Phyre2

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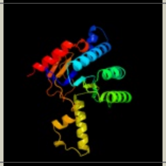
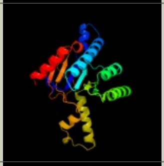
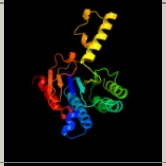
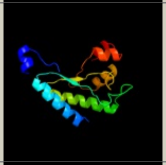
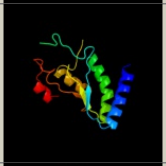
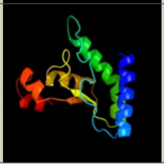
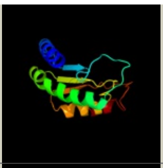
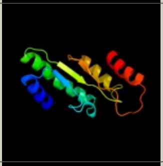
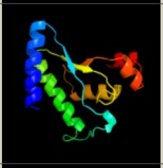
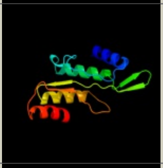
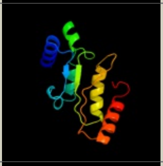
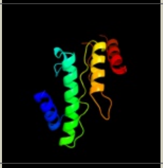
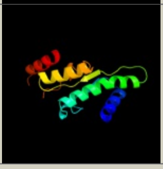
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2vg2C_	Alignment		100.0	41	**PDB header:**transferase **Chain:** C: **PDB Molecule:**undecaprenyl pyrophosphate synthetase; **PDBTitle:** rv2361 with ipp
2	d1ueha_	Alignment		100.0	97	**Fold:**Undecaprenyl diphosphate synthase **Superfamily:**Undecaprenyl diphosphate synthase **Family:**Undecaprenyl diphosphate synthase
3	c2vfwB_	Alignment		100.0	33	**PDB header:**transferase **Chain:** B: **PDB Molecule:**short-chain z-isoprenyl diphosphate synthetase; **PDBTitle:** rv1086 native
4	c1jp3A_	Alignment		100.0	95	**PDB header:**transferase **Chain:** A: **PDB Molecule:**undecaprenyl pyrophosphate synthase; **PDBTitle:** structure of e.coli undecaprenyl pyrophosphate synthase
5	d1f75a_	Alignment		100.0	38	**Fold:**Undecaprenyl diphosphate synthase **Superfamily:**Undecaprenyl diphosphate synthase **Family:**Undecaprenyl diphosphate synthase
6	c2d2rA_	Alignment		100.0	41	**PDB header:**transferase **Chain:** A: **PDB Molecule:**undecaprenyl pyrophosphate synthase; **PDBTitle:** crystal structure of helicobacter pylori undecaprenyl pyrophosphate2 synthase
7	c3ugsB_	Alignment		100.0	38	**PDB header:**transferase **Chain:** B: **PDB Molecule:**undecaprenyl pyrophosphate synthase; **PDBTitle:** crystal structure of a probable undecaprenyl diphosphate synthase2 (upps) from campylobacter jejuni
8	c3bdkB_	Alignment		92.3	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**d-mannonate dehydratase; **PDBTitle:** crystal structure of streptococcus suis mannonate2 dehydratase complexed with substrate analogue
9	c3cnyA_	Alignment		91.4	8	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**inositol catabolism protein iole; **PDBTitle:** crystal structure of a putative inositol catabolism protein iole2 (iole, lp_3607) from lactobacillus plantarum wcfs1 at 1.85 a3 resolution
10	d1tz9a_	Alignment		85.7	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**UxuA-like
11	c2ou4C_	Alignment		84.2	9	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**d-tagatose 3-epimerase; **PDBTitle:** crystal structure of d-tagatose 3-epimerase from2 pseudomonas cichorii

12	c2hk1D_	Alignment		84.1	12	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**d-psicose 3-epimerase; **PDBTitle:** crystal structure of d-psicose 3-epimerase (dpease) in the presence of2 d-fructose
13	c2nuxB_	Alignment		81.3	9	**PDB header:**lyase **Chain:** B: **PDB Molecule:**2-keto-3-deoxygluconate/2-keto-3-deoxy-6-phospho gluconate **PDBTitle:** 2-keto-3-deoxygluconate aldolase from sulfolobus acidocaldarius,2 native structure in p6522 at 2.5 a resolution
14	c3dx5A_	Alignment		79.6	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**uncharacterized protein asbf; **PDBTitle:** crystal structure of the probable 3-dhs dehydratase asbf involved in2 the petrobactin synthesis from bacillus anthracis
15	c3eb2A_	Alignment		77.4	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative dihydrodipicolinate synthetase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 rhodopseudomonas palustris at 2.0a resolution
16	c3b4uB_	Alignment		75.9	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from agrobacterium2 tumefaciens str. c58
17	c3fluD_	Alignment		75.3	20	**PDB header:**lyase **Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from the pathogen2 neisseria meningitidis
18	c2rfgB_	Alignment		73.9	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from hahella2 chejuensis at 1.5a resolution
19	c3cqkB_	Alignment		73.5	16	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**l-ribulose-5-phosphate 3-epimerase ulae; **PDBTitle:** crystal structure of l-xylulose-5-phosphate 3-epimerase ulae (form b)2 complex with zn2+ and sulfate
20	c3d0cB_	Alignment		73.4	17	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 oceanobacillus iheyensis at 1.9 a resolution
21	c3qxbB_	Alignment	not modelled	72.1	9	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative xylose isomerase; **PDBTitle:** crystal structure of a putative xylose isomerase (yp_426450.1) from2 rhodospirillum rubrum atcc 11170 at 1.90 a resolution
22	c3si9B_	Alignment	not modelled	70.7	19	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from bartonella2 henselae
23	c2zdsB_	Alignment	not modelled	66.6	15	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**putative dna-binding protein; **PDBTitle:** crystal structure of sco6571 from streptomyces coelicolor2 a3(2)
24	c3pueA_	Alignment	not modelled	63.5	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of the complex of dhydrodipicolinate synthase from2 acinetobacter baumannii with lysine at 2.6a resolution
25	c3s5oA_	Alignment	not modelled	59.4	10	**PDB header:**lyase **Chain:** A: **PDB Molecule:**4-hydroxy-2-oxoglutarate aldolase, mitochondrial; **PDBTitle:** crystal structure of human 4-hydroxy-2-oxoglutarate aldolase bound to2 pyruvate
26	c2r8wB_	Alignment	not modelled	57.4	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**agr_c_1641p; **PDBTitle:** the crystal structure of dihydrodipicolinate synthase (atu0899) from2 agrobacterium tumefaciens str. c58
27	c3cprB_	Alignment	not modelled	56.4	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthetase; **PDBTitle:** the crystal structure of corynebacterium glutamicum2 dihydrodipicolinate synthase to 2.2 a resolution
						Fold:TIM beta/alpha-barrel

28	d1bxba_	Alignment	not modelled	55.5	9	**Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
29	c2v9dB_	Alignment	not modelled	54.9	17	**PDB header:**lyase **Chain:** B: **PDB Molecule:**yage; **PDBTitle:** crystal structure of yage, a prophage protein belonging to2 the dihydrodipicolinic acid synthase family from e. coli3 k12
30	c3fkkA_	Alignment	not modelled	52.6	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**l-2-keto-3-deoxyarabonate dehydratase; **PDBTitle:** structure of l-2-keto-3-deoxyarabonate dehydratase
31	c3kwsB_	Alignment	not modelled	52.3	3	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative sugar isomerase; **PDBTitle:** crystal structure of putative sugar isomerase (yp_001305149.1) from2 parabacteroides distasonis atcc 8503 at 1.68 a resolution
32	d1m5wa_	Alignment	not modelled	51.6	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Pyridoxine 5'-phosphate synthase **Family:**Pyridoxine 5'-phosphate synthase
33	c3qfeB_	Alignment	not modelled	51.3	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative dihydrodipicolinate synthase family protein; **PDBTitle:** crystal structures of a putative dihydrodipicolinate synthase family2 protein from coccidioides immitis
34	c3noeA_	Alignment	not modelled	49.5	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from pseudomonas2 aeruginosa
35	d1xxxa1	Alignment	not modelled	49.2	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
36	c3n2xB_	Alignment	not modelled	48.4	18	**PDB header:**lyase **Chain:** B: **PDB Molecule:**uncharacterized protein yage; **PDBTitle:** crystal structure of yage, a prophage protein belonging to the2 dihydrodipicolinic acid synthase family from e. coli k12 in complex3 with pyruvate
37	c3ktcB_	Alignment	not modelled	46.8	8	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**xylose isomerase; **PDBTitle:** crystal structure of putative sugar isomerase (yp_050048.1) from2 erwinia carotovora atroseptica scri1043 at 1.54 a resolution
38	c2ehhE_	Alignment	not modelled	46.6	16	**PDB header:**lyase **Chain:** E: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 aquifex aeolicus
39	c3h5dD_	Alignment	not modelled	46.6	13	**PDB header:**lyase **Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** dihydrodipicolinate synthase from drug-resistant streptococcus2 pneumoniae
40	c2vc6A_	Alignment	not modelled	45.3	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** structure of mosa from s. meliloti with pyruvate bound
41	c3bi8A_	Alignment	not modelled	44.1	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** structure of dihydrodipicolinate synthase from clostridium2 botulinum
42	c2r94B_	Alignment	not modelled	43.7	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**2-keto-3-deoxy-(6-phospho-)gluconate aldolase; **PDBTitle:** crystal structure of kd(p)ga from t.tenax
43	c2zvrA_	Alignment	not modelled	42.9	9	**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
44	c2ksnA_	Alignment	not modelled	41.9	20	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ubiquitin domain-containing protein 2; **PDBTitle:** solution structure of the n-terminal domain of dc-ubp/ubtd2
45	d1hl2a_	Alignment	not modelled	41.9	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
46	d1vhua_	Alignment	not modelled	41.7	15	**Fold:**Macro domain-like **Superfamily:**Macro domain-like **Family:**Macro domain
47	d1i60a_	Alignment	not modelled	41.6	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**IolI-like
48	d1bxca_	Alignment	not modelled	39.3	7	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
49	c3daqB_	Alignment	not modelled	38.9	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from methicillin-2 resistant staphylococcus aureus
50	d1otha2	Alignment	not modelled	37.7	21	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
51	c2ejaB_	Alignment	not modelled	37.6	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**uroporphyrinogen decarboxylase; **PDBTitle:** crystal structure of uroporphyrinogen decarboxylase from2 aquifex aeolicus
52	d1o5ka_	Alignment	not modelled	37.5	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
53	c3g0sA_	Alignment	not modelled	36.0	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** dihydrodipicolinate synthase from salmonella typhimurium lt2

54	c3na8A_	Alignment	not modelled	35.9	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative dihydrodipicolinate synthetase; **PDBTitle:** crystal structure of a putative dihydrodipicolinate synthetase from2 pseudomonas aeruginosa
55	c3dz1A_	Alignment	not modelled	35.7	22	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 rhodopseudomonas palustris at 1.87a resolution
56	c3lciA_	Alignment	not modelled	34.7	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**n-acetylneuraminate lyase; **PDBTitle:** the d-sialic acid aldolase mutant v251w
57	c3bzjA_	Alignment	not modelled	33.3	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uv endonuclease; **PDBTitle:** uvde k229l
58	c1xhoB_	Alignment	not modelled	33.2	19	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**chorismate mutase; **PDBTitle:** chorismate mutase from clostridium thermocellum cth-682
59	d1xhoa_	Alignment	not modelled	33.2	19	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**Chorismate mutase
60	c3vh1A_	Alignment	not modelled	31.8	20	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**ubiquitin-like modifier-activating enzyme atg7; **PDBTitle:** crystal structure of saccharomyces cerevisiae atg7 (1-595)
61	c3gk0H_	Alignment	not modelled	31.4	15	**PDB header:**transferase **Chain:** H: **PDB Molecule:**pyridoxine 5'-phosphate synthase; **PDBTitle:** crystal structure of pyridoxal phosphate biosynthetic2 protein from burkholderia pseudomallei
62	d1fnja_	Alignment	not modelled	31.2	22	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**Chorismate mutase
63	c3q71A_	Alignment	not modelled	30.9	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly [adp-ribose] polymerase 14; **PDBTitle:** human parp14 (artd8) - macro domain 2 in complex with adenosine-5-2 diphosphoribose
64	c3grfA_	Alignment	not modelled	30.8	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** x-ray structure of ornithine transcarbamoylase from giardia2 lamblia
65	d1vk1a_	Alignment	not modelled	29.8	60	**Fold:**ParB/Sulfiredoxin **Superfamily:**ParB/Sulfiredoxin **Family:**Hypothetical protein PF0380
66	c1ut8B_	Alignment	not modelled	28.1	8	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**exodeoxyribonuclease; **PDBTitle:** divalent metal ions (zinc) bound to t5 5'-exonuclease
67	c2yxgD_	Alignment	not modelled	27.7	18	**PDB header:**lyase **Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihyrodipicolinate synthase (dapa)
68	d1dbfa_	Alignment	not modelled	25.6	22	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**Chorismate mutase
69	c2pfuA_	Alignment	not modelled	25.6	10	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**biopolymer transport exbd protein; **PDBTitle:** nmr strcuture determination of the periplasmic domain of exbd from2 e.coli
70	c2f9iC_	Alignment	not modelled	25.5	16	**PDB header:**transferase **Chain:** C: **PDB Molecule:**acetyl-coenzyme a carboxylase carboxyl **PDBTitle:** crystal structure of the carboxyltransferase subunit of acc2 from staphylococcus aureus
71	c3gzaB_	Alignment	not modelled	24.6	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative alpha-l-fucosidase; **PDBTitle:** crystal structure of putative alpha-l-fucosidase (np_812709.1) from2 bacteroides thetaiotaomicron vpi-5482 at 1.60 a resolution
72	d1cmwa2	Alignment	not modelled	24.5	10	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**5' to 3' exonuclease catalytic domain
73	d1xkya1	Alignment	not modelled	23.2	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
74	d2f9ya1	Alignment	not modelled	22.9	16	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
75	d2a6na1	Alignment	not modelled	22.7	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
76	c3lmzA_	Alignment	not modelled	22.5	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative sugar isomerase; **PDBTitle:** crystal structure of putative sugar isomerase. (yp_001305105.1) from2 parabacteroides distasonis atcc 8503 at 1.44 a resolution
77	c3e96B_	Alignment	not modelled	22.4	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 bacillus clausii
78	c3ngfA_	Alignment	not modelled	22.3	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ap endonuclease, family 2; **PDBTitle:** crystal structure of ap endonuclease, family 2 from brucella2 melitensis
79	d1nw9b_	Alignment	not modelled	21.7	16	**Fold:**Caspase-like **Superfamily:**Caspase-like **Family:**Caspase catalytic domain

80	c3ju2A_	Alignment	not modelled	21.6	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein smc04130; **PDBTitle:** crystal structure of protein smc04130 from sinorhizobium meliloti 1021
81	d1xima_	Alignment	not modelled	21.5	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
82	c2qtzA_	Alignment	not modelled	20.6	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**methionine synthase reductase; **PDBTitle:** crystal structure of the nadp+-bound fad-containing fnr-like module of2 human methionine synthase reductase
83	c3gqeA_	Alignment	not modelled	19.4	13	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**non-structural protein 3; **PDBTitle:** crystal structure of macro domain of venezuelan equine encephalitis2 virus
84	c3q6zA_	Alignment	not modelled	16.3	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly [adp-ribose] polymerase 14; **PDBTitle:** human parp14 (artd8)-macro domain 1 in complex with adenosine-5-2 diphosphoribose
85	d1f1ja_	Alignment	not modelled	16.1	16	**Fold:**Caspase-like **Superfamily:**Caspase-like **Family:**Caspase catalytic domain
86	d1fmta2	Alignment	not modelled	16.1	17	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
87	d2eyqa6	Alignment	not modelled	15.9	9	**Fold:**TRCF domain-like **Superfamily:**TRCF domain-like **Family:**TRCF domain
88	d1wsca1	Alignment	not modelled	15.7	16	**Fold:**AMMECR1-like **Superfamily:**AMMECR1-like **Family:**AMMECR1-like
89	c2bpoA_	Alignment	not modelled	15.6	9	**PDB header:**reductase **Chain:** A: **PDB Molecule:**nadph-cytochrom p450 reductase; **PDBTitle:** crystal structure of the yeast cpr triple mutant: d74g,2 y75f, k78a.
90	c1nmqB_	Alignment	not modelled	15.6	20	**PDB header:**apoptosis, hydrolase **Chain:** B: **PDB Molecule:**caspase-3; **PDBTitle:** extendend tethering: in situ assembly of inhibitors
91	c3lerA_	Alignment	not modelled	15.5	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 campylobacter jejuni subsp. jejuni nctc 11168
92	d1w3ia_	Alignment	not modelled	15.2	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
93	c2btdA_	Alignment	not modelled	15.0	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pts-dependent dihydroxyacetone kinase; **PDBTitle:** crystal structure of dhal from e. coli
94	d1bg4a_	Alignment	not modelled	14.9	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
95	c3eyxB_	Alignment	not modelled	14.5	36	**PDB header:**lyase **Chain:** B: **PDB Molecule:**carbonic anhydrase; **PDBTitle:** crystal structure of carbonic anhydrase nce103 from2 saccharomyces cerevisiae
96	d2pp4a1	Alignment	not modelled	14.4	13	**Fold:**TAFH domain-like **Superfamily:**TAFH domain-like **Family:**TAFH domain-like
97	d1yvka1	Alignment	not modelled	14.4	17	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
98	c2x7vA_	Alignment	not modelled	14.3	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable endonuclease 4; **PDBTitle:** crystal structure of thermotoga maritima endonuclease iv in2 the presence of zinc
99	d2q02a1	Alignment	not modelled	13.7	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**IolI-like