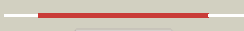
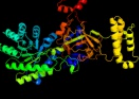
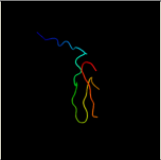
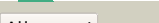
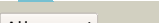
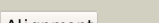
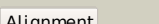
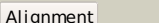
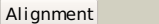
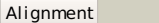
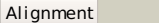
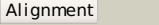
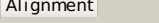
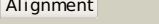
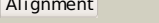
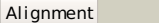
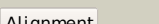
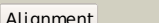
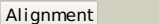
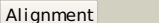
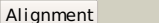
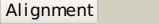
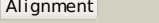
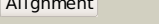
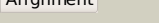


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3nzqB_	 Alignment		100.0	100	PDB header: lyase Chain: B: PDB Molecule: biosynthetic arginine decarboxylase; PDBTitle: crystal structure of biosynthetic arginine decarboxylase adc (spea)2 from escherichia coli, northeast structural genomics consortium3 target er600
2	c3n2oA_	 Alignment		100.0	55	PDB header: lyase Chain: A: PDB Molecule: biosynthetic arginine decarboxylase; PDBTitle: x-ray crystal structure of arginine decarboxylase complexed with2 arginine from vibrio vulnificus
3	c3nzpA_	 Alignment		100.0	35	PDB header: lyase Chain: A: PDB Molecule: arginine decarboxylase; PDBTitle: crystal structure of the biosynthetic arginine decarboxylase spea from2 campylobacter jejuni, northeast structural genomics consortium target3 br53
4	c2o0tB_	 Alignment		100.0	24	PDB header: lyase Chain: B: PDB Molecule: diaminopimelate decarboxylase; PDBTitle: the three dimensional structure of diaminopimelate decarboxylase from2 mycobacterium tuberculosis reveals a tetrameric enzyme organisation
5	c1tufA_	 Alignment		100.0	22	PDB header: lyase Chain: A: PDB Molecule: diaminopimelate decarboxylase; PDBTitle: crystal structure of diaminopimelate decarboxylase from m.2 jannaschi
6	c1knwA_	 Alignment		100.0	19	PDB header: lyase Chain: A: PDB Molecule: diaminopimelate decarboxylase; PDBTitle: crystal structure of diaminopimelate decarboxylase
7	c1d7kB_	 Alignment		100.0	20	PDB header: lyase Chain: B: PDB Molecule: human ornithine decarboxylase; PDBTitle: crystal structure of human ornithine decarboxylase at 2.12 angstroms resolution
8	c2on3A_	 Alignment		100.0	20	PDB header: lyase Chain: A: PDB Molecule: ornithine decarboxylase; PDBTitle: a structural insight into the inhibition of human and2 leishmania donovani ornithine decarboxylases by 3-aminooxy-3 1-aminopropane
9	c3n2bD_	 Alignment		100.0	23	PDB header: lyase Chain: D: PDB Molecule: diaminopimelate decarboxylase; PDBTitle: 1.8 angstrom resolution crystal structure of diaminopimelate2 decarboxylase (lysa) from vibrio cholerae.
10	c2qghA_	 Alignment		100.0	21	PDB header: lyase Chain: A: PDB Molecule: diaminopimelate decarboxylase; PDBTitle: crystal structure of diaminopimelate decarboxylase from helicobacter2 pylori complexed with l-lysine
11	c3btnA_	 Alignment		100.0	19	PDB header: biosynthetic protein Chain: A: PDB Molecule: antizyme inhibitor 1; PDBTitle: crystal structure of antizyme inhibitor, an ornithine2 decarboxylase homologous protein

12	c2p3eA_	Alignment		100.0	22	PDB header: lyase Chain: A: PDB Molecule: diaminopimelate decarboxylase; PDBTitle: crystal structure of aq1208 from aquifex aeolicus
13	c2pljA_	Alignment		100.0	25	PDB header: lyase Chain: A: PDB Molecule: lysine/ornithine decarboxylase; PDBTitle: crystal structure of lysine/ornithine decarboxylase complexed with2 putrescine from vibrio vulnificus
14	c2j66A_	Alignment		100.0	19	PDB header: lyase Chain: A: PDB Molecule: btrk; PDBTitle: structural characterisation of btrk decarboxylase from2 butirosin biosynthesis
15	c2yxxA_	Alignment		100.0	22	PDB header: lyase Chain: A: PDB Molecule: diaminopimelate decarboxylase; PDBTitle: crystal structure analysis of diaminopimelate decarboxylate (lysa)
16	c2nvaH_	Alignment		100.0	24	PDB header: lyase Chain: H: PDB Molecule: arginine decarboxylase, a207r protein; PDBTitle: the x-ray crystal structure of the paramecium bursaria2 chlorella virus arginine decarboxylase bound to agmatine
17	d1twia2	Alignment		100.0	23	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel Family: Alanine racemase-like, N-terminal domain
18	c3mt1B_	Alignment		100.0	18	PDB header: lyase Chain: B: PDB Molecule: putative carboxynorspermidine decarboxylase protein; PDBTitle: crystal structure of putative carboxynorspermidine decarboxylase2 protein from sinorhizobium meliloti
19	c3n29A_	Alignment		100.0	17	PDB header: lyase Chain: A: PDB Molecule: carboxynorspermidine decarboxylase; PDBTitle: crystal structure of carboxynorspermidine decarboxylase complexed with2 norspermidine from campylobacter jejuni
20	d1knwa2	Alignment		100.0	18	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel Family: Alanine racemase-like, N-terminal domain
21	d1hkva2	Alignment	not modelled	100.0	23	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel Family: Alanine racemase-like, N-terminal domain
22	c1njjC_	Alignment	not modelled	100.0	21	PDB header: lyase Chain: C: PDB Molecule: ornithine decarboxylase; PDBTitle: crystal structure determination of t. brucei ornithine2 decarboxylase bound to d-ornithine and to g418
23	d1d7ka2	Alignment	not modelled	100.0	19	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel Family: Alanine racemase-like, N-terminal domain
24	d1f3ta2	Alignment	not modelled	100.0	22	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel Family: Alanine racemase-like, N-terminal domain
25	d7odca2	Alignment	not modelled	100.0	22	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel Family: Alanine racemase-like, N-terminal domain
26	c3anuA_	Alignment	not modelled	99.9	11	PDB header: lyase Chain: A: PDB Molecule: d-serine dehydratase; PDBTitle: crystal structure of d-serine dehydratase from chicken kidney
27	c3gwqB_	Alignment	not modelled	99.9	14	PDB header: lyase Chain: B: PDB Molecule: d-serine deaminase; PDBTitle: crystal structure of a putative d-serine deaminase (bx_e_a4060) from2 burkholderia xenovorans lb400 at 2.00 a resolution
28	c3llxA_	Alignment	not modelled	99.8	13	PDB header: isomerase Chain: A: PDB Molecule: predicted amino acid aldolase or racemase; PDBTitle: crystal structure of an ala racemase-like protein (il1761) from2 idiomarina loihiensis at 1.50 a resolution

29	c1xfcB_	Alignment	not modelled	99.8	17	PDB header: isomerase Chain: B: PDB Molecule: alanine racemase; PDBTitle: the 1.9 a crystal structure of alanine racemase from mycobacterium2 tuberculosis contains a conserved entryway into the active site
30	c3kw3B_	Alignment	not modelled	99.7	10	PDB header: isomerase Chain: B: PDB Molecule: alanine racemase; PDBTitle: crystal structure of alanine racemase from bartonella henselae with2 covalently bound pyridoxal phosphate
31	c3oo2B_	Alignment	not modelled	99.6	11	PDB header: isomerase Chain: B: PDB Molecule: alanine racemase 1; PDBTitle: 2.37 angstrom resolution crystal structure of an alanine racemase2 (alr) from staphylococcus aureus subsp. aureus col
32	c2dy3B_	Alignment	not modelled	99.6	15	PDB header: isomerase Chain: B: PDB Molecule: alanine racemase; PDBTitle: crystal structure of alanine racemase from corynebacterium glutamicum
33	c1w8gA_	Alignment	not modelled	99.5	14	PDB header: plp-binding protein Chain: A: PDB Molecule: hypothetical upf0001 protein yggs; PDBTitle: crystal structure of e. coli k-12 yggs
34	c1vftA_	Alignment	not modelled	99.4	16	PDB header: isomerase Chain: A: PDB Molecule: alanine racemase; PDBTitle: crystal structure of l-cycloserine-bound form of alanine2 racemase from d-cycloserine-producing streptomyces3 lavendulae
35	d1hkva1	Alignment	not modelled	99.4	27	Fold: Domain of alpha and beta subunits of F1 ATP synthase-like Superfamily: Alanine racemase C-terminal domain-like Family: Eukaryotic ODC-like
36	d1vfa2	Alignment	not modelled	99.4	19	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel Family: Alanine racemase-like, N-terminal domain
37	c3oo2A_	Alignment	not modelled	99.4	10	PDB header: isomerase Chain: A: PDB Molecule: alanine racemase 1; PDBTitle: 2.37 angstrom resolution crystal structure of an alanine racemase2 (alr) from staphylococcus aureus subsp. aureus col
38	c3r79B_	Alignment	not modelled	99.3	15	PDB header: structure genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an uncharacterized protein from agrobacterium2 tumefaciens
39	c3e6eC_	Alignment	not modelled	99.3	12	PDB header: isomerase Chain: C: PDB Molecule: alanine racemase; PDBTitle: crystal structure of alanine racemase from e.faecalis2 complex with cycloserine
40	d1rcqa2	Alignment	not modelled	99.2	15	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel Family: Alanine racemase-like, N-terminal domain
41	c3hurA_	Alignment	not modelled	99.2	13	PDB header: isomerase Chain: A: PDB Molecule: alanine racemase; PDBTitle: crystal structure of alanine racemase from oenococcus oeni
42	c2odoC_	Alignment	not modelled	99.2	14	PDB header: isomerase Chain: C: PDB Molecule: alanine racemase; PDBTitle: crystal structure of pseudomonas fluorescens alanine racemase
43	c3cpgA_	Alignment	not modelled	99.2	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an unknown protein from bifidobacterium2 adolescentis
44	d1bd0a2	Alignment	not modelled	99.2	11	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel Family: Alanine racemase-like, N-terminal domain
45	d1knwa1	Alignment	not modelled	99.2	22	Fold: Domain of alpha and beta subunits of F1 ATP synthase-like Superfamily: Alanine racemase C-terminal domain-like Family: Eukaryotic ODC-like
46	d1twia1	Alignment	not modelled	99.1	22	Fold: Domain of alpha and beta subunits of F1 ATP synthase-like Superfamily: Alanine racemase C-terminal domain-like Family: Eukaryotic ODC-like
47	c3mubB_	Alignment	not modelled	99.0	16	PDB header: isomerase Chain: B: PDB Molecule: alanine racemase; PDBTitle: the crystal structure of alanine racemase from streptococcus2 pneumoniae
48	d7odca1	Alignment	not modelled	99.0	23	Fold: Domain of alpha and beta subunits of F1 ATP synthase-like Superfamily: Alanine racemase C-terminal domain-like Family: Eukaryotic ODC-like
49	c1niuA_	Alignment	not modelled	98.9	12	PDB header: isomerase Chain: A: PDB Molecule: alanine racemase; PDBTitle: alanine racemase with bound inhibitor derived from l-2 cycloserine
50	c2rjgC_	Alignment	not modelled	98.9	12	PDB header: isomerase Chain: C: PDB Molecule: alanine racemase; PDBTitle: crystal structure of biosynthetic alaine racemase from escherichia2 coli
51	c3co8B_	Alignment	not modelled	98.8	14	PDB header: isomerase Chain: B: PDB Molecule: alanine racemase; PDBTitle: crystal structure of alanine racemase from oenococcus oeni
52	d1d7ka1	Alignment	not modelled	98.7	23	Fold: Domain of alpha and beta subunits of F1 ATP synthase-like Superfamily: Alanine racemase C-terminal domain-like Family: Eukaryotic ODC-like
53	d1f3ta1	Alignment	not modelled	98.7	22	Fold: Domain of alpha and beta subunits of F1 ATP synthase-like Superfamily: Alanine racemase C-terminal domain-like Family: Eukaryotic ODC-like
54	d1ct5a_	Alignment	not modelled	97.8	13	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel Family: "Hypothetical" protein ybl036c
						Fold: Domain of alpha and beta subunits of F1 ATP synthase-like

55	d1njib1	Alignment	not modelled	97.7	26	Superfamily: Alanine racemase C-terminal domain-like Family: Eukaryotic ODC-like
56	c2vd9A	Alignment	not modelled	96.9	14	PDB header: isomerase Chain: A: PDB Molecule: alanine racemase; PDBTitle: the crystal structure of alanine racemase from bacillus2 anthracis (ba0252) with bound l-ala-p
57	d2toda1	Alignment	not modelled	96.8	24	Fold: Domain of alpha and beta subunits of F1 ATP synthase-like Superfamily: Alanine racemase C-terminal domain-like Family: Eukaryotic ODC-like
58	c2zq0B	Alignment	not modelled	74.1	13	PDB header: hydrolase Chain: B: PDB Molecule: alpha-glucosidase (alpha-glucosidase sub); PDBTitle: crystal structure of subb complexed with acarbose
59	d1z41a1	Alignment	not modelled	70.2	15	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
60	c2k2eA	Alignment		68.0	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein bp2786; PDBTitle: solution nmr structure of bordetella pertussis protein2 bp2786, a mth938-like domain. northeast structural3 genomics consortium target ber31
61	c1us2A	Alignment	not modelled	67.9	19	PDB header: hydrolase Chain: A: PDB Molecule: endo-beta-1,4-xylanase; PDBTitle: xylanase10c (mutant e385a) from cellvibrio japonicus in2 complex with xylopentaose
62	c1iszA	Alignment	not modelled	64.6	20	PDB header: hydrolase Chain: A: PDB Molecule: endo-1,4-beta-d-xylanase; PDBTitle: crystal structure of xylanase from streptomyces2 olivaceoviridis e-86 complexed with galactose
63	c2gm2A	Alignment	not modelled	64.6	31	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein; PDBTitle: nmr structure of xanthomonas campestris xcc1710: northeast2 structural genomics consortium target xcr35
64	c2h1xB	Alignment	not modelled	60.0	21	PDB header: hydrolase Chain: B: PDB Molecule: 5-hydroxyisourate hydrolase (formerly known as PDBTitle: crystal structure of 5-hydroxyisourate hydrolase (formerly2 known as trp, transthyretin related protein)
65	d2dexx3	Alignment		58.3	18	Fold: Pentatein, beta/alpha-propeller Superfamily: Pentatein Family: Peptidylarginine deiminase Pad4, catalytic C-terminal domain
66	d1l1ea	Alignment	not modelled	57.4	11	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
67	d1r85a	Alignment	not modelled	53.7	19	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
68	d1tf3a3	Alignment	not modelled	51.9	55	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
69	c3hrdE	Alignment	not modelled	51.4	28	PDB header: oxidoreductase Chain: E: PDB Molecule: nicotinate dehydrogenase large molybdopterin PDBTitle: crystal structure of nicotinate dehydrogenase
70	d2fk8a1	Alignment	not modelled	50.7	11	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
71	d2ha9a1	Alignment	not modelled	49.1	14	Fold: PFL-like glycyl radical enzymes Superfamily: PFL-like glycyl radical enzymes Family: SP0239-like
72	c2q5xA	Alignment	not modelled	48.3	18	PDB header: hydrolase Chain: A: PDB Molecule: ribosome-inactivating protein; PDBTitle: crystal structure of lychnin a type 1 ribosome inactivating2 protein (rip)
73	c2w54F	Alignment	not modelled	46.7	27	PDB header: oxidoreductase Chain: F: PDB Molecule: xanthine dehydrogenase; PDBTitle: crystal structure of xanthine dehydrogenase from2 rhodobacter capsulatus in complex with bound inhibitor3 pterin-6-aldehyde
74	c3kruC	Alignment	not modelled	45.9	13	PDB header: oxidoreductase Chain: C: PDB Molecule: nadh:flavin oxidoreductase/nadh oxidase; PDBTitle: crystal structure of the thermostable old yellow enzyme from2 thermoanaerobacter pseudethanolicus e39
75	d1ps9a1	Alignment	not modelled	45.2	14	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
76	c3eubl	Alignment	not modelled	44.1	20	PDB header: oxidoreductase Chain: L: PDB Molecule: xanthine dehydrogenase/oxidase; PDBTitle: crystal structure of desulfo-xanthine oxidase with xanthine
77	c3gr7A	Alignment	not modelled	43.5	20	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh dehydrogenase; PDBTitle: structure of oye from geobacillus kaustophilus, hexagonal2 crystal form
78	c3hf3A	Alignment	not modelled	42.8	26	PDB header: oxidoreductase Chain: A: PDB Molecule: chromate reductase; PDBTitle: old yellow enzyme from thermus scotoductus sa-01

79	c1ps9A	 Alignment	not modelled	41.5	16	PDB header: oxidoreductase Chain: A: PDB Molecule: 2,4-dienoyl-coa reductase; PDBTitle: the crystal structure and reaction mechanism of e. coli 2,4-2 dienoyl coa reductase
80	d1v97a5	 Alignment	not modelled	40.2	20	Fold: Molybdenum cofactor-binding domain Superfamily: Molybdenum cofactor-binding domain Family: Molybdenum cofactor-binding domain
81	c1wygA	 Alignment	not modelled	39.8	20	PDB header: oxidoreductase Chain: A: PDB Molecule: xanthine dehydrogenase/oxidase; PDBTitle: crystal structure of a rat xanthine dehydrogenase triple mutant2 (c535a, c992r and c1324s)
82	d1jsca3	 Alignment	not modelled	39.4	20	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
83	c2b5dX	 Alignment	not modelled	39.4	9	PDB header: hydrolase Chain: X: PDB Molecule: alpha-amylase; PDBTitle: crystal structure of the novel alpha-amylase amyc from thermotoga2 maritima
84	d1jrob2	 Alignment	not modelled	39.1	27	Fold: Molybdenum cofactor-binding domain Superfamily: Molybdenum cofactor-binding domain Family: Molybdenum cofactor-binding domain
85	c2zvra	 Alignment	not modelled	37.9	17	PDB header: isomerase Chain: A: PDB Molecule: uncharacterized protein tm_0416; PDBTitle: crystal structure of a d-tagatose 3-epimerase-related2 protein from thermotoga maritima
86	d1vyra	 Alignment	not modelled	37.8	14	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
87	d2ji7a3	 Alignment	not modelled	37.5	25	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
88	d1ffvb2	 Alignment	not modelled	36.9	29	Fold: Molybdenum cofactor-binding domain Superfamily: Molybdenum cofactor-binding domain Family: Molybdenum cofactor-binding domain
89	d1qo7a	 Alignment	not modelled	36.4	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase
90	c1ydoC	 Alignment	not modelled	36.4	18	PDB header: lyase Chain: C: PDB Molecule: hmg-coa lyase; PDBTitle: crystal structure of the bacillus subtilis hmg-coa lyase, northeast2 structural genomics target sr181.
91	d1rm6a2	 Alignment	not modelled	35.4	17	Fold: Molybdenum cofactor-binding domain Superfamily: Molybdenum cofactor-binding domain Family: Molybdenum cofactor-binding domain
92	c2h90A	 Alignment	not modelled	35.1	19	PDB header: oxidoreductase Chain: A: PDB Molecule: xenobiotic reductase a; PDBTitle: xenobiotic reductase a in complex with coumarin
93	d2glka1	 Alignment	not modelled	34.6	18	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
94	d1kpga	 Alignment	not modelled	34.5	13	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
95	d1n62b2	 Alignment	not modelled	33.4	27	Fold: Molybdenum cofactor-binding domain Superfamily: Molybdenum cofactor-binding domain Family: Molybdenum cofactor-binding domain
96	c1sb3D	 Alignment	not modelled	31.9	17	PDB header: oxidoreductase Chain: D: PDB Molecule: 4-hydroxybenzoyl-coa reductase alpha subunit; PDBTitle: structure of 4-hydroxybenzoyl-coa reductase from thauera2 aromatica
97	c2gpzC	 Alignment	not modelled	31.1	22	PDB header: hydrolase Chain: C: PDB Molecule: transthyretin-like protein; PDBTitle: transthyretin-like protein from salmonella dublin
98	d1xlma	 Alignment	not modelled	30.9	19	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
99	d1vlba4	 Alignment	not modelled	30.6	15	Fold: Molybdenum cofactor-binding domain Superfamily: Molybdenum cofactor-binding domain Family: Molybdenum cofactor-binding domain
100	c2fk8A	 Alignment	not modelled	30.5	11	PDB header: transferase Chain: A: PDB Molecule: methoxy mycolic acid synthase 4; PDBTitle: crystal structure of hma (mmaa4) from mycobacterium tuberculosis2 complexed with s-adenosylmethionine
101	d1bxca	 Alignment	not modelled	30.1	17	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
102	d1wxma1	 Alignment	not modelled	29.8	30	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ras-binding domain, RBD
103	c1kblA	 Alignment	not modelled	29.7	18	PDB header: transferase Chain: A: PDB Molecule: pyruvate phosphate dikinase; PDBTitle: pyruvate phosphate dikinase
104	d2b5dx2	 Alignment	not modelled	29.2	9	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: AmyC N-terminal domain-like
105	d1qt1a	 Alignment	not modelled	29.0	18	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase

106	dlw32a_	Alignment	not modelled	28.4	17	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
107	dls4ea2	Alignment	not modelled	28.4	19	Fold: Ferredoxin-like Superfamily: GHMP Kinase, C-terminal domain Family: Galactokinase
108	c2ojlB_	Alignment	not modelled	28.2	22	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of q7waf1_borpa from bordetella parapertussis.2 northeast structural genomics target bpr68.
109	c3dtyA_	Alignment	not modelled	27.6	14	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, gfo/ldh/moca family; PDBTitle: crystal structure of an oxidoreductase from pseudomonas2 syringae
110	c1ffvB_	Alignment	not modelled	27.5	29	PDB header: hydrolase Chain: B: PDB Molecule: cutl, molybdoprotein of carbon monoxide PDBTitle: carbon monoxide dehydrogenase from hydrogenophaga2 pseudoflava
111	cljscA_	Alignment	not modelled	27.4	20	PDB header: lyase Chain: A: PDB Molecule: acetohydroxy-acid synthase; PDBTitle: crystal structure of the catalytic subunit of yeast2 acetohydroxyacid synthase: a target for herbicidal3 inhibitors
112	c1t3qB_	Alignment	not modelled	27.4	25	PDB header: oxidoreductase Chain: B: PDB Molecule: quinoline 2-oxidoreductase large subunit; PDBTitle: crystal structure of quinoline 2-oxidoreductase from pseudomonas2 putida 86
113	c1n62E_	Alignment	not modelled	27.3	27	PDB header: oxidoreductase Chain: E: PDB Molecule: carbon monoxide dehydrogenase large chain; PDBTitle: crystal structure of the mo,cu-co dehydrogenase (codh), n-2 butylisocyanide-bound state
114	d2fi9a1	Alignment	not modelled	26.4	24	Fold: MTH938-like Superfamily: MTH938-like Family: MTH938-like
115	d1lqaa_	Alignment	not modelled	25.7	18	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
116	c1tx2A_	Alignment	not modelled	25.5	24	PDB header: transferase Chain: A: PDB Molecule: dhps, dihydropteroate synthase; PDBTitle: dihydropteroate synthetase, with bound inhibitor manic, from bacillus2 anthracis
117	d1tx2a_	Alignment	not modelled	25.5	24	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
118	c2p10D_	Alignment	not modelled	25.3	11	PDB header: hydrolase Chain: D: PDB Molecule: ml19387 protein; PDBTitle: crystal structure of a putative phosphonopyruvate hydrolase (ml19387)2 from mesorhizobium loti maff303099 at 2.15 a resolution
119	c3dexA_	Alignment	not modelled	24.9	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: sav_2001; PDBTitle: crystal structure of sav_2001 protein from streptomyces2 avermitilis, northeast structural genomics consortium3 target svr107.
120	d1bxbA_	Alignment	not modelled	24.4	18	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase