

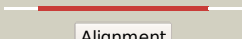

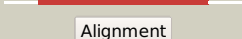



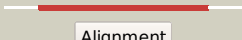

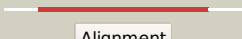













Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2251 (-) _2525413_2527002
Date	Mon Aug 5 13:25:38 BST 2019
Unique Job ID	3e9d93c3a89fbfc6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4bc9C_	 Alignment		100.0	30	PDB header: transferase Chain: C; PDB Molecule: alkyldihydroxyacetonephosphate synthase, peroxisomal; PDBTitle: mammalian alkyldihydroxyacetonephosphate synthase: wild-type, adduct2 with cyanoethyl
2	c2uuvC_	 Alignment		100.0	32	PDB header: transferase Chain: C; PDB Molecule: alkyldihydroxyacetonephosphate synthase; PDBTitle: alkyldihydroxyacetonephosphate synthase in p1
3	c3pm9A_	 Alignment		100.0	20	PDB header: oxidoreductase Chain: A; PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative dehydrogenase (rpa1076) from2 rhodopseudomonas palustris cga009 at 2.57 a resolution
4	c1ahuB_	 Alignment		100.0	15	PDB header: flavoenzyme Chain: B; PDB Molecule: vanillyl-alcohol oxidase; PDBTitle: structure of the octameric flavoenzyme vanillyl-alcohol2 oxidase in complex with p-cresol
5	c5fxpA_	 Alignment		100.0	16	PDB header: oxidoreductase Chain: A; PDB Molecule: eugenol oxidase; PDBTitle: crystal structure of eugenol oxidase in complex with2 vanillin
6	c1f0xA_	 Alignment		100.0	18	PDB header: oxidoreductase Chain: A; PDB Molecule: d-lactate dehydrogenase; PDBTitle: crystal structure of d-lactate dehydrogenase, a peripheral membrane2 respiratory enzyme.
7	c1wveB_	 Alignment		100.0	17	PDB header: oxidoreductase Chain: B; PDB Molecule: 4-cresol dehydrogenase [hydroxylating] PDBTitle: p-cresol methylhydroxylase: alteration of the structure of2 the flavoprotein subunit upon its binding to the3 cytochrome subunit
8	c3bw7A_	 Alignment		100.0	14	PDB header: oxidoreductase Chain: A; PDB Molecule: cytokinin dehydrogenase 1; PDBTitle: maize cytokinin oxidase/dehydrogenase complexed with the allenic2 cytokinin analog ha-1
9	c4oaalB_	 Alignment		100.0	17	PDB header: oxidoreductase Chain: B; PDB Molecule: cytokinin dehydrogenase 4; PDBTitle: crystal structure of maize cytokinin oxidase/dehydrogenase 4 (zmcko4)2 in complex with phenylurea inhibitor cppu in alternative spacegroup
10	c4ml8C_	 Alignment		100.0	15	PDB header: oxidoreductase Chain: C; PDB Molecule: cytokinin oxidase 2; PDBTitle: structure of maize cytokinin oxidase/dehydrogenase 2 (zmcko2)
11	c6f73B_	 Alignment		100.0	16	PDB header: flavoprotein Chain: B; PDB Molecule: mtvao615; PDBTitle: crystal structure of vao-type flavoprotein mtvao615 at ph 5.0 from2 myceliophthora thermophila c1

12	c3vteA_	Alignment		100.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: tetrahydrocannabinolic acid synthase; PDBTitle: crystal structure of tetrahydrocannabinolic acid synthase from2 cannabis sativa
13	c6f74B_	Alignment		100.0	11	PDB header: flavoprotein Chain: B: PDB Molecule: alcohol oxidase; PDBTitle: crystal structure of vao-type flavoprotein mtvao713 from2 myceliophthora thermophila c1
14	c3w8wA_	Alignment		100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: putative fad-dependent oxygenase encm; PDBTitle: the crystal structure of encm
15	c2exrA_	Alignment		100.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: cytokinin dehydrogenase 7; PDBTitle: x-ray structure of cytokinin oxidase/dehydrogenase (ckx) from2 arabidopsis thaliana at5g21482
16	c2bvfa_	Alignment		100.0	16	PDB header: oxidase Chain: A: PDB Molecule: 6-hydroxy-d-nicotine oxidase; PDBTitle: crystal structure of 6-hydroxy-d-nicotine oxidase from2 arthrobacter nicotinovorans. crystal form 3 (p1)
17	c6c80B_	Alignment		100.0	17	PDB header: immune system Chain: B: PDB Molecule: cytokinin oxidase luckx1.1; PDBTitle: crystal structure of a flax cytokinin oxidase
18	c3rjaA_	Alignment		100.0	12	PDB header: oxidoreductase Chain: A: PDB Molecule: carbohydrate oxidase; PDBTitle: crystal structure of carbohydrate oxidase from microdochium nivale in2 complex with substrate analogue
19	c5l6fa_	Alignment		100.0	13	PDB header: oxidoreductase Chain: A: PDB Molecule: fad linked oxidase-like protein; PDBTitle: xylooligosaccharide oxidase from myceliophthora thermophila c1 in2 complex with xylobiose
20	c3tsja_	Alignment		100.0	12	PDB header: allergen, oxidoreductase Chain: A: PDB Molecule: pollen allergen phl p 4; PDBTitle: crystal structure of phl p 4, a grass pollen allergen with glucose2 dehydrogenase activity
21	c4ud8B_	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: B: PDB Molecule: fad-binding and bbe domain-containing protein; PDBTitle: atbbe15
22	c6eo5A_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: ppbbe-like 1 d396n; PDBTitle: physcomitrella patens bbe-like 1 variant d396n
23	c3fwaA_	Alignment	not modelled	100.0	14	PDB header: flavoprotein Chain: A: PDB Molecule: reticuline oxidase; PDBTitle: structure of berberine bridge enzyme, c166a variant in complex with2 (s)-reticuline
24	c3d2ha_	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: berberine bridge-forming enzyme; PDBTitle: structure of berberine bridge enzyme from eschscholzia californica,2 monoclinic crystal form
25	c1zr6A_	Alignment	not modelled	100.0	11	PDB header: oxidoreductase Chain: A: PDB Molecule: glucooligosaccharide oxidase; PDBTitle: the crystal structure of an acremonium strictum glucooligosaccharide2 oxidase reveals a novel flavinylation
26	c4fdoA_	Alignment	not modelled	100.0	13	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: A: PDB Molecule: oxidoreductase dpre1; PDBTitle: mycobacterium tuberculosis dpre1 in complex with ct319
27	c3popD_	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: D: PDB Molecule: gilr oxidase; PDBTitle: the crystal structure of gilr, an oxidoreductase that catalyzes the2 terminal step of gilvocarcin biosynthesis
28	c5d79B_	Alignment	not modelled	100.0	13	PDB header: oxidoreductase Chain: B: PDB Molecule: berberine bridge enzyme-like protein; PDBTitle: structure of bbe-like #28 from arabidopsis thaliana
						PDB header: oxidoreductase

29	c2ipiD_	Alignment	not modelled	100.0	16	Chain: D: PDB Molecule: aclacinomycin oxidoreductase (aknox); PDBTitle: crystal structure of aclacinomycin oxidoreductase
30	c5i1wD_	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: D: PDB Molecule: crmk; PDBTitle: crystal structure of crmk, a flavoenzyme involved in the shunt product2 recycling mechanism in caerulomycin biosynthesis
31	c2y3rC_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: C: PDB Molecule: taml; PDBTitle: structure of the tirandamycin-bound fad-dependent tirandamycin oxidase2 taml in p21 space group
32	c2wdwB_	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: B: PDB Molecule: putative hexose oxidase; PDBTitle: the native crystal structure of the primary hexose oxidase (2 dbv29) in antibiotic a40926 biosynthesis
33	c2vfvA_	Alignment	not modelled	100.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: xylitol oxidase; PDBTitle: alditol oxidase from streptomyces coelicolor a3(2): complex2 with sulphite
34	c1i19B_	Alignment	not modelled	100.0	11	PDB header: oxidoreductase Chain: B: PDB Molecule: cholesterol oxidase; PDBTitle: crystal structure of cholesterol oxidase from b.sterolicum
35	c3js8A_	Alignment	not modelled	100.0	13	PDB header: oxidoreductase Chain: A: PDB Molecule: cholesterol oxidase; PDBTitle: solvent-stable cholesterol oxidase
36	d1f0xa2	Alignment	not modelled	100.0	26	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: FAD-linked oxidases, N-terminal domain
37	d1e8ga2	Alignment	not modelled	100.0	18	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: FAD-linked oxidases, N-terminal domain
38	d1wvfa2	Alignment	not modelled	100.0	17	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: FAD-linked oxidases, N-terminal domain
39	d1w1oa2	Alignment	not modelled	100.0	19	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: FAD-linked oxidases, N-terminal domain
40	d2i0ka2	Alignment	not modelled	100.0	16	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: FAD-linked oxidases, N-terminal domain
41	d1hska1	Alignment	not modelled	100.0	17	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase (MurB), N-terminal domain
42	d1luxya1	Alignment	not modelled	100.0	11	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase (MurB), N-terminal domain
43	d1e8ga1	Alignment	not modelled	100.0	15	Fold: Ferredoxin-like Superfamily: FAD-linked oxidases, C-terminal domain Family: Vanillyl-alcohol oxidase-like
44	c4pytA_	Alignment	not modelled	100.0	13	PDB header: oxidoreductase Chain: A: PDB Molecule: udp-n-acetylenolpyruvoylglucosamine reductase; PDBTitle: crystal structure of a murb family ep-udp-n-acetylglucosamine2 reductase
45	c1hska_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: udp-n-acetylenolpyruvoylglucosamine reductase; PDBTitle: crystal structure of s. aureus murb
46	c2yvsa_	Alignment	not modelled	100.0	22	PDB header: oxidoreductase Chain: A: PDB Molecule: glycolate oxidase subunit glce; PDBTitle: crystal structure of glycolate oxidase subunit glce from thermus2 thermophilus hb8
47	d1wvfa1	Alignment	not modelled	100.0	15	Fold: Ferredoxin-like Superfamily: FAD-linked oxidases, C-terminal domain Family: Vanillyl-alcohol oxidase-like
48	c4jayC_	Alignment	not modelled	100.0	22	PDB header: oxidoreductase Chain: C: PDB Molecule: udp-n-acetylenolpyruvoylglucosamine reductase; PDBTitle: crystal structure of p. aeruginosa murb in complex with nadp+
49	d1f0xa1	Alignment	not modelled	99.9	13	Fold: Ferredoxin-like Superfamily: FAD-linked oxidases, C-terminal domain Family: D-lactate dehydrogenase
50	c1mbbA_	Alignment	not modelled	99.9	14	PDB header: oxidoreductase Chain: A: PDB Molecule: uridine diphospho-n-acetylenolpyruvylglucosamine PDBTitle: oxidoreductase
51	c3i99A_	Alignment	not modelled	99.9	13	PDB header: oxidoreductase Chain: A: PDB Molecule: udp-n-acetylenolpyruvoylglucosamine reductase; PDBTitle: the crystal structure of the udp-n-acetylenolpyruvoylglucosamine2 reductase from the vibrio cholerae o1 biovar tor
52	c5jzxB_	Alignment	not modelled	99.9	17	PDB header: oxidoreductase Chain: B: PDB Molecule: udp-n-acetylenolpyruvoylglucosamine reductase; PDBTitle: crystal structure of udp-n-acetylenolpyruvoylglucosamine reductase2 (murb) from mycobacterium tuberculosis
53	c2gquA_	Alignment	not modelled	99.8	16	PDB header: oxidoreductase Chain: A: PDB Molecule: udp-n-acetylenolpyruvylglucosamine reductase; PDBTitle: crystal structure of udp-n-acetylenolpyruvylglucosamine2 reductase (murb) from thermus caldophilus
						Fold: Ferredoxin-like

54	d1w1oa1	Alignment	not modelled	99.1	15	Superfamily: FAD-linked oxidases, C-terminal domain Family: Cytokinin dehydrogenase 1
55	c5y6qB	Alignment	not modelled	97.8	18	PDB header: oxidoreductase Chain: B: PDB Molecule: aldehyde oxidase medium subunit; PDBTitle: crystal structure of an aldehyde oxidase from methylobacillus sp.2 ky4400
56	c5g5hB	Alignment	not modelled	97.6	20	PDB header: oxidoreductase Chain: B: PDB Molecule: putative xanthine dehydrogenase yags fad-binding subunit; PDBTitle: escherichia coli periplasmic aldehyde oxidase r440h mutant
57	d1ffvc2	Alignment	not modelled	97.5	21	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like
58	c1n62C	Alignment	not modelled	97.4	22	PDB header: oxidoreductase Chain: C: PDB Molecule: carbon monoxide dehydrogenase medium chain; PDBTitle: crystal structure of the mo,cu-co dehydrogenase (codh), n-2 butylisocyanide-bound state
59	c1ffuF	Alignment	not modelled	97.4	22	PDB header: hydrolase Chain: F: PDB Molecule: cutm, flavoprotein of carbon monoxide PDBTitle: carbon monoxide dehydrogenase from hydrogenophaga2 pseudoflava which lacks the mo-pyranopterin moiety of the3 molybdenum cofactor
60	c1t3qF	Alignment	not modelled	97.3	21	PDB header: oxidoreductase Chain: F: PDB Molecule: quinoline 2-oxidoreductase medium subunit; PDBTitle: crystal structure of quinoline 2-oxidoreductase from pseudomonas2 putida 86
61	d1n62c2	Alignment	not modelled	97.2	22	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like
62	c3hrdC	Alignment	not modelled	97.1	26	PDB header: oxidoreductase Chain: C: PDB Molecule: nicotinate dehydrogenase fad-subunit; PDBTitle: crystal structure of nicotinate dehydrogenase
63	d1t3qc2	Alignment	not modelled	97.1	22	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like
64	c4zohB	Alignment	not modelled	97.0	26	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase fad-binding subunit; PDBTitle: crystal structure of glyceraldehyde oxidoreductase
65	d1v97a6	Alignment	not modelled	97.0	17	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like
66	d3b9jb2	Alignment	not modelled	96.9	18	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like
67	c1rm6E	Alignment	not modelled	96.8	24	PDB header: oxidoreductase Chain: E: PDB Molecule: 4-hydroxybenzoyl-coa reductase beta subunit; PDBTitle: structure of 4-hydroxybenzoyl-coa reductase from thauera2 aromatica
68	c2w3rG	Alignment	not modelled	96.7	27	PDB header: oxidoreductase Chain: G: PDB Molecule: xanthine dehydrogenase; PDBTitle: crystal structure of xanthine dehydrogenase (desulfo form)2 from rhodobacter capsulatus in complex with hypoxanthine
69	c3etrM	Alignment	not modelled	96.7	14	PDB header: oxidoreductase Chain: M: PDB Molecule: xanthine dehydrogenase/oxidase; PDBTitle: crystal structure of xanthine oxidase in complex with lumazine
70	c3b9jj	Alignment	not modelled	96.6	14	PDB header: oxidoreductase Chain: J: PDB Molecule: xanthine oxidase; PDBTitle: structure of xanthine oxidase with 2-hydroxy-6-methylpurine
71	d1jroa4	Alignment	not modelled	96.4	26	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like
72	d1rm6b2	Alignment	not modelled	96.4	24	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like
73	c1wygA	Alignment	not modelled	96.3	19	PDB header: oxidoreductase Chain: A: PDB Molecule: xanthine dehydrogenase/oxidase; PDBTitle: crystal structure of a rat xanthine dehydrogenase triple mutant2 (c535a, c992r and c1324s)
74	c4uhxA	Alignment	not modelled	94.9	23	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde oxidase; PDBTitle: human aldehyde oxidase in complex with phthalazine and thioridazine
75	c3zyvA	Alignment	not modelled	94.4	16	PDB header: oxidoreductase Chain: A: PDB Molecule: aox3; PDBTitle: crystal structure of the mouse liver aldehyde oxidase 3 (maox3)
76	d2i0ka1	Alignment	not modelled	82.3	9	Fold: Ferredoxin-like Superfamily: FAD-linked oxidases, C-terminal domain Family: Cholesterol oxidase
77	c6je8A	Alignment	not modelled	79.7	29	PDB header: hydrolase Chain: A: PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: crystal structure of a beta-n-acetylhexosaminidase
78	d1jaka1	Alignment	not modelled	79.0	24	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
79	c5oarB	Alignment	not modelled	78.2	33	PDB header: hydrolase Chain: B: PDB Molecule: beta-hexosaminidase; PDBTitle: crystal structure of native beta-n-acetylhexosaminidase

						isolated from2 aspergillus oryzae
80	c3nsnA_	Alignment	not modelled	78.2	19	PDB header: hydrolase Chain: A: PDB Molecule: n-acetylglucosaminidase; PDBTitle: crystal structure of insect beta-n-acetyl-d-hexosaminidase ofhex12 complexed with tmg-chitotriomycin
81	c4h04B_	Alignment	not modelled	77.9	29	PDB header: hydrolase Chain: B: PDB Molecule: lacto-n-biosidase; PDBTitle: lacto-n-biosidase from bifidobacterium bifidum
82	c2mzqA_	Alignment	not modelled	77.2	19	PDB header: rna binding protein Chain: A: PDB Molecule: single-strand telomeric dna-binding protein gbp2; PDBTitle: nmr structure of the rrm3 domain of gbp2
83	c3gh7A_	Alignment	not modelled	76.6	29	PDB header: hydrolase Chain: A: PDB Molecule: beta-hexosaminidase; PDBTitle: crystal structure of beta-hexosaminidase from paenibacillus sp. ts122 in complex with galnac
84	d1yhta1	Alignment	not modelled	76.2	29	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
85	c2yl8A_	Alignment	not modelled	76.0	33	PDB header: hydrolase Chain: A: PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: inhibition of the pneumococcal virulence factor strh and2 molecular insights into n-glycan recognition and3 hydrolysis
86	d1qbaa3	Alignment	not modelled	75.9	29	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
87	c6ezrA_	Alignment	not modelled	75.7	19	PDB header: hydrolase Chain: A: PDB Molecule: beta-n-acetylglucosaminidase nag2; PDBTitle: crystal structure of gh20 exo beta-n-acetylglucosaminidase from vibrio2 harveyi
88	c2ylaA_	Alignment	not modelled	75.4	19	PDB header: hydrolase Chain: A: PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: inhibition of the pneumococcal virulence factor strh and2 molecular insights into n-glycan recognition and3 hydrolysis
89	c1nouA_	Alignment	not modelled	75.3	29	PDB header: hydrolase Chain: A: PDB Molecule: beta-hexosaminidase beta chain; PDBTitle: native human lysosomal beta-hexosaminidase isoform b
90	c1no8A_	Alignment	not modelled	75.3	18	PDB header: rna binding protein Chain: A: PDB Molecule: aly; PDBTitle: solution structure of the nuclear factor aly rbd domain
91	d1no8a_	Alignment	not modelled	75.3	18	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
92	c1m04A_	Alignment	not modelled	75.2	24	PDB header: hydrolase Chain: A: PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: mutant streptomyces plicatus beta-hexosaminidase (d313n) in complex2 with product (glcnac)
93	c3rcnA_	Alignment	not modelled	75.2	29	PDB header: hydrolase Chain: A: PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: crystal structure of beta-n-acetylhexosaminidase from arthrobacter2 aurescens
94	d1nowa1	Alignment	not modelled	75.2	29	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
95	c2gxE_	Alignment	not modelled	74.5	24	PDB header: hydrolase Chain: E: PDB Molecule: beta-hexosaminidase alpha chain; PDBTitle: crystallographic structure of human beta-hexosaminidase a
96	d2gxa1	Alignment	not modelled	74.4	24	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
97	c3lmyA_	Alignment	not modelled	73.4	29	PDB header: hydrolase Chain: A: PDB Molecule: beta-hexosaminidase subunit beta; PDBTitle: the crystal structure of beta-hexosaminidase b in complex with2 pyrimethamine
98	c1qbaA_	Alignment	not modelled	73.3	29	PDB header: glycosyl hydrolase Chain: A: PDB Molecule: chitobiase; PDBTitle: bacterial chitobiase, glycosyl hydrolase family 20
99	c4pysB_	Alignment	not modelled	72.7	43	PDB header: hydrolase Chain: B: PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: the crystal structure of beta-n-acetylhexosaminidase from bacteroides2 fragilis nctc 9343
100	c3rpmA_	Alignment	not modelled	72.3	33	PDB header: hydrolase Chain: A: PDB Molecule: beta-n-acetyl-hexosaminidase; PDBTitle: crystal structure of the first gh20 domain of a novel beta-n-acetyl-2 hexosaminidase strh from streptococcus pneumoniae r6
101	c2dhgA_	Alignment	not modelled	71.9	17	PDB header: rna binding protein Chain: A: PDB Molecule: trna selenocysteine associated protein (secp43); PDBTitle: solution structure of the c-terminal rna recognition motif2 in trna selenocysteine associated protein
102	c4wikA_	Alignment	not modelled	71.0	18	PDB header: transcription Chain: A: PDB Molecule: splicing factor, proline- and glutamine-rich; PDBTitle: human splicing factor, construct 2
103	c6em5o_	Alignment	not modelled	68.6	21	PDB header: ribosome Chain: O: PDB Molecule: 60s ribosomal protein l16-a; PDBTitle: state d architectural model (nsa1-tap flag-ytm1) - visualizing the2 assembly pathway of nucleolar pre-60s ribosomes
104	c2epoB_	Alignment	not modelled	68.6	24	PDB header: hydrolase Chain: B: PDB Molecule: n-acetyl-beta-d-glucosaminidase; PDBTitle: n-acetyl-b-d-glucosaminidase (gcna) from streptococcus gordonii
105	c2dgxA_	Alignment	not modelled	68.3	11	PDB header: rna binding protein Chain: A: PDB Molecule: kiaa0430 protein; PDBTitle: solution structure of the rna recognition motif in kiaa04302 protein

106	c3s8sA_	Alignment	not modelled	66.7	11	PDB header: transcription Chain: A: PDB Molecule: histone-lysine n-methyltransferase setd1a; PDBTitle: crystal structure of the rrm domain of human setd1a
107	d1b93a_	Alignment	not modelled	65.2	21	Fold: Methylglyoxal synthase-like Superfamily: Methylglyoxal synthase-like Family: Methylglyoxal synthase, MgsA
108	c2dnoA_	Alignment	not modelled	65.0	23	PDB header: rna binding protein Chain: A: PDB Molecule: trinucleotide repeat containing 4 variant; PDBTitle: solution structure of rna binding domain in trinucleotide2 repeat containing 4 variant
109	d1fhta_	Alignment	not modelled	61.8	17	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
110	c5ac4A_	Alignment	not modelled	60.0	19	PDB header: hydrolase Chain: A: PDB Molecule: n-acetyl-beta-d-glucosaminidase; PDBTitle: gh20c, beta-hexosaminidase from streptococcus pneumoniae in complex2 with gainac
111	c3s01A_	Alignment	not modelled	59.9	13	PDB header: rna binding protein Chain: A: PDB Molecule: heterogeneous nuclear ribonucleoprotein l; PDBTitle: crystal structure of a heterogeneous nuclear ribonucleoprotein l2 (hnrpl) from mus musculus at 2.15 a resolution
112	c2fy1A_	Alignment	not modelled	59.8	22	PDB header: structural protein/rna Chain: A: PDB Molecule: rna-binding motif protein, y chromosome, family 1 member PDBTitle: a dual mode of rna recognition by the rbmy protein
113	c2do0A_	Alignment	not modelled	59.0	15	PDB header: rna binding protein Chain: A: PDB Molecule: heterogeneous nuclear ribonucleoprotein m; PDBTitle: solution structure of the rna binding domain of 2 heterogeneous nuclear ribonucleoprotein m
114	c2m70A_	Alignment	not modelled	58.7	16	PDB header: protein binding Chain: A: PDB Molecule: poly(a)-binding protein 1; PDBTitle: structural determination of the citrus sinensis poly(a)-binding2 protein cspabp1
115	d1x5oa1	Alignment	not modelled	58.3	15	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
116	c2mzsA_	Alignment	not modelled	57.6	18	PDB header: rna binding protein Chain: A: PDB Molecule: protein hrb1; PDBTitle: nmr structure of the rrm2 domain of hrb1
117	c2mkkA_	Alignment	not modelled	57.4	10	PDB header: translation regulator/rna Chain: A: PDB Molecule: cytoplasmic polyadenylation element-binding protein 1; PDBTitle: structural model of tandem rrm domains of cytoplasmic polyadenylation2 element binding protein 1 (cpeb1) in complex with rna
118	d2k3ka1	Alignment	not modelled	56.8	15	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
119	d2bi7a1	Alignment	not modelled	55.5	23	Fold: Nucleotide-binding domain Superfamily: Nucleotide-binding domain Family: UDP-galactopyranose mutase, N-terminal domain
120	d1vmda_	Alignment	not modelled	55.4	17	Fold: Methylglyoxal synthase-like Superfamily: Methylglyoxal synthase-like Family: Methylglyoxal synthase, MgsA