

Phyre2

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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2vfvA_	Alignment		100.0	28	PDB header: oxidoreductase Chain: A: PDB Molecule: xylitol oxidase; PDBTitle: alditol oxidase from streptomyces coelicolor a3(2): complex2 with sulphite
2	c4fdoA_	Alignment		100.0	20	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: A: PDB Molecule: oxidoreductase dpre1; PDBTitle: mycobacterium tuberculosis dpre1 in complex with ct319
3	c1i19B_	Alignment		100.0	22	PDB header: oxidoreductase Chain: B: PDB Molecule: cholesterol oxidase; PDBTitle: crystal structure of cholesterol oxidase from b.sterolicum
4	c3js8A_	Alignment		100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: cholesterol oxidase; PDBTitle: solvent-stable cholesterol oxidase
5	c4bc9C_	Alignment		100.0	16	PDB header: transferase Chain: C: PDB Molecule: alkyldihydroxyacetonephosphate synthase, peroxisomal; PDBTitle: mammalian alkyldihydroxyacetonephosphate synthase: wild-type, adduct2 with cyanoethyl
6	c4ml8C_	Alignment		100.0	16	PDB header: oxidoreductase Chain: C: PDB Molecule: cytokinin oxidase 2; PDBTitle: structure of maize cytokinin oxidase/dehydrogenase 2 (zmcko2)
7	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
8	c3pm9A_	Alignment		100.0	15	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
9	c3w8wA_	Alignment		100.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: putative fad-dependent oxygenase encm; PDBTitle: the crystal structure of encm
10	c4qaalB_	Alignment		100.0	16	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
11	c6f74B_	Alignment		100.0	10	PDB header: flavoprotein Chain: B: PDB Molecule: alcohol oxidase; PDBTitle: crystal structure of vao-type flavoprotein mtvao713 from2 myceliophthora thermophila c1

12	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
13	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
14	c2bvfa_	Alignment		100.0	17	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)
15	c3vteA_	Alignment		100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: tetrahydrocannabinolic acid synthase; PDBTitle: crystal structure of tetrahydrocannabinolic acid synthase from2 cannabis sativa
16	c4ud8B_	Alignment		100.0	15	PDB header: oxidoreductase Chain: B: PDB Molecule: fad-binding and bbe domain-containing protein; PDBTitle: atbbe15
17	c2exra_	Alignment		100.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: cytokinin dehydrogenase 7; PDBTitle: x-ray structure of cytokinin oxidase/dehydrogenase (ckx) from2 arabidopsis thaliana at5g21482
18	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
19	c5d79B_	Alignment		100.0	15	PDB header: oxidoreductase Chain: B: PDB Molecule: berberine bridge enzyme-like protein; PDBTitle: structure of bbe-like #28 from arabidopsis thaliana
20	c6eo5A_	Alignment		100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: ppbbe-like 1 d396n; PDBTitle: physcomitrella patens bbe-like 1 variant d396n
21	c1wveB_	Alignment	not modelled	100.0	12	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
22	c3rjaA_	Alignment	not modelled	100.0	13	PDB header: oxidoreductase Chain: A: PDB Molecule: carbohydrate oxidase; PDBTitle: crystal structure of carbohydrate oxidase from microdochium nivale in2 complex with substrate analogue
23	c1zr6A_	Alignment	not modelled	100.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: glucooligosaccharide oxidase; PDBTitle: the crystal structure of an acremonium strictum glucooligosaccharide2 oxidase reveals a novel flavinylation
24	c3popD_	Alignment	not modelled	100.0	11	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
25	c3tsja_	Alignment	not modelled	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
26	c2ipiD_	Alignment	not modelled	100.0	14	PDB header: oxidoreductase Chain: D: PDB Molecule: aclacinomycin oxidoreductase (aknox); PDBTitle: crystal structure of aclacinomycin oxidoreductase
27	c3fwaA_	Alignment	not modelled	100.0	17	PDB header: flavoprotein Chain: A: PDB Molecule: reticuline oxidase; PDBTitle: structure of berberine bridge enzyme, c166a variant in complex with2 (s)-reticuline
28	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

29	c2y3rC	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: C: PDB Molecule: taml; PDBTitle: structure of the tirandamycin-bound fad-dependent tirandamycin oxidase2 taml in p21 space group
30	c2wdwB	Alignment	not modelled	100.0	13	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
31	c5i1wD	Alignment	not modelled	100.0	15	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
32	c5fxpA	Alignment	not modelled	100.0	12	PDB header: oxidoreductase Chain: A: PDB Molecule: eugenol oxidase; PDBTitle: crystal structure of eugenol oxidase in complex with2 vanillin
33	c2uuvC	Alignment	not modelled	100.0	15	PDB header: transferase Chain: C: PDB Molecule: alkyldihydroxyacetonephosphate synthase; PDBTitle: alkyldihydroxyacetonephosphate synthase in p1
34	c1ahuB	Alignment	not modelled	100.0	13	PDB header: flavoenzyme Chain: B: PDB Molecule: vanillyl-alcohol oxidase; PDBTitle: structure of the octameric flavoenzyme vanillyl-alcohol2 oxidase in complex with p-cresol
35	c1f0xA	Alignment	not modelled	100.0	12	PDB header: oxidoreductase Chain: A: PDB Molecule: d-lactate dehydrogenase; PDBTitle: crystal structure of d-lactate dehydrogenase, a peripheral membrane2 respiratory enzyme.
36	d2i0ka2	Alignment	not modelled	100.0	25	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: FAD-linked oxidases, N-terminal domain
37	d1wvfa2	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
38	d1w1oa2	Alignment	not modelled	100.0	21	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: FAD-linked oxidases, N-terminal domain
39	d1e8ga2	Alignment	not modelled	100.0	20	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	18	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: FAD-linked oxidases, N-terminal domain
41	d1luxya1	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
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	19	PDB header: oxidoreductase Chain: A: PDB Molecule: udp-n-acetylenolpyruvylglucosamine reductase; PDBTitle: crystal structure of a murb family ep-udp-n-acetylglucosamine2 reductase
44	c1hska	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: udp-n-acetylenolpyruvylglucosamine reductase; PDBTitle: crystal structure of s. aureus murb
45	c4jayC	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: C: PDB Molecule: udp-n-acetylenolpyruvylglucosamine reductase; PDBTitle: crystal structure of p. aeruginosa murb in complex with nadp+
46	c1mbbA	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: uridine diphospho-n-acetylenolpyruvylglucosamine PDBTitle: oxidoreductase
47	c3i99A	Alignment	not modelled	99.9	15	PDB header: oxidoreductase Chain: A: PDB Molecule: udp-n-acetylenolpyruvylglucosamine reductase; PDBTitle: the crystal structure of the udp-n-acetylenolpyruvylglucosamine2 reductase from the vibrio cholerae o1 biovar tor
48	c5jzxB	Alignment	not modelled	99.9	18	PDB header: oxidoreductase Chain: B: PDB Molecule: udp-n-acetylenolpyruvylglucosamine reductase; PDBTitle: crystal structure of udp-n-acetylenolpyruvylglucosamine reductase2 (murb) from mycobacterium tuberculosis
49	c2yvsa	Alignment	not modelled	99.9	19	PDB header: oxidoreductase Chain: A: PDB Molecule: glycolate oxidase subunit glce; PDBTitle: crystal structure of glycolate oxidase subunit glce from thermus2 thermophilus hb8
50	d2i0ka1	Alignment	not modelled	99.9	18	Fold: Ferredoxin-like Superfamily: FAD-linked oxidases, C-terminal domain Family: Cholesterol oxidase
51	c2gquA	Alignment	not modelled	99.8	18	PDB header: oxidoreductase Chain: A: PDB Molecule: udp-n-acetylenolpyruvylglucosamine reductase; PDBTitle: crystal structure of udp-n-acetylenolpyruvylglucosamine2 reductase (murb) from thermus caldophilus
52	d1w1oa1	Alignment	not modelled	99.0	11	Fold: Ferredoxin-like Superfamily: FAD-linked oxidases, C-terminal domain Family: Cytokinin dehydrogenase 1
53	d1e8ga1	Alignment	not modelled	98.4	9	Fold: Ferredoxin-like Superfamily: FAD-linked oxidases, C-terminal domain Family: Vanillyl-alcohol oxidase-like

54	d1f0xa1	Alignment	not modelled	98.2	10	Fold: Ferredoxin-like Superfamily: FAD-linked oxidases, C-terminal domain Family: D-lactate dehydrogenase
55	d1wvfa1	Alignment	not modelled	98.2	8	Fold: Ferredoxin-like Superfamily: FAD-linked oxidases, C-terminal domain Family: Vanillyl-alcohol oxidase-like
56	d1ffvc2	Alignment	not modelled	97.7	16	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like
57	c5y6qB_	Alignment	not modelled	97.6	18	PDB header: oxidoreductase Chain: B: PDB Molecule: aldehyde oxidase medium subunit; PDBTitle: crystal structure of an aldehyde oxidase from methylobacillus sp.2 ky4400
58	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
59	d1v97a6	Alignment	not modelled	97.5	12	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like
60	d3b9jb2	Alignment	not modelled	97.4	13	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like
61	d1n62c2	Alignment	not modelled	97.4	19	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like
62	c1ffuF_	Alignment	not modelled	97.3	17	PDB header: hydrolase Chain: F: PDB Molecule: cutm, flavoprotein of carbon monoxide dehydrogenase from hydrogenophaga2 pseudoflava which lacks the mo-pyranopterin moiety of the3 molybdenum cofactor
63	c1n62C_	Alignment	not modelled	97.3	20	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
64	c1t3qF_	Alignment	not modelled	97.3	20	PDB header: oxidoreductase Chain: F: PDB Molecule: quinoline 2-oxidoreductase medium subunit; PDBTitle: crystal structure of quinoline 2-oxidoreductase from pseudomonas2 putida 86
65	c3etrM_	Alignment	not modelled	96.9	13	PDB header: oxidoreductase Chain: M: PDB Molecule: xanthine dehydrogenase/oxidase; PDBTitle: crystal structure of xanthine oxidase in complex with lumazine
66	c1rm6E_	Alignment	not modelled	96.8	16	PDB header: oxidoreductase Chain: E: PDB Molecule: 4-hydroxybenzoyl-coa reductase beta subunit; PDBTitle: structure of 4-hydroxybenzoyl-coa reductase from thauera2 aromatica
67	c3b9jl_	Alignment	not modelled	96.8	13	PDB header: oxidoreductase Chain: J: PDB Molecule: xanthine oxidase; PDBTitle: structure of xanthine oxidase with 2-hydroxy-6-methylpurine
68	d1t3qc2	Alignment	not modelled	96.8	18	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like
69	c3hrdC_	Alignment	not modelled	96.6	11	PDB header: oxidoreductase Chain: C: PDB Molecule: nicotinate dehydrogenase fad-subunit; PDBTitle: crystal structure of nicotinate dehydrogenase
70	c4zohB_	Alignment	not modelled	96.1	11	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase fad-binding subunit; PDBTitle: crystal structure of glyceraldehyde oxidoreductase
71	c1wygA_	Alignment	not modelled	95.6	15	PDB header: oxidoreductase Chain: A: PDB Molecule: xanthine dehydrogenase/oxidase; PDBTitle: crystal structure of a rat xanthine dehydrogenase triple mutant2 (c535a, c992r and c1324s)
72	d1jroa4	Alignment	not modelled	95.6	12	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like
73	c2w3rG_	Alignment	not modelled	95.6	16	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
74	d1rm6b2	Alignment	not modelled	95.1	19	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like
75	c4uhxA_	Alignment	not modelled	93.8	18	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde oxidase; PDBTitle: human aldehyde oxidase in complex with phthalazine and thioridazine
76	c2uval_	Alignment	not modelled	91.2	31	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	c2vkhH_	Alignment	not modelled	89.6	31	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	c2wvaA_	Alignment	not modelled	88.8	12	PDB header: oxidoreductase Chain: A: PDB Molecule: aox3;

78	c2zyvA	Alignment	not modelled	88.9	12	PDBTitle: crystal structure of the mouse liver aldehyde oxidase 3 (maox3) PDB header: transferase
79	c4b3yB	Alignment	not modelled	86.3	28	Chain: B: PDB Molecule: fatty acid synthase; PDBTitle: cryo-em structure of the mycobacterial fatty acid synthase
80	d1kx9b	Alignment	not modelled	61.2	17	Fold: alpha-alpha superhelix Superfamily: Chemosensory protein Csp2 Family: Chemosensory protein Csp2
81	d1jaka1	Alignment	not modelled	61.1	29	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
82	c3komB	Alignment	not modelled	60.9	11	PDB header: transferase Chain: B: PDB Molecule: transketolase; PDBTitle: crystal structure of apo transketolase from francisella tularensis
83	c2gvsA	Alignment	not modelled	60.9	29	PDB header: lipid binding protein Chain: A: PDB Molecule: chemosensory protein csp-sg4; PDBTitle: nmr solution structure of cspsg4
84	d1n8va	Alignment	not modelled	60.8	17	Fold: alpha-alpha superhelix Superfamily: Chemosensory protein Csp2 Family: Chemosensory protein Csp2
85	d1yhta1	Alignment	not modelled	58.7	29	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
86	c6je8A	Alignment	not modelled	58.2	33	PDB header: hydrolase Chain: A: PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: crystal structure of a beta-n-acetylhexosaminidase
87	c5oarB	Alignment	not modelled	57.2	29	PDB header: hydrolase Chain: B: PDB Molecule: beta-hexosaminidase; PDBTitle: crystal structure of native beta-n-acetylhexosaminidase isolated from <i>Aspergillus oryzae</i>
88	c4h04B	Alignment	not modelled	54.8	14	PDB header: hydrolase Chain: B: PDB Molecule: lacto-n-biosidase; PDBTitle: lacto-n-biosidase from bifidobacterium bifidum
89	c3gh7A	Alignment	not modelled	54.2	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
90	c3nsnA	Alignment	not modelled	53.3	29	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	52.7	29	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
92	c2yl8A	Alignment	not modelled	52.3	24	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	c2ylaA	Alignment	not modelled	51.6	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
94	d2gjxa1	Alignment	not modelled	50.9	38	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
95	d1nowa1	Alignment	not modelled	50.7	33	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
96	c1nouA	Alignment	not modelled	49.9	33	PDB header: hydrolase Chain: A: PDB Molecule: beta-hexosaminidase beta chain; PDBTitle: native human lysosomal beta-hexosaminidase isoform b
97	c1m04A	Alignment	not modelled	49.2	29	PDB header: hydrolase Chain: A: PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: mutant streptomyces plicatus beta-hexosaminidase (d313n) in complex2 with product (glcnac)
98	c6ezrA	Alignment	not modelled	48.1	38	PDB header: hydrolase Chain: A: PDB Molecule: beta-n-acetylglucosaminidase nag2; PDBTitle: crystal structure of gh20 exo beta-n-acetylglucosaminidase from vibrio2 harveyi
99	c2gjxE	Alignment	not modelled	47.9	38	PDB header: hydrolase Chain: E: PDB Molecule: beta-hexosaminidase alpha chain; PDBTitle: crystallographic structure of human beta-hexosaminidase a
100	c3rcnA	Alignment	not modelled	46.3	29	PDB header: hydrolase Chain: A: PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: crystal structure of beta-n-acetylhexosaminidase from arthrobacter2 aureescens
101	c3lmyA	Alignment	not modelled	45.7	33	PDB header: hydrolase Chain: A: PDB Molecule: beta-hexosaminidase subunit beta; PDBTitle: the crystal structure of beta-hexosaminidase b in complex with2 pyrimethamine
102	c3rpmA	Alignment	not modelled	44.8	24	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	c4pysB	Alignment	not modelled	41.3	38	PDB header: hydrolase Chain: B: PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: the crystal structure of beta-n-acetylhexosaminidase from bacteroides2 fragilis nctc 9343
104	c2bp7F	Alignment	not modelled	40.3	8	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	c1qbaA_	Alignment	not modelled	36.2	29	PDB header: glycosyl hydrolase Chain: A: PDB Molecule: chitobiase; PDBTitle: bacterial chitobiase, glycosyl hydrolase family 20
106	c3m7iA_	Alignment	not modelled	35.2	12	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
107	c3zihB_	Alignment	not modelled	33.2	16	PDB header: cell cycle Chain: B: PDB Molecule: cell division protein sepf; PDBTitle: bacillus subtilis sepf, c-terminal domain
108	d1qupa2	Alignment	not modelled	33.0	14	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
109	d1umdb1	Alignment	not modelled	31.4	11	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase Pyr module
110	c2epoB_	Alignment	not modelled	31.4	24	PDB header: hydrolase Chain: B: PDB Molecule: n-acetyl-beta-d-glucosaminidase; PDBTitle: n-acetyl-b-d-glucosaminidase (gcna) from streptococcus gordonii
111	c1um9D_	Alignment	not modelled	30.6	9	PDB header: oxidoreductase Chain: D: PDB Molecule: 2-oxo acid dehydrogenase beta subunit; PDBTitle: branched-chain 2-oxo acid dehydrogenase (e1) from thermus2 thermophilus hb8 in apo-form
112	c1qupA_	Alignment	not modelled	29.4	8	PDB header: chaperone Chain: A: PDB Molecule: superoxide dismutase 1 copper chaperone; PDBTitle: crystal structure of the copper chaperone for superoxide dismutase
113	c5fkvA_	Alignment	not modelled	29.3	29	PDB header: transferase Chain: A: PDB Molecule: dna polymerase iii subunit alpha; PDBTitle: cryo-em structure of the e. coli replicative dna polymerase complex2 bound to dna (dna polymerase iii alpha, beta, epsilon, tau complex)
114	d1ik6a1	Alignment	not modelled	29.3	15	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase Pyr module
115	c1ik6A_	Alignment	not modelled	28.6	10	PDB header: oxidoreductase Chain: A: PDB Molecule: pyruvate dehydrogenase; PDBTitle: 3d structure of the e1beta subunit of pyruvate2 dehydrogenase from the archeon pyrobaculum aerophilum
116	d1poib_	Alignment	not modelled	27.6	25	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: CoA transferase beta subunit-like
117	d1w85b1	Alignment	not modelled	26.4	15	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase Pyr module
118	c6a8mA_	Alignment	not modelled	26.0	7	PDB header: dna binding protein Chain: A: PDB Molecule: fact complex subunit spt16; PDBTitle: n-terminal domain of fact complex subunit spt16 from eremothecium2 gossypii (ashbya gossypii)
119	d2ozlb1	Alignment	not modelled	25.8	19	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase Pyr module
120	c2hnhA_	Alignment	not modelled	25.7	29	PDB header: transferase Chain: A: PDB Molecule: dna polymerase iii alpha subunit; PDBTitle: crystal structure of the catalytic alpha subunit of e. coli2 replicative dna polymerase iii