Phyre^2

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Description	P76280
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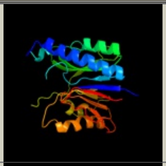
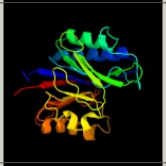
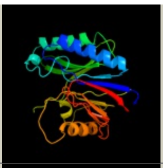
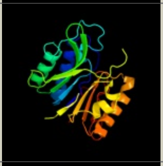
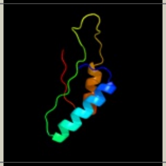
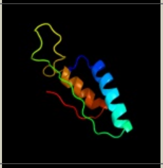
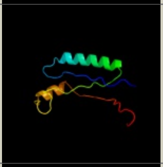
Detailed template information

#	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	c2e2kC_	Alignment		100.0	12	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**formamidase; **PDBTitle:** helicobacter pylori formamidase amif contains a fine-tuned cysteine-2 glutamate-lysine catalytic triad
3	c2e11B_	Alignment		100.0	15	**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
4	c1emsB_	Alignment		100.0	13	**PDB header:**antitumor protein **Chain:** B: **PDB Molecule:**nit-fragile histidine triad fusion protein; **PDBTitle:** crystal structure of the c. elegans nitfhit protein
5	c2plqA_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aliphatic amidase; **PDBTitle:** crystal structure of the amidase from geobacillus pallidus rapc8
6	c2w1vA_	Alignment		100.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nitrilase homolog 2; **PDBTitle:** crystal structure of mouse nitrilase-2 at 1.4a resolution
7	d1uf5a_	Alignment		100.0	18	**Fold:**Carbon-nitrogen hydrolase **Superfamily:**Carbon-nitrogen hydrolase **Family:**Carbamilase
8	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
9	c3hkxA_	Alignment		100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**amidase; **PDBTitle:** crystal structure analysis of an amidase from nesterenkonia sp.
10	d1f89a_	Alignment		100.0	15	**Fold:**Carbon-nitrogen hydrolase **Superfamily:**Carbon-nitrogen hydrolase **Family:**Nitrilase
11	d1emsa2	Alignment		100.0	13	**Fold:**Carbon-nitrogen hydrolase **Superfamily:**Carbon-nitrogen hydrolase **Family:**Nitrilase

12	c3n05B_	Alignment		100.0	16	**PDB header:**ligase **Chain:** B: **PDB Molecule:**nh(3)-dependent nad(+) synthetase; **PDBTitle:** crystal structure of nh3-dependent nad+ synthetase from streptomyces2 avermitilis
13	d1j31a_	Alignment		100.0	18	**Fold:**Carbon-nitrogen hydrolase **Superfamily:**Carbon-nitrogen hydrolase **Family:**Carbamilase
14	c3ilvA_	Alignment		100.0	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamine-dependent nad(+) synthetase; **PDBTitle:** crystal structure of a glutamine-dependent nad(+) synthetase2 from cytophaga hutchinsonii
15	d1d9ea_	Alignment		74.3	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I DAHP synthetase
16	d1uf3a_	Alignment		74.2	11	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**TT1561-like
17	c3stgA_	Alignment		67.0	9	**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
18	d1o60a_	Alignment		66.9	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I DAHP synthetase
19	c3dx5A_	Alignment		62.5	4	**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
20	c3sz8D_	Alignment		57.8	13	**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
21	c2qw5B_	Alignment	not modelled	57.1	14	**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
22	c3qxbB_	Alignment	not modelled	56.9	13	**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
23	d1vlia2	Alignment	not modelled	53.8	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**NeuB-like
24	c1vliA_	Alignment	not modelled	50.3	9	**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
25	d2zdra2	Alignment	not modelled	49.5	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**NeuB-like
26	c2ou4C_	Alignment	not modelled	47.5	3	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**d-tagatose 3-epimerase; **PDBTitle:** crystal structure of d-tagatose 3-epimerase from2 pseudomonas cichorii
27	d1yx1a1	Alignment	not modelled	47.0	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**KguE-like
						Fold:TIM beta/alpha-barrel

28	d1i60a_	Alignment	not modelled	46.2	11	**Superfamily:**Xylose isomerase-like **Family:**IolI-like
29	c3pnxF_	Alignment	not modelled	45.4	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
30	c2ei9A_	Alignment	not modelled	44.9	6	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**non-ltr retrotransposon r1bmks orf2 protein; **PDBTitle:** crystal structure of r1bm endonuclease domain
31	d2vgna3	Alignment	not modelled	41.7	22	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**ERF1/Dom34 C-terminal domain-like
32	c3s5oA_	Alignment	not modelled	41.2	15	**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
33	c1xuzA_	Alignment	not modelled	39.2	13	**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
34	d1oi7a1	Alignment	not modelled	39.0	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
35	d1wdua_	Alignment	not modelled	38.7	7	**Fold:**DNase I-like **Superfamily:**DNase I-like **Family:**DNase I-like
36	d2nu7a1	Alignment	not modelled	34.6	5	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
37	c2r94B_	Alignment	not modelled	31.8	6	**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
38	c2zdsB_	Alignment	not modelled	31.7	14	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**putative dna-binding protein; **PDBTitle:** crystal structure of sco6571 from streptomyces coelicolor2 a3(2)
39	c3qfnA_	Alignment	not modelled	30.8	4	**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
40	c3ngfA_	Alignment	not modelled	29.4	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ap endonuclease, family 2; **PDBTitle:** crystal structure of ap endonuclease, family 2 from brucella2 melitensis
41	c3bi8A_	Alignment	not modelled	28.8	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** structure of dihydrodipicolinate synthase from clostridium2 botulinum
42	c3ju2A_	Alignment	not modelled	28.0	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein smc04130; **PDBTitle:** crystal structure of protein smc04130 from sinorhizobium meliloti 1021
43	d1x52a1	Alignment	not modelled	27.3	16	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**ERF1/Dom34 C-terminal domain-like
44	d2yvta1	Alignment	not modelled	25.9	27	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**TT1561-like
45	c1vs1B_	Alignment	not modelled	25.2	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**3-deoxy-7-phosphoheptulonate synthase; **PDBTitle:** crystal structure of 3-deoxy-d-arabino-heptulosonate-7-2 phosphate synthase (dahp synthase) from aeropyrum pernix3 in complex with mn2+ and pep
46	d1w3ia_	Alignment	not modelled	24.7	4	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
47	c3obyB_	Alignment	not modelled	24.2	8	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein pelota homolog; **PDBTitle:** crystal structure of archaeoglobus fulgidus pelota reveals inter-2 domain structural plasticity
48	c1s3mA_	Alignment	not modelled	23.8	0	**PDB header:**phosphodiesterase **Chain:** A: **PDB Molecule:**hypothetical protein mj0936; **PDBTitle:** structural and functional characterization of a novel2 archaeal phosphodiesterase
49	d1s3la_	Alignment	not modelled	23.8	0	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**YfcE-like
50	c3obwA_	Alignment	not modelled	22.5	7	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein pelota homolog; **PDBTitle:** crystal structure of two archaeal pelotas reveal inter-domain2 structural plasticity
51	c3agjB_	Alignment	not modelled	22.5	19	**PDB header:**translation/hydrolase **Chain:** B: **PDB Molecule:**protein pelota homolog; **PDBTitle:** crystal structure of archaeal pelota and gtp-bound ef1 alpha complex
52	c3agjD_	Alignment	not modelled	22.5	19	**PDB header:**translation/hydrolase **Chain:** D: **PDB Molecule:**protein pelota homolog; **PDBTitle:** crystal structure of archaeal pelota and gtp-bound ef1 alpha complex
						PDB header:lyase

53	c3fkkA_	Alignment	not modelled	21.4	11	**Chain:** A: **PDB Molecule:**l-2-keto-3-deoxyarabonate dehydratase; **PDBTitle:** structure of l-2-keto-3-deoxyarabonate dehydratase
54	c1su1A_	Alignment	not modelled	20.0	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein yfce; **PDBTitle:** structural and biochemical characterization of yfce, a2 phosphoesterase from e. coli
55	d1su1a_	Alignment	not modelled	20.0	14	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**YfcE-like
56	c3kwsB_	Alignment	not modelled	19.6	9	**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
57	c2nuxB_	Alignment	not modelled	19.4	13	**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
58	c2j63B_	Alignment	not modelled	19.4	18	**PDB header:**lyase **Chain:** B: **PDB Molecule:**ap-endonuclease; **PDBTitle:** crystal structure of ap endonuclease lmap from leishmania2 major
59	c3pg8B_	Alignment	not modelled	19.2	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phospho-2-dehydro-3-deoxyheptonate aldolase; **PDBTitle:** truncated form of 3-deoxy-d-arabino-heptulosonate 7-phosphate synthase2 from thermotoga maritima
60	c3cnyA_	Alignment	not modelled	18.8	5	**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
61	c3p94A_	Alignment	not modelled	18.7	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**gdsl-like lipase; **PDBTitle:** crystal structure of a gdsl-like lipase (bdi_0976) from2 parabacteroides distasonis atcc 8503 at 1.93 a resolution
62	c1zcoA_	Alignment	not modelled	18.6	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**2-dehydro-3-deoxyphosphoheptonate aldolase; **PDBTitle:** crystal structure of pyrococcus furiosus 3-deoxy-d-arabino-2 heptulosonate 7-phosphate synthase
63	c2vyeA_	Alignment	not modelled	18.5	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**replicative dna helicase; **PDBTitle:** crystal structure of the dnac-ssdna complex
64	d1sgva1	Alignment	not modelled	18.4	19	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**PUA domain
65	c2zsmA_	Alignment	not modelled	18.4	17	**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
66	c2hk1D_	Alignment	not modelled	18.2	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
67	d2csua1	Alignment	not modelled	18.1	11	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
68	c2vgmA_	Alignment	not modelled	17.0	22	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**dom34; **PDBTitle:** structure of yeast dom34 : a protein related to translation2 termination factor erf1 and involved in no-go decay.
69	c3dmyA_	Alignment	not modelled	16.6	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein fdra; **PDBTitle:** crystal structure of a predicated acyl-coa synthetase from e.coli
70	c3noeA_	Alignment	not modelled	16.3	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from pseudomonas2 aeruginosa
71	c3e96B_	Alignment	not modelled	15.9	8	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 bacillus clausii
72	c2hnhA_	Alignment	not modelled	15.9	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna polymerase iii alpha subunit; **PDBTitle:** crystal structure of the catalytic alpha subunit of e. coli2 replicative dna polymerase iii
73	d1q7ra_	Alignment	not modelled	15.7	24	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
74	d1iuka_	Alignment	not modelled	15.7	9	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
75	c3l44A_	Alignment	not modelled	15.6	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate-1-semialdehyde 2,1-aminomutase 1; **PDBTitle:** crystal structure of bacillus anthracis heml-1, glutamate semialdehyde2 aminotransferase
76	c3bleA_	Alignment	not modelled	15.2	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**citramalate synthase from leptospira interrogans; **PDBTitle:** crystal structure of the catalytic domain of licms in2 complexed with malonate
77	c3na8A_	Alignment	not modelled	15.0	8	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative dihydrodipicolinate synthetase;

77	c3na8A_	Alignment	not modelled	15.0	8	**PDBTitle:** crystal structure of a putative dihydrodipicolinate synthetase from2 pseudomonas aeruginosa
78	c3rqzC_	Alignment	not modelled	14.8	6	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**metallophosphoesterase; **PDBTitle:** crystal structure of metallophosphoesterase from sphaerobacter2 thermophilus
79	d2gsaa_	Alignment	not modelled	14.2	11	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
80	c3g8rA_	Alignment	not modelled	14.2	11	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**probable spore coat polysaccharide biosynthesis protein e; **PDBTitle:** crystal structure of putative spore coat polysaccharide biosynthesis2 protein e from chromobacterium violaceum atcc 12472
81	c3si9B_	Alignment	not modelled	14.1	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from bartonella2 henselae
82	c3fluD_	Alignment	not modelled	14.0	10	**PDB header:**lyase **Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from the pathogen2 neisseria meningitidis
83	c3pueA_	Alignment	not modelled	14.0	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
84	c2o14A_	Alignment	not modelled	13.9	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein yxim; **PDBTitle:** x-ray crystal structure of protein yxim_bacsu from bacillus2 subtilis. northeast structural genomics consortium target3 sr595
85	c3t4cD_	Alignment	not modelled	13.8	16	**PDB header:**transferase **Chain:** D: **PDB Molecule:**2-dehydro-3-deoxyphosphooctonate aldolase 1; **PDBTitle:** crystal structure of 2-dehydro-3-deoxyphosphooctonate aldolase from2 burkholderia ambifaria
86	d1g5ba_	Alignment	not modelled	13.8	10	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Protein serine/threonine phosphatase
87	d1f74a_	Alignment	not modelled	13.7	8	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
88	c3fs2A_	Alignment	not modelled	13.6	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-dehydro-3-deoxyphosphooctonate aldolase; **PDBTitle:** crystal structure of 2-dehydro-3-deoxyphosphooctonate2 aldolase from bruciella melitensis at 1.85a resolution
89	c3mcaB_	Alignment	not modelled	13.6	22	**PDB header:**translation regulation/hydrolase **Chain:** B: **PDB Molecule:**protein dom34; **PDBTitle:** structure of the dom34-hbs1 complex and implications for its role in2 no-go decay
90	c2v9dB_	Alignment	not modelled	13.3	10	**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
91	d1k77a_	Alignment	not modelled	12.9	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Hypothetical protein YgbM (EC1530)
92	c1jvnB_	Alignment	not modelled	12.8	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**bifunctional histidine biosynthesis protein hishf; **PDBTitle:** crystal structure of imidazole glycerol phosphate synthase: a tunnel2 through a (beta/alpha)8 barrel joins two active sites
93	c3eb2A_	Alignment	not modelled	12.5	8	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative dihydrodipicolinate synthetase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 rhodopseudomonas palustris at 2.0a resolution
94	c2cjdA_	Alignment	not modelled	12.5	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**l-lysine-epsilon aminotransferase; **PDBTitle:** lysine aminotransferase from m. tuberculosis in external2 aldimine form
95	c3i4jC_	Alignment	not modelled	12.5	8	**PDB header:**transferase **Chain:** C: **PDB Molecule:**aminotransferase, class iii; **PDBTitle:** crystal structure of aminotransferase, class iii from2 deinococcus radiodurans
96	c2cy8A_	Alignment	not modelled	12.3	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**d-phenylglycine aminotransferase; **PDBTitle:** crystal structure of d-phenylglycine aminotransferase (d-phgat) from2 pseudomonas strutzeri st-201
97	d2qi2a3	Alignment	not modelled	12.1	7	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**ERF1/Dom34 C-terminal domain-like
98	d1xkya1	Alignment	not modelled	12.0	6	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
99	c2yxgD_	Alignment	not modelled	11.9	14	**PDB header:**lyase **Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihyrodipicolinate synthase (dapa)