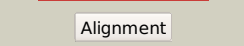


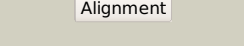








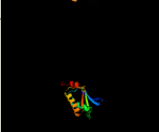



Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1365c_(rsfA)_1537789_1538175
 Date Wed Jul 31 22:05:46 BST 2019
 Unique Job ID 131d532fa68f4e29





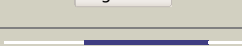
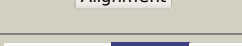
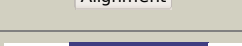
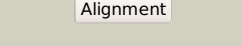

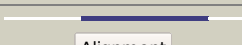

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3t6oA_	 Alignment		99.9	18	PDB header: transport protein Chain: A: PDB Molecule: sulfate transporter/antisigma-factor antagonist stas; PDBTitle: the structure of an anti-sigma-factor antagonist (stas) domain protein2 from planctomyces limnophilus.
2	c4hylB_	 Alignment		99.9	19	PDB header: transcription regulator Chain: B: PDB Molecule: stage ii sporulation protein; PDBTitle: the crystal structure of an anti-sigma-factor antagonist from2 haliangium ochraceum dsm 14365
3	d1th8b_	 Alignment		99.9	22	Fold: Spollaa-like Superfamily: Spollaa-like Family: Anti-sigma factor antagonist Spollaa
4	d1lauza_	 Alignment		99.9	21	Fold: Spollaa-like Superfamily: Spollaa-like Family: Anti-sigma factor antagonist Spollaa
5	d1vc1a_	 Alignment		99.9	23	Fold: Spollaa-like Superfamily: Spollaa-like Family: Anti-sigma factor antagonist Spollaa
6	c4xs5D_	 Alignment		99.9	17	PDB header: transport protein Chain: D: PDB Molecule: sulfate transporter/antisigma-factor antagonist stas; PDBTitle: crystal structure of sulfate transporter/antisigma-factor antagonist2 stas from dyadobacter fermentans dsm 18053
7	c3f43A_	 Alignment		99.9	16	PDB header: transcription Chain: A: PDB Molecule: putative anti-sigma factor antagonist tm1081; PDBTitle: crystal structure of a putative anti-sigma factor antagonist (tm1081)2 from thermotoga maritima at 1.59 a resolution
8	d1h4xa_	 Alignment		99.9	17	Fold: Spollaa-like Superfamily: Spollaa-like Family: Anti-sigma factor antagonist Spollaa
9	c2vy9A_	 Alignment		99.8	14	PDB header: gene regulation Chain: A: PDB Molecule: anti-sigma-factor antagonist; PDBTitle: molecular architecture of the stressosome, a signal2 integration and transduction hub
10	c3mglA_	 Alignment		99.8	20	PDB header: transport protein Chain: A: PDB Molecule: sulfate permease family protein; PDBTitle: crystal structure of permease family protein from vibrio cholerae
11	c2klnA_	 Alignment		99.8	16	PDB header: transport protein Chain: A: PDB Molecule: probable sulphate-transport transmembrane protein, cog0659; PDBTitle: solution structure of stas domain of rv1739c from m. tuberculosis

12	c3oirA_	Alignment		99.8	14	PDB header: transport protein Chain: A: PDB Molecule: sulfate transporter sulfate transporter family protein; PDBTitle: crystal structure of sulfate transporter family protein from wolinnella2 succinogenes
13	c5ezbB_	Alignment		99.8	15	PDB header: transport protein Chain: B: PDB Molecule: chicken prestin stas domain,chicken prestin stas domain; PDBTitle: chicken prestin stas domain
14	c3ny7A_	Alignment		99.8	9	PDB header: membrane protein Chain: A: PDB Molecule: sulfate transporter; PDBTitle: stas domain of ychm bound to acp
15	c3lloA_	Alignment		99.7	15	PDB header: motor protein Chain: A: PDB Molecule: prestine; PDBTitle: crystal structure of the stas domain of motor protein prestin (anion2 transporter slc26a5)
16	c6rtfA_	Alignment		99.7	20	PDB header: membrane protein Chain: A: PDB Molecule: solute carrier family 26 member 9,solute carrier family 26 PDBTitle: structure of murine solute carrier 26 family member a9 (slc26a9) anion2 transporter in an intermediate state
17	c6ic4K_	Alignment		99.6	21	PDB header: protein transport Chain: K: PDB Molecule: ttg2e; PDBTitle: cryo-em structure of the a. baumannii mla complex at 8.7 a resolution
18	c3lkiB_	Alignment		99.5	14	PDB header: transport protein Chain: B: PDB Molecule: antisigma-factor antagonist stas; PDBTitle: crystal structure of the c-terminal domain of anti-sigma factor2 antagonist stas from rhodobacter sphaeroides
19	c5da0A_	Alignment		99.2	19	PDB header: transport protein Chain: A: PDB Molecule: sulphate transporter; PDBTitle: structure of the the slc26 transporter slc26dg in complex with a2 nanobody
20	d2q3la1	Alignment		96.3	12	Fold: Spollaa-like Superfamily: Spollaa-like Family: Sfri0576-like
21	c3ih9A_	Alignment	not modelled	95.1	20	PDB header: hydrolase Chain: A: PDB Molecule: salt-tolerant glutaminase; PDBTitle: crystal structure analysis of mglu in its tris form
22	c3bl4B_	Alignment	not modelled	90.8	16	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a protein with unknown function (arth_0117) from2 arthrobacter sp. fb24 at 2.20 a resolution
23	c3bezC_	Alignment	not modelled	88.9	13	PDB header: hydrolase Chain: C: PDB Molecule: protease 4; PDBTitle: crystal structure of escherichia coli signal peptide peptidase (sppa),2 semet crystals
24	c2pr7A_	Alignment	not modelled	78.8	17	PDB header: hydrolase Chain: A: PDB Molecule: haloacid dehalogenase/epoxide hydrolase family; PDBTitle: crystal structure of uncharacterized protein (np_599989.1) from2 corynebacterium glutamicum atcc 13032 kitasato at 1.44 a resolution
25	c3rstH_	Alignment	not modelled	77.0	11	PDB header: hydrolase Chain: H: PDB Molecule: signal peptide peptidase sppa; PDBTitle: crystal structure of bacillus subtilis signal peptide peptidase a
26	d2ooka1	Alignment	not modelled	71.9	14	Fold: Spollaa-like Superfamily: Spollaa-like Family: Sfri0576-like
27	c3ghfA_	Alignment	not modelled	59.0	15	PDB header: cell cycle Chain: A: PDB Molecule: septum site-determining protein minc; PDBTitle: crystal structure of the septum site-determining protein minc from2 salmonella typhimurium
28	c3kthD_	Alignment	not modelled	50.9	11	PDB header: hydrolase Chain: D: PDB Molecule: atp-dependent clp protease proteolytic subunit; PDBTitle: structure of clpp from bacillus subtilis in orthorombic

						crystal form
29	c2cbyG_	Alignment	not modelled	48.4	15	PDB header: hydrolase Chain: G: PDB Molecule: atp-dependent clp protease proteolytic subunit 1; PDBTitle: crystal structure of the atp-dependent clp protease proteolytic2 subunit 1 (clpp1) from mycobacterium tuberculosis
30	c4yajA_	Alignment	not modelled	47.7	19	PDB header: ligase Chain: A: PDB Molecule: alpha subunit of acetyl-coenzyme a synthetase PDBTitle: ca. korarchaeum cryptofilum dinucleotide forming acetyl-coenzyme a2 synthetase 1 (apo form)
31	d1tg6a1	Alignment	not modelled	43.4	14	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Clp protease, ClpP subunit
32	c4umfC_	Alignment	not modelled	39.6	11	PDB header: hydrolase Chain: C: PDB Molecule: 3-deoxy-d-manno-octulosonate 8-phosphate phosphatase kdsc; PDBTitle: crystal structure of 3-deoxy-d-manno-octulosonate 8-2 phosphate phosphatase from moraxella catarrhalis in3 complex with magnesium ion, phosphate ion and kdo molecule
33	c3kc2A_	Alignment	not modelled	39.3	17	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein ykr070w; PDBTitle: crystal structure of mitochondrial had-like phosphatase from2 saccharomyces cerevisiae
34	c2deoA_	Alignment	not modelled	35.2	9	PDB header: hydrolase Chain: A: PDB Molecule: 441aa long hypothetical nfd protein; PDBTitle: 1510-n membrane protease specific for a stomatin homolog from2 pyrococcus horikoshii
35	c4eogA_	Alignment	not modelled	34.7	13	PDB header: dna binding protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of csx1 of pyrococcus furiosus
36	d2csua3	Alignment	not modelled	33.9	12	Fold: Flavodoxin-like Superfamily: Succinyl-CoA synthetase domains Family: Succinyl-CoA synthetase domains
37	c2yx6C_	Alignment	not modelled	31.6	15	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: hypothetical protein ph0822; PDBTitle: crystal structure of ph0822
38	c4olqD_	Alignment	not modelled	30.9	18	PDB header: lyase Chain: D: PDB Molecule: enoyl-coa hydratase/isomerase family protein; PDBTitle: crystal structure of a putative enoyl-coa hydratase/isomerase family2 protein from hyphomonas neptunium
39	c1tg6G_	Alignment	not modelled	30.6	11	PDB header: hydrolase Chain: G: PDB Molecule: putative atp-dependent clp protease proteolytic subunit; PDBTitle: crystallography and mutagenesis point to an essential role for the n-2 terminus of human mitochondrial clpp
40	d1t3va_	Alignment	not modelled	28.9	15	Fold: Ribonuclease H-like motif Superfamily: Nitrogenase accessory factor-like Family: MTH1175-like
41	d1o13a_	Alignment	not modelled	27.6	15	Fold: Ribonuclease H-like motif Superfamily: Nitrogenase accessory factor-like Family: MTH1175-like
42	d2cbya1	Alignment	not modelled	27.4	19	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Clp protease, ClpP subunit
43	c2dfwA_	Alignment	not modelled	25.7	19	PDB header: hydrolase Chain: A: PDB Molecule: salt-tolerant glutaminase; PDBTitle: crystal structure of a major fragment of the salt-tolerant2 glutaminase from micrococcus luteus k-3
44	d1yg6a1	Alignment	not modelled	22.9	7	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Clp protease, ClpP subunit
45	c3qmjA_	Alignment	not modelled	20.7	14	PDB header: lyase Chain: A: PDB Molecule: enoyl-coa hydratase, echa8_6; PDBTitle: crystal structure of enoyl-coa hydratase echa8_6 from mycobacterium2 marinum
46	c2csuB_	Alignment	not modelled	20.6	12	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: 457aa long hypothetical protein; PDBTitle: crystal structure of ph0766 from pyrococcus horikoshii ot3
47	d1y7oa1	Alignment	not modelled	19.6	11	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Clp protease, ClpP subunit
48	c2w3pB_	Alignment	not modelled	19.4	11	PDB header: lyase Chain: B: PDB Molecule: benzoyl-coa-dihydrodiol lyase; PDBTitle: boxc crystal structure
49	c2mwgB_	Alignment	not modelled	18.8	10	PDB header: protein binding Chain: B: PDB Molecule: blue-light photoreceptor; PDBTitle: full-length solution structure of ytvA, a low-photoreceptor protein2 and regulator of bacterial stress response
50	c2wfbA_	Alignment	not modelled	18.1	20	PDB header: biosynthetic protein Chain: A: PDB Molecule: putative uncharacterized protein orp; PDBTitle: high resolution structure of the apo form of the orange2 protein (orp) from desulfovibrio gigas
51	c4hgnB_	Alignment	not modelled	17.6	13	PDB header: hydrolase Chain: B: PDB Molecule: 2-keto-3-deoxy-d-manno-octulosonate 8-phosphate PDBTitle: crystal structure of 2-keto-3-deoxyoctulosonate 8-phosphate2 phosphohydrolase from bacteroides thetaiotaomicron
52	d1rdua_	Alignment	not modelled	17.1	20	Fold: Ribonuclease H-like motif Superfamily: Nitrogenase accessory factor-like Family: MTH1175-like
						PDB header: hydrolase Chain: A: PDB Molecule: fucosyltransferase 1; fucosyltransferase 1; fucosyltransferase 1

53	c2wmhA_	Alignment	not modelled	16.9	6	PDBTitle: crystal structure of the catalytic module of a family 982 glycoside hydrolase from streptococcus pneumoniae tigr4 in3 complex with the h-disaccharide blood group antigen.
54	c6g4qB_	Alignment	not modelled	16.6	16	PDB header: ligase Chain: B: PDB Molecule: succinate--coa ligase [adp-forming] subunit beta, PDBTitle: structure of human adp-forming succinyl-coa ligase complex sucg1-2 suc1a2
55	d1e01a_	Alignment	not modelled	16.1	17	Fold: Ribonuclease H-like motif Superfamily: Nitrogenase accessory factor-like Family: MTH1175-like
56	c2ej5B_	Alignment	not modelled	16.1	7	PDB header: lyase Chain: B: PDB Molecule: enoyl-coa hydratase subunit ii; PDBTitle: crystal structure of gk2038 protein (enoyl-coa hydratase subunit ii)2 from geobacillus kaustophilus
57	c2hroA_	Alignment	not modelled	14.8	9	PDB header: transferase Chain: A: PDB Molecule: phosphoenolpyruvate-protein phosphotransferase; PDBTitle: structure of the full-length enzyme i of the pts system from2 staphylococcus carnosus
58	d1ptma_	Alignment	not modelled	13.4	10	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: PdxA-like
59	c2j5iF_	Alignment	not modelled	13.3	12	PDB header: lyase Chain: F: PDB Molecule: p-hydroxycinnamoyl coa hydratase/lyase; PDBTitle: crystal structure of hydroxycinnamoyl-coa hydratase-lyase
60	c6iqsD_	Alignment	not modelled	13.1	5	PDB header: hydrolase Chain: D: PDB Molecule: tail-specific protease; PDBTitle: crystal structure of prc with I245a and I340g mutations in complex2 with nlpi
61	c6k4fU_	Alignment	not modelled	12.6	21	PDB header: biosynthetic protein Chain: U: PDB Molecule: duf1987 domain-containing protein; PDBTitle: siac of pseudomonas aeruginosa
62	d1s1ma2	Alignment	not modelled	12.1	12	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
63	c3isaA_	Alignment	not modelled	11.2	29	PDB header: hydrolase Chain: A: PDB Molecule: putative enoyl-coa hydratase/isomerase; PDBTitle: crystal structure of putative enoyl-coa hydratase/isomerase from2 bordetella parapertussis
64	c2qtdA_	Alignment	not modelled	11.1	5	PDB header: oxidoreductase Chain: A: PDB Molecule: uncharacterized protein mj0327; PDBTitle: crystal structure of a putative dinitrogenase (mj0327) from2 methanocaldococcus jannaschii dsm at 1.70 a resolution
65	c4wczB_	Alignment	not modelled	10.9	13	PDB header: isomerase Chain: B: PDB Molecule: enoyl-coa hydratase/isomerase; PDBTitle: crystal structure of a putative enoyl-coa hydratase/isomerase from2 novosphingobium aromaticivorans
66	c2dgdD_	Alignment	not modelled	10.8	10	PDB header: lyase Chain: D: PDB Molecule: 223aa long hypothetical arylmalonate decarboxylase; PDBTitle: crystal structure of st0656, a function unknown protein from2 sulfobolus tokodaii
67	c3re1B_	Alignment	not modelled	10.8	22	PDB header: lyase Chain: B: PDB Molecule: uroporphyrinogen-iii synthetase; PDBTitle: crystal structure of uroporphyrinogen iii synthase from pseudomonas2 syringae pv. tomato dc3000
68	d2f0ca1	Alignment	not modelled	10.6	15	Fold: Virus attachment protein globular domain Superfamily: Virus attachment protein globular domain Family: Lactophage receptor-binding protein head domain
69	d1sg4a1	Alignment	not modelled	10.1	4	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Crotonase-like
70	d1tqya1	Alignment	not modelled	10.0	7	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
71	d2nu7b1	Alignment	not modelled	9.9	9	Fold: Flavodoxin-like Superfamily: Succinyl-CoA synthetase domains Family: Succinyl-CoA synthetase domains
72	c3uosH_	Alignment	not modelled	9.9	17	PDB header: ribosome Chain: H: PDB Molecule: 50s ribosomal protein l10; PDBTitle: crystal structure of release factor rf3 trapped in the gtp state on a2 rotated conformation of the ribosome (without viomycin)
73	d2bufa1	Alignment	not modelled	9.7	9	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: N-acetyl-l-glutamate kinase
74	c2hwgA_	Alignment	not modelled	9.6	7	PDB header: transferase Chain: A: PDB Molecule: phosphoenolpyruvate-protein phosphotransferase; PDBTitle: structure of phosphorylated enzyme i of the phosphoenolpyruvate:sugar2 phosphotransferase system
75	d1fmfa_	Alignment	not modelled	9.1	15	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
76	d1czan4	Alignment	not modelled	9.0	11	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Hexokinase
77	c5udtD_	Alignment	not modelled	9.0	15	PDB header: transferase Chain: D: PDB Molecule: lactate racemization operon protein lare; PDBTitle: lare, a sulfur transferase involved in synthesis of the cofactor for2 lactate racemase, in complex with amp
78	d1bg3a2	Alignment	not modelled	8.9	9	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Hexokinase

79	c2ppyE	 Alignment	not modelled	8.8	13	PDB header: lyase Chain: E: PDB Molecule: enoyl-coa hydratase; PDBTitle: crystal structure of enoyl-coa hydrates (gk_1992) from geobacillus2 kaustophilus hta426
80	d1ro5a	 Alignment	not modelled	8.8	8	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: Autoinducer synthetase
81	c3igxA	 Alignment	not modelled	8.6	17	PDB header: transferase Chain: A: PDB Molecule: transaldolase; PDBTitle: 1.85 angstrom resolution crystal structure of transaldolase b (tala)2 from francisella tularensis.
82	c5wybB	 Alignment	not modelled	8.6	18	PDB header: isomerase Chain: B: PDB Molecule: probable enoyl-coa hydratase/isomerase; PDBTitle: structure of pseudomonas aeruginosa dspi
83	c3i47A	 Alignment	not modelled	8.4	11	PDB header: lyase Chain: A: PDB Molecule: enoyl coa hydratase/isomerase (crotonase); PDBTitle: crystal structure of putative enoyl coa hydratase/isomerase2 (crotonase) from legionella pneumophila subsp. pneumophila str.3 philadelphia 1
84	c2b5oA	 Alignment	not modelled	8.4	14	PDB header: oxidoreductase Chain: A: PDB Molecule: ferredoxin--nadp reductase; PDBTitle: ferredoxin-nadp reductase
85	c3mn1B	 Alignment	not modelled	8.3	14	PDB header: hydrolase Chain: B: PDB Molecule: probable yrbi family phosphatase; PDBTitle: crystal structure of probable yrbi family phosphatase from pseudomonas2 syringae pv.phaseolica 1448a
86	c3rsiA	 Alignment	not modelled	8.3	4	PDB header: isomerase Chain: A: PDB Molecule: putative enoyl-coa hydratase/isomerase; PDBTitle: the structure of a putative enoyl-coa hydratase/isomerase from2 mycobacterium abscessus atcc 19977 / dsm 44196
87	d1ys9a1	 Alignment	not modelled	8.3	19	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
88	c6me1B	 Alignment	not modelled	8.2	10	PDB header: ligase Chain: B: PDB Molecule: succinate--coa ligase [adp-forming] subunit beta; PDBTitle: succinyl-coa synthase from campylobacter jejuni
89	c4es6A	 Alignment	not modelled	8.1	20	PDB header: lyase Chain: A: PDB Molecule: uroporphyrinogen-iii synthase; PDBTitle: crystal structure of hemd (pa5259) from pseudomonas aeruginosa (pao1)2 at 2.22 a resolution
90	c4u0gG	 Alignment	not modelled	8.1	11	PDB header: hydrolase/antibiotic Chain: G: PDB Molecule: atp-dependent clp protease proteolytic subunit 2; PDBTitle: crystal structure of m. tuberculosis clpp1p2 bound to adep and agonist
91	c2bg5C	 Alignment	not modelled	8.0	12	PDB header: transferase Chain: C: PDB Molecule: phosphoenolpyruvate-protein kinase; PDBTitle: crystal structure of the phosphoenolpyruvate-binding enzyme i-domain2 from the thermoanaerobacter tengcongensis pep: sugar3 phosphotransferase system (pts)
92	c3efaA	 Alignment	not modelled	7.9	18	PDB header: transferase Chain: A: PDB Molecule: putative acetyltransferase; PDBTitle: crystal structure of putative n-acetyltransferase from lactobacillus2 plantarum
93	c3n1uA	 Alignment	not modelled	7.7	13	PDB header: hydrolase Chain: A: PDB Molecule: hydrolase, had superfamily, subfamily iii a; PDBTitle: structure of putative had superfamily (subfamily iii a) hydrolase from2 legionella pneumophila
94	c3gkuB	 Alignment	not modelled	7.6	15	PDB header: rna binding protein Chain: B: PDB Molecule: probable rna-binding protein; PDBTitle: crystal structure of a probable rna-binding protein from clostridium2 symbiosum atcc 14940
95	c2hx1D	 Alignment	not modelled	7.6	8	PDB header: hydrolase Chain: D: PDB Molecule: predicted sugar phosphatases of the had superfamily; PDBTitle: crystal structure of possible sugar phosphatase, had superfamily2 (zp_00311070.1) from cytophaga hutchinsonii atcc 33406 at 2.10 a3 resolution
96	d2qale1	 Alignment	not modelled	7.4	22	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Translational machinery components
97	c5ve2J	 Alignment	not modelled	7.1	4	PDB header: isomerase,lyase Chain: J: PDB Molecule: enoyl-coa hydratase; PDBTitle: crystal structure of enoyl-coa hydratase/isomerase from2 pseudoalteromonas atlantica t6c at 2.3 a resolution.
98	c3trrA	 Alignment	not modelled	7.0	9	PDB header: isomerase Chain: A: PDB Molecule: probable enoyl-coa hydratase/isomerase; PDBTitle: crystal structure of a probable enoyl-coa hydratase/isomerase from2 mycobacterium abscessus
99	c2q8fA	 Alignment	not modelled	6.9	10	PDB header: transferase Chain: A: PDB Molecule: [pyruvate dehydrogenase [lipoamide]] kinase isozyme 1; PDBTitle: structure of pyruvate dehydrogenase kinase isoform 1