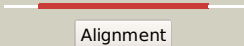

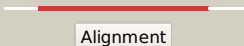

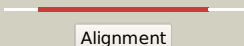







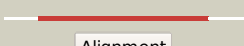











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0063 (-)_66920_68359
Date	Tue Jul 23 14:50:09 BST 2019
Unique Job ID	e66f27eed0780754

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6f73B_	 Alignment		100.0	22	PDB header: flavoprotein Chain: B; PDB Molecule: mtvao615; PDBTitle: crystal structure of vao-type flavoprotein mtvao615 at ph 5.0 from2 myceliophthora thermophila c1
2	c6f74B_	 Alignment		100.0	21	PDB header: flavoprotein Chain: B; PDB Molecule: alcohol oxidase; PDBTitle: crystal structure of vao-type flavoprotein mtvao713 from2 myceliophthora thermophila c1
3	c3w8wA_	 Alignment		100.0	27	PDB header: oxidoreductase Chain: A; PDB Molecule: putative fad-dependent oxygenase encm; PDBTitle: the crystal structure of encm
4	c3vteA_	 Alignment		100.0	24	PDB header: oxidoreductase Chain: A; PDB Molecule: tetrahydrocannabinolic acid synthase; PDBTitle: crystal structure of tetrahydrocannabinolic acid synthase from2 cannabis sativa
5	c2bvfa_	 Alignment		100.0	23	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)
6	c6eo5A_	 Alignment		100.0	26	PDB header: oxidoreductase Chain: A; PDB Molecule: ppbbe-like 1 d396n; PDBTitle: physcomitrella patens bbe-like 1 variant d396n
7	c4ud8B_	 Alignment		100.0	21	PDB header: oxidoreductase Chain: B; PDB Molecule: fad-binding and bbe domain-containing protein; PDBTitle: atbbe15
8	c5l6fA_	 Alignment		100.0	27	PDB header: oxidoreductase Chain: A; PDB Molecule: fad linked oxidase-like protein; PDBTitle: xylooligosaccharide oxidase from myceliophthora thermophila c1 in2 complex with xylobiose
9	c3rjaA_	 Alignment		100.0	24	PDB header: oxidoreductase Chain: A; PDB Molecule: carbohydrate oxidase; PDBTitle: crystal structure of carbohydrate oxidase from microdochium nivale in2 complex with substrate analogue
10	c3tsja_	 Alignment		100.0	18	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
11	c3d2hA_	 Alignment		100.0	21	PDB header: oxidoreductase Chain: A; PDB Molecule: berberine bridge-forming enzyme; PDBTitle: structure of berberine bridge enzyme from eschscholzia californica,2 monoclinic crystal form

12	c4oa1B_	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
13	c3fwaA_	Alignment		100.0	21	PDB header: flavoprotein Chain: A: PDB Molecule: reticuline oxidase; PDBTitle: structure of berberine bridge enzyme, c166a variant in complex with2 (s)-reticuline
14	c1zr6A_	Alignment		100.0	25	PDB header: oxidoreductase Chain: A: PDB Molecule: glucooligosaccharide oxidase; PDBTitle: the crystal structure of an acremonium strictum glucooligosaccharide2 oxidase reveals a novel flavinylation
15	c5i1wD_	Alignment		100.0	22	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
16	c2wdwB_	Alignment		100.0	26	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
17	c3popD_	Alignment		100.0	21	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
18	c5d79B_	Alignment		100.0	23	PDB header: oxidoreductase Chain: B: PDB Molecule: berberine bridge enzyme-like protein; PDBTitle: structure of bbe-like #28 from arabidopsis thaliana
19	c4ml8C_	Alignment		100.0	17	PDB header: oxidoreductase Chain: C: PDB Molecule: cytokinin oxidase 2; PDBTitle: structure of maize cytokinin oxidase/dehydrogenase 2 (zmcko2)
20	c2ipiD_	Alignment		100.0	24	PDB header: oxidoreductase Chain: D: PDB Molecule: aclacinomycin oxidoreductase (aknox); PDBTitle: crystal structure of aclacinomycin oxidoreductase
21	c2y3rC_	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: C: PDB Molecule: taml; PDBTitle: structure of the tirandamycin-bound fad-dependent tirandamycin oxidase2 taml in p21 space group
22	c3bw7A_	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: cytokinin dehydrogenase 1; PDBTitle: maize cytokinin oxidase/dehydrogenase complexed with the allenic2 cytokinin analog ha-1
23	c6c80B_	Alignment	not modelled	100.0	18	PDB header: immune system Chain: B: PDB Molecule: cytokinin oxidase luckx1.1; PDBTitle: crystal structure of a flax cytokinin oxidase
24	c4bc9C_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: C: PDB Molecule: alkyldihydroxyacetonephosphate synthase, peroxisomal; PDBTitle: mammalian alkyldihydroxyacetonephosphate synthase: wild-type, adduct2 with cyanoethyl
25	c3pm9A_	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative dehydrogenase (rpa1076) from2 rhodospseudomonas palustris cga009 at 2.57 a resolution
26	c1wveB_	Alignment	not modelled	100.0	16	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
27	c2exrA_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: cytokinin dehydrogenase 7; PDBTitle: x-ray structure of cytokinin oxidase/dehydrogenase (ckx) from2 arabidopsis thaliana at5g21482
28	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

29	c5fxpA	Alignment	not modelled	100.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: eugenol oxidase; PDBTitle: crystal structure of eugenol oxidase in complex with2 vanillin
30	c2vfvA	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: xylitol oxidase; PDBTitle: alditol oxidase from streptomyces coelicolor a3(2): complex2 with sulphite
31	c1i19B	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: B: PDB Molecule: cholesterol oxidase; PDBTitle: crystal structure of cholesterol oxidase from b.sterolicum
32	c3js8A	Alignment	not modelled	100.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: cholesterol oxidase; PDBTitle: solvent-stable cholesterol oxidase
33	c1ahuB	Alignment	not modelled	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
34	c2uuvC	Alignment	not modelled	100.0	13	PDB header: transferase Chain: C: PDB Molecule: alkyldihydroxyacetonephosphate synthase; PDBTitle: alkyldihydroxyacetonephosphate synthase in p1
35	c1f0xA	Alignment	not modelled	100.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: d-lactate dehydrogenase; PDBTitle: crystal structure of d-lactate dehydrogenase, a peripheral membrane2 respiratory enzyme.
36	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
37	d1w1oa2	Alignment	not modelled	100.0	28	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: FAD-linked oxidases, N-terminal domain
38	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
39	d2i0ka2	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	d1f0xa2	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
41	d1uxya1	Alignment	not modelled	100.0	13	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	d1hska1	Alignment	not modelled	100.0	18	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	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
44	c4jayC	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: C: PDB Molecule: udp-n-acetylenolpyruvoylglucosamine reductase; PDBTitle: crystal structure of p. aeruginosa murb in complex with nadp+
45	c1hska	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: udp-n-acetylenolpyruvoylglucosamine reductase; PDBTitle: crystal structure of s. aureus murb
46	c1mbbA	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: uridine diphospho-n-acetylenolpyruvylglucosamine PDBTitle: oxidoreductase
47	c2yvsA	Alignment	not modelled	99.9	20	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	c2gquA	Alignment	not modelled	99.9	17	PDB header: oxidoreductase Chain: A: PDB Molecule: udp-n-acetylenolpyruvylglucosamine reductase; PDBTitle: crystal structure of udp-n-acetylenolpyruvylglucosamine2 reductase (murb) from thermus caldophilus
51	d1w1oa1	Alignment	not modelled	98.8	14	Fold: Ferredoxin-like Superfamily: FAD-linked oxidases, C-terminal domain Family: Cytokinin dehydrogenase 1
52	d1wvfa1	Alignment	not modelled	98.4	13	Fold: Ferredoxin-like Superfamily: FAD-linked oxidases, C-terminal domain Family: Vanillyl-alcohol oxidase-like
53	d1e8ga1	Alignment	not modelled	98.2	14	Fold: Ferredoxin-like Superfamily: FAD-linked oxidases, C-terminal domain Family: Vanillyl-alcohol oxidase-like

54	d1f0xa1	Alignment	not modelled	98.1	15	Fold: Ferredoxin-like Superfamily: FAD-linked oxidases, C-terminal domain Family: D-lactate dehydrogenase
55	c5g5hb	Alignment	not modelled	95.9	13	PDB header: oxidoreductase Chain: B: PDB Molecule: putative xanthine dehydrogenase yags fad-binding subunit; PDBTitle: escherichia coli periplasmic aldehyde oxidase r440h mutant
56	c1n62c	Alignment	not modelled	95.9	19	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
57	d1ffvc2	Alignment	not modelled	95.8	15	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like
58	c1ffuF	Alignment	not modelled	95.6	14	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
59	c1t3qF	Alignment	not modelled	95.6	16	PDB header: oxidoreductase Chain: F: PDB Molecule: quinoline 2-oxidoreductase medium subunit; PDBTitle: crystal structure of quinoline 2-oxidoreductase from pseudomonas2 putida 86
60	c3hrdC	Alignment	not modelled	95.6	9	PDB header: oxidoreductase Chain: C: PDB Molecule: nicotinate dehydrogenase fad-subunit; PDBTitle: crystal structure of nicotinate dehydrogenase
61	c3etrM	Alignment	not modelled	95.5	9	PDB header: oxidoreductase Chain: M: PDB Molecule: xanthine dehydrogenase/oxidase; PDBTitle: crystal structure of xanthine oxidase in complex with lumazine
62	d1v97a6	Alignment	not modelled	95.5	9	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like
63	c3b9jj	Alignment	not modelled	95.5	9	PDB header: oxidoreductase Chain: J: PDB Molecule: xanthine oxidase; PDBTitle: structure of xanthine oxidase with 2-hydroxy-6-methylpurine
64	c5y6qB	Alignment	not modelled	95.1	8	PDB header: oxidoreductase Chain: B: PDB Molecule: aldehyde oxidase medium subunit; PDBTitle: crystal structure of an aldehyde oxidase from methylobacillus sp.2 ky4400
65	d1n62c2	Alignment	not modelled	95.1	20	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like
66	d1jroa4	Alignment	not modelled	94.7	12	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like
67	c4zohB	Alignment	not modelled	94.6	13	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase fad-binding subunit; PDBTitle: crystal structure of glyceraldehyde oxidoreductase
68	d3b9jb2	Alignment	not modelled	94.6	9	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	94.3	17	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like
70	d2i0ka1	Alignment	not modelled	94.2	14	Fold: Ferredoxin-like Superfamily: FAD-linked oxidases, C-terminal domain Family: Cholesterol oxidase
71	c1rm6E	Alignment	not modelled	94.1	20	PDB header: oxidoreductase Chain: E: PDB Molecule: 4-hydroxybenzoyl-coa reductase beta subunit; PDBTitle: structure of 4-hydroxybenzoyl-coa reductase from thauera2 aromatica
72	d1rm6b2	Alignment	not modelled	94.1	21	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	92.9	9	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	c2w3rG	Alignment	not modelled	91.9	11	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
75	c4uhxA	Alignment	not modelled	89.9	12	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde oxidase; PDBTitle: human aldehyde oxidase in complex with phthalazine and thioridazine
76	c2uval	Alignment	not modelled	89.8	33	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
77	c2vkzH	Alignment	not modelled	87.9	36	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
78	c4h3vB	Alignment	not modelled	87.1	22	PDB header: transferase Chain: B: PDB Molecule: fatty acid synthase;

78	c4b3yB	Alignment	not modelled	87.1	42	PDBTitle: cryo-em structure of the mycobacterial fatty acid synthase PDB header: oxidoreductase
79	c3zyvA	Alignment	not modelled	82.9	11	Chain: A; PDB Molecule: aox3; PDBTitle: crystal structure of the mouse liver aldehyde oxidase 3 (maox3)
80	d1jaka1	Alignment	not modelled	60.3	24	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
81	c2gvsA	Alignment	not modelled	59.6	24	PDB header: lipid binding protein Chain: A; PDB Molecule: chemosensory protein csp-sg4; PDBTitle: nmr solution structure of cspsg4
82	c2pq4B	Alignment	not modelled	59.1	37	PDB header: chaperone/oxidoreductase Chain: B; PDB Molecule: periplasmic nitrate reductase precursor; PDBTitle: nmr solution structure of napd in complex with napa1-352 signal peptide
83	c6je8A	Alignment	not modelled	57.3	24	PDB header: hydrolase Chain: A; PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: crystal structure of a beta-n-acetylhexosaminidase
84	c5oarB	Alignment	not modelled	56.7	33	PDB header: hydrolase Chain: B; PDB Molecule: beta-hexosaminidase; PDBTitle: crystal structure of native beta-n-acetylhexosaminidase isolated from <i>Aspergillus oryzae</i>
85	d1kx9b	Alignment	not modelled	54.7	24	Fold: alpha-alpha superhelix Superfamily: Chemosensory protein Csp2 Family: Chemosensory protein Csp2
86	d1yhta1	Alignment	not modelled	54.6	24	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
87	d1n8va	Alignment	not modelled	54.3	24	Fold: alpha-alpha superhelix Superfamily: Chemosensory protein Csp2 Family: Chemosensory protein Csp2
88	c2yl8A	Alignment	not modelled	53.8	10	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	c4h04B	Alignment	not modelled	53.6	29	PDB header: hydrolase Chain: B; PDB Molecule: lacto-n-biosidase; PDBTitle: lacto-n-biosidase from bifidobacterium bifidum
90	c3nsnA	Alignment	not modelled	53.3	14	PDB header: hydrolase Chain: A; PDB Molecule: n-acetylglucosaminidase; PDBTitle: crystal structure of insect beta-n-acetyl-d-hexosaminidase of hex12 complexed with tmg-chitotriomycin
91	d1qbaa3	Alignment	not modelled	52.6	29	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
92	c2ylaA	Alignment	not modelled	52.4	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
93	c1qupA	Alignment	not modelled	52.0	11	PDB header: chaperone Chain: A; PDB Molecule: superoxide dismutase 1 copper chaperone; PDBTitle: crystal structure of the copper chaperone for superoxide dismutase
94	c2e76D	Alignment	not modelled	51.5	23	PDB header: photosynthesis Chain: D; PDB Molecule: cytochrome b6-f complex iron-sulfur subunit; PDBTitle: crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from <i>M. lamosus</i>
95	c3gh7A	Alignment	not modelled	51.4	24	PDB header: hydrolase Chain: A; PDB Molecule: beta-hexosaminidase; PDBTitle: crystal structure of beta-hexosaminidase from <i>Paenibacillus</i> sp. ts122 in complex with galnac
96	d2gjxa1	Alignment	not modelled	51.0	19	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
97	d1nowa1	Alignment	not modelled	50.7	24	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
98	c1nouA	Alignment	not modelled	48.6	24	PDB header: hydrolase Chain: A; PDB Molecule: beta-hexosaminidase beta chain; PDBTitle: native human lysosomal beta-hexosaminidase isoform b
99	c2gjxE	Alignment	not modelled	47.8	19	PDB header: hydrolase Chain: E; PDB Molecule: beta-hexosaminidase alpha chain; PDBTitle: crystallographic structure of human beta-hexosaminidase a
100	c1m04A	Alignment	not modelled	46.7	24	PDB header: hydrolase Chain: A; PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: mutant streptomyces plicatus beta-hexosaminidase (d313n) in complex2 with product (glcnac)
101	c6ezrA	Alignment	not modelled	46.5	24	PDB header: hydrolase Chain: A; PDB Molecule: beta-n-acetylglucosaminidase nag2; PDBTitle: crystal structure of gh20 exo beta-n-acetylglucosaminidase from <i>Vibrio</i> sp. harveyi
102	c3lmyA	Alignment	not modelled	45.9	24	PDB header: hydrolase Chain: A; PDB Molecule: beta-hexosaminidase subunit beta; PDBTitle: the crystal structure of beta-hexosaminidase b in complex with2 pyrimethamine
103	c3rcnA	Alignment	not modelled	43.6	38	PDB header: hydrolase Chain: A; PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: crystal structure of beta-n-acetylhexosaminidase from <i>Arthrobacter</i> sp. aureus
104	c3rnnA	Alignment	not modelled	43.5	10	PDB header: hydrolase Chain: A; PDB Molecule: beta-n-acetylhexosaminidase;

104	c3pma_	Alignment	not modelled	43.5	10	PDBTitle: crystal structure of the first gh20 domain of a novel beta-n-acetyl-2 hexosaminidase strh from streptococcus pneumoniae r6 PDB header: hydrolase
105	c4pysB_	Alignment	not modelled	40.8	33	Chain: B: PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: the crystal structure of beta-n-acetylhexosaminidase from bacteroides2 fragilis nctc 9343
106	c1jk9D_	Alignment	not modelled	40.4	11	PDB header: oxidoreductase Chain: D: PDB Molecule: copper chaperone for superoxide dismutase; PDBTitle: heterodimer between h48f-yso1 and yccs
107	c2bp7F_	Alignment	not modelled	38.9	13	PDB header: oxidoreductase Chain: F: PDB Molecule: 2-oxoisovalerate dehydrogenase beta subunit; PDBTitle: new crystal form of the pseudomonas putida branched-chain2 dehydrogenase (e1)
108	d1kjq2	Alignment	not modelled	38.4	8	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
109	d1umdb1	Alignment	not modelled	37.8	15	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase Pyr module
110	c3m7iA_	Alignment	not modelled	37.6	8	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
111	c4fukB_	Alignment	not modelled	35.4	18	PDB header: hydrolase Chain: B: PDB Molecule: methionine aminopeptidase; PDBTitle: aminopeptidase from trypanosoma brucei
112	c1qbaA_	Alignment	not modelled	34.9	29	PDB header: glycosyl hydrolase Chain: A: PDB Molecule: chitobiase; PDBTitle: bacterial chitobiase, glycosyl hydrolase family 20
113	d2r8oa1	Alignment	not modelled	33.3	15	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like Pyr module
114	c2yswB_	Alignment	not modelled	33.0	16	PDB header: lyase Chain: B: PDB Molecule: 3-dehydroquinate dehydratase; PDBTitle: crystal structure of the 3-dehydroquinate dehydratase from aquifex2 aeolicus vf5
115	d1k6a1	Alignment	not modelled	33.0	15	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase Pyr module
116	c2epoB_	Alignment	not modelled	32.7	19	PDB header: hydrolase Chain: B: PDB Molecule: n-acetyl-beta-d-glucosaminidase; PDBTitle: n-acetyl-b-d-glucosaminidase (gcna) from streptococcus gordonii
117	d1itza2	Alignment	not modelled	31.5	11	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like Pyr module
118	d1w85b1	Alignment	not modelled	31.0	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	d1gpua2	Alignment	not modelled	29.6	11	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like Pyr module
120	d1qupa2	Alignment	not modelled	29.1	17	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain