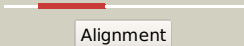
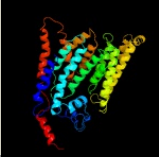
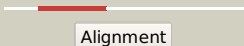

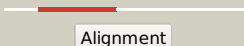




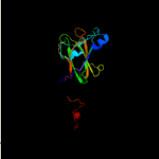


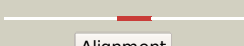




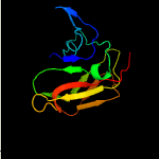






Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0236c_(-)_282649_286851
Date	Tue Jul 23 14:50:29 BST 2019
Unique Job ID	1271df2e1f60eb99

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3wajA_	 Alignment		99.2	16	PDB header: transferase Chain: A: PDB Molecule: transmembrane oligosaccharyl transferase; PDBTitle: crystal structure of the archaeoglobus fulgidus2 oligosaccharyltransferase (o29867_arcfu) complex with zn and sulfate
2	c3rceA_	 Alignment		98.6	14	PDB header: transferase/peptide Chain: A: PDB Molecule: oligosaccharide transferase to n-glycosylate proteins; PDBTitle: bacterial oligosaccharyltransferase pglb
3	c5f15A_	 Alignment		98.5	17	PDB header: transferase Chain: A: PDB Molecule: 4-amino-4-deoxy-l-arabinose (l-ara4n) transferase; PDBTitle: crystal structure of arnt from cupriavidus metallidurans bound to2 undecaprenyl phosphate
4	c6eznF_	 Alignment		97.8	19	PDB header: membrane protein Chain: F: PDB Molecule: dolichyl-diphosphooligosaccharide--protein PDBTitle: cryo-em structure of the yeast oligosaccharyltransferase (ost) complex
5	c5xnrA_	 Alignment		95.6	16	PDB header: lyase Chain: A: PDB Molecule: alyq; PDBTitle: truncated alyq with cbm32 and alginate lyase domains
6	c5zu5A_	 Alignment		94.6	15	PDB header: lyase Chain: A: PDB Molecule: alginate lyase; PDBTitle: crystal structure of a full length alginate lyase with cbm domain
7	c6orfA_	 Alignment		94.3	20	PDB header: hydrolase Chain: A: PDB Molecule: spgh29; PDBTitle: crystal structure of spgh29
8	c4a44A_	 Alignment		94.0	17	PDB header: hydrolase Chain: A: PDB Molecule: alpha-n-acetylglucosaminidase family protein; PDBTitle: cpgh89cbm32-5, from clostridium perfringens, in complex with the tn2 antigen
9	c2rv9A_	 Alignment		93.8	20	PDB header: hydrolase Chain: A: PDB Molecule: glucanase; PDBTitle: solution structure of chitosan-binding module 1 derived from2 chitosanase/glucanase from paenibacillus sp. ik-5
10	c4cuaB_	 Alignment		93.4	18	PDB header: hydrolase Chain: B: PDB Molecule: beta-galactosidase; PDBTitle: unravelling the multiple functions of the architecturally2 intricate streptococcus pneumoniae beta-galactosidase, bgaa
11	c3mo4B_	 Alignment		93.2	15	PDB header: hydrolase Chain: B: PDB Molecule: alpha-1,3/4-fucosidase; PDBTitle: the crystal structure of an alpha-(1-3,4)-fucosidase from2 bifidobacterium longum subsp. infantis atcc 15697

12	c2j1aA_	Alignment		92.9	13	PDB header: hydrolase Chain: A: PDB Molecule: hyaluronidase; PDBTitle: structure of cbm32 from clostridium perfringens beta-n-2 acetylhexosaminidase gh84c in complex with galactose
13	c5k9hA_	Alignment		92.7	9	PDB header: hydrolase Chain: A: PDB Molecule: 0940_gh29; PDBTitle: crystal structure of a glycoside hydrolase 29 family member from an2 unknown rumen bacterium
14	d1w8oa2	Alignment		92.3	23	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: Galactose-binding domain
15	c2j1sB_	Alignment		92.3	13	PDB header: carbohydrate-binding protein Chain: B: PDB Molecule: fucolectin-related protein; PDBTitle: structure of a streptococcus pneumoniae fucose binding2 module in complex with fucose
16	c3eypB_	Alignment		92.2	15	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative alpha-l-fucosidase; PDBTitle: crystal structure of putative alpha-l-fucosidase from bacteroides2 thetaiotaomicron
17	c2jdaA_	Alignment		91.8	16	PDB header: sugar-binding protein Chain: A: PDB Molecule: yecbm32; PDBTitle: structure of a pectin binding carbohydrate binding module2 determined in a monoclinic crystal form.
18	d1tvga_	Alignment		91.6	19	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: APC10-like
19	c2j22A_	Alignment		91.6	12	PDB header: carbohydrate-binding protein Chain: A: PDB Molecule: fucolectin-related protein; PDBTitle: structure of a streptococcus pneumoniae fucose binding2 module, spx-3
20	c5zu6A_	Alignment		91.4	15	PDB header: lyase Chain: A: PDB Molecule: cbm32 domain; PDBTitle: a cbm32 derived from alginate lyase b (alyb-ou02)
21	c4txwA_	Alignment	not modelled	90.9	17	PDB header: carbohydrate-binding module Chain: A: PDB Molecule: hyaluronoglucosaminidase; PDBTitle: crystal structure of cbm32-4 from the clostridium perfringens nagh
22	c3hnmD_	Alignment	not modelled	90.6	11	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: putative chitobiase; PDBTitle: crystal structure of protein bt_411 (putative chitobiase, fragment2 298-461) from bacteroides thetaiotaomicron, northeast structural3 genomics consortium target btr319d
23	c2yc2A_	Alignment	not modelled	89.8	13	PDB header: transport protein Chain: A: PDB Molecule: intraflagellar transport protein 25; PDBTitle: intraflagellar transport complex 25-27 from chlamydomonas
24	c3cqoC_	Alignment	not modelled	89.7	19	PDB header: sugar binding protein Chain: C: PDB Molecule: fbp32; PDBTitle: crystal structure of a f-lectin (fucolectin) from morone saxatilis2 (striped bass) serum
25	c2vz1A_	Alignment	not modelled	88.2	9	PDB header: oxidoreductase Chain: A: PDB Molecule: galactose oxidase; PDBTitle: premat-galactose oxidase
26	c3le0A_	Alignment	not modelled	88.2	14	PDB header: blood clotting Chain: A: PDB Molecule: platelet aggregation factor sm-hpaf; PDBTitle: lectin domain of lectinolysin complexed with glycerol
27	c6p2rB_	Alignment	not modelled	86.9	10	PDB header: transferase Chain: B: PDB Molecule: dolichyl-phosphate-mannose--protein mannosyltransferase 2; PDBTitle: structure of s. cerevisiae protein o-mannosyltransferase pmt1-pmt22 complex bound to the sugar donor
28	c2y9iB_	Alignment	not modelled	86.5	23	PDB header: sugar binding protein Chain: B: PDB Molecule: carbohydrate binding family 6; PDBTitle: cbm62 in complex with xyloglucan oligosaccharide

29	c5msxA	Alignment	not modelled	85.6	9	PDB header: hydrolase Chain: A: PDB Molecule: putative endo-1,4-beta-xylanase; PDBTitle: glycoside hydrolase bt_3662
30	c4a42B	Alignment	not modelled	85.1	12	PDB header: hydrolase Chain: B: PDB Molecule: alpha-n-acetylglucosaminidase family protein; PDBTitle: cpgh89cbm32-6 produced by clostridium perfringens
31	c6p25A	Alignment	not modelled	83.5	14	PDB header: transferase Chain: A: PDB Molecule: dolichyl-phosphate-mannose--protein mannosyltransferase 1; PDBTitle: structure of s. cerevisiae protein o-mannosyltransferase pmt1-pmt22 complex bound to the sugar donor and a peptide acceptor
32	c4a6oB	Alignment	not modelled	82.5	14	PDB header: hydrolase Chain: B: PDB Molecule: alpha-n-acetylglucosaminidase family protein; PDBTitle: cpgh89cbm32-4, produced by clostridium perfringens, in2 complex with glcnac-alpha-1,4-galactose
33	c4lqrA	Alignment	not modelled	80.8	19	PDB header: sugar binding protein Chain: A: PDB Molecule: glycosyl hydrolase, family 31/fibronectin type iii domain PDBTitle: structure of cbm32-3 from a family 31 glycoside hydrolase from2 clostridium perfringens
34	c2orxA	Alignment	not modelled	80.6	13	PDB header: signaling protein, membrane protein Chain: A: PDB Molecule: neuropilin-1; PDBTitle: structural basis for ligand binding and heparin mediated activation of2 neuropilin
35	c2v72A	Alignment	not modelled	80.3	19	PDB header: sugar-binding protein Chain: A: PDB Molecule: exo-alpha-sialidase; PDBTitle: the structure of the family 32 cbm from c. perfringens nanj2 in complex with galactose
36	c5h9xA	Alignment	not modelled	79.2	10	PDB header: hydrolase Chain: A: PDB Molecule: beta-1,3-glucanase; PDBTitle: crystal structure of gh family 64 laminaripentaose-producing beta-1,3-2 glucanase from paenibacillus barengoltzii
37	c2kd7A	Alignment	not modelled	75.3	17	PDB header: cell adhesion Chain: A: PDB Molecule: putative chitobiase; PDBTitle: solution nmr structure of f5/8 type c-terminal domain of a2 putative chitobiase from bacteroides thetaiotaomicron.3 northeast structural genomics consortium target btr324b
38	c2ls6A	Alignment	not modelled	73.1	14	PDB header: hydrolase Chain: A: PDB Molecule: hyaluronoglucosaminidase; PDBTitle: solution nmr structure of a non-canonical galactose-binding cbm32 from2 clostridium perfringens
39	d1gqpa	Alignment	not modelled	71.6	16	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: APC10-like
40	d1jhja	Alignment	not modelled	70.9	20	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: APC10-like
41	d1k3ia2	Alignment	not modelled	70.9	11	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: Galactose-binding domain
42	c1gqpB	Alignment	not modelled	69.5	16	PDB header: cell cycle Chain: B: PDB Molecule: doc1/apc10; PDBTitle: apc10/doc1 subunit of s. cerevisiae
43	c2qqjA	Alignment	not modelled	68.8	16	PDB header: signaling protein Chain: A: PDB Molecule: neuropilin-2; PDBTitle: crystal structure of the b1b2 domains from human neuropilin-2
44	c2berA	Alignment	not modelled	66.3	22	PDB header: hydrolase Chain: A: PDB Molecule: bacterial sialidase; PDBTitle: y370g active site mutant of the sialidase from2 micromonospora viridifaciens in complex with beta-neu5ac3 (sialic acid).
45	c4pqqA	Alignment	not modelled	64.5	16	PDB header: protein binding Chain: A: PDB Molecule: muskelin; PDBTitle: the crystal structure of discoidin domain from muskelin
46	c2k9yB	Alignment	not modelled	62.9	39	PDB header: transferase Chain: B: PDB Molecule: ephrin type-a receptor 2; PDBTitle: epha2 dimeric structure in the lipidic bicelle at ph 5.0
47	c2k9yA	Alignment	not modelled	62.7	39	PDB header: transferase Chain: A: PDB Molecule: ephrin type-a receptor 2; PDBTitle: epha2 dimeric structure in the lipidic bicelle at ph 5.0
48	d1k12a	Alignment	not modelled	57.3	19	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: Fucose binding lectin
49	c2w1sB	Alignment	not modelled	56.1	17	PDB header: hydrolase Chain: B: PDB Molecule: hyaluronoglucosaminidase; PDBTitle: unique ligand binding specificity of a family 322 carbohydrate-binding module from the mu toxin produced by3 clostridium perfringens
50	c3mogA	Alignment	not modelled	54.4	24	PDB header: oxidoreductase Chain: A: PDB Molecule: probable 3-hydroxybutyryl-coa dehydrogenase; PDBTitle: crystal structure of 3-hydroxybutyryl-coa dehydrogenase from2 escherichia coli k12 substr. mg1655
51	c3ctvA	Alignment	not modelled	45.9	28	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-hydroxyacyl-coa dehydrogenase; PDBTitle: crystal structure of central domain of 3-hydroxyacyl-coa dehydrogenase2 from archaeoglobus fulgidus
52	c2wtbA	Alignment	not modelled	42.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: fatty acid multifunctional protein (atmfp2); PDBTitle: arabidopsis thaliana multifunctional protein, mfp2
						PDB header: oxidoreductase

53	c1zciA_	Alignment	not modelled	40.1	15	Chain: A: PDB Molecule: peroxisomal bifunctional enzyme; PDBTitle: crystal structure of 3-hydroxyacyl-coa dehydrogenase
54	c2x58B_	Alignment	not modelled	38.4	15	PDB header: oxidoreductase Chain: B: PDB Molecule: peroxisomal bifunctional enzyme; PDBTitle: the crystal structure of mfe1 liganded with coa
55	c1zeja_	Alignment	not modelled	35.1	17	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-hydroxyacyl-coa dehydrogenase; PDBTitle: crystal structure of the 3-hydroxyacyl-coa dehydrogenase (hbd-9.2 af2017) from archaeoglobus fulgidus dsm 4304 at 2.00 a resolution
56	d1wdka1	Alignment	not modelled	35.0	12	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: HCDH C-domain-like
57	c2d3tB_	Alignment	not modelled	32.7	13	PDB header: lyase, oxidoreductase/transferase Chain: B: PDB Molecule: fatty oxidation complex alpha subunit; PDBTitle: fatty acid beta-oxidation multienzyme complex from2 pseudomonas fragi, form v
58	c3jsbA_	Alignment	not modelled	31.6	11	PDB header: rna binding protein Chain: A: PDB Molecule: rna-directed rna polymerase; PDBTitle: crystal structure of the n-terminal domain of the lymphocytic2 choriomeningitis virus l protein
59	c4miwA_	Alignment	not modelled	30.6	21	PDB header: viral protein, transferase Chain: A: PDB Molecule: rna-directed rna polymerase l; PDBTitle: high-resolution structure of the n-terminal endonuclease domain of the2 lassa virus l polymerase
60	c5lnk2_	Alignment	not modelled	29.9	38	PDB header: oxidoreductase Chain: 2: PDB Molecule: mitochondrial complex i, 24 kda subunit; PDBTitle: entire ovine respiratory complex i
61	c4oyuB_	Alignment	not modelled	29.1	14	PDB header: protein binding Chain: B: PDB Molecule: muskelin; PDBTitle: crystal structure of the n-terminal domains of muskelin
62	c5awwG_	Alignment	not modelled	28.3	24	PDB header: protein transport/immune system Chain: G: PDB Molecule: putative preprotein translocase, secg subunit; PDBTitle: precise resting state of thermus thermophilus secyeg
63	c4b3hA_	Alignment	not modelled	28.2	10	PDB header: oxidoreductase/transferase Chain: A: PDB Molecule: fatty acid beta-oxidation complex alpha-chain fadb; PDBTitle: crystal structure of mycobacterium tuberculosis fatty acid2 beta-oxidation complex
64	c5zqzC_	Alignment	not modelled	28.1	13	PDB header: lyase,hydrolase/transferase Chain: C: PDB Molecule: trifunctional enzyme subunit alpha, mitochondrial; PDBTitle: structure of human mitochondrial trifunctional protein, tetramer
65	c4i1tA_	Alignment	not modelled	27.5	50	PDB header: viral protein Chain: A: PDB Molecule: rna-directed rna polymerase l; PDBTitle: crystal structure of the cap-snatching endonuclease from pichinde2 virus
66	c5t2tB_	Alignment	not modelled	26.9	10	PDB header: transferase Chain: B: PDB Molecule: rna-directed rna polymerase l; PDBTitle: crystal structure of lymphocytic choriomeningitis mammarenavirus2 endonuclease bound to compound l742001
67	c4f4mA_	Alignment	not modelled	25.3	10	PDB header: hydrolase regulator Chain: A: PDB Molecule: papain peptidoglycan amidase effector tse1; PDBTitle: structure of the type vi peptidoglycan amidase effector tse1 (c30a)2 from pseudomonas aeruginosa
68	c4f0wA_	Alignment	not modelled	24.8	10	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of type effector tse1 c30a mutant from pseudomonas2 aeruginosa
69	d2fug21	Alignment	not modelled	24.1	21	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: NQO2-like
70	c2xqxB_	Alignment	not modelled	23.2	13	PDB header: sugar binding protein Chain: B: PDB Molecule: endo-beta-n-acetylglucosaminidase d; PDBTitle: structure of the family 32 carbohydrate-binding module from2 streptococcus pneumoniae endod
71	d2v4jc1	Alignment	not modelled	23.0	35	Fold: DsrC, the gamma subunit of dissimilatory sulfite reductase Superfamily: DsrC, the gamma subunit of dissimilatory sulfite reductase Family: DsrC, the gamma subunit of dissimilatory sulfite reductase
72	c6hrdD_	Alignment	not modelled	22.9	23	PDB header: oxidoreductase Chain: D: PDB Molecule: 3-hydroxybutyryl-coa dehydrogenase; PDBTitle: crystal structure of m. tuberculosis fadb2 (rv0468)
73	c6iunB_	Alignment	not modelled	22.7	23	PDB header: oxidoreductase Chain: B: PDB Molecule: enoyl-coa hydratase/delta(3)-cis-delta(2)-trans-enoyl-coa PDBTitle: crystal structure of enoyl-coa hydratase (ech) from ralstonia eutropha2 h16 in complex with nad
74	c1yx3A_	Alignment	not modelled	22.4	35	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein dsrC; PDBTitle: nmr structure of allochromatium vinosum dsrC: northeast2 structural genomics consortium target op4
75	c2a5wC_	Alignment	not modelled	22.0	35	PDB header: oxidoreductase Chain: C: PDB Molecule: sulfite reductase, desulfoviridin-type subunit gamma PDBTitle: crystal structure of the oxidized gamma-subunit of the dissimilatory2 sulfite reductase (dsrC) from archaeoglobus fulgidus
76	c1m75B_	Alignment	not modelled	21.3	28	PDB header: oxidoreductase Chain: B: PDB Molecule: 3-hydroxyacyl-coa dehydrogenase; PDBTitle: crystal structure of the n208s mutant of l-3-hydroxyacyl-coa2 dehydrogenase in complex with nad and acetoacetyl-coa
77	c5n6mA_	Alignment	not modelled	19.4	13	PDB header: membrane protein Chain: A: PDB Molecule: apolipoprotein n-acyltransferase; PDBTitle: structure of the membrane integral lipoprotein n-acyltransferase lnt2 from p. aeruginosa

78	d1wdka2	Alignment	not modelled	18.9	41	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: HCDH C-domain-like
79	c3j6vl	Alignment	not modelled	18.9	54	PDB header: ribosome Chain: I: PDB Molecule: 28s ribosomal protein s9, mitochondrial; PDBTitle: cryo-em structure of the small subunit of the mammalian mitochondrial2 ribosome
80	d1ji8a	Alignment	not modelled	18.2	35	Fold: DsrC, the gamma subunit of dissimilatory sulfite reductase Superfamily: DsrC, the gamma subunit of dissimilatory sulfite reductase Family: DsrC, the gamma subunit of dissimilatory sulfite reductase
81	d3hdha1	Alignment	not modelled	17.8	31	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: HCDH C-domain-like
82	d1m1ha2	Alignment	not modelled	17.6	20	Fold: Ferredoxin-like Superfamily: N-utilization substance G protein NusG, N-terminal domain Family: N-utilization substance G protein NusG, N-terminal domain
83	c3waiA	Alignment	not modelled	17.2	22	PDB header: transferase, transport protein Chain: A: PDB Molecule: maltose-binding periplasmic protein, transmembrane PDBTitle: crystal structure of the c-terminal globular domain of2 oligosaccharyltransferase (afaglb-l, o29867_arcfu) from archaeoglobus3 fulgidus as a mbp fusion
84	c4hxc	Alignment	not modelled	17.0	22	PDB header: rna/rna binding protein/hydrolase Chain: C: PDB Molecule: histone rna hairpin-binding protein; PDBTitle: structure of mrna stem-loop, human stem-loop binding protein and2 3'hexo ternary complex
85	c6ez3C	Alignment	not modelled	16.1	16	PDB header: rna binding protein Chain: C: PDB Molecule: cyclo(l-leucyl-l-leucyl) synthase; PDBTitle: structure of cdps from staphylococcus haemolyticus
86	c5lc5E	Alignment	not modelled	15.9	38	PDB header: oxidoreductase Chain: E: PDB Molecule: snadh dehydrogenase [ubiquinone] flavoprotein 2, PDBTitle: structure of mammalian respiratory complex i, class2
87	c6btmF	Alignment	not modelled	15.8	13	PDB header: membrane protein Chain: F: PDB Molecule: alternative complex iii subunit f; PDBTitle: structure of alternative complex iii from flavobacterium johnsoniae2 (wild type)
88	c3rqsB	Alignment	not modelled	15.0	31	PDB header: oxidoreductase Chain: B: PDB Molecule: hydroxyacyl-coenzyme a dehydrogenase, mitochondrial; PDBTitle: crystal structure of human l-3- hydroxyacyl-coa dehydrogenase2 (ec1.1.1.35) from mitochondria at the resolution 2.0 a, northeast3 structural genomics consortium target hr487, mitochondrial protein4 partnership
89	c1cygA	Alignment	not modelled	14.9	12	PDB header: glycosyltransferase Chain: A: PDB Molecule: cyclodextrin glucanotransferase; PDBTitle: cyclodextrin glucanotransferase (e.c.2.4.1.19) (cgtase)
90	d1f0ya1	Alignment	not modelled	14.7	31	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: HCDH C-domain-like
91	c1oy8A	Alignment	not modelled	14.5	17	PDB header: membrane protein Chain: A: PDB Molecule: acriflavine resistance protein b; PDBTitle: structural basis of multiple drug binding capacity of the acrb2 multidrug efflux pump
92	c3k6jA	Alignment	not modelled	13.9	13	PDB header: oxidoreductase Chain: A: PDB Molecule: protein f01g10.3, confirmed by transcript evidence; PDBTitle: crystal structure of the dehydrogenase part of multifunctional enzyme 12 from c.elegans
93	c5mv0D	Alignment	not modelled	13.7	21	PDB header: viral protein Chain: D: PDB Molecule: l protein; PDBTitle: structure of an n-terminal domain of a reptarenavirus l protein
94	d1iwga8	Alignment	not modelled	13.6	20	Fold: Multidrug efflux transporter AcrB transmembrane domain Superfamily: Multidrug efflux transporter AcrB transmembrane domain Family: Multidrug efflux transporter AcrB transmembrane domain
95	c5nz8A	Alignment	not modelled	13.3	26	PDB header: hydrolase Chain: A: PDB Molecule: cellodextrin phosphorylase; PDBTitle: clostridium thermocellum cellodextrin phosphorylase with cellotetraose2 and phosphate bound
96	c1i8qA	Alignment	not modelled	13.0	20	PDB header: lyase Chain: A: PDB Molecule: hyaluronate lyase; PDBTitle: crystal structure of streptococcus agalactiae hyaluronate lyase2 complexed with enzyme product, unsaturated disaccharide hyaluronan
97	c4kueA	Alignment	not modelled	13.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-hydroxybutyryl-coa dehydrogenase; PDBTitle: crystal structure of 3-hydroxybutyryl-coa dehydrogenase from2 clostridium butyricum
98	c2qtsA	Alignment	not modelled	12.7	22	PDB header: membrane protein Chain: A: PDB Molecule: acid-sensing ion channel; PDBTitle: structure of an acid-sensing ion channel 1 at 1.9 a resolution and low2 ph
99	c3wbzD	Alignment	not modelled	12.3	14	PDB header: transferase Chain: D: PDB Molecule: likely histidyl trna-specific guanylyltransferase; PDBTitle: crystal structure of c. albicans trna(his) guanylyltransferase (thg1)2 with atp