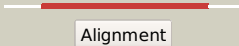



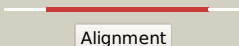

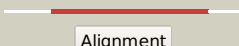

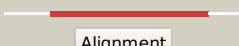

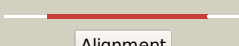

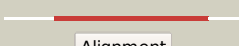









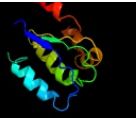




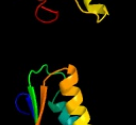





Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0516c_(-)_608062_608538
Date	Fri Jul 26 01:50:06 BST 2019
Unique Job ID	a57f4a21c2313bc3

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	20	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	21	Fold: Spollaa-like Superfamily: Spollaa-like Family: Anti-sigma factor antagonist Spollaa
4	c3f43A_	 Alignment		99.9	14	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
5	c4xs5D_	 Alignment		99.8	9	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
6	d1vc1a_	 Alignment		99.8	26	Fold: Spollaa-like Superfamily: Spollaa-like Family: Anti-sigma factor antagonist Spollaa
7	c3mg1A_	 Alignment		99.8	12	PDB header: transport protein Chain: A: PDB Molecule: sulfate permease family protein; PDBTitle: crystal structure of permease family protein from vibrio cholerae
8	d1lauza_	 Alignment		99.8	18	Fold: Spollaa-like Superfamily: Spollaa-like Family: Anti-sigma factor antagonist Spollaa
9	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
10	c2vy9A_	 Alignment		99.8	17	PDB header: gene regulation Chain: A: PDB Molecule: anti-sigma-factor antagonist; PDBTitle: molecular architecture of the stressosome, a signal2 integration and transduction hub
11	d1h4xa_	 Alignment		99.8	16	Fold: Spollaa-like Superfamily: Spollaa-like Family: Anti-sigma factor antagonist Spollaa

12	c2klnA	Alignment		99.8	13	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
13	c3ny7A	Alignment		99.7	13	PDB header: membrane protein Chain: A: PDB Molecule: sulfate transporter; PDBTitle: stas domain of ychm bound to acp
14	c5ezbB	Alignment		99.7	14	PDB header: transport protein Chain: B: PDB Molecule: chicken prestin stas domain,chicken prestin stas domain; PDBTitle: chicken prestin stas domain
15	c3lloA	Alignment		99.6	16	PDB header: motor protein Chain: A: PDB Molecule: prestine; PDBTitle: crystal structure of the stas domain of motor protein prestin (anion2 transporter slc26a5)
16	c6ic4K	Alignment		99.5	17	PDB header: protein transport Chain: K: PDB Molecule: ttg2e; PDBTitle: cryo-em structure of the a. baumannii mla complex at 8.7 a resolution
17	c3lklB	Alignment		99.4	18	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
18	c5da0A	Alignment		99.0	13	PDB header: transport protein Chain: A: PDB Molecule: sulphate transporter; PDBTitle: structure of the the slc26 transporter slc26dg in complex with a2 nanobody
19	c3ih9A	Alignment		96.8	18	PDB header: hydrolase Chain: A: PDB Molecule: salt-tolerant glutaminase; PDBTitle: crystal structure analysis of mglu in its tris form
20	c3bl4B	Alignment		92.8	19	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
21	c2pr7A	Alignment	not modelled	80.2	9	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
22	d2csua3	Alignment	not modelled	74.3	7	Fold: Flavodoxin-like Superfamily: Succinyl-CoA synthetase domains Family: Succinyl-CoA synthetase domains
23	c6k4fU	Alignment	not modelled	60.9	21	PDB header: biosynthetic protein Chain: U: PDB Molecule: duf1987 domain-containing protein; PDBTitle: siac of pseudomonas aeruginosa
24	c2dfwA	Alignment	not modelled	58.4	11	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
25	d2nu7b1	Alignment	not modelled	51.9	8	Fold: Flavodoxin-like Superfamily: Succinyl-CoA synthetase domains Family: Succinyl-CoA synthetase domains
26	d1ccwa	Alignment	not modelled	51.2	19	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
27	c2deoA	Alignment	not modelled	48.1	15	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
28	c3n07B	Alignment	not modelled	44.5	11	PDB header: hydrolase Chain: B: PDB Molecule: 3-deoxy-d-manno-octulosonate 8-phosphate phosphatase; PDBTitle: structure of putative 3-deoxy-d-manno-octulosonate 8-phosphate2 phosphatase from vibrio cholerae

29	c4umfC	Alignment	not modelled	43.0	10	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
30	c3kc2A	Alignment	not modelled	42.0	5	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein ykr070w; PDBTitle: crystal structure of mitochondrial had-like phosphatase from2 saccharomyces cerevisiae
31	c2csuB	Alignment	not modelled	41.2	7	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: 457aa long hypothetical protein; PDBTitle: crystal structure of ph0766 from pyrococcus horikoshii ot3
32	c4hgnB	Alignment	not modelled	35.3	11	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
33	c3ghfA	Alignment	not modelled	31.5	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
34	c2q5cA	Alignment	not modelled	30.8	8	PDB header: transcription Chain: A: PDB Molecule: ntrc family transcriptional regulator; PDBTitle: crystal structure of ntrc family transcriptional regulator from2 clostridium acetobutylicum
35	c1tg6G	Alignment	not modelled	29.9	15	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
36	c4e8iA	Alignment	not modelled	29.4	16	PDB header: transferase Chain: A: PDB Molecule: lincosamide resistance protein; PDBTitle: crystal structure of lincosamide antibiotic adenylyltransferase lina,2 apo
37	c4yajA	Alignment	not modelled	27.4	5	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)
38	c3mn1B	Alignment	not modelled	26.7	18	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
39	d2pjuA1	Alignment	not modelled	26.1	5	Fold: Chelatase-like Superfamily: PrpR receptor domain-like Family: PrpR receptor domain-like
40	c2pjuD	Alignment	not modelled	26.1	5	PDB header: transcription Chain: D: PDB Molecule: propionate catabolism operon regulatory protein; PDBTitle: crystal structure of propionate catabolism operon regulatory protein2 prpr
41	d1tg6a1	Alignment	not modelled	26.0	15	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Clp protease, ClpP subunit
42	d2cbya1	Alignment	not modelled	25.6	6	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Clp protease, ClpP subunit
43	d1t3va	Alignment	not modelled	25.6	6	Fold: Ribonuclease H-like motif Superfamily: Nitrogenase accessory factor-like Family: MTH1175-like
44	c6r62A	Alignment	not modelled	25.1	11	PDB header: lyase Chain: A: PDB Molecule: hpch/hpai aldolase; PDBTitle: crystal structure of a class ii pyruvate aldolase from sphingomonas2 wittichii rw1 in complex with hydroxypyruvate
45	d1izca	Alignment	not modelled	25.1	8	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: HpCH/Hpai aldolase
46	c1izcA	Alignment	not modelled	25.1	8	PDB header: lyase Chain: A: PDB Molecule: macrophomate synthase intermolecular diels-alderase; PDBTitle: crystal structure analysis of macrophomate synthase
47	c4e1pA	Alignment	not modelled	24.6	17	PDB header: dna binding protein Chain: A: PDB Molecule: protein lsr2; PDBTitle: crystal structure of the dimerization domain of lsr2 from2 mycobacterium tuberculosis in the p 1 21 1 space group
48	c4e1rA	Alignment	not modelled	24.6	17	PDB header: dna binding protein Chain: A: PDB Molecule: protein lsr2; PDBTitle: crystal structure of the dimerization domain of lsr2 from2 mycobacterium tuberculosis in the p 31 2 1 space group
49	c4jcuU	Alignment	not modelled	22.2	21	PDB header: hydrolase Chain: U: PDB Molecule: atp-dependent clp protease proteolytic subunit; PDBTitle: clpp1 from listeria monocytogenes
50	c2p9iH	Alignment	not modelled	21.2	12	PDB header: structural genomics, unknown function Chain: H: PDB Molecule: hypothetical protein aq2171; PDBTitle: crystal structure of aq2171 from aquifex aeolicus
51	c2yx6C	Alignment	not modelled	21.1	6	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: hypothetical protein ph0822; PDBTitle: crystal structure of ph0822
52	c3q94B	Alignment	not modelled	20.2	16	PDB header: lyase Chain: B: PDB Molecule: fructose-bisphosphate aldolase, class ii; PDBTitle: the crystal structure of fructose 1,6-bisphosphate aldolase from2 bacillus anthracis str. 'ames ancestor'
53	c2v5jB	Alignment	not modelled	19.1	13	PDB header: lyase Chain: B: PDB Molecule: 2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase;

						PDBTitle: apo class ii aldolase hpch
54	c3kthD	Alignment	not modelled	18.4	11	PDB header: hydrolase Chain: D: PDB Molecule: atp-dependent clp protease proteolytic subunit; PDBTitle: structure of clpp from bacillus subtilis in orthorhombic crystal form
55	d1o13a	Alignment	not modelled	18.1	6	Fold: Ribonuclease H-like motif Superfamily: Nitrogenase accessory factor-like Family: MTH1175-like
56	c1wloA	Alignment	not modelled	18.0	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: supe protein; PDBTitle: solution structure of the hypothetical protein from thermus2 thermophilus hb8
57	d1rq0a	Alignment	not modelled	17.9	23	Fold: Release factor Superfamily: Release factor Family: Release factor
58	c3bezC	Alignment	not modelled	17.9	20	PDB header: hydrolase Chain: C: PDB Molecule: protease 4; PDBTitle: crystal structure of escherichia coli signal peptide peptidase (sppa),2 semet crystals
59	d1yg6a1	Alignment	not modelled	17.7	13	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Clp protease, ClpP subunit
60	c3rstH	Alignment	not modelled	16.8	13	PDB header: hydrolase Chain: H: PDB Molecule: signal peptide peptidase sppa; PDBTitle: crystal structure of bacillus subtilis signal peptide peptidase a
61	c3n1uA	Alignment	not modelled	16.8	18	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
62	c3cwcB	Alignment	not modelled	16.7	8	PDB header: transferase Chain: B: PDB Molecule: putative glycerate kinase 2; PDBTitle: crystal structure of putative glycerate kinase 2 from salmonella2 typhimurium lt2
63	c2cbyG	Alignment	not modelled	15.7	8	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
64	c2r8zC	Alignment	not modelled	15.7	13	PDB header: hydrolase Chain: C: PDB Molecule: 3-deoxy-d-manno-octulosonate 8-phosphate phosphatase; PDBTitle: crystal structure of yrbi phosphatase from escherichia coli in complex2 with a phosphate and a calcium ion
65	d1eol1a	Alignment	not modelled	15.6	12	Fold: Ribonuclease H-like motif Superfamily: Nitrogenase accessory factor-like Family: MTH1175-like
66	c3sdoB	Alignment	not modelled	15.2	26	PDB header: oxidoreductase Chain: B: PDB Molecule: nitrilotriacetate monooxygenase; PDBTitle: structure of a nitrilotriacetate monooxygenase from burkholderia2 pseudomallei
67	c3pm6B	Alignment	not modelled	15.1	23	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
68	d2bufa1	Alignment	not modelled	14.3	12	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: N-acetyl-l-glutamate kinase
69	c2olsA	Alignment	not modelled	13.7	14	PDB header: transferase Chain: A: PDB Molecule: phosphoenolpyruvate synthase; PDBTitle: the crystal structure of the phosphoenolpyruvate synthase from2 neisseria meningitidis
70	d2q3la1	Alignment	not modelled	13.6	14	Fold: Spollaa-like Superfamily: Spollaa-like Family: Sfri0576-like
71	d1rdua	Alignment	not modelled	13.4	12	Fold: Ribonuclease H-like motif Superfamily: Nitrogenase accessory factor-like Family: MTH1175-like
72	c3p2ID	Alignment	not modelled	13.4	12	PDB header: hydrolase Chain: D: PDB Molecule: atp-dependent clp protease proteolytic subunit; PDBTitle: crystal structure of atp-dependent clp protease subunit p from2 francisella tularensis
73	c2hx1D	Alignment	not modelled	13.4	10	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
74	c2vvtA	Alignment	not modelled	13.3	14	PDB header: lyase Chain: A: PDB Molecule: yfau, 2-keto-3-deoxy sugar aldolase; PDBTitle: crystal structure of yfau, a metal ion dependent class ii2 aldolase from escherichia coli k12 - mg-pyruvate product3 complex
75	c6g61A	Alignment	not modelled	13.2	8	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin o1, mitochondrial; PDBTitle: crystal structure of thioredoxin o1 from arabidopsis thaliana in2 oxidized state
76	d1gqea	Alignment	not modelled	12.8	12	Fold: Release factor Superfamily: Release factor Family: Release factor
77	c3c3mA	Alignment	not modelled	12.7	10	PDB header: signaling protein Chain: A: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of the n-terminal domain of response regulator2 receiver protein from methanoculleus marisnigri jr1
78	d7rega2	Alignment	not modelled	12.6	11	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain

						Family: Cobalamin (vitamin B12)-binding domain
79	d3bula2	Alignment	not modelled	12.5	9	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
80	c3luaA	Alignment	not modelled	12.1	11	PDB header: transcription regulator Chain: A; PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of a signal receiver domain of two component signal2 transduction (histidine kinase) from clostridium thermocellum
81	d1lowxa	Alignment	not modelled	12.0	15	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
82	c6ak1B	Alignment	not modelled	11.8	19	PDB header: oxidoreductase Chain: B; PDB Molecule: dimethyl-sulfide monooxygenase; PDBTitle: crystal structure of dmoa from hyphomicrobium sulfonivorans
83	c2vm2C	Alignment	not modelled	11.7	11	PDB header: oxidoreductase Chain: C; PDB Molecule: thioredoxin h isoform 1.; PDBTitle: crystal structure of barley thioredoxin h isoform 1 crystallized using2 peg as precipitant
84	d1qyia	Alignment	not modelled	11.6	12	Fold: HAD-like Superfamily: HAD-like Family: Hypothetical protein MW1667 (SA1546)
85	c2qtdA	Alignment	not modelled	10.3	9	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
86	c2cftA	Alignment	not modelled	10.0	13	PDB header: phosphatase Chain: A; PDB Molecule: pyridoxal phosphate phosphatase; PDBTitle: crystal structure of human pyridoxal 5'-phosphate2 phosphatase with its substrate
87	d2f6ia1	Alignment	not modelled	9.8	11	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Clp protease, ClpP subunit
88	d1ni8a	Alignment	not modelled	9.7	21	Fold: H-NS histone-like proteins Superfamily: H-NS histone-like proteins Family: H-NS histone-like proteins
89	c2wfbA	Alignment	not modelled	9.6	11	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
90	c3khtA	Alignment	not modelled	9.4	7	PDB header: signaling protein Chain: A; PDB Molecule: response regulator; PDBTitle: crystal structure of response regulator from hahella chejuensis
91	d1u6ka1	Alignment	not modelled	9.3	24	Fold: F420-dependent methylenetetrahydromethanopterin dehydrogenase (MTD) Superfamily: F420-dependent methylenetetrahydromethanopterin dehydrogenase (MTD) Family: F420-dependent methylenetetrahydromethanopterin dehydrogenase (MTD)
92	d1u7pa	Alignment	not modelled	9.1	9	Fold: HAD-like Superfamily: HAD-like Family: Magnesium-dependent phosphatase-1, Mdp1
93	c1xrsB	Alignment	not modelled	8.9	16	PDB header: isomerase Chain: B; PDB Molecule: d-lysine 5,6-aminomutase beta subunit; PDBTitle: crystal structure of lysine 5,6-aminomutase in complex with plp,2 cobalamin, and 5'-deoxyadenosine
94	c3qz6A	Alignment	not modelled	8.5	13	PDB header: lyase Chain: A; PDB Molecule: hpch/hpai aldolase; PDBTitle: the crystal structure of hpch/hpai aldolase from desulfitobacterium2 hafniense dcb-2
95	c5tlcA	Alignment	not modelled	8.0	9	PDB header: oxidoreductase Chain: A; PDB Molecule: dibenzothiophene desulfurization enzyme a; PDBTitle: crystal structure of bdsa from bacillus subtilis wu-s2b
96	d1dxea	Alignment	not modelled	7.9	15	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Hpch/Hpal aldolase
97	c3d5cX	Alignment	not modelled	7.7	17	PDB header: ribosome Chain: X; PDB Molecule: peptide chain release factor 1; PDBTitle: structural basis for translation termination on the 70s ribosome. this2 file contains the 30s subunit, release factor 1 (rf1), two trna, and3 mrna molecules of the second 70s ribosome. the entire crystal4 structure contains two 70s ribosomes as described in remark 400.
98	d1to6a	Alignment	not modelled	7.7	11	Fold: Glycerate kinase I Superfamily: Glycerate kinase I Family: Glycerate kinase I
99	d1kjna	Alignment	not modelled	7.6	16	Fold: Hypothetical protein MTH777 (MT0777) Superfamily: Hypothetical protein MTH777 (MT0777) Family: Hypothetical protein MTH777 (MT0777)