
















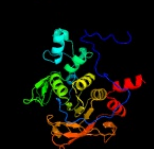






Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1475c_acn_1663221_1666052
Date	Fri Aug 2 13:30:05 BST 2019
Unique Job ID	6c52ce9bead7e5c7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2b3yB_	 Alignment		100.0	52	PDB header: lyase Chain: B; PDB Molecule: iron-responsive element binding protein 1; PDBTitle: structure of a monoclinic crystal form of human cytosolic aconitase2 (irp1)
2	c5acnA_	 Alignment		100.0	29	PDB header: lyase(carbon-oxygen) Chain: A; PDB Molecule: aconitase; PDBTitle: structure of activated aconitase. formation of the (4fe-4s) cluster in2 the crystal
3	d2b3ya2	 Alignment		100.0	51	Fold: Aconitase iron-sulfur domain Superfamily: Aconitase iron-sulfur domain Family: Aconitase iron-sulfur domain
4	d1acoa2	 Alignment		100.0	31	Fold: Aconitase iron-sulfur domain Superfamily: Aconitase iron-sulfur domain Family: Aconitase iron-sulfur domain
5	c4kp1A_	 Alignment		100.0	25	PDB header: isomerase Chain: A; PDB Molecule: isopropylmalate/citramalate isomerase large subunit; PDBTitle: crystal structure of ipm isomerase large subunit from methanococcus2 jannaschii (mj0499)
6	c4kp2A_	 Alignment		100.0	24	PDB header: lyase Chain: A; PDB Molecule: homoaconitase large subunit; PDBTitle: crystal structure of homoaconitase large subunit from methanococcus2 jannaschii (mj1003)
7	d1l5ja3	 Alignment		100.0	22	Fold: Aconitase iron-sulfur domain Superfamily: Aconitase iron-sulfur domain Family: Aconitase iron-sulfur domain
8	c1l5jB_	 Alignment		100.0	23	PDB header: lyase Chain: B; PDB Molecule: aconitate hydratase 2; PDBTitle: crystal structure of e. coli aconitase b.
9	d2b3ya1	 Alignment		100.0	52	Fold: The "swivelling" beta/beta/alpha domain Superfamily: LeuD/IlvD-like Family: LeuD-like
10	d1acoa1	 Alignment		100.0	26	Fold: The "swivelling" beta/beta/alpha domain Superfamily: LeuD/IlvD-like Family: LeuD-like
11	d1l5ja2	 Alignment		100.0	22	Fold: The "swivelling" beta/beta/alpha domain Superfamily: LeuD/IlvD-like Family: LeuD-like

12	c3vbaE_	Alignment		100.0	29	PDB header: lyase Chain: E; PDB Molecule: isopropylmalate/citramalate isomerase small subunit; PDBTitle: crystal structure of methanogen 3-isopropylmalate isomerase small2 subunit
13	c2pkpA_	Alignment		100.0	30	PDB header: lyase Chain: A; PDB Molecule: homoaconitase small subunit; PDBTitle: crystal structure of 3-isopropylmalate dehydratase (leud)2 from methanocaldococcus jannaschii dsm2661 (mj1271)
14	d1v7la_	Alignment		100.0	36	Fold: The "swivelling" beta/beta/alpha domain Superfamily: LeuD/IlvD-like Family: LeuD-like
15	c2hcuA_	Alignment		100.0	25	PDB header: lyase Chain: A; PDB Molecule: 3-isopropylmalate dehydratase small subunit; PDBTitle: crystal structure of smu.1381 (or leud) from streptococcus mutans
16	c3q3wB_	Alignment		100.0	25	PDB header: transferase Chain: B; PDB Molecule: 3-isopropylmalate dehydratase small subunit; PDBTitle: isopropylmalate isomerase small subunit from campylobacter jejuni.
17	c3h5jA_	Alignment		100.0	27	PDB header: lyase Chain: A; PDB Molecule: 3-isopropylmalate dehydratase small subunit; PDBTitle: leud_1-168 small subunit of isopropylmalate isomerase (rv2987c) from mycobacterium tuberculosis
18	d1cfla1	Alignment		72.3	14	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Arrestin/Vps26-like
19	d1g4ma1	Alignment		71.5	34	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Arrestin/Vps26-like
20	d2r4qa1	Alignment		71.4	32	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: PTS system IIB component-like Family: PTS system, Fructose specific IIB subunit-like
21	c4zwc_	Alignment	not modelled	59.2	16	PDB header: signaling protein Chain: C; PDB Molecule: chimera protein of human rhodopsin, mouse s-arrestin, and PDBTitle: crystal structure of rhodopsin bound to arrestin by femtosecond x-ray2 laser
22	c4zwa_	Alignment	not modelled	59.1	16	PDB header: signaling protein Chain: A; PDB Molecule: chimera protein of human rhodopsin, mouse s-arrestin, and PDBTitle: crystal structure of rhodopsin bound to arrestin by femtosecond x-ray2 laser
23	c4jxdA_	Alignment	not modelled	54.4	15	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
24	c3qm3C_	Alignment	not modelled	52.6	26	PDB header: lyase Chain: C; PDB Molecule: fructose-bisphosphate aldolase; PDBTitle: 1.85 angstrom resolution crystal structure of fructose-bisphosphate2 aldolase (fba) from campylobacter jejuni
25	c5dleD_	Alignment	not modelled	50.3	21	PDB header: transferase Chain: D; PDB Molecule: pts system, fructose-specific iibc component; PDBTitle: crystal structure from a domain (thr161-f265) from fructose-specific2 iibc component (pts system) from borrelia burgdorferi
26	d1dosa_	Alignment	not modelled	50.0	19	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class II FBP aldolase
27	c2kyrA_	Alignment	not modelled	49.3	27	PDB header: transferase Chain: A; PDB Molecule: fructose-like phosphotransferase enzyme iib component 1; PDBTitle: solution structure of enzyme iib subunit of pts system from2 escherichia coli k12. northeast structural genomics

						consortium target3 er315/ontario center for structural proteomics target ec0544
28	d2r48a1	Alignment	not modelled	48.9	33	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: PTS system IIB component-like Family: PTS system, Fructose specific IIB subunit-like
29	c6bk9A	Alignment	not modelled	48.8	22	PDB header: signaling protein Chain: A: PDB Molecule: visual arrestin; PDBTitle: crystal structure of squid arrestin
30	c4e6nC	Alignment	not modelled	48.6	25	PDB header: protein binding Chain: C: PDB Molecule: metallophosphoesterase; PDBTitle: crystal structure of bacterial pnkp-c/hen1-n heterodimer
31	c2m1zA	Alignment	not modelled	46.0	27	PDB header: transferase Chain: A: PDB Molecule: lmo0427 protein; PDBTitle: solution structure of uncharacterized protein lmo0427
32	c4y0bA	Alignment	not modelled	40.3	11	PDB header: protein binding Chain: A: PDB Molecule: double clp-n motif protein; PDBTitle: the structure of arabidopsis clpt1
33	c3elfA	Alignment	not modelled	31.4	25	PDB header: lyase Chain: A: PDB Molecule: fructose-bisphosphate aldolase; PDBTitle: structural characterization of tetrameric mycobacterium tuberculosis2 fructose 1,6-bisphosphate aldolase - substrate binding and catalysis3 mechanism of a class iia bacterial aldolase
34	d1t3va	Alignment	not modelled	29.6	15	Fold: Ribonuclease H-like motif Superfamily: Nitrogenase accessory factor-like Family: MTH1175-like
35	c5ze4A	Alignment	not modelled	28.1	18	PDB header: lyase Chain: A: PDB Molecule: dihydroxy-acid dehydratase, chloroplastic; PDBTitle: the structure of holo- structure of dhad complex with [2fe-2s] cluster
36	c6ez3C	Alignment	not modelled	25.8	22	PDB header: rna binding protein Chain: C: PDB Molecule: cyclo(l-leucyl-l-leucyl) synthase; PDBTitle: structure of cdps from staphylococcus haemolyticus
37	d1o13a	Alignment	not modelled	25.4	15	Fold: Ribonuclease H-like motif Superfamily: Nitrogenase accessory factor-like Family: MTH1175-like
38	d1mxaa1	Alignment	not modelled	23.9	23	Fold: S-adenosylmethionine synthetase Superfamily: S-adenosylmethionine synthetase Family: S-adenosylmethionine synthetase
39	d1k6ka	Alignment	not modelled	22.6	30	Fold: Double Clp-N motif Superfamily: Double Clp-N motif Family: Double Clp-N motif
40	c2yx6C	Alignment	not modelled	22.2	12	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: hypothetical protein ph0822; PDBTitle: crystal structure of ph0822
41	d1rdua	Alignment	not modelled	21.9	22	Fold: Ribonuclease H-like motif Superfamily: Nitrogenase accessory factor-like Family: MTH1175-like
42	c5n5xL	Alignment	not modelled	21.5	16	PDB header: transcription Chain: L: PDB Molecule: rna polymerase i-specific transcription initiation factor PDBTitle: crystal structure of s. cerevisiae core factor at 3.2a resolution
43	c5n5xl	Alignment	not modelled	21.5	16	PDB header: transcription Chain: I: PDB Molecule: rna polymerase i-specific transcription initiation factor PDBTitle: crystal structure of s. cerevisiae core factor at 3.2a resolution
44	d2p02a1	Alignment	not modelled	20.7	21	Fold: S-adenosylmethionine synthetase Superfamily: S-adenosylmethionine synthetase Family: S-adenosylmethionine synthetase
45	c4wwsE	Alignment	not modelled	20.3	32	PDB header: oxidoreductase Chain: E: PDB Molecule: putative heme-dependent peroxidase lmo2113; PDBTitle: structure of chlorite dismutase-like protein from listeria2 monocytogenes
46	d1gvfa	Alignment	not modelled	20.2	21	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class II FBP aldolase
47	c5yudA	Alignment	not modelled	19.8	33	PDB header: immune system Chain: A: PDB Molecule: baculoviral iap repeat-containing protein 1e; PDBTitle: flagellin derivative in complex with the nlr protein naip5
48	c5u2IA	Alignment	not modelled	19.3	22	PDB header: protein binding Chain: A: PDB Molecule: heat shock protein 104; PDBTitle: crystal structure of the hsp104 n-terminal domain from candida2 albicans
49	c3iz5Q	Alignment	not modelled	18.9	22	PDB header: ribosome Chain: Q: PDB Molecule: 60s ribosomal protein l5 (l18p); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
50	c5gkmA	Alignment	not modelled	18.9	16	PDB header: chaperone Chain: A: PDB Molecule: at5g51070/k3k7_27; PDBTitle: crystal structure of the n-terminal domain of caseinolytic protease2 associated chaperone clpd from arabidopsis thaliana
51	d1qm4a1	Alignment	not modelled	18.7	18	Fold: S-adenosylmethionine synthetase Superfamily: S-adenosylmethionine synthetase Family: S-adenosylmethionine synthetase
52	c4y0cB	Alignment	not modelled	18.4	19	PDB header: protein binding Chain: B: PDB Molecule: clp protease-related protein at4g12060, chloroplastic; PDBTitle: the structure of arabidopsis clpt2
						Fold: IlvD/EDD N-terminal domain-like

53	d2gp4a2	Alignment	not modelled	18.0	18	Superfamily: lvD/EDD N-terminal domain-like Family: lvD/EDD N-terminal domain-like
54	c6b5bA	Alignment	not modelled	17.7	33	PDB header: immune system Chain: A: PDB Molecule: baculoviral iap repeat-containing protein 1e; PDBTitle: cryo-em structure of the naip5-nlr4-flagellin inflammasome
55	c2wbrA	Alignment	not modelled	17.5	31	PDB header: dna-binding protein Chain: A: PDB Molecule: gw182; PDBTitle: the rrm domain in gw182 proteins contributes to mirna-2 mediated gene silencing
56	d1eo1a	Alignment	not modelled	17.5	23	Fold: Ribonuclease H-like motif Superfamily: Nitrogenase accessory factor-like Family: MTH1175-like
57	c2gp4A	Alignment	not modelled	16.9	14	PDB header: lyase Chain: A: PDB Molecule: 6-phosphogluconate dehydratase; PDBTitle: structure of [fes]cluster-free apo form of 6-phosphogluconate2 dehydratase from shewanella oneidensis
58	c4hn9B	Alignment	not modelled	16.4	21	PDB header: transport protein Chain: B: PDB Molecule: iron complex transport system substrate-binding protein; PDBTitle: crystal structure of iron abc transporter solute-binding protein from2 eubacterium eligens
59	d1t0tv	Alignment	not modelled	16.3	27	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Chlorite dismutase-like
60	d1uk8a	Alignment	not modelled	16.1	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carbon-carbon bond hydrolase
61	c4lkrA	Alignment	not modelled	16.1	23	PDB header: transferase Chain: A: PDB Molecule: purine nucleoside phosphorylase deo-type; PDBTitle: crystal structure of deo-3 gene product from shewanella oneidensis2 mr-1, nysgrc target 029437
62	c6hu9r	Alignment	not modelled	16.0	22	PDB header: oxidoreductase/electron transport Chain: R: PDB Molecule: cytochrome b-c1 complex subunit 7; PDBTitle: iii2-iv2 mitochondrial respiratory supercomplex from s. cerevisiae
63	c4zo3A	Alignment	not modelled	15.9	13	PDB header: hydrolase Chain: A: PDB Molecule: acylhomoserine lactonase; PDBTitle: aidc, a dizinc quorum-quenching lactonase, in complex with a product2 n-hexnoyl-l-homoserine
64	c2dfjA	Alignment	not modelled	15.6	31	PDB header: hydrolase Chain: A: PDB Molecule: diadenosinetetraphosphatase; PDBTitle: crystal structure of the diadenosine tetraphosphate2 hydrolase from shigella flexneri 2a
65	c3cf4A	Alignment	not modelled	15.3	18	PDB header: oxidoreductase Chain: A: PDB Molecule: acetyl-coa decarboxylase/synthase alpha subunit; PDBTitle: structure of the codh component of the m. barkeri acds complex
66	c2wfbA	Alignment	not modelled	15.2	17	PDB header: biosynthetic protein Chain: A: PDB Molecule: putative uncharacterized protein orp; PDBTitle: high resolution structure of the apo form of the orange2 protein (orp) from desulfovibrio gigas
67	c6emwX	Alignment	not modelled	14.4	21	PDB header: chaperone Chain: X: PDB Molecule: atp-dependent clp protease atp-binding subunit clpc; PDBTitle: structure of s.aureus clpc in complex with meca
68	c2oxlA	Alignment	not modelled	14.2	21	PDB header: gene regulation Chain: A: PDB Molecule: hypothetical protein ymgb; PDBTitle: structure and function of the e. coli protein ymgb: a protein critical2 for biofilm formation and acid resistance
69	d1iuka	Alignment	not modelled	14.1	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
70	c4oc8A	Alignment	not modelled	13.9	14	PDB header: hydrolase Chain: A: PDB Molecule: restriction endonuclease aspbhi; PDBTitle: dna modification-dependent restriction endonuclease aspbhi
71	d2ac7a1	Alignment	not modelled	13.9	23	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
72	d1p90a	Alignment	not modelled	13.6	15	Fold: Ribonuclease H-like motif Superfamily: Nitrogenase accessory factor-like Family: Nitrogenase accessory factor
73	d1vdha	Alignment	not modelled	13.4	23	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Chlorite dismutase-like
74	c4m3nA	Alignment	not modelled	13.1	18	PDB header: transferase Chain: A: PDB Molecule: purine nucleoside phosphorylase deo-type; PDBTitle: crystal structure of purine nucleoside phosphorylase from meiothermus2 ruber dsm 1279, nysgrc target 029804.
75	c4dtfA	Alignment	not modelled	13.0	21	PDB header: toxin Chain: A: PDB Molecule: vgrg protein; PDBTitle: structure of a vgrg vibrio cholerae toxin acd domain in complex with2 amp-pnp and mg++
76	c3qpbB	Alignment	not modelled	12.8	25	PDB header: transferase Chain: B: PDB Molecule: uridine phosphorylase; PDBTitle: crystal structure of streptococcus pyogenes uridine phosphorylase2 reveals a subclass of the np-i superfamily
77	c5oynB	Alignment	not modelled	12.6	14	PDB header: lyase Chain: B: PDB Molecule: dehydratase, ilvd/edd family; PDBTitle: crystal structure of d-xylonate dehydratase in holo-form
78	c4irfA	Alignment	not modelled	12.5	10	PDB header: chaperone Chain: A: PDB Molecule: malarial clpb2 atpase/hsp101 protein;

78	c4h1A	Alignment	not modelled	12.3	10	PDBTitle: preliminary structural investigations of a malarial protein secretion2 system PDB header: photosynthesis
79	c5x56A	Alignment	not modelled	12.4	15	Chain: A: PDB Molecule: photosystem ii repair protein psb27-h1, chloroplastic; PDBTitle: crystal structure of psb27 from arabidopsis thaliana
80	c5guiA	Alignment	not modelled	12.4	20	PDB header: chaperone Chain: A: PDB Molecule: chaperone protein clpc1, chloroplastic; PDBTitle: crystal structure of the n-terminal domain of caseinolytic protease2 associated chaperone clpc1 from arabidopsis thaliana
81	c2w9mB	Alignment	not modelled	12.3	35	PDB header: dna replication Chain: B: PDB Molecule: polymerase x; PDBTitle: structure of family x dna polymerase from deinococcus2 radiodurans
82	c3fh2A	Alignment	not modelled	12.2	15	PDB header: hydrolase Chain: A: PDB Molecule: probable atp-dependent protease (heat shock protein); PDBTitle: the crystal structure of the probable atp-dependent protease (heat2 shock protein) from corynebacterium glutamicum
83	d1hyua4	Alignment	not modelled	11.9	27	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: PDI-like
84	c2jz2A	Alignment	not modelled	11.9	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ssl0352 protein; PDBTitle: solution nmr structure of ssl0352 protein from synechocystis sp. pcc2 6803. northeast structural genomics consortium target sgr42
85	c4xb6D	Alignment	not modelled	11.8	36	PDB header: transferase Chain: D: PDB Molecule: alpha-d-ribose 1-methylphosphonate 5-phosphate c-p lyase; PDBTitle: structure of the e. coli c-p lyase core complex
86	d2aioa1	Alignment	not modelled	11.5	17	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Zn metallo-beta-lactamase
87	c4oe4A	Alignment	not modelled	11.4	27	PDB header: oxidoreductase Chain: A: PDB Molecule: delta-1-pyrroline-5-carboxylate dehydrogenase, PDBTitle: crystal structure of yeast ald4a1 complexed with nad+
88	c2y69R	Alignment	not modelled	11.1	14	PDB header: electron transport Chain: R: PDB Molecule: cytochrome c oxidase subunit 5a; PDBTitle: bovine heart cytochrome c oxidase re-refined with molecular oxygen
89	d1v54e	Alignment	not modelled	11.0	14	Fold: alpha-alpha superhelix Superfamily: Cytochrome c oxidase subunit E Family: Cytochrome c oxidase subunit E
90	c3fz5C	Alignment	not modelled	10.9	14	PDB header: isomerase Chain: C: PDB Molecule: possible 2-hydroxychromene-2-carboxylate isomerase; PDBTitle: crystal structure of possible 2-hydroxychromene-2-carboxylate2 isomerase from rhodobacter sphaeroides
91	c2kmfA	Alignment	not modelled	10.7	35	PDB header: photosynthesis Chain: A: PDB Molecule: photosystem ii 11 kda protein; PDBTitle: solution structure of psb27 from cyanobacterial photosystem2 ii
92	c2r2dC	Alignment	not modelled	10.6	30	PDB header: hydrolase Chain: C: PDB Molecule: zn-dependent hydrolases; PDBTitle: structure of a quorum-quenching lactonase (aiib) from agrobacterium2 tumefaciens
93	d1vhwa	Alignment	not modelled	10.6	18	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
94	c1xovA	Alignment	not modelled	10.5	14	PDB header: hydrolase Chain: A: PDB Molecule: ply protein; PDBTitle: the crystal structure of the listeria monocytogenes bacteriophage psa2 endolysin plypsa
95	d2ghra1	Alignment	not modelled	10.5	13	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: HTS-like
96	c3c52B	Alignment	not modelled	10.4	14	PDB header: lyase Chain: B: PDB Molecule: fructose-bisphosphate aldolase; PDBTitle: class ii fructose-1,6-bisphosphate aldolase from helicobacter pylori2 in complex with phosphoglycolohydroxamic acid, a competitive3 inhibitor
97	c1z34A	Alignment	not modelled	10.4	18	PDB header: transferase Chain: A: PDB Molecule: purine nucleoside phosphorylase; PDBTitle: crystal structure of trichomonas vaginalis purine nucleoside2 phosphorylase complexed with 2-fluoro-2'-deoxyadenosine
98	c3l4gl	Alignment	not modelled	10.2	30	PDB header: ligase Chain: I: PDB Molecule: phenylalanyl-trna synthetase alpha chain; PDBTitle: crystal structure of homo sapiens cytoplasmic phenylalanyl-trna2 synthetase
99	c4d98A	Alignment	not modelled	10.2	23	PDB header: transferase Chain: A: PDB Molecule: purine nucleoside phosphorylase deo-type; PDBTitle: crystal structure of the hexameric purine nucleoside phosphorylase2 from bacillus subtilis in space group h32 at ph 7.5