










#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2uuvC_	Alignment		100.0	21	PDB header: transferase Chain: C: PDB Molecule: alkyl dihydroxyacetonephosphate synthase; PDBTitle: alkyl dihydroxyacetonephosphate synthase in p1
2	c1f0xA_	Alignment		100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: d-lactate dehydrogenase; PDBTitle: crystal structure of d-lactate dehydrogenase, a peripheral2 membrane respiratory enzyme.
3	c1ahuB_	Alignment		100.0	17	PDB header: flavoenzyme Chain: B: PDB Molecule: vanillyl-alcohol oxidase; PDBTitle: structure of the octameric flavoenzyme vanillyl-alcohol2 oxidase in complex with p-cresol
4	c3pm9A_	Alignment		100.0	21	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	15	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	c3bw7A_	Alignment		100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: cytokinin dehydrogenase 1; PDBTitle: maize cytokinin oxidase/dehydrogenase complexed with the allenic2 cytokinin analog ha-1
7	c2bvfA_	Alignment		100.0	16	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)
8	c2exrA_	Alignment		100.0	16	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	c3fwaA_	Alignment		100.0	13	PDB header: flavoprotein Chain: A: PDB Molecule: reticuline oxidase; PDBTitle: structure of berberine bridge enzyme, c166a variant in complex with2 (s)-reticuline
10	c1zr6A_	Alignment		100.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: glucosylglycosaccharide oxidase; PDBTitle: the crystal structure of an acremonium strictum glucosylglycosaccharide2 oxidase reveals a novel flavinylation
11	c3d2hA_	Alignment		100.0	13	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	c2vfvA_	Alignment		100.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: xylitol oxidase; PDBTitle: alditol oxidase from streptomyces coelicolor a3(2): complex2 with sulphite
13	c2ipiD_	Alignment		100.0	16	PDB header: oxidoreductase Chain: D: PDB Molecule: aclacinomycin oxidoreductase (aknox); PDBTitle: crystal structure of aclacinomycin oxidoreductase
14	c3popD_	Alignment		100.0	15	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
15	c1i19B_	Alignment		100.0	16	PDB header: oxidoreductase Chain: B: PDB Molecule: cholesterol oxidase; PDBTitle: crystal structure of cholesterol oxidase from b.sterolicum
16	c2wdwB_	Alignment		100.0	17	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	c2y3rC_	Alignment		100.0	14	PDB header: oxidoreductase Chain: C: PDB Molecule: taml; PDBTitle: structure of the tirandamycin-bound fad-dependent2 tirandamycin oxidase taml in p21 space group
18	d1f0xa2	Alignment		100.0	18	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: FAD-linked oxidases, N-terminal domain
19	d1e8ga2	Alignment		100.0	16	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: FAD-linked oxidases, N-terminal domain
20	d1wvfa2	Alignment		100.0	15	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: FAD-linked oxidases, N-terminal domain
21	c3js8A_	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: cholesterol oxidase; PDBTitle: solvent-stable cholesterol oxidase
22	d1w1oa2	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
23	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
24	c2yvsA_	Alignment	not modelled	100.0	31	PDB header: oxidoreductase Chain: A: PDB Molecule: glycolate oxidase subunit glce; PDBTitle: crystal structure of glycolate oxidase subunit glce from thermus2 thermophilus hb8
25	d1uxya1	Alignment	not modelled	100.0	12	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase (MurB), N-terminal domain
26	d1hska1	Alignment	not modelled	100.0	15	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase (MurB), N-terminal domain
27	c1hskA_	Alignment	not modelled	99.9	15	PDB header: oxidoreductase Chain: A: PDB Molecule: udp-n-acetylenolpyruvoylglucosamine reductase; PDBTitle: crystal structure of s. aureus murb
28	c1mbbA_	Alignment	not modelled	99.9	13	PDB header: oxidoreductase Chain: A: PDB Molecule: uridine diphospho-n-acetylenolpyruvylglucosamine PDBTitle: oxidoreductase
						PDB header: oxidoreductase

29	c3i99A	Alignment	not modelled	99.9	12	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
30	c2gquA	Alignment	not modelled	99.7	19	PDB header: oxidoreductase Chain: A: PDB Molecule: udp-n-acetylenolpyruvyglucosamine reductase; PDBTitle: crystal structure of udp-n-acetylenolpyruvyglucosamine2 reductase (murb) from thermus caldophilus
31	d1f0xa1	Alignment	not modelled	99.7	17	Fold: Ferredoxin-like Superfamily: FAD-linked oxidases, C-terminal domain Family: D-lactate dehydrogenase
32	d1e8ga1	Alignment	not modelled	99.6	18	Fold: Ferredoxin-like Superfamily: FAD-linked oxidases, C-terminal domain Family: Vanillyl-alcohol oxidase-like
33	d1wvfa1	Alignment	not modelled	99.6	14	Fold: Ferredoxin-like Superfamily: FAD-linked oxidases, C-terminal domain Family: Vanillyl-alcohol oxidase-like
34	c1ffuF	Alignment	not modelled	97.2	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
35	d1ffvc2	Alignment	not modelled	97.1	14	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	97.1	12	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	d1n62c2	Alignment	not modelled	96.7	11	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like
38	c3hrdC	Alignment	not modelled	96.6	13	PDB header: oxidoreductase Chain: C: PDB Molecule: nicotinate dehydrogenase fad-subunit; PDBTitle: crystal structure of nicotinate dehydrogenase
39	c1t3qF	Alignment	not modelled	96.6	16	PDB header: oxidoreductase Chain: F: PDB Molecule: quinoline 2-oxidoreductase medium subunit; PDBTitle: crystal structure of quinoline 2-oxidoreductase from pseudomonas2 putida 86
40	d1t3qc2	Alignment	not modelled	96.5	15	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like
41	c2w3rG	Alignment	not modelled	96.4	14	PDB header: oxidoreductase Chain: G: PDB Molecule: xanthine dehydrogenase; PDBTitle: crystal structure of xanthine dehydrogenase (desulfo form)2 from rhodobacter capsulatus in complex with hypoxanthine
42	d1w1oa1	Alignment	not modelled	96.3	21	Fold: Ferredoxin-like Superfamily: FAD-linked oxidases, C-terminal domain Family: Cytokinin dehydrogenase 1
43	c1rm6E	Alignment	not modelled	96.3	16	PDB header: oxidoreductase Chain: E: PDB Molecule: 4-hydroxybenzoyl-coa reductase beta subunit; PDBTitle: structure of 4-hydroxybenzoyl-coa reductase from thauera2 aromatica
44	d1v97a6	Alignment	not modelled	96.2	12	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like
45	d3b9jb2	Alignment	not modelled	96.1	12	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like
46	d1jroa4	Alignment	not modelled	96.0	12	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like
47	c3etrM	Alignment	not modelled	95.9	12	PDB header: oxidoreductase Chain: M: PDB Molecule: xanthine dehydrogenase/oxidase; PDBTitle: crystal structure of xanthine oxidase in complex with2 lumazine
48	c3b9jj	Alignment	not modelled	95.9	12	PDB header: oxidoreductase Chain: J: PDB Molecule: xanthine oxidase; PDBTitle: structure of xanthine oxidase with 2-hydroxy-6-methylpurine
49	d1rm6b2	Alignment	not modelled	95.3	15	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like
50	c1wygA	Alignment	not modelled	94.6	13	PDB header: oxidoreductase Chain: A: PDB Molecule: xanthine dehydrogenase/oxidase; PDBTitle: crystal structure of a rat xanthine dehydrogenase triple mutant2 (c535a, c992r and c1324s)
51	d1yhta1	Alignment	not modelled	68.8	14	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
52	d1jaka1	Alignment	not modelled	68.8	19	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
53	c3nsnA	Alignment	not modelled	67.2	14	PDB header: hydrolase Chain: A: PDB Molecule: n-acetylglucosaminidase; PDBTitle: crystal structure of insect beta-n-acetyl-d-hexosaminidase ofhex12 complexed with tmg-chitotriomycin

54	c2yl8A	Alignment	not modelled	66.3	14	PDB header: hydrolase Chain: A: PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: inhibition of the pneumococcal virulence factor strh and2 molecular insights into n-glycan recognition and3 hydrolysis
55	d2gja1	Alignment	not modelled	66.2	14	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
56	c3rcnA	Alignment	not modelled	66.1	19	PDB header: hydrolase Chain: A: PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: crystal structure of beta-n-acetylhexosaminidase from arthrobacter2 aurescens
57	d1qbaa3	Alignment	not modelled	65.9	10	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
58	c3gh7A	Alignment	not modelled	65.1	10	PDB header: hydrolase Chain: A: PDB Molecule: beta-hexosaminidase; PDBTitle: crystal structure of beta-hexosaminidase from paenibacillus2 sp. ts12 in complex with galnac
59	c1m04A	Alignment	not modelled	64.7	24	PDB header: hydrolase Chain: A: PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: mutant streptomyces plicatus beta-hexosaminidase (d313n) in complex2 with product (glcnac)
60	d1nowa1	Alignment	not modelled	64.7	5	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
61	c2ylaA	Alignment	not modelled	64.1	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
62	c1nouA	Alignment	not modelled	63.3	5	PDB header: hydrolase Chain: A: PDB Molecule: beta-hexosaminidase beta chain; PDBTitle: native human lysosomal beta-hexosaminidase isoform b
63	c2gjxE	Alignment	not modelled	62.8	14	PDB header: hydrolase Chain: E: PDB Molecule: beta-hexosaminidase alpha chain; PDBTitle: crystallographic structure of human beta-hexosaminidase a
64	c3lmyA	Alignment	not modelled	62.2	5	PDB header: hydrolase Chain: A: PDB Molecule: beta-hexosaminidase subunit beta; PDBTitle: the crystal structure of beta-hexosaminidase b in complex with2 pyrimethamine
65	c1qbaA	Alignment	not modelled	61.8	10	PDB header: glycosyl hydrolase Chain: A: PDB Molecule: chitinase; PDBTitle: bacterial chitinase, glycosyl hydrolase family 20
66	c3dedB	Alignment	not modelled	61.2	15	PDB header: membrane protein Chain: B: PDB Molecule: probable hemolysin; PDBTitle: c-terminal domain of probable hemolysin from chromobacterium violaceum
67	c3rpmA	Alignment	not modelled	60.9	14	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
68	d2bi7a1	Alignment	not modelled	57.6	12	Fold: Nucleotide-binding domain Superfamily: Nucleotide-binding domain Family: UDP-galactopyranose mutase, N-terminal domain
69	d3deda1	Alignment	not modelled	54.4	15	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like
70	c2epoB	Alignment	not modelled	54.1	19	PDB header: hydrolase Chain: B: PDB Molecule: n-acetyl-beta-d-glucosaminidase; PDBTitle: n-acetyl-b-d-glucosaminidase (gcna) from streptococcus gordonii
71	d2pls1	Alignment	not modelled	50.4	14	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like
72	d2i0ka1	Alignment	not modelled	43.3	29	Fold: Ferredoxin-like Superfamily: FAD-linked oxidases, C-terminal domain Family: Cholesterol oxidase
73	d2nqwa1	Alignment	not modelled	42.6	15	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like
74	d2o1ra1	Alignment	not modelled	34.7	10	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like
75	c3e0dA	Alignment	not modelled	34.1	17	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
76	c1qupA	Alignment	not modelled	29.4	7	PDB header: chaperone Chain: A: PDB Molecule: superoxide dismutase 1 copper chaperone; PDBTitle: crystal structure of the copper chaperone for superoxide2 dismutase
77	c2hnhA	Alignment	not modelled	29.3	17	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
78	c2gjaA	Alignment	not modelled	26.5	10	PDB header: motor protein Chain: A: PDB Molecule: hypothetical protein pp4397; PDBTitle: crystal structure of a pilz-containing protein (pp4397) from2 pseudomonas putida kt2440 at 2.25 a resolution
79	c2x24B	Alignment	not modelled	25.5	18	PDB header: ligase Chain: B: PDB Molecule: acetyl-coa carboxylase; PDBTitle: bovine acc2 ct domain in complex with inhibitor

80	dli8ta1	Alignment	not modelled	24.0	13	Fold: Nucleotide-binding domain Superfamily: Nucleotide-binding domain Family: UDP-galactopyranose mutase, N-terminal domain
81	c2k2pA	Alignment	not modelled	23.9	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein atu1203; PDBTitle: solution nmr structure of protein atu1203 from agrobacterium2 tumefaciens. northeast structural genomics consortium (nesg) target3 att10, ontario center for structural proteomics target atc1183
82	d1fe0a	Alignment	not modelled	23.8	17	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
83	d2p13a1	Alignment	not modelled	23.5	16	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like
84	c1jk9D	Alignment	not modelled	21.9	7	PDB header: oxidoreductase Chain: D: PDB Molecule: copper chaperone for superoxide dismutase; PDBTitle: heterodimer between h48f-ysod1 and yccs
85	c3ff6D	Alignment	not modelled	21.3	18	PDB header: ligase Chain: D: PDB Molecule: acetyl-coa carboxylase 2; PDBTitle: human acc2 ct domain with cp-640186
86	d1qupa2	Alignment	not modelled	21.2	20	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
87	c2rq7A	Alignment	not modelled	19.6	26	PDB header: hydrolase Chain: A: PDB Molecule: atp synthase epsilon chain; PDBTitle: solution structure of the epsilon subunit chimera combining2 the n-terminal beta-sandwich domain from t. elongatus bp-13 f1 and the c-terminal alpha-helical domain from spinach4 chloroplast f1
88	c2f9iD	Alignment	not modelled	19.5	12	PDB header: transferase Chain: D: PDB Molecule: acetyl-coenzyme a carboxylase carboxyl PDBTitle: crystal structure of the carboxyltransferase subunit of acc2 from staphylococcus aureus
89	d2z15a1	Alignment	not modelled	18.5	13	Fold: BTG domain-like Superfamily: BTG domain-like Family: BTG domain-like
90	c2hldH	Alignment	not modelled	18.2	14	PDB header: hydrolase Chain: H: PDB Molecule: atp synthase delta chain, mitochondrial; PDBTitle: crystal structure of yeast mitochondrial f1-atpase
91	c3tgoD	Alignment	not modelled	16.9	9	PDB header: membrane protein Chain: D: PDB Molecule: lipoprotein 34; PDBTitle: crystal structure of the e. coli bamcd complex
92	d3e9va1	Alignment	not modelled	16.8	17	Fold: BTG domain-like Superfamily: BTG domain-like Family: BTG domain-like
93	d1cooa	Alignment	not modelled	16.5	21	Fold: SAM domain-like Superfamily: C-terminal domain of RNA polymerase alpha subunit Family: C-terminal domain of RNA polymerase alpha subunit
94	c1xtyD	Alignment	not modelled	16.3	8	PDB header: hydrolase Chain: D: PDB Molecule: peptidyl-trna hydrolase; PDBTitle: crystal structure of sulfolobus solfataricus peptidyl-trna2 hydrolase
95	d1sb6a	Alignment	not modelled	16.1	26	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
96	c2crlA	Alignment	not modelled	16.1	20	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
97	c2e1mA	Alignment	not modelled	15.9	16	PDB header: oxidoreductase Chain: A: PDB Molecule: l-glutamate oxidase; PDBTitle: crystal structure of l-glutamate oxidase from streptomyces sp. x-119-6
98	c1x3lA	Alignment	not modelled	15.8	17	PDB header: transferase Chain: A: PDB Molecule: hypothetical protein ph0495; PDBTitle: crystal structure of the ph0495 protein from pyrococcus horikoshii2 ot3
99	c2kt2A	Alignment	not modelled	15.5	16	PDB header: oxidoreductase Chain: A: PDB Molecule: mercuric reductase; PDBTitle: structure of nmera, the n-terminal hma domain of tn501 mercuric2 reductase