

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1f0xA_	 Alignment		100.0	98	PDB header: oxidoreductase Chain: A: PDB Molecule: d-lactate dehydrogenase; PDBTitle: crystal structure of d-lactate dehydrogenase, a peripheral2 membrane respiratory enzyme.
2	c1ahuB_	 Alignment		100.0	12	PDB header: flavoenzyme Chain: B: PDB Molecule: vanillyl-alcohol oxidase; PDBTitle: structure of the octameric flavoenzyme vanillyl-alcohol2 oxidase in complex with p-cresol
3	c2uuvC_	 Alignment		100.0	15	PDB header: transferase Chain: C: PDB Molecule: alkyl dihydroxyacetonephosphate synthase; PDBTitle: alkyl dihydroxyacetonephosphate synthase in p1
4	c3pm9A_	 Alignment		100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative dehydrogenase (rpa1076) from2 rhodopseudomonas palustris cga009 at 2.57 a resolution
5	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
6	d1f0xa2	 Alignment		100.0	100	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: FAD-linked oxidases, N-terminal domain
7	c3bw7A_	 Alignment		100.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: cytokinin dehydrogenase 1; PDBTitle: maize cytokinin oxidase/dehydrogenase complexed with the allenic2 cytokinin analog ha-1
8	c2exrA_	 Alignment		100.0	11	PDB header: oxidoreductase Chain: A: PDB Molecule: cytokinin dehydrogenase 7; PDBTitle: x-ray structure of cytokinin oxidase/dehydrogenase (ckx)2 from arabidopsis thaliana at5g21482
9	c1zr6A_	 Alignment		100.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: glucosylglycosyltransferase; PDBTitle: the crystal structure of an acremonium strictum glucosylglycosyltransferase2 reveals a novel flavinylation
10	c3fwaA_	 Alignment		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
11	c2bvfa_	 Alignment		100.0	13	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)

12	c3d2hA_	Alignment		100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: berberine bridge-forming enzyme; PDBTitle: structure of berberine bridge enzyme from eschscholzia californica,2 monoclinic crystal form
13	c2ipiD_	Alignment		100.0	12	PDB header: oxidoreductase Chain: D: PDB Molecule: aclacinomycin oxidoreductase (aknox); PDBTitle: crystal structure of aclacinomycin oxidoreductase
14	d1f0xa1	Alignment		100.0	100	Fold: Ferredoxin-like Superfamily: FAD-linked oxidases, C-terminal domain Family: D-lactate dehydrogenase
15	c3popD_	Alignment		100.0	13	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
16	c2wdwB_	Alignment		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
17	d1wvfa2	Alignment		100.0	12	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: FAD-linked oxidases, N-terminal domain
18	d1e8ga2	Alignment		100.0	12	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: FAD-linked oxidases, N-terminal domain
19	c2y3rC_	Alignment		100.0	13	PDB header: oxidoreductase Chain: C: PDB Molecule: taml; PDBTitle: structure of the tirandamycin-bound fad-dependent2 tirandamycin oxidase taml in p21 space group
20	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
21	cli19B_	Alignment	not modelled	100.0	11	PDB header: oxidoreductase Chain: B: PDB Molecule: cholesterol oxidase; PDBTitle: crystal structure of cholesterol oxidase from b.sterolicum
22	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
23	c3js8A_	Alignment	not modelled	100.0	13	PDB header: oxidoreductase Chain: A: PDB Molecule: cholesterol oxidase; PDBTitle: solvent-stable cholesterol oxidase
24	d1hska1	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
25	d2i0ka2	Alignment	not modelled	100.0	16	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: FAD-linked oxidases, N-terminal domain
26	d1e8ga1	Alignment	not modelled	100.0	11	Fold: Ferredoxin-like Superfamily: FAD-linked oxidases, C-terminal domain Family: Vanillyl-alcohol oxidase-like
27	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
28	c1hska_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: udp-n-acetylenolpyruvoylglucosamine reductase; PDBTitle: crystal structure of s. aureus murB
						Fold: Ferredoxin-like

29	d1wvfa1	Alignment	not modelled	100.0	12	Superfamily: FAD-linked oxidases, C-terminal domain Family: Vanillyl-alcohol oxidase-like
30	c2yvsA	Alignment	not modelled	99.9	17	PDB header: oxidoreductase Chain: A: PDB Molecule: glycolate oxidase subunit glce; PDBTitle: crystal structure of glycolate oxidase subunit glce from thermus2 thermophilus hb8
31	c1mbbA	Alignment	not modelled	99.9	17	PDB header: oxidoreductase Chain: A: PDB Molecule: uridine diphospho-n-acetylenolpyruvylglucosamine PDBTitle: oxidoreductase
32	c3i99A	Alignment	not modelled	99.9	14	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
33	c2gquA	Alignment	not modelled	99.7	17	PDB header: oxidoreductase Chain: A: PDB Molecule: udp-n-acetylenolpyruvylglucosamine reductase; PDBTitle: crystal structure of udp-n-acetylenolpyruvylglucosamine2 reductase (murb) from thermus caldophilus
34	d1ffvc2	Alignment	not modelled	97.7	17	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like
35	d3b9jb2	Alignment	not modelled	97.6	19	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like
36	c1n62C	Alignment	not modelled	97.5	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
37	c1t3qF	Alignment	not modelled	97.5	14	PDB header: oxidoreductase Chain: F: PDB Molecule: quinoline 2-oxidoreductase medium subunit; PDBTitle: crystal structure of quinoline 2-oxidoreductase from pseudomonas2 putida 86
38	c1ffuF	Alignment	not modelled	97.5	16	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
39	d1n62c2	Alignment	not modelled	97.5	15	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like
40	c3hrdC	Alignment	not modelled	97.5	18	PDB header: oxidoreductase Chain: C: PDB Molecule: nicotinate dehydrogenase fad-subunit; PDBTitle: crystal structure of nicotinate dehydrogenase
41	d1v97a6	Alignment	not modelled	97.4	21	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like
42	d1t3qc2	Alignment	not modelled	97.4	14	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like
43	c3etrM	Alignment	not modelled	97.3	20	PDB header: oxidoreductase Chain: M: PDB Molecule: xanthine dehydrogenase/oxidase; PDBTitle: crystal structure of xanthine oxidase in complex with2 lumazine
44	c3b9jl	Alignment	not modelled	97.3	20	PDB header: oxidoreductase Chain: J: PDB Molecule: xanthine oxidase; PDBTitle: structure of xanthine oxidase with 2-hydroxy-6-methyl purine
45	c2w3rG	Alignment	not modelled	97.2	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
46	d1jroa4	Alignment	not modelled	97.2	17	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like
47	c1rm6E	Alignment	not modelled	97.1	16	PDB header: oxidoreductase Chain: E: PDB Molecule: 4-hydroxybenzoyl-coa reductase beta subunit; PDBTitle: structure of 4-hydroxybenzoyl-coa reductase from thauera2 aromatica
48	d1rm6b2	Alignment	not modelled	96.7	18	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like
49	c1wygA	Alignment	not modelled	96.7	18	PDB header: oxidoreductase Chain: A: PDB Molecule: xanthine dehydrogenase/oxidase; PDBTitle: crystal structure of a rat xanthine dehydrogenase triple mutant2 (c535a, c992r and c1324s)
50	d1w1oa1	Alignment	not modelled	96.3	15	Fold: Ferredoxin-like Superfamily: FAD-linked oxidases, C-terminal domain Family: Cytokinin dehydrogenase 1
51	c3dedB	Alignment	not modelled	78.6	13	PDB header: membrane protein Chain: B: PDB Molecule: probable hemolysin; PDBTitle: c-terminal domain of probable hemolysin from chromobacterium violaceum
52	d1jaka1	Alignment	not modelled	71.1	5	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
53	d1nowa1	Alignment	not modelled	70.1	10	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain

54	d1qbaa3	Alignment	not modelled	68.8	10	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
55	c2yl8A_	Alignment	not modelled	68.3	0	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
56	d1yhta1	Alignment	not modelled	68.2	10	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
57	d2z67a1	Alignment	not modelled	68.1	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: SepSecS-Ilike
58	c1nouA_	Alignment	not modelled	68.0	10	PDB header: hydrolase Chain: A: PDB Molecule: beta-hexosaminidase beta chain; PDBTitle: native human lysosomal beta-hexosaminidase isoform b
59	c1m04A_	Alignment	not modelled	67.9	5	PDB header: hydrolase Chain: A: PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: mutant streptomyces plicatus beta-hexosaminidase (d313n) in complex2 with product (glcnac)
60	c2ylaA_	Alignment	not modelled	67.8	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
61	c3rcnA_	Alignment	not modelled	67.7	5	PDB header: hydrolase Chain: A: PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: crystal structure of beta-n-acetylhexosaminidase from arthrobacter2 aureusens
62	d2gixa1	Alignment	not modelled	67.6	10	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
63	d3deda1	Alignment	not modelled	67.0	13	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like
64	c3gh7A_	Alignment	not modelled	66.8	0	PDB header: hydrolase Chain: A: PDB Molecule: beta-hexosaminidase; PDBTitle: crystal structure of beta-hexosaminidase from paenibacillus2 sp. ts12 in complex with galnac
65	c3nsnA_	Alignment	not modelled	66.0	10	PDB header: hydrolase Chain: A: PDB Molecule: n-acetylglucosaminidase; PDBTitle: crystal structure of insect beta-n-acetyl-d-hexosaminidase ofhex12 complexed with tmg-chitotriomycin
66	c2gjxE_	Alignment	not modelled	65.3	10	PDB header: hydrolase Chain: E: PDB Molecule: beta-hexosaminidase alpha chain; PDBTitle: crystallographic structure of human beta-hexosaminidase a
67	c3lmyA_	Alignment	not modelled	64.7	10	PDB header: hydrolase Chain: A: PDB Molecule: beta-hexosaminidase subunit beta; PDBTitle: the crystal structure of beta-hexosaminidase b in complex with2 pyrimethamine
68	c3rpmA_	Alignment	not modelled	64.4	0	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
69	d2nqwa1	Alignment	not modelled	64.2	15	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like
70	c1qbaA_	Alignment	not modelled	62.3	10	PDB header: glycosyl hydrolase Chain: A: PDB Molecule: chitobiase; PDBTitle: bacterial chitobiase, glycosyl hydrolase family 20
71	c2epoB_	Alignment	not modelled	55.8	14	PDB header: hydrolase Chain: B: PDB Molecule: n-acetyl-beta-d-glucosaminidase; PDBTitle: n-acetyl-b-d-glucosaminidase (gcna) from streptococcus gordonii
72	c2x24B_	Alignment	not modelled	47.8	22	PDB header: ligase Chain: B: PDB Molecule: acetyl-coa carboxylase; PDBTitle: bovine acc2 ct domain in complex with inhibitor
73	d2o1ra1	Alignment	not modelled	46.0	16	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like
74	d2plsai	Alignment	not modelled	45.6	17	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like
75	d1wo8a1	Alignment	not modelled	43.7	24	Fold: Methylglyoxal synthase-like Superfamily: Methylglyoxal synthase-like Family: Methylglyoxal synthase, MgsA
76	c3ff6D_	Alignment	not modelled	42.3	22	PDB header: ligase Chain: D: PDB Molecule: acetyl-coa carboxylase 2; PDBTitle: human acc2 ct domain with cp-640186
77	c2yv1A_	Alignment	not modelled	42.2	15	PDB header: ligase Chain: A: PDB Molecule: succinyl-coa ligase [adp-forming] subunit alpha; PDBTitle: crystal structure of succinyl-coa synthetase alpha chain from2 methanocaldococcus jannaschii dsm 2661
78	c2yswB_	Alignment	not modelled	42.0	13	PDB header: lyase Chain: B: PDB Molecule: 3-dehydroquinate dehydratase; PDBTitle: crystal structure of the 3-dehydroquinate dehydratase from aquifex2 aeolicus vf5
79	d1pixa3	Alignment	not modelled	41.6	17	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
80	d2bi7a1	Alianment	not modelled	39.9	11	Fold: Nucleotide-binding domain Superfamily: Nucleotide-binding domain

						Family: UDP-galactopyranose mutase, N-terminal domain
81	d1b93a_	Alignment	not modelled	37.7	6	Fold: Methylglyoxal synthase-like Superfamily: Methylglyoxal synthase-like Family: Methylglyoxal synthase, MgsA
82	d1vmda_	Alignment	not modelled	37.1	0	Fold: Methylglyoxal synthase-like Superfamily: Methylglyoxal synthase-like Family: Methylglyoxal synthase, MgsA
83	d1umdb1	Alignment	not modelled	33.9	19	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase Pyr module
84	d2p5ia1	Alignment	not modelled	33.8	17	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: LplA-like
85	d1ik6a1	Alignment	not modelled	33.7	26	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase Pyr module
86	c2uval_	Alignment	not modelled	33.3	17	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
87	c1oi7A_	Alignment	not modelled	32.9	16	PDB header: synthetase Chain: A: PDB Molecule: succinyl-coa synthetase alpha chain; PDBTitle: the crystal structure of succinyl-coa synthetase alpha2 subunit from thermus thermophilus
88	d2ozlb1	Alignment	not modelled	32.8	15	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase Pyr module
89	d1js3a_	Alignment	not modelled	32.6	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Pyridoxal-dependent decarboxylase
90	d2r2za1	Alignment	not modelled	31.7	7	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like
91	c3s01A_	Alignment	not modelled	30.4	3	PDB header: rna binding protein Chain: A: PDB Molecule: heterogeneous nuclear ribonucleoprotein I; PDBTitle: crystal structure of a heterogeneous nuclear ribonucleoprotein I2 (hnrlp) from mus musculus at 2.15 a resolution
92	c2yv2A_	Alignment	not modelled	30.3	21	PDB header: ligase Chain: A: PDB Molecule: succinyl-coa synthetase alpha chain; PDBTitle: crystal structure of succinyl-coa synthetase alpha chain from2 aeropyrum pernix k1
93	c3mwdB_	Alignment	not modelled	29.6	10	PDB header: transferase Chain: B: PDB Molecule: atp-citrate synthase; PDBTitle: truncated human atp-citrate lyase with citrate bound
94	c3e0dA_	Alignment	not modelled	29.5	4	PDB header: transferase/dna Chain: A: PDB Molecule: dna polymerase iii subunit alpha; PDBTitle: insights into the replisome from the crystal structure of2 the ternary complex of the eubacterial dna polymerase iii3 alpha-subunit
95	c1od4C_	Alignment	not modelled	29.4	17	PDB header: ligase Chain: C: PDB Molecule: acetyl-coenzyme a carboxylase; PDBTitle: acetyl-coa carboxylase carboxyltransferase domain
96	c2jlhA_	Alignment	not modelled	29.2	19	PDB header: protein transport Chain: A: PDB Molecule: yop proteins translocation protein u; PDBTitle: crystal structure of the cytoplasmic domain of yersinia2 pestis yscu n263a mutant
97	c3if2B_	Alignment	not modelled	28.0	10	PDB header: transferase Chain: B: PDB Molecule: aminotransferase; PDBTitle: crystal structure of putative amino-acid aminotransferase2 (yp_265399.1) from psychrobacter arcticum 273-4 at 2.50 a resolution
98	c2dgaA_	Alignment	not modelled	26.7	3	PDB header: rna binding protein Chain: A: PDB Molecule: kiaa0430 protein; PDBTitle: solution structure of the rna recognition motif in kiaa04302 protein
99	d2r8oa1	Alignment	not modelled	26.4	14	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like Pyr module
100	d1jmta_	Alignment	not modelled	25.6	11	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Splicing factor U2AF subunits
101	c2nhhA_	Alignment	not modelled	25.6	4	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
102	d1zoda1	Alignment	not modelled	25.6	4	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
103	c2dnoA_	Alignment	not modelled	25.5	3	PDB header: rna binding protein Chain: A: PDB Molecule: trinucleotide repeat containing 4 variant; PDBTitle: solution structure of rna binding domain in trinucleotide2 repeat containing 4 variant
104	c3ez4B_	Alignment	not modelled	25.2	10	PDB header: transferase Chain: B: PDB Molecule: 3-methyl-2-oxobutanoate hydroxymethyltransferase; PDBTitle: crystal structure of 3-methyl-2-oxobutanoate2 hydroxymethyltransferase from burkholderia pseudomallei
105	d1liza2	Alignment	not modelled	25.1	12	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding)

					Family: TK-like Pyr module
106	d1qs0b1	Alignment	not modelled	24.6	19 Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase Pyr module
107	c1pixB	Alignment	not modelled	24.4	17 PDB header: lyase Chain: B: PDB Molecule: glutaconyl-coa decarboxylase a subunit; PDBTitle: crystal structure of the carboxyltransferase subunit of the2 bacterial ion pump glutaconyl-coenzyme a decarboxylase
108	c3l1bA	Alignment	not modelled	24.0	17 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the crystal structure of the protein pa3983 with unknown2 function from pseudomonas aeruginosa pao1
109	d1w85b1	Alignment	not modelled	23.3	15 Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase Pyr module
110	d2rk5a1	Alignment	not modelled	23.0	11 Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like
111	d1c7ga	Alignment	not modelled	23.0	22 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Beta-eliminating lyases
112	c3glmD	Alignment	not modelled	22.2	8 PDB header: lyase Chain: D: PDB Molecule: glutaconyl-coa decarboxylase subunit a; PDBTitle: glutaconyl-coa decarboxylase a subunit from clostridium2 symbiosum co-crystallized with crotonyl-coa
113	c3bzrA	Alignment	not modelled	22.1	15 PDB header: membrane protein, protein transport Chain: A: PDB Molecule: escu; PDBTitle: crystal structure of escu c-terminal domain with n262d mutation, space2 group p 41 21 2
114	d3bzra1	Alignment	not modelled	22.1	15 Fold: EscU C-terminal domain-like Superfamily: EscU C-terminal domain-like Family: EscU C-terminal domain-like
115	d1knxa1	Alignment	not modelled	21.6	21 Fold: MurF and HprK N-domain-like Superfamily: HprK N-terminal domain-like Family: HPr kinase/phoshatase HprK N-terminal domain
116	c3e02A	Alignment	not modelled	21.6	4 PDB header: metal binding protein Chain: A: PDB Molecule: uncharacterized protein duf849; PDBTitle: crystal structure of a duf849 family protein (bx_e_c0271) from2 burkholderia xenovorans lb400 at 1.90 a resolution
117	c3h0jA	Alignment	not modelled	21.3	17 PDB header: transferase Chain: A: PDB Molecule: acetyl-coa carboxylase; PDBTitle: crystal structure of the carboxyltransferase domain of2 acetyl-coenzyme a carboxylase in complex with compound 2
118	c1uytC	Alignment	not modelled	21.2	17 PDB header: transferase Chain: C: PDB Molecule: acetyl-coa carboxylase; PDBTitle: acetyl-coa carboxylase carboxyltransferase domain
119	d1sffa	Alignment	not modelled	20.9	13 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
120	d2o3ga1	Alignment	not modelled	20.8	19 Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like