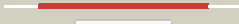



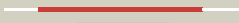

















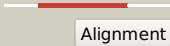

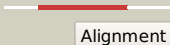

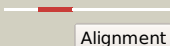
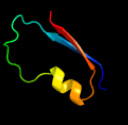




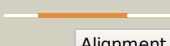

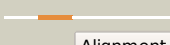
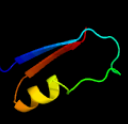




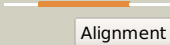
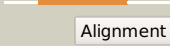
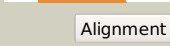
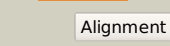
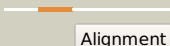
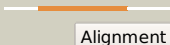

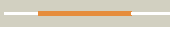


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1170_(mshB)_1300309_1301220
Date	Wed Jul 31 22:05:25 BST 2019
Unique Job ID	ea6f380e0d22efab

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1q7tA_	 Alignment		100.0	100	PDB header: hydrolase Chain: A: PDB Molecule: hypothetical protein rv1170; PDBTitle: rv1170 (mshb) from mycobacterium tuberculosis
2	d1q74a_	 Alignment		100.0	99	Fold: LmbE-like Superfamily: LmbE-like Family: LmbE-like
3	c3we7A_	 Alignment		100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein ph0499; PDBTitle: crystal structure of diacetylchitobiose deacetylase from pyrococcus2 horikoshii
4	c5bmoB_	 Alignment		100.0	31	PDB header: hydrolase Chain: B: PDB Molecule: putative uncharacterized protein Inmx; PDBTitle: Inmx protein, a putative glcnac-pi de-n-acetylase from streptomyces2 atroolivaceus
5	c5cgzA_	 Alignment		100.0	23	PDB header: lyase Chain: A: PDB Molecule: 4-oxalmesaconate hydratase; PDBTitle: crystal structure of galb, the 4-carboxy-2-hydroxymuconate hydratase,2 from pseudomonas putida kt2440
6	c3dfmA_	 Alignment		100.0	25	PDB header: hydrolase Chain: A: PDB Molecule: teicoplanin pseudoaglycone deacetylase orf2; PDBTitle: the crystal structure of the zinc inhibited form of2 teicoplanin deacetylase orf2
7	c3dfiA_	 Alignment		100.0	27	PDB header: hydrolase Chain: A: PDB Molecule: pseudoaglycone deacetylase dbv21; PDBTitle: the crystal structure of antimicrobial reagent a40926 pseudoaglycone2 deacetylase dbv21
8	d1uana_	 Alignment		100.0	32	Fold: LmbE-like Superfamily: LmbE-like Family: LmbE-like
9	c2ixdB_	 Alignment		100.0	23	PDB header: hydrolase Chain: B: PDB Molecule: lmbE-related protein; PDBTitle: crystal structure of the putative deacetylase bc1534 from bacillus2 cereus
10	c3beoA_	 Alignment		94.9	16	PDB header: isomerase Chain: A: PDB Molecule: udp-n-acetylglucosamine 2-epimerase; PDBTitle: a structural basis for the allosteric regulation of non-2 hydrolyzing udp-glcnac 2-epimerases
11	c1t9gR_	 Alignment		94.2	16	PDB header: oxidoreductase, electron transport Chain: R: PDB Molecule: electron transfer flavoprotein alpha-subunit, PDBTitle: structure of the human mcad:etf complex

12	d1efva1	 Alignment		93.8	16	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
13	c1efvA	 Alignment		92.2	16	PDB header: electron transport Chain: A: PDB Molecule: electron transfer flavoprotein; PDBTitle: three-dimensional structure of human electron transfer2 flavoprotein to 2.1 a resolution
14	d1dxqa	 Alignment		90.8	26	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Quinone reductase
15	d1qrda	 Alignment		89.6	23	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Quinone reductase
16	c4gi5B	 Alignment		89.5	28	PDB header: oxidoreductase Chain: B: PDB Molecule: quinone reductase; PDBTitle: crystal structure of a putative quinone reductase from klebsiella2 pneumoniae (target psi-013613)
17	c3ih5A	 Alignment		87.4	21	PDB header: electron transport Chain: A: PDB Molecule: electron transfer flavoprotein alpha-subunit; PDBTitle: crystal structure of electron transfer flavoprotein alpha-subunit from2 bacteroides thetaiotaomicron
18	d1d4aa	 Alignment		87.0	27	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Quinone reductase
19	c4hwgA	 Alignment		86.5	15	PDB header: isomerase Chain: A: PDB Molecule: udp-n-acetylglucosamine 2-epimerase; PDBTitle: structure of udp-n-acetylglucosamine 2-epimerase from rickettsia2 bellii
20	d1o94c	 Alignment		85.6	20	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
21	d1f0ka	 Alignment	not modelled	85.1	17	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Peptidoglycan biosynthesis glycosyltransferase MurG
22	c1o94D	 Alignment	not modelled	85.0	23	PDB header: electron transport Chain: D: PDB Molecule: electron transfer flavoprotein alpha-subunit; PDBTitle: ternary complex between trimethylamine dehydrogenase and2 electron transferring flavoprotein
23	d3clsc1	 Alignment	not modelled	85.0	25	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
24	c3clrD	 Alignment	not modelled	84.6	27	PDB header: electron transport Chain: D: PDB Molecule: electron transfer flavoprotein subunit alpha; PDBTitle: crystal structure of the r236a etf mutant from m. methylotrophus
25	c3f2vA	 Alignment	not modelled	83.8	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: general stress protein 14; PDBTitle: crystal structure of the general stress protein 14 (tde0354) in2 complex with fnn from treponema denticola, northeast structural3 genomics consortium target tdr58.
26	d3clsd1	 Alignment	not modelled	83.1	23	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
27	d2qwxal	 Alignment	not modelled	81.7	18	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Quinone reductase
						PDB header: flavoprotein Chain: E: PDB Molecule: electron transfer flavoprotein small

28	c5ol2E_	Alignment	not modelled	81.7	29	subunit; PDBTitle: the electron transferring flavoprotein/butyryl-coa dehydrogenase2 complex from clostridium difficile
29	c4nesA_	Alignment	not modelled	80.6	14	PDB header: isomerase Chain: A: PDB Molecule: udp-n-acetylglucosamine 2-epimerase; PDBTitle: crystal structure of methanocaldococcus jannaschii udp-glcna2 2- epimerase in complex with udp-glcna2 and udp
30	c3ot5D_	Alignment	not modelled	80.3	15	PDB header: isomerase Chain: D: PDB Molecule: udp-n-acetylglucosamine 2-epimerase; PDBTitle: 2.2 angstrom resolution crystal structure of putative udp-n-2 acetylglucosamine 2-epimerase from listeria monocytogenes
31	d1efpb_	Alignment	not modelled	79.9	20	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
32	c3ha2B_	Alignment	not modelled	79.6	14	PDB header: oxidoreductase Chain: B: PDB Molecule: nadph-quinone reductase; PDBTitle: crystal structure of protein (nadph-quinone reductase) from2 p.pentosaaceus, northeast structural genomics consortium target ptr24a
33	c5w8sA_	Alignment	not modelled	77.4	20	PDB header: transferase Chain: A: PDB Molecule: lipid-a-disaccharide synthase; PDBTitle: lipid a disaccharide synthase (lpxb)-7 solubilizing mutations
34	d1rrva_	Alignment	not modelled	76.6	17	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Gtf glycosyltransferase
35	c4l2iA_	Alignment	not modelled	75.2	21	PDB header: electron transport Chain: A: PDB Molecule: electron transfer flavoprotein alpha subunit; PDBTitle: electron transferring flavoprotein of acidaminococcus fermentans:2 towards a mechanism of flavin-based electron bifurcation
36	c3dzcA_	Alignment	not modelled	73.8	15	PDB header: isomerase Chain: A: PDB Molecule: udp-n-acetylglucosamine 2-epimerase; PDBTitle: 2.35 angstrom resolution structure of webc (vc0917), a udp-n-2 acetylglucosamine 2-epimerase from vibrio cholerae.
37	c5lvaA_	Alignment	not modelled	72.8	14	PDB header: oxidoreductase Chain: A: PDB Molecule: nad(p)h-fmn oxidoreductase; PDBTitle: crystal structure of thermophilic tryptophan halogenase (th-hal)2 enzyme from streptomycin violaceusniger.
38	c3s2uA_	Alignment	not modelled	72.6	18	PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine--n-acetylmuramyl-(pentapeptide) PDBTitle: crystal structure of the pseudomonas aeruginosa murg:udp-glcna2 substrate complex
39	d1i3ca_	Alignment	not modelled	72.3	10	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
40	c6fahB_	Alignment	not modelled	72.2	30	PDB header: flavoprotein Chain: B: PDB Molecule: cafeyl-coa reductase-etf complex subunit card; PDBTitle: molecular basis of the flavin-based electron-bifurcating cafeyl-coa2 reductase reaction
41	c3eywA_	Alignment	not modelled	72.1	14	PDB header: transport protein Chain: A: PDB Molecule: c-terminal domain of glutathione-regulated potassium-efflux PDBTitle: crystal structure of the c-terminal domain of e. coli kefc in complex2 with keff
42	d1v4va_	Alignment	not modelled	70.9	16	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDP-N-acetylglucosamine 2-epimerase
43	c5ql5B_	Alignment	not modelled	67.5	12	PDB header: transferase Chain: B: PDB Molecule: sterol 3-beta-glucosyltransferase; PDBTitle: sterol 3-beta-glucosyltransferase (ugt51) from saccharomyces2 cerevisiae (strain atcc 204508 / s288c): udpg complex
44	c6fahE_	Alignment	not modelled	66.1	14	PDB header: flavoprotein Chain: E: PDB Molecule: cafeyl-coa reductase-etf complex subunit care; PDBTitle: molecular basis of the flavin-based electron-bifurcating cafeyl-coa2 reductase reaction
45	c3ia7A_	Alignment	not modelled	65.5	15	PDB header: transferase Chain: A: PDB Molecule: calg4; PDBTitle: crystal structure of calg4, the calicheamicin glycosyltransferase
46	d2acva1	Alignment	not modelled	63.8	9	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like
47	d1di6a_	Alignment	not modelled	61.9	26	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
48	c2r60A_	Alignment	not modelled	61.9	33	PDB header: transferase Chain: A: PDB Molecule: glycosyl transferase, group 1; PDBTitle: structure of apo sucrose phosphate synthase (sps) of2 halothermothrix orenii
49	c1telA_	Alignment	not modelled	60.2	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ribulose biphosphate carboxylase, large subunit; PDBTitle: crystal structure of a rubisco-like protein from chlorobium2 tepidum
50	d1ej7l1	Alignment	not modelled	58.4	20	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
51	c3fk4A_	Alignment	not modelled	57.9	24	PDB header: isomerase Chain: A: PDB Molecule: rubisco-like protein; PDBTitle: crystal structure of rubisco-like protein from bacillus2 cereus atcc 14579
						PDB header: transferase

52	c5du2B_	Alignment	not modelled	57.6	21	Chain: B: PDB Molecule: espg2 glycosyltransferase; PDBTitle: structural analysis of espg2 glycosyltransferase
53	d1efvb_	Alignment	not modelled	56.8	15	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
54	c9rubB_	Alignment	not modelled	56.4	25	PDB header: lyase(carbon-carbon) Chain: B: PDB Molecule: ribulose-1,5-bisphosphate carboxylase; PDBTitle: crystal structure of activated ribulose-1,5-bisphosphate carboxylase2 complexed with its substrate, ribulose-1,5-bisphosphate
55	c6hunA_	Alignment	not modelled	55.7	29	PDB header: photosynthesis Chain: A: PDB Molecule: ribulose bisphosphate carboxylase; PDBTitle: dimeric archeal rubisco from hyperthermus butylicus
56	c4r3uD_	Alignment	not modelled	55.2	14	PDB header: isomerase Chain: D: PDB Molecule: 2-hydroxyisobutyryl-coa mutase small subunit; PDBTitle: crystal structure of 2-hydroxyisobutyryl-coa mutase
57	d1wdda1	Alignment	not modelled	55.0	20	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
58	c2iyaB_	Alignment	not modelled	54.7	11	PDB header: transferase Chain: B: PDB Molecule: oleandomycin glycosyltransferase; PDBTitle: the crystal structure of macrolide glycosyltransferases: a blueprint2 for antibiotic engineering
59	c1rldB_	Alignment	not modelled	54.7	20	PDB header: lyase(carbon-carbon) Chain: B: PDB Molecule: ribulose 1,5 bisphosphate carboxylase/oxygenase (large PDBTitle: solid-state phase transition in the crystal structure of ribulose 1,5-2 biphosphate carboxylase(/slash)oxygenase
60	d1bwva1	Alignment	not modelled	54.3	30	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
61	c3wrbB_	Alignment	not modelled	54.3	16	PDB header: oxidoreductase Chain: B: PDB Molecule: gallate dioxygenase; PDBTitle: crystal structure of the anaerobic h124f desb-gallate complex
62	c1bwvA_	Alignment	not modelled	54.3	30	PDB header: lyase Chain: A: PDB Molecule: protein (ribulose bisphosphate carboxylase); PDBTitle: activated ribulose 1,5-bisphosphate carboxylase/oxygenase (rubisco)2 complexed with the reaction intermediate analogue 2-carboxyarabinitol3 1,5-bisphosphate
63	d1svda1	Alignment	not modelled	53.9	20	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
64	c2yxbA_	Alignment	not modelled	53.6	11	PDB header: isomerase Chain: A: PDB Molecule: coenzyme b12-dependent mutase; PDBTitle: crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
65	c1jqoA_	Alignment	not modelled	53.4	17	PDB header: lyase Chain: A: PDB Molecule: phosphoenolpyruvate carboxylase; PDBTitle: crystal structure of c4-form phosphoenolpyruvate carboxylase from2 maize
66	d1jqoa_	Alignment	not modelled	53.4	17	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate carboxylase
67	c5macD_	Alignment	not modelled	53.0	20	PDB header: lyase Chain: D: PDB Molecule: ribulose-1,5-bisphosphate carboxylase-oxygenase type iii; PDBTitle: crystal structure of decameric methanococcoides burtonii rubisco2 complexed with 2-carboxyarabinitol bisphosphate
68	c3iaaB_	Alignment	not modelled	52.3	25	PDB header: transferase Chain: B: PDB Molecule: calg2; PDBTitle: crystal structure of calg2, calicheamicin glycosyltransferase, tdp2 bound form
69	c5enzA_	Alignment	not modelled	52.1	15	PDB header: isomerase Chain: A: PDB Molecule: udp-glcna2 2-epimerase; PDBTitle: s. aureus mnaa-udp co-structure
70	c3jx9B_	Alignment	not modelled	51.9	19	PDB header: isomerase Chain: B: PDB Molecule: putative phosphoheptose isomerase; PDBTitle: crystal structure of putative phosphoheptose isomerase2 (yp_001815198.1) from exiguobacterium sp. 255-15 at 1.95 a resolution
71	c1rcxH_	Alignment	not modelled	51.4	20	PDB header: lyase (carbon-carbon) Chain: H: PDB Molecule: ribulose bisphosphate carboxylase/oxygenase; PDBTitle: non-activated spinach rubisco in complex with its substrate2 ribulose-1,5-bisphosphate
72	d8ruca1	Alignment	not modelled	51.2	20	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
73	c2qygC_	Alignment	not modelled	50.8	22	PDB header: unknown function Chain: C: PDB Molecule: ribulose bisphosphate carboxylase-like protein 2; PDBTitle: crystal structure of a rubisco-like protein rlp2 from rhodospseudomonas2 palustris
74	c2oemA_	Alignment	not modelled	50.4	29	PDB header: isomerase Chain: A: PDB Molecule: 2,3-diketo-5-methylthiopentyl-1-phosphate enolase; PDBTitle: crystal structure of a rubisco-like protein from geobacillus2 kaustophilus liganded with mg2+ and 2,3-diketohexane 1-phosphate
75	d1rbla1	Alignment	not modelled	50.3	22	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain PDB header: lyase

76	c2d69B_	Alignment	not modelled	50.1	27	Chain: B: PDB Molecule: ribulose bisphosphate carboxylase; PDBTitle: crystal structure of the complex of sulfate ion and octameric2 ribulose-1,5-bisphosphate carboxylase/oxygenase (rubisco) from3 pyrococcus horikoshii ot3 (form-2 crystal)
77	c1gehE_	Alignment	not modelled	49.6	25	PDB header: lyase Chain: E: PDB Molecule: ribulose-1,5-bisphosphate carboxylase/oxygenase; PDBTitle: crystal structure of archaeal rubisco (ribulose 1,5-bisphosphate2 carboxylase/oxygenase)
78	c5ol2D_	Alignment	not modelled	49.1	20	PDB header: flavoprotein Chain: D: PDB Molecule: electron transfer flavoprotein large subunit; PDBTitle: the electron transferring flavoprotein/butyryl-coa dehydrogenase2 complex from clostridium difficile
79	d5ruba1	Alignment	not modelled	49.0	25	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
80	c5iejA_	Alignment	not modelled	48.8	22	PDB header: protein Chain: A: PDB Molecule: sdrG; PDBTitle: solution structure of the bef3-activated conformation of sdrG from2 pseudomonas melonis fr1
81	c3qi7A_	Alignment	not modelled	48.2	10	PDB header: transcription Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of a putative transcriptional regulator2 (yp_001089212.1) from clostridium difficile 630 at 1.86 a resolution
82	d1gk8a1	Alignment	not modelled	48.0	17	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
83	c2zviB_	Alignment	not modelled	47.6	17	PDB header: isomerase Chain: B: PDB Molecule: 2,3-diketo-5-methylthiopentyl-1-phosphate PDBTitle: crystal structure of 2,3-diketo-5-methylthiopentyl-1-2 phosphate enolase from bacillus subtilis
84	d1bxna1	Alignment	not modelled	47.2	24	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
85	d1y5ea1	Alignment	not modelled	46.3	28	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
86	c2rusB_	Alignment	not modelled	45.0	25	PDB header: lyase(carbon-carbon) Chain: B: PDB Molecule: rubisco (ribulose-1,5-bisphosphate carboxylase(/slash)) PDBTitle: crystal structure of the ternary complex of ribulose-1,5-bisphosphate2 carboxylase, mg(ii), and activator co2 at 2.3-angstroms resolution
87	d1geha1	Alignment	not modelled	44.6	25	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
88	c5c2gD_	Alignment	not modelled	44.5	25	PDB header: lyase Chain: D: PDB Molecule: form ii rubisco; PDBTitle: gws1b rubisco: form ii rubisco derived from uncultivated2 gallionellacea species (cabp-bound).
89	d1f6da_	Alignment	not modelled	44.4	16	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDP-N-acetylglucosamine 2-epimerase
90	d2d69a1	Alignment	not modelled	43.6	27	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
91	c3okaA_	Alignment	not modelled	43.2	25	PDB header: transferase Chain: A: PDB Molecule: gdp-mannose-dependent alpha-(1-6)-phosphatidylinositol PDBTitle: crystal structure of corynebacterium glutamicum pimB' in complex with2 gdp-man (triclinic crystal form)
92	c5xvmB_	Alignment	not modelled	43.1	13	PDB header: transferase Chain: B: PDB Molecule: sterol 3-beta-glucosyltransferase; PDBTitle: sterol 3-beta-glucosyltransferase (ugt51) from saccharomyces2 cerevisiae (strain atcc 204508 / s288c)
93	d1mkza_	Alignment	not modelled	43.0	16	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
94	d1ykwa1	Alignment	not modelled	42.1	18	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
95	c3nwrA_	Alignment	not modelled	41.4	22	PDB header: lyase Chain: A: PDB Molecule: a rubisco-like protein; PDBTitle: crystal structure of a rubisco-like protein from burkholderia fungorum
96	c5xt2C_	Alignment	not modelled	38.9	18	PDB header: dna binding protein Chain: C: PDB Molecule: response regulator fixj; PDBTitle: crystal structures of full-length fixj from b. japonicum crystallized2 in space group p212121
97	d1jqna_	Alignment	not modelled	37.6	19	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate carboxylase
98	c5nlmB_	Alignment	not modelled	37.1	11	PDB header: transferase Chain: B: PDB Molecule: indoxyl udp-glucosyltransferase; PDBTitle: complex between a udp-glucosyltransferase from polygonum tinctorium2 capable of glucosylating indoxyl and indoxyl sulfate
99	c2ohiB_	Alignment	not modelled	36.5	6	PDB header: oxidoreductase Chain: B: PDB Molecule: type a flavoprotein fpra; PDBTitle: crystal structure of coenzyme f420h2 oxidase (fpra), a diiron2 flavoprotein, reduced state
100	c3u7iB_	Alignment	not modelled	35.7	13	PDB header: oxidoreductase Chain: B: PDB Molecule: fmn-dependent nadh-azoreductase 1; PDBTitle: the crystal structure of fmn-dependent nadh-azoreductase 1 (gbaa0966)2 from bacillus anthracis str. ames

						ancestor
101	c3lteH_	Alignment	not modelled	32.8	24	PDB header: transcription Chain: H: PDB Molecule: response regulator; PDBTitle: crystal structure of response regulator (signal receiver domain) from2 bermanella marisrubri
102	d1k68a_	Alignment	not modelled	32.6	16	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
103	c4fzrA_	Alignment	not modelled	32.4	12	PDB header: transferase Chain: A: PDB Molecule: ssf6; PDBTitle: crystal structure of ssf6, streptomyces sp. sf25752 glycosyltransferase
104	c5brjA_	Alignment	not modelled	32.1	21	PDB header: signaling protein Chain: A: PDB Molecule: two component response regulator; PDBTitle: structure of the bacteriophytochrome response regulator atbr
105	c2csuB_	Alignment	not modelled	31.6	15	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: 457aa long hypothetical protein; PDBTitle: crystal structure of ph0766 from pyrococcus horikoshii ot3
106	c2q9uB_	Alignment	not modelled	31.1	14	PDB header: oxidoreductase Chain: B: PDB Molecule: a-type flavoprotein; PDBTitle: crystal structure of the flavodiiron protein from giardia2 intestinalis
107	c2jimH_	Alignment	not modelled	30.4	8	PDB header: transferase Chain: H: PDB Molecule: glycosyl transferase, group 1 family protein; PDBTitle: crystal structure of a family gt4 glycosyltransferase from bacillus2 anthracis orf ba1558.
108	d1s8na_	Alignment	not modelled	29.9	25	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
109	c5okiA_	Alignment	not modelled	29.6	25	PDB header: replication Chain: A: PDB Molecule: dna polymerase epsilon catalytic subunit a; PDBTitle: crystal structure of the ctf18-1-8 module from ctf18-rfc in complex2 with a 63 kda fragment of dna polymerase epsilon
110	d1a04a2	Alignment	not modelled	29.5	18	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
111	d1uuya_	Alignment	not modelled	29.1	16	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
112	d1o6ca_	Alignment	not modelled	28.7	15	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDP-N-acetylglucosamine 2-epimerase
113	d2afwa1	Alignment	not modelled	28.2	19	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Glutaminyl-peptide cyclotransferase-like
114	d1efpa1	Alignment	not modelled	27.9	13	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
115	c6qrgB_	Alignment	not modelled	26.7	9	PDB header: signaling protein Chain: B: PDB Molecule: oxygen-binding diiron protein; PDBTitle: apo conformation of chemotaxis sensor odp
116	c3d0qB_	Alignment	not modelled	26.6	17	PDB header: transferase Chain: B: PDB Molecule: protein calg3; PDBTitle: crystal structure of calg3 from micromonospora echinospora determined2 in space group i222
117	c5dldA_	Alignment	not modelled	26.3	21	PDB header: isomerase Chain: A: PDB Molecule: udp-n-acetylglucosamine 2-epimerase; PDBTitle: crystal structure of a udp-n-acetylglucosamine 2-epimerase from2 burkholderia vietnamiensis complexed with udp-glcnaac and udp
118	d1k66a_	Alignment	not modelled	26.3	21	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
119	d1e5da2	Alignment	not modelled	26.1	11	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: ROO N-terminal domain-like
120	d1dkua2	Alignment	not modelled	25.8	21	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosylpyrophosphate synthetase-like