

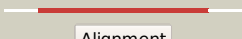

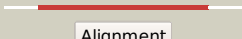



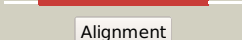



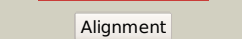

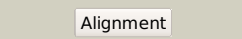

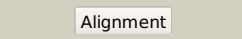

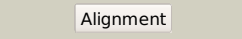

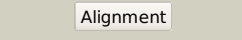



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3790_(-)_4235957_4237342
Date	Fri Aug 9 18:20:49 BST 2019
Unique Job ID	02e642758a342408

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4fdoA_	 Alignment		100.0	100	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: A: PDB Molecule: oxidoreductase dpre1; PDBTitle: mycobacterium tuberculosis dpre1 in complex with ct319
2	c2vfvA_	 Alignment		100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: xylitol oxidase; PDBTitle: alditol oxidase from streptomyces coelicolor a3(2): complex2 with sulphite
3	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
4	c4ml8C_	 Alignment		100.0	15	PDB header: oxidoreductase Chain: C: PDB Molecule: cytokinin oxidase 2; PDBTitle: structure of maize cytokinin oxidase/dehydrogenase 2 (zmcko2)
5	c3bw7A_	 Alignment		100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: cytokinin dehydrogenase 1; PDBTitle: maize cytokinin oxidase/dehydrogenase complexed with the allenic2 cytokinin analog ha-1
6	c3pm9A_	 Alignment		100.0	13	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
7	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
8	c2bvfa_	 Alignment		100.0	18	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)
9	c1i19B_	 Alignment		100.0	14	PDB header: oxidoreductase Chain: B: PDB Molecule: cholesterol oxidase; PDBTitle: crystal structure of cholesterol oxidase from b.sterolicum
10	c3vteA_	 Alignment		100.0	13	PDB header: oxidoreductase Chain: A: PDB Molecule: tetrahydrocannabinolic acid synthase; PDBTitle: crystal structure of tetrahydrocannabinolic acid synthase from2 cannabis sativa
11	c4bc9C_	 Alignment		100.0	14	PDB header: transferase Chain: C: PDB Molecule: alkyldihydroxyacetonephosphate synthase, peroxisomal; PDBTitle: mammalian alkyldihydroxyacetonephosphate synthase: wild-type, adduct2 with cyanoethyl

12	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
13	c3w8wA_	Alignment		100.0	17	PDB header: oxidoreductase Chain: A; PDB Molecule: putative fad-dependent oxygenase encm; PDBTitle: the crystal structure of encm
14	c3js8A_	Alignment		100.0	18	PDB header: oxidoreductase Chain: A; PDB Molecule: cholesterol oxidase; PDBTitle: solvent-stable cholesterol oxidase
15	c1wveB_	Alignment		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
16	c5l6fA_	Alignment		100.0	15	PDB header: oxidoreductase Chain: A; PDB Molecule: fad linked oxidase-like protein; PDBTitle: xylooligosaccharide oxidase from myceliophthora thermophila c1 in2 complex with xylobiose
17	c4ud8B_	Alignment		100.0	11	PDB header: oxidoreductase Chain: B; PDB Molecule: fad-binding and bbe domain-containing protein; PDBTitle: atbbe15
18	c6eo5A_	Alignment		100.0	14	PDB header: oxidoreductase Chain: A; PDB Molecule: ppbbe-like 1 d396n; PDBTitle: physcomitrella patens bbe-like 1 variant d396n
19	c3tjsA_	Alignment		100.0	13	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
20	c3rjaA_	Alignment		100.0	14	PDB header: oxidoreductase Chain: A; PDB Molecule: carbohydrate oxidase; PDBTitle: crystal structure of carbohydrate oxidase from microdochium nivale in2 complex with substrate analogue
21	c1zr6A_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: A; PDB Molecule: glucooligosaccharide oxidase; PDBTitle: the crystal structure of an acremonium strictum glucooligosaccharide2 oxidase reveals a novel flavinylation
22	c6f73B_	Alignment	not modelled	100.0	15	PDB header: flavoprotein Chain: B; PDB Molecule: mtvao615; PDBTitle: crystal structure of vao-type flavoprotein mtvao615 at ph 5.0 from2 myceliophthora thermophila c1
23	c6f74B_	Alignment	not modelled	100.0	14	PDB header: flavoprotein Chain: B; PDB Molecule: alcohol oxidase; PDBTitle: crystal structure of vao-type flavoprotein mtvao713 from2 myceliophthora thermophila c1
24	c3fwaA_	Alignment	not modelled	100.0	15	PDB header: flavoprotein Chain: A; PDB Molecule: reticuline oxidase; PDBTitle: structure of berberine bridge enzyme, c166a variant in complex with2 (s)-reticuline
25	c3d2hA_	Alignment	not modelled	100.0	14	PDB header: oxidoreductase Chain: A; PDB Molecule: berberine bridge-forming enzyme; PDBTitle: structure of berberine bridge enzyme from eschscolzia californica,2 monoclinic crystal form
26	c5d79B_	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: B; PDB Molecule: berberine bridge enzyme-like protein; PDBTitle: structure of bbe-like #28 from arabidopsis thaliana
27	c3popD_	Alignment	not modelled	100.0	17	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	c5i1wD_	Alignment	not modelled	100.0	14	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
						PDB header: oxidoreductase

29	c5fxpA	Alignment	not modelled	100.0	11	Chain: A: PDB Molecule: eugenol oxidase; PDBTitle: crystal structure of eugenol oxidase in complex with2 vanillin
30	c2y3rC	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: C: PDB Molecule: tamli; PDBTitle: structure of the tirandamycin-bound fad-dependent tirandamycin oxidase2 tamli in p21 space group
31	c2ipiD	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: D: PDB Molecule: aclacinomycin oxidoreductase (aknox); PDBTitle: crystal structure of aclacinomycin oxidoreductase
32	c2wdwB	Alignment	not modelled	100.0	15	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	c1ahuB	Alignment	not modelled	100.0	11	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	c2uuuC	Alignment	not modelled	100.0	11	PDB header: transferase Chain: C: PDB Molecule: alkyldihydroxyacetonephosphate synthase; PDBTitle: alkyldihydroxyacetonephosphate synthase in p1
35	c1f0xA	Alignment	not modelled	100.0	11	PDB header: oxidoreductase Chain: A: PDB Molecule: d-lactate dehydrogenase; PDBTitle: crystal structure of d-lactate dehydrogenase, a peripheral membrane2 respiratory enzyme.
36	d1w1oa2	Alignment	not modelled	100.0	27	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: FAD-linked oxidases, N-terminal domain
37	d2i0ka2	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
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	d1e8ga2	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
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	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	21	PDB header: oxidoreductase Chain: A: PDB Molecule: udp-n-acetylenolpyruvylglucosamine reductase; PDBTitle: crystal structure of a murb family ep-udp-n-acetylglucosamine2 reductase
44	c4jayC	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: C: PDB Molecule: udp-n-acetylenolpyruvylglucosamine 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-acetylenolpyruvylglucosamine reductase; PDBTitle: crystal structure of s. aureus murb
46	c1mbbA	Alignment	not modelled	99.9	16	PDB header: oxidoreductase Chain: A: PDB Molecule: uridine diphospho-n-acetylenolpyruvylglucosamine PDBTitle: oxidoreductase
47	c2yvsA	Alignment	not modelled	99.9	18	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	14	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
49	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
50	c2gquA	Alignment	not modelled	99.8	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	d2i0ka1	Alignment	not modelled	99.6	10	Fold: Ferredoxin-like Superfamily: FAD-linked oxidases, C-terminal domain Family: Cholesterol oxidase
52	d1w1oa1	Alignment	not modelled	98.5	10	Fold: Ferredoxin-like Superfamily: FAD-linked oxidases, C-terminal domain Family: Cytokinin dehydrogenase 1
53	d1e8ga1	Alignment	not modelled	98.3	10	Fold: Ferredoxin-like Superfamily: FAD-linked oxidases, C-terminal domain Family: Vanillyl-alcohol oxidase-like

54	d1wvfa1	Alignment	not modelled	98.2	10	Fold: Ferredoxin-like Superfamily: FAD-linked oxidases, C-terminal domain Family: Vanillyl-alcohol oxidase-like
55	d1ffvc2	Alignment	not modelled	97.9	16	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like
56	c5y6qB	Alignment	not modelled	97.4	20	PDB header: oxidoreductase Chain: B: PDB Molecule: aldehyde oxidase medium subunit; PDBTitle: crystal structure of an aldehyde oxidase from methylobacillus sp.2 ky4400
57	c1t3qF	Alignment	not modelled	97.4	18	PDB header: oxidoreductase Chain: F: PDB Molecule: quinoline 2-oxidoreductase medium subunit; PDBTitle: crystal structure of quinoline 2-oxidoreductase from pseudomonas2 putida 86
58	c1ffuF	Alignment	not modelled	97.4	17	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	c1n62C	Alignment	not modelled	97.4	17	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
60	d1v97a6	Alignment	not modelled	97.3	10	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like
61	c3hrdC	Alignment	not modelled	97.3	16	PDB header: oxidoreductase Chain: C: PDB Molecule: nicotinate dehydrogenase fad-subunit; PDBTitle: crystal structure of nicotinate dehydrogenase
62	d1t3qc2	Alignment	not modelled	97.3	18	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like
63	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
64	d1n62c2	Alignment	not modelled	97.1	17	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like
65	c4zohB	Alignment	not modelled	97.1	14	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase fad-binding subunit; PDBTitle: crystal structure of glyceraldehyde oxidoreductase
66	c5g5hB	Alignment	not modelled	96.8	18	PDB header: oxidoreductase Chain: B: PDB Molecule: putative xanthine dehydrogenase yags fad-binding subunit; PDBTitle: escherichia coli periplasmic aldehyde oxidase r440h mutant
67	c3etrM	Alignment	not modelled	96.8	8	PDB header: oxidoreductase Chain: M: PDB Molecule: xanthine dehydrogenase/oxidase; PDBTitle: crystal structure of xanthine oxidase in complex with lumazine
68	c3b9jj	Alignment	not modelled	96.7	8	PDB header: oxidoreductase Chain: J: PDB Molecule: xanthine oxidase; PDBTitle: structure of xanthine oxidase with 2-hydroxy-6-methylpurine
69	d1f0xa1	Alignment	not modelled	96.7	8	Fold: Ferredoxin-like Superfamily: FAD-linked oxidases, C-terminal domain Family: D-lactate dehydrogenase
70	d1jroa4	Alignment	not modelled	96.6	17	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like
71	c1rm6E	Alignment	not modelled	96.4	15	PDB header: oxidoreductase Chain: E: PDB Molecule: 4-hydroxybenzoyl-coa reductase beta subunit; PDBTitle: structure of 4-hydroxybenzoyl-coa reductase from thauera2 aromatica
72	c2w3rG	Alignment	not modelled	96.2	18	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	c1wygA	Alignment	not modelled	96.0	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)
74	d1rm6b2	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
75	c4uhxA	Alignment	not modelled	93.4	9	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde oxidase; PDBTitle: human aldehyde oxidase in complex with phthalazine and thioridazine
76	c3zyvA	Alignment	not modelled	92.8	6	PDB header: oxidoreductase Chain: A: PDB Molecule: aox3; PDBTitle: crystal structure of the mouse liver aldehyde oxidase 3 (maox3)
77	c2uval	Alignment	not modelled	91.0	23	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	c2vzrH	Alignment	not modelled	88.1	20	PDB header: transferase Chain: H: PDB Molecule: fatty acid synthase subunit beta;

78	c4vsk1	Alignment	not modelled	89.1	29	PDBTitle: structure of the cerulenin-inhibited fungal fatty acid synthase type I2 multienzyme complex PDB header: transferase
79	c4b3yB	Alignment	not modelled	79.1	28	Chain: B: PDB Molecule: fatty acid synthase; PDBTitle: cryo-em structure of the mycobacterial fatty acid synthase
80	c2gvsA	Alignment	not modelled	72.7	24	PDB header: lipid binding protein Chain: A: PDB Molecule: chemosensory protein csp-sg4; PDBTitle: nmr solution structure of cspsg4
81	d1n8va	Alignment	not modelled	69.6	21	Fold: alpha-alpha superhelix Superfamily: Chemosensory protein Csp2 Family: Chemosensory protein Csp2
82	d1kx9b	Alignment	not modelled	69.3	21	Fold: alpha-alpha superhelix Superfamily: Chemosensory protein Csp2 Family: Chemosensory protein Csp2
83	c1jk9D	Alignment	not modelled	61.0	7	PDB header: oxidoreductase Chain: D: PDB Molecule: copper chaperone for superoxide dismutase; PDBTitle: heterodimer between h48f-ysoD1 and yccs
84	c1qupA	Alignment	not modelled	60.3	7	PDB header: chaperone Chain: A: PDB Molecule: superoxide dismutase 1 copper chaperone; PDBTitle: crystal structure of the copper chaperone for superoxide dismutase
85	d1itza2	Alignment	not modelled	55.6	12	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like Pyr module
86	c2bp7F	Alignment	not modelled	41.1	16	PDB header: oxidoreductase Chain: F: PDB Molecule: 2-oxoisovalerate dehydrogenase beta subunit; PDBTitle: new crystal form of the pseudomonas putida branched-chain2 dehydrogenase (e1)
87	c2r8pA	Alignment	not modelled	40.1	7	PDB header: transferase Chain: A: PDB Molecule: transketolase 1; PDBTitle: transketolase from e. coli in complex with substrate d-fructose-6-2 phosphate
88	d2r8oa1	Alignment	not modelled	39.8	4	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like Pyr module
89	d1umdb1	Alignment	not modelled	38.9	7	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase Pyr module
90	c4wxcC	Alignment	not modelled	37.3	9	PDB header: lyase Chain: C: PDB Molecule: biotin and thiamin synthesis associated; PDBTitle: crystal structure of hydG: a maturase of the [fefe]-hydrogenase
91	c4usiC	Alignment	not modelled	35.5	14	PDB header: signaling protein Chain: C: PDB Molecule: nitrogen regulatory protein pii; PDBTitle: nitrogen regulatory protein pii from chlamydomonas2 reinhardtii in complex with mgatp and 2-oxoglutarate
92	c3komB	Alignment	not modelled	35.2	11	PDB header: transferase Chain: B: PDB Molecule: transketolase; PDBTitle: crystal structure of apo transketolase from francisella tularensis
93	c6je8A	Alignment	not modelled	34.7	14	PDB header: hydrolase Chain: A: PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: crystal structure of a beta-n-acetylhexosaminidase
94	c4r25A	Alignment	not modelled	34.6	12	PDB header: transcription Chain: A: PDB Molecule: nitrogen regulatory pii-like protein; PDBTitle: structure of b. subtilis glnK
95	d1qupa2	Alignment	not modelled	34.6	9	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
96	c5oarB	Alignment	not modelled	33.3	24	PDB header: hydrolase Chain: B: PDB Molecule: beta-hexosaminidase; PDBTitle: crystal structure of native beta-n-acetylhexosaminidase isolated from2 aspergillus oryzae
97	c3ncpD	Alignment	not modelled	33.0	18	PDB header: signaling protein Chain: D: PDB Molecule: nitrogen regulatory protein p-ii (glnb-2); PDBTitle: glnK2 from archaeoglobus fulgidus
98	c3bzqA	Alignment	not modelled	32.8	24	PDB header: signaling protein/transcription Chain: A: PDB Molecule: nitrogen regulatory protein p-ii; PDBTitle: high resolution crystal structure of nitrogen regulatory protein2 (rv2919c) of mycobacterium tuberculosis
99	d1jaka1	Alignment	not modelled	32.6	19	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
100	c3hylB	Alignment	not modelled	32.5	13	PDB header: transferase Chain: B: PDB Molecule: transketolase; PDBTitle: crystal structure of transketolase from bacillus anthracis
101	c2rd5D	Alignment	not modelled	31.9	18	PDB header: protein binding Chain: D: PDB Molecule: pii protein; PDBTitle: structural basis for the regulation of n-acetylglutamate kinase by pii2 in arabidopsis thaliana
102	c2crlA	Alignment	not modelled	31.8	5	PDB header: chaperone Chain: A: PDB Molecule: copper chaperone for superoxide dismutase; PDBTitle: the apo form of hma domain of copper chaperone for2 superoxide dismutase
103	d1gpua2	Alignment	not modelled	31.3	14	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like Pyr module
						Fold: Thiamin diphosphate-binding fold (THDP-binding)

104	d1w85b1	Alignment	not modelled	30.9	15	Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase Pyr module
105	c4h04B	Alignment	not modelled	30.3	24	PDB header: hydrolase Chain: B: PDB Molecule: lacto-n-biosidase; PDBTitle: lacto-n-biosidase from bifidobacterium bifidum
106	d1ik6a1	Alignment	not modelled	29.9	15	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase Pyr module
107	d2bi7a1	Alignment	not modelled	29.4	16	Fold: Nucleotide-binding domain Superfamily: Nucleotide-binding domain Family: UDP-galactopyranose mutase, N-terminal domain
108	c2yl8A	Alignment	not modelled	29.4	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
109	c4c7vA	Alignment	not modelled	29.3	11	PDB header: transferase Chain: A: PDB Molecule: transketolase; PDBTitle: apo transketolase from lactobacillus salivarius at 2.2a resolution
110	d2piia	Alignment	not modelled	29.2	17	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Prokaryotic signal transducing protein
111	c6a8mA	Alignment	not modelled	29.0	10	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)
112	c4ozlA	Alignment	not modelled	28.7	18	PDB header: signaling protein Chain: A: PDB Molecule: nitrogen regulatory protein p-ii; PDBTitle: glnk2 from haloferax mediterranei complexed with amp
113	c3nsnA	Alignment	not modelled	28.3	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
114	c3m7iA	Alignment	not modelled	28.2	9	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
115	d1yhta1	Alignment	not modelled	27.9	14	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
116	c2ylaA	Alignment	not modelled	26.7	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
117	d1o6da	Alignment	not modelled	26.3	11	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: YbeA-like
118	d1poib	Alignment	not modelled	26.3	26	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: CoA transferase beta subunit-like
119	d1fe0a	Alignment	not modelled	25.9	28	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
120	c3gh7A	Alignment	not modelled	25.9	14	PDB header: hydrolase Chain: A: PDB Molecule: beta-hexosaminidase; PDBTitle: crystal structure of beta-hexosaminidase from paenibacillus sp. ts122 in complex with galnac