

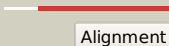



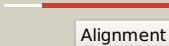

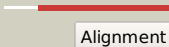

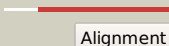




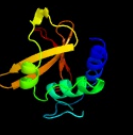


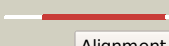


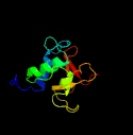


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1566c_(-)_1773934_1774626
Date	Fri Aug 2 13:30:15 BST 2019
Unique Job ID	f091e462cb6cfc80

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2xivA_	 Alignment		100.0	48	PDB header: structural protein Chain: A; PDB Molecule: hypothetical invasion protein; PDBTitle: structure of rv1477, hypothetical invasion protein of mycobacterium2 tuberculosis
2	c3gt2A_	 Alignment		100.0	84	PDB header: unknown function Chain: A; PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the p60 domain from m. avium paratuberculosis2 antigen map1272c
3	c3pbIA_	 Alignment		100.0	49	PDB header: hydrolase Chain: A; PDB Molecule: invasion protein; PDBTitle: structure of the peptidoglycan hydrolase ripb (rv1478) from2 mycobacterium tuberculosis at 1.6 resolution
4	c3i86A_	 Alignment		100.0	53	PDB header: hydrolase Chain: A; PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the p60 domain from m. avium subspecies2 paratuberculosis antigen map1204
5	c6biqA_	 Alignment		100.0	24	PDB header: hydrolase Chain: A; PDB Molecule: clan ca, family c40, nlp/p60 superfamily cysteine PDBTitle: structure of nlp2 from trichomonas vaginalis
6	c4fdyA_	 Alignment		100.0	28	PDB header: hydrolase Chain: A; PDB Molecule: similar to lipoprotein, nlp/p60 family; PDBTitle: crystal structure of a similar to lipoprotein, nlp/p60 family2 (sav0400) from staphylococcus aureus subsp. aureus mu50 at 2.23 a3 resolution
7	c2fg0B_	 Alignment		100.0	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
8	d2evra2	 Alignment		100.0	29	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: NlpC/P60
9	c3npgB_	 Alignment		100.0	29	PDB header: hydrolase Chain: B; PDB Molecule: putative dipeptidyl-peptidase vi; PDBTitle: crystal structure of a putative dipeptidyl-peptidase vi (bacova_00612)2 from bacteroides ovatus at 1.72 a resolution
10	c4hpeA_	 Alignment		100.0	28	PDB header: hydrolase Chain: A; PDB Molecule: putative cell wall hydrolase tn916-like,ctn1-orf17; PDBTitle: crystal structure of a putative cell wall hydrolase (cd630_03720) from2 clostridium difficile 630 at 2.38 a resolution
11	c3h41A_	 Alignment		100.0	33	PDB header: hydrolase Chain: A; PDB Molecule: nlp/p60 family protein; PDBTitle: crystal structure of a nlp/p60 family protein (bce_2878) from2 bacillus cereus atcc 10987 at 1.79 a resolution

12	c6b8cA_	Alignment		100.0	34	PDB header: hydrolase Chain: A: PDB Molecule: nlp/p60; PDBTitle: crystal structure of nlp/p60 domain of peptidoglycan hydrolase saga
13	c2k1gA_	Alignment		100.0	25	PDB header: lipoprotein Chain: A: PDB Molecule: lipoprotein spr; PDBTitle: solution nmr structure of lipoprotein spr from escherichia coli k12.2 northeast structural genomics target er541-37-162
14	c4xcmB_	Alignment		99.9	28	PDB header: hydrolase Chain: B: PDB Molecule: cell wall-binding endopeptidase-related protein; PDBTitle: crystal structure of the putative nlp/p60 d,l endopeptidase from t.2 thermophilus
15	c3m1uB_	Alignment		99.8	27	PDB header: hydrolase Chain: B: PDB Molecule: putative gamma-d-glutamyl-l-diamino acid endopeptidase; PDBTitle: crystal structure of a putative gamma-d-glutamyl-l-diamino acid2 endopeptidase (dву_0896) from desulfovibrio vulgaris hildenborough at3 1.75 a resolution
16	c2p1gA_	Alignment		99.1	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative xylanase; PDBTitle: crystal structure of a putative xylanase from bacteroides fragilis
17	c2kytA_	Alignment		98.2	24	PDB header: hydrolase Chain: A: PDB Molecule: group xvi phospholipase a2; PDBTitle: solution structure of the h-rev107 n-terminal domain
18	c2lktA_	Alignment		98.1	33	PDB header: hydrolase Chain: A: PDB Molecule: retinoic acid receptor responder protein 3; PDBTitle: solution structure of n-terminal domain of human tig3 in 2 m urea
19	c3kw0D_	Alignment		97.5	21	PDB header: hydrolase Chain: D: PDB Molecule: cysteine peptidase; PDBTitle: crystal structure of cysteine peptidase (np_982244.1) from bacillus2 cereus atcc 10987 at 2.50 a resolution
20	d2if6a1	Alignment		96.2	11	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: YiiX-like
21	c4hzbA_	Alignment	not modelled	95.8	22	PDB header: hydrolase Chain: A: PDB Molecule: putative cytoplasmic protein; PDBTitle: crystal structure of the type vi semet effector-immunity complex tae3-2 tai3 from ralstonia pickettii
22	c2lrjA_	Alignment	not modelled	93.2	32	PDB header: biosynthetic protein Chain: A: PDB Molecule: staphyloxanthin biosynthesis protein, putative; PDBTitle: nmr solution structure of staphyloxanthin biosynthesis protein
23	c4eyzB_	Alignment	not modelled	93.0	42	PDB header: hydrolase Chain: B: PDB Molecule: cellulosome-related protein module from ruminococcus PDBTitle: crystal structure of an uncommon cellulosome-related protein module2 from ruminococcus flavefaciens that resembles papain-like cysteine3 peptidases
24	c4pa5A_	Alignment	not modelled	92.3	18	PDB header: transferase Chain: A: PDB Molecule: protein-glutamine gamma-glutamyltransferase; PDBTitle: tgl - a bacterial spore coat transglutaminase - cystamine complex
25	c5udmA_	Alignment	not modelled	92.2	17	PDB header: hydrolase Chain: A: PDB Molecule: phage-associated cell wall hydrolase; PDBTitle: phage-associated cell wall hydrolase plypy from streptococcus2 pyogenes, space group p6522
26	c2k3aA_	Alignment	not modelled	92.0	18	PDB header: hydrolase Chain: A: PDB Molecule: chap domain protein; PDBTitle: nmr solution structure of staphylococcus saprophyticus chap2 (cysteine, histidine-dependent amidohydrolases/peptidases)3 domain protein. northeast structural genomics consortium4 target syr11
27	d2im9a1	Alignment	not modelled	90.1	15	Fold: Cysteine proteinases Superfamily: Cysteine proteinases

						Family: Lpg0564-like
28	c2im9A	Alignment	not modelled	90.1	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of protein lpg0564 from legionella pneumophila str.2 philadelphia 1, pfam duf1460
29	c4h4jA	Alignment	not modelled	89.7	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a n-acetylmuramoyl-l-alanine amidase2 (bacuni_02947) from bacteroides uniformis atcc 8492 at 1.15 a3 resolution
30	c4f4mA	Alignment	not modelled	84.7	42	PDB header: hydrolase regulator Chain: A: PDB Molecule: papain peptidoglycan amidase effector tse1; PDBTitle: structure of the type vi peptidoglycan amidase effector tse1 (c30a)2 from pseudomonas aeruginosa
31	c4f0wA	Alignment	not modelled	83.8	42	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of type effector tse1 c30a mutant from pseudomonas2 aeruginosa
32	c2q1dX	Alignment	not modelled	81.5	20	PDB header: lyase Chain: X: PDB Molecule: 2-keto-3-deoxy-d-arabinonate dehydratase; PDBTitle: 2-keto-3-deoxy-d-arabinonate dehydratase complexed with magnesium and2 2,5-dioxopentanoate
33	c4yxBA	Alignment	not modelled	76.7	16	PDB header: protein transport Chain: A: PDB Molecule: flagellar motor switch protein flim,flagellar motor switch PDBTitle: flim(spoa)::flin fusion protein
34	d1nkqa	Alignment	not modelled	74.5	37	Fold: FAH Superfamily: FAH Family: FAH
35	d2io8a2	Alignment	not modelled	74.0	33	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: CHAP domain
36	d1o9ya	Alignment	not modelled	74.0	16	Fold: Surface presentation of antigens (SPOA) Superfamily: Surface presentation of antigens (SPOA) Family: Surface presentation of antigens (SPOA)
37	c4cgkA	Alignment	not modelled	73.3	11	PDB header: cell cycle Chain: A: PDB Molecule: secreted 45 kda protein; PDBTitle: crystal structure of the essential protein pcsb from streptococcus2 pneumoniae
38	c3eopB	Alignment	not modelled	73.1	9	PDB header: unknown function Chain: B: PDB Molecule: thymocyte nuclear protein 1; PDBTitle: crystal structure of the duf55 domain of human thymocyte nuclear2 protein 1
39	c4nubA	Alignment	not modelled	72.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: 50s ribosomal protein l16 arginine hydroxylase; PDBTitle: crystal structure of escherichia coli ribosomal oxygenase ycfd
40	c4dbhA	Alignment	not modelled	71.5	22	PDB header: isomerase Chain: A: PDB Molecule: 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase; PDBTitle: crystal structure of cg1458 with inhibitor
41	d1gtta1	Alignment	not modelled	71.4	33	Fold: FAH Superfamily: FAH Family: FAH
42	d1sawa	Alignment	not modelled	71.2	26	Fold: FAH Superfamily: FAH Family: FAH
43	c3r6oA	Alignment	not modelled	71.0	26	PDB header: isomerase Chain: A: PDB Molecule: 2-hydroxyhepta-2,4-diene-1, 7-dioateisomerase; PDBTitle: crystal structure of a probable 2-hydroxyhepta-2,4-diene-1, 7-2 dioateisomerase from mycobacterium abscessus
44	c3s52A	Alignment	not modelled	70.9	26	PDB header: hydrolase Chain: A: PDB Molecule: putative fumarylacetoacetate hydrolase family protein; PDBTitle: crystal structure of a putative fumarylacetoacetate hydrolase family2 protein from yersinia pestis co92
45	d2gbsa1	Alignment	not modelled	70.8	41	Fold: PUA domain-like Superfamily: PUA domain-like Family: Atu2648/PH1033-like
46	c4maqB	Alignment	not modelled	69.8	44	PDB header: hydrolase Chain: B: PDB Molecule: putative fumarylpyruvate hydrolase; PDBTitle: crystal structure of a putative fumarylpyruvate hydrolase from2 burkholderia cenocepacia
47	c4olkB	Alignment	not modelled	69.3	13	PDB header: hydrolase Chain: B: PDB Molecule: endolysin; PDBTitle: the chap domain of lysgh15
48	d2ar1a1	Alignment	not modelled	68.3	13	Fold: PUA domain-like Superfamily: PUA domain-like Family: Atu2648/PH1033-like
49	cli7oC	Alignment	not modelled	68.1	30	PDB header: isomerase, lyase Chain: C: PDB Molecule: 4-hydroxyphenylacetate degradation bifunctional PDBTitle: crystal structure of hpce
50	c5xrwD	Alignment	not modelled	67.7	14	PDB header: motor protein Chain: D: PDB Molecule: flii; PDBTitle: crystal structure of flagellar motor switch complex from h. pylori
51	c3qdfA	Alignment	not modelled	67.6	41	PDB header: isomerase Chain: A: PDB Molecule: 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase; PDBTitle: crystal structure of 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase2 from mycobacterium marinum
						Fold: PUA domain-like

52	d1zcea1	Alignment	not modelled	67.6	32	Superfamily: PUA domain-like Family: Atu2648/PH1033-like
53	d2eyqa1	Alignment	not modelled	67.1	22	Fold: SH3-like barrel Superfamily: CarD-like Family: CarD-like
54	c6jvwA	Alignment	not modelled	66.4	42	PDB header: hydrolase Chain: A: PDB Molecule: maleylypyruvate hydrolase; PDBTitle: crystal structure of maleylypyruvate hydrolase from sphingobium sp.2 syk-6 in complex with manganese (ii) ion and pyruvate
55	c4rgkA	Alignment	not modelled	65.0	23	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
56	c2dbiA	Alignment	not modelled	64.9	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ybiu; PDBTitle: crystal structure of a hypothetical protein jw0805 from2 escherichia coli
57	d1o6aa	Alignment	not modelled	64.9	19	Fold: Surface presentation of antigens (SPOA) Superfamily: Surface presentation of antigens (SPOA) Family: Surface presentation of antigens (SPOA)
58	c3uepB	Alignment	not modelled	64.8	24	PDB header: protein transport Chain: B: PDB Molecule: yscq-c, type iii secretion protein; PDBTitle: crystal structure of yscq-c from yersinia pseudotuberculosis
59	d2csga1	Alignment	not modelled	64.7	18	Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: YbiU-like
60	d1gta2	Alignment	not modelled	64.7	33	Fold: FAH Superfamily: FAH Family: FAH
61	c4cswA	Alignment	not modelled	64.2	18	PDB header: oxidoreductase Chain: A: PDB Molecule: cupin 4 family protein; PDBTitle: rhodothermus marinus ycf-d-like ribosomal protein I16 arginyl2 hydroxylase
62	c4lt5A	Alignment	not modelled	63.8	23	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
63	d1nr9a	Alignment	not modelled	63.0	33	Fold: FAH Superfamily: FAH Family: FAH
64	d2g2xa1	Alignment	not modelled	62.7	13	Fold: PUA domain-like Superfamily: PUA domain-like Family: Atu2648/PH1033-like
65	d2evea1	Alignment	not modelled	62.4	13	Fold: PUA domain-like Superfamily: PUA domain-like Family: Atu2648/PH1033-like
66	d1hyoa2	Alignment	not modelled	62.2	39	Fold: FAH Superfamily: FAH Family: FAH
67	c2nnzA	Alignment	not modelled	60.3	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: solution structure of the hypothetical protein af2241 from2 archaeoglobus fulgidus
68	c4tt9A	Alignment	not modelled	59.9	14	PDB header: protein transport Chain: A: PDB Molecule: surface presentation of antigens protein spa0; PDBTitle: structure of the c-terminal spa domain of shigella flexneri spa33
69	c3l53F	Alignment	not modelled	59.6	41	PDB header: structural genomics, unknown function Chain: F: PDB Molecule: putative fumarylacetoacetate isomerase/hydrolase; PDBTitle: crystal structure of a putative fumarylacetoacetate2 isomerase/hydrolase from oleispira antarctica
70	c5xrwA	Alignment	not modelled	58.6	23	PDB header: motor protein Chain: A: PDB Molecule: flin; PDBTitle: crystal structure of flagellar motor switch complex from h. pylori
71	c3kopB	Alignment	not modelled	57.5	23	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of protein with a cyclophilin-like fold2 (yp_831253.1) from arthrobacter sp. fb24 at 1.90 a resolution
72	c1hyoB	Alignment	not modelled	57.0	30	PDB header: hydrolase Chain: B: PDB Molecule: fumarylacetoacetate hydrolase; PDBTitle: crystal structure of fumarylacetoacetate hydrolase2 complexed with 4-(hydroxymethylphosphinoyl)-3-oxo-butanoic3 acid
73	d2ba0a2	Alignment	not modelled	56.8	24	Fold: Barrel-sandwich hybrid Superfamily: Ribosomal L27 protein-like Family: ECR1 N-terminal domain-like
74	c2dfuB	Alignment	not modelled	56.6	30	PDB header: isomerase Chain: B: PDB Molecule: probable 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase; PDBTitle: crystal structure of the 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase2 from thermus thermophilus hb8
75	d1vrba1	Alignment	not modelled	56.2	14	Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: Asparaginyl hydroxylase-like
76	c6iyvB	Alignment	not modelled	56.0	25	PDB header: hydrolase Chain: B: PDB Molecule: 5-oxopent-3-ene-1,2,5-tricarboxylate decarboxylase; PDBTitle: fumarylacetoacetate hydrolase (eafah) from psychrophilic2 exiguobacterium antarcticum
77	d1zx8a1	Alignment	not modelled	56.0	20	Fold: Cyclophilin-like Superfamily: Cyclophilin-like

						Family: TM1367-like
78	c5t1qB_	Alignment	not modelled	55.3	21	PDB header: hydrolase Chain: B: PDB Molecule: n-acetylmuramoyl-l-alanine amidase domain-containing PDBTitle: 2.15 angstrom crystal structure of n-acetylmuramoyl-l-alanine amidase2 from staphylococcus aureus.
79	c4qkuC_	Alignment	not modelled	53.6	26	PDB header: hydrolase Chain: C: PDB Molecule: hydrolase; PDBTitle: crystal structure of a putative hydrolase from burkholderia2 cenocepacia
80	c4yxaB_	Alignment	not modelled	52.7	19	PDB header: protein transport Chain: B: PDB Molecule: surface presentation of antigens protein spao; PDBTitle: complex of spao(spoa1,2 semet) and orgb(apar)::t4lysozyme fusion2 protein
81	c3lzkC_	Alignment	not modelled	51.1	32	PDB header: hydrolase Chain: C: PDB Molecule: fumarylacetoacetate hydrolase family protein; PDBTitle: the crystal structure of a probably aromatic amino acid2 degradation protein from sinorhizobium meliloti 1021
82	c3uyjA_	Alignment	not modelled	50.3	15	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
83	c1wzoC_	Alignment	not modelled	49.7	22	PDB header: isomerase Chain: C: PDB Molecule: hpce; PDBTitle: crystal structure of the hpce from thermus thermophilus hb8
84	c2xxzA_	Alignment	not modelled	49.6	19	PDB header: oxidoreductase Chain: A: PDB Molecule: lysine-specific demethylase 6b; PDBTitle: crystal structure of the human jmjd3 jumonji domain
85	c4diqA_	Alignment	not modelled	49.5	26	PDB header: oxidoreductase Chain: A: PDB Molecule: lysine-specific demethylase no66; PDBTitle: crystal structure of human no66
86	c2ioaA_	Alignment	not modelled	48.6	33	PDB header: ligase, hydrolase Chain: A: PDB Molecule: bifunctional glutathionylspermidine synthetase/amidase incomplex with mg2+ and adp and3 phosphinate inhibitor
87	c5eqnA_	Alignment	not modelled	48.0	18	PDB header: hydrolase Chain: A: PDB Molecule: frbj; PDBTitle: structure of phosphonate hydroxylase
88	c4l5gA_	Alignment	not modelled	47.0	35	PDB header: transcription Chain: A: PDB Molecule: card; PDBTitle: crystal structure of thermus thermophilus card
89	c3al6A_	Alignment	not modelled	45.0	19	PDB header: unknown function Chain: A: PDB Molecule: jmjc domain-containing protein c2orf60; PDBTitle: crystal structure of human tyw5
90	c2lqkA_	Alignment	not modelled	44.6	32	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator; PDBTitle: nmr solution structure of the n-terminal domain of the cdnl protein2 from thermus thermophilus
91	c2wbqA_	Alignment	not modelled	44.4	19	PDB header: oxidoreductase Chain: A: PDB Molecule: l-arginine beta-hydroxylase; PDBTitle: crystal structure of vioc in complex with (2s,3s)-2 hydroxyarginine
92	d1wpga1	Alignment	not modelled	44.2	16	Fold: Double-stranded beta-helix Superfamily: Calcium ATPase, transduction domain A Family: Calcium ATPase, transduction domain A
93	c6gmaA_	Alignment	not modelled	43.8	29	PDB header: protein binding Chain: A: PDB Molecule: rb1-inducible coiled-coil protein 1; PDBTitle: crystal structure of the fip200 c-terminal region
94	c6exhA_	Alignment	not modelled	42.3	31	PDB header: oxidoreductase Chain: A: PDB Molecule: l-lysine 4-hydroxylase; PDBTitle: crystal structure of the complex fe(ii)/alpha-ketoglutarate dependent2 dioxygenase kdo5 with fe(ii)/succinate/(4r)-4-hydroxy-l-lysine
95	c2vpmB_	Alignment	not modelled	41.3	14	PDB header: ligase Chain: B: PDB Molecule: trypanothione synthetase; PDBTitle: trypanothione synthetase
96	c4ne0B_	Alignment	not modelled	41.3	25	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
97	d2phla2	Alignment	not modelled	40.1	11	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Germin/Seed storage 7S protein
98	d1j3pa_	Alignment	not modelled	39.4	18	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Glucose-6-phosphate isomerase, GPI
99	c3nnlB_	Alignment	not modelled	38.9	19	PDB header: biosynthetic protein Chain: B: PDB Molecule: cura; PDBTitle: halogenase domain from cura module (crystal form iii)
100	c3l2hD_	Alignment	not modelled	38.6	25	PDB header: isomerase Chain: D: PDB Molecule: putative sugar phosphate isomerase; PDBTitle: crystal structure of putative sugar phosphate isomerase (afe_0303)2 from acidithiobacillus ferrooxidans atcc 23270 at 1.85 a resolution
101	c6dawA_	Alignment	not modelled	38.3	19	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
102	c6ar2B_	Alignment	not modelled	38.1	24	PDB header: membrane protein Chain: B: PDB Molecule: sarcolemmal membrane-associated protein;

						PDBTitle: structure of human slmap fha domain in complex with pmst2
103	c3ibmB	Alignment	not modelled	37.9	11	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
104	c4kbmB	Alignment	not modelled	37.8	32	PDB header: transferase/transcription Chain: B: PDB Molecule: rna polymerase-binding transcription factor card; PDBTitle: structure of the mtb card/rnap beta subunit b1-b2 domains complex
105	d1jr7a	Alignment	not modelled	37.4	6	Fold: Double-stranded beta-helix Superfamily: Clavaminatase synthase-like Family: Gab protein (hypothetical protein YgaT)
106	c2eyqA	Alignment	not modelled	36.8	22	PDB header: hydrolase Chain: A: PDB Molecule: transcription-repair coupling factor; PDBTitle: crystal structure of escherichia coli transcription-repair2 coupling factor
107	d2jfga2	Alignment	not modelled	36.2	17	Fold: MurD-like peptide ligases, peptide-binding domain Superfamily: MurD-like peptide ligases, peptide-binding domain Family: MurCDEF C-terminal domain
108	c6f6jC	Alignment	not modelled	35.9	6	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
109	c2og5A	Alignment	not modelled	35.8	19	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxygenase; PDBTitle: crystal structure of asparagine oxygenase (asno)
110	c4gg1A	Alignment	not modelled	35.3	25	PDB header: oxidoreductase Chain: A: PDB Molecule: acireductone dioxygenase; PDBTitle: acireductone dioxygenase from bacillus anthracis with three cadmium2 ions
111	d1ds1a	Alignment	not modelled	35.1	25	Fold: Double-stranded beta-helix Superfamily: Clavaminatase synthase-like Family: Clavaminatase synthase
112	c2xdvA	Alignment	not modelled	34.6	30	PDB header: nuclear protein Chain: A: PDB Molecule: myc-induced nuclear antigen; PDBTitle: crystal structure of the catalytic domain of flj14393
113	c4ne0A	Alignment	not modelled	34.5	24	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
114	c2lt1A	Alignment	not modelled	34.3	30	PDB header: transcription Chain: A: PDB Molecule: card protein; PDBTitle: solution nmr structure of the 72-residue n-terminal domain of2 myxococcus xanthus card
115	d2z1ea2	Alignment	not modelled	33.2	31	Fold: PurM C-terminal domain-like Superfamily: PurM C-terminal domain-like Family: PurM C-terminal domain-like
116	d1c0aa2	Alignment	not modelled	32.8	50	Fold: DCoH-like Superfamily: GAD domain-like Family: GAD domain
117	d2pyta1	Alignment	not modelled	32.8	16	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: EutQ-like
118	c4xbzB	Alignment	not modelled	32.5	19	PDB header: oxidoreductase Chain: B: PDB Molecule: evdo1; PDBTitle: crystal structure of evdo1 from micromonospora carbonacea var.2 aurantiaca
119	c3al6C	Alignment	not modelled	32.0	24	PDB header: unknown function Chain: C: PDB Molecule: jmjc domain-containing protein c2orf60; PDBTitle: crystal structure of human tyw5
120	d1a3xa1	Alignment	not modelled	31.3	16	Fold: PK beta-barrel domain-like Superfamily: PK beta-barrel domain-like Family: Pyruvate kinase beta-barrel domain