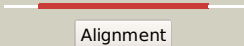

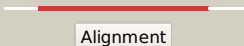

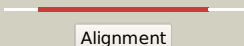







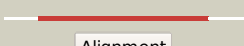











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1257c_(-)_1404723_1406090
Date	Wed Jul 31 22:05:35 BST 2019
Unique Job ID	16b4546592d23080

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3pm9A_	 Alignment		100.0	28	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
2	c4bc9C_	 Alignment		100.0	19	PDB header: transferase Chain: C: PDB Molecule: alkyldihydroxyacetonephosphate synthase, peroxisomal; PDBTitle: mammalian alkyldihydroxyacetonephosphate synthase: wild-type, adduct2 with cyanoethyl
3	c1wveB_	 Alignment		100.0	20	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
4	c5fxpA_	 Alignment		100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: eugenol oxidase; PDBTitle: crystal structure of eugenol oxidase in complex with2 vanillin
5	c3bw7A_	 Alignment		100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: cytokinin dehydrogenase 1; PDBTitle: maize cytokinin oxidase/dehydrogenase complexed with the allenic2 cytokinin analog ha-1
6	c1ahuB_	 Alignment		100.0	17	PDB header: flavoenzyme Chain: B: PDB Molecule: vanillyl-alcohol oxidase; PDBTitle: structure of the octameric flavoenzyme vanillyl-alcohol2 oxidase in complex with p-cresol
7	c4oalB_	 Alignment		100.0	18	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
8	c4ml8C_	 Alignment		100.0	15	PDB header: oxidoreductase Chain: C: PDB Molecule: cytokinin oxidase 2; PDBTitle: structure of maize cytokinin oxidase/dehydrogenase 2 (zmcko2)
9	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
10	c2exrA_	 Alignment		100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: cytokinin dehydrogenase 7; PDBTitle: x-ray structure of cytokinin oxidase/dehydrogenase (ckx) from2 arabidopsis thaliana at5g21482
11	c3w8wA_	 Alignment		100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: putative fad-dependent oxygenase encm; PDBTitle: the crystal structure of encm

12	c4ud8B_	Alignment		100.0	16	PDB header: oxidoreductase Chain: B: PDB Molecule: fad-binding and bbe domain-containing protein; PDBTitle: atbbe15
13	c2uuvC_	Alignment		100.0	20	PDB header: transferase Chain: C: PDB Molecule: alkyldihydroxyacetonephosphate synthase; PDBTitle: alkyldihydroxyacetonephosphate synthase in p1
14	c3tstA_	Alignment		100.0	17	PDB header: allergen, oxidoreductase Chain: A: PDB Molecule: pollen allergen phi p 4; PDBTitle: crystal structure of phi p 4, a grass pollen allergen with glucose2 dehydrogenase activity
15	c6c80B_	Alignment		100.0	18	PDB header: immune system Chain: B: PDB Molecule: cytokinin oxidase luckx1.1; PDBTitle: crystal structure of a flax cytokinin oxidase
16	c2bvfa_	Alignment		100.0	19	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	c6eo5A_	Alignment		100.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: ppbbe-like 1 d396n; PDBTitle: physcomitrella patens bbe-like 1 variant d396n
18	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
19	c1f0xA_	Alignment		100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: d-lactate dehydrogenase; PDBTitle: crystal structure of d-lactate dehydrogenase, a peripheral membrane2 respiratory enzyme.
20	c3fwaA_	Alignment		100.0	16	PDB header: flavoprotein Chain: A: PDB Molecule: reticuline oxidase; PDBTitle: structure of berberine bridge enzyme, c166a variant in complex with2 (s)-reticuline
21	c6f74B_	Alignment	not modelled	100.0	13	PDB header: flavoprotein Chain: B: PDB Molecule: alcohol oxidase; PDBTitle: crystal structure of vao-type flavoprotein mtvao713 from2 myceliophthora thermophila c1
22	c3rjaA_	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: carbohydrate oxidase; PDBTitle: crystal structure of carbohydrate oxidase from microdochium nivale in2 complex with substrate analogue
23	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
24	c5l6fA_	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: fad linked oxidase-like protein; PDBTitle: xylooligosaccharide oxidase from myceliophthora thermophila c1 in2 complex with xylobiose
25	c1zr6A_	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: glucooligosaccharide oxidase; PDBTitle: the crystal structure of an acremonium strictum glucooligosaccharide2 oxidase reveals a novel flavinylation
26	c5d79B_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: B: PDB Molecule: berberine bridge enzyme-like protein; PDBTitle: structure of bbe-like #28 from arabidopsis thaliana
27	c5j1wD_	Alignment	not modelled	100.0	16	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
28	c3popD_	Alignment	not modelled	100.0	14	PDB header: oxidoreductase Chain: D: PDB Molecule: gilr oxidase; PDBTitle: the crystal structure of gilr, an oxidoreductase that catalyzes the2 terminal step of gilvocarin biosynthesis

29	c2ipiD	Alignment	not modelled	100.0	14	PDB header: oxidoreductase Chain: D: PDB Molecule: aclacinomycin oxidoreductase (aknox); PDBTitle: crystal structure of aclacinomycin oxidoreductase
30	c4fdoA	Alignment	not modelled	100.0	16	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: A: PDB Molecule: oxidoreductase dpre1; PDBTitle: mycobacterium tuberculosis dpre1 in complex with ct319
31	c2y3rC	Alignment	not modelled	100.0	14	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	14	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	20	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	14	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	14	PDB header: oxidoreductase Chain: A: PDB Molecule: cholesterol oxidase; PDBTitle: solvent-stable cholesterol oxidase
36	d1wvfa2	Alignment	not modelled	100.0	24	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	22	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: FAD-linked oxidases, N-terminal domain
38	d1w1oa2	Alignment	not modelled	100.0	24	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: FAD-linked oxidases, N-terminal domain
39	d1f0xa2	Alignment	not modelled	100.0	23	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	22	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	26	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	d1uxya1	Alignment	not modelled	100.0	16	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	c1hskA	Alignment	not modelled	100.0	25	PDB header: oxidoreductase Chain: A: PDB Molecule: udp-n-acetylenolpyruvoylglucosamine reductase; PDBTitle: crystal structure of s. aureus murb
44	c4pytA	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: udp-n-acetylenolpyruvoylglucosamine reductase; PDBTitle: crystal structure of a murb family ep-udp-n-acetylglucosamine2 reductase
45	c4jayC	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: C: PDB Molecule: udp-n-acetylenolpyruvoylglucosamine reductase; PDBTitle: crystal structure of p. aeruginosa murb in complex with nadp+
46	c1mbbA	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: uridine diphospho-n-acetylenolpyruvylglucosamine PDBTitle: oxidoreductase
47	c2yvsA	Alignment	not modelled	99.9	31	PDB header: oxidoreductase Chain: A: PDB Molecule: glycolate oxidase subunit glce; PDBTitle: crystal structure of glycolate oxidase subunit glce from thermus2 thermophilus hb8
48	c3i99A	Alignment	not modelled	99.9	16	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
49	c5jzxB	Alignment	not modelled	99.9	19	PDB header: oxidoreductase Chain: B: PDB Molecule: udp-n-acetylenolpyruvoylglucosamine reductase; PDBTitle: crystal structure of udp-n-acetylenolpyruvoylglucosamine reductase2 (murb) from mycobacterium tuberculosis
50	d1e8ga1	Alignment	not modelled	99.9	16	Fold: Ferredoxin-like Superfamily: FAD-linked oxidases, C-terminal domain Family: Vanillyl-alcohol oxidase-like
51	d1wvfa1	Alignment	not modelled	99.9	17	Fold: Ferredoxin-like Superfamily: FAD-linked oxidases, C-terminal domain Family: Vanillyl-alcohol oxidase-like
52	c2gquA	Alignment	not modelled	99.8	21	PDB header: oxidoreductase Chain: A: PDB Molecule: udp-n-acetylenolpyruvylglucosamine reductase; PDBTitle: crystal structure of udp-n-acetylenolpyruvylglucosamine2 reductase (murb) from thermus caldophilus
53	d1f0xa1	Alignment	not modelled	99.8	18	Fold: Ferredoxin-like Superfamily: FAD-linked oxidases, C-terminal domain Family: D-lactate dehydrogenase
						Fold: Ferredoxin-like

54	d1w1oa1	Alignment	not modelled	99.3	15	Superfamily: FAD-linked oxidases, C-terminal domain Family: Cytokinin dehydrogenase 1
55	d1v97a6	Alignment	not modelled	97.3	13	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like
56	d1ffvc2	Alignment	not modelled	97.2	14	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like
57	d3b9jb2	Alignment	not modelled	97.2	13	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	97.1	15	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	c3etrM	Alignment	not modelled	97.1	12	PDB header: oxidoreductase Chain: M: PDB Molecule: xanthine dehydrogenase/oxidase; PDBTitle: crystal structure of xanthine oxidase in complex with lumazine
60	c3b9jj	Alignment	not modelled	97.1	12	PDB header: oxidoreductase Chain: J: PDB Molecule: xanthine oxidase; PDBTitle: structure of xanthine oxidase with 2-hydroxy-6-methylpurine
61	c1ffuF	Alignment	not modelled	97.0	15	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
62	c5g5hB	Alignment	not modelled	96.9	12	PDB header: oxidoreductase Chain: B: PDB Molecule: putative xanthine dehydrogenase yags fad-binding subunit; PDBTitle: escherichia coli periplasmic aldehyde oxidase r440h mutant
63	c5y6qB	Alignment	not modelled	96.9	16	PDB header: oxidoreductase Chain: B: PDB Molecule: aldehyde oxidase medium subunit; PDBTitle: crystal structure of an aldehyde oxidase from methylobacillus sp.2 ky4400
64	d2i0ka1	Alignment	not modelled	96.9	12	Fold: Ferredoxin-like Superfamily: FAD-linked oxidases, C-terminal domain Family: Cholesterol oxidase
65	d1n62c2	Alignment	not modelled	96.8	15	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like
66	c1t3qF	Alignment	not modelled	96.7	12	PDB header: oxidoreductase Chain: F: PDB Molecule: quinoline 2-oxidoreductase medium subunit; PDBTitle: crystal structure of quinoline 2-oxidoreductase from pseudomonas2 putida 86
67	c3hrdC	Alignment	not modelled	96.5	16	PDB header: oxidoreductase Chain: C: PDB Molecule: nicotinate dehydrogenase fad-subunit; PDBTitle: crystal structure of nicotinate dehydrogenase
68	d1jroa4	Alignment	not modelled	96.5	15	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like
69	d1t3qc2	Alignment	not modelled	96.1	11	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like
70	c1rm6E	Alignment	not modelled	96.1	16	PDB header: oxidoreductase Chain: E: PDB Molecule: 4-hydroxybenzoyl-coa reductase beta subunit; PDBTitle: structure of 4-hydroxybenzoyl-coa reductase from thauera2 aromatica
71	c4zohB	Alignment	not modelled	96.0	14	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase fad-binding subunit; PDBTitle: crystal structure of glyceraldehyde oxidoreductase
72	c2w3rG	Alignment	not modelled	95.5	14	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
73	d1rm6b2	Alignment	not modelled	93.9	18	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like
74	c1wygA	Alignment	not modelled	93.6	11	PDB header: oxidoreductase Chain: A: PDB Molecule: xanthine dehydrogenase/oxidase; PDBTitle: crystal structure of a rat xanthine dehydrogenase triple mutant2 (c535a, c992r and c1324s)
75	c3zyvA	Alignment	not modelled	92.5	16	PDB header: oxidoreductase Chain: A: PDB Molecule: aox3; PDBTitle: crystal structure of the mouse liver aldehyde oxidase 3 (maox3)
76	c4uhxA	Alignment	not modelled	85.2	18	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde oxidase; PDBTitle: human aldehyde oxidase in complex with phthalazine and thioridazine
77	c2uval	Alignment	not modelled	84.4	28	PDB header: transferase Chain: I: PDB Molecule: fatty acid synthase beta subunits; PDBTitle: crystal structure of fatty acid synthase from thermomyces2 lanuginosus at 3.1 angstrom resolution. this file contains3 the beta subunits of the fatty acid synthase. the entire4 crystal structure consists of one heterododecameric fatty5 acid synthase and is described in remark 400
78	c2vkhH	Alignment	not modelled	83.7	23	PDB header: transferase Chain: H: PDB Molecule: fatty acid synthase subunit beta; PDBTitle: structure of the cerulenin-inhibited fungal fatty acid

						synthase type i2 multienzyme complex
79	c4b3yB_	Alignment	not modelled	77.6	26	PDB header: transferase Chain: B: PDB Molecule: fatty acid synthase; PDBTitle: cryo-em structure of the mycobacterial fatty acid synthase
80	c1qupA_	Alignment	not modelled	76.3	10	PDB header: chaperone Chain: A: PDB Molecule: superoxide dismutase 1 copper chaperone; PDBTitle: crystal structure of the copper chaperone for superoxide dismutase
81	c1jk9D_	Alignment	not modelled	72.3	9	PDB header: oxidoreductase Chain: D: PDB Molecule: copper chaperone for superoxide dismutase; PDBTitle: heterodimer between h48f-yosd1 and yccs
82	d1yhta1	Alignment	not modelled	68.4	10	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
83	c5oarB_	Alignment	not modelled	68.4	19	PDB header: hydrolase Chain: B: PDB Molecule: beta-hexosaminidase; PDBTitle: crystal structure of native beta-n-acetylhexosaminidase isolated from2 aspergillus oryzae
84	d1jaka1	Alignment	not modelled	68.2	24	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
85	c6je8A_	Alignment	not modelled	67.7	14	PDB header: hydrolase Chain: A: PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: crystal structure of a beta-n-acetylhexosaminidase
86	c4h04B_	Alignment	not modelled	66.2	14	PDB header: hydrolase Chain: B: PDB Molecule: lacto-n-biosidase; PDBTitle: lacto-n-biosidase from bifidobacterium bifidum
87	c3nsnA_	Alignment	not modelled	66.2	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
88	d1qbaa3	Alignment	not modelled	65.3	19	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
89	d2qjxa1	Alignment	not modelled	63.5	19	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
90	c2yl8A_	Alignment	not modelled	63.1	5	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
91	d1nowa1	Alignment	not modelled	62.6	19	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
92	c3gh7A_	Alignment	not modelled	62.2	14	PDB header: hydrolase Chain: A: PDB Molecule: beta-hexosaminidase; PDBTitle: crystal structure of beta-hexosaminidase from paenibacillus sp. ts122 in complex with galnac
93	c1m04A_	Alignment	not modelled	62.2	24	PDB header: hydrolase Chain: A: PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: mutant streptomyces plicatus beta-hexosaminidase (d313n) in complex2 with product (glcnac)
94	c2ylaA_	Alignment	not modelled	62.1	14	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
95	c1nouA_	Alignment	not modelled	61.6	19	PDB header: hydrolase Chain: A: PDB Molecule: beta-hexosaminidase beta chain; PDBTitle: native human lysosomal beta-hexosaminidase isoform b
96	c3rcnA_	Alignment	not modelled	61.2	10	PDB header: hydrolase Chain: A: PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: crystal structure of beta-n-acetylhexosaminidase from arthrobacter2 aureus
97	c6ezrA_	Alignment	not modelled	60.8	19	PDB header: hydrolase Chain: A: PDB Molecule: beta-n-acetylglucosaminidase nag2; PDBTitle: crystal structure of gh20 exo beta-n-acetylglucosaminidase from vibrio2 harveyi
98	c2qjxE_	Alignment	not modelled	60.3	19	PDB header: hydrolase Chain: E: PDB Molecule: beta-hexosaminidase alpha chain; PDBTitle: crystallographic structure of human beta-hexosaminidase a
99	c1qbaA_	Alignment	not modelled	57.9	19	PDB header: glycosyl hydrolase Chain: A: PDB Molecule: chitobiase; PDBTitle: bacterial chitobiase, glycosyl hydrolase family 20
100	c3lmyA_	Alignment	not modelled	57.7	19	PDB header: hydrolase Chain: A: PDB Molecule: beta-hexosaminidase subunit beta; PDBTitle: the crystal structure of beta-hexosaminidase b in complex with2 pyrimethamine
101	c4pysB_	Alignment	not modelled	56.9	29	PDB header: hydrolase Chain: B: PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: the crystal structure of beta-n-acetylhexosaminidase from bacteroides2 fragilis nctc 9343
102	c3rpmA_	Alignment	not modelled	53.5	5	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
103	c2epoB_	Alignment	not modelled	46.9	19	PDB header: hydrolase Chain: B: PDB Molecule: n-acetyl-beta-d-glucosaminidase; PDBTitle: n-acetyl-b-d-glucosaminidase (gcna) from streptococcus gordonii
104	c2bp7F_	Alignment	not modelled	46.2	17	PDB header: oxidoreductase Chain: F: PDB Molecule: 2-oxoisovalerate dehydrogenase beta subunit; PDBTitle: new crystal form of the pseudomonas putida branched-

						chain2 dehydrogenase (e1)
105	c2yswB_	Alignment	not modelled	45.7	13	PDB header: lyase Chain: B: PDB Molecule: 3-dehydroquinatase dehydratase; PDBTitle: crystal structure of the 3-dehydroquinatase dehydratase from aquifex2 aeolicus vf5
106	d1rlka_	Alignment	not modelled	44.4	12	Fold: Peptidyl-tRNA hydrolase II Superfamily: Peptidyl-tRNA hydrolase II Family: Peptidyl-tRNA hydrolase II
107	c2gvsA_	Alignment	not modelled	40.3	25	PDB header: lipid binding protein Chain: A: PDB Molecule: chemosensory protein csp-sg4; PDBTitle: nmr solution structure of cspsg4
108	c2zv3E_	Alignment	not modelled	40.3	12	PDB header: hydrolase Chain: E: PDB Molecule: peptidyl-tRNA hydrolase; PDBTitle: crystal structure of project mj0051 from methanocaldococcus2 jannaschii dsm 2661
109	c1itzC_	Alignment	not modelled	39.5	16	PDB header: transferase Chain: C: PDB Molecule: transketolase; PDBTitle: maize transketolase in complex with tpp
110	d1kx9b_	Alignment	not modelled	39.4	21	Fold: alpha-alpha superhelix Superfamily: Chemosensory protein Csp2 Family: Chemosensory protein Csp2
111	d2r8oa1	Alignment	not modelled	39.3	15	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like Pyr module
112	d1umdb1	Alignment	not modelled	39.2	19	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase Pyr module
113	d1n8va_	Alignment	not modelled	38.2	19	Fold: alpha-alpha superhelix Superfamily: Chemosensory protein Csp2 Family: Chemosensory protein Csp2
114	d1ik6a1	Alignment	not modelled	35.8	22	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase Pyr module
115	d1w85b1	Alignment	not modelled	34.3	19	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase Pyr module
116	c3m7iA_	Alignment	not modelled	32.5	16	PDB header: transferase Chain: A: PDB Molecule: transketolase; PDBTitle: crystal structure of transketolase in complex with thiamine2 diphosphate, ribose-5-phosphate(pyranose form) and magnesium ion
117	c4r25A_	Alignment	not modelled	32.3	14	PDB header: transcription Chain: A: PDB Molecule: nitrogen regulatory pii-like protein; PDBTitle: structure of b. subtilis glnk
118	d2ozb1	Alignment	not modelled	31.6	22	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase Pyr module
119	c5ac4A_	Alignment	not modelled	31.1	29	PDB header: hydrolase Chain: A: PDB Molecule: n-acetyl-beta-d-glucosaminidase; PDBTitle: gh20c, beta-hexosaminidase from streptococcus pneumoniae in complex2 with gainac
120	c3komB_	Alignment	not modelled	30.8	13	PDB header: transferase Chain: B: PDB Molecule: transketolase; PDBTitle: crystal structure of apo transketolase from francisella tularensis