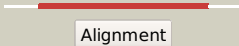



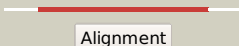



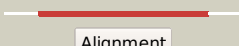

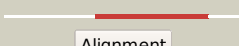

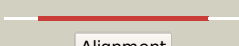












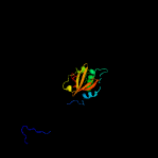


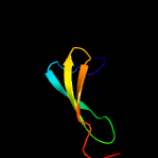
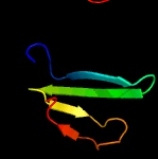



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1478 (-)_1668425_1669150
Date	Fri Aug 2 13:30:06 BST 2019
Unique Job ID	5d749ffb6d01f7dd

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2xivA_	 Alignment		100.0	59	PDB header: structural protein Chain: A: PDB Molecule: hypothetical invasion protein; PDBTitle: structure of rv1477, hypothetical invasion protein of mycobacterium2 tuberculosis
2	c3pbiA_	 Alignment		100.0	99	PDB header: hydrolase Chain: A: PDB Molecule: invasion protein; PDBTitle: structure of the peptidoglycan hydrolase ripb (rv1478) from2 mycobacterium tuberculosis at 1.6 resolution
3	c6biqA_	 Alignment		100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: clan ca, family c40, nlp/p60 superfamily cysteine PDBTitle: structure of nlp2 from trichomonas vaginalis
4	c3gt2A_	 Alignment		100.0	54	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the p60 domain from m. avium paratuberculosis2 antigen map1272c
5	c3nfpB_	 Alignment		100.0	28	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
6	c3i86A_	 Alignment		100.0	85	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the p60 domain from m. avium subspecies2 paratuberculosis antigen map1204
7	c3h41A_	 Alignment		100.0	20	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
8	c2fg0B_	 Alignment		100.0	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
9	d2evra2	 Alignment		100.0	30	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: NlpC/P60
10	c4fdyA_	 Alignment		100.0	26	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
11	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

12	c6b8cA	Alignment		100.0	39	PDB header: hydrolase Chain: A: PDB Molecule: nlp/p60; PDBTitle: crystal structure of nlp/p60 domain of peptidoglycan hydrolase saga
13	c3m1uB	Alignment		100.0	19	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 (dvu_0896) from desulfovibrio vulgaris hildenborough at3 1.75 a resolution
14	c2k1gA	Alignment		100.0	31	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
15	c4xcmB	Alignment		100.0	30	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
16	c2p1gA	Alignment		99.5	29	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	32	PDB header: hydrolase Chain: A: PDB Molecule: group xvi phospholipase a2; PDBTitle: solution structure of the h-rev107 n-terminal domain
18	c2lktA	Alignment		98.0	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		97.9	20	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	c4h4jA	Alignment		97.5	30	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
21	d2if6a1	Alignment	not modelled	96.8	17	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: YiiX-like
22	c2lrjA	Alignment	not modelled	96.6	35	PDB header: biosynthetic protein Chain: A: PDB Molecule: staphyloxanthin biosynthesis protein, putative; PDBTitle: nmr solution structure of staphyloxanthin biosynthesis protein
23	c5udmA	Alignment	not modelled	96.6	25	PDB header: hydrolase Chain: A: PDB Molecule: phage-associated cell wall hydrolase; PDBTitle: phage-associated cell wall hydrolase plppy from streptococcus2 pyogenes, space group p6522
24	c4hzbA	Alignment	not modelled	96.5	29	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
25	c2k3aA	Alignment	not modelled	95.8	36	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
26	c5t1qB	Alignment	not modelled	95.7	30	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.
27	c4f4mA	Alignment	not modelled	95.6	26	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

28	c4f0wA	Alignment	not modelled	95.5	26	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of type effector tse1 c30a mutant from pseudomonas aeruginosa
29	d2im9a1	Alignment	not modelled	94.2	22	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Lpg0564-like
30	c2im9A	Alignment	not modelled	94.2	22	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
31	d2io8a2	Alignment	not modelled	93.7	19	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: CHAP domain
32	c4olkB	Alignment	not modelled	92.6	19	PDB header: hydrolase Chain: B: PDB Molecule: endolysin; PDBTitle: the chap domain of lysgh15
33	c4pa5A	Alignment	not modelled	90.5	14	PDB header: transferase Chain: A: PDB Molecule: protein-glutamine gamma-glutamyltransferase; PDBTitle: tgl - a bacterial spore coat transglutaminase - cystamine complex
34	c4eyzB	Alignment	not modelled	90.1	50	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
35	c4krtA	Alignment	not modelled	88.0	11	PDB header: hydrolase Chain: A: PDB Molecule: autolytic lysozyme; PDBTitle: x-ray structure of endolysin from clostridium perfringens phage2 phism101
36	c2krsA	Alignment	not modelled	84.3	6	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: probable enterotoxin; PDBTitle: solution nmr structure of sh3 domain from cpf_0587 (fragment2 415-479) from clostridium perfringens. northeast structural3 genomics consortium (nesg) target cpr74a.
37	c2kt8A	Alignment	not modelled	83.3	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: probable surface protein; PDBTitle: solution nmr structure of the cpe1231(468-535) protein from2 clostridium perfringens, northeast structural genomics3 consortium target cpr82b
38	d1o9ya	Alignment	not modelled	74.9	14	Fold: Surface presentation of antigens (SPOA) Superfamily: Surface presentation of antigens (SPOA) Family: Surface presentation of antigens (SPOA)
39	d2gbsa1	Alignment	not modelled	74.6	36	Fold: PUA domain-like Superfamily: PUA domain-like Family: Atu2648/PH1033-like
40	c4cgkA	Alignment	not modelled	74.4	18	PDB header: cell cycle Chain: A: PDB Molecule: secreted 45 kda protein; PDBTitle: crystal structure of the essential protein pcsb from streptococcus pneumoniae
41	d1we3o	Alignment	not modelled	74.0	21	Fold: GroES-like Superfamily: GroES-like Family: GroES
42	c5xrwD	Alignment	not modelled	73.9	4	PDB header: motor protein Chain: D: PDB Molecule: flyi; PDBTitle: crystal structure of flagellar motor switch complex from h. pylori
43	c2kybA	Alignment	not modelled	73.5	18	PDB header: toxin Chain: A: PDB Molecule: mannosyl-glycoprotein endo-beta-n-acetylglucosamidase PDBTitle: solution structure of cpr82g from clostridium perfringens. north east2 structural genomics consortium target cpr82g
44	c2dfuB	Alignment	not modelled	71.8	17	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
45	c2kq8A	Alignment	not modelled	71.8	9	PDB header: hydrolase Chain: A: PDB Molecule: cell wall hydrolase; PDBTitle: solution nmr structure of a domain from bt9727_4915 from2 bacillus thuringiensis, northeast structural genomics3 consortium target bur95a
46	c4yxbA	Alignment	not modelled	71.2	9	PDB header: protein transport Chain: A: PDB Molecule: flagellar motor switch protein flim,flagellar motor switch PDBTitle: flim(spoa)::flin fusion protein
47	d2ba0a2	Alignment	not modelled	71.1	23	Fold: Barrel-sandwich hybrid Superfamily: Ribosomal L27 protein-like Family: ECR1 N-terminal domain-like
48	d1zcea1	Alignment	not modelled	70.7	30	Fold: PUA domain-like Superfamily: PUA domain-like Family: Atu2648/PH1033-like
49	d1o6aa	Alignment	not modelled	69.2	23	Fold: Surface presentation of antigens (SPOA) Superfamily: Surface presentation of antigens (SPOA) Family: Surface presentation of antigens (SPOA)
50	d1gtta1	Alignment	not modelled	68.4	21	Fold: FAH Superfamily: FAH Family: FAH
51	d1nkqa	Alignment	not modelled	65.6	18	Fold: FAH Superfamily: FAH Family: FAH
52	c2uopB	Alignment	not modelled	64.5	12	PDB header: protein transport Chain: B: PDB Molecule: yscq-c, type iii secretion protein;

52	c3uepB	Alignment	not modelled	64.3	13	PDBTitle: crystal structure of yscq-c from yersinia pseudotuberculosis PDB header: isomerase
53	c4dbhA	Alignment	not modelled	64.3	24	Chain: A: PDB Molecule: 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase; PDBTitle: crystal structure of cg1458 with inhibitor
54	c2q1dX	Alignment	not modelled	63.3	17	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 and 2 2,5-dioxopentanoate
55	c4pj1V	Alignment	not modelled	62.6	28	PDB header: chaperone Chain: V: PDB Molecule: 10 kda heat shock protein, mitochondrial; PDBTitle: crystal structure of the human mitochondrial chaperonin symmetrical2 'football' complex
56	d2ar1a1	Alignment	not modelled	62.5	9	Fold: PUA domain-like Superfamily: PUA domain-like Family: Atu2648/PH1033-like
57	c3eopB	Alignment	not modelled	61.4	13	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
58	c4tt9A	Alignment	not modelled	61.4	12	PDB header: protein transport Chain: A: PDB Molecule: surface presentation of antigens protein spa0; PDBTitle: structure of the c-terminal spa0 domain of shigella flexneri spa33
59	d1aono	Alignment	not modelled	60.8	18	Fold: GroES-like Superfamily: GroES-like Family: GroES
60	c2ioaA	Alignment	not modelled	60.3	27	PDB header: ligase, hydrolase Chain: A: PDB Molecule: bifunctional glutathionylspermidine PDBTitle: e. coli bifunctional glutathionylspermidine2 synthetase/amidase incomplex with mg2+ and adp and3 phosphinate inhibitor
61	c5xrwA	Alignment	not modelled	59.8	12	PDB header: motor protein Chain: A: PDB Molecule: flin; PDBTitle: crystal structure of flagellar motor switch complex from h. pylori
62	c3qdfA	Alignment	not modelled	59.6	24	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
63	c2vpmB	Alignment	not modelled	59.3	18	PDB header: ligase Chain: B: PDB Molecule: trypanothione synthetase; PDBTitle: trypanothione synthetase
64	d1p3ha	Alignment	not modelled	59.0	26	Fold: GroES-like Superfamily: GroES-like Family: GroES
65	c4yxaB	Alignment	not modelled	57.4	17	PDB header: protein transport Chain: B: PDB Molecule: surface presentation of antigens protein spa0; PDBTitle: complex of spa0(spa01,2 semet) and orgb(apar)::t4lysozyme fusion2 protein
66	c4rgkA	Alignment	not modelled	57.1	21	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
67	d2hd9a1	Alignment	not modelled	56.9	21	Fold: PUA domain-like Superfamily: PUA domain-like Family: Atu2648/PH1033-like
68	c1i7oC	Alignment	not modelled	56.8	18	PDB header: isomerase, lyase Chain: C: PDB Molecule: 4-hydroxyphenylacetate degradation bifunctional PDBTitle: crystal structure of hpce
69	c2dbiA	Alignment	not modelled	56.8	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ybiu; PDBTitle: crystal structure of a hypothetical protein jw0805 from2 escherichia coli
70	c5eqnA	Alignment	not modelled	56.5	18	PDB header: hydrolase Chain: A: PDB Molecule: frbj; PDBTitle: structure of phosphonate hydroxylase
71	d2csga1	Alignment	not modelled	56.2	13	Fold: Double-stranded beta-helix Superfamily: Clavaminatase synthase-like Family: YbiU-like
72	d2g2xa1	Alignment	not modelled	55.2	14	Fold: PUA domain-like Superfamily: PUA domain-like Family: Atu2648/PH1033-like
73	d2evea1	Alignment	not modelled	52.9	13	Fold: PUA domain-like Superfamily: PUA domain-like Family: Atu2648/PH1033-like
74	c3s52A	Alignment	not modelled	52.4	18	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
75	d1sawa	Alignment	not modelled	52.0	21	Fold: FAH Superfamily: FAH Family: FAH
76	c1wzoC	Alignment	not modelled	51.5	12	PDB header: isomerase Chain: C: PDB Molecule: hpce; PDBTitle: crystal structure of the hpce from thermus thermophilus hb8
77	c3kopB	Alignment	not modelled	51.3	13	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein;

77	c3k0pb	Alignment	not modelled	51.5	15	PDBTitle: crystal structure of protein with a cyclophilin-like fold2 (yp_831253.1) from arthrobacter sp. fb24 at 1.90 a resolution
78	d2eyqa1	Alignment	not modelled	50.7	26	Fold: SH3-like barrel Superfamily: CarD-like Family: CarD-like
79	c6exhA	Alignment	not modelled	50.5	38	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
80	d1jr7a	Alignment	not modelled	49.3	12	Fold: Double-stranded beta-helix Superfamily: Clavaminatase synthase-like Family: Gab protein (hypothetical protein YgaT)
81	d1qtta2	Alignment	not modelled	49.0	18	Fold: FAH Superfamily: FAH Family: FAH
82	d2fcta1	Alignment	not modelled	48.5	24	Fold: Double-stranded beta-helix Superfamily: Clavaminatase synthase-like Family: PhyH-like
83	c2opwA	Alignment	not modelled	48.4	23	PDB header: oxidoreductase Chain: A; PDB Molecule: phyhd1 protein; PDBTitle: crystal structure of human phytanoyl-coa dioxygenase phyhd1 (apo)
84	c2l8ka	Alignment	not modelled	47.1	17	PDB header: viral protein Chain: A; PDB Molecule: non-structural protein 7; PDBTitle: nmr structure of the arterivirus nonstructural protein 7 alpha (nsp72 alpha)
85	c4maqB	Alignment	not modelled	47.0	29	PDB header: hydrolase Chain: B; PDB Molecule: putative fumarylpyruvate hydrolase; PDBTitle: crystal structure of a putative fumarylpyruvate hydrolase from2 burkholderia cenocepacia
86	c6dawA	Alignment	not modelled	45.7	25	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
87	d1wpqa1	Alignment	not modelled	45.6	16	Fold: Double-stranded beta-helix Superfamily: Calcium ATPase, transduction domain A Family: Calcium ATPase, transduction domain A
88	c6gmaA	Alignment	not modelled	45.4	17	PDB header: protein binding Chain: A; PDB Molecule: rb1-inducible coiled-coil protein 1; PDBTitle: crystal structure of the fip200 c-terminal region
89	c2wbqA	Alignment	not modelled	44.6	25	PDB header: oxidoreductase Chain: A; PDB Molecule: l-arginine beta-hydroxylase; PDBTitle: crystal structure of vioc in complex with (2s,3s)-2 hydroxyarginine
90	c3nnlB	Alignment	not modelled	44.6	31	PDB header: biosynthetic protein Chain: B; PDB Molecule: cura; PDBTitle: halogenase domain from cura module (crystal form iii)
91	c4ne0B	Alignment	not modelled	44.4	31	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
92	c3r6oA	Alignment	not modelled	44.0	34	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
93	c5zm4B	Alignment	not modelled	41.0	22	PDB header: oxidoreductase Chain: B; PDB Molecule: dioxygenase anda; PDBTitle: fe(ii)/(alpha)ketoglutarate-dependent dioxygenase anda with2 preandiloid c
94	c6iywB	Alignment	not modelled	40.7	23	PDB header: hydrolase Chain: B; PDB Molecule: 5-oxopent-3-ene-1,2,5-tricarboxylate decarboxylase; PDBTitle: fumarylacetoacetate hydrolase (eafah) from psychrophilic2 exiguobacterium antarcticum
95	c6jvwA	Alignment	not modelled	39.8	18	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
96	d1ds1a	Alignment	not modelled	39.4	25	Fold: Double-stranded beta-helix Superfamily: Clavaminatase synthase-like Family: Clavaminatase synthase
97	c2p5dA	Alignment	not modelled	39.0	22	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: upf0310 protein mjec136; PDBTitle: crystal structure of mjec136 from methanocaldococcus2 jannaschii dsm 2661
98	c5m0tA	Alignment	not modelled	38.7	24	PDB header: oxidoreductase Chain: A; PDB Molecule: alpha-ketoglutarate-dependent non-heme iron oxygenase eash; PDBTitle: alpha-ketoglutarate-dependent non-heme iron oxygenase eash
99	c6f6jC	Alignment	not modelled	38.6	13	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
100	c4zonB	Alignment	not modelled	38.4	22	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: B; PDB Molecule: verruculogen synthase; PDBTitle: structure of ftmox1 with fumitremorgen b complex
101	d1nr9a	Alignment	not modelled	38.2	24	Fold: FAH Superfamily: FAH Family: FAH
102	c4naoA	Alignment	not modelled	38.1	22	PDB header: oxidoreductase Chain: A; PDB Molecule: putative oxygenase;

						PDBTitle: crystal structure of eash
103	c2og5A_	Alignment	not modelled	37.9	19	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxygenase; PDBTitle: crystal structure of asparagine oxygenase (asno)
104	c4lt5A_	Alignment	not modelled	37.8	31	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
105	c4ne0A_	Alignment	not modelled	37.4	29	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
106	c4xbzB_	Alignment	not modelled	36.6	27	PDB header: oxidoreductase Chain: B: PDB Molecule: evdo1; PDBTitle: crystal structure of evdo1 from micromonospora carbonacea var.2 aurantiaca
107	c4nubA_	Alignment	not modelled	36.0	32	PDB header: oxidoreductase Chain: A: PDB Molecule: 50s ribosomal protein l16 arginine hydroxylase; PDBTitle: crystal structure of escherichia coli ribosomal oxygenase ycfd
108	c4kbmB_	Alignment	not modelled	35.7	35	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
109	d1otja_	Alignment	not modelled	34.3	18	Fold: Double-stranded beta-helix Superfamily: Clavaminatase synthase-like Family: TauD/TfdA-like
110	c4mhuB_	Alignment	not modelled	34.1	18	PDB header: oxidoreductase Chain: B: PDB Molecule: ectoine hydroxylase; PDBTitle: crystal structure of ectd from s. alaskensis with bound fe
111	d1knwa1	Alignment	not modelled	33.6	24	Fold: Domain of alpha and beta subunits of F1 ATP synthase-like Superfamily: Alanine racemase C-terminal domain-like Family: Eukaryotic ODC-like
112	c5yboA_	Alignment	not modelled	33.4	17	PDB header: oxidoreductase Chain: A: PDB Molecule: prha; PDBTitle: fe(ii)/(alpha)ketoglutarate-dependent dioxygenase prha in complex with2 preaustinoid a1
113	c3lzkC_	Alignment	not modelled	33.3	27	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
114	c6b8wB_	Alignment	not modelled	32.6	4	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.
115	c2hc8A_	Alignment	not modelled	32.6	26	PDB header: transport protein Chain: A: PDB Molecule: cation-transporting atpase, p-type; PDBTitle: structure of the a. fulgidus copa a-domain
116	c4me8A_	Alignment	not modelled	31.3	13	PDB header: hydrolase Chain: A: PDB Molecule: signal peptidase i; PDBTitle: crystal structure of a signal peptidase i (ef3073) from enterococcus2 faecalis v583 at 2.27 a resolution
117	d1c0aa2	Alignment	not modelled	30.2	50	Fold: DCoH-like Superfamily: GAD domain-like Family: GAD domain
118	d1hyoa2	Alignment	not modelled	30.0	36	Fold: FAH Superfamily: FAH Family: FAH
119	d1l0wa2	Alignment	not modelled	29.4	40	Fold: DCoH-like Superfamily: GAD domain-like Family: GAD domain
120	c2kijA_	Alignment	not modelled	29.1	24	PDB header: hydrolase Chain: A: PDB Molecule: copper-transporting atpase 1; PDBTitle: solution structure of the actuator domain of the copper-2 transporting atpase atp7a