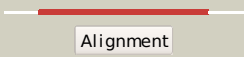

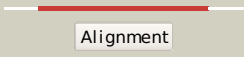

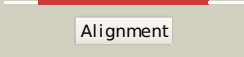

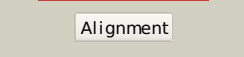

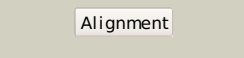

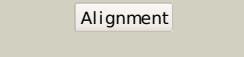

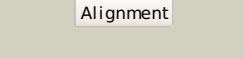

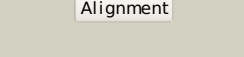
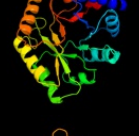


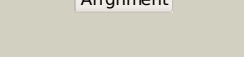

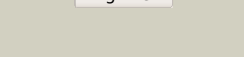







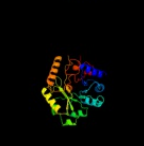

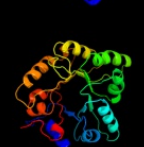


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1w8gA_</a>	 Alignment		100.0	100	<b>PDB header:</b> plp-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical upf0001 protein yggs; <b>PDBTitle:</b> crystal structure of e. coli k-12 yggs
2	<a href="#">c3cpaA_</a>	 Alignment		100.0	33	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of an unknown protein from bifidobacterium2 adolescentis
3	<a href="#">c3r79B_</a>	 Alignment		100.0	38	<b>PDB header:</b> structure genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of an uncharacterized protein from agrobacterium2 tumefaciens
4	<a href="#">d1ct5a_</a>	 Alignment		100.0	36	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> PLP-binding barrel <b>Family:</b> "Hypothetical" protein ybl036c
5	<a href="#">c1xfcb_</a>	 Alignment		100.0	15	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> alanine racemase; <b>PDBTitle:</b> the 1.9 Å crystal structure of alanine racemase from mycobacterium2 tuberculosis contains a conserved entryway into the active site
6	<a href="#">d1bd0a2</a>	 Alignment		100.0	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> PLP-binding barrel <b>Family:</b> Alanine racemase-like, N-terminal domain
7	<a href="#">d1vfsa2</a>	 Alignment		100.0	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> PLP-binding barrel <b>Family:</b> Alanine racemase-like, N-terminal domain
8	<a href="#">c3e6eC_</a>	 Alignment		100.0	16	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> alanine racemase; <b>PDBTitle:</b> crystal structure of alanine racemase from e. faecalis2 complex with cycloserine
9	<a href="#">c3oo2A_</a>	 Alignment		100.0	13	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> alanine racemase 1; <b>PDBTitle:</b> 2.37 Å resolution crystal structure of an alanine racemase2 (alr) from staphylococcus aureus subsp. aureus col
10	<a href="#">c2dy3B_</a>	 Alignment		100.0	17	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> alanine racemase; <b>PDBTitle:</b> crystal structure of alanine racemase from corynebacterium glutamicum
11	<a href="#">c3mubB_</a>	 Alignment		100.0	18	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> alanine racemase; <b>PDBTitle:</b> the crystal structure of alanine racemase from streptococcus2 pneumoniae

12	<a href="#">d1rcqa2</a>	Alignment		100.0	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> PLP-binding barrel <b>Family:</b> Alanine racemase-like, N-terminal domain
13	<a href="#">c1niuA</a>	Alignment		100.0	17	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> alanine racemase; <b>PDBTitle:</b> alanine racemase with bound inhibitor derived from l-2 cycloserine
14	<a href="#">c3kw3B</a>	Alignment		100.0	13	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> alanine racemase; <b>PDBTitle:</b> crystal structure of alanine racemase from bartonella henselae with 2 covalently bound pyridoxal phosphate
15	<a href="#">c1vftA</a>	Alignment		100.0	17	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> alanine racemase; <b>PDBTitle:</b> crystal structure of l-cycloserine-bound form of alanine 2 racemase from d-cycloserine-producing streptomyces 3 lavendulae
16	<a href="#">c3oo2B</a>	Alignment		100.0	13	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> alanine racemase 1; <b>PDBTitle:</b> 2.37 angstrom resolution crystal structure of an alanine racemase 2 (alr) from staphylococcus aureus subsp. aureus col
17	<a href="#">c3co8B</a>	Alignment		100.0	13	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> alanine racemase; <b>PDBTitle:</b> crystal structure of alanine racemase from oenococcus oeni
18	<a href="#">c3hurA</a>	Alignment		100.0	19	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> alanine racemase; <b>PDBTitle:</b> crystal structure of alanine racemase from oenococcus oeni
19	<a href="#">c2vd9A</a>	Alignment		100.0	18	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> alanine racemase; <b>PDBTitle:</b> the crystal structure of alanine racemase from bacillus 2 anthracis (ba0252) with bound l-ala-p
20	<a href="#">c2rjgC</a>	Alignment		100.0	11	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> alanine racemase; <b>PDBTitle:</b> crystal structure of biosynthetic alaine racemase from escherichia 2 coli
21	<a href="#">c2odoC</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> alanine racemase; <b>PDBTitle:</b> crystal structure of pseudomonas fluorescens alanine racemase
22	<a href="#">c3anuA</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> d-serine dehydratase; <b>PDBTitle:</b> crystal structure of d-serine dehydratase from chicken kidney
23	<a href="#">c3l1xA</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> predicted amino acid aldolase or racemase; <b>PDBTitle:</b> crystal structure of an ala racemase-like protein (il1761) from 2 idiomarina loihiensis at 1.50 a resolution
24	<a href="#">c3gwqB</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> d-serine deaminase; <b>PDBTitle:</b> crystal structure of a putative d-serine deaminase (bx_e_a4060) from 2 burkholderia xenovorans lb400 at 2.00 a resolution
25	<a href="#">c2qghA</a>	Alignment	not modelled	100.0	9	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> diaminopimelate decarboxylase; <b>PDBTitle:</b> crystal structure of diaminopimelate decarboxylase from helicobacter 2 pylori complexed with l-lysine
26	<a href="#">c2j66A</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> btrk; <b>PDBTitle:</b> structural characterisation of btrk decarboxylase from 2 butirosin biosynthesis
27	<a href="#">c2p3eA</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> diaminopimelate decarboxylase; <b>PDBTitle:</b> crystal structure of aq1208 from aquifex aeolicus
28	<a href="#">c3n2bD</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> diaminopimelate decarboxylase; <b>PDBTitle:</b> 1.8 angstrom resolution crystal structure of

						diaminopimelate2 decarboxylase (lysa) from vibrio cholerae.
29	<a href="#">c1tufA_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> diaminopimelate decarboxylase; <b>PDBTitle:</b> crystal structure of diaminopimelate decarboxylase from m.2 jannaschi
30	<a href="#">c1njjC_</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> ornithine decarboxylase; <b>PDBTitle:</b> crystal structure determination of t. brucei ornithine2 decarboxylase bound to d-ornithine and to g418
31	<a href="#">d1twia2</a>	Alignment	not modelled	99.9	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> PLP-binding barrel <b>Family:</b> Alanine racemase-like, N-terminal domain
32	<a href="#">c2nvaH_</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> lyase <b>Chain:</b> H: <b>PDB Molecule:</b> arginine decarboxylase, a207r protein; <b>PDBTitle:</b> the x-ray crystal structure of the paramecium bursaria2 chlorella virus arginine decarboxylase bound to agmatine
33	<a href="#">d1hkva2</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> PLP-binding barrel <b>Family:</b> Alanine racemase-like, N-terminal domain
34	<a href="#">d7odca2</a>	Alignment	not modelled	99.9	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> PLP-binding barrel <b>Family:</b> Alanine racemase-like, N-terminal domain
35	<a href="#">d1f3ta2</a>	Alignment	not modelled	99.9	12	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> PLP-binding barrel <b>Family:</b> Alanine racemase-like, N-terminal domain
36	<a href="#">c2pljA_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> lysine/ornithine decarboxylase; <b>PDBTitle:</b> crystal structure of lysine/ornithine decarboxylase complexed with2 putrescine from vibrio vulnificus
37	<a href="#">c2o0tB_</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> diaminopimelate decarboxylase; <b>PDBTitle:</b> the three dimensional structure of diaminopimelate decarboxylase from2 mycobacterium tuberculosis reveals a tetrameric enzyme organisation
38	<a href="#">c1knwA_</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> diaminopimelate decarboxylase; <b>PDBTitle:</b> crystal structure of diaminopimelate decarboxylase
39	<a href="#">d1d7ka2</a>	Alignment	not modelled	99.8	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> PLP-binding barrel <b>Family:</b> Alanine racemase-like, N-terminal domain
40	<a href="#">c2yxxA_</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> diaminopimelate decarboxylase; <b>PDBTitle:</b> crystal structure analysis of diaminopimelate decarboxylate (lysa)
41	<a href="#">c2on3A_</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> ornithine decarboxylase; <b>PDBTitle:</b> a structural insight into the inhibition of human and2 leishmania donovani ornithine decarboxylases by 3-aminooxy-3 1-aminopropane
42	<a href="#">c3nzqB_</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> biosynthetic arginine decarboxylase; <b>PDBTitle:</b> crystal structure of biosynthetic arginine decarboxylase adc (spea)2 from escherichia coli, northeast structural genomics consortium3 target er600
43	<a href="#">c3btaA_</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> antizyme inhibitor 1; <b>PDBTitle:</b> crystal structure of antizyme inhibitor, an ornithine2 decarboxylase homologous protein
44	<a href="#">c3n2oA_</a>	Alignment	not modelled	99.7	11	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> biosynthetic arginine decarboxylase; <b>PDBTitle:</b> x-ray crystal structure of arginine decarboxylase complexed with2 arginine from vibrio vulnificus
45	<a href="#">c1d7kB_</a>	Alignment	not modelled	99.7	12	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> human ornithine decarboxylase; <b>PDBTitle:</b> crystal structure of human ornithine decarboxylase at 2.12 angstroms resolution
46	<a href="#">c3nzpA_</a>	Alignment	not modelled	99.6	13	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> arginine decarboxylase; <b>PDBTitle:</b> crystal structure of the biosynthetic arginine decarboxylase spea from2 campylobacter jejuni, northeast structural genomics consortium target3 br53
47	<a href="#">d1knwa2</a>	Alignment	not modelled	99.6	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> PLP-binding barrel <b>Family:</b> Alanine racemase-like, N-terminal domain
48	<a href="#">c3n29A_</a>	Alignment	not modelled	99.5	11	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> carboxynorspermidine decarboxylase; <b>PDBTitle:</b> crystal structure of carboxynorspermidine decarboxylase complexed with2 norspermidine from campylobacter jejuni
49	<a href="#">c3mt1B_</a>	Alignment	not modelled	99.1	13	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> putative carboxynorspermidine decarboxylase protein; <b>PDBTitle:</b> crystal structure of putative carboxynorspermidine decarboxylase2 protein from sinorhizobium meliloti
50	<a href="#">d1rpxa_</a>	Alignment	not modelled	95.4	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> D-ribulose-5-phosphate 3-epimerase
51	<a href="#">d2flia1</a>	Alignment	not modelled	94.6	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> D-ribulose-5-phosphate 3-epimerase
52	<a href="#">c2h90A_</a>	Alignment	not modelled	94.4	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> xenobiotic reductase a; <b>PDBTitle:</b> xenobiotic reductase a in complex with coumarin
53	<a href="#">d1h1ya_</a>	Alignment	not modelled	93.6	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> D-ribulose-5-phosphate 3-epimerase

54	<a href="#">c3hf3A_</a>	Alignment	not modelled	92.1	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> chromate reductase; <b>PDBTitle:</b> old yellow enzyme from thermus scotoductus sa-01
55	<a href="#">d1tqja_</a>	Alignment	not modelled	92.0	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> D-ribulose-5-phosphate 3-epimerase
56	<a href="#">c3ct7E_</a>	Alignment	not modelled	91.5	16	<b>PDB header:</b> isomerase <b>Chain:</b> E: <b>PDB Molecule:</b> d-allulose-6-phosphate 3-epimerase; <b>PDBTitle:</b> crystal structure of d-allulose 6-phosphate 3-epimerase2 from escherichia coli k-12
57	<a href="#">d1djqa1</a>	Alignment	not modelled	91.2	10	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
58	<a href="#">d1ps9a1</a>	Alignment	not modelled	91.2	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
59	<a href="#">c2y85D_</a>	Alignment	not modelled	91.0	12	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> phosphoribosyl isomerase a; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis phosphoribosyl2 isomerase with bound rcdrp
60	<a href="#">d1tqxa_</a>	Alignment	not modelled	87.9	12	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> D-ribulose-5-phosphate 3-epimerase
61	<a href="#">c1djnB_</a>	Alignment	not modelled	87.6	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> trimethylamine dehydrogenase; <b>PDBTitle:</b> structural and biochemical characterization of recombinant wild type2 trimethylamine dehydrogenase from methylophilus methylotrophus (sp.3 w3a1)
62	<a href="#">c3inpA_</a>	Alignment	not modelled	86.7	10	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> d-ribulose-phosphate 3-epimerase; <b>PDBTitle:</b> 2.05 angstrom resolution crystal structure of d-ribulose-phosphate 3-2 epimerase from francisella tularensis.
63	<a href="#">c3k30B_</a>	Alignment	not modelled	86.3	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> histamine dehydrogenase; <b>PDBTitle:</b> histamine dehydrogenase from nocardioodes simplex
64	<a href="#">c2vwtA_</a>	Alignment	not modelled	85.8	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> yfau, 2-keto-3-deoxy sugar aldolase; <b>PDBTitle:</b> crystal structure of yfau, a metal ion dependent class ii2 aldolase from escherichia coli k12 - mg-pyruvate product3 complex
65	<a href="#">c1ps9A_</a>	Alignment	not modelled	82.9	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 2,4-dienoyl-coa reductase; <b>PDBTitle:</b> the crystal structure and reaction mechanism of e. coli 2,4-2 dienoyl coa reductase
66	<a href="#">c3qz6A_</a>	Alignment	not modelled	80.7	10	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> hpch/hpai aldolase; <b>PDBTitle:</b> the crystal structure of hpch/hpai aldolase from desulfotobacterium2 hafniense dcb-2
67	<a href="#">d1dxea_</a>	Alignment	not modelled	79.7	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> HpcH/Hpal aldolase
68	<a href="#">c2v5jB_</a>	Alignment	not modelled	79.4	12	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase; <b>PDBTitle:</b> apo class ii aldolase hpch
69	<a href="#">c1izcA_</a>	Alignment	not modelled	79.1	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> macrophomate synthase intermolecular diels-alderase; <b>PDBTitle:</b> crystal structure analysis of macrophomate synthase
70	<a href="#">d1izca_</a>	Alignment	not modelled	79.1	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> HpcH/Hpal aldolase
71	<a href="#">d1qapa1</a>	Alignment	not modelled	76.1	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Nicotinate/Quinolinate PRTase C-terminal domain-like <b>Family:</b> NadC C-terminal domain-like
72	<a href="#">d1v6ta_</a>	Alignment	not modelled	75.6	14	<b>Fold:</b> 7-stranded beta/alpha barrel <b>Superfamily:</b> Glycoside hydrolase/deacetylase <b>Family:</b> LamB/YcsF-like
73	<a href="#">d2dfa1</a>	Alignment	not modelled	72.3	19	<b>Fold:</b> 7-stranded beta/alpha barrel <b>Superfamily:</b> Glycoside hydrolase/deacetylase <b>Family:</b> LamB/YcsF-like
74	<a href="#">d1o4ua1</a>	Alignment	not modelled	70.7	12	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Nicotinate/Quinolinate PRTase C-terminal domain-like <b>Family:</b> NadC C-terminal domain-like
75	<a href="#">c3cu2A_</a>	Alignment	not modelled	67.5	6	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ribulose-5-phosphate 3-epimerase; <b>PDBTitle:</b> crystal structure of ribulose-5-phosphate 3-epimerase (yp_718263.1)2 from haemophilus somnus 129pt at 1.91 a resolution
76	<a href="#">c3gr7A_</a>	Alignment	not modelled	64.9	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadh dehydrogenase; <b>PDBTitle:</b> structure of oye from geobacillus kaustophilus, hexagonal2 crystal form
77	<a href="#">c3l5aA_</a>	Alignment	not modelled	62.5	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadh/flavin oxidoreductase/nadh oxidase; <b>PDBTitle:</b> crystal structure of a probable nadh-dependent flavin oxidoreductase2 from staphylococcus aureus
78	<a href="#">c3kruC_</a>	Alignment	not modelled	61.7	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> nadh:flavin oxidoreductase/nadh oxidase; <b>PDBTitle:</b> crystal structure of the thermostable old yellow enzyme from2 thermoanaerobacter pseudethanolicus e39
79	<a href="#">d1vyra_</a>	Alignment	not modelled	58.3	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases

						<b>Family:</b> FMN-linked oxidoreductases
80	<a href="#">c2gq8A</a>	Alignment	not modelled	57.6	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase, fmn-binding; <b>PDBTitle:</b> structure of sye1, an oye homologue from s. ondeidensis, in complex2 with p-hydroxyacetophenone
81	<a href="#">d1qo2a</a>	Alignment	not modelled	56.9	12	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phoshate binding barrel <b>Family:</b> Histidine biosynthesis enzymes
82	<a href="#">c3qc3B</a>	Alignment	not modelled	56.2	16	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> d-ribulose-5-phosphate-3-epimerase; <b>PDBTitle:</b> crystal structure of a d-ribulose-5-phosphate-3-epimerase (np_954699)2 from homo sapiens at 2.20 a resolution
83	<a href="#">c2yciX</a>	Alignment	not modelled	55.7	9	<b>PDB header:</b> transferase <b>Chain:</b> X: <b>PDB Molecule:</b> 5-methyltetrahydrofolate corrinoid/iron sulfur protein <b>PDBTitle:</b> methyltransferase native
84	<a href="#">c2c3zA</a>	Alignment	not modelled	52.5	12	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> indole-3-glycerol phosphate synthase; <b>PDBTitle:</b> crystal structure of a truncated variant of indole-3-2 glycerol phosphate synthase from sulfolobus solfataricus
85	<a href="#">d1y0ea</a>	Alignment	not modelled	51.0	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phoshate binding barrel <b>Family:</b> NanE-like
86	<a href="#">c2x5eA</a>	Alignment	not modelled	48.9	15	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> upf0271 protein pa4511; <b>PDBTitle:</b> crystal structure of the hypothetical protein pa4511 from2 pseudomonas aeruginosa
87	<a href="#">d1qpoa1</a>	Alignment	not modelled	47.1	8	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Nicotinate/Quinolinate PRTase C-terminal domain-like <b>Family:</b> NadC C-terminal domain-like
88	<a href="#">d1gwja</a>	Alignment	not modelled	46.8	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
89	<a href="#">d1gvfa</a>	Alignment	not modelled	45.2	12	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class II FBP aldolase
90	<a href="#">d1z41a1</a>	Alignment	not modelled	44.6	12	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
91	<a href="#">d1vc4a</a>	Alignment	not modelled	42.8	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phoshate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
92	<a href="#">c2zviB</a>	Alignment	not modelled	42.8	15	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> 2,3-diketo-5-methylthiopentyl-1-phosphate <b>PDBTitle:</b> crystal structure of 2,3-diketo-5-methylthiopentyl-1-2 phosphate enolase from bacillus subtilis
93	<a href="#">c2vkzH</a>	Alignment	not modelled	40.7	12	<b>PDB header:</b> transferase <b>Chain:</b> H: <b>PDB Molecule:</b> fatty acid synthase subunit beta; <b>PDBTitle:</b> structure of the cerulenin-inhibited fungal fatty acid2 synthase type i multienzyme complex
94	<a href="#">d1vzwa1</a>	Alignment	not modelled	39.7	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phoshate binding barrel <b>Family:</b> Histidine biosynthesis enzymes
95	<a href="#">c2v82A</a>	Alignment	not modelled	39.0	13	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-dehydro-3-deoxy-6-phosphogalactonate aldolase; <b>PDBTitle:</b> kdpgal complexed to kdpgal
96	<a href="#">c1vadD</a>	Alignment	not modelled	38.4	12	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> regulatory protein teni; <b>PDBTitle:</b> structure of teni from bacillus subtilis
97	<a href="#">c2qv5A</a>	Alignment	not modelled	36.4	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein atu2773; <b>PDBTitle:</b> crystal structure of uncharacterized protein atu2773 from2 agrobacterium tumefaciens c58
98	<a href="#">d1wbha1</a>	Alignment	not modelled	36.4	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
99	<a href="#">c2dzaA</a>	Alignment	not modelled	35.3	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydropteroate synthase; <b>PDBTitle:</b> crystal structure of dihydropteroate synthase from thermus2 thermophilus hb8 in complex with 4-aminobenzoate
100	<a href="#">c2oemA</a>	Alignment	not modelled	34.5	15	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> 2,3-diketo-5-methylthiopentyl-1-phosphate enolase; <b>PDBTitle:</b> crystal structure of a rubisco-like protein from geobacillus2 kaustophilus liganded with mg2+ and 2,3-diketohehexane 1-phosphate
101	<a href="#">d1ka9f</a>	Alignment	not modelled	34.4	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phoshate binding barrel <b>Family:</b> Histidine biosynthesis enzymes
102	<a href="#">c1rr2A</a>	Alignment	not modelled	33.0	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> transcarboxylase 5s subunit; <b>PDBTitle:</b> propionibacterium shermanii transcarboxylase 5s subunit bound to 2-2 ketobutyric acid
103	<a href="#">d1ajza</a>	Alignment	not modelled	32.8	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Dihydropteroate synthetase-like <b>Family:</b> Dihydropteroate synthetase
104	<a href="#">c3atyA</a>	Alignment	not modelled	31.1	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> prostaglandin f2a synthase; <b>PDBTitle:</b> crystal structure of tcoye
105	<a href="#">c2ifaA</a>	Alignment	not modelled	26.9	10	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate racemase;

105	<a href="#">c2j1qA_</a>	Alignment	not modelled	20.9	10	<b>PDBTitle:</b> crystal structure of staphylococcus aureus glutamate2 racemase in complex with d-glutamate <b>PDB header:</b> oxidoreductase
106	<a href="#">c3gkaB_</a>	Alignment	not modelled	26.6	15	<b>Chain:</b> B: <b>PDB Molecule:</b> n-ethylmaleimide reductase; <b>PDBTitle:</b> crystal structure of n-ethylmaleimidine reductase from2 burkholderia pseudomallei
107	<a href="#">d1thfd_</a>	Alignment	not modelled	23.0	10	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Histidine biosynthesis enzymes
108	<a href="#">d2zdra2</a>	Alignment	not modelled	21.6	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> NeuB-like
109	<a href="#">c3ju3A_</a>	Alignment	not modelled	21.6	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> probable 2-oxoacid ferredoxin oxidoreductase, alpha chain; <b>PDBTitle:</b> crystal structure of alpha chain of probable 2-oxoacid ferredoxin2 oxidoreductase from thermoplasma acidophilum
110	<a href="#">c2x7vA_</a>	Alignment	not modelled	20.1	7	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable endonuclease 4; <b>PDBTitle:</b> crystal structure of thermotoga maritima endonuclease iv in2 the presence of zinc