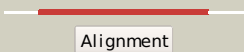

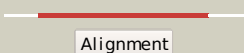

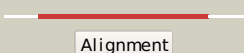

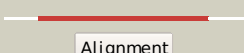



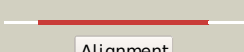

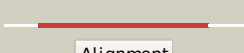

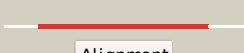


















#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3os4A_</a>	 Alignment		100.0	72	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nicotinate phosphoribosyltransferase; <b>PDBTitle:</b> the crystal structure of nicotinate phosphoribosyltransferase from2 yersinia pestis
2	<a href="#">c2im5C_</a>	 Alignment		100.0	38	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> nicotinate phosphoribosyltransferase; <b>PDBTitle:</b> crystal structure of nicotinate phosphoribosyltransferase2 from porphyromonas gingivalis
3	<a href="#">c1vlpA_</a>	 Alignment		100.0	33	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nicotinate phosphoribosyltransferase; <b>PDBTitle:</b> crystal structure of a putative nicotinate phosphoribosyltransferase2 (yor209c, npt1) from saccharomyces cerevisiae at 1.75 a resolution
4	<a href="#">c1ybeA_</a>	 Alignment		100.0	33	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nicotinate phosphoribosyltransferase; <b>PDBTitle:</b> crystal structure of a nicotinate phosphoribosyltransferase
5	<a href="#">c1yirA_</a>	 Alignment		100.0	51	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nicotinate phosphoribosyltransferase 2; <b>PDBTitle:</b> crystal structure of a nicotinate phosphoribosyltransferase
6	<a href="#">c2f7fA_</a>	 Alignment		100.0	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nicotinate phosphoribosyltransferase, putative; <b>PDBTitle:</b> crystal structure of enterococcus faecalis putative nicotinate2 phosphoribosyltransferase, new york structural genomics consortium
7	<a href="#">c2e5cA_</a>	 Alignment		100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nicotinamide phosphoribosyltransferase; <b>PDBTitle:</b> crystal structure of human nmprtase complexed with 5'-phosphoribosyl-2' 1'-pyrophosphate
8	<a href="#">c2i14B_</a>	 Alignment		100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> nicotinate-nucleotide pyrophosphorylase; <b>PDBTitle:</b> crystal structure of nicotinate-nucleotide2 pyrophosphorylase from pyrococcus furiosus
9	<a href="#">d1yira1</a>	 Alignment		100.0	55	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Nicotinate/Quinolinate PRTase C-terminal domain-like <b>Family:</b> Monomeric nicotinate phosphoribosyltransferase C-terminal domain
10	<a href="#">d1ybea1</a>	 Alignment		100.0	37	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Nicotinate/Quinolinate PRTase C-terminal domain-like <b>Family:</b> Monomeric nicotinate phosphoribosyltransferase C-terminal domain
11	<a href="#">c1ytkA_</a>	 Alignment		100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nicotinate phosphoribosyltransferase from thermoplasma <b>PDBTitle:</b> crystal structure of a nicotinate phosphoribosyltransferase from2 thermoplasma acidophilum with nicotinate mononucleotide

12	<a href="#">d1vlpA2</a>	Alignment		100.0	35	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Nicotinate/Quinolinate PRTase C-terminal domain-like <b>Family:</b> Monomeric nicotinate phosphoribosyltransferase C-terminal domain
13	<a href="#">d2f7fa1</a>	Alignment		100.0	25	<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
14	<a href="#">d1ytda1</a>	Alignment		100.0	22	<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
15	<a href="#">d2i14a1</a>	Alignment		100.0	22	<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
16	<a href="#">d1yira2</a>	Alignment		100.0	45	<b>Fold:</b> alpha/beta-Hammerhead <b>Superfamily:</b> Nicotinate/Quinolinate PRTase N-terminal domain-like <b>Family:</b> Monomeric nicotinate phosphoribosyltransferase N-terminal domain-like
17	<a href="#">d1vlpA1</a>	Alignment		100.0	31	<b>Fold:</b> alpha/beta-Hammerhead <b>Superfamily:</b> Nicotinate/Quinolinate PRTase N-terminal domain-like <b>Family:</b> Monomeric nicotinate phosphoribosyltransferase N-terminal domain-like
18	<a href="#">d1ybea2</a>	Alignment		100.0	28	<b>Fold:</b> alpha/beta-Hammerhead <b>Superfamily:</b> Nicotinate/Quinolinate PRTase N-terminal domain-like <b>Family:</b> Monomeric nicotinate phosphoribosyltransferase N-terminal domain-like
19	<a href="#">d2f7fa2</a>	Alignment		100.0	21	<b>Fold:</b> alpha/beta-Hammerhead <b>Superfamily:</b> Nicotinate/Quinolinate PRTase N-terminal domain-like <b>Family:</b> NadC N-terminal domain-like
20	<a href="#">c1x1oC</a>	Alignment		99.9	17	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> nicotinate-nucleotide pyrophosphorylase; <b>PDBTitle:</b> crystal structure of project id tt0268 from thermus thermophilus hb8
21	<a href="#">c2b7pA</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable nicotinate-nucleotide pyrophosphorylase; <b>PDBTitle:</b> crystal structure of quinolinic acid phosphoribosyltransferase from2 helicobacter pylori
22	<a href="#">c3l0gD</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> nicotinate-nucleotide pyrophosphorylase; <b>PDBTitle:</b> crystal structure of nicotinate-nucleotide pyrophosphorylase from2 ehrlchia chaffeensis at 2.05a resolution
23	<a href="#">c1qpoA</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> quinolinate acid phosphoribosyl transferase; <b>PDBTitle:</b> quinolinate phosphoribosyl transferase (qaprtase) apo-enzyme from2 mycobacterium tuberculosis
24	<a href="#">c3pajA</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nicotinate-nucleotide pyrophosphorylase, carboxylating; <b>PDBTitle:</b> 2.00 angstrom resolution crystal structure of a quinolinate2 phosphoribosyltransferase from vibrio cholerae o1 biovar eltor str.3 n16961
25	<a href="#">c2jbmA</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nicotinate-nucleotide pyrophosphorylase; <b>PDBTitle:</b> qprtase structure from human
26	<a href="#">c1o4uA</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> type ii quinolic acid phosphoribosyltransferase; <b>PDBTitle:</b> crystal structure of a nicotinate nucleotide pyrophosphorylase2 (tm1645) from thermotoga maritima at 2.50 a resolution
27	<a href="#">c1qapA</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> glycosyltransferase <b>Chain:</b> A: <b>PDB Molecule:</b> quinolinic acid phosphoribosyltransferase;

						<b>PDBTitle:</b> quinolinic acid phosphoribosyltransferase with bound2 quinolinic acid
28	<a href="#">c3tqvA_</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nicotinate-nucleotide pyrophosphorylase; <b>PDBTitle:</b> structure of the nicotinate-nucleotide pyrophosphorylase from2 francisella tularensis.
29	<a href="#">d2i14a2</a>	Alignment	not modelled	99.8	13	<b>Fold:</b> alpha/beta-Hammerhead <b>Superfamily:</b> Nicotinate/Quinolinate PRTase N-terminal domain-like <b>Family:</b> NadC N-terminal domain-like
30	<a href="#">c3gnnA_</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nicotinate-nucleotide pyrophosphorylase; <b>PDBTitle:</b> crystal structure of nicotinate-nucleotide2 pyrophosphorylase from burkholderi pseudomallei
31	<a href="#">d1ytda2</a>	Alignment	not modelled	99.7	19	<b>Fold:</b> alpha/beta-Hammerhead <b>Superfamily:</b> Nicotinate/Quinolinate PRTase N-terminal domain-like <b>Family:</b> NadC N-terminal domain-like
32	<a href="#">c3c2vA_</a>	Alignment	not modelled	99.6	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nicotinate-nucleotide pyrophosphorylase; <b>PDBTitle:</b> crystal structure of the quinolinate phosphoribosyl2 transferase (bna6) from saccharomyces cerevisiae complexed3 with prpp and the inhibitor phthalate
33	<a href="#">d1qapa1</a>	Alignment	not modelled	99.6	18	<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
34	<a href="#">d1qpoa1</a>	Alignment	not modelled	99.5	18	<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
35	<a href="#">d1o4ua1</a>	Alignment	not modelled	97.7	9	<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
36	<a href="#">d1gwja_</a>	Alignment	not modelled	73.6	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
37	<a href="#">d1rpxa_</a>	Alignment	not modelled	72.7	8	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> D-ribulose-5-phosphate 3-epimerase
38	<a href="#">c3cu2A_</a>	Alignment	not modelled	72.1	10	<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
39	<a href="#">d2flia1</a>	Alignment	not modelled	62.7	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> D-ribulose-5-phosphate 3-epimerase
40	<a href="#">c3absD_</a>	Alignment	not modelled	58.3	20	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> ethanolamine ammonia-lyase light chain; <b>PDBTitle:</b> crystal structure of ethanolamine ammonia-lyase from escherichia coli2 complexed with adeninylpentylcobalamin and ethanolamine
41	<a href="#">d2j9ga1</a>	Alignment	not modelled	57.6	20	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Rudiment single hybrid motif <b>Family:</b> BC C-terminal domain-like
42	<a href="#">c3inpA_</a>	Alignment	not modelled	57.3	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.
43	<a href="#">d1ulza1</a>	Alignment	not modelled	57.2	18	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Rudiment single hybrid motif <b>Family:</b> BC C-terminal domain-like
44	<a href="#">d1vyra_</a>	Alignment	not modelled	54.3	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
45	<a href="#">d1icpa_</a>	Alignment	not modelled	53.9	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
46	<a href="#">c3qjaA_</a>	Alignment	not modelled	51.9	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 the mycobacterium tuberculosis indole-3-glycerol2 phosphate synthase (trpc) in apo form
47	<a href="#">c1ni4D_</a>	Alignment	not modelled	51.9	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> pyruvate dehydrogenase e1 component: beta <b>PDBTitle:</b> human pyruvate dehydrogenase
48	<a href="#">d2ozlb2</a>	Alignment	not modelled	51.5	18	<b>Fold:</b> TK C-terminal domain-like <b>Superfamily:</b> TK C-terminal domain-like <b>Family:</b> Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
49	<a href="#">d1xi3a_</a>	Alignment	not modelled	50.5	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Thiamin phosphate synthase <b>Family:</b> Thiamin phosphate synthase
50	<a href="#">d1a53a_</a>	Alignment	not modelled	48.9	24	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
51	<a href="#">d1tqxa_</a>	Alignment	not modelled	47.0	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> D-ribulose-5-phosphate 3-epimerase
						<b>Fold:</b> TIM beta/alpha-barrel

52	<a href="#">dlvhca_</a>	Alignment	not modelled	45.8	6	<b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
53	<a href="#">dl1qja_</a>	Alignment	not modelled	44.9	9	<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="#">c3labA_</a>	Alignment	not modelled	44.3	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative kdpG (2-keto-3-deoxy-6-phosphogluconate) <b>PDBTitle:</b> crystal structure of a putative kdpG (2-keto-3-deoxy-6-2 phosphogluconate) aldolase from oleispira antarctica
55	<a href="#">dlmxsa_</a>	Alignment	not modelled	44.3	3	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
56	<a href="#">dlwbha1</a>	Alignment	not modelled	44.0	12	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
57	<a href="#">c2h90A_</a>	Alignment	not modelled	43.9	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
58	<a href="#">dlvjia_</a>	Alignment	not modelled	42.1	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
59	<a href="#">c2v82A_</a>	Alignment	not modelled	41.1	11	<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
60	<a href="#">dlxya1</a>	Alignment	not modelled	40.5	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> NanE-like
61	<a href="#">c3ct7E_</a>	Alignment	not modelled	40.2	12	<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
62	<a href="#">c3dl2A_</a>	Alignment	not modelled	40.1	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin-conjugating enzyme e2 variant 3; <b>PDBTitle:</b> hexagonal structure of the Idh domain of human ubiquitin-2 conjugating enzyme e2-like isoform a
63	<a href="#">dlr0ma1</a>	Alignment	not modelled	39.5	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Enolase C-terminal domain-like <b>Family:</b> D-glucarate dehydratase-like
64	<a href="#">dl1uca_</a>	Alignment	not modelled	39.3	22	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> Bacterial luciferase (alkanal monooxygenase)
65	<a href="#">c2c3zA_</a>	Alignment	not modelled	38.3	26	<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
66	<a href="#">dlh1ya_</a>	Alignment	not modelled	37.3	8	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> D-ribulose-5-phosphate 3-epimerase
67	<a href="#">d2tpsa_</a>	Alignment	not modelled	36.3	8	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Thiamin phosphate synthase <b>Family:</b> Thiamin phosphate synthase
68	<a href="#">clwueA_</a>	Alignment	not modelled	36.3	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> mandelate racemase/muconate lactonizing enzyme family <b>PDBTitle:</b> crystal structure of protein gi:29375081, unknown member of enolase2 superfamily from enterococcus faecalis v583
69	<a href="#">dl1vaa3</a>	Alignment	not modelled	36.2	23	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> C-terminal fragment of elongation factor SelB
70	<a href="#">d7reqa2</a>	Alignment	not modelled	35.5	15	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Cobalamin (vitamin B12)-binding domain <b>Family:</b> Cobalamin (vitamin B12)-binding domain
71	<a href="#">c3anyB_</a>	Alignment	not modelled	35.3	16	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> ethanolamine ammonia-lyase light chain; <b>PDBTitle:</b> crystal structure of ethanolamine ammonia-lyase from escherichia coli2 complexed with cn-cbl and (r)-2-amino-1-propanol
72	<a href="#">c2h9aA_</a>	Alignment	not modelled	34.5	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> carbon monoxide dehydrogenase corrinoid/iron- <b>PDBTitle:</b> corrinoid iron-sulfur protein
73	<a href="#">c3o63B_</a>	Alignment	not modelled	32.6	7	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> probable thiamine-phosphate pyrophosphorylase; <b>PDBTitle:</b> crystal structure of thiamin phosphate synthase from mycobacterium2 tuberculosis
74	<a href="#">dlwuea1</a>	Alignment	not modelled	32.5	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Enolase C-terminal domain-like <b>Family:</b> D-glucarate dehydratase-like
75	<a href="#">c3atyA_</a>	Alignment	not modelled	31.6	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> prostaglandin f2a synthase; <b>PDBTitle:</b> crystal structure of tcoye
76	<a href="#">clm6vE_</a>	Alignment	not modelled	30.8	18	<b>PDB header:</b> ligase <b>Chain:</b> E: <b>PDB Molecule:</b> carbamoyl phosphate synthetase large chain; <b>PDBTitle:</b> crystal structure of the g359f (small subunit) point mutant of2 carbamoyl phosphate synthetase
77	<a href="#">c3qc3B_</a>	Alignment	not modelled	27.6	9	<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
78	<a href="#">dlwufal</a>	Alignment	not modelled	27.5	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Enolase C-terminal domain-like <b>Family:</b> D-glucarate dehydratase-like
79	<a href="#">c2bdqA</a>	Alignment	not modelled	27.3	13	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> copper homeostasis protein cutc; <b>PDBTitle:</b> crystal structure of the putative copper homeostasis2 protein cutc from streptococcus agalactiae, northeast3 strucural genomics target sar15.
80	<a href="#">dljsdal</a>	Alignment	not modelled	26.2	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Enolase C-terminal domain-like <b>Family:</b> D-glucarate dehydratase-like
81	<a href="#">c3gkxB</a>	Alignment	not modelled	25.4	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative arsc family related protein; <b>PDBTitle:</b> crystal structure of putative arsc family related protein from2 bacteroides fragilis
82	<a href="#">dlxcfa</a>	Alignment	not modelled	24.9	8	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phoshate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
83	<a href="#">clhvxA</a>	Alignment	not modelled	24.6	5	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-amylase; <b>PDBTitle:</b> bacillus stearothermophilus alpha-amylase
84	<a href="#">c2j7pA</a>	Alignment	not modelled	22.2	12	<b>PDB header:</b> signal recognition <b>Chain:</b> A: <b>PDB Molecule:</b> signal recognition particle protein; <b>PDBTitle:</b> gmppnp-stabilized ng domain complex of the srp gtpases ffh2 and ftsy
85	<a href="#">clhyhA</a>	Alignment	not modelled	22.1	17	<b>PDB header:</b> oxidoreductase (choh(d)-nad+(a)) <b>Chain:</b> A: <b>PDB Molecule:</b> l-2-hydroxysocaproate dehydrogenase; <b>PDBTitle:</b> crystal structure of l-2-hydroxysocaproate dehydrogenase from2 lactobacillus confusus at 2.2 angstroms resolution-an example of3 strong asymmetry between subunits
86	<a href="#">clojuA</a>	Alignment	not modelled	21.7	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> malate dehydrogenase; <b>PDBTitle:</b> 2.8 a resolution structure of malate dehydrogenase from2 archaeoglobus fulgidus in complex with etheno-nad.
87	<a href="#">c3kwpA</a>	Alignment	not modelled	21.6	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> predicted methyltransferase; <b>PDBTitle:</b> crystal structure of putative methyltransferase from lactobacillus2 brevis
88	<a href="#">clvadD</a>	Alignment	not modelled	21.5	4	<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
89	<a href="#">c3m4wH</a>	Alignment	not modelled	21.0	44	<b>PDB header:</b> signaling protein/signaling protein <b>Chain:</b> H: <b>PDB Molecule:</b> sigma-e factor negative regulatory protein; <b>PDBTitle:</b> structural basis for the negative regulation of bacterial stress2 response by rseb
90	<a href="#">clzfaA</a>	Alignment	not modelled	20.4	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> inosine monophosphate dehydrogenase; <b>PDBTitle:</b> inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
91	<a href="#">c3gkaB</a>	Alignment	not modelled	19.5	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> n-ethylmaleimide reductase; <b>PDBTitle:</b> crystal structure of n-ethylmaleimidine reductase from2 burkholderia pseudomallei
92	<a href="#">c2ekcA</a>	Alignment	not modelled	19.4	13	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> structural study of project id aq_1548 from aquifex aeolicus vf5
93	<a href="#">dlbqga1</a>	Alignment	not modelled	18.9	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Enolase C-terminal domain-like <b>Family:</b> D-glucarate dehydratase-like
94	<a href="#">dlfuia1</a>	Alignment	not modelled	18.5	23	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Fucl/AraA C-terminal domain-like <b>Family:</b> L-fucose isomerase, C-terminal domain
95	<a href="#">clsjaA</a>	Alignment	not modelled	18.3	13	<b>PDB header:</b> lyase, isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acylamino acid racemase; <b>PDBTitle:</b> x-ray structure of o-succinylbenzoate synthase complexed2 with n-acetylmethionine
96	<a href="#">c3q58A</a>	Alignment	not modelled	18.1	12	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetylmannosamine-6-phosphate 2-epimerase; <b>PDBTitle:</b> structure of n-acetylmannosamine-6-phosphate epimerase from salmonella2 enterica
97	<a href="#">d2dfaa1</a>	Alignment	not modelled	18.0	21	<b>Fold:</b> 7-stranded beta/alpha barrel <b>Superfamily:</b> Glycoside hydrolase/deacetylase <b>Family:</b> LamB/YcsF-like
98	<a href="#">d2f9ya1</a>	Alignment	not modelled	17.9	20	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Biotin dependent carboxylase carboxyltransferase domain
99	<a href="#">dltwda</a>	Alignment	not modelled	17.7	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> CutC-like <b>Family:</b> CutC-like