Phyre2

Email	l.a.kelley@imperial.ac.uk
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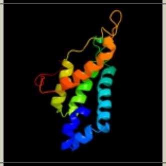
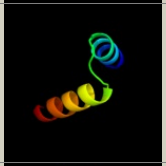
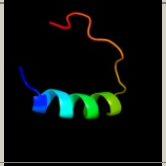
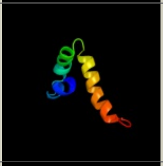
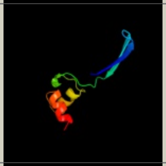
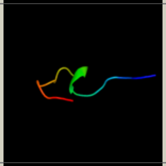
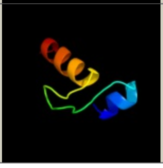
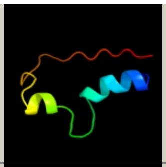
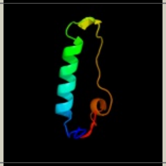
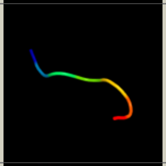
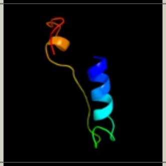
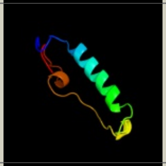
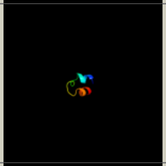
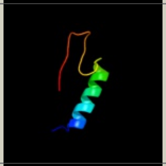
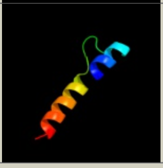
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2iafa1	Alignment		100.0	43	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Serine metabolism enzymes domain **Family:**Serine dehydratase beta chain-like
2	c1ygyA_	Alignment		99.7	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** crystal structure of d-3-phosphoglycerate dehydrogenase from2 mycobacterium tuberculosis
3	d1ygya4	Alignment		99.4	16	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Serine metabolism enzymes domain **Family:**SerA intervening domain-like
4	c2hp0A_	Alignment		98.1	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ids-epimerase; **PDBTitle:** crystal structure of iminodisuccinate epimerase
5	d1szqa_	Alignment		97.6	15	**Fold:**2-methylcitrate dehydratase PrpD **Superfamily:**2-methylcitrate dehydratase PrpD **Family:**2-methylcitrate dehydratase PrpD
6	c3u4gA_	Alignment		58.6	31	**PDB header:**transferase **Chain:** A: **PDB Molecule:**namn:dmb phosphoribosyltransferase; **PDBTitle:** the structure of cobt from pyrococcus horikoshii
7	c3s1sA_	Alignment		36.0	31	**PDB header:**hydrolase, transferase **Chain:** A: **PDB Molecule:**restriction endonuclease bpusi; **PDBTitle:** characterization and crystal structure of the type iig restriction2 endonuclease bpusi
8	d1ug2a_	Alignment		34.1	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Myb/SANT domain
9	d2i7pa1	Alignment		31.2	29	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Fumble-like
10	d1no5a_	Alignment		27.2	22	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Catalytic subunit of bi-partite nucleotidyltransferase
11	c2kelB_	Alignment		24.3	19	**PDB header:**transcription repressor **Chain:** B: **PDB Molecule:**uncharacterized protein 56b; **PDBTitle:** structure of the transcription regulator svtr from the2 hyperthermophilic archaeal virus sirv1

12	c2rkbE_	Alignment		21.8	14	**PDB header:**lyase **Chain:** E: **PDB Molecule:**serine dehydratase-like; **PDBTitle:** serine dehydratase like-1 from human cancer cells
13	c1knyA_	Alignment		21.7	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**kanamycin nucleotidyltransferase; **PDBTitle:** kanamycin nucleotidyltransferase
14	c1yy3A_	Alignment		18.2	57	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**s-adenosylmethionine:trna ribosyltransferase- **PDBTitle:** structure of s-adenosylmethionine:trna ribosyltransferase-2 isomerase (quea)
15	c2rffA_	Alignment		15.6	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative nucleotidyltransferase; **PDBTitle:** crystal structure of a putative nucleotidyltransferase2 (np_343093.1) from sulfolobus solfataricus at 1.40 a3 resolution
16	d1knya2	Alignment		15.5	20	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Kanamycin nucleotidyltransferase (KNTase), N-terminal domain
17	d1jb0l_	Alignment		14.5	35	**Fold:**Photosystem I reaction center subunit XI, PsaL **Superfamily:**Photosystem I reaction center subunit XI, PsaL **Family:**Photosystem I reaction center subunit XI, PsaL
18	c2k9iB_	Alignment		14.3	14	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**plasmid prn1, complete sequence; **PDBTitle:** nmr structure of plasmid copy control protein orf56 from2 sulfolobus islandicus
19	c2zfdB_	Alignment		12.6	24	**PDB header:**signaling protein/transferase **Chain:** B: **PDB Molecule:**putative uncharacterized protein t20l15_90; **PDBTitle:** the crystal structure of plant specific calcium binding protein atcbl22 in complex with the regulatory domain of atcipk14
20	c2k3qA_	Alignment		11.6	22	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**tusp1; **PDBTitle:** solution structure of the n-terminal domain (tusp1-n) of the2 egg case silk from nephila antipodiana
21	c2ddhA_	Alignment	not modelled	11.2	38	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**acyl-coa oxidase; **PDBTitle:** crystal structure of acyl-coa oxidase complexed with 3-oh-dodecanoate
22	d1h72c1	Alignment	not modelled	11.2	27	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**GHMP Kinase, N-terminal domain
23	c3lr6A_	Alignment	not modelled	10.9	33	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**major ampullate spidroin 1; **PDBTitle:** self-assembly of spider silk proteins is controlled by a ph-sensitive2 relay
24	d1gg2g_	Alignment	not modelled	10.5	25	**Fold:**Non-globular all-alpha subunits of globular proteins **Superfamily:**Transducin (heterotrimeric G protein), gamma chain **Family:**Transducin (heterotrimeric G protein), gamma chain
25	d1ylqa1	Alignment	not modelled	10.4	28	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Catalytic subunit of bi-partite nucleotidyltransferase
26	c2fonA_	Alignment	not modelled	10.2	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**peroxisomal acyl-coa oxidase 1a; **PDBTitle:** x-ray crystal structure of leacx1, an acyl-coa oxidase from2 lycopersicon esculentum (tomato)
27	c1u9pA_	Alignment	not modelled	10.2	17	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**parc; **PDBTitle:** permuted single-chain arc
28	c1qoyA_	Alignment	not modelled	10.1	10	**PDB header:**toxin **Chain:** A: **PDB Molecule:**hemolysin e; **PDBTitle:** e.coli hemolysin e (hlye, clya, shea)
						PDB header:transferase

29	c3mwdA_	Alignment	not modelled	10.0	31	**Chain:** A: **PDB Molecule:**atp-citrate synthase; **PDBTitle:** truncated human atp-citrate lyase with citrate bound
30	c1k97A_	Alignment	not modelled	10.0	12	**PDB header:**ligase **Chain:** A: **PDB Molecule:**argininosuccinate synthase; **PDBTitle:** crystal structure of e. coli argininosuccinate synthetase in complex2 with aspartate and citrulline
31	d1k61a_	Alignment	not modelled	9.8	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
32	d1b65a_	Alignment	not modelled	9.4	17	**Fold:**DmpA/ArgJ-like **Superfamily:**DmpA/ArgJ-like **Family:**DmpA-like
33	d1wota_	Alignment	not modelled	9.3	24	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Catalytic subunit of bi-partite nucleotidyltransferase
34	d1omwg_	Alignment	not modelled	9.2	25	**Fold:**Non-globular all-alpha subunits of globular proteins **Superfamily:**Transducin (heterotrimeric G protein), gamma chain **Family:**Transducin (heterotrimeric G protein), gamma chain
35	c2fgyA_	Alignment	not modelled	9.0	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**carboxysome shell polypeptide; **PDBTitle:** beta carbonic anhydrase from the carboxysomal shell of2 halothiobacillus neapolitanus (csosca)
36	d1j20a1	Alignment	not modelled	8.8	14	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
37	d1ee8a1	Alignment	not modelled	8.8	13	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Middle domain of MutM-like DNA repair proteins
38	c1uf2A_	Alignment	not modelled	8.7	43	**PDB header:**virus **Chain:** A: **PDB Molecule:**core protein p3; **PDBTitle:** the atomic structure of rice dwarf virus (rdv)
39	d1uf2a_	Alignment	not modelled	8.7	43	**Fold:**Reovirus inner layer core protein p3 **Superfamily:**Reovirus inner layer core protein p3 **Family:**Phytoreovirus core
40	d1xhmb1	Alignment	not modelled	8.7	27	**Fold:**Non-globular all-alpha subunits of globular proteins **Superfamily:**Transducin (heterotrimeric G protein), gamma chain **Family:**Transducin (heterotrimeric G protein), gamma chain
41	c1xhmB_	Alignment	not modelled	8.6	27	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**guanine nucleotide-binding protein g(i)/g(s) **PDBTitle:** the crystal structure of a biologically active peptide2 (sigk) bound to a g protein beta:gamma heterodimer
42	d1ncfb3	Alignment	not modelled	8.6	40	**Fold:**TNF receptor-like **Superfamily:**TNF receptor-like **Family:**TNF receptor-like
43	c3ibqA_	Alignment	not modelled	8.6	30	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyridoxal kinase; **PDBTitle:** crystal structure of pyridoxal kinase from lactobacillus2 plantarum in complex with atp
44	d1gotg_	Alignment	not modelled	8.5	8	**Fold:**Non-globular all-alpha subunits of globular proteins **Superfamily:**Transducin (heterotrimeric G protein), gamma chain **Family:**Transducin (heterotrimeric G protein), gamma chain
45	d1rypa_	Alignment	not modelled	8.3	7	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
46	c2w4eA_	Alignment	not modelled	8.3	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mutt/nudix family protein; **PDBTitle:** structure of an n-terminally truncated nudix hydrolase2 dr2204 from deinococcus radiodurans
47	d1w32a_	Alignment	not modelled	8.2	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
48	d1fi6a_	Alignment	not modelled	8.0	20	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Eps15 homology domain (EH domain)
49	c2crnA_	Alignment	not modelled	8.0	16	**PDB header:**immune system **Chain:** A: **PDB Molecule:**ubash3a protein; **PDBTitle:** solution structure of the uba domain of human ubash3a2 protein
50	d1tbge_	Alignment	not modelled	7.9	8	**Fold:**Non-globular all-alpha subunits of globular proteins **Superfamily:**Transducin (heterotrimeric G protein), gamma chain **Family:**Transducin (heterotrimeric G protein), gamma chain
51	d1ng7a_	Alignment	not modelled	7.9	27	**Fold:**Soluble domain of poliovirus core protein 3a **Superfamily:**Soluble domain of poliovirus core protein 3a **Family:**Soluble domain of poliovirus core protein 3a
52	c2dagA_	Alignment	not modelled	7.8	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ubiquitin carboxyl-terminal hydrolase 5; **PDBTitle:** solution structure of the first uba domain in the human2 ubiquitin specific protease 5 (isopeptidase 5)
53	d1n93x_	Alignment	not modelled	7.8	24	**Fold:**P40 nucleoprotein **Superfamily:**P40 nucleoprotein **Family:**P40 nucleoprotein
54	c1n93X_	Alignment	not modelled	7.8	24	**PDB header:**viral protein **Chain:** X: **PDB Molecule:**p40 nucleoprotein; **PDBTitle:** crystal structure of the borna disease virus nucleoprotein
55	c1kh2D_	Alignment	not modelled	7.6	15	**PDB header:**ligase **Chain:** D: **PDB Molecule:**argininosuccinate synthetase; **PDBTitle:** crystal structure of thermus thermophilus hb82 argininosuccinate synthetase in complex with atp

56	d1h0ha2	Alignment	not modelled	7.5	23	**Fold:**Formate dehydrogenase/DMSO reductase, domains 1-3 **Superfamily:**Formate dehydrogenase/DMSO reductase, domains 1-3 **Family:**Formate dehydrogenase/DMSO reductase, domains 1-3
57	d1x2na1	Alignment	not modelled	7.5	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
58	c1w07A_	Alignment	not modelled	7.4	31	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**acyl-coa oxidase; **PDBTitle:** arabidopsis thaliana acyl-coa oxidase 1
59	d1k47a1	Alignment	not modelled	7.4	25	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**GHMP Kinase, N-terminal domain
60	d2i7na2	Alignment	not modelled	7.1	31	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Fumble-like
61	c3a24A_	Alignment	not modelled	7.1	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-galactosidase; **PDBTitle:** crystal structure of bt1871 retaining glycosidase
62	d2raqa1	Alignment	not modelled	7.1	11	**Fold:**Ferredoxin-like **Superfamily:**MTH889-like **Family:**MTH889-like
63	c2iifA_	Alignment	not modelled	7.1	14	**PDB header:**recombination/dna **Chain:** A: **PDB Molecule:**integration host factor; **PDBTitle:** single chain integration host factor mutant protein (scihf2-2 k45ae) in complex with dna
64	c2x3dC_	Alignment	not modelled	7.0	16	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**sso6206; **PDBTitle:** crystal structure of sso6206 from sulfolobus solfataricus p2
65	d1fh9a_	Alignment	not modelled	6.9	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
66	c3iz5w_	Alignment	not modelled	6.9	40	**PDB header:**ribosome **Chain:** W: **PDB Molecule:**60s ribosomal protein l22 (l22e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
67	c3l0zC_	Alignment	not modelled	6.7	13	**PDB header:**transferase **Chain:** C: **PDB Molecule:**putative nicotinate-nucleotide-dimethylbenzimidazole **PDBTitle:** crystal structure of a putative nicotinate-nucleotide-2 dimethylbenzimidazole phosphoribosyltransferase from3 methanocaldococcus jannaschii dsm 2661
68	c3noyA_	Alignment	not modelled	6.6	42	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; **PDBTitle:** crystal structure of ispg (gcpe)
69	c2gefA_	Alignment	not modelled	6.4	50	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protease vp4; **PDBTitle:** crystal structure of a novel viral protease with a2 serine/lysine catalytic dyad mechanism
70	d2r5yb1	Alignment	not modelled	6.4	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
71	c1p5jA_	Alignment	not modelled	6.3	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**l-serine dehydratase; **PDBTitle:** crystal structure analysis of human serine dehydratase
72	d1p5ja_	Alignment	not modelled	6.3	19	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
73	c2jyaA_	Alignment	not modelled	6.3	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu1810; **PDBTitle:** nmr solution structure of protein atu1810 from agrobacterium2 tumefaciens. northeast structural genomics consortium target atr23,3 ontario centre for structural proteomics target atc1776
74	d1j6ua3	Alignment	not modelled	6.3	33	**Fold:**Ribokinase-like **Superfamily:**MurD-like peptide ligases, catalytic domain **Family:**MurCDEF
75	d1r85a_	Alignment	not modelled	6.2	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
76	d1w85i_	Alignment	not modelled	6.2	22	**Fold:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Superfamily:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Family:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
77	d1yrnb_	Alignment	not modelled	6.2	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
78	c2jugB_	Alignment	not modelled	6.2	33	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**tubc protein; **PDBTitle:** multienzyme docking in hybrid megasynthetases
79	c3sz8D_	Alignment	not modelled	6.2	10	**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
80	c2wscL_	Alignment	not modelled	6.2	24	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**photosystem i reaction center subunit xi,

						PDBTitle: improved model of plant photosystem i
81	d1exta3	Alignment	not modelled	6.2	40	**Fold:**TNF receptor-like **Superfamily:**TNF receptor-like **Family:**TNF receptor-like
82	c2i7pA_	Alignment	not modelled	6.1	31	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pantothenate kinase 3; **PDBTitle:** crystal structure of human pank3 in complex with accoa
83	c2f5xC_	Alignment	not modelled	6.1	20	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**bugd; **PDBTitle:** structure of periplasmic binding protein bugd
84	c2y8sE_	Alignment	not modelled	6.1	63	**PDB header:**membrane protein **Chain:** E: **PDB Molecule:**rhoptry neck protein 2; **PDBTitle:** co-structure of an ama1 mutant (y230a) with a surface2 exposed region of ron2 from toxoplasma gondii
85	c2cooA_	Alignment	not modelled	6.0	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lipoamide acyltransferase component of branched- **PDBTitle:** solution structure of the e3_binding domain of2 dihydrolipoamide branched chaintransacylase
86	c2iirJ_	Alignment	not modelled	6.0	12	**PDB header:**transferase **Chain:** J: **PDB Molecule:**acetate kinase; **PDBTitle:** acetate kinase from a hypothermophile thermotoga maritima
87	d1lxna_	Alignment	not modelled	5.9	24	**Fold:**Ferredoxin-like **Superfamily:**MTH1187/YkoF-like **Family:**MTH1187-like
88	c3no9C_	Alignment	not modelled	5.9	14	**PDB header:**lyase **Chain:** C: **PDB Molecule:**fumarate hydratase class ii; **PDBTitle:** crystal structure of apo fumarate hydratase from mycobacterium2 tuberculosis
89	c2lk2A_	Alignment	not modelled	5.9	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**homeobox protein tgif1; **PDBTitle:** solution nmr structure of homeobox domain (171-248) of human homeobox2 protein tgif1, northeast structural genomics consortium target3 hr4411b
90	d1huua_	Alignment	not modelled	5.8	16	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
91	c2w1oA_	Alignment	not modelled	5.8	25	**PDB header:**translation **Chain:** A: **PDB Molecule:**60s acidic ribosomal protein p2; **PDBTitle:** nmr structure of dimerization domain of human ribosomal2 protein p2
92	c3ugsB_	Alignment	not modelled	5.7	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**undecaprenyl pyrophosphate synthase; **PDBTitle:** crystal structure of a probable undecaprenyl diphosphate synthase2 (upps) from campylobacter jejuni
93	d2sici_	Alignment	not modelled	5.7	63	**Fold:**Subtilisin inhibitor **Superfamily:**Subtilisin inhibitor **Family:**Subtilisin inhibitor
94	d1pwha_	Alignment	not modelled	5.6	20	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
95	d2nrha1	Alignment	not modelled	5.6	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**CoaX-like
96	d1pvla_	Alignment	not modelled	5.6	18	**Fold:**Leukocidin-like **Superfamily:**Leukocidin-like **Family:**Leukocidin (pore-forming toxin)
97	d2gkea2	Alignment	not modelled	5.5	23	**Fold:**Diaminopimelate epimerase-like **Superfamily:**Diaminopimelate epimerase-like **Family:**Diaminopimelate epimerase
98	c1p4eB_	Alignment	not modelled	5.5	33	**PDB header:**dna binding protein/recombination/dna **Chain:** B: **PDB Molecule:**recombinase flp protein; **PDBTitle:** flpe w330f mutant-dna holliday junction complex
99	c3beyC_	Alignment	not modelled	5.5	20	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**conserved protein o27018; **PDBTitle:** crystal structure of the protein o27018 from methanobacterium2 thermoautotrophicum. northeast structural genomics consortium target3 tt217