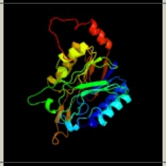
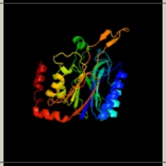
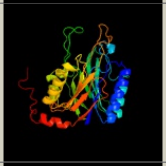
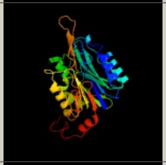
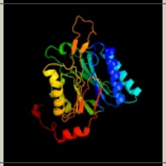
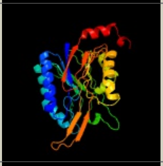
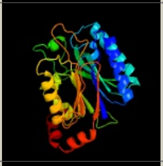
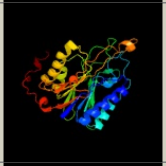
Phyre^2

Email	mdejesus@rockefeller.edu
Description	RVBD0480c_(-)_568967_569809
Date	Tue Jul 23 14:50:56 BST 2019
Unique Job ID	a62a31a44e006b1d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2vhiG_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**cg3027-pa; **PDBTitle:** crystal structure of a pyrimidine degrading enzyme from2 drosophila melanogaster
2	c1emsB_	Alignment		100.0	28	**PDB header:**antitumor protein **Chain:** B: **PDB Molecule:**nit-fragile histidine triad fusion protein; **PDBTitle:** crystal structure of the c. elegans nitfhit protein
3	c2vhhA_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cg3027-pa; **PDBTitle:** crystal structure of a pyrimidine degrading enzyme from2 drosophila melanogaster
4	c2w1vA_	Alignment		100.0	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nitrilase homolog 2; **PDBTitle:** crystal structure of mouse nitrilase-2 at 1.4a resolution
5	c6ftqA_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-ureidopropionase; **PDBTitle:** crystal structure of human beta-ureidopropionase (beta-alanine2 synthase) - mutant t299c
6	c5h8lM_	Alignment		100.0	21	**PDB header:**hydrolase **Chain:** M: **PDB Molecule:**n-carbamoylputrescine amidohydrolase; **PDBTitle:** crystal structure of medicago truncatula n-carbamoylputrescine2 amidohydrolase (mtcpa) c158s mutant in complex with putrescine
7	d1uf5a_	Alignment		100.0	24	**Fold:**Carbon-nitrogen hydrolase **Superfamily:**Carbon-nitrogen hydrolase **Family:**Carbamilase
8	c2plqA_	Alignment		100.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aliphatic amidase; **PDBTitle:** crystal structure of the amidase from geobacillus pallidus rapc8
9	c2e2kC_	Alignment		100.0	17	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**formamidase; **PDBTitle:** helicobacter pylori formamidase amif contains a fine-tuned cysteine-2 glutamate-lysine catalytic triad
10	c4hg3C_	Alignment		100.0	28	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**probable hydrolase nit2; **PDBTitle:** structural insights into yeast nit2: wild-type yeast nit2 in complex2 with alpha-ketoglutarate
11	c2e11B_	Alignment		100.0	29	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hydrolase; **PDBTitle:** the crystal structure of xc1258 from xanthomonas campestris: a cn-2 hydrolase superfamily protein with an arsenic adduct in the active3 site

12	c6mg6D_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**carbon-nitrogen hydrolase; **PDBTitle:** crystal structure of carbon-nitrogen hydrolase from helicobacter2 pylori g27
13	d1emsa2	Alignment		100.0	28	**Fold:**Carbon-nitrogen hydrolase **Superfamily:**Carbon-nitrogen hydrolase **Family:**Nitrilase
14	c5khaA_	Alignment		100.0	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamine-dependent nad+ synthetase; **PDBTitle:** structure of glutamine-dependent nad+ synthetase from acinetobacter2 baumannii in complex with adenosine diphosphate (adp)
15	c3dlaD_	Alignment		100.0	21	**PDB header:**ligase **Chain:** D: **PDB Molecule:**glutamine-dependent nad(+) synthetase; **PDBTitle:** x-ray crystal structure of glutamine-dependent nad+ synthetase from2 mycobacterium tuberculosis bound to naad+ and don
16	d1f89a_	Alignment		100.0	25	**Fold:**Carbon-nitrogen hydrolase **Superfamily:**Carbon-nitrogen hydrolase **Family:**Nitrilase
17	c3wuyA_	Alignment		100.0	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nitrilase; **PDBTitle:** crystal structure of nit6803
18	c4f4hA_	Alignment		100.0	23	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamine dependent nad+ synthetase; **PDBTitle:** crystal structure of a glutamine dependent nad+ synthetase from2 burkholderia thailandensis
19	d1j31a_	Alignment		100.0	26	**Fold:**Carbon-nitrogen hydrolase **Superfamily:**Carbon-nitrogen hydrolase **Family:**Carbamilase
20	c3n05B_	Alignment		100.0	25	**PDB header:**ligase **Chain:** B: **PDB Molecule:**nh(3)-dependent nad(+) synthetase; **PDBTitle:** crystal structure of nh3-dependent nad+ synthetase from streptomyces2 avermitilis
21	c3hkxA_	Alignment	not modelled	100.0	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**amidase; **PDBTitle:** crystal structure analysis of an amidase from nesterenkonia sp.
22	c3ilvA_	Alignment	not modelled	100.0	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamine-dependent nad(+) synthetase; **PDBTitle:** crystal structure of a glutamine-dependent nad(+) synthetase2 from cytophaga hutchinsonii
23	c4cyyA_	Alignment	not modelled	100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pantetheinase; **PDBTitle:** the structure of vanin-1: defining the link between metabolic disease,2 oxidative stress and inflammation
24	c5vrhA_	Alignment	not modelled	100.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**apolipoprotein n-acyltransferase; **PDBTitle:** apolipoprotein n-acyltransferase c387s active site mutant
25	c5n6mA_	Alignment	not modelled	100.0	20	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**apolipoprotein n-acyltransferase; **PDBTitle:** structure of the membrane integral lipoprotein n-acyltransferase lnt2 from p. aeruginosa
26	c5hyyA_	Alignment	not modelled	100.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nta1p; **PDBTitle:** crystal structure of n-terminal amidase
27	c2csuB_	Alignment	not modelled	78.2	9	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**457aa long hypothetical protein; **PDBTitle:** crystal structure of ph0766 from pyrococcus horikoshii ot3
28	d1s3la_	Alignment	not modelled	74.1	18	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**YfcE-like
						PDB header:phosphodiesterase

29	c1s3mA_	Alignment	not modelled	73.3	18	**Chain:** A: **PDB Molecule:**hypothetical protein mj0936; **PDBTitle:** structural and functional characterization of a novel2 archaeal phosphodiesterase
30	c3qfnA_	Alignment	not modelled	70.9	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of streptococcal asymmetric ap4a hydrolase and2 phosphodiesterase spr1479/saph in complex with inorganic phosphate
31	d1uf3a_	Alignment	not modelled	68.8	22	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**TT1561-like
32	d1i60a_	Alignment	not modelled	60.9	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**IolI-like
33	c1su1A_	Alignment	not modelled	59.9	27	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein yfce; **PDBTitle:** structural and biochemical characterization of yfce, a phosphoesterase2 from e. coli
34	d1su1a_	Alignment	not modelled	59.9	27	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**YfcE-like
35	d1o60a_	Alignment	not modelled	58.1	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I DAHP synthetase
36	c6ncsB_	Alignment	not modelled	56.0	18	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**n-acetylneuraminic acid (sialic acid) synthetase; **PDBTitle:** crystal structure of n-acetylneuraminic acid (sialic acid) synthetase2 from leptospira borgpetersenii serovar hardjo-bovis in complex with3 citrate
37	d1d9ea_	Alignment	not modelled	54.7	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I DAHP synthetase
38	d1t70a_	Alignment	not modelled	46.8	16	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**DR1281-like
39	d1gsaa1	Alignment	not modelled	42.9	11	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**Prokaryotic glutathione synthetase, N-terminal domain
40	c5zfsA_	Alignment	not modelled	42.4	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**d-allulose-3-epimerase; **PDBTitle:** crystal structure of arthrobacter globiformis m30 sugar epimerase2 which can produce d-allulose from d-fructose
41	c3stgA_	Alignment	not modelled	40.6	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-dehydro-3-deoxyphosphooctonate aldolase; **PDBTitle:** crystal structure of a58p, del(n59), and loop 7 truncated mutant of 3-2 deoxy-d-manno-octulosonate 8-phosphate synthase (kdo8ps) from3 neisseria meningitidis
42	c4lu0A_	Alignment	not modelled	39.6	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-dehydro-3-deoxyphosphooctonate aldolase; **PDBTitle:** crystal structure of 2-keto-3-deoxy-d-manno-octulosonate-8-phosphate2 synthase from pseudomonas aeruginosa.
43	c2fu3A_	Alignment	not modelled	36.8	11	**PDB header:**biosynthetic protein/structural protein **Chain:** A: **PDB Molecule:**gephyrin; **PDBTitle:** crystal structure of gephyrin e-domain
44	c4k3zA_	Alignment	not modelled	36.5	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-erythrulose 4-phosphate dehydrogenase; **PDBTitle:** crystal structure of d-erythrulose 4-phosphate dehydrogenase from2 brucella melitensis, solved by iodide sad
45	c3dx5A_	Alignment	not modelled	36.0	9	**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
46	c2ou4C_	Alignment	not modelled	34.8	14	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**d-tagatose 3-epimerase; **PDBTitle:** crystal structure of d-tagatose 3-epimerase from2 pseudomonas cichorii
47	c3vniC_	Alignment	not modelled	34.5	6	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**xylose isomerase domain protein tim barrel; **PDBTitle:** crystal structures of d-psicose 3-epimerase from clostridium2 cellulolyticum h10 and its complex with ketohexose sugars
48	c4r8kC_	Alignment	not modelled	33.4	11	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the guinea pig l-asparaginase 1 catalytic domain
49	c2qw5B_	Alignment	not modelled	33.0	10	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**xylose isomerase-like tim barrel; **PDBTitle:** crystal structure of a putative sugar phosphate isomerase/epimerase2 (ava4194) from anabaena variabilis atcc 29413 at 1.78 a resolution
50	c4yajA_	Alignment	not modelled	32.8	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**alpha subunit of acetyl-coenzyme a synthetase **PDBTitle:** ca. korarchaeum cryptofilum dinucleotide forming acetyl-coenzyme a2 synthetase 1 (apo form)
51	c3wqoB_	Alignment	not modelled	30.1	10	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein mj1311; **PDBTitle:** crystal structure of d-tagatose 3-epimerase-like protein
52	c2ei9A_	Alignment	not modelled	29.2	23	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**non-ltr retrotransposon r1bmks orf2 protein;

						PDBTitle: crystal structure of r1bm endonuclease domain
53	d4pgaa_	Alignment	not modelled	29.1	13	**Fold:**Glutaminase/Asparaginase **Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase
54	d1t71a_	Alignment	not modelled	28.6	15	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**DR1281-like
55	c2ejcA_	Alignment	not modelled	28.6	9	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pantoate--beta-alanine ligase; **PDBTitle:** crystal structure of pantoate--beta-alanine ligase (panc)2 from thermotoga maritima
56	d1agxa_	Alignment	not modelled	28.5	13	**Fold:**Glutaminase/Asparaginase **Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase
57	d2zdra2	Alignment	not modelled	28.1	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**NeuB-like
58	c2p2dA_	Alignment	not modelled	27.8	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**l-asparaginase i; **PDBTitle:** crystal structure and allosteric regulation of the cytoplasmic2 escherichia coli l-asparaginase i
59	d1v8fa_	Alignment	not modelled	27.0	21	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Pantothenate synthetase (Pantoate-beta-alanine ligase, PanC)
60	d1ihoa_	Alignment	not modelled	26.9	18	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Pantothenate synthetase (Pantoate-beta-alanine ligase, PanC)
61	d2yvta1	Alignment	not modelled	26.7	18	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**TT1561-like
62	c5hmqE_	Alignment	not modelled	26.2	15	**PDB header:**lyase **Chain:** E: **PDB Molecule:**4-hydroxyphenylpyruvate dioxygenase; **PDBTitle:** xylose isomerase-like tim barrel/4-hydroxyphenylpyruvate dioxygenase2 fusion protein
63	c3mxtA_	Alignment	not modelled	25.3	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pantothenate synthetase; **PDBTitle:** crystal structure of pantoate-beta-alanine ligase from campylobacter2 jejuni
64	c3uk2B_	Alignment	not modelled	25.3	9	**PDB header:**ligase **Chain:** B: **PDB Molecule:**pantothenate synthetase; **PDBTitle:** the structure of pantothenate synthetase from burkholderia2 thailandensis
65	c3vylB_	Alignment	not modelled	25.2	14	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**l-ribulose 3-epimerase; **PDBTitle:** structure of l-ribulose 3-epimerase
66	c1gshA_	Alignment	not modelled	25.1	11	**PDB header:**glutathione biosynthesis ligase **Chain:** A: **PDB Molecule:**glutathione biosynthetic ligase; **PDBTitle:** structure of escherichia coli glutathione synthetase at ph 7.5
67	d2vgna3	Alignment	not modelled	24.6	11	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**ERF1/Dom34 C-terminal domain-like
68	c2zdsB_	Alignment	not modelled	24.5	14	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**putative dna-binding protein; **PDBTitle:** crystal structure of sco6571 from streptomyces coelicolor a3(2)
69	c3o3cD_	Alignment	not modelled	24.3	13	**PDB header:**transferase **Chain:** D: **PDB Molecule:**glycogen [starch] synthase isoform 2; **PDBTitle:** glycogen synthase basal state udp complex
70	c2nqqA_	Alignment	not modelled	24.3	10	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**molybdopterin biosynthesis protein moea; **PDBTitle:** moea r137q
71	c3qxbB_	Alignment	not modelled	23.9	11	**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
72	c3guzB_	Alignment	not modelled	23.0	18	**PDB header:**ligase **Chain:** B: **PDB Molecule:**pantothenate synthetase; **PDBTitle:** structural and substrate-binding studies of pantothenate2 synthenate (ps)provide insights into homotropic inhibition3 by pantoate in ps's
73	c3rqzC_	Alignment	not modelled	22.7	29	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**metallophosphoesterase; **PDBTitle:** crystal structure of metallophosphoesterase from sphaerobacter2 thermophilus
74	c5g2rA_	Alignment	not modelled	22.2	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**molybdopterin biosynthesis protein cnx1; **PDBTitle:** crystal structure of the mo-insertase domain cnx1e from2 arabidopsis thaliana
75	c3n8hA_	Alignment	not modelled	22.1	12	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pantothenate synthetase; **PDBTitle:** crystal structure of pantoate-beta-alanine ligase from francisella2 tularensis
76	c3aytA_	Alignment	not modelled	21.8	15	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein tthb071; **PDBTitle:** tthb071 protein from thermus thermophilus hb8
77	d2a40b1	Alignment	not modelled	21.1	17	**Fold:**DNase I-like **Superfamily:**DNase I-like **Family:**DNase I-like
78	d2ocda1	Alignment	not modelled	21.1	8	**Fold:**Glutaminase/Asparaginase **Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase

79	c4f1hA_	Alignment	not modelled	20.9	10	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**tyrosyl-dna phosphodiesterase 2; **PDBTitle:** crystal structure of tdp2 from danio rerio complexed with a single2 strand dna
80	d1yx1a1	Alignment	not modelled	20.8	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**KguE-like
81	c3sz8D_	Alignment	not modelled	20.8	14	**PDB header:**transferase **Chain:** D: **PDB Molecule:**2-dehydro-3-deoxyphosphooctonate aldolase 2; **PDBTitle:** crystal structure of 2-dehydro-3-deoxyphosphooctonate aldolase from2 burkholderia pseudomallei
82	c3tebA_	Alignment	not modelled	20.4	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endonuclease/exonuclease/phosphatase; **PDBTitle:** endonuclease/exonuclease/phosphatase family protein from leptotrichia2 buccalis c-1013-b
83	c6bngB_	Alignment	not modelled	20.4	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**2-dehydro-3-deoxyphosphooctonate aldolase; **PDBTitle:** structure of 2-dehydro-3-deoxyphosphooctonate aldolase from2 acinetobacter baumannii
84	c3pnxF_	Alignment	not modelled	20.3	8	**PDB header:**transferase **Chain:** F: **PDB Molecule:**putative sulfurtransferase dsre; **PDBTitle:** crystal structure of a putative sulfurtransferase dsre (swol_2425)2 from syntrophomonas wolfei str. goettingen at 1.92 a resolution
85	c2o14A_	Alignment	not modelled	20.3	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein yxim; **PDBTitle:** x-ray crystal structure of protein yxim_bacsu from bacillus subtilis.2 northeast structural genomics consortium target sr595
86	c5d95A_	Alignment	not modelled	19.5	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminotransferase class-iii; **PDBTitle:** structure of thermostable omega-transaminase
87	c2nydB_	Alignment	not modelled	19.4	12	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**upf0135 protein sa1388; **PDBTitle:** crystal structure of staphylococcus aureus hypothetical protein sa1388
88	c1xuzA_	Alignment	not modelled	18.4	18	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**polysialic acid capsule biosynthesis protein siac; **PDBTitle:** crystal structure analysis of sialic acid synthase (neub)from2 neisseria meningitidis, bound to mn2+, phosphoenolpyruvate, and n-3 acetyl mannosaminitol
89	d1vlia2	Alignment	not modelled	17.5	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**NeuB-like
90	c2odrC_	Alignment	not modelled	16.9	20	**PDB header:**ligase **Chain:** C: **PDB Molecule:**phosphoseryl-trna synthetase; **PDBTitle:** methanococcus maripaludis phosphoseryl-trna synthetase
91	c4s1aB_	Alignment	not modelled	16.7	11	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a hypothetical protein cthe_0052 from2 ruminiclostridium thermocellum atcc 27405
92	c1vliA_	Alignment	not modelled	16.4	17	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**spore coat polysaccharide biosynthesis protein spse; **PDBTitle:** crystal structure of spore coat polysaccharide biosynthesis protein2 spse (bsu37870) from bacillus subtilis at 2.38 a resolution
93	c3ju2A_	Alignment	not modelled	15.7	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein smc04130; **PDBTitle:** crystal structure of protein smc04130 from sinorhizobium meliloti 1021
94	c2issF_	Alignment	not modelled	15.7	10	**PDB header:**lyase, transferase **Chain:** F: **PDB Molecule:**glutamine amidotransferase subunit pdxt; **PDBTitle:** structure of the plp synthase holoenzyme from thermotoga maritima
95	c2odrB_	Alignment	not modelled	15.6	14	**PDB header:**ligase **Chain:** B: **PDB Molecule:**phosphoseryl-trna synthetase; **PDBTitle:** methanococcus maripaludis phosphoseryl-trna synthetase
96	c5tnvA_	Alignment	not modelled	15.5	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ap endonuclease, family protein 2; **PDBTitle:** crystal structure of a xylose isomerase-like tim barrel protein from2 mycobacterium smegmatis in complex with magnesium
97	c2zsmA_	Alignment	not modelled	15.3	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate-1-semialdehyde 2,1-aminomutase; **PDBTitle:** crystal structure of glutamate-1-semialdehyde 2,1-2 aminomutase from aeropyrum pernix, hexagonal form
98	d1x52a1	Alignment	not modelled	15.2	7	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**ERF1/Dom34 C-terminal domain-like
99	c3cnyA_	Alignment	not modelled	15.1	15	**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