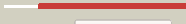



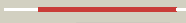








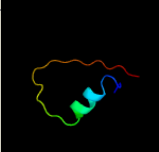










Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0487 (-)_576790_577341
Date	Fri Jul 26 01:50:02 BST 2019
Unique Job ID	bcd6f36597f121fc

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2plga1	 Alignment		98.7	16	Fold: Secretion chaperone-like Superfamily: Type III secretory system chaperone-like Family: TII0839-like
2	d1jyoa_	 Alignment		97.1	11	Fold: Secretion chaperone-like Superfamily: Type III secretory system chaperone-like Family: Type III secretory system chaperone
3	c4g6tA_	 Alignment		94.0	12	PDB header: chaperone Chain: A: PDB Molecule: type iii chaperone protein shca; PDBTitle: structure of the hopa1-scha chaperone-effector complex
4	c3epuB_	 Alignment		93.8	13	PDB header: chaperone Chain: B: PDB Molecule: stm2138 virulence chaperone; PDBTitle: crystal structure of stm2138, a novel virulence chaperone in2 salmonella
5	d1k3ea_	 Alignment		93.7	10	Fold: Secretion chaperone-like Superfamily: Type III secretory system chaperone-like Family: Type III secretory system chaperone
6	d1ttwa_	 Alignment		91.9	13	Fold: Secretion chaperone-like Superfamily: Type III secretory system chaperone-like Family: Type III secretory system chaperone
7	c6j7aB_	 Alignment		67.2	29	PDB header: oxidoreductase Chain: B: PDB Molecule: heme oxygenase 1, nadph--cytochrome p450 reductase; PDBTitle: fusion protein of heme oxygenase-1 and nadph cytochrome p450 reductase2 (17aa)
8	d1xkpc1	 Alignment		56.8	21	Fold: Secretion chaperone-like Superfamily: Type III secretory system chaperone-like Family: Type III secretory system chaperone
9	d1ul7a_	 Alignment		56.3	29	Fold: TBP-like Superfamily: KA1-like Family: Kinase associated domain 1, KA1
10	c4akxA_	 Alignment		55.8	25	PDB header: transport protein Chain: A: PDB Molecule: spcu; PDBTitle: structure of the heterodimeric complex exou-spcu from the type iii2 secretion system (t3ss) of pseudomonas aeruginosa
11	c3tu3A_	 Alignment		55.3	25	PDB header: toxin/toxin chaperone Chain: A: PDB Molecule: exou chaperone; PDBTitle: 1.92 angstrom resolution crystal structure of the full-length spcu in2 complex with full-length exou from the type iii secretion system of3 pseudomonas aeruginosa

12	c1j9zB_	Alignment		52.6	29	PDB header: oxidoreductase Chain: B: PDB Molecule: nadph-cytochrome p450 reductase; PDBTitle: cypor-w677g
13	c6efvA_	Alignment		45.3	25	PDB header: flavoprotein Chain: A: PDB Molecule: sulfite reductase [nadph] flavoprotein alpha-component; PDBTitle: the nadph-dependent sulfite reductase flavoprotein adopts an extended2 conformation that is unique to this diflavin reductase
14	d1ja1a2	Alignment		44.2	29	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like
15	d2akja1	Alignment		43.5	15	Fold: Ferredoxin-like Superfamily: Nitrite/Sulfite reductase N-terminal domain-like Family: Duplicated SiR/NiR-like domains 1 and 3
16	c2j58G_	Alignment		39.7	18	PDB header: membrane protein Chain: G: PDB Molecule: outer membrane lipoprotein wza; PDBTitle: the structure of wza
17	d2b3aa1	Alignment		37.2	32	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ras-binding domain, RBD
18	d1b1ca_	Alignment		36.4	29	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like
19	c3hr4C_	Alignment		35.1	16	PDB header: oxidoreductase/metal binding protein Chain: C: PDB Molecule: nitric oxide synthase, inducible; PDBTitle: human inos reductase and calmodulin complex
20	c3qrzC_	Alignment		34.7	26	PDB header: hormone receptor Chain: C: PDB Molecule: abscisic acid receptor pyl5; PDBTitle: crystal structure of native abscisic acid receptor pyl5 at 2.62 angstrom
21	c5gxuA_	Alignment	not modelled	32.9	26	PDB header: oxidoreductase Chain: A: PDB Molecule: nadph--cytochrome p450 reductase 2; PDBTitle: cystal structure of arabidopsis atr2
22	c2zc0C_	Alignment	not modelled	32.8	16	PDB header: transferase Chain: C: PDB Molecule: alanine glyoxylate transaminase; PDBTitle: crystal structure of an archaeal alanine:glyoxylate aminotransferase
23	c2w85A_	Alignment	not modelled	29.9	20	PDB header: protein transport Chain: A: PDB Molecule: peroxisomal membrane anchor protein pex14; PDBTitle: structure of pex14 in complex with pex19
24	d1ef5a_	Alignment	not modelled	29.9	21	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ras-binding domain, RBD
25	c4oxxA_	Alignment	not modelled	28.8	16	PDB header: electron transport Chain: A: PDB Molecule: cindoxin; PDBTitle: crystal structure of cindoxin, surface entropy reduction mutant
26	c2lqjA_	Alignment	not modelled	27.1	15	PDB header: hydrolase Chain: A: PDB Molecule: mg2+ transport protein; PDBTitle: solution structure of the c-terminal domain of the mgtc protein from2 mycobacterium tuberculosis
27	c2w8iG_	Alignment	not modelled	26.8	15	PDB header: membrane protein Chain: G: PDB Molecule: putative outer membrane lipoprotein wza; PDBTitle: crystal structure of wza24-345.
28	c2bpoA_	Alignment	not modelled	26.2	13	PDB header: reductase Chain: A: PDB Molecule: nadph-cytochrom p450 reductase; PDBTitle: crystal structure of the yeast cpr triple mutant: d74g, y75f, k78a.
						Fold: TBP-like

29	d1v5sa_	Alignment	not modelled	25.9	27	Superfamily: KA1-like Family: Kinase associated domain 1, KA1
30	d2dloa2	Alignment	not modelled	25.5	33	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
31	c2m1mA_	Alignment	not modelled	25.3	30	PDB header: transcription Chain: A: PDB Molecule: auxin-induced protein iaa4; PDBTitle: solution structure of the psiaa4 oligomerization domain reveals2 interaction modes for transcription factors in early auxin response
32	d1lfda_	Alignment	not modelled	25.2	23	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ras-binding domain, RBD
33	d1n8ja_	Alignment	not modelled	24.5	20	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
34	d1erna1	Alignment	not modelled	24.5	17	Fold: Immunoglobulin-like beta-sandwich Superfamily: Fibronectin type III Family: Fibronectin type III
35	c4r2nA_	Alignment	not modelled	22.7	19	PDB header: transferase Chain: A: PDB Molecule: putative phenylalanine aminotransferase; PDBTitle: crystal structure of rv3772 in complex with its substrate
36	c3cbfA_	Alignment	not modelled	22.2	14	PDB header: transferase Chain: A: PDB Molecule: alpha-aminodipate aminotransferase; PDBTitle: crystal structure of lysn, alpha-aminoadipate2 aminotransferase, from thermus thermophilus hb27
37	c2i7aA_	Alignment	not modelled	22.2	33	PDB header: hydrolase Chain: A: PDB Molecule: calpain 13; PDBTitle: domain iv of human calpain 13
38	c4h5bB_	Alignment	not modelled	20.8	27	PDB header: unknown function Chain: B: PDB Molecule: dr_1245 protein; PDBTitle: crystal structure of dr_1245 from deinococcus radiodurans
39	c5mtzA_	Alignment	not modelled	20.8	26	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease z; PDBTitle: crystal structure of a long form rnase z from yeast
40	c3l34H_	Alignment	not modelled	20.5	45	PDB header: transferase Chain: H: PDB Molecule: sensor protein; PDBTitle: the crystal structure of a two-component sensor domain (2nd2 form) from pseudomonas aeruginosa pa01
41	c1tlIA_	Alignment	not modelled	19.9	31	PDB header: oxidoreductase Chain: A: PDB Molecule: nitric-oxide synthase, brain; PDBTitle: crystal structure of rat neuronal nitric-oxide synthase2 reductase module at 2.3 a resolution.
42	c2w8wA_	Alignment	not modelled	19.5	14	PDB header: transferase Chain: A: PDB Molecule: serine palmitoyltransferase; PDBTitle: n100y spt with plp-ser
43	d1g8fa1	Alignment	not modelled	19.1	20	Fold: PUA domain-like Superfamily: PUA domain-like Family: ATP sulfurylase N-terminal domain
44	c2iufA_	Alignment	not modelled	18.1	25	PDB header: oxidoreductase Chain: A: PDB Molecule: catalase; PDBTitle: the structures of penicillium vitale catalase: resting2 state, oxidised state (compound i) and complex with3 aminotriazole
45	c2v2gC_	Alignment	not modelled	17.7	14	PDB header: oxidoreductase Chain: C: PDB Molecule: peroxiredoxin 6; PDBTitle: crystal structure of the c45s mutant of the peroxiredoxin 62 of arenicola marina. monoclinic form
46	d1lbaa_	Alignment	not modelled	17.5	6	Fold: N-acetylmuramoyl-L-alanine amidase-like Superfamily: N-acetylmuramoyl-L-alanine amidase-like Family: N-acetylmuramoyl-L-alanine amidase-like
47	c5ykjA_	Alignment	not modelled	17.2	29	PDB header: transferase Chain: A: PDB Molecule: peroxiredoxin prx1, mitochondrial; PDBTitle: structural basis of the thiol resolving mechanism in yeast2 mitochondrial 1-cys peroxiredoxin via glutathione/thioredoxin systems
48	c5jayB_	Alignment	not modelled	17.0	12	PDB header: transferase Chain: B: PDB Molecule: 8-amino-7-oxononoate synthase; PDBTitle: crystal structure of an 8-amino-7-oxononoate synthase from2 burkholderia xenovorans
49	c3ly1C_	Alignment	not modelled	16.9	15	PDB header: transferase Chain: C: PDB Molecule: putative histidinol-phosphate aminotransferase; PDBTitle: crystal structure of putative histidinol-phosphate aminotransferase2 (yp_050345.1) from erwinia carotovora atroseptica scri1043 at 1.80 a3 resolution
50	c3hwjA_	Alignment	not modelled	16.7	29	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase mycbp2; PDBTitle: crystal structure of the second phr domain of mouse myc-binding2 protein 2 (mycbp-2)
51	c3no8A_	Alignment	not modelled	16.3	21	PDB header: isomerase regulator Chain: A: PDB Molecule: btb/poz domain-containing protein 2; PDBTitle: crystal structure of the phr domain from human btb2 protein
52	c4g0zA_	Alignment	not modelled	15.7	23	PDB header: gene regulation Chain: A: PDB Molecule: protein argonaute 1; PDBTitle: crystal structure of arabidopsis thaliana ago1 mid domain in complex2 with gmp
53	c2va0E_	Alignment	not modelled	15.2	43	PDB header: transferase Chain: E: PDB Molecule: abfs arabinofuranosidase two component system sensor PDBTitle: differential regulation of the xylan degrading apparatus of2 cellvibrio japonicus by a novel two component system
54	c4pqjB_	Alignment	not modelled	14.9	23	PDB header: dna binding protein Chain: B: PDB Molecule: truncated replication protein repa;

						PDBTitle: n-terminal domain of dna binding protein
55	c4r7fA_	Alignment	not modelled	14.6	32	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a hypothetical protein (parmer_01801) from <i>2 parabacteroides merdae</i> atcc 43184 at 2.30 a resolution
56	d1uula_	Alignment	not modelled	14.5	24	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
57	c3tqxA_	Alignment	not modelled	14.3	15	PDB header: transferase Chain: A: PDB Molecule: 2-amino-3-ketobutyrate coenzyme a ligase; PDBTitle: structure of the 2-amino-3-ketobutyrate coenzyme a ligase (kbl) from <i>2 coxiella burnetii</i>
58	c3kh0A_	Alignment	not modelled	14.3	28	PDB header: signaling protein Chain: A: PDB Molecule: ral guanine nucleotide dissociation stimulator; PDBTitle: crystal structure of the ras-association (ra) domain of ralgs
59	c5ovqL_	Alignment	not modelled	14.2	24	PDB header: oxidoreductase Chain: L: PDB Molecule: peroxiredoxin; PDBTitle: crystal structure of the peroxiredoxin (ahpc2) from the <i>2 hyperthermophilic bacteria aquifex aeolicus</i> vf
60	c2m6rA_	Alignment	not modelled	14.1	9	PDB header: electron transport Chain: A: PDB Molecule: flavodoxin; PDBTitle: apo_yqca
61	d1n0ua5	Alignment	not modelled	14.0	9	Fold: Ferredoxin-like Superfamily: EF-G C-terminal domain-like Family: EF-G/eEF-2 domains III and V
62	c3zrrB_	Alignment	not modelled	13.8	14	PDB header: transferase Chain: B: PDB Molecule: serine-pyruvate aminotransferase (agxt); PDBTitle: crystal structure and substrate specificity of a thermophilic <i>2 archaeal serine : pyruvate aminotransferase</i> from <i>3 sulfobolus3 solfataricus</i>
63	c2e5aA_	Alignment	not modelled	13.8	18	PDB header: ligase Chain: A: PDB Molecule: lipoyltransferase 1; PDBTitle: crystal structure of bovine lipoyltransferase in complex <i>2 with lipoyl-amp</i>
64	c3ej6D_	Alignment	not modelled	13.7	8	PDB header: oxidoreductase Chain: D: PDB Molecule: catalase-3; PDBTitle: <i>neurospora crassa catalase-3 crystal structure</i>
65	c1r6xA_	Alignment	not modelled	13.7	20	PDB header: transferase Chain: A: PDB Molecule: atp:sulfate adenyllyltransferase; PDBTitle: the crystal structure of a truncated form of yeast atp2 sulfurylase, lacking the c-terminal aps kinase-like domain, <i>3 in complex with sulfate</i>
66	c6ambB_	Alignment	not modelled	13.3	32	PDB header: signaling protein Chain: B: PDB Molecule: afadin; PDBTitle: crystal structure of the afadin ra1 domain in complex with hras
67	c2mukX_	Alignment	not modelled	13.2	33	PDB header: transcription Chain: X: PDB Molecule: auxin-responsive protein iaa17; PDBTitle: <i>1h, 13c, and 15n chemical shift assignments for aux/iaa17</i>
68	d2rgfa_	Alignment	not modelled	13.2	28	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ras-binding domain, RBD
69	c3w6gP_	Alignment	not modelled	13.1	20	PDB header: oxidoreductase Chain: P: PDB Molecule: probable peroxiredoxin; PDBTitle: structure of peroxiredoxin from anaerobic hyperthermophilic archaeon <i>2 pyrococcus horikoshii</i>
70	c1g8gB_	Alignment	not modelled	13.0	20	PDB header: transferase Chain: B: PDB Molecule: sulfate adenyllyltransferase; PDBTitle: atp sulfurylase from <i>s. cerevisiae</i> : the binary product complex with <i>2 aps</i>
71	c3ftbA_	Alignment	not modelled	12.8	20	PDB header: transferase Chain: A: PDB Molecule: histidinol-phosphate aminotransferase; PDBTitle: the crystal structure of the histidinol-phosphate aminotransferase <i>2 from clostridium acetobutylicum</i>
72	d2o3bb1	Alignment	not modelled	12.6	23	Fold: Nuclease A inhibitor (NuiA) Superfamily: Nuclease A inhibitor (NuiA) Family: Nuclease A inhibitor (NuiA)
73	d1oxja2	Alignment	not modelled	12.5	22	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: PHAT domain
74	d1lf6a2	Alignment	not modelled	12.4	14	Fold: Supersandwich Superfamily: Galactose mutarotase-like Family: Bacterial glucoamylase N-terminal domain-like
75	d1rp3b_	Alignment	not modelled	12.3	26	Fold: Non-globular all-alpha subunits of globular proteins Superfamily: Anti-sigma factor FlgM Family: Anti-sigma factor FlgM
76	c6i52A_	Alignment	not modelled	12.2	38	PDB header: dna binding protein Chain: A: PDB Molecule: replication factor a protein 3; PDBTitle: yeast rpa bound to ssdna
77	c4xlqA_	Alignment	not modelled	12.1	22	PDB header: hydrolase Chain: A: PDB Molecule: structure-specific endonuclease subunit slx1; PDBTitle: <i>c. glabrata slx1 in complex with slx4ccd</i> .
78	c1m8pB_	Alignment	not modelled	12.1	11	PDB header: transferase Chain: B: PDB Molecule: sulfate adenyllyltransferase; PDBTitle: crystal structure of <i>p. chrysogenum atp sulfurylase</i> in the t-state
79	d2q3la1	Alignment	not modelled	12.1	11	Fold: Spollaa-like Superfamily: Spollaa-like Family: Sfri0576-like

80	c4davA	Alignment	not modelled	12.0	11	PDB header: hydrolase/dna Chain: A: PDB Molecule: sugar fermentation stimulation protein homolog; PDBTitle: the structure of pyrococcus furiosus sfsa in complex with dna
81	d1ae9a	Alignment	not modelled	11.1	18	Fold: DNA breaking-rejoining enzymes Superfamily: DNA breaking-rejoining enzymes Family: Lambda integrase-like, catalytic core
82	c2z5cA	Alignment	not modelled	11.0	29	PDB header: chaperone/hydrolase Chain: A: PDB Molecule: protein ypl144w; PDBTitle: crystal structure of a novel chaperone complex for yeast 20s2 proteasome assembly
83	d1zsqa2	Alignment	not modelled	10.5	36	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Myotubularin-like phosphatases
84	c5b3kA	Alignment	not modelled	10.5	16	PDB header: electron transport Chain: A: PDB Molecule: uncharacterized protein pa3435; PDBTitle: c101a mutant of flavodoxin from pseudomonas aeruginosa
85	d2grea2	Alignment	not modelled	10.3	21	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
86	d1x6va1	Alignment	not modelled	9.8	13	Fold: PUA domain-like Superfamily: PUA domain-like Family: ATP sulfurylase N-terminal domain
87	c6h82b	Alignment	not modelled	9.8	30	PDB header: virus Chain: B: PDB Molecule: vp4; PDBTitle: cryo-em structure of the archaeal extremophilic internal membrane2 containing haloarcula hispanica icosahedral virus 2 (hhiv-2) at 3.783 angstroms resolution.
88	c5bndA	Alignment	not modelled	9.7	44	PDB header: transport protein Chain: A: PDB Molecule: abc transporter, atp-binding protein; PDBTitle: crystal structure of the c-terminal domain of tagh
89	c5ha0A	Alignment	not modelled	9.6	5	PDB header: transport protein Chain: A: PDB Molecule: lipocalin ai-4; PDBTitle: crystal structure of the ltbp1 leukotriene d4 complex
90	d1qmva	Alignment	not modelled	9.4	25	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
91	c1sy9B	Alignment	not modelled	9.4	36	PDB header: calcium-binding protein Chain: B: PDB Molecule: cyclic-nucleotide-gated olfactory channel; PDBTitle: structure of calmodulin complexed with a fragment of the2 olfactory cng channel
92	c4mafH	Alignment	not modelled	9.0	15	PDB header: transferase Chain: H: PDB Molecule: atp sulfurylase; PDBTitle: soybean atp sulfurylase
93	d1aiha	Alignment	not modelled	9.0	9	Fold: DNA breaking-rejoining enzymes Superfamily: DNA breaking-rejoining enzymes Family: Lambda integrase-like, catalytic core
94	d1s28a	Alignment	not modelled	8.9	22	Fold: Secretion chaperone-like Superfamily: Type III secretory system chaperone-like Family: Type III secretory system chaperone
95	c6drhC	Alignment	not modelled	8.7	17	PDB header: toxin Chain: C: PDB Molecule: adp-ribosyl-(dinitrogen reductase) hydrolase; PDBTitle: adp-ribosyltransferase toxin/immunity pair
96	d1vhea2	Alignment	not modelled	8.7	23	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
97	c5c6kB	Alignment	not modelled	8.5	19	PDB header: hydrolase Chain: B: PDB Molecule: integrase; PDBTitle: bacteriophage p2 integrase catalytic domain
98	c4gekG	Alignment	not modelled	8.5	18	PDB header: transferase Chain: G: PDB Molecule: trna (cmo5u34)-methyltransferase; PDBTitle: crystal structure of wild-type cmoa from e.coli
99	c4nj7P	Alignment	not modelled	8.4	33	PDB header: protein binding Chain: P: PDB Molecule: auxin response factor 7; PDBTitle: pb1 domain of atarf7 - semet derivative