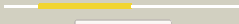

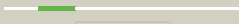












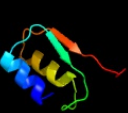



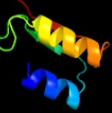
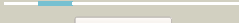



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0874c (-)_972549_973709
Date	Fri Jul 26 01:50:46 BST 2019
Unique Job ID	d1f0b9c9690a2f37

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1zfa_	 Alignment		71.3	15	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine monophosphate dehydrogenase; PDBTitle: inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
2	d1rq2a2	 Alignment		56.6	14	Fold: Bacillus chorismate mutase-like Superfamily: Tubulin C-terminal domain-like Family: Tubulin, C-terminal domain
3	d2vapa2	 Alignment		55.9	19	Fold: Bacillus chorismate mutase-like Superfamily: Tubulin C-terminal domain-like Family: Tubulin, C-terminal domain
4	d1w5fa2	 Alignment		52.0	21	Fold: Bacillus chorismate mutase-like Superfamily: Tubulin C-terminal domain-like Family: Tubulin, C-terminal domain
5	c2zauB_	 Alignment		49.1	15	PDB header: transferase Chain: B: PDB Molecule: selenide, water dikinase; PDBTitle: crystal structure of an n-terminally truncated2 selenophosphate synthetase from aquifex aeolicus
6	c4ldaF_	 Alignment		46.1	6	PDB header: transcription Chain: F: PDB Molecule: tadz; PDBTitle: crystal structure of a chey-like protein (tadz) from pseudomonas2 aeruginosa pao1 at 2.70 a resolution
7	c2ayxA_	 Alignment		45.9	14	PDB header: transferase Chain: A: PDB Molecule: sensor kinase protein rcsc; PDBTitle: solution structure of the e.coli rcsc c-terminus (residues2 700-949) containing linker region and phosphoreceiver3 domain
8	c3b2nA_	 Alignment		42.5	10	PDB header: transcription Chain: A: PDB Molecule: uncharacterized protein q99uf4; PDBTitle: crystal structure of dna-binding response regulator, luxr family, from2 staphylococcus aureus
9	c1ny5A_	 Alignment		37.9	8	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigm54 activator (aaa+ atpase) in the inactive2 state
10	c6ifhA_	 Alignment		36.8	15	PDB header: transferase Chain: A: PDB Molecule: sporulation initiation phosphotransferase f; PDBTitle: unphosphorylated spo0f from paenisporosarcina sp. tg-14
11	c4r3uD_	 Alignment		36.5	6	PDB header: isomerase Chain: D: PDB Molecule: 2-hydroxyisobutyryl-coa mutase small subunit; PDBTitle: crystal structure of 2-hydroxyisobutyryl-coa mutase

12	c4z87B_	Alignment		35.8	15	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: structure of the imp dehydrogenase from ashbya gossypii bound to gdp
13	c5uicA_	Alignment		34.9	13	PDB header: transcription Chain: A: PDB Molecule: two-component response regulator; PDBTitle: structure of the francisella response regulator receiver domain, qseb
14	c5ep0A_	Alignment		32.0	18	PDB header: transcription Chain: A: PDB Molecule: putative repressor protein luxo; PDBTitle: quorum-sensing signal integrator luxo - receiver+catalytic domains
15	c5lwkB_	Alignment		30.7	16	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulatory protein; PDBTitle: maer response regulator bound to beryllium trifluoride
16	d1ys7a2	Alignment		30.0	19	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
17	c3hv2B_	Alignment		27.9	18	PDB header: signaling protein Chain: B: PDB Molecule: response regulator/hd domain protein; PDBTitle: crystal structure of signal receiver domain of hd domain-containing2 protein from pseudomonas fluorescens pf-5
18	d1g2oa_	Alignment		27.8	33	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
19	c3cu5B_	Alignment		27.5	8	PDB header: transcription regulator Chain: B: PDB Molecule: two component transcriptional regulator, arac family; PDBTitle: crystal structure of a two component transcriptional regulator arac2 from clostridium phytofermentans isdg
20	d1peya_	Alignment		27.2	20	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
21	c4rndB_	Alignment	not modelled	26.7	10	PDB header: hydrolase Chain: B: PDB Molecule: v-type proton atpase subunit f; PDBTitle: crystal structure of the subunit df-assembly of the eukaryotic v-2 atpase.
22	c3dzdA_	Alignment	not modelled	26.2	8	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4 in the inactive2 state
23	d2zoda1	Alignment	not modelled	26.0	10	Fold: Bacillus chorismate mutase-like Superfamily: PurM N-terminal domain-like Family: PurM N-terminal domain-like
24	c4e7pA_	Alignment	not modelled	25.8	16	PDB header: transcription regulator Chain: A: PDB Molecule: response regulator; PDBTitle: crystal structure of receiver domain of putative narl family response2 regulator spr1814 from streptococcus pneumoniae in the presence of3 the phosphoryl analog beryllifluoride
25	c6ekhY_	Alignment	not modelled	25.7	20	PDB header: metal binding protein Chain: Y: PDB Molecule: chemotaxis protein chey; PDBTitle: crystal structure of activated chey from methanococcus maripaludis
26	c3rqIA_	Alignment	not modelled	25.5	8	PDB header: transcription Chain: A: PDB Molecule: response regulator protein; PDBTitle: crystal structure of a response regulator protein from burkholderia2 pseudomallei with a phosphorylated aspartic acid, calcium ion and3 citrate
27	d1dbfa_	Alignment	not modelled	24.8	15	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: Chorismate mutase
28	c3eulB_	Alignment	not modelled	24.8	24	PDB header: transcription Chain: B: PDB Molecule: possible nitrate/nitrite response transcriptional PDBTitle: structure of the signal receiver domain of the putative

						response2 regulator narI from mycobacterium tuberculosis
29	c2rjnA	Alignment	not modelled	24.5	16	PDB header: hydrolase Chain: A: PDB Molecule: response regulator receiver:metal-dependent PDBTitle: crystal structure of an uncharacterized protein q2bku2 from2 neptuniibacter caesariensis
30	c1y80A	Alignment	not modelled	23.6	9	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: predicted cobalamin binding protein; PDBTitle: structure of a corrinoid (factor iim)-binding protein from moorella2 thermoacetica
31	c4qpiC	Alignment	not modelled	23.6	10	PDB header: signaling protein/dna binding protein Chain: C: PDB Molecule: cell cycle response regulator ctra; PDBTitle: 2.7 angstrom structure of a phosphotransferase in complex with a2 receiver domain
32	c2yxbA	Alignment	not modelled	23.4	8	PDB header: isomerase Chain: A: PDB Molecule: coenzyme b12-dependent mutase; PDBTitle: crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
33	d1qe5a	Alignment	not modelled	23.1	26	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
34	d1u0sy	Alignment	not modelled	22.2	10	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
35	c4k40B	Alignment	not modelled	21.6	14	PDB header: hydrolase Chain: B: PDB Molecule: gdsI-like lipase/acylhydrolase family protein; PDBTitle: peptidoglycan o-acetylerase in action, 0 min
36	d1ofua2	Alignment	not modelled	20.8	16	Fold: Bacillus chorismate mutase-like Superfamily: Tubulin C-terminal domain-like Family: Tubulin, C-terminal domain
37	c5i4cA	Alignment	not modelled	20.6	4	PDB header: gene regulation Chain: A: PDB Molecule: transcriptional regulatory protein rcsb; PDBTitle: crystal structure of non-phosphorylated receiver domain of the stress2 response regulator rcsb from escherichia coli
38	c4q7eA	Alignment	not modelled	20.6	18	PDB header: signaling protein Chain: A: PDB Molecule: response regulator of a two component regulatory system; PDBTitle: non-phosphorylated hemr receiver domain from leptospira biflexa
39	d1krwa	Alignment	not modelled	20.0	14	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
40	c4s05B	Alignment	not modelled	20.0	24	PDB header: transcription/dna Chain: B: PDB Molecule: dna-binding transcriptional regulator basr; PDBTitle: crystal structure of non-phosphorylated receiver domain in complex with pmra2 box dna
41	c3u0aA	Alignment	not modelled	19.6	18	PDB header: transferase Chain: A: PDB Molecule: selenide, water dikinase; PDBTitle: the crystal structure of selenophosphate synthetase from e. coli
42	d2zaua1	Alignment	not modelled	19.4	15	Fold: Bacillus chorismate mutase-like Superfamily: PurM N-terminal domain-like Family: PurM N-terminal domain-like
43	d1jbea	Alignment	not modelled	19.3	12	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
44	d1b74a1	Alignment	not modelled	19.0	12	Fold: ATC-like Superfamily: Aspartate/glutamate racemase Family: Aspartate/glutamate racemase
45	d2e7ya1	Alignment	not modelled	18.2	4	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: RNase Z-like
46	c3w9sB	Alignment	not modelled	18.2	24	PDB header: signaling protein/antimicrobial protein Chain: B: PDB Molecule: ompr family response regulator in two-component regulatory PDBTitle: crystal structure analysis of the n-terminal receiver domain of2 response regulator pmra
47	d3c9ua1	Alignment	not modelled	18.0	12	Fold: Bacillus chorismate mutase-like Superfamily: PurM N-terminal domain-like Family: PurM N-terminal domain-like
48	d1ny5a1	Alignment	not modelled	17.8	8	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
49	c5wlpA	Alignment	not modelled	17.8	13	PDB header: protein transport Chain: A: PDB Molecule: autophagy-related protein 32; PDBTitle: solution structure of the pseudo-receiver domain of atg32
50	d1ufya	Alignment	not modelled	16.9	23	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: Chorismate mutase
51	c6grgD	Alignment	not modelled	15.8	8	PDB header: biosynthetic protein Chain: D: PDB Molecule: microcin b17-processing protein mcbd; PDBTitle: e. coli microcin synthetase mcbcd complex with promccb17, adp and2 phosphate bound
52	c1ys7B	Alignment	not modelled	15.5	19	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulatory protein prra; PDBTitle: crystal structure of the response regulator protein prra complexed2 with mg2+
53	c1w59B	Alignment	not modelled	15.5	17	PDB header: cell division Chain: B: PDB Molecule: cell division protein ftsz homolog 1; PDBTitle: ftsz dimer, empty (m. jannaschii)
54	d1kgsa2	Alignment	not modelled	15.2	10	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related

55	d1vk3a2	Alignment	not modelled	14.6	9	Fold: Bacillus chorismate mutase-like Superfamily: PurM N-terminal domain-like Family: PurM N-terminal domain-like
56	c5mg5P	Alignment	not modelled	14.6	23	PDB header: transferase Chain: P: PDB Molecule: hydroxymethylglutaryl-coa synthase; PDBTitle: a multi-component acyltransferase phlabc from pseudomonas protegens2 soaked with the monoacetylphloroglucinol (mapg)
57	c3kcnA	Alignment	not modelled	14.2	8	PDB header: lyase Chain: A: PDB Molecule: adenylate cyclase homolog; PDBTitle: the crystal structure of adenylyate cyclase from2 rhodopirellula baltica
58	c2x3eA	Alignment	not modelled	13.9	17	PDB header: transferase Chain: A: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] synthase 3; PDBTitle: crystal structure of 3-oxoacyl-(acyl carrier protein) synthase iii,2 fabh from pseudomonas aeruginosa pao1
59	d1dbwa	Alignment	not modelled	13.8	6	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
60	c2vxyA	Alignment	not modelled	13.5	16	PDB header: cell cycle Chain: A: PDB Molecule: cell division protein ftsz; PDBTitle: the structure of ftsz from bacillus subtilis at 1.7a2 resolution
61	c5l16A	Alignment	not modelled	13.4	13	PDB header: transferase Chain: A: PDB Molecule: putative selenophosphate synthetase; PDBTitle: crystal structure of n-terminus truncated selenophosphate synthetase2 from leishmania major
62	c6m8oA	Alignment	not modelled	13.4	14	PDB header: signaling protein Chain: A: PDB Molecule: dna-binding response regulator; PDBTitle: crystal structure of the receiver domain of lytr from staphylococcus2 aureus
63	c3cz5B	Alignment	not modelled	13.3	14	PDB header: transcription regulator Chain: B: PDB Molecule: two-component response regulator, luxr family; PDBTitle: crystal structure of two-component response regulator, luxr family,2 from aurantimonas sp. si85-9a1
64	d1s0aa	Alignment	not modelled	13.2	27	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
65	d1xpmA1	Alignment	not modelled	13.2	9	Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
66	d1mvoa	Alignment	not modelled	13.1	27	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
67	c2wztA	Alignment	not modelled	12.9	12	PDB header: oxidoreductase Chain: A: PDB Molecule: aldo-keto reductase; PDBTitle: crystal structure of a mycobacterium aldo-keto reductase in its apo2 and liganded form
68	c3wrbB	Alignment	not modelled	12.8	9	PDB header: oxidoreductase Chain: B: PDB Molecule: gallate dioxygenase; PDBTitle: crystal structure of the anaerobic h124f desb-gallate complex
69	c2zwmA	Alignment	not modelled	12.7	17	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein yycf; PDBTitle: crystal structure of yycf receiver domain from bacillus2 subtilis
70	c1u24A	Alignment	not modelled	12.7	20	PDB header: hydrolase Chain: A: PDB Molecule: myo-inositol hexaphosphate phosphohydrolase; PDBTitle: crystal structure of selenomonas ruminantium phytase
71	d1yioa2	Alignment	not modelled	12.3	14	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
72	d1qh8a	Alignment	not modelled	12.2	18	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein
73	c3s3lB	Alignment	not modelled	12.0	15	PDB header: transferase Chain: B: PDB Molecule: cerj; PDBTitle: crystal structure of cerj from streptomyces tendae
74	c1zxuA	Alignment	not modelled	11.9	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: at5g01750 protein; PDBTitle: x-ray structure of protein from arabidopsis thaliana at5g01750
75	d2q4ma1	Alignment	not modelled	11.9	15	Fold: Tubby C-terminal domain-like Superfamily: Tubby C-terminal domain-like Family: At5g01750-like
76	c5ieJA	Alignment	not modelled	11.9	13	PDB header: protein Chain: A: PDB Molecule: sdrG; PDBTitle: solution structure of the bef3-activated conformation of sdrG from2 pseudomonas melonis fr1
77	c5lhaC	Alignment	not modelled	11.8	23	PDB header: transferase Chain: C: PDB Molecule: omega transaminase; PDBTitle: amine transaminase crystal structure from an uncultivated pseudomonas2 species in the pmp-bound form
78	c2qr3A	Alignment	not modelled	11.8	16	PDB header: transcription Chain: A: PDB Molecule: two-component system response regulator; PDBTitle: crystal structure of the n-terminal signal receiver domain of two-2 component system response regulator from bacteroides fragilis
79	c3jteA	Alignment	not modelled	11.6	8	PDB header: protein binding Chain: A: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of response regulator receiver domain protein from2 clostridium thermocellum

80	c6erkB	Alignment	not modelled	11.4	27	PDB header: transferase Chain: B: PDB Molecule: aminotransferase; PDBTitle: crystal structure of diaminopelargonic acid aminotransferase from2 psychrobacter cryohalolentis
81	c3snkA	Alignment	not modelled	11.3	8	PDB header: signaling protein Chain: A: PDB Molecule: response regulator chey-like protein; PDBTitle: crystal structure of a response regulator chey-like protein (mll6475)2 from mesorhizobium loti at 2.02 a resolution
82	d2uube2	Alignment	not modelled	11.3	30	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Ribosomal S5 protein, N-terminal domain
83	d1qh8b	Alignment	not modelled	11.0	9	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein
84	c2ynmC	Alignment	not modelled	10.9	16	PDB header: oxidoreductase Chain: C: PDB Molecule: light-independent protochlorophyllide reductase subunit n; PDBTitle: structure of the adpxalf3-stabilized transition state of the2 nitrogenase-like dark-operative protochlorophyllide oxidoreductase3 complex from prochlorococcus marinus with its substrate4 protochlorophyllide a
85	c2qv0A	Alignment	not modelled	10.8	14	PDB header: transcription Chain: A: PDB Molecule: protein mrke; PDBTitle: crystal structure of the response regulatory domain of protein mrke2 from klebsiella pneumoniae
86	d2pl1a1	Alignment	not modelled	10.8	14	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
87	c3crnA	Alignment	not modelled	10.8	14	PDB header: signaling protein Chain: A: PDB Molecule: response regulator receiver domain protein, chey-like; PDBTitle: crystal structure of response regulator receiver domain protein (chey-2 like) from methanospirillum hungatei jf-1
88	d1pkpa2	Alignment	not modelled	10.6	22	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Ribosomal S5 protein, N-terminal domain
89	c3fd5B	Alignment	not modelled	10.6	18	PDB header: transferase Chain: B: PDB Molecule: selenide, water dikinase 1; PDBTitle: crystal structure of human selenophosphate synthetase 12 complex with ampcp
90	d1ccwa	Alignment	not modelled	10.4	2	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
91	c5n6yD	Alignment	not modelled	10.2	14	PDB header: oxidoreductase Chain: D: PDB Molecule: nitrogenase vanadium-iron protein alpha chain; PDBTitle: azotobacter vinelandii vanadium nitrogenase
92	c3nhzA	Alignment	not modelled	10.2	19	PDB header: dna binding protein Chain: A: PDB Molecule: two component system transcriptional regulator mtra; PDBTitle: structure of n-terminal domain of mtra
93	c3t6kB	Alignment	not modelled	10.2	14	PDB header: signaling protein Chain: B: PDB Molecule: response regulator receiver; PDBTitle: crystal structure of a putative response regulator (caur_3799) from2 chloroflexus aurantiacus j-10-fl at 1.86 a resolution
94	c2yxzA	Alignment	not modelled	10.1	12	PDB header: transferase Chain: A: PDB Molecule: thiamin-monophosphate kinase; PDBTitle: crystal structure of tt0281 from thermus thermophilus hb8
95	c6cboB	Alignment	not modelled	10.0	30	PDB header: transferase Chain: B: PDB Molecule: c-6' aminotransferase; PDBTitle: x-ray structure of genb1 from micromonospora echinospora in complex2 with neamine and plp (as the external aldimine)
96	c2jrlA	Alignment	not modelled	10.0	8	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: solution structure of the beryll fluoride-activated ntrc4 receiver2 domain dimer
97	d1m1nb	Alignment	not modelled	10.0	7	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein
98	d1xhoa	Alignment	not modelled	9.9	8	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: Chorismate mutase
99	c1xhoB	Alignment	not modelled	9.9	8	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: chorismate mutase; PDBTitle: chorismate mutase from clostridium thermocellum cth-682