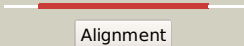

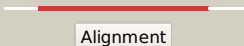

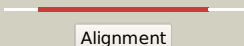







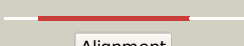











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3633_(-)_4071970_4072845
Date	Fri Aug 9 18:20:32 BST 2019
Unique Job ID	57b5b5727c40f50a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4naoA_	 Alignment		100.0	22	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxygenase; PDBTitle: crystal structure of eash
2	c5daqA_	 Alignment		100.0	22	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
3	c5m0tA_	 Alignment		100.0	27	PDB header: oxidoreductase Chain: A: PDB Molecule: alpha-ketoglutarate-dependent non-heme iron oxygenase eash; PDBTitle: alpha-ketoglutarate-dependent non-heme iron oxygenase eash
4	c4zonB_	 Alignment		100.0	23	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: B: PDB Molecule: verruculogen synthase; PDBTitle: structure of ftmox1 with fumitremorgen b complex
5	c5zm4B_	 Alignment		100.0	28	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	26	PDB header: oxidoreductase Chain: A: PDB Molecule: prha; PDBTitle: fe(ii)/(alpha)ketoglutarate-dependent dioxygenase prha in complex with2 preaustinoi d a1
7	c6ec3C_	 Alignment		100.0	22	PDB header: transferase, oxidoreductase Chain: C: PDB Molecule: methyltransferase domain-containing protein; PDBTitle: crystal structure of evdm1
8	c4xbzB_	 Alignment		100.0	17	PDB header: oxidoreductase Chain: B: PDB Molecule: evdo1; PDBTitle: crystal structure of evdo1 from micromonospora carbonacea var.2 aurantiaca
9	d2fcta1	 Alignment		100.0	18	Fold: Double-stranded beta-helix Superfamily: Clavaminat synthase-like Family: PhyH-like
10	c3emrA_	 Alignment		100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: ectd; PDBTitle: crystal structure analysis of the ectoine hydroxylase ectd from2 salibacillus salexigens
11	c3gjbA_	 Alignment		100.0	16	PDB header: biosynthetic protein Chain: A: PDB Molecule: cytc3; PDBTitle: cytc3 with fe(ii) and alpha-ketoglutarate

12	c4mhuB_	Alignment		100.0	19	PDB header: oxidoreductase Chain: B: PDB Molecule: ectoine hydroxylase; PDBTitle: crystal structure of ectd from s. alaskensis with bound fe
13	c5erlD_	Alignment		100.0	27	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
14	c2opwA_	Alignment		100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: phyhd1 protein; PDBTitle: crystal structure of human phytanoyl-coa dioxygenase phyhd1 (apo)
15	c5epaE_	Alignment		100.0	22	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	17	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	17	Fold: Double-stranded beta-helix Superfamily: Clavaminate synthase-like Family: PhyH-like
18	c3nnlB_	Alignment		100.0	17	PDB header: biosynthetic protein Chain: B: PDB Molecule: cura; PDBTitle: halogenase domain from cura module (crystal form iii)
19	c4xc9B_	Alignment		100.0	20	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidase/hydroxylase; PDBTitle: crystal structure of apo hygx from streptomyces hygrosopicus
20	c4xaaA_	Alignment		100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxygenase; PDBTitle: crystal structure of avio1 from streptomyces viridochromogenes tue57
21	c4xabA_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: evdo2; PDBTitle: crystal structure of evdo2 from micromonospora carbonacea var.2 aurantiaca
22	c2rdsA_	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: 1-deoxypentalenic acid 11-beta hydroxylase; fe(ii)/alpha- PDBTitle: crystal structure of ptlh with fe/oxalylglycine and ent-1-2 deoxypentalenic acid bound
23	c4iw3J_	Alignment	not modelled	99.4	22	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	c2g19A_	Alignment	not modelled	99.3	17	PDB header: oxidoreductase Chain: A: PDB Molecule: egl nine homolog 1; PDBTitle: cellular oxygen sensing: crystal structure of hypoxia-inducible factor2 prolyl hydroxylase (phd2)
25	c6f0wA_	Alignment	not modelled	99.3	16	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	c6iuqA_	Alignment	not modelled	99.2	20	PDB header: oxidoreductase Chain: A: PDB Molecule: prolyl 4-hydroxylase; PDBTitle: crystal structure and expression patterns of prolyl 4-hydroxylases2 from phytophthora capsici
27	c3ouiA_	Alignment	not modelled	99.1	19	PDB header: oxidoreductase Chain: A: PDB Molecule: egl nine homolog 1; PDBTitle: phd2-r717 with 40787422
28	d2csga1	Alianment	not modelled	98.9	16	Fold: Double-stranded beta-helix Superfamily: Clavaminate synthase-like

						Family:YbiU-like
29	c3rgkA	Alignment	not modelled	98.9	15	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
30	c2dbiA	Alignment	not modelled	98.8	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ybiu; PDBTitle: crystal structure of a hypothetical protein jw0805 from2 escherichia coli
31	c5c5tB	Alignment	not modelled	98.6	8	PDB header: oxidoreductase Chain: B: PDB Molecule: prolyl 4-hydroxylase; PDBTitle: the crystal structure of viral collagen prolyl hydroxylase vcph from2 paramecium bursaria chlorella virus-1 - 2og complex
32	c3dkqB	Alignment	not modelled	98.5	15	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
33	c2jijA	Alignment	not modelled	98.5	15	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
34	c3itqB	Alignment	not modelled	98.4	17	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	c3bvcA	Alignment	not modelled	97.9	12	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
36	c6ax6B	Alignment	not modelled	97.9	14	PDB header: oxidoreductase Chain: B: PDB Molecule: procollagen lysyl hydroxylase and glycosyltransferase; PDBTitle: the crystal structure of a lysyl hydroxylase from acanthamoeba2 polyphaga mimivirus
37	d1oiha	Alignment	not modelled	97.8	24	Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: TauD/TfdA-like
38	d1otja	Alignment	not modelled	97.8	22	Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: TauD/TfdA-like
39	c3mguA	Alignment	not modelled	97.8	12	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
40	c3r1jB	Alignment	not modelled	97.8	24	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
41	c3kt4A	Alignment	not modelled	97.6	15	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
42	c5hsxB	Alignment	not modelled	97.6	18	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
43	c5vn6B	Alignment	not modelled	97.5	18	PDB header: oxidoreductase Chain: B: PDB Molecule: taurine dioxygenase; PDBTitle: crystal structure of taurine dioxygenase from burkholderia ambifaria
44	c4j5iH	Alignment	not modelled	97.5	22	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
45	c2iuwA	Alignment	not modelled	97.4	18	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
46	c6npcB	Alignment	not modelled	97.4	17	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
47	d2iuwa1	Alignment	not modelled	97.4	16	Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: AlkB-like
48	c6d1oD	Alignment	not modelled	97.4	16	PDB header: oxidoreductase Chain: D: PDB Molecule: (r)-phenoxypropionate/alpha-ketoglutarate-dioxygenase; PDBTitle: ft_5 dioxygenase apoenzyme
49	d1nx4a	Alignment	not modelled	97.3	24	Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: gamma-Butyrobetaine hydroxylase
50	c6dchA	Alignment	not modelled	97.3	20	PDB header: oxidoreductase Chain: A: PDB Molecule: scoe protein; PDBTitle: structure of isonitrile biosynthesis enzyme scoe
51	c4y0eB	Alignment	not modelled	97.3	23	PDB header: oxidoreductase Chain: B: PDB Molecule: putative dioxygenase; PDBTitle: x-ray crystal structure of a putative dioxygenase from mycobacterium2 abscessus
52	c3ms5A	Alignment	not modelled	97.2	15	PDB header: oxidoreductase Chain: A: PDB Molecule: gamma-butyrobetaine dioxygenase; PDBTitle: crystal structure of human gamma-butyrobetaine,2-oxoglutarate2 dioxygenase 1 (bbox1)

53	c3pvjB_	Alignment	not modelled	97.2	27	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
54	c5bkeF_	Alignment	not modelled	97.1	20	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-oxalylglycine
55	c3eatX_	Alignment	not modelled	97.0	20	PDB header: oxidoreductase Chain: X: PDB Molecule: pyoverdine biosynthesis protein pvcb; PDBTitle: crystal structure of the pvcb (pa2255) protein from2 pseudomonas aeruginosa
56	c4qkbA_	Alignment	not modelled	96.8	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)
57	c4nhyC_	Alignment	not modelled	96.8	11	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	c5j92B_	Alignment	not modelled	96.7	21	PDB header: oxidoreductase 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
59	c4lt5A_	Alignment	not modelled	96.5	18	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	c5ylbA_	Alignment	not modelled	96.5	16	PDB header: oxidoreductase Chain: A: PDB Molecule: uncharacterized protein p8a3.02c; PDBTitle: crystal structure of ofd2 from schizosaccharomyces pombe at 1.80 a
61	c4nj4A_	Alignment	not modelled	96.4	11	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: A: PDB Molecule: rna demethylase alkbh5; PDBTitle: crystal structure of human alkbh5
62	c3btzA_	Alignment	not modelled	96.0	13	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
63	c6fxyA_	Alignment	not modelled	95.7	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
64	d1y0za_	Alignment	not modelled	95.6	18	Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: gamma-Butyrobetaine hydroxylase
65	c4diqA_	Alignment	not modelled	95.5	9	PDB header: oxidoreductase Chain: A: PDB Molecule: lysine-specific demethylase no66; PDBTitle: crystal structure of human no66
66	c5xoiA_	Alignment	not modelled	95.4	15	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, 2og-fe oxygenase family protein, putative, PDBTitle: the structure of osalkbh1
67	c3pl0B_	Alignment	not modelled	95.3	15	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
68	c5jqyA_	Alignment	not modelled	95.2	12	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)
69	d2fdia1	Alignment	not modelled	94.8	15	Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: AlkB-like
70	c3rcqA_	Alignment	not modelled	94.1	12	PDB header: oxidoreductase Chain: A: PDB Molecule: aspartyl/asparaginyl beta-hydroxylase; PDBTitle: crystal structure of human aspartate beta-hydroxylase isoform a
71	c6n1fD_	Alignment	not modelled	94.0	12	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
72	d1dcsa_	Alignment	not modelled	93.4	13	Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: Penicillin synthase-like
73	c5lunC_	Alignment	not modelled	92.9	16	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 oxalylglycine and arginine
74	c2xdvA_	Alignment	not modelled	92.6	14	PDB header: nuclear protein Chain: A: PDB Molecule: myc-induced nuclear antigen; PDBTitle: crystal structure of the catalytic domain of flj14393
75	c6jyvA_	Alignment	not modelled	89.5	22	PDB header: metal binding protein Chain: A: PDB Molecule: probable iron/ascorbate oxidoreductase; PDBTitle: structure of an isopenicillin n synthase from pseudomonas aeruginosa2 pao1 PDB header: oxidoreductase

76	c4nubA	Alignment	not modelled	89.1	12	Chain: A: PDB Molecule: 50s ribosomal protein l16 arginine hydroxylase; PDBTitle: crystal structure of escherichia coli ribosomal oxygenase ycfD
77	c4cswA	Alignment	not modelled	88.6	14	PDB header: oxidoreductase Chain: A: PDB Molecule: cupin 4 family protein; PDBTitle: rhodothermus marinus ycfD-like ribosomal protein l16 arginyl2 hydroxylase
78	d1w9ya1	Alignment	not modelled	87.7	17	Fold: Double-stranded beta-helix Superfamily: Clavaminic synthase-like Family: Penicillin synthase-like
79	c6b8wB	Alignment	not modelled	86.3	12	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.
80	c5gj9A	Alignment	not modelled	84.6	18	PDB header: oxidoreductase Chain: A: PDB Molecule: 1-aminocyclopropane-1-carboxylate oxidase 2; PDBTitle: crystal structure of arabidopsis thaliana aco2 in complex with poa
81	d1vrba1	Alignment	not modelled	83.9	16	Fold: Double-stranded beta-helix Superfamily: Clavaminic synthase-like Family: Asparaginyl hydroxylase-like
82	c4p7xA	Alignment	not modelled	81.9	18	PDB header: oxidoreductase Chain: A: PDB Molecule: l-proline cis-4-hydroxylase; PDBTitle: l-pipecolic acid-bound l-proline cis-4-hydroxylase
83	c3on7C	Alignment	not modelled	80.8	14	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
84	c2og5A	Alignment	not modelled	80.3	16	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxygenase; PDBTitle: crystal structure of asparagine oxygenase (asno)
85	d1gp6a	Alignment	not modelled	80.1	13	Fold: Double-stranded beta-helix Superfamily: Clavaminic synthase-like Family: Penicillin synthase-like
86	d2bnma2	Alignment	not modelled	80.0	16	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1459-like
87	d1y9qa2	Alignment	not modelled	79.3	14	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Probable transcriptional regulator VC1968, C-terminal domain
88	d1odma	Alignment	not modelled	78.1	16	Fold: Double-stranded beta-helix Superfamily: Clavaminic synthase-like Family: Penicillin synthase-like
89	c2bnoA	Alignment	not modelled	77.9	14	PDB header: oxidoreductase Chain: A: PDB Molecule: epoxidase; PDBTitle: the structure of hydroxypropylphosphonic acid epoxidase from s.2 wedmorenis.
90	c3ibmB	Alignment	not modelled	76.9	7	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: cupin 2, conserved barrel domain protein; PDBTitle: crystal structure of cupin 2 domain-containing protein hha1_0468 from2 halorhodospira halophila
91	c3h7yA	Alignment	not modelled	76.7	26	PDB header: biosynthetic protein Chain: A: PDB Molecule: bacilysin biosynthesis protein bacb; PDBTitle: crystal structure of bacb, an enzyme involved in bacilysin synthesis,2 in tetragonal form
92	c3cewA	Alignment	not modelled	76.3	18	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
93	c5o7yA	Alignment	not modelled	76.1	14	PDB header: oxidoreductase Chain: A: PDB Molecule: thebaine 6-o-demethylase; PDBTitle: thebaine 6-o-demethylase (t6odm) from papaver somniferum in complex2 with succinate
94	c4xaeB	Alignment	not modelled	71.5	16	PDB header: oxidoreductase Chain: B: PDB Molecule: feruloyl coa ortho-hydroxylase 1; PDBTitle: structure of feruloyl-coa 6-hydroxylase (f6h) from arabidopsis2 thaliana
95	c4ne0A	Alignment	not modelled	71.0	18	PDB header: hydrolase Chain: A: PDB Molecule: l-arginine beta-hydroxylase; PDBTitle: crystal structure of non-heme iron oxygenase orp d157a mutant in2 complex with (3s)-hydroxy-l-arg
96	d1ds1a	Alignment	not modelled	71.0	22	Fold: Double-stranded beta-helix Superfamily: Clavaminic synthase-like Family: Clavaminic synthase
97	c5u57B	Alignment	not modelled	70.1	22	PDB header: oxidoreductase Chain: B: PDB Molecule: (s)-2-hydroxypropylphosphonic acid epoxidase; PDBTitle: psf4 in complex with fe2+ and (s)-2-hpp
98	c4i4aA	Alignment	not modelled	70.0	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: similar to unknown protein; PDBTitle: crystal structure of plu4264 protein from photorhabdus luminescens
99	d1jr7a	Alignment	not modelled	68.7	13	Fold: Double-stranded beta-helix Superfamily: Clavaminic synthase-like Family: Gab protein (hypothetical protein YgaT)
100	d2ix0a3	Alignment	not modelled	67.5	23	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
						PDB header: oxidoreductase Chain: B: PDB Molecule: alkylated dna repair protein alkB homolog 8;

101	c3thtB_	Alignment	not modelled	65.9	17	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
102	c2fqpD_	Alignment	not modelled	63.6	12	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
103	d1dgwa_	Alignment	not modelled	63.3	11	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Germin/Seed storage 7S protein
104	c6nwoD_	Alignment	not modelled	62.6	21	PDB header: transcription Chain: D: PDB Molecule: transcriptional regulator bgar; PDBTitle: structures of the transcriptional regulator bgar, a lactose sensor.
105	c3o27B_	Alignment	not modelled	59.5	16	PDB header: dna binding protein Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: the crystal structure of c68 from the hybrid virus-plasmid pssvx
106	d2f4pa1	Alignment	not modelled	59.0	10	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: TM1287-like
107	c6f6jC_	Alignment	not modelled	57.2	17	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
108	c3h8uA_	Alignment	not modelled	57.0	27	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
109	d1uika1	Alignment	not modelled	54.1	15	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Germin/Seed storage 7S protein
110	d1e5ra_	Alignment	not modelled	53.7	19	Fold: Double-stranded beta-helix Superfamily: Clavaminate synthase-like Family: Type II Proline 3-hydroxylase (proline oxidase)
111	c5eqnA_	Alignment	not modelled	53.1	12	PDB header: hydrolase Chain: A: PDB Molecule: frbj; PDBTitle: structure of phosphonate hydroxylase
112	c2gu9B_	Alignment	not modelled	52.5	17	PDB header: immune system Chain: B: PDB Molecule: tetracenomycin polyketide synthesis protein; PDBTitle: crystal structure of xc5357 from xanthomonas campestris: a2 putative tetracenomycin polyketide synthesis protein3 adopting a novel cupin subfamily structure
113	c4e2gE_	Alignment	not modelled	52.3	15	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 spheroobacter2 thermophilus
114	c3al6C_	Alignment	not modelled	51.4	16	PDB header: unknown function Chain: C: PDB Molecule: jnjc domain-containing protein c2orf60; PDBTitle: crystal structure of human tyw5
115	d1uija1	Alignment	not modelled	50.8	11	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Germin/Seed storage 7S protein
116	c5c3qB_	Alignment	not modelled	48.8	10	PDB header: oxidoreductase Chain: B: PDB Molecule: thymine dioxygenase; PDBTitle: crystal structure of the full-length neurospora crassa t7h in complex2 with alpha-kg and thymine (t)
117	c2fg0B_	Alignment	not modelled	48.7	26	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
118	d1od5a2	Alignment	not modelled	48.3	10	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Germin/Seed storage 7S protein
119	c5j7mB_	Alignment	not modelled	48.1	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
120	c6m9sC_	Alignment	not modelled	48.0	19	PDB header: oxidoreductase Chain: C: PDB Molecule: sznf; PDBTitle: crystal structure of semet sznf from streptomyces achromogenes var.2 streptozoticus nr1 2697