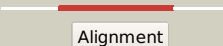




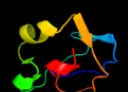

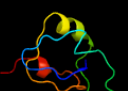
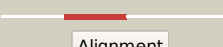













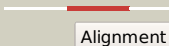
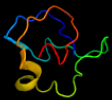



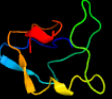


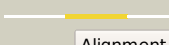

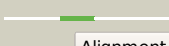

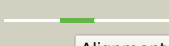





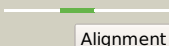
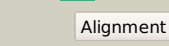
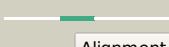
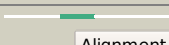
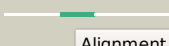

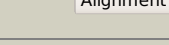
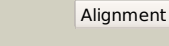


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0990c_(-)_1107447_1108103
Date	Wed Jul 31 22:05:05 BST 2019
Unique Job ID	41896c0f150b25c2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3teeA_	 Alignment		99.4	20	PDB header: chaperone Chain: A: PDB Molecule: flagella basal body p-ring formation protein flga; PDBTitle: crystal structure of salmonella flga in open form
2	c3frnA_	 Alignment		99.2	26	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: flagellar protein flga; PDBTitle: crystal structure of flagellar protein flga from thermotoga maritima2 msb8
3	d2zdra1	 Alignment		98.0	20	Fold: beta-clip Superfamily: AFP III-like domain Family: AFP III-like domain
4	d1vlia1	 Alignment		97.8	6	Fold: beta-clip Superfamily: AFP III-like domain Family: AFP III-like domain
5	c1xuzA_	 Alignment		97.7	20	PDB header: biosynthetic protein Chain: A: PDB Molecule: polysialic acid capsule biosynthesis protein sialc; PDBTitle: crystal structure analysis of sialic acid synthase (neub)from2 neisseria meningitidis, bound to mn2+, phosphoenolpyruvate, and n-3 acetyl mannosaminitol
6	c3g8rA_	 Alignment		97.4	19	PDB header: biosynthetic protein Chain: A: PDB Molecule: probable spore coat polysaccharide biosynthesis protein e; PDBTitle: crystal structure of putative spore coat polysaccharide biosynthesis2 protein e from chromobacterium violaceum atcc 12472
7	c1vlia_	 Alignment		97.4	8	PDB header: biosynthetic protein Chain: A: PDB Molecule: spore coat polysaccharide biosynthesis protein spse; PDBTitle: crystal structure of spore coat polysaccharide biosynthesis protein2 spse (bsu37870) from bacillus subtilis at 2.38 a resolution
8	d1lopsa_	 Alignment		96.6	27	Fold: beta-clip Superfamily: AFP III-like domain Family: AFP III-like domain
9	d1c8aa2	 Alignment		96.2	25	Fold: beta-clip Superfamily: AFP III-like domain Family: AFP III-like domain
10	c1wvoA_	 Alignment		95.7	20	PDB header: transferase Chain: A: PDB Molecule: sialic acid synthase; PDBTitle: solution structure of rsgi ruh-029, an antifreeze protein2 like domain in human n-acetylneuraminic acid phosphate3 synthase gene.
11	d3nlaa_	 Alignment		95.7	25	Fold: beta-clip Superfamily: AFP III-like domain Family: AFP III-like domain

12	c1c8aA	 Alignment		94.9	25	PDB header: antifreeze protein Chain: A: PDB Molecule: protein (antifreeze protein type iii); PDBTitle: nmr structure of intramolecular dimer antifreeze protein2 rd3, 40 sa structures
13	c3upyB	 Alignment		92.1	20	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of the brucella abortus enzyme catalyzing the first2 committed step of the methylerythritol 4-phosphate pathway.
14	d1ucsa	 Alignment		85.0	23	Fold: beta-clip Superfamily: AFP III-like domain Family: AFP III-like domain
15	d1hg7a	 Alignment		81.6	25	Fold: beta-clip Superfamily: AFP III-like domain Family: AFP III-like domain
16	c3k3sG	 Alignment		72.0	21	PDB header: hydrolase Chain: G: PDB Molecule: altronate hydrolase; PDBTitle: crystal structure of altronate hydrolase (fragment 1-84) from shigella2 flexneri.
17	c6chgC	 Alignment		57.2	33	PDB header: transferase Chain: C: PDB Molecule: histone-lysine n-methyltransferase, h3 lysine-4 specific; PDBTitle: crystal structure of the yeast compass catalytic module
18	c5ht6B	 Alignment		57.0	27	PDB header: transferase Chain: B: PDB Molecule: histone-lysine n-methyltransferase 2e; PDBTitle: crystal structure of the set domain of the human ml152 methyltransferase
19	c4z4pA	 Alignment		51.3	20	PDB header: transferase Chain: A: PDB Molecule: histone-lysine n-methyltransferase 2d; PDBTitle: structure of the ml14 set domain
20	d2g46a1	 Alignment		51.1	13	Fold: beta-clip Superfamily: SET domain Family: Viral histone H3 Lysine 27 Methyltransferase
21	c3f9xA	 Alignment	not modelled	50.9	27	PDB header: transferase Chain: A: PDB Molecule: histone-lysine n-methyltransferase setd8; PDBTitle: structural insights into lysine multiple methylation by set domain2 methyltransferases, set8-y334f / h4-lys20me2 / adohcy
22	d2f69a2	 Alignment	not modelled	49.0	13	Fold: beta-clip Superfamily: SET domain Family: Histone lysine methyltransferases
23	c2w5zA	 Alignment	not modelled	47.9	33	PDB header: transferase Chain: A: PDB Molecule: histone-lysine n-methyltransferase hrx; PDBTitle: ternary complex of the mixed lineage leukaemia (ml1) set2 domain with the cofactor product s-adenosylhomocysteine3 and histone peptide.
24	d1h3ia2	 Alignment	not modelled	44.2	13	Fold: beta-clip Superfamily: SET domain Family: Histone lysine methyltransferases
25	c3opeA	 Alignment	not modelled	42.9	40	PDB header: transferase Chain: A: PDB Molecule: probable histone-lysine n-methyltransferase ash11; PDBTitle: structural basis of auto-inhibitory mechanism of histone2 methyltransferase
26	c6bx3E	 Alignment	not modelled	42.3	33	PDB header: gene regulation/transferase Chain: E: PDB Molecule: histone-lysine n-methyltransferase, h3 lysine-4 specific; PDBTitle: structure of histone h3k4 methyltransferase
27	c3h6IA	 Alignment	not modelled	42.2	20	PDB header: transferase Chain: A: PDB Molecule: histone-lysine n-methyltransferase setd2; PDBTitle: methyltransferase domain of human set domain-containing protein 2
28	c6agoA	 Alignment	not modelled	42.0	40	PDB header: transferase/gene regulation Chain: A: PDB Molecule: histone-lysine n-methyltransferase ash11; PDBTitle: crystal structure of mrg15-ash11 histone

						methyltransferase complex
29	c4o30B_	Alignment	not modelled	41.7	33	PDB header: transferase Chain: B: PDB Molecule: histone-lysine n-methyltransferase atxr6, putative; PDBTitle: crystal structure of atxr5 in complex with histone h3.1 and adohcy
30	c5h6zA_	Alignment	not modelled	41.1	7	PDB header: transcription Chain: A: PDB Molecule: set domain-containing protein 7; PDBTitle: crystal structure of set7, a novel histone methyltransferase in2 schizosaccharomyces pombe
31	c4mi0A_	Alignment	not modelled	39.6	20	PDB header: transferase Chain: A: PDB Molecule: histone-lysine n-methyltransferase ezh2; PDBTitle: human enhancer of zeste (drosophila) homolog 2(ezh2)
32	c4rz0B_	Alignment	not modelled	39.5	13	PDB header: transferase Chain: B: PDB Molecule: pfl0690c; PDBTitle: crystal structure of plasmodium falciparum putative histone2 methyltransferase pfl0690c
33	c3bo5A_	Alignment	not modelled	39.0	33	PDB header: transferase Chain: A: PDB Molecule: histone-lysine n-methyltransferase setmar; PDBTitle: crystal structure of methyltransferase domain of human histone-lysine2 n-methyltransferase setmar
34	c3ooiA_	Alignment	not modelled	38.6	40	PDB header: transferase Chain: A: PDB Molecule: histone-lysine n-methyltransferase, h3 lysine-36 and h4 PDBTitle: crystal structure of human histone-lysine n-methyltransferase nsd1 set2 domain in complex with s-adenosyl-l-methionine
35	c2r3aA_	Alignment	not modelled	38.2	20	PDB header: transferase Chain: A: PDB Molecule: histone-lysine n-methyltransferase suv39h2; PDBTitle: methyltransferase domain of human suppressor of variegation2 3-9 homolog 2
36	d1ml9a_	Alignment	not modelled	37.6	40	Fold: beta-clip Superfamily: SET domain Family: Histone lysine methyltransferases
37	c3hnaA_	Alignment	not modelled	36.1	13	PDB header: hydrolase/hydrolase regulator Chain: A: PDB Molecule: histone-lysine n-methyltransferase, h3 lysine-9 specific 5; PDBTitle: crystal structure of catalytic domain of human euchromatic histone2 methyltransferase 1 in complex with sah and mono-methylated h3k93 peptide
38	c2o8jC_	Alignment	not modelled	34.4	27	PDB header: transferase Chain: C: PDB Molecule: histone-lysine n-methyltransferase, h3 lysine-9 PDBTitle: human euchromatic histone methyltransferase 2
39	c1xqhE_	Alignment	not modelled	34.3	13	PDB header: transferase Chain: E: PDB Molecule: histone-lysine n-methyltransferase, h3 lysine-4 PDBTitle: crystal structure of a ternary complex of the2 methyltransferase set9 (also known as set7/9) with a p533 peptide and sah
40	c3n71A_	Alignment	not modelled	31.5	8	PDB header: transcription Chain: A: PDB Molecule: histone lysine methyltransferase smyd1; PDBTitle: crystal structure of cardiac specific histone methyltransferase smyd1
41	d1mvha_	Alignment	not modelled	31.2	33	Fold: beta-clip Superfamily: SET domain Family: Histone lysine methyltransferases
42	c1mvhA_	Alignment	not modelled	31.2	33	PDB header: transferase Chain: A: PDB Molecule: cryptic loci regulator 4; PDBTitle: structure of the set domain histone lysine2 methyltransferase clr4
43	c3lazB_	Alignment	not modelled	31.1	7	PDB header: lyase Chain: B: PDB Molecule: d-galactarate dehydratase; PDBTitle: the crystal structure of the n-terminal domain of d-2 galactarate dehydratase from escherichia coli cft073
44	c4ldgA_	Alignment	not modelled	29.7	27	PDB header: unknown function Chain: A: PDB Molecule: protein with a set domain within carboxy region; PDBTitle: crystal structure of cpset8 from cryptosporidium, cgd4_370
45	c2qpwA_	Alignment	not modelled	28.8	20	PDB header: transcription Chain: A: PDB Molecule: pr domain zinc finger protein 2; PDBTitle: methyltransferase domain of human pr domain-containing2 protein 2
46	c3s8pA_	Alignment	not modelled	28.3	33	PDB header: transferase Chain: A: PDB Molecule: histone-lysine n-methyltransferase suv420h1; PDBTitle: crystal structure of the set domain of human histone-lysine n-2 methyltransferase suv420h1 in complex with s-adenosyl-l-methionine
47	c6a5mA_	Alignment	not modelled	27.0	20	PDB header: gene regulation Chain: A: PDB Molecule: histone-lysine n-methyltransferase, h3 lysine-9 specific PDBTitle: crystal structure of arabidopsis thaliana suvh6 in complex with sam,2 form 2
48	c4yt1B_	Alignment	not modelled	26.1	16	PDB header: transcription Chain: B: PDB Molecule: transcription elongation factor spt5; PDBTitle: structure of the kow2-kow3 domain of transcription elongation factor2 spt5.
49	c3rayA_	Alignment	not modelled	25.9	40	PDB header: transcription Chain: A: PDB Molecule: pr domain-containing protein 11; PDBTitle: crystal structure of methyltransferase domain of human pr domain-2 containing protein 11
50	c3rq4A_	Alignment	not modelled	25.7	33	PDB header: transferase Chain: A: PDB Molecule: histone-lysine n-methyltransferase suv420h2; PDBTitle: crystal structure of suppressor of variegation 4-20 homolog 2 PDB header: transferase

51	c1h3iB_	Alignment	not modelled	23.4	13	Chain: B: PDB Molecule: histone h3 lysine 4 specific methyltransferase; PDBTitle: crystal structure of the histone methyltransferase set7/9
52	c4nj5A_	Alignment	not modelled	23.1	33	PDB header: metal binding protein Chain: A: PDB Molecule: probable histone-lysine n-methyltransferase, h3 lysine-9 PDBTitle: crystal structure of suvh9
53	c3ep0A_	Alignment	not modelled	22.1	21	PDB header: transferase Chain: A: PDB Molecule: pr domain zinc finger protein 12; PDBTitle: methyltransferase domain of human pr domain-containing2 protein 12
54	c3qwvA_	Alignment	not modelled	21.8	23	PDB header: transferase Chain: A: PDB Molecule: set and mynd domain-containing protein 2; PDBTitle: crystal structure of histone lysine methyltransferase smyd2 in complex2 with the cofactor product adohcy
55	c3mekA_	Alignment	not modelled	19.0	46	PDB header: transferase Chain: A: PDB Molecule: set and mynd domain-containing protein 3; PDBTitle: crystal structure of human histone-lysine n-methyltransferase smyd3 in2 complex with s-adenosyl-l-methionine
56	d2h2ja2	Alignment	not modelled	18.9	7	Fold: beta-clip Superfamily: SET domain Family: RuBisCo LSMT catalytic domain
57	c6fndC_	Alignment	not modelled	17.0	33	PDB header: transferase Chain: C: PDB Molecule: apical complex lysine methyltransferase; PDBTitle: crystal structure of toxoplasma gondii akmt
58	c3oxgA_	Alignment	not modelled	16.0	46	PDB header: transferase Chain: A: PDB Molecule: set and mynd domain-containing protein 3; PDBTitle: human lysine methyltransferase smyd3 in complex with adohcy (form iii)
59	c1wzoC_	Alignment	not modelled	15.9	23	PDB header: isomerase Chain: C: PDB Molecule: hpce; PDBTitle: crystal structure of the hpce from thermus thermophilus hb8
60	d1nkqa_	Alignment	not modelled	14.8	16	Fold: FAH Superfamily: FAH Family: FAH
61	c4qeoA_	Alignment	not modelled	14.3	40	PDB header: transcription/dna Chain: A: PDB Molecule: histone-lysine n-methyltransferase, h3 lysine-9 specific PDBTitle: crystal structure of kryptonite in complex with mchh dna, h3(1-15)2 peptide and sah
62	c4e5sC_	Alignment	not modelled	14.1	27	PDB header: hydrolase Chain: C: PDB Molecule: mccflike protein (ba_5613); PDBTitle: crystal structure of mccflike protein (ba_5613) from bacillus2 anthracis str. ames
63	d1gtta2	Alignment	not modelled	14.1	20	Fold: FAH Superfamily: FAH Family: FAH
64	c3db5A_	Alignment	not modelled	13.8	23	PDB header: transferase Chain: A: PDB Molecule: pr domain zinc finger protein 4; PDBTitle: crystal structure of methyltransferase domain of human pr domain-2 containing protein 4
65	c6jvwA_	Alignment	not modelled	13.3	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
66	d1sawa_	Alignment	not modelled	12.4	12	Fold: FAH Superfamily: FAH Family: FAH
67	d1hh2p1	Alignment	not modelled	12.2	19	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
68	c2hj1A_	Alignment	not modelled	12.1	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a 3d domain-swapped dimer of protein hi0395 from2 haemophilus influenzae
69	d2hj1a1	Alignment	not modelled	12.1	20	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: HI0395-like
70	c3gjzB_	Alignment	not modelled	12.0	20	PDB header: immune system Chain: B: PDB Molecule: microcin immunity protein mccf; PDBTitle: crystal structure of microcin immunity protein mccf from bacillus2 anthracis str. ames
71	c5zz5D_	Alignment	not modelled	11.6	18	PDB header: gene regulation Chain: D: PDB Molecule: redox-sensing transcriptional repressor rex; PDBTitle: redox-sensing transcriptional repressor rex
72	d2do3a1	Alignment	not modelled	11.6	13	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: SPT5 KOW domain-like
73	c6iywB_	Alignment	not modelled	11.5	20	PDB header: hydrolase Chain: B: PDB Molecule: 5-oxopent-3-ene-1,2,5-tricarboxylate decarboxylase; PDBTitle: fumarylacetoacetate hydrolase (eafah) from psychrophilic2 exiguobacterium antarcticum
74	c5ij7B_	Alignment	not modelled	11.4	20	PDB header: transferase/transferase inhibitor Chain: B: PDB Molecule: enhancer of zeste homolog 2 (ezh2),histone-lysine n- PDBTitle: structure of hs/acpcr2 in complex with a pyridone inhibitor
75	c3qdfA_	Alignment	not modelled	11.4	19	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
76	c2I55A_	Alignment	not modelled	11.3	13	PDB header: metal binding protein Chain: A: PDB Molecule: silb,silver efflux protein, mfp component of the three PDBTitle: solution structure of the c-terminal domain of silb from cupriavidus2 metallidurans
77	c5f1yA_	Alignment	not modelled	11.1	21	PDB header: hydrolase Chain: A: PDB Molecule: mccc family protein; PDBTitle: crystal structure of ba3275, the member of s66 family of serine2 peptidases
78	c3tlgB_	Alignment	not modelled	10.7	27	PDB header: hydrolase Chain: B: PDB Molecule: mccf; PDBTitle: microcin c7 self immunity protein mccf in the inactive mutant apo2 state
79	c4h1hB_	Alignment	not modelled	10.5	18	PDB header: hydrolase Chain: B: PDB Molecule: lmo1638 protein; PDBTitle: crystal structure of mccf homolog from listeria monocytogenes egd-e
80	d1e0ta3	Alignment	not modelled	9.8	24	Fold: Pyruvate kinase C-terminal domain-like Superfamily: PK C-terminal domain-like Family: Pyruvate kinase, C-terminal domain
81	c6f0kA_	Alignment	not modelled	9.1	14	PDB header: membrane protein Chain: A: PDB Molecule: cytochrome c family protein; PDBTitle: alternative complex iii
82	c4maqB_	Alignment	not modelled	9.0	16	PDB header: hydrolase Chain: B: PDB Molecule: putative fumarylpyruvate hydrolase; PDBTitle: crystal structure of a putative fumarylpyruvate hydrolase from2 burkholderia cenocepacia
83	c5wg6C_	Alignment	not modelled	9.0	20	PDB header: transferase/transferase inhibitor Chain: C: PDB Molecule: histone-lysine n-methyltransferase ezh2,polycomb protein PDBTitle: human polycomb repressive complex 2 in complex with gsk126 inhibitor
84	c3qxyA_	Alignment	not modelled	8.6	31	PDB header: transferase Chain: A: PDB Molecule: n-lysine methyltransferase setd6; PDBTitle: human setd6 in complex with rela lys310
85	c2e6zA_	Alignment	not modelled	8.2	31	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor spt5; PDBTitle: solution structure of the second kow motif of human2 transcription elongation factor spt5
86	c1zrsB_	Alignment	not modelled	8.1	18	PDB header: hydrolase Chain: B: PDB Molecule: hypothetical protein; PDBTitle: wild-type ld-carboxypeptidase
87	c4dbhA_	Alignment	not modelled	8.0	14	PDB header: isomerase Chain: A: PDB Molecule: 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase; PDBTitle: crystal structure of cg1458 with inhibitor
88	d2g50a3	Alignment	not modelled	7.8	16	Fold: Pyruvate kinase C-terminal domain-like Superfamily: PK C-terminal domain-like Family: Pyruvate kinase, C-terminal domain
89	c1ri9A_	Alignment	not modelled	7.5	19	PDB header: signaling protein Chain: A: PDB Molecule: fyn-binding protein; PDBTitle: structure of a helically extended sh3 domain of the t cell2 adapter protein adap
90	d1ri9a_	Alignment	not modelled	7.5	19	Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain
91	c1p0yA_	Alignment	not modelled	7.5	23	PDB header: transferase Chain: A: PDB Molecule: ribulose-1,5 bisphosphate carboxylase/oxygenase PDBTitle: crystal structure of the set domain of lsmt bound to2 melysine and adohcy
92	d1hr0w_	Alignment	not modelled	7.3	26	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
93	c4hkrB_	Alignment	not modelled	7.2	9	PDB header: transport protein Chain: B: PDB Molecule: calcium release-activated calcium channel protein 1; PDBTitle: calcium release-activated calcium (crac) channel orai
94	d1ah9a_	Alignment	not modelled	6.9	32	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
95	d2auna2	Alignment	not modelled	6.8	12	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: LD-carboxypeptidase A N-terminal domain-like
96	c6flqF_	Alignment	not modelled	6.5	22	PDB header: transcription Chain: F: PDB Molecule: transcription termination/antitermination protein nusa; PDBTitle: cryoem structure of e.coli rna polymerase paused elongation complex2 bound to nusa
97	c3zr6A_	Alignment	not modelled	6.5	30	PDB header: hydrolase Chain: A: PDB Molecule: galactocerebrosidase; PDBTitle: structure of galactocerebrosidase from mouse in complex with galactose
98	c4ql5A_	Alignment	not modelled	6.4	26	PDB header: translation Chain: A: PDB Molecule: translation initiation factor if-1; PDBTitle: crystal structure of translation initiation factor if-1 from2 streptococcus pneumoniae tigr4
99	c3i4oA_	Alignment	not modelled	6.1	26	PDB header: translation Chain: A: PDB Molecule: translation initiation factor if-1; PDBTitle: crystal structure of translation initiation factor 1 from2 mycobacterium tuberculosis