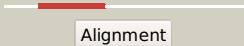

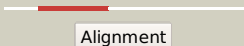

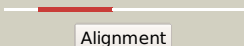







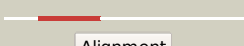
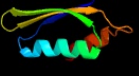

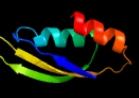






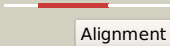

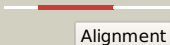

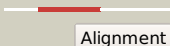













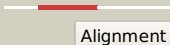


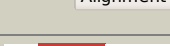
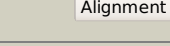
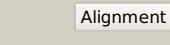




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3013 (-) _3371825_3372481
Date	Thu Aug 8 16:20:18 BST 2019
Unique Job ID	b247f2a2f42b52f0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ibwA_	 Alignment		98.4	17	PDB header: transferase Chain: A: PDB Molecule: gtp pyrophosphokinase; PDBTitle: crystal structure of the act domain from gtp pyrophosphokinase of2 chlorobium tepidum. northeast structural genomics consortium target3 ctr148a
2	d1sc6a3	 Alignment		97.5	20	Fold: Ferredoxin-like Superfamily: ACT-like Family: Phosphoglycerate dehydrogenase, regulatory (C-terminal) domain
3	d1ygya3	 Alignment		97.4	29	Fold: Ferredoxin-like Superfamily: ACT-like Family: Phosphoglycerate dehydrogenase, regulatory (C-terminal) domain
4	d1u8sa2	 Alignment		97.3	14	Fold: Ferredoxin-like Superfamily: ACT-like Family: Glycine cleavage system transcriptional repressor
5	c1u8sB_	 Alignment		97.0	13	PDB header: transcription Chain: B: PDB Molecule: glycine cleavage system transcriptional PDBTitle: crystal structure of putative glycine cleavage system2 transcriptional repressor
6	c2lvwA_	 Alignment		96.9	9	PDB header: transferase Chain: A: PDB Molecule: acetolactate synthase isozyme 1 small subunit; PDBTitle: solution nmr studies of the dimeric regulatory subunit ilvn of the2 e.coli acetohydroxyacid synthase i (ahas i)
7	c3n0vD_	 Alignment		96.7	9	PDB header: hydrolase Chain: D: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (pp_0327)2 from pseudomonas putida kt2440 at 2.25 a resolution
8	d1zpvA1	 Alignment		96.6	16	Fold: Ferredoxin-like Superfamily: ACT-like Family: SP0238-like
9	c5uscB_	 Alignment		96.1	14	PDB header: hydrolase Chain: B: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase tyra from bacillus2 anthracis in complex with nad and l-tyrosine
10	c6dzsD_	 Alignment		96.0	25	PDB header: oxidoreductase Chain: D: PDB Molecule: homoserine dehydrogenase; PDBTitle: mycobacterial homoserine dehydrogenase thra in complex with nadp
11	d2f06a2	 Alignment		95.8	21	Fold: Ferredoxin-like Superfamily: ACT-like Family: BT0572-like

12	c2nyiB_	 Alignment		95.6	19	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: unknown protein; PDBTitle: crystal structure of an unknown protein from galdieria sulphuraria
13	d1u8sa1	 Alignment		95.2	13	Fold: Ferredoxin-like Superfamily: ACT-like Family: Glycine cleavage system transcriptional repressor
14	c1tdjA_	 Alignment		95.1	14	PDB header: allostery Chain: A: PDB Molecule: biosynthetic threonine deaminase; PDBTitle: threonine deaminase (biosynthetic) from e. coli
15	d2f1fa1	 Alignment		94.3	16	Fold: Ferredoxin-like Superfamily: ACT-like Family: IlvH-like
16	d2f06a1	 Alignment		94.0	23	Fold: Ferredoxin-like Superfamily: ACT-like Family: BT0572-like
17	c2f1fA_	 Alignment		93.9	18	PDB header: transferase Chain: A: PDB Molecule: acetolactate synthase isozyme iii small subunit; PDBTitle: crystal structure of the regulatory subunit of acetohydroxyacid2 synthase isozyme iii from e. coli
18	c3o1lB_	 Alignment		93.9	16	PDB header: hydrolase Chain: B: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (pspto_4314)2 from pseudomonas syringae pv. tomato str. dc3000 at 2.20 a resolution
19	c1ygyA_	 Alignment		92.8	28	PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: crystal structure of d-3-phosphoglycerate dehydrogenase from2 mycobacterium tuberculosis
20	d2fgca2	 Alignment		91.9	18	Fold: Ferredoxin-like Superfamily: ACT-like Family: IlvH-like
21	c2f06B_	 Alignment	not modelled	91.6	23	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of protein bt0572 from bacteroides thetaiotaomicron
22	c1y7pB_	 Alignment	not modelled	91.3	14	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein af1403; PDBTitle: 1.9 a crystal structure of a protein of unknown function2 af1403 from archaeoglobus fulgidus, probable metabolic3 regulator
23	c3mtjA_	 Alignment	not modelled	91.3	25	PDB header: oxidoreductase Chain: A: PDB Molecule: homoserine dehydrogenase; PDBTitle: the crystal structure of a homoserine dehydrogenase from thiobacillus2 denitrificans to 2.15a
24	d2pc6a2	 Alignment	not modelled	91.0	17	Fold: Ferredoxin-like Superfamily: ACT-like Family: IlvH-like
25	c2fgcA_	 Alignment	not modelled	90.4	18	PDB header: transferase Chain: A: PDB Molecule: acetolactate synthase, small subunit; PDBTitle: crystal structure of acetolactate synthase- small subunit from2 thermotoga maritima
26	c1ybaC_	 Alignment	not modelled	90.0	21	PDB header: oxidoreductase Chain: C: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: the active form of phosphoglycerate dehydrogenase
27	c3nrbd_	 Alignment	not modelled	89.3	20	PDB header: hydrolase Chain: D: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (puru_2 pp_1943) from pseudomonas putida kt2440 at 2.05 a resolution
28	c3louB_	 Alignment	not modelled	89.1	14	PDB header: hydrolase Chain: B: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of formyltetrahydrofolate deformylase (yp_105254.1)2 from burkholderia mallei atcc 23344 at 1.90 a

						resolution
29	c3w7bB_	Alignment	not modelled	83.2	29	PDB header: hydrolase Chain: B: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of formyltetrahydrofolate deformylase from thermus2 thermophilus hb8
30	c3luyA_	Alignment	not modelled	82.8	19	PDB header: isomerase Chain: A: PDB Molecule: probable chorismate mutase; PDBTitle: putative chorismate mutase from bifidobacterium adolescentis
31	c3e98B_	Alignment	not modelled	80.5	15	PDB header: unknown function Chain: B: PDB Molecule: gaf domain of unknown function; PDBTitle: crystal structure of a gaf domain containing protein that belongs to2 pfam duf484 family (pa5279) from pseudomonas aeruginosa at 2.43 a3 resolution
32	c2pc6C_	Alignment	not modelled	80.2	17	PDB header: lyase Chain: C: PDB Molecule: probable acetolactate synthase isozyme iii (small subunit); PDBTitle: crystal structure of putative acetolactate synthase- small subunit2 from nitrosomonas europaea
33	d1phza1	Alignment	not modelled	80.2	14	Fold: Ferredoxin-like Superfamily: ACT-like Family: Phenylalanine metabolism regulatory domain
34	c2qmxB_	Alignment	not modelled	80.0	15	PDB header: ligase Chain: B: PDB Molecule: prephenate dehydratase; PDBTitle: the crystal structure of l-phe inhibited prephenate dehydratase from2 chlorobium tepidum t1s
35	c3k5pA_	Alignment	not modelled	79.4	22	PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: crystal structure of amino acid-binding act: d-isomer specific 2-2 hydroxyacid dehydrogenase catalytic domain from brucella melitensis
36	c3obiC_	Alignment	not modelled	75.2	22	PDB header: hydrolase Chain: C: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (np_949368)2 from rhodopseudomonas palustris cga009 at 1.95 a resolution
37	d1tdja2	Alignment	not modelled	67.5	16	Fold: Ferredoxin-like Superfamily: ACT-like Family: Allosteric threonine deaminase C-terminal domain
38	c4qprA_	Alignment	not modelled	67.2	17	PDB header: transferase Chain: A: PDB Molecule: sensor protein kdpd; PDBTitle: crystal structure of gaf domain of potassium sensor histidine kinase2 kdpd from escherichia coli
39	c5xhxA_	Alignment	not modelled	66.6	17	PDB header: transcription Chain: A: PDB Molecule: helix-turn-helix transcriptional regulator; PDBTitle: crystal structure of vqsr lbd domain from pseudomonas aeruginosa
40	d2qmwa2	Alignment	not modelled	64.6	13	Fold: Ferredoxin-like Superfamily: ACT-like Family: Phenylalanine metabolism regulatory domain
41	c3mahA_	Alignment	not modelled	57.9	11	PDB header: transferase Chain: A: PDB Molecule: aspartokinase; PDBTitle: a putative c-terminal regulatory domain of aspartate kinase from2 porphyromonas gingivalis w83.
42	c2dtjA_	Alignment	not modelled	50.3	14	PDB header: transferase Chain: A: PDB Molecule: aspartokinase; PDBTitle: crystal structure of regulatory subunit of aspartate kinase2 from corynebacterium glutamicum
43	c3mwbA_	Alignment	not modelled	45.4	16	PDB header: lyase Chain: A: PDB Molecule: prephenate dehydratase; PDBTitle: the crystal structure of prephenate dehydratase in complex with l-phe2 from arthrobacter aureescens to 2.0a
44	d1tdja3	Alignment	not modelled	38.7	32	Fold: Ferredoxin-like Superfamily: ACT-like Family: Allosteric threonine deaminase C-terminal domain
45	c3l76B_	Alignment	not modelled	37.3	20	PDB header: transferase Chain: B: PDB Molecule: aspartokinase; PDBTitle: crystal structure of aspartate kinase from synechocystis
46	c5jk5A_	Alignment	not modelled	32.6	13	PDB header: oxidoreductase Chain: A: PDB Molecule: phenylalanine-4-hydroxylase; PDBTitle: phenylalanine hydroxylase from dictyostelium - bh2 complex
47	c2mdaB_	Alignment	not modelled	32.0	27	PDB header: oxidoreductase Chain: B: PDB Molecule: tyrosine 3-monooxygenase; PDBTitle: the solution structure of the regulatory domain of tyrosine2 hydroxylase
48	c2vjwA_	Alignment	not modelled	31.9	13	PDB header: hydrolase Chain: A: PDB Molecule: gaf family protein; PDBTitle: crystal structure of the second gaf domain of devs from2 mycobacterium smegmatis
49	c3eeaB_	Alignment	not modelled	30.7	15	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: gaf domain/hd domain protein; PDBTitle: the crystal structure of the gaf domain/hd domain protein2 from geobacter sulfurreducens
50	d1mw7a_	Alignment	not modelled	28.5	14	Fold: YebC-like Superfamily: YebC-like Family: YebC-like
51	d2c0ga1	Alignment	not modelled	27.9	40	Fold: ERP29 C domain-like Superfamily: ERP29 C domain-like Family: ERP29 C domain-like
52	c4f3qA_	Alignment	not modelled	26.5	13	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein cbu_1566; PDBTitle: structure of a yebc family protein (cbu_1566) from coxiella burnetii
53	d1rwua_	Alignment	not modelled	25.7	10	Fold: Ferredoxin-like Superfamily: YbeD/HP0495-like Family: YbeD-like

54	c1rwuA	Alignment	not modelled	25.7	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical upf0250 protein ybed; PDBTitle: solution structure of conserved protein ybed from e. coli
55	d2hmfA2	Alignment	not modelled	25.1	24	Fold: Ferredoxin-like Superfamily: ACT-like Family: Aspartokinase allosteric domain-like
56	c2k4mA	Alignment	not modelled	24.4	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0146 protein mth_1000; PDBTitle: solution nmr structure of m. thermoautotrophicum protein mth_1000,2 northeast structural genomics consortium target tr8
57	c3ci6B	Alignment	not modelled	24.2	9	PDB header: transferase Chain: B: PDB Molecule: phosphoenolpyruvate-protein phosphotransferase; PDBTitle: crystal structure of the gaf domain from acinetobacter2 phosphoenolpyruvate-protein phosphotransferase
58	c3bfrA	Alignment	not modelled	24.0	11	PDB header: oxidoreductase Chain: A: PDB Molecule: superoxide dismutase [mn]; PDBTitle: the crystal structure of sod2 from saccharomyces cerevisiae
59	d1m0sa2	Alignment	not modelled	23.5	19	Fold: Ferredoxin-like Superfamily: D-ribose-5-phosphate isomerase (RpiA), lid domain Family: D-ribose-5-phosphate isomerase (RpiA), lid domain
60	d1g7da	Alignment	not modelled	23.3	47	Fold: ERP29 C domain-like Superfamily: ERP29 C domain-like Family: ERP29 C domain-like
61	d1o8ba2	Alignment	not modelled	23.2	24	Fold: Ferredoxin-like Superfamily: D-ribose-5-phosphate isomerase (RpiA), lid domain Family: D-ribose-5-phosphate isomerase (RpiA), lid domain
62	c4br6B	Alignment	not modelled	22.8	9	PDB header: oxidoreductase Chain: B: PDB Molecule: superoxide dismutase; PDBTitle: crystal structure of chaetomium thermophilum mnsod
63	c2jsxA	Alignment	not modelled	21.4	20	PDB header: chaperone Chain: A: PDB Molecule: protein napd; PDBTitle: solution structure of the e. coli tat proofreading2 chaperone protein napd
64	c2yy3B	Alignment	not modelled	19.5	16	PDB header: translation Chain: B: PDB Molecule: elongation factor 1-beta; PDBTitle: crystal structure of translation elongation factor ef-1 beta from2 pyrococcus horikoshii
65	c4c7uB	Alignment	not modelled	18.7	11	PDB header: oxidoreductase Chain: B: PDB Molecule: superoxide dismutase [mn] 1, mitochondrial; PDBTitle: crystal structure of manganese superoxide dismutase from arabidopsis2 thaliana
66	d1uerc2	Alignment	not modelled	15.9	12	Fold: Fe,Mn superoxide dismutase (SOD), C-terminal domain Superfamily: Fe,Mn superoxide dismutase (SOD), C-terminal domain Family: Fe,Mn superoxide dismutase (SOD), C-terminal domain
67	c4bwiA	Alignment	not modelled	15.8	12	PDB header: transferase Chain: A: PDB Molecule: phytochrome-like protein cph2; PDBTitle: structure of the phytochrome cph2 from synechocystis sp. pcc6803
68	d2hmfA3	Alignment	not modelled	15.8	15	Fold: Ferredoxin-like Superfamily: ACT-like Family: Aspartokinase allosteric domain-like
69	c5aweA	Alignment	not modelled	14.1	26	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative acetoin utilization protein, acetoin PDBTitle: crystal structure of a hypothetical protein, ttha0829 from thermus2 thermophilus hb8, composed of cystathionine-beta-synthase (cbs) and3 aspartate-kinase chorismate-mutase tyra (act) domains
70	c4lubA	Alignment	not modelled	13.8	11	PDB header: lyase Chain: A: PDB Molecule: putative prephenate dehydratase; PDBTitle: x-ray structure of prephenate dehydratase from streptococcus mutans
71	d1idsa2	Alignment	not modelled	13.8	16	Fold: Fe,Mn superoxide dismutase (SOD), C-terminal domain Superfamily: Fe,Mn superoxide dismutase (SOD), C-terminal domain Family: Fe,Mn superoxide dismutase (SOD), C-terminal domain
72	c1lkzB	Alignment	not modelled	13.6	26	PDB header: isomerase Chain: B: PDB Molecule: ribose 5-phosphate isomerase a; PDBTitle: crystal structure of d-ribose-5-phosphate isomerase (rpiA) from2 escherichia coli.
73	d1mnga2	Alignment	not modelled	13.0	18	Fold: Fe,Mn superoxide dismutase (SOD), C-terminal domain Superfamily: Fe,Mn superoxide dismutase (SOD), C-terminal domain Family: Fe,Mn superoxide dismutase (SOD), C-terminal domain
74	d1kona	Alignment	not modelled	12.8	22	Fold: YebC-like Superfamily: YebC-like Family: YebC-like
75	c3s1tB	Alignment	not modelled	12.8	13	PDB header: transferase Chain: B: PDB Molecule: aspartokinase; PDBTitle: structure of the regulatory domain of aspartokinase (rv3709c; ak-beta)2 in complex with threonine from mycobacterium tuberculosis
76	c3p96A	Alignment	not modelled	12.3	22	PDB header: hydrolase Chain: A: PDB Molecule: phosphoserine phosphatase serb; PDBTitle: crystal structure of phosphoserine phosphatase serb from mycobacterium2 avium, native form
77	d2cdqa2	Alignment	not modelled	11.8	12	Fold: Ferredoxin-like Superfamily: ACT-like Family: Aspartokinase allosteric domain-like
78	c3h1sB	Alignment	not modelled	11.3	16	PDB header: oxidoreductase Chain: B: PDB Molecule: superoxide dismutase; PDBTitle: crystal structure of superoxide dismutase from francisella tularensis2 subsp. tularensis schu s4

79	d2nyba2	Alignment	not modelled	10.8	15	Fold: Fe,Mn superoxide dismutase (SOD), C-terminal domain Superfamily: Fe,Mn superoxide dismutase (SOD), C-terminal domain Family: Fe,Mn superoxide dismutase (SOD), C-terminal domain
80	d1b06a2	Alignment	not modelled	10.7	16	Fold: Fe,Mn superoxide dismutase (SOD), C-terminal domain Superfamily: Fe,Mn superoxide dismutase (SOD), C-terminal domain Family: Fe,Mn superoxide dismutase (SOD), C-terminal domain
81	d1gv3a2	Alignment	not modelled	10.4	10	Fold: Fe,Mn superoxide dismutase (SOD), C-terminal domain Superfamily: Fe,Mn superoxide dismutase (SOD), C-terminal domain Family: Fe,Mn superoxide dismutase (SOD), C-terminal domain
82	c5uf2A_	Alignment	not modelled	10.4	14	PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose 5 phosphate isomerase a from neisseria2 gonorrhoeae
83	c3p01A_	Alignment	not modelled	9.9	19	PDB header: signaling protein Chain: A: PDB Molecule: two-component response regulator; PDBTitle: crystal structure of two-component response regulator from nostoc sp.2 pcc 7120
84	c3kwmC_	Alignment	not modelled	9.4	19	PDB header: isomerase Chain: C: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose-5-isomerase a
85	c3trcA_	Alignment	not modelled	9.2	16	PDB header: transferase Chain: A: PDB Molecule: phosphoenolpyruvate-protein phosphotransferase; PDBTitle: structure of the gaf domain from a phosphoenolpyruvate-protein2 phosphotransferase (ptsp) from coxiella burnetii
86	c4x84C_	Alignment	not modelled	9.2	24	PDB header: isomerase Chain: C: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose-5-phosphate isomerase a from pseudomonas2 aeruginosa
87	c2ns6A_	Alignment	not modelled	9.1	27	PDB header: hydrolase Chain: A: PDB Molecule: mobilization protein a; PDBTitle: crystal structure of the minimal relaxase domain of moba from plasmid2 r1162
88	c3fijA_	Alignment	not modelled	9.1	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein conserved in bacteria with a PDBTitle: crystal structure of uncharacterized protein conserved in bacteria2 with a cystatin-like fold (yp_168589.1) from silicibacter pomeroyi3 dss-3 at 2.00 a resolution
89	d1wb8a2	Alignment	not modelled	8.9	16	Fold: Fe,Mn superoxide dismutase (SOD), C-terminal domain Superfamily: Fe,Mn superoxide dismutase (SOD), C-terminal domain Family: Fe,Mn superoxide dismutase (SOD), C-terminal domain
90	d2nv0a1	Alignment	not modelled	8.6	23	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
91	c5irdA_	Alignment	not modelled	8.5	18	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of rv1466 from mycobacterium tuberculosis, a2 protein associated with [fe-s] complex assembly and repair - seattle3 structural genomics center for infectious disease target4 mytud.17486.a
92	c2qybA_	Alignment	not modelled	8.4	14	PDB header: membrane protein Chain: A: PDB Molecule: membrane protein, putative; PDBTitle: crystal structure of the gaf domain region of putative membrane2 protein from geobacter sulfurreducens pca
93	c1s6cB_	Alignment	not modelled	8.3	65	PDB header: transport protein Chain: B: PDB Molecule: potassium voltage-gated channel subfamily d member 2; PDBTitle: crystal structure of the complex between kchip1 and kv4.2 n1-30
94	c4n8oA_	Alignment	not modelled	7.7	24	PDB header: membrane protein Chain: A: PDB Molecule: cell division protein ftsx; PDBTitle: crystal structure of mycobacterial ftsx extracellular domain, bromide2 derivative
95	d1pv8a_	Alignment	not modelled	7.6	24	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: 5-aminolaevulinatase, ALAD (porphobilinogen synthase)
96	d1zvpa2	Alignment	not modelled	7.4	18	Fold: Ferredoxin-like Superfamily: ACT-like Family: VC0802-like
97	d2p4ka2	Alignment	not modelled	7.2	16	Fold: Fe,Mn superoxide dismutase (SOD), C-terminal domain Superfamily: Fe,Mn superoxide dismutase (SOD), C-terminal domain Family: Fe,Mn superoxide dismutase (SOD), C-terminal domain
98	c6eepA_	Alignment	not modelled	7.1	19	PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose-5-phosphate isomerase from legionella2 pneumophila
99	c1nrnR_	Alignment	not modelled	7.0	83	PDB header: serine proteinase/receptor Chain: R: PDB Molecule: receptor based peptide nrs; PDBTitle: crystallographic structures of thrombin complexed with2 thrombin receptor peptides: existence of expected and3 novel binding modes