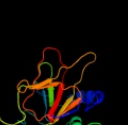
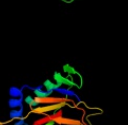
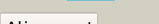
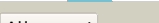
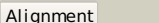
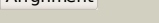
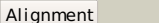
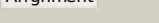
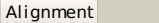
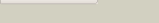
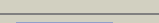
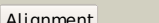
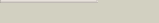
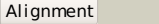
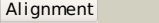
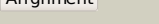
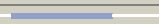


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3dkqB_	 Alignment		100.0	54	PDB header: oxidoreductase Chain: B; PDB Molecule: pkhd-type hydroxylase sbal_3634; PDBTitle: crystal structure of putative oxygenase (yp_001051978.1) from <i>Shewanella baltica</i> OS155 at 2.26 Å resolution
2	c2jijA_	 Alignment		100.0	17	PDB header: hydrolase Chain: A; PDB Molecule: prolyl-4 hydroxylase; PDBTitle: crystal structure of the apo form of Chlamydomonas reinhardtii prolyl-4 hydroxylase type I
3	c3itqB_	 Alignment		100.0	19	PDB header: oxidoreductase Chain: B; PDB Molecule: prolyl 4-hydroxylase, alpha subunit domain protein; PDBTitle: crystal structure of a prolyl 4-hydroxylase from <i>Bacillus anthracis</i>
4	c3ouiA_	 Alignment		99.9	16	PDB header: oxidoreductase Chain: A; PDB Molecule: egl nine homolog 1; PDBTitle: phd2-r717 with 40787422
5	c2g19A_	 Alignment		99.9	12	PDB header: oxidoreductase Chain: A; PDB Molecule: egl nine homolog 1; PDBTitle: cellular oxygen sensing: crystal structure of hypoxia-2 inducible factor prolyl hydroxylase (phd2)
6	c3kt4A_	 Alignment		99.6	13	PDB header: oxidoreductase Chain: A; PDB Molecule: pkhd-type hydroxylase tpa1; PDBTitle: crystal structure of tpa1 from <i>Saccharomyces cerevisiae</i> , α2 component of the messenger ribonucleoprotein complex
7	c3gjbA_	 Alignment		99.0	13	PDB header: biosynthetic protein Chain: A; PDB Molecule: cytc3; PDBTitle: cytc3 with Fe(II) and α-ketoglutarate
8	c3bvcA_	 Alignment		98.8	17	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein ISM_01780; PDBTitle: crystal structure of uncharacterized protein ISM_01780 from <i>Roseovarius nubinhibens</i> ISM
9	d2fcta1	 Alignment		98.7	14	Fold: Double-stranded beta-helix Superfamily: Clavaminate synthase-like Family: PhyH-like
10	c3emrA_	 Alignment		98.7	15	PDB header: oxidoreductase Chain: A; PDB Molecule: ectd; PDBTitle: crystal structure analysis of the ectoine hydroxylase EctD from <i>Salibacillus salicigenus</i>
11	d2fdia1	 Alignment		98.6	19	Fold: Double-stranded beta-helix Superfamily: Clavaminate synthase-like Family: AlkB-like
						PDB header: oxidoreductase

12	c3thtB_	Alignment		98.6	15	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
13	c2opwA_	Alignment		98.6	14	PDB header: oxidoreductase Chain: A: PDB Molecule: phyhd1 protein; PDBTitle: crystal structure of human phytanoyl-coa dioxygenase phyhd1 (apo)
14	c3nnlB_	Alignment		98.5	17	PDB header: biosynthetic protein Chain: B: PDB Molecule: cura; PDBTitle: halogenase domain from cura module (crystal form iii)
15	d2alxa1	Alignment		98.5	16	Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: PhyH-like
16	c2iuwA_	Alignment		98.4	19	PDB header: oxidoreductase Chain: A: PDB Molecule: alkylated repair protein alkb homolog 3; PDBTitle: crystal structure of human abh3 in complex with iron ion2 and 2-oxoglutarate
17	d2iuwa1	Alignment		98.3	18	Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: AlkB-like
18	c2rdsA_	Alignment		98.3	10	PDB header: oxidoreductase Chain: A: PDB Molecule: 1-deoxypentalenic acid 11-beta hydroxylase; fe(ii)/alpha- PDBTitle: crystal structure of pth with fe/oxalylglycine and ent-1-2 deoxypentalenic acid bound
19	c3btzA_	Alignment		98.0	14	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
20	d1w9ya1	Alignment		96.8	17	Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: Penicillin synthase-like
21	d1odma_	Alignment	not modelled	96.1	18	Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: Penicillin synthase-like
22	d1dcsa_	Alignment	not modelled	95.0	18	Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: Penicillin synthase-like
23	d1oiha_	Alignment	not modelled	94.8	20	Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: TauD/TfdA-like
24	c3pl0B_	Alignment	not modelled	94.7	37	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
25	d1gp6a_	Alignment	not modelled	94.5	19	Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: Penicillin synthase-like
26	c3on7C_	Alignment	not modelled	93.7	17	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
27	c3ooxA_	Alignment	not modelled	93.4	21	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
28	d1vrba1	Alignment	not modelled	93.2	17	Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: Asparaginyl hydroxylase-like
						PDB header: oxidoreductase

29	c3eatX_	Alignment	not modelled	92.8	20	Chain: X: PDB Molecule: pyoverdine biosynthesis protein pvcb; PDBTitle: crystal structure of the pvcb (pa2255) protein from2 pseudomonas aeruginosa
30	c3r1jB_	Alignment	not modelled	91.0	22	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
31	c2dbiA_	Alignment	not modelled	89.9	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ybiu; PDBTitle: crystal structure of a hypothetical protein jw0805 from2 escherichia coli
32	c3rcqA_	Alignment	not modelled	88.1	13	PDB header: oxidoreductase Chain: A: PDB Molecule: aspartyl/asparaginyl beta-hydroxylase; PDBTitle: crystal structure of human aspartate beta-hydroxylase isoform a
33	d2csqa1	Alignment	not modelled	88.1	20	Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: YbiU-like
34	d1h2ka_	Alignment	not modelled	87.3	20	Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: Hypoxia-inducible factor HIF inhibitor (FIH1)
35	c3ms5A_	Alignment	not modelled	82.3	27	PDB header: oxidoreductase Chain: A: PDB Molecule: gamma-butyrobetaine dioxygenase; PDBTitle: crystal structure of human gamma-butyrobetaine,2-oxoglutarate2 dioxygenase 1 (bbox1)
36	c2xdvA_	Alignment	not modelled	81.4	18	PDB header: nuclear protein Chain: A: PDB Molecule: myc-induced nuclear antigen; PDBTitle: crystal structure of the catalytic domain of flj14393
37	d1nx4a_	Alignment	not modelled	70.5	19	Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: gamma-Butyrobetaine hydroxylase
38	c3uyiA_	Alignment	not modelled	68.9	18	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
39	c3ht2A_	Alignment	not modelled	66.7	14	PDB header: lyase Chain: A: PDB Molecule: remf protein; PDBTitle: zink containing polyketide cyclase remf from streptomyces2 resistomycificus
40	c3al6A_	Alignment	not modelled	66.4	22	PDB header: unknown function Chain: A: PDB Molecule: jmjC domain-containing protein c2orf60; PDBTitle: crystal structure of human tyw5
41	d1yfua1	Alignment	not modelled	60.4	20	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: 3-hydroxyanthranilic acid dioxygenase-like
42	d1otja_	Alignment	not modelled	55.9	16	Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: TauD/TfdA-like
43	d3bb6a1	Alignment	not modelled	55.6	12	Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: TehB-like
44	c2og5A_	Alignment	not modelled	53.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxygenase; PDBTitle: crystal structure of asparagine oxygenase (asno)
45	d2bnma2	Alignment	not modelled	52.7	18	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1459-like
46	c3pviB_	Alignment	not modelled	49.0	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
47	d1y0za_	Alignment	not modelled	47.2	24	Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: gamma-Butyrobetaine hydroxylase
48	d1sfna_	Alignment	not modelled	47.1	13	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: YlbA-like
49	d1jr7a_	Alignment	not modelled	46.9	23	Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: Gab protein (hypothetical protein YgaT)
50	d1ds1a_	Alignment	not modelled	46.8	30	Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: Clavamate synthase
51	c2bnoA_	Alignment	not modelled	45.7	20	PDB header: oxidoreductase Chain: A: PDB Molecule: epoxidase; PDBTitle: the structure of hydroxypropylphosphonic acid epoxidase2 from s. wedmorens.
52	d1pzqa_	Alignment	not modelled	44.4	32	Fold: Dimerisation interlock Superfamily: Docking domain A of the erythromycin polyketide synthase (DEBS) Family: Docking domain A of the erythromycin polyketide synthase (DEBS)
53	c3ibmB_	Alignment	not modelled	43.4	10	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 hhal_0468 from2 halorhodospira halophila
54	c3rnsA_	Alignment	not modelled	40.7	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: cupin 2 conserved barrel domain protein; PDBTitle: cupin 2 conserved barrel domain protein from leptotrichia buccalis

55	c3bcwB	 Alignment	not modelled	38.4	27	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a duf861 family protein with a rmlc-like cupin2 fold (bb1179) from bordetella bronchiseptica rb50 at 1.60 a3 resolution
56	c2pfbB	 Alignment	not modelled	36.3	30	PDB header: unknown function Chain: B: PDB Molecule: cupin 2, conserved barrel domain protein; PDBTitle: crystal structure of a rmlc-like cupin (sfri_3105) from shewanella2 frigidimarina ncimb 400 at 1.90 a resolution
57	c3lwcA	 Alignment	not modelled	35.6	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of structural genomics, unknown function2 (yp_766765.1) from rhizobium leguminosarum bv. viciae 3841 at 1.40 a3 resolution
58	c3kvaA	 Alignment	not modelled	35.1	19	PDB header: h3k4me3 binding protein, transferase Chain: A: PDB Molecule: jmc domain-containing histone demethylation protein 1d; PDBTitle: structure of kaa1718 jumonji domain in complex with alpha-2 ketoglutarate
59	c3k3nA	 Alignment	not modelled	34.4	19	PDB header: oxidoreductase Chain: A: PDB Molecule: phd finger protein 8; PDBTitle: crystal structure of the catalytic core domain of human phf8
60	c2i45C	 Alignment	not modelled	32.9	19	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of protein nmb1881 from neisseria meningitidis
61	c2fqpd	 Alignment	not modelled	31.6	21	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
62	c2wbqA	 Alignment	not modelled	30.4	16	PDB header: oxidoreductase Chain: A: PDB Molecule: l-arginine beta-hydroxylase; PDBTitle: crystal structure of vioc in complex with (2s,3s)-2 hydroxyarginine
63	d1o5ua	 Alignment	not modelled	29.9	27	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Hypothetical protein TM1112
64	c3h7yA	 Alignment	not modelled	29.9	9	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
65	c3fjsC	 Alignment	not modelled	29.8	21	PDB header: biosynthetic protein Chain: C: PDB Molecule: uncharacterized protein with rmlc-like cupin fold; PDBTitle: crystal structure of a putative biosynthetic protein with rmlc-like2 cupin fold (reut_b4087) from ralstonia eutropha jmp134 at 1.90 a3 resolution
66	d1j58a	 Alignment	not modelled	29.4	19	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
67	c3pu3A	 Alignment	not modelled	29.0	14	PDB header: protein binding Chain: A: PDB Molecule: phd finger protein 2; PDBTitle: phf2 jumonji domain-nog complex
68	c2q30C	 Alignment	not modelled	28.7	22	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
69	c3i38E	 Alignment	not modelled	28.3	20	PDB header: chaperone Chain: E: PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
70	c3i38C	 Alignment	not modelled	28.3	20	PDB header: chaperone Chain: C: PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
71	c3i38A	 Alignment	not modelled	28.1	20	PDB header: chaperone Chain: A: PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
72	c3i38G	 Alignment	not modelled	28.1	20	PDB header: chaperone Chain: G: PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
73	d1dgwa	 Alignment	not modelled	26.8	17	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
74	d1vj2a	 Alignment	not modelled	26.0	20	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1459-like
75	c2yu1A	 Alignment	not modelled	25.5	33	PDB header: oxidoreductase Chain: A: PDB Molecule: jmc domain-containing histone demethylation protein 1a; PDBTitle: crystal structure of hjhdm1a complexed with a-ketoglutarate
76	d1v70a	 Alignment	not modelled	25.1	18	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1287-like
77	c3k2oB	 Alignment	not modelled	24.7	14	PDB header: oxidoreductase Chain: B: PDB Molecule: bifunctional arginine demethylase and lysyl-hydroxylase PDBTitle: structure of an oxygenase
78	c3i38L	 Alignment	not modelled	24.5	19	PDB header: chaperone Chain: L: PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
		 Alignment				Fold: Double-stranded beta-helix

79	d1uija1	Alignment	not modelled	24.0	14	Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
80	c3kv4A	Alignment	not modelled	23.7	19	PDB header: h3k4me3 binding protein, transferase Chain: A: PDB Molecule: phd finger protein 8; PDBTitle: structure of phf8 in complex with histone h3
81	dlyhfa1	Alignment	not modelled	22.9	12	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1287-like
82	c3kv5D	Alignment	not modelled	22.7	19	PDB header: h3k4me3 binding protein, transferase Chain: D: PDB Molecule: jmjc domain-containing histone demethylation PDBTitle: structure of kiaa1718, human jumonji demethylase, in complex2 with n-oxalylglycine
83	c3i38D	Alignment	not modelled	21.3	20	PDB header: chaperone Chain: D: PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
84	c2ozia	Alignment	not modelled	20.9	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein rpa4178; PDBTitle: structural genomics, the crystal structure of a putative2 protein rpa4178 from rhodopseudomonas palustris cga009
85	c3i38J	Alignment	not modelled	20.8	20	PDB header: chaperone Chain: J: PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
86	d3dl3a1	Alignment	not modelled	20.3	15	Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: TehB-like
87	c2ozjB	Alignment	not modelled	19.8	21	PDB header: unknown function Chain: B: PDB Molecule: cupin 2, conserved barrel; PDBTitle: crystal structure of a cupin superfamily protein (dsy2733) from2 desulfitobacterium hafniense dcb-2 at 1.60 a resolution
88	c3i38H	Alignment	not modelled	19.6	19	PDB header: chaperone Chain: H: PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
89	d1j3pa	Alignment	not modelled	19.2	16	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Glucose-6-phosphate isomerase, GPI
90	c3d89A	Alignment	not modelled	19.2	7	PDB header: electron transport Chain: A: PDB Molecule: rieske domain-containing protein; PDBTitle: crystal structure of a soluble rieske ferredoxin from mus musculus
91	c3i38K	Alignment	not modelled	18.2	20	PDB header: chaperone Chain: K: PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
92	d1jm1a	Alignment	not modelled	17.7	16	Fold: ISP domain Superfamily: ISP domain Family: Rieske iron-sulfur protein (ISP)
93	d1xjva1	Alignment	not modelled	17.2	15	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
94	c2opkC	Alignment	not modelled	17.2	13	PDB header: isomerase Chain: C: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a putative mannose-6-phosphate isomerase2 (reut_a1446) from ralstonia eutropha jmp134 at 2.10 a resolution
95	c3i38B	Alignment	not modelled	17.2	19	PDB header: chaperone Chain: B: PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
96	c3d82A	Alignment	not modelled	16.9	20	PDB header: metal binding protein Chain: A: PDB Molecule: cupin 2, conserved barrel domain protein; PDBTitle: crystal structure of a cupin-2 domain containing protein (sfri_3543)2 from shewanella frigidimarina ncimb 400 at 2.05 a resolution
97	d1rc6a	Alignment	not modelled	16.3	16	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: YlbA-like
98	d1zrra1	Alignment	not modelled	15.7	19	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Acireductone dioxygenase
99	d1vm9a	Alignment	not modelled	14.9	15	Fold: ISP domain Superfamily: ISP domain Family: Rieske iron-sulfur protein (ISP)