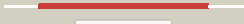



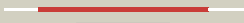

















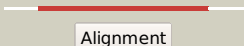




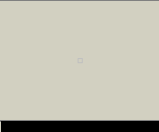






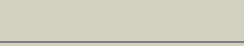

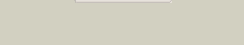

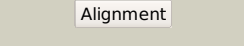

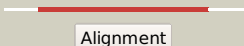
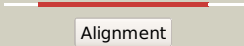
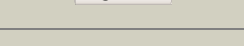
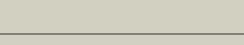
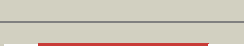




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0812_(-)_906426_907295
Date	Fri Jul 26 01:50:39 BST 2019
Unique Job ID	3a0f0e734bf23f15

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4ce5A_	 Alignment		100.0	19	PDB header: transferase Chain: A: PDB Molecule: at-omegata; PDBTitle: first crystal structure of an (r)-selective omega-transaminase2 from aspergillus terreus
2	c3wwjE_	 Alignment		100.0	19	PDB header: transferase Chain: E: PDB Molecule: (r)-amine transaminase; PDBTitle: crystal structure of an engineered sitagliptin-producing transaminase,2 ata-117-rd11
3	c4tviB_	 Alignment		100.0	19	PDB header: transferase Chain: B: PDB Molecule: aminotransferase, class iv; PDBTitle: x-ray crystal structure of an aminotransferase from brucella abortus2 bound to the co-factor plp
4	c5cm0A_	 Alignment		100.0	24	PDB header: transferase Chain: A: PDB Molecule: branched-chain transaminase; PDBTitle: crystal structure of branched-chain aminotransferase from thermophilic2 archaea geoglobus acetivorans
5	d1i2ka_	 Alignment		100.0	20	Fold: D-aminoacid aminotransferase-like PLP-dependent enzymes Superfamily: D-aminoacid aminotransferase-like PLP-dependent enzymes Family: D-aminoacid aminotransferase-like PLP-dependent enzymes
6	c3u0gA_	 Alignment		100.0	18	PDB header: transferase Chain: A: PDB Molecule: putative branched-chain amino acid aminotransferase ilve; PDBTitle: crystal structure of branched-chain amino acid aminotransferase from2 burkholderia pseudomallei
7	d1iyea_	 Alignment		100.0	21	Fold: D-aminoacid aminotransferase-like PLP-dependent enzymes Superfamily: D-aminoacid aminotransferase-like PLP-dependent enzymes Family: D-aminoacid aminotransferase-like PLP-dependent enzymes
8	c1wrvB_	 Alignment		100.0	17	PDB header: transferase Chain: B: PDB Molecule: branched-chain amino acid aminotransferase; PDBTitle: crystal structure of t.th.hb8 branched-chain amino acid2 aminotransferase
9	c5ce8B_	 Alignment		100.0	21	PDB header: transferase Chain: B: PDB Molecule: branched-chain amino acid aminotransferase; PDBTitle: crystal structure of branched-chain aminotransferase from thermophilic2 archaea thermoproteus uzoniensis
10	d1daaa_	 Alignment		100.0	19	Fold: D-aminoacid aminotransferase-like PLP-dependent enzymes Superfamily: D-aminoacid aminotransferase-like PLP-dependent enzymes Family: D-aminoacid aminotransferase-like PLP-dependent enzymes
11	c5k3wA_	 Alignment		100.0	42	PDB header: transferase Chain: A: PDB Molecule: cputa1; PDBTitle: structural characterisation of fold iv-transaminase, cputa1, from2 curtobacterium pusillum

12	c6h65A	 Alignment		100.0	18	PDB header: transferase Chain: A: PDB Molecule: branched-chain-amino-acid aminotransferase; PDBTitle: crystal structure of the branched-chain-amino-acid aminotransferase2 from haliangium ochraceum
13	c2xpfB	 Alignment		100.0	25	PDB header: lyase Chain: B: PDB Molecule: 4-amino-4-deoxychorismate lyase; PDBTitle: crystal structure of putative aminodeoxychorismate lyase2 from pseudomonas aeruginosa
14	c3cswB	 Alignment		100.0	19	PDB header: transferase Chain: B: PDB Molecule: putative branched-chain-amino-acid aminotransferase; PDBTitle: crystal structure of a putative branched-chain amino acid2 aminotransferase (tm0831) from thermotoga maritima at 2.15 a3 resolution
15	c6nstD	 Alignment		100.0	22	PDB header: transferase Chain: D: PDB Molecule: branched-chain-amino-acid aminotransferase; PDBTitle: crystal structure of branched chain amino acid aminotransferase from2 pseudomonas aeruginosa
16	c6gkrC	 Alignment		100.0	19	PDB header: transferase Chain: C: PDB Molecule: branched-chain-amino-acid aminotransferase; PDBTitle: crystal structure of branched-chain amino acid aminotransferase from2 thermobaculum terrenum in plp-form (holo-form)
17	c4m0jA	 Alignment		100.0	28	PDB header: transferase Chain: A: PDB Molecule: d-amino acid aminotransferase; PDBTitle: crystal structure of a d-amino acid aminotransferase from burkholderia2 thailandensis e264
18	c6bb9A	 Alignment		100.0	22	PDB header: lyase Chain: A: PDB Molecule: 4-amino-4-deoxychorismate lyase; PDBTitle: the crystal structure of 4-amino-4-deoxychorismate lyase from2 salmonella typhimurium lt2
19	c4jxuB	 Alignment		100.0	21	PDB header: transferase Chain: B: PDB Molecule: putative aminotransferase; PDBTitle: structure of aminotransferase ilve2 from sinorhizobium meliloti2 complexed with plp
20	c3dtfB	 Alignment		100.0	21	PDB header: transferase Chain: B: PDB Molecule: branched-chain amino acid aminotransferase; PDBTitle: structural analysis of mycobacterial branched chain aminotransferase-2 implications for inhibitor design
21	c4dqnA	 Alignment	not modelled	100.0	18	PDB header: transferase Chain: A: PDB Molecule: putative branched-chain amino acid aminotransferase ilve; PDBTitle: crystal structure of the branched-chain aminotransferase from2 streptococcus mutans
22	d2a1ha1	 Alignment	not modelled	100.0	18	Fold: D-aminoacid aminotransferase-like PLP-dependent enzymes Superfamily: D-aminoacid aminotransferase-like PLP-dependent enzymes Family: D-aminoacid aminotransferase-like PLP-dependent enzymes
23	c3uzbA	 Alignment	not modelled	100.0	19	PDB header: transferase Chain: A: PDB Molecule: branched-chain-amino-acid aminotransferase; PDBTitle: crystal structures of branched-chain aminotransferase from deinococcus2 radiodurans complexes with alpha-ketoisocaproate and l-glutamate3 suggest its radio-resistance for catalysis
24	c2abjG	 Alignment	not modelled	100.0	18	PDB header: transferase Chain: G: PDB Molecule: branched-chain-amino-acid aminotransferase, cytosolic; PDBTitle: crystal structure of human branched chain amino acid transaminase in a2 complex with an inhibitor, c16h10n2o4f3scl, and pyridoxal 5'3 phosphate.
25	c3luIA	 Alignment	not modelled	100.0	22	PDB header: lyase Chain: A: PDB Molecule: 4-amino-4-deoxychorismate lyase; PDBTitle: crystal structure of putative 4-amino-4-deoxychorismate lyase.2 (yp_094631.1) from legionella pneumophila subsp. pneumophila str.3 philadelphia 1 at 1.78 a resolution
26	c2zgiA	 Alignment	not modelled	100.0	22	PDB header: lyase Chain: A: PDB Molecule: putative 4-amino-4-deoxychorismate lyase; PDBTitle: crystal structure of putative 4-amino-4-deoxychorismate lyase
27	c3snoA	 Alignment	not modelled	100.0	37	PDB header: transferase Chain: A: PDB Molecule: hypothetical aminotransferase; PDBTitle: crystal structure of a putative aminotransferase (ncgl2491) from2 corynebacterium glutamicum atcc 13032 at 1.60 a

						resolution
28	c3qqmD_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: D: PDB Molecule: mlr3007 protein; PDBTitle: crystal structure of a putative amino-acid aminotransferase2 (np_104211.1) from mesorhizobium loti at 2.30 a resolution
29	c3cebA_	Alignment	not modelled	100.0	20	PDB header: lyase Chain: A: PDB Molecule: d-aminoacid aminotransferase-like plp-dependent enzyme; PDBTitle: crystal structure of a putative 4-amino-4-deoxychorismate lyase2 (hs_0128) from haemophilus somnus 129pt at 2.40 a resolution
30	c4k6nA_	Alignment	not modelled	100.0	14	PDB header: lyase Chain: A: PDB Molecule: aminodeoxychorismate lyase; PDBTitle: crystal structure of yeast 4-amino-4-deoxychorismate lyase
31	d1aw9a2	Alignment	not modelled	49.8	11	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
32	d1jlvA2	Alignment	not modelled	49.4	13	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
33	d1ljra2	Alignment	not modelled	48.4	11	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
34	c3zjIA_	Alignment	not modelled	47.5	8	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: crystal structure of the thioredoxin-like protein bc3987
35	d2r48a1	Alignment	not modelled	47.1	16	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: PTS system IIB component-like Family: PTS system, Fructose specific IIB subunit-like
36	d2r4qa1	Alignment	not modelled	45.1	22	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: PTS system IIB component-like Family: PTS system, Fructose specific IIB subunit-like
37	d1axda2	Alignment	not modelled	44.6	9	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
38	c4tr1A_	Alignment	not modelled	38.2	10	PDB header: oxidoreductase Chain: A: PDB Molecule: glutaredoxin 3; PDBTitle: crystal structure of gsh-bound cgrx2/c15s
39	d1k3ya2	Alignment	not modelled	37.1	16	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
40	d1pn9a2	Alignment	not modelled	34.8	13	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
41	d2fnoa2	Alignment	not modelled	33.6	11	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
42	d1v2aa2	Alignment	not modelled	31.8	13	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
43	d1gnwa2	Alignment	not modelled	31.6	8	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
44	c4ielB_	Alignment	not modelled	30.7	9	PDB header: transferase Chain: B: PDB Molecule: glutathione s-transferase, n-terminal domain protein; PDBTitle: crystal structure of a glutathione s-transferase family protein from2 burkholderia ambifaria, target efi-507141, with bound glutathione
45	d1oyja2	Alignment	not modelled	30.0	18	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
46	d1r5aa2	Alignment	not modelled	29.6	14	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
47	c4jbbA_	Alignment	not modelled	29.0	12	PDB header: transferase Chain: A: PDB Molecule: putative glutathione s-transferase; PDBTitle: crystal structure of glutathione s-transferase a6tby7(target efi-2 507184) from klebsiella pneumoniae mgh 78578, gsh complex
48	c4gxzB_	Alignment	not modelled	28.2	7	PDB header: isomerase Chain: B: PDB Molecule: suppression of copper sensitivity protein; PDBTitle: crystal structure of a periplasmic thioredoxin-like protein from2 salmonella enterica serovar typhimurium
49	d1e6ba2	Alignment	not modelled	28.2	8	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
50	c2kixA_	Alignment	not modelled	25.4	5	PDB header: oxidoreductase Chain: A: PDB Molecule: glutaredoxin; PDBTitle: solution structure of glutaredoxin from bartonella henselae str.2 houston
51	c2mvfA_	Alignment	not modelled	23.9	22	PDB header: ribosomal protein Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: structural insight into an essential assembly factor network on the2 pre-ribosome
52	d1t1va_	Alignment	not modelled	23.2	4	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: SH3BGR (SH3-binding, glutamic acid-rich protein-like)
						Fold: Thioredoxin fold

53	d1r7ha_	Alignment	not modelled	23.2	15	Superfamily: Thioredoxin-like Family: Thioltransferase
54	d1nm3a1	Alignment	not modelled	22.1	15	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
55	d1ev4a2	Alignment	not modelled	21.2	13	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
56	c5xxuE	Alignment	not modelled	20.9	9	PDB header: ribosome Chain: E: PDB Molecule: ribosomal protein es4; PDBTitle: small subunit of toxoplasma gondii ribosome
57	d1pd212	Alignment	not modelled	20.0	13	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
58	c6k4eB	Alignment	not modelled	19.7	14	PDB header: signaling protein Chain: B: PDB Molecule: hamp domain-containing protein; PDBTitle: siaa-pp2c domain of pseudomonas aeruginosa
59	d1h75a_	Alignment	not modelled	19.3	8	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
60	c2cb1A	Alignment	not modelled	19.2	12	PDB header: lyase Chain: A: PDB Molecule: o-acetyl homoserine sulfhydrylase; PDBTitle: crystal structure of o-acetyl homoserine sulfhydrylase2 from thermus thermophilus hb8,oah2.
61	d2c4ja2	Alignment	not modelled	19.0	5	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
62	c4ri7A	Alignment	not modelled	18.7	6	PDB header: transferase Chain: A: PDB Molecule: phi class glutathione transferase gstf1; PDBTitle: crystal structure of poplar glutathione transferase f1 mutant ser 132 cys
63	d1xw6a2	Alignment	not modelled	18.4	6	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
64	d1tw9a2	Alignment	not modelled	18.3	13	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
65	c6em5r_	Alignment	not modelled	17.8	21	PDB header: ribosome Chain: R: PDB Molecule: 60s ribosomal protein l19-a; PDBTitle: state d architectural model (nsa1-tap flag-ytm1) - visualizing the2 assembly pathway of nucleolar pre-60s ribosomes
66	c3ic4A	Alignment	not modelled	17.7	13	PDB header: oxidoreductase Chain: A: PDB Molecule: glutaredoxin (grx-1); PDBTitle: the crystal structure of the glutaredoxin(grx-1) from archaeoglobus2 fulgidus
67	c5dleD	Alignment	not modelled	17.4	18	PDB header: transferase Chain: D: PDB Molecule: pts system, fructose-specific iiabc component; PDBTitle: crystal structure from a domain (thr161-f265) from fructose-specific2 iiabc component (pts system) from borrelia burgdorferi
68	c3ipzA	Alignment	not modelled	16.6	9	PDB header: electron transport, oxidoreductase Chain: A: PDB Molecule: monothiol glutaredoxin-s14, chloroplastic; PDBTitle: crystal structure of arabidopsis monothiol glutaredoxin atgrxcp
69	d1fova_	Alignment	not modelled	16.4	8	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
70	d2gsta2	Alignment	not modelled	16.2	8	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
71	d1tu7a2	Alignment	not modelled	16.0	2	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
72	c3qmxA	Alignment	not modelled	15.9	6	PDB header: electron transport Chain: A: PDB Molecule: glutaredoxin a; PDBTitle: x-ray crystal structure of synechocystis sp. pcc 6803 glutaredoxin a
73	c6f01B	Alignment	not modelled	15.9	8	PDB header: transferase Chain: B: PDB Molecule: glutathione s-transferase f9; PDBTitle: arabidopsis thaliana gstf9, gso3 and gsoh bound
74	c1jlvA	Alignment	not modelled	15.6	14	PDB header: transferase Chain: A: PDB Molecule: glutathione transferase gst1-3; PDBTitle: anopheles dirus species b glutathione s-transferases 1-3
75	d1fhea2	Alignment	not modelled	15.0	11	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
76	c1ua5A	Alignment	not modelled	14.9	4	PDB header: transferase Chain: A: PDB Molecule: glutathione s-transferase; PDBTitle: non-fusion gst from s. japonicum in complex with glutathione
77	d2gk3a1	Alignment	not modelled	14.7	32	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: STM3548-like
78	c2kd2A	Alignment	not modelled	14.6	18	PDB header: apoptosis Chain: A: PDB Molecule: fas apoptotic inhibitory molecule 1; PDBTitle: nmr structure of faim-ctd
79	c2m1zA	Alignment	not modelled	14.2	21	PDB header: transferase Chain: A: PDB Molecule: lmo0427 protein; PDBTitle: solution structure of uncharacterized protein lmo0427

80	d2hqya2	Alignment	not modelled	13.6	14	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: FemXAB nonribosomal peptidyltransferases
81	d1jlwa2	Alignment	not modelled	13.6	11	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
82	d1ml6a2	Alignment	not modelled	13.5	11	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
83	c4jxdA_	Alignment	not modelled	13.4	12	PDB header: transferase Chain: A: PDB Molecule: fructose-like phosphotransferase enzyme iib component 3; PDBTitle: crystal structure of predicted fructose specific iib from escherichia2 coli
84	d1k0dd2	Alignment	not modelled	13.3	9	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
85	d2nv0a1	Alignment	not modelled	13.2	21	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
86	c2jl4A_	Alignment	not modelled	12.9	12	PDB header: isomerase Chain: A: PDB Molecule: maleylpyruvate isomerase; PDBTitle: holo structure of maleyl pyruvate isomerase, a bacterial2 glutathione-s-transferase in zeta class
87	c4pqia_	Alignment	not modelled	12.8	8	PDB header: transferase Chain: A: PDB Molecule: in2-1 family protein, glutathione transferase lambda3; PDBTitle: crystal structure of glutathione transferase lambda3 from populus2 trichocarpa
88	c3h1nA_	Alignment	not modelled	12.7	14	PDB header: transferase Chain: A: PDB Molecule: probable glutathione s-transferase; PDBTitle: crystal structure of probable glutathione s-transferase from2 bordetella bronchiseptica rb50
89	c3zf7g_	Alignment	not modelled	12.4	7	PDB header: ribosome Chain: G: PDB Molecule: PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
90	d1b48a2	Alignment	not modelled	12.2	13	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
91	d2fhea2	Alignment	not modelled	12.1	9	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
92	d2gsqa2	Alignment	not modelled	12.1	18	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
93	d2cvda2	Alignment	not modelled	12.1	11	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
94	c6cfzj_	Alignment	not modelled	12.0	31	PDB header: nuclear protein Chain: J: PDB Molecule: spc34; PDBTitle: structure of the dash/dam1 complex shows its role at the yeast2 kinetochore-microtubule interface
95	d1duga2	Alignment	not modelled	11.9	5	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
96	c2agaA_	Alignment	not modelled	11.2	8	PDB header: transcription Chain: A: PDB Molecule: machado-joseph disease protein 1; PDBTitle: de-ubiquitinating function of ataxin-3: insights from the2 solution structure of the josephin domain
97	c6hq9A_	Alignment	not modelled	11.2	15	PDB header: hydrolase Chain: A: PDB Molecule: dna excision repair protein ercc-6-like 2; PDBTitle: crystal structure of the tudor domain of human ercc6-l2
98	c4h5fB_	Alignment	not modelled	11.1	13	PDB header: transport protein Chain: B: PDB Molecule: amino acid abc superfamily atp binding cassette PDBTitle: crystal structure of an amino acid abc transporter substrate-binding2 protein from streptococcus pneumoniae canada mdr_19a bound to l-3 arginine, form 1
99	c5g5aC_	Alignment	not modelled	11.1	14	PDB header: transferase Chain: C: PDB Molecule: glutathione s-transferase u25; PDBTitle: glutathione transferase u25 from arabidopsis thaliana in complex with2 glutathione disulfide