

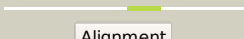
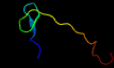
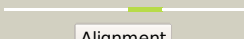
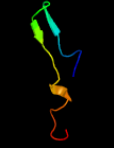
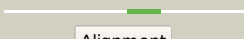
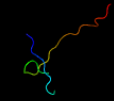

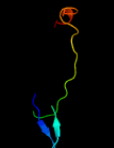





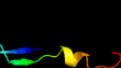



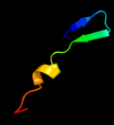

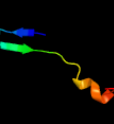
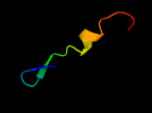
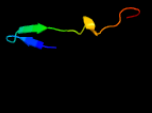
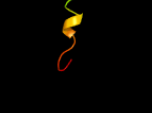

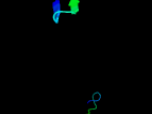

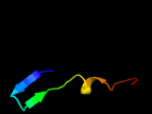
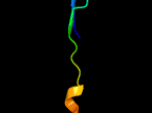
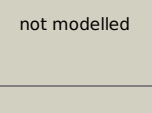


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0988 (-) _1105120_1106280
Date	Wed Jul 31 22:05:05 BST 2019
Unique Job ID	435bf4f090b943e2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2icha1	 Alignment		100.0	35	Fold: Atth-like Superfamily: Atth-like Family: Atth-like
2	d1tvna1	 Alignment		66.7	13	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
3	c2b4rQ_	 Alignment		62.4	24	PDB header: oxidoreductase Chain: Q; PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: crystal structure of glyceraldehyde-3-phosphate dehydrogenase from2 plasmodium falciparum at 2.25 angstrom resolution reveals intriguing3 extra electron density in the active site
4	d1egza_	 Alignment		54.6	13	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
5	c5fipA_	 Alignment		54.1	17	PDB header: hydrolase Chain: A; PDB Molecule: gh5 cellulase; PDBTitle: discovery and characterization of a novel thermostable and2 highly halotolerant gh5 cellulase from an icelandic hot3 spring isolate
6	d1whva_	 Alignment		50.2	23	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
7	d1g01a_	 Alignment		50.1	16	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
8	c2i5pO_	 Alignment		47.3	20	PDB header: oxidoreductase Chain: O; PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase 1; PDBTitle: crystal structure of glyceraldehyde-3-phosphate2 dehydrogenase isoform 1 from k. marxianus
9	c2d2iO_	 Alignment		44.9	35	PDB header: oxidoreductase Chain: O; PDB Molecule: glyceraldehyde 3-phosphate dehydrogenase; PDBTitle: crystal structure of nadp-dependent glyceraldehyde-3-2 phosphate dehydrogenase from synechococcus sp. complexed3 with nadp+
10	c3b20R_	 Alignment		43.9	35	PDB header: oxidoreductase Chain: R; PDB Molecule: glyceraldehyde 3-phosphate dehydrogenase (nadp+); PDBTitle: crystal structure of glyceraldehyde-3-phosphate dehydrogenase2 complexed with nadpfrom synechococcus elongatus"
11	c3docD_	 Alignment		43.7	35	PDB header: oxidoreductase Chain: D; PDB Molecule: glyceraldehyde 3-phosphate dehydrogenase; PDBTitle: crystal structure of trka glyceraldehyde-3-phosphate dehydrogenase2 from brucella melitensis

12	c4dibF_	Alignment		43.3	30	PDB header: oxidoreductase Chain: F: PDB Molecule: glyceraldehyde 3-phosphate dehydrogenase; PDBTitle: the crystal structure of glyceraldehyde-3-phosphate dehydrogenase from2 bacillus anthracis str. Sterne
13	c1rm4O_	Alignment		42.2	30	PDB header: oxidoreductase Chain: O: PDB Molecule: glyceraldehyde 3-phosphate dehydrogenase a; PDBTitle: crystal structure of recombinant photosynthetic glyceraldehyde-3-2 phosphate dehydrogenase a4 isoform, complexed with nadp
14	c2pkrl_	Alignment		41.5	30	PDB header: oxidoreductase Chain: I: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase aor; PDBTitle: crystal structure of (a+cte)4 chimeric form of photosynthetic2 glyceraldehyde-3-phosphate dehydrogenase, complexed with nadp
15	c1hdgO_	Alignment		41.1	40	PDB header: oxidoreductase (aldehy(d)-nad(a)) Chain: O: PDB Molecule: holo-d-glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: the crystal structure of holo-glyceraldehyde-3-phosphate dehydrogenase2 from the hyperthermophilic bacterium thermotoga maritima at 2.53 angstroms resolution
16	c3h9eO_	Alignment		39.9	30	PDB header: oxidoreductase Chain: O: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase, testis-specific; PDBTitle: crystal structure of human sperm-specific glyceraldehyde-3-phosphate2 dehydrogenase (gapds) complex with nad and phosphate
17	c2x5kO_	Alignment		39.9	25	PDB header: oxidoreductase Chain: O: PDB Molecule: d-erythrose-4-phosphate dehydrogenase; PDBTitle: structure of an active site mutant of the d-erythrose-4-phosphate2 dehydrogenase from e. coli
18	c1s7cA_	Alignment		38.7	25	PDB header: structural genomics, oxidoreductase Chain: A: PDB Molecule: glyceraldehyde 3-phosphate dehydrogenase a; PDBTitle: crystal structure of mes buffer bound form of glyceraldehyde 3-2 phosphate dehydrogenase from escherichia coli
19	c1ihxD_	Alignment		38.4	25	PDB header: oxidoreductase Chain: D: PDB Molecule: glyceraldehyde 3-phosphate dehydrogenase; PDBTitle: crystal structure of two d-glyceraldehyde-3-phosphate2 dehydrogenase complexes: a case of asymmetry
20	c3hjaB_	Alignment		38.3	30	PDB header: oxidoreductase Chain: B: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: crystal structure of glyceraldehyde-3-phosphate dehydrogenase from2 borrelia burgdorferi
21	c6ok4A_	Alignment	not modelled	36.7	30	PDB header: oxidoreductase Chain: A: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: crystal structure of glyceraldehyde-3-phosphate dehydrogenase (gapdh)2 from chlamydia trachomatis with bound nad
22	c3sthA_	Alignment	not modelled	34.2	25	PDB header: oxidoreductase Chain: A: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: crystal structure of glyceraldehyde-3-phosphate dehydrogenase from2 toxoplasma gondii
23	c2gd1P_	Alignment	not modelled	31.2	35	PDB header: oxidoreductase(aldehyde(d)-nad(a)) Chain: P: PDB Molecule: apo-d-glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: coenzyme-induced conformational changes in glyceraldehyde-3-2 phosphate dehydrogenase from bacillus stearothermophilus
24	c3cieC_	Alignment	not modelled	27.5	42	PDB header: oxidoreductase Chain: C: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: crystal structure of glyceraldehyde 3-phosphate2 dehydrogenase from cryptosporidium parvum
25	c5sydA_	Alignment	not modelled	24.1	15	PDB header: oxidoreductase Chain: A: PDB Molecule: azurin, chimeric construct; PDBTitle: circularly permuted azurin (cpaz) based on p. aeruginosa azurin2 sequence
26	c5ld5C_	Alignment	not modelled	24.0	27	PDB header: oxidoreductase Chain: C: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: crystal structure of a bacterial dehydrogenase at 2.19 angstroms2 resolution
27	d1xnka1	Alignment	not modelled	23.3	17	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases

						Family:Xylanase/endoglucanase 11/12
28	c2dvya_	Alignment	not modelled	22.3	26	PDB header: hydrolase Chain: A: PDB Molecule: restriction endonuclease pabi; PDBTitle: crystal structure of restriction endonucleases pabi
29	c2cksB_	Alignment	not modelled	22.1	19	PDB header: hydrolase Chain: B: PDB Molecule: endoglucanase e-5; PDBTitle: x-ray crystal structure of the catalytic domain of thermobifida fusca2 endoglucanase cel5a (e5)
30	c5uhxA_	Alignment	not modelled	21.1	18	PDB header: hydrolase Chain: A: PDB Molecule: carbohydrate-active enzyme; PDBTitle: structure of cellulase cel5c_1
31	d1ei5a1	Alignment	not modelled	19.8	26	Fold: Streptavidin-like Superfamily: D-aminopeptidase, middle and C-terminal domains Family: D-aminopeptidase, middle and C-terminal domains
32	c4xzbA_	Alignment	not modelled	19.8	17	PDB header: hydrolase Chain: A: PDB Molecule: cel4; PDBTitle: endo-glucanase gscel4 p1
33	c2r5iL_	Alignment	not modelled	19.1	19	PDB header: viral protein Chain: L: PDB Molecule: l1 protein; PDBTitle: pentamer structure of major capsid protein l1 of human papilloma virus2 type 18
34	c5jyfB_	Alignment	not modelled	19.0	42	PDB header: oxidoreductase Chain: B: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: structures of streptococcus agalactiae gbs gapdh in different2 enzymatic states
35	d1r44a_	Alignment	not modelled	18.8	56	Fold: Hedgehog/DD-peptidase Superfamily: Hedgehog/DD-peptidase Family: VanX-like
36	c5ihsA_	Alignment	not modelled	17.8	22	PDB header: hydrolase Chain: A: PDB Molecule: endoglucanase, glycoside hydrolase family 5 protein; PDBTitle: structure of chu_2103 from cytophaga hutchinsonii
37	c4htyA_	Alignment	not modelled	17.2	24	PDB header: hydrolase Chain: A: PDB Molecule: cellulase; PDBTitle: crystal structure of a metagenome-derived cellulase cel5a
38	c4hcgA_	Alignment	not modelled	16.7	7	PDB header: oxidoreductase Chain: A: PDB Molecule: cupredoxin 1; PDBTitle: uncharacterized cupredoxin-like domain protein cupredoxin_1 with zinc2 bound from bacillus anthracis
39	c5ur0B_	Alignment	not modelled	15.6	33	PDB header: oxidoreductase Chain: B: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: crystallographic structure of glyceraldehyde-3-phosphate dehydrogenase2 from naegleria gruberi
40	c4o2hB_	Alignment	not modelled	15.1	41	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: protein bcam1869; PDBTitle: crystal structure of bcam1869 protein (rsam homolog) from burkholderia2 cenocepacia
41	c2ep7B_	Alignment	not modelled	14.9	31	PDB header: oxidoreductase Chain: B: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: structural study of project id aq_1065 from aquifex aeolicus vf5
42	c2dcjA_	Alignment	not modelled	14.6	22	PDB header: hydrolase Chain: A: PDB Molecule: xylanase j; PDBTitle: a two-domain structure of alkaliphilic xynj from bacillus sp. 41m-1
43	d2pyta1	Alignment	not modelled	14.5	13	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: EutQ-like
44	c1cerC_	Alignment	not modelled	14.5	33	PDB header: oxidoreductase (aldehyde(d)-nad(a)) Chain: C: PDB Molecule: holo-d-glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: determinants of enzyme thermostability observed in the2 molecular structure of thermus aquaticus d-glyceraldehyde-3 3-phosphate dehydrogenase at 2.5 angstroms resolution
45	c3hq4R_	Alignment	not modelled	14.4	35	PDB header: oxidoreductase Chain: R: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase 1; PDBTitle: crystal structure of c151s mutant of glyceraldehyde-3-phosphate2 dehydrogenase 1 (gapdh1) complexed with nad from staphylococcus3 aureus mrsa252 at 2.2 angstrom resolution
46	c1obfO_	Alignment	not modelled	14.0	38	PDB header: glycolytic pathway Chain: O: PDB Molecule: glyceraldehyde 3-phosphate dehydrogenase; PDBTitle: the crystal structure of glyceraldehyde 3-phosphate2 dehydrogenase from alcaligenes xylooxidans at 1.7 a3 resolution.
47	c5j9gB_	Alignment	not modelled	13.4	41	PDB header: oxidoreductase Chain: B: PDB Molecule: glyceraldehyde-3-p dehydrogenase; PDBTitle: structure of lactobacillus acidophilus glyceraldehyde-3-phosphate2 dehydrogenase at 2.21 angstrom resolution
48	c1i32D_	Alignment	not modelled	12.8	33	PDB header: oxidoreductase Chain: D: PDB Molecule: glyceraldehyde 3-phosphate dehydrogenase; PDBTitle: leishmania mexicana glyceraldehyde-3-phosphate2 dehydrogenase in complex with inhibitors
49	d1wuba_	Alignment	not modelled	11.8	18	Fold: Streptavidin-like Superfamily: Ycel-like Family: Ycel-like
50	d1y0ga_	Alignment	not modelled	11.7	26	Fold: Streptavidin-like Superfamily: Ycel-like Family: Ycel-like
51	c4nx6A_	Alignment	not modelled	11.6	30	PDB header: oxidoreductase Chain: A: PDB Molecule: glyceraldehyde 3-phosphate dehydrogenase;

51	c4qxvA	Alignment	not modelled	11.0	30	PDBTitle: crystal structure of glyceraldehyde-3-phosphate dehydrogenase from <i>Streptococcus agalactiae</i> nem316 at 2.46 angstrom resolution
52	c3ctrA	Alignment	not modelled	11.6	31	PDB header: hydrolase Chain: A; PDB Molecule: poly(a)-specific ribonuclease parn; PDBTitle: crystal structure of the poly(a)-specific 2 ribonuclease parn bound to m7gtp
53	c5lhxA	Alignment	not modelled	11.6	22	PDB header: structural protein Chain: A; PDB Molecule: serine/threonine-protein kinase plk4; PDBTitle: pb3 domain of <i>Drosophila melanogaster</i> plk4 (sak)
54	c3pzvB	Alignment	not modelled	11.4	17	PDB header: hydrolase Chain: B; PDB Molecule: endoglucanase; PDBTitle: c2 crystal form of the endo-1,4-beta-glucanase from <i>Bacillus subtilis</i> 168
55	c2r5kE	Alignment	not modelled	11.2	20	PDB header: viral protein Chain: E; PDB Molecule: major capsid protein I1; PDBTitle: pentamer structure of major capsid protein I1 of human papilloma virus 2 type 11
56	d7a3ha	Alignment	not modelled	11.0	14	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
57	c5xf9F	Alignment	not modelled	11.0	8	PDB header: oxidoreductase Chain: F; PDB Molecule: nad-reducing hydrogenase; PDBTitle: crystal structure of nad+-reducing [nife]-hydrogenase in the air-2 oxidized state
58	d1cc3a	Alignment	not modelled	10.6	13	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
59	c5ixhB	Alignment	not modelled	10.6	18	PDB header: unknown function Chain: B; PDB Molecule: ycei-like domain protein; PDBTitle: crystal structure of <i>Burkholderia cenocepacia</i> bcna
60	c6f0kA	Alignment	not modelled	10.4	25	PDB header: membrane protein Chain: A; PDB Molecule: cytochrome c family protein; PDBTitle: alternative complex iii
61	c2aanA	Alignment	not modelled	10.1	14	PDB header: electron transport Chain: A; PDB Molecule: auracyanin a; PDBTitle: auracyanin a: a "blue" copper protein from the green thermophilic 2 photosynthetic bacterium, <i>Chloroflexus aurantiacus</i>
62	c3hpeB	Alignment	not modelled	9.7	25	PDB header: transport protein Chain: B; PDB Molecule: conserved hypothetical secreted protein; PDBTitle: crystal structure of ycei (hp1286) from <i>Helicobacter pylori</i>
63	c5i2uB	Alignment	not modelled	9.3	20	PDB header: hydrolase Chain: B; PDB Molecule: cellulase; PDBTitle: crystal structure of a novel halo-tolerant cellulase from soil 2 metagenome
64	c2z5cA	Alignment	not modelled	9.3	18	PDB header: chaperone/hydrolase Chain: A; PDB Molecule: protein ypl144w; PDBTitle: crystal structure of a novel chaperone complex for yeast 20s 2 proteasome assembly
65	c2fgsA	Alignment	not modelled	9.3	17	PDB header: lipid binding protein Chain: A; PDB Molecule: putative periplasmic protein; PDBTitle: crystal structure of <i>Campylobacter jejuni</i> ycei protein, 2 structural genomics
66	c3q34A	Alignment	not modelled	9.3	22	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: ycei-like family protein; PDBTitle: the crystal structure of ycei-like family protein from <i>Pseudomonas</i> 2 <i>syringae</i>
67	d1ecea	Alignment	not modelled	9.0	15	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
68	d1plqa2	Alignment	not modelled	8.9	14	Fold: DNA clamp Superfamily: DNA clamp Family: DNA polymerase processivity factor
69	c4f2eA	Alignment	not modelled	8.4	10	PDB header: metal transport Chain: A; PDB Molecule: cupa; PDBTitle: crystal structure of the <i>Streptococcus pneumoniae</i> d39 copper chaperone 2 cupa with cu(i)
70	c3bvdC	Alignment	not modelled	8.4	59	PDB header: oxidoreductase Chain: C; PDB Molecule: cytochrome c oxidase polypeptide 2a; PDBTitle: structure of surface-engineered cytochrome ba3 oxidase from <i>Thermus</i> 2 <i>thermophilus</i> under xenon pressure, 100psi 5min
71	d1xmec1	Alignment	not modelled	8.4	59	Fold: Single transmembrane helix Superfamily: Bacterial ba3 type cytochrome c oxidase subunit IIa Family: Bacterial ba3 type cytochrome c oxidase subunit IIa
72	c5ixgD	Alignment	not modelled	8.3	17	PDB header: unknown function Chain: D; PDB Molecule: ycei; PDBTitle: crystal structure of <i>Burkholderia cenocepacia</i> bcnb
73	c6amgA	Alignment	not modelled	8.2	18	PDB header: metal binding protein Chain: A; PDB Molecule: cytochrome p460; PDBTitle: cyt p460 of <i>Nitrosomonas</i> sp. al212
74	d1miau4	Alignment	not modelled	8.0	21	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
75	c4bjrA	Alignment	not modelled	7.9	40	PDB header: ligase Chain: A; PDB Molecule: pup--protein ligase, prokaryotic ubiquitin-like protein PDBTitle: crystal structure of the complex between prokaryotic 2 ubiquitin-like protein pup and its ligase pafa
76	c2h47C	Alignment	not modelled	7.9	13	PDB header: oxidoreductase/electron transport Chain: C; PDB Molecule: azurin; PDBTitle: crystal structure of an electron transfer complex between 2 aromatic amine dehydrogenase and azurin from <i>Alcaligenes</i> 3 <i>faecalis</i> (form 1)
						PDB header: structural genomics, unknown function Chain: A; PDB Molecule: putative periplasmic protein;

77	c2mqcA_	Alignment	not modelled	7.8	21	Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: nmr structure of the protein bvu_0925 from bacteroides vulgatus atcc2 8482
78	d1ajoa_	Alignment	not modelled	7.7	38	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Glycosyl hydrolases family 16
79	c4y66C_	Alignment	not modelled	7.6	18	PDB header: cell cycle Chain: C: PDB Molecule: mnd1; PDBTitle: crystal structure of giardia lamblia hop2-mnd1 complex
80	c4g6tB_	Alignment	not modelled	7.5	18	PDB header: chaperone Chain: B: PDB Molecule: type iii effector hopa1; PDBTitle: structure of the hopa1-scha chaperone-effector complex
81	c1kjkA_	Alignment	not modelled	7.3	7	PDB header: viral protein Chain: A: PDB Molecule: integrase; PDBTitle: solution structure of the lambda integrase amino-terminal2 domain
82	d1z1ba1	Alignment	not modelled	7.3	7	Fold: DNA-binding domain Superfamily: DNA-binding domain Family: lambda integrase N-terminal domain
83	c2x34A_	Alignment	not modelled	6.7	11	PDB header: carbohydrate-binding protein Chain: A: PDB Molecule: cellulose-binding protein, x158; PDBTitle: structure of a polyisoprenoid binding domain from saccharophagus2 degradans implicated in plant cell wall breakdown
84	c4nohA_	Alignment	not modelled	6.7	19	PDB header: lipid binding protein Chain: A: PDB Molecule: lipoprotein, putative; PDBTitle: 1.5 angstrom crystal structure of putative lipoprotein from bacillus2 anthracis.
85	c3iyjE_	Alignment	not modelled	6.6	20	PDB header: virus Chain: E: PDB Molecule: major capsid protein I1; PDBTitle: bovine papillomavirus type 1 outer capsid
86	c2l9uB_	Alignment	not modelled	6.4	30	PDB header: membrane protein Chain: B: PDB Molecule: receptor tyrosine-protein kinase erb3-3; PDBTitle: spatial structure of dimeric erb3 transmembrane domain
87	c2l9uA_	Alignment	not modelled	6.4	30	PDB header: membrane protein Chain: A: PDB Molecule: receptor tyrosine-protein kinase erb3-3; PDBTitle: spatial structure of dimeric erb3 transmembrane domain
88	c1jauA_	Alignment	not modelled	6.3	50	PDB header: viral protein Chain: A: PDB Molecule: transmembrane glycoprotein (gp41); PDBTitle: nmr solution structure of the trp-rich peptide of hiv gp412 bound to dpc micelles
89	c4fd7A_	Alignment	not modelled	6.3	19	PDB header: transferase Chain: A: PDB Molecule: putative arylalkylamine n-acetyltransferase 7; PDBTitle: crystal structure of insect putative arylalkylamine n-2 acetyltransferase 7 from the yellow fever mosquito aedes aegypt
90	c4kmaA_	Alignment	not modelled	6.3	41	PDB header: protein binding Chain: A: PDB Molecule: gm14141p; PDBTitle: crystal structure of drosophila suppressor of fused
91	c6igdG_	Alignment	not modelled	6.3	19	PDB header: structural protein Chain: G: PDB Molecule: major capsid protein I1; PDBTitle: crystal structure of hpv58/33 chimeric I1 pentamer
92	c3pm6B_	Alignment	not modelled	6.2	18	PDB header: lyase Chain: B: PDB Molecule: putative fructose-bisphosphate aldolase; PDBTitle: crystal structure of a putative fructose-1,6-biphosphate aldolase from2 coccidioides immitis solved by combined sad mr
93	d2c0ha1	Alignment	not modelled	6.2	23	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
94	d1dzla_	Alignment	not modelled	6.1	20	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Group I dsDNA viruses Family: Papovaviridae-like VP
95	c1dzlA_	Alignment	not modelled	6.1	20	PDB header: virus Chain: A: PDB Molecule: late major capsid protein I1; PDBTitle: I1 protein of human papillomavirus 16
96	d2diga1	Alignment	not modelled	6.0	23	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: Tudor domain
97	c5b0uB_	Alignment	not modelled	6.0	28	PDB header: luminescent protein Chain: B: PDB Molecule: oplophorus-luciferin 2-monooxygenase catalytic subunit; PDBTitle: crystal structure of the mutated 19 kda protein of oplophorus2 luciferase (nanokaz)
98	d1cuoa_	Alignment	not modelled	5.9	16	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
99	d1m1la_	Alignment	not modelled	5.9	41	Fold: Suppressor of Fused, N-terminal domain Superfamily: Suppressor of Fused, N-terminal domain Family: Suppressor of Fused, N-terminal domain