

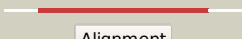













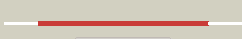







Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0186_(bglS)_216267_218342
Date	Tue Jul 23 14:50:23 BST 2019
Unique Job ID	cd19be9ee65ca242

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5wabD_	 Alignment		100.0	35	PDB header: hydrolase Chain: D: PDB Molecule: putative beta-glucosidase; PDBTitle: crystal structure of bifidobacterium adolescentis gh3 beta-glucosidase
2	c4i3gB_	 Alignment		100.0	39	PDB header: hydrolase Chain: B: PDB Molecule: beta-glucosidase; PDBTitle: crystal structure of desr, a beta-glucosidase from streptomyces2 venezuelae in complex with d-glucose.
3	c3ac0B_	 Alignment		100.0	31	PDB header: hydrolase Chain: B: PDB Molecule: beta-glucosidase i; PDBTitle: crystal structure of beta-glucosidase from kluyveromyces marxianus in2 complex with glucose
4	c5wabC_	 Alignment		100.0	35	PDB header: hydrolase Chain: C: PDB Molecule: putative beta-glucosidase; PDBTitle: crystal structure of bifidobacterium adolescentis gh3 beta-glucosidase
5	c5yotB_	 Alignment		100.0	30	PDB header: hydrolase Chain: B: PDB Molecule: isoprimeverose-producing enzyme; PDBTitle: isoprimeverose-producing enzyme from aspergillus oryzae in complex2 with isoprimeverose
6	c5nbsA_	 Alignment		100.0	34	PDB header: hydrolase Chain: A: PDB Molecule: beta-glucosidase; PDBTitle: structural studies of a glycoside hydrolase family 3 beta-glucosidase2 from the model fungus neurospora crassa
7	c3zz1A_	 Alignment		100.0	30	PDB header: hydrolase Chain: A: PDB Molecule: beta-d-glucoside glucohydrolase; PDBTitle: crystal structure of a glycoside hydrolase family 3 beta-glucosidase,2 bgl1 from hypocrea jecorina at 2.1a resolution.
8	c4iidB_	 Alignment		100.0	35	PDB header: hydrolase Chain: B: PDB Molecule: beta-glucosidase 1; PDBTitle: crystal structure of beta-glucosidase 1 from aspergillus aculeatus in2 complex with 1-deoxynojirimycin
9	c4d0jD_	 Alignment		100.0	36	PDB header: hydrolase Chain: D: PDB Molecule: beta-glucosidase; PDBTitle: crystal structure of glycoside hydrolase family 3 beta-2 glucosidase cel3a from the moderately thermophilic fungus3 rasamsonia emersonii
10	c2x41A_	 Alignment		100.0	34	PDB header: hydrolase Chain: A: PDB Molecule: beta-glucosidase; PDBTitle: structure of beta-glucosidase 3b from thermotoga neapolitana in2 complex with glucose
11	c5z87B_	 Alignment		100.0	31	PDB header: hydrolase Chain: B: PDB Molecule: emgh1; PDBTitle: structural of a novel b-glucosidase emgh1 at 2.3 angstrom from2 erythrobacter marinus

12	c6q7jB_	Alignment		100.0	28	PDB header: hydrolase Chain: B: PDB Molecule: exo-1,4-beta-xylosidase xlnD; PDBTitle: gh3 exo-beta-xylosidase (xlnD) in complex with xylobiose aziridine2 activity based probe
13	c3u48A_	Alignment		100.0	28	PDB header: hydrolase Chain: A: PDB Molecule: jmb19063; PDBTitle: from soil to structure: a novel dimeric family 3-beta-glucosidase2 isolated from compost using metagenomic analysis
14	c4zo9B_	Alignment		100.0	25	PDB header: hydrolase Chain: B: PDB Molecule: lin1840 protein; PDBTitle: crystal structure of mutant (d270a) beta-glucosidase from listeria2 innocua in complex with laminaribiose
15	c5z9sB_	Alignment		100.0	31	PDB header: hydrolase Chain: B: PDB Molecule: glycosyl hydrolase family 3 protein; PDBTitle: functional and structural characterization of a beta-glucosidase2 involved in saponin metabolism from intestinal bacteria
16	c5a7mA_	Alignment		100.0	28	PDB header: hydrolase Chain: A: PDB Molecule: beta-xylosidase; PDBTitle: the structure of hypocrea jecorina beta-xylosidase xyl3a (bx11)
17	c5tf0B_	Alignment		100.0	27	PDB header: hydrolase Chain: B: PDB Molecule: glycosyl hydrolase family 3 n-terminal domain protein; PDBTitle: crystal structure of glycosyl hydrolase family 3 n-terminal domain2 protein from bacteroides intestinalis
18	c5jp0A_	Alignment		100.0	26	PDB header: hydrolase Chain: A: PDB Molecule: beta-glucosidase bogh3b; PDBTitle: bacteroides ovatus xyloglucan pul gh3b with bound glucose
19	c3f93D_	Alignment		100.0	25	PDB header: hydrolase Chain: D: PDB Molecule: beta-glucosidase; PDBTitle: crystal structure of exo-1,3/1,4-beta-glucanase (exop) from2 pseudoalteromonas sp. bb1
20	c1ex1A_	Alignment		100.0	28	PDB header: hydrolase Chain: A: PDB Molecule: protein (beta-d-glucan exohydrolase isoenzyme exo1); PDBTitle: beta-d-glucan exohydrolase from barley
21	c5m6gA_	Alignment	not modelled	100.0	30	PDB header: hydrolase Chain: A: PDB Molecule: beta-glucosidase; PDBTitle: crystal structure glucan 1,4-beta-glucosidase from saccharopolyspora2 erythraea
22	c3bmxB_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: B: PDB Molecule: uncharacterized lipoprotein ybbd; PDBTitle: beta-n-hexosaminidase (ybbd) from bacillus subtilis
23	c3lk6A_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: lipoprotein ybbd; PDBTitle: beta-n-hexosaminidase n318d mutant (ybbd_n318d) from bacillus subtilis
24	c5vqdA_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: beta-glucoside phosphorylase bglx; PDBTitle: beta-glucoside phosphorylase bglx
25	c4zm6A_	Alignment	not modelled	100.0	19	PDB header: hydrolase, transferase Chain: A: PDB Molecule: n-acetyl-beta-d glucosaminidase; PDBTitle: a unique gcn5-related glucosamine n-acetyltransferase region exist in2 the fungal multi-domain gh3 beta-n-acetylglucosaminidase
26	c3sqlB_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: B: PDB Molecule: glycosyl hydrolase family 3; PDBTitle: crystal structure of glycoside hydrolase from synechococcus
27	c5k6lA_	Alignment	not modelled	100.0	26	PDB header: hydrolase Chain: A: PDB Molecule: b-glucosidase; PDBTitle: structure of a gh3 b-glucosidase from cow rumen metagenome
28	c5wvpA_	Alignment	not modelled	100.0	28	PDB header: hydrolase Chain: A: PDB Molecule: beta-glucosidase; PDBTitle: expression, characterization and crystal structure of a novel beta-2 glucosidase from paenibacillus barengoltzii

29	d1x38a1	Alignment	not modelled	100.0	28	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: NagZ-like
30	c5bzaA	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: crystal structure of cbsa from thermotoga neapolitana
31	c3wo8B	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: B: PDB Molecule: beta-n-acetylglucosaminidase; PDBTitle: crystal structure of the beta-n-acetylglucosaminidase from thermotoga2 maritima
32	c4yyfC	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: C: PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: the crystal structure of a glycosyl hydrolase of gh3 family member2 from [mycobacterium smegmatis str. mc2 155
33	c5bu9B	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: B: PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: crystal structure of beta-n-acetylhexosaminidase from beutenbergia2 cavernae dsm 12333
34	c4g6cA	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: beta-hexosaminidase 1; PDBTitle: crystal structure of beta-hexosaminidase 1 from burkholderia2 cenocepacia j2315
35	c5iobC	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: C: PDB Molecule: beta-glucosidase-related glycosidases; PDBTitle: crystal structure of beta-n-acetylglucosaminidase-like protein from2 corynebacterium glutamicum
36	c5g1mA	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: beta-hexosaminidase; PDBTitle: crystal structure of nagz from pseudomonas aeruginosa
37	c3tevA	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: glycosyl hydrolase, family 3; PDBTitle: the crystal structure of glycosyl hydrolase from deinococcus2 radiodurans r1
38	c4gvgB	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: B: PDB Molecule: beta-hexosaminidase; PDBTitle: crystal structure of salmonella typhimurium family 3 glycoside2 hydrolase (nagz)
39	d1tr9a	Alignment	not modelled	100.0	18	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: NagZ-like
40	d1x38a2	Alignment	not modelled	100.0	29	Fold: Flavodoxin-like Superfamily: Beta-D-glucan exohydrolase, C-terminal domain Family: Beta-D-glucan exohydrolase, C-terminal domain
41	d1w8oa1	Alignment	not modelled	97.9	22	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: E-set domains of sugar-utilizing enzymes
42	c2l0dA	Alignment	not modelled	97.0	18	PDB header: cell adhesion Chain: A: PDB Molecule: cell surface protein; PDBTitle: solution nmr structure of putative cell surface protein ma_4588 (272-2 376 domain) from methanosarcina acetivorans, northeast structural3 genomics consortium target mvr254a
43	c2kl6A	Alignment	not modelled	96.9	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of the cardb domain of pf1109 from2 pyrococcus furiosus. northeast structural genomics3 consortium target pfr193a
44	d2q3za2	Alignment	not modelled	96.4	13	Fold: Immunoglobulin-like beta-sandwich Superfamily: Transglutaminase, two C-terminal domains Family: Transglutaminase, two C-terminal domains
45	c5vhvB	Alignment	not modelled	96.2	18	PDB header: hydrolase/dna Chain: B: PDB Molecule: alkylpurine dna glycosylase alk; PDBTitle: pseudomonas fluorescens alkylpurine dna glycosylase alk bound to dna2 containing an oxocarbenium-intermediate analog
46	c1l9mB	Alignment	not modelled	96.0	11	PDB header: transferase Chain: B: PDB Molecule: protein-glutamine glutamyltransferase e3; PDBTitle: three-dimensional structure of the human transglutaminase 32 enzyme: binding of calcium ions change structure for3 activation
47	c4zlgA	Alignment	not modelled	96.0	26	PDB header: transferase Chain: A: PDB Molecule: putative b-glycan phosphorylase; PDBTitle: cellobionic acid phosphorylase - gluconic acid complex
48	c2x3bB	Alignment	not modelled	95.6	26	PDB header: hydrolase Chain: B: PDB Molecule: toxic extracellular endopeptidase; PDBTitle: asap1 inactive mutant e294a, an extracellular toxic zinc2 metalloendopeptidase
49	d1ex0a2	Alignment	not modelled	95.5	11	Fold: Immunoglobulin-like beta-sandwich Superfamily: Transglutaminase, two C-terminal domains Family: Transglutaminase, two C-terminal domains
50	d1g0da2	Alignment	not modelled	95.1	13	Fold: Immunoglobulin-like beta-sandwich Superfamily: Transglutaminase, two C-terminal domains Family: Transglutaminase, two C-terminal domains
51	d1vija2	Alignment	not modelled	94.7	11	Fold: Immunoglobulin-like beta-sandwich Superfamily: Transglutaminase, two C-terminal domains Family: Transglutaminase, two C-terminal domains
52	d2vza2	Alignment	not modelled	94.6	19	Fold: Immunoglobulin-like beta-sandwich Superfamily: beta-Galactosidase/glucuronidase domain Family: beta-Galactosidase/glucuronidase domain
53	c2kutA	Alignment	not modelled	94.5	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of gmr58a from geobacter metallireducens.2 northeast structural genomics consortium target gmr58a
54	c2qsvA	Alignment	not modelled	93.4	27	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of protein of unknown function from

						porphyromonas2_gingivalis_w83
55	c4cucA	Alignment	not modelled	93.0	12	PDB header: hydrolase Chain: A: PDB Molecule: beta-galactosidase; PDBTitle: unravelling the multiple functions of the architecturally intricate2 streptococcus pneumoniae beta-galactosidase, bgaa.
56	c3isyA	Alignment	not modelled	92.4	21	PDB header: protein binding Chain: A: PDB Molecule: intracellular proteinase inhibitor; PDBTitle: crystal structure of an intracellular proteinase inhibitor (ipi,2 bsu11130) from bacillus subtilis at 2.61 a resolution
57	c5z6pB	Alignment	not modelled	91.9	13	PDB header: hydrolase Chain: B: PDB Molecule: b-agarase; PDBTitle: the crystal structure of an agarase, agwh50c
58	c2h47C	Alignment	not modelled	91.1	18	PDB header: oxidoreductase/electron transport Chain: C: PDB Molecule: azurin; PDBTitle: crystal structure of an electron transfer complex between2 aromatic amine dehydrogenase and azurin from alcaligenes3 faecalis (form 1)
59	c4bq3A	Alignment	not modelled	90.9	16	PDB header: hydrolase Chain: A: PDB Molecule: b-agarase; PDBTitle: structural analysis of an exo-beta-agarase
60	d2ccwa1	Alignment	not modelled	90.2	9	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
61	c3fcsA	Alignment	not modelled	89.8	20	PDB header: cell adhesion/blood clotting Chain: A: PDB Molecule: integrin, alpha 2b; PDBTitle: structure of complete ectodomain of integrin aiibb3
62	c1kv3F	Alignment	not modelled	89.0	13	PDB header: transferase Chain: F: PDB Molecule: protein-glutamine gamma-glutamyltransferase; PDBTitle: human tissue transglutaminase in gdp bound form
63	c3rgbA	Alignment	not modelled	88.3	31	PDB header: oxidoreductase Chain: A: PDB Molecule: methane monooxygenase subunit b2; PDBTitle: crystal structure of particulate methane monooxygenase from2 methylococcus capsulatus (bath)
64	d1v7wa2	Alignment	not modelled	88.1	30	Fold: Supersandwich Superfamily: Galactose mutarotase-like Family: Glycosyltransferase family 36 N-terminal domain
65	c5t9gD	Alignment	not modelled	87.7	13	PDB header: hydrolase Chain: D: PDB Molecule: glycoside hydrolase; PDBTitle: crystal structure of bugh2cwt in complex with galactoisofagomine
66	c2cqtA	Alignment	not modelled	87.1	26	PDB header: transferase Chain: A: PDB Molecule: cellobiose phosphorylase; PDBTitle: crystal structure of cellvibrio gilvus cellobiose phosphorylase2 crystallized from sodium/potassium phosphate
67	c1yewL	Alignment	not modelled	86.9	31	PDB header: oxidoreductase, membrane protein Chain: I: PDB Molecule: particulate methane monooxygenase, b subunit; PDBTitle: crystal structure of particulate methane monooxygenase
68	c3ay2A	Alignment	not modelled	86.4	12	PDB header: antitumor protein, antiviral protein Chain: A: PDB Molecule: lipid modified azurin protein; PDBTitle: crystal structure of neisserial azurin
69	d7mdha1	Alignment	not modelled	85.2	26	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
70	d1cc3a	Alignment	not modelled	84.8	9	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
71	c2aanA	Alignment	not modelled	84.7	18	PDB header: electron transport Chain: A: PDB Molecule: auracyanin a; PDBTitle: auracyanin a: a "blue" copper protein from the green thermophilic2 photosynthetic bacterium, chloroflexus aurantiacus
72	c2a74B	Alignment	not modelled	84.7	14	PDB header: immune system Chain: B: PDB Molecule: complement component c3c; PDBTitle: human complement component c3c
73	c1v7wA	Alignment	not modelled	84.1	24	PDB header: transferase Chain: A: PDB Molecule: chitobiose phosphorylase; PDBTitle: crystal structure of vibrio proteolyticus chitobiose phosphorylase in2 complex with glcnac
74	d5mdha1	Alignment	not modelled	84.0	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
75	d1civa1	Alignment	not modelled	83.6	26	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
76	c1g0dA	Alignment	not modelled	83.4	13	PDB header: transferase Chain: A: PDB Molecule: protein-glutamine gamma-glutamyltransferase; PDBTitle: crystal structure of red sea bream transglutaminase
77	c2e6jA	Alignment	not modelled	83.3	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hydin protein; PDBTitle: solution structure of the c-terminal papd-like domain from2 human hydin protein
78	c2ys4A	Alignment	not modelled	83.2	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hydrocephalus-inducing protein homolog; PDBTitle: solution structure of the n-terminal papd-like domain of2 hydin protein from human
79	c1b8vA	Alignment	not modelled	83.1	28	PDB header: oxidoreductase Chain: A: PDB Molecule: protein (malate dehydrogenase); PDBTitle: malate dehydrogenase from aquaspirillum arcticum
80	c5mdhB	Alignment	not modelled	83.1	24	PDB header: oxidoreductase Chain: B: PDB Molecule: malate dehydrogenase; PDBTitle: crystal structure of ternary complex of porcine cytoplasmic malate2 dehydrogenase alpha-ketomalonnate and tnad at 2.4 angstroms resolution

81	c5t98B	Alignment	not modelled	82.7	19	PDB header: hydrolase Chain: B: PDB Molecule: glycoside hydrolase; PDBTitle: crystal structure of bugh2awt
82	d2co7b1	Alignment	not modelled	82.7	29	Fold: Immunoglobulin-like beta-sandwich Superfamily: PapD-like Family: Pilus chaperone
83	d1y7ta1	Alignment	not modelled	82.6	28	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
84	d4ubpb	Alignment	not modelled	82.4	38	Fold: beta-clip Superfamily: Urease, beta-subunit Family: Urease, beta-subunit
85	c1f13A	Alignment	not modelled	82.3	13	PDB header: coagulation factor Chain: A: PDB Molecule: cellular coagulation factor xiii zymogen; PDBTitle: recombinant human cellular coagulation factor xiii
86	d1ejxb	Alignment	not modelled	82.3	40	Fold: beta-clip Superfamily: Urease, beta-subunit Family: Urease, beta-subunit
87	d1b8pa1	Alignment	not modelled	81.6	28	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
88	c4acqA	Alignment	not modelled	80.5	15	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: alpha-2-macroglobulin; PDBTitle: alpha-2 macroglobulin
89	c7mdhA	Alignment	not modelled	80.4	26	PDB header: chloroplastic malate dehydrogenase Chain: A: PDB Molecule: protein (malate dehydrogenase); PDBTitle: structural basis for light acitvation of a chloroplast enzyme. the2 structure of sorghum nadp-malate dehydrogenase in its oxidized form
90	d1joia	Alignment	not modelled	79.7	13	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
91	d1nwpa	Alignment	not modelled	79.3	12	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
92	c4acqC	Alignment	not modelled	78.9	15	PDB header: hydrolase inhibitor Chain: C: PDB Molecule: alpha-2-macroglobulin; PDBTitle: alpha-2 macroglobulin
93	c4h7pA	Alignment	not modelled	78.9	24	PDB header: oxidoreductase Chain: A: PDB Molecule: malate dehydrogenase; PDBTitle: crystal structure of a putative cytosolic malate dehydrogenase from2 leishmania major friedlin
94	c4fxkB	Alignment	not modelled	78.4	12	PDB header: immune system Chain: B: PDB Molecule: complement c4-a alpha chain; PDBTitle: human complement c4
95	c5nufA	Alignment	not modelled	78.1	19	PDB header: oxidoreductase Chain: A: PDB Molecule: malate dehydrogenase 1, cytoplasmic; PDBTitle: cytosolic malate dehydrogenase 1
96	c5zi3A	Alignment	not modelled	77.9	23	PDB header: oxidoreductase Chain: A: PDB Molecule: malate dehydrogenase; PDBTitle: mdh3 wild type, apo-form
97	c1wziA	Alignment	not modelled	77.4	28	PDB header: oxidoreductase Chain: A: PDB Molecule: malate dehydrogenase; PDBTitle: structural basis for alteration of cofactor specificity of malate2 dehydrogenase from thermus flavus
98	c1hyhA	Alignment	not modelled	77.2	20	PDB header: oxidoreductase (choh(d)-nad+(a)) Chain: A: PDB Molecule: l-2-hydroxyisocaproate dehydrogenase; PDBTitle: crystal structure of l-2-hydroxyisocaproate dehydrogenase from2 lactobacillus confusus at 2.2 angstroms resolution-an example of3 strong asymmetry between subunits
99	d1a5za1	Alignment	not modelled	76.8	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
100	d1llda1	Alignment	not modelled	76.6	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
101	d1e9ya1	Alignment	not modelled	76.5	38	Fold: beta-clip Superfamily: Urease, beta-subunit Family: Urease, beta-subunit
102	d1lazca	Alignment	not modelled	76.4	9	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
103	c3zhnA	Alignment	not modelled	76.3	25	PDB header: toxin Chain: A: PDB Molecule: pa_0080; PDBTitle: crystal structure of the t6ss lipoprotein tssj1 from2 pseudomonas aeruginosa
104	c4uupB	Alignment	not modelled	75.7	26	PDB header: oxidoreductase Chain: B: PDB Molecule: malate dehydrogenase; PDBTitle: reconstructed ancestral trichomonad malate dehydrogenase in2 complex with nadh, so4, and po4
105	c3qgaD	Alignment	not modelled	74.9	30	PDB header: hydrolase Chain: D: PDB Molecule: fusion of urease beta and gamma subunits; PDBTitle: 3.0 a model of iron containing urease urea2b2 from helicobacter2 mustelae
106	c3qbtH	Alignment	not modelled	74.6	19	PDB header: protein transport/hydrolase Chain: H: PDB Molecule: inositol polyphosphate 5-phosphatase ocr1-1; PDBTitle: crystal structure of ocr1 540-678 in complex with rab8a:gppnhp

107	c4uunA	Alignment	not modelled	74.2	24	PDB header: oxidoreductase Chain: A; PDB Molecule: l-lactate dehydrogenase; PDBTitle: trichomonas vaginalis lactate dehydrogenase in complex with nadh
108	c5xyrA	Alignment	not modelled	74.0	17	PDB header: lyase Chain: A; PDB Molecule: chemokine protease c; PDBTitle: crystal structure of a serine protease from streptococcus species
109	c3rfrL	Alignment	not modelled	73.9	18	PDB header: oxidoreductase Chain: I; PDB Molecule: pmob; PDBTitle: crystal structure of particulate methane monooxygenase (pmmo) from 2 methylocystis sp. strain m
110	d1i0za1	Alignment	not modelled	73.8	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
111	d2ldxa1	Alignment	not modelled	73.8	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
112	d1ldma1	Alignment	not modelled	73.7	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
113	c3wsvC	Alignment	not modelled	73.6	18	PDB header: oxidoreductase Chain: C; PDB Molecule: l-lactate dehydrogenase; PDBTitle: crystal structure of minor l-lactate dehydrogenase from enterococcus2 mundtii in the ligands-unbound form
114	c4q3nA	Alignment	not modelled	73.1	19	PDB header: hydrolase Chain: A; PDB Molecule: mgs-m5; PDBTitle: crystal structure of mgs-m5, a lactate dehydrogenase enzyme from a2 medee basin deep-sea metagenome library
115	c8ldhA	Alignment	not modelled	72.8	16	PDB header: oxidoreductase Chain: A; PDB Molecule: m4 apo-lactate dehydrogenase; PDBTitle: refined crystal structure of dogfish m4 apo-lactate dehydrogenase
116	c1e1cA	Alignment	not modelled	72.7	18	PDB header: isomerase Chain: A; PDB Molecule: methylmalonyl-coa mutase alpha chain; PDBTitle: methylmalonyl-coa mutase h244a mutant
117	c1e9zA	Alignment	not modelled	71.9	38	PDB header: hydrolase Chain: A; PDB Molecule: urease subunit alpha; PDBTitle: crystal structure of helicobacter pylori urease
118	c3fn9B	Alignment	not modelled	71.9	8	PDB header: hydrolase Chain: B; PDB Molecule: putative beta-galactosidase; PDBTitle: crystal structure of putative beta-galactosidase from bacteroides2 fragilis
119	c1mldA	Alignment	not modelled	71.9	20	PDB header: oxidoreductase(nad(a)-choh(d)) Chain: A; PDB Molecule: malate dehydrogenase; PDBTitle: refined structure of mitochondrial malate dehydrogenase2 from porcine heart and the consensus structure for 3 dicarboxylic acid oxidoreductases
120	c4djmA	Alignment	not modelled	71.1	21	PDB header: chaperone Chain: A; PDB Molecule: drab; PDBTitle: crystal structure of the e. coli chaperone drab