resolution
44	c5vn6B_	Alignment	not modelled	97.3	21	PDB header: oxidoreductase Chain: B: PDB Molecule: taurine dioxygenase; PDBTitle: crystal structure of taurine dioxygenase from burkholderia ambifaria
45	c6ax6B_	Alignment	not modelled	97.2	12	PDB header: oxidoreductase Chain: B: PDB Molecule: procollagen lysyl hydroxylase and glycosyltransferase; PDBTitle: the crystal structure of a lysyl hydroxylase from acanthamoeba2 polyphaga mimivirus
46	c6d1oD_	Alignment	not modelled	97.1	19	PDB header: oxidoreductase Chain: D: PDB Molecule: (r)-phenoxypropionate/alpha-ketoglutarate-dioxygenase; PDBTitle: ft_5 dioxygenase apoenzyme
47	c6dchA_	Alignment	not modelled	97.1	18	PDB header: oxidoreductase Chain: A: PDB Molecule: scoe protein; PDBTitle: structure of isonitrile biosynthesis enzyme scoe
48	c5bkeF_	Alignment	not modelled	97.1	19	PDB header: oxidoreductase Chain: F: PDB Molecule: alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate PDBTitle: crystal structure of aad-2 in complex with mn(ii) and n-oxalyglycine
49	c3eatX_	Alignment	not modelled	97.0	15	PDB header: oxidoreductase Chain: X: PDB Molecule: pyoverdine biosynthesis protein pvcb; PDBTitle: crystal structure of the pvcb (pa2255) protein from2 pseudomonas aeruginosa
50	c4y0eB_	Alignment	not modelled	97.0	25	PDB header: oxidoreductase Chain: B: PDB Molecule: putative dioxygenase; PDBTitle: x-ray crystal structure of a putative dioxygenase from mycobacterium2 abscessus
51	d1nx4a_	Alignment	not modelled	96.9	23	Fold: Double-stranded beta-helix Superfamily: Clavaminatase synthase-like Family: gamma-Butyrobetaine hydroxylase
52	c3pvjB_	Alignment	not modelled	96.8	19	PDB header: oxidoreductase Chain: B: PDB Molecule: alpha-ketoglutarate-dependent taurine dioxygenase; PDBTitle: crystal structure of the fe(ii)/alpha-ketoglutarate dependent taurine2 dioxygenase from pseudomonas putida kt2440 PDB header: oxidoreductase

53	c5j92B_	Alignment	not modelled	96.6	21	Chain: B: PDB Molecule: putative alpha kg dependent 2,4-d dioxygenase; PDBTitle: crystal structure of a putative alpha-ketoglutarate dependent 2,4-d2 dioxygenase from burkholderia xenovorans
54	c3ms5A_	Alignment	not modelled	96.4	18	PDB header: oxidoreductase Chain: A: PDB Molecule: gamma-butyrobetaine dioxygenase; PDBTitle: crystal structure of human gamma-butyrobetaine,2-oxoglutarate2 dioxygenase 1 (bbox1)
55	c4qkB_	Alignment	not modelled	96.2	12	PDB header: oxidoreductase Chain: A: PDB Molecule: alpha-ketoglutarate-dependent dioxygenase alkb homolog 7, PDBTitle: crystal structure of seleno-methionine labelled human alkbh7 in2 complex with alpha-ketoglutarate and mn(ii)
56	c6npcB_	Alignment	not modelled	96.1	20	PDB header: oxidoreductase Chain: B: PDB Molecule: tmpa, 2-trimethylaminoethylphosphonate hydroxylase; PDBTitle: x-ray crystal structure of tmpa, 2-trimethylaminoethylphosphonate2 hydroxylase, with fe, 2og, and 2-trimethylaminoethylphosphonate
57	c4nhyC_	Alignment	not modelled	95.9	15	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: C: PDB Molecule: 2-oxoglutarate and iron-dependent oxygenase domain- PDBTitle: crystal structure of human ogfod1, 2-oxoglutarate and iron-dependent2 oxygenase domain containing 1, in complex with pyridine-2,4-3 dicarboxylic acid (2,4-pdca)
58	d2iuwa1	Alignment	not modelled	95.7	13	Fold: Double-stranded beta-helix Superfamily: Clavaminatase synthase-like Family: AlkB-like
59	c4lt5A_	Alignment	not modelled	95.5	14	PDB header: oxidoreductase/dna Chain: A: PDB Molecule: naegleria tet-like dioxygenase; PDBTitle: structure of a naegleria tet-like dioxygenase in complex with 5-2 methylcytosine dna
60	c6n1fD_	Alignment	not modelled	94.5	15	PDB header: oxidoreductase Chain: D: PDB Molecule: oxidoreductase, 2og-fe(ii) oxygenase family; PDBTitle: crystal structure of oxidoreductase, 2og-fe(ii) oxygenase family, from2 burkholderia pseudomallei
61	c3btzA_	Alignment	not modelled	93.8	16	PDB header: oxidoreductase/dna Chain: A: PDB Molecule: alpha-ketoglutarate-dependent dioxygenase alkb homolog 2; PDBTitle: crystal structure of human abh2 cross-linked to dsdna
62	c6fxyA_	Alignment	not modelled	93.1	14	PDB header: transferase Chain: A: PDB Molecule: procollagen-lysine,2-oxoglutarate 5-dioxygenase 3; PDBTitle: crystal structure of full-length human lysyl hydroxylase lh3 -2 cocrystal with fe2+, mn2+, udp-gal - structure from long-wavelength3 s-sad
63	c5ylbA_	Alignment	not modelled	92.2	15	PDB header: oxidoreductase Chain: A: PDB Molecule: uncharacterized protein p8a3.02c; PDBTitle: crystal structure of ofd2 from schizosaccharomyces pombe at 1.80 a
64	c2iuwA_	Alignment	not modelled	91.2	16	PDB header: oxidoreductase Chain: A: PDB Molecule: alkylated repair protein alkb homolog 3; PDBTitle: crystal structure of human abh3 in complex with iron ion and 2-2 oxoglutarate
65	c4p7xA_	Alignment	not modelled	91.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: l-proline cis-4-hydroxylase; PDBTitle: l-pipecolic acid-bound l-proline cis-4-hydroxylase
66	c5jqvA_	Alignment	not modelled	91.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: aspartyl/asparaginyl beta-hydroxylase; PDBTitle: aspartyl/asparaginyl beta-hydroxylase (asph) oxygenase and tpr domains2 in complex with manganese, n-oxalylglycine and factor x substrate3 peptide fragment(39mer-4ser)
67	c4nj4A_	Alignment	not modelled	84.0	15	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: A: PDB Molecule: rna demethylase alkbh5; PDBTitle: crystal structure of human alkbh5
68	c3rcqA_	Alignment	not modelled	82.8	16	PDB header: oxidoreductase Chain: A: PDB Molecule: aspartyl/asparaginyl beta-hydroxylase; PDBTitle: crystal structure of human aspartate beta-hydroxylase isoform a
69	c6b8wB_	Alignment	not modelled	82.5	13	PDB header: transcription Chain: B: PDB Molecule: xre family transcriptional regulator; PDBTitle: 1.9 angstrom resolution crystal structure of cupin_2 domain (pfam2 07883) of xre family transcriptional regulator from enterobacter3 cloacae.
70	d1y9qa2	Alignment	not modelled	79.4	14	Fold: Double-stranded beta-helix Superfamily: RmC-like cupins Family: Probable transcriptional regulator VC1968, C-terminal domain
71	d1e5ra_	Alignment	not modelled	75.8	18	Fold: Double-stranded beta-helix Superfamily: Clavaminatase synthase-like Family: Type II Proline 3-hydroxylase (proline oxidase)
72	c6jyvA_	Alignment	not modelled	75.8	20	PDB header: metal binding protein Chain: A: PDB Molecule: probable iron/ascorbate oxidoreductase; PDBTitle: structure of an isopenicillin n synthase from pseudomonas aeruginosa2 pao1
73	c3on7C_	Alignment	not modelled	75.4	13	PDB header: oxidoreductase Chain: C: PDB Molecule: oxidoreductase, iron/ascorbate family; PDBTitle: crystal structure of a putative oxygenase (so_2589) from shewanella2 oneidensis at 2.20 a resolution
74	c3thtB_	Alignment	not modelled	74.8	23	PDB header: oxidoreductase Chain: B: PDB Molecule: alkylated dna repair protein alkb homolog 8; PDBTitle: crystal structure and rna binding properties of the rrm/alkb domains2 in human abh8, an enzyme catalyzing trna hypermodification, northeast3 structural genomics consortium target hr5601b
75	c3w20B_	Alignment	not modelled	74.7	14	PDB header: oxidoreductase Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a novel n-substituted l-amino acid

						dioxygenase2 from burkholderia ambifaria ammd PDB header: biosynthetic protein
76	c3h7yA_	Alignment	not modelled	74.4	22	Chain: A: PDB Molecule: bacilysin biosynthesis protein bacb; PDBTitle: crystal structure of bacb, an enzyme involved in bacilysin synthesis,2 in tetragonal form
77	d2bnma2	Alignment	not modelled	73.8	14	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1459-like
78	d1jr7a_	Alignment	not modelled	71.8	18	Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: Gab protein (hypothetical protein YgaT)
79	d1vrba1	Alignment	not modelled	71.7	15	Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: Asparaginyl hydroxylase-like
80	c3cewA_	Alignment	not modelled	69.8	9	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized cupin protein; PDBTitle: crystal structure of a cupin protein (bf4112) from bacteroides2 fragilis. northeast structural genomics consortium target bfr205
81	c5j7mB_	Alignment	not modelled	69.1	17	PDB header: unknown function Chain: B: PDB Molecule: cupin 2 conserved barrel domain protein; PDBTitle: crystal structure of cupin 2 conserved barrel domain protein from2 kribbella flavida dsm 17836
82	c4ne0A_	Alignment	not modelled	67.3	10	PDB header: hydrolase Chain: A: PDB Molecule: l-arginine beta-hydroxylase; PDBTitle: crystal structure of non-heme iron oxygenase orfp d157a mutant in2 complex with (3s)-hydroxy-l-arg
83	c2bnoA_	Alignment	not modelled	65.1	14	PDB header: oxidoreductase Chain: A: PDB Molecule: epoxidase; PDBTitle: the structure of hydroxypropylphosphonic acid epoxidase from s.2 wedmorenis.
84	c5u57B_	Alignment	not modelled	65.0	11	PDB header: oxidoreductase Chain: B: PDB Molecule: (s)-2-hydroxypropylphosphonic acid epoxidase; PDBTitle: psf4 in complex with fe2+ and (s)-2-hpp
85	d2fdia1	Alignment	not modelled	63.6	12	Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: AlkB-like
86	c3ibmB_	Alignment	not modelled	62.5	8	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: cupin 2, conserved barrel domain protein; PDBTitle: crystal structure of a cupin 2 domain-containing protein hha1_0468 from2 halorhodospira halophila
87	c4i4aA_	Alignment	not modelled	61.9	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: similar to unknown protein; PDBTitle: crystal structure of plu4264 protein from photorhabdus luminescens
88	d1y0za_	Alignment	not modelled	61.6	17	Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: gamma-Butyrobetaine hydroxylase
89	d2ix0a3	Alignment	not modelled	61.5	19	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
90	d1w9ya1	Alignment	not modelled	58.2	13	Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: Penicillin synthase-like
91	c2fqpD_	Alignment	not modelled	53.2	15	PDB header: metal binding protein Chain: D: PDB Molecule: hypothetical protein bp2299; PDBTitle: crystal structure of a cupin domain (bp2299) from bordetella pertussis2 tohama i at 1.80 a resolution
92	d1gp6a_	Alignment	not modelled	52.5	12	Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: Penicillin synthase-like
93	d1x82a_	Alignment	not modelled	51.7	13	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Glucose-6-phosphate isomerase, GPI
94	c5eqnA_	Alignment	not modelled	51.4	21	PDB header: hydrolase Chain: A: PDB Molecule: frbj; PDBTitle: structure of phosphonate hydroxylase
95	c2fg0B_	Alignment	not modelled	51.0	28	PDB header: hydrolase Chain: B: PDB Molecule: cog0791: cell wall-associated hydrolases (invasion- PDBTitle: crystal structure of a putative gamma-d-glutamyl-l-diamino acid2 endopeptidase (npun_r0659) from nostoc punctiforme pcc 73102 at 1.793 a resolution
96	d2evra2	Alignment	not modelled	50.7	35	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: NlpC/P60
97	d2f4pa1	Alignment	not modelled	50.1	8	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1287-like
98	c6nwoD_	Alignment	not modelled	49.8	6	PDB header: transcription Chain: D: PDB Molecule: transcriptional regulator bgar; PDBTitle: structures of the transcriptional regulator bgar, a lactose sensor.
99	c4e2gE_	Alignment	not modelled	49.6	11	PDB header: structural genomics, unknown function Chain: E: PDB Molecule: cupin 2 conserved barrel domain protein; PDBTitle: crystal structure of cupin fold protein sthe2323 from sphaerobacter2 thermophilus
100	c4rd7A_	Alignment	not modelled	49.1	9	PDB header: unknown function Chain: A: PDB Molecule: cupin 2 conserved barrel domain protein; PDBTitle: the crystal structure of a cupin 2 conserved barrel domain protein2 from salinispora arenicola cns-205
101	c3kgzA_	Alignment	not modelled	47.9	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: cupin 2 conserved barrel domain protein; PDBTitle: crystal structure of a cupin 2 conserved barrel domain

						protein from2 rhodospseudomonas palustris
102	c3uyjA_	Alignment	not modelled	46.7	9	PDB header: oxidoreductase Chain: A: PDB Molecule: lysine-specific demethylase 8; PDBTitle: crystal structure of jmjD5 catalytic core domain in complex with2 nickle and alpha-kg
103	c3h8uA_	Alignment	not modelled	46.3	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized conserved protein with double-stranded PDBTitle: crystal structure of uncharacterized conserved protein with double-2 stranded beta-helix domain (yp_001338853.1) from klebsiella3 pneumoniae subsp. pneumoniae mgh 78578 at 1.80 a resolution
104	c5lunC_	Alignment	not modelled	45.2	14	PDB header: oxidoreductase Chain: C: PDB Molecule: 2-oxoglutarate-dependent ethylene/succinate-forming enzyme; PDBTitle: ethylene forming enzyme from pseudomonas syringae pv. phaseolicola -2 p1 ultra-high resolution crystal form in complex with iron, n-3 oxalyglycine and arginine
105	c6m9sC_	Alignment	not modelled	43.4	19	PDB header: oxidoreductase Chain: C: PDB Molecule: sznf; PDBTitle: crystal structure of semet sznf from streptomyces achromogenes var.2 streptozoticus nrml 2697
106	c3a16C_	Alignment	not modelled	43.2	10	PDB header: unknown function Chain: C: PDB Molecule: jmjc domain-containing protein c2orf60; PDBTitle: crystal structure of human tyw5
107	d1ds1a_	Alignment	not modelled	42.6	29	Fold: Double-stranded beta-helix Superfamily: Clavaminatase synthase-like Family: Clavaminatase synthase
108	c2oa2A_	Alignment	not modelled	42.6	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: bh2720 protein; PDBTitle: crystal structure of bh2720 (10175341) from bacillus halodurans at2 1.41 a resolution
109	c5bxxA_	Alignment	not modelled	41.6	15	PDB header: lyase Chain: A: PDB Molecule: l-ectoine synthase; PDBTitle: crystal structure of the ectoine synthase from the cold-adapted marine2 bacterium sphingopyxis alaskensis
110	c6dawA_	Alignment	not modelled	41.2	27	PDB header: oxidoreductase Chain: A: PDB Molecule: non-heme iron hydroxylase; PDBTitle: x-ray crystal structure of napi l-arginine desaturase bound to fe(ii),2 l-arginine, and acetate
111	c6cboB_	Alignment	not modelled	40.7	13	PDB header: transferase Chain: B: PDB Molecule: c-6' aminotransferase; PDBTitle: x-ray structure of genb1 from micromonospora echinospora in complex2 with neamine and plp (as the external aldimine)
112	c4ne0B_	Alignment	not modelled	40.4	11	PDB header: hydrolase Chain: B: PDB Molecule: l-arginine beta-hydroxylase; PDBTitle: crystal structure of non-heme iron oxygenase orfp d157a mutant in2 complex with (3s)-hydroxy-l-arg
113	c6f6jC_	Alignment	not modelled	40.2	18	PDB header: oxidoreductase Chain: C: PDB Molecule: l-lysine 3-hydroxylase; PDBTitle: crystal structure of the fe(ii)/alpha-ketoglutarate dependent2 dioxygenase kdo1 with fe(ii)/succinate/(3s)-3-hydroxy-l-lysine
114	d1j3pa_	Alignment	not modelled	40.0	17	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Glucose-6-phosphate isomerase, GPI
115	c2q30C_	Alignment	not modelled	39.8	9	PDB header: unknown function Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a rmlc-like cupin protein (dde_2303) from2 desulfovibrio desulfuricans subsp. at 1.94 a resolution
116	c4diqA_	Alignment	not modelled	39.6	12	PDB header: oxidoreductase Chain: A: PDB Molecule: lysine-specific demethylase no66; PDBTitle: crystal structure of human no66
117	c2og5A_	Alignment	not modelled	39.2	23	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxygenase; PDBTitle: crystal structure of asparagine oxygenase (asno)
118	c4bifC_	Alignment	not modelled	39.1	12	PDB header: lyase Chain: C: PDB Molecule: cupin 2 conserved barrel domain protein; PDBTitle: biochemical and structural characterisation of a novel2 manganese-dependent hydroxynitrile lyase from bacteria
119	c3ooxA_	Alignment	not modelled	39.1	24	PDB header: oxidoreductase Chain: A: PDB Molecule: putative 2og-fe(ii) oxygenase family protein; PDBTitle: crystal structure of a putative 2og-fe(ii) oxygenase family protein2 (cc_0200) from caulobacter crescentus at 1.44 a resolution
120	c4nubA_	Alignment	not modelled	38.7	8	PDB header: oxidoreductase Chain: A: PDB Molecule: 50s ribosomal protein l16 arginine hydroxylase; PDBTitle: crystal structure of escherichia coli ribosomal oxygenase ycfD