Phyre2

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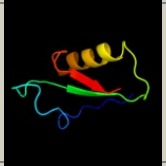
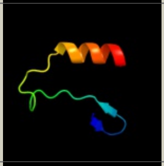
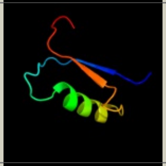
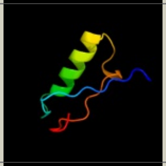
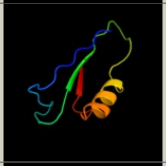
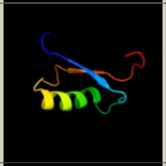
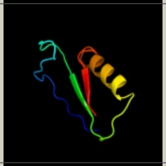
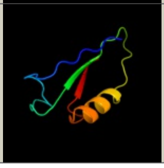
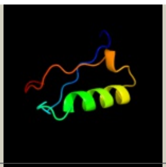
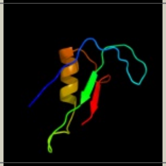
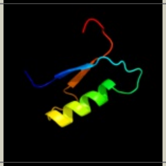
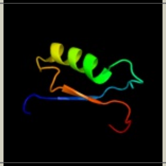
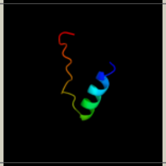
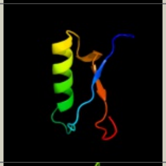
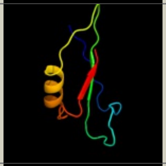
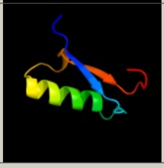
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1yh5a1	Alignment		100.0	98	**Fold:**YggU-like **Superfamily:**YggU-like **Family:**YggU-like
2	d1jrma_	Alignment		99.9	23	**Fold:**YggU-like **Superfamily:**YggU-like **Family:**YggU-like
3	c3t5sA_	Alignment		85.5	13	**PDB header:**immune system **Chain:** A: **PDB Molecule:**macrophage migration inhibitory factor; **PDBTitle:** structure of macrophage migration inhibitory factor from giardia2 lamblia
4	d1t6aa_	Alignment		75.7	36	**Fold:**TBP-like **Superfamily:**Rbstp2229 protein **Family:**Rbstp2229 protein
5	d1ffvb2	Alignment		64.3	4	**Fold:**Molybdenum cofactor-binding domain **Superfamily:**Molybdenum cofactor-binding domain **Family:**Molybdenum cofactor-binding domain
6	d1v97a5	Alignment		63.1	13	**Fold:**Molybdenum cofactor-binding domain **Superfamily:**Molybdenum cofactor-binding domain **Family:**Molybdenum cofactor-binding domain
7	d2gdga1	Alignment		61.5	18	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MIF-related
8	d1n62b2	Alignment		59.0	9	**Fold:**Molybdenum cofactor-binding domain **Superfamily:**Molybdenum cofactor-binding domain **Family:**Molybdenum cofactor-binding domain
9	c3hrdF_	Alignment		56.8	7	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**nicotinate dehydrogenase medium molybdopterin **PDBTitle:** crystal structure of nicotinate dehydrogenase
10	c3b64A_	Alignment		53.6	9	**PDB header:**cytokine **Chain:** A: **PDB Molecule:**macrophage migration inhibitory factor-like **PDBTitle:** macrophage migration inhibitory factor (mif) from2 /leishmania major
11	d1fima_	Alignment		51.8	18	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MIF-related

12	c3eubL_	Alignment		49.7	13	**PDB header:**oxidoreductase **Chain:** L: **PDB Molecule:**xanthine dehydrogenase/oxidase; **PDBTitle:** crystal structure of desulfo-xanthine oxidase with xanthine
13	d1gd0a_	Alignment		48.3	18	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MIF-related
14	d1t3qb2	Alignment		48.1	16	**Fold:**Molybdenum cofactor-binding domain **Superfamily:**Molybdenum cofactor-binding domain **Family:**Molybdenum cofactor-binding domain
15	c1n62E_	Alignment		47.4	9	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**carbon monoxide dehydrogenase large chain; **PDBTitle:** crystal structure of the mo,cu-co dehydrogenase (codh), n-2 butylisocyanide-bound state
16	c1ffvB_	Alignment		46.9	4	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cutl, molybdoprotein of carbon monoxide **PDBTitle:** carbon monoxide dehydrogenase from hydrogenophaga2 pseudoflava
17	d1b24a1	Alignment		46.4	37	**Fold:**Homing endonuclease-like **Superfamily:**Homing endonucleases **Family:**Group I mobile intron endonuclease
18	d1jrob2	Alignment		46.3	11	**Fold:**Molybdenum cofactor-binding domain **Superfamily:**Molybdenum cofactor-binding domain **Family:**Molybdenum cofactor-binding domain
19	c3fwtA_	Alignment		41.6	9	**PDB header:**cytokine **Chain:** A: **PDB Molecule:**macrophage migration inhibitory factor-like **PDBTitle:** crystal structure of leishmania major mif2
20	c1sb3D_	Alignment		40.9	9	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**4-hydroxybenzoyl-coa reductase alpha subunit; **PDBTitle:** structure of 4-hydroxybenzoyl-coa reductase from thauera2 aromatica
21	d1dpta_	Alignment	not modelled	40.6	14	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MIF-related
22	d1hfoa_	Alignment	not modelled	37.7	12	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MIF-related
23	c3gacD_	Alignment	not modelled	37.6	20	**PDB header:**cytokine **Chain:** D: **PDB Molecule:**macrophage migration inhibitory factor-like **PDBTitle:** structure of mif with hpp
24	c1t3qB_	Alignment	not modelled	37.5	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**quinoline 2-oxidoreductase large subunit; **PDBTitle:** crystal structure of quinoline 2-oxidoreductase from pseudomonas2 putida 86
25	c2w54F_	Alignment	not modelled	37.1	11	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**xanthine dehydrogenase; **PDBTitle:** crystal structure of xanthine dehydrogenase from2 rhodobacter capsulatus in complex with bound inhibitor3 pterin-6-aldehyde
26	d1rm6a2	Alignment	not modelled	36.7	9	**Fold:**Molybdenum cofactor-binding domain **Superfamily:**Molybdenum cofactor-binding domain **Family:**Molybdenum cofactor-binding domain
27	c2xczA_	Alignment	not modelled	30.0	7	**PDB header:**immune system **Chain:** A: **PDB Molecule:**possible atls1-like light-inducible protein; **PDBTitle:** crystal structure of macrophage migration inhibitory factor2 homologue from prochlorococcus marinus
28	d1uiza_	Alignment	not modelled	28.1	20	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF

						Family:MIF-related
29	c2os5C_	Alignment	not modelled	27.7	11	**PDB header:**cytokine **Chain:** C: **PDB Molecule:**acemif; **PDBTitle:** macrophage migration inhibitory factor from ancylostoma ceylanicum
30	c2l0kA_	Alignment	not modelled	26.8	35	**PDB header:**transcription **Chain:** A: **PDB Molecule:**stage iii sporulation protein d; **PDBTitle:** nmr solution structure of a transcription factor spoiiid in complex2 with dna
31	c3abfB_	Alignment	not modelled	25.1	10	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**4-oxalocrotonate tautomerase; **PDBTitle:** crystal structure of a 4-oxalocrotonate tautomerase homologue2 (tthb242)
32	c1wygA_	Alignment	not modelled	24.9	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**xanthine dehydrogenase/oxidase; **PDBTitle:** crystal structure of a rat xanthine dehydrogenase triple mutant2 (c535a, c992r and c1324s)
33	d1otfa_	Alignment	not modelled	24.0	5	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**4-oxalocrotonate tautomerase-like
34	c3glaA_	Alignment	not modelled	23.9	13	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**low molecular weight heat shock protein; **PDBTitle:** crystal structure of the hspa from xanthomonas axonopodis
35	c3m20A_	Alignment	not modelled	23.4	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**4-oxalocrotonate tautomerase, putative; **PDBTitle:** crystal structure of dmpi from archaeoglobus fulgidus determined to2 2.37 angstroms resolution
36	c3mb2G_	Alignment	not modelled	22.2	19	**PDB header:**isomerase **Chain:** G: **PDB Molecule:**4-oxalocrotonate tautomerase family enzyme - alpha subunit; **PDBTitle:** kinetic and structural characterization of a heterohexamer 4-2 oxalocrotonate tautomerase from chloroflexus aurantiacus j-10-fl:3 implications for functional and structural diversity in the4 tautomerase superfamily
37	d1xdpa2	Alignment	not modelled	21.4	14	**Fold:**PHP14-like **Superfamily:**PHP14-like **Family:**PPK middle domain-like
38	d1bjpa_	Alignment	not modelled	21.4	5	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**4-oxalocrotonate tautomerase-like
39	c3p1tB_	Alignment	not modelled	20.9	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative histidinol-phosphate aminotransferase; **PDBTitle:** crystal structure of a putative aminotransferase (bpsl1724) from2 burkholderia pseudomallei k96243 at 2.60 a resolution
40	d1gyxa_	Alignment	not modelled	20.1	10	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**4-oxalocrotonate tautomerase-like
41	c2x4kB_	Alignment	not modelled	18.7	10	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**4-oxalocrotonate tautomerase; **PDBTitle:** crystal structure of sar1376, a putative 4-oxalocrotonate2 tautomerase from the methicillin-resistant staphylococcus3 aureus (mrsa)
42	c2op8A_	Alignment	not modelled	18.6	5	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**probable tautomerase ywhb; **PDBTitle:** crystal structure of ywhb- homologue of 4-oxalocrotonate tautomerase
43	d1oeya_	Alignment	not modelled	18.3	9	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**PB1 domain
44	d1qbjc_	Alignment	not modelled	18.1	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Z-DNA binding domain
45	d1mwwa_	Alignment	not modelled	18.0	19	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**Hypothetical protein HI1388.1
46	d2aala1	Alignment	not modelled	17.8	14	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MSAD-like
47	c3ry0A_	Alignment	not modelled	17.7	10	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative tautomerase; **PDBTitle:** crystal structure of tomn, a 4-oxalocrotonate tautomerase homologue in2 tomaymycin biosynthetic pathway
48	d2gxba1	Alignment	not modelled	17.1	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Z-DNA binding domain
49	d1qgpa_	Alignment	not modelled	17.1	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Z-DNA binding domain
50	c1z2zB_	Alignment	not modelled	16.9	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**probable trna pseudouridine synthase d; **PDBTitle:** crystal structure of the putative trna pseudouridine2 synthase d (trud) from methanosarcina mazei, northeast3 structural genomics target mar1
51	c3fkdC_	Alignment	not modelled	16.9	27	**PDB header:**lyase **Chain:** C: **PDB Molecule:**l-threonine-o-3-phosphate decarboxylase; **PDBTitle:** the crystal structure of l-threonine-o-3-phosphate2 decarboxylase from porphyromonas gingivalis
52	c2kvrA_	Alignment	not modelled	16.7	8	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ubiquitin carboxyl-terminal hydrolase 7; **PDBTitle:** solution nmr structure of human ubiquitin specific protease2 usp7 ubl domain (residues 537-664). nesg target hr4395c/3 sgc-toronto

53	c2ormA_	Alignment	not modelled	15.6	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**probable tautomerase hp0924; **PDBTitle:** crystal structure of the 4-oxalocrotonate tautomerase homologue dmpi2 from helicobacter pylori.
54	c1sb7A_	Alignment	not modelled	14.9	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**trna pseudouridine synthase d; **PDBTitle:** crystal structure of the e.coli pseudouridine synthase trud
55	d1szwa_	Alignment	not modelled	14.9	19	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**tRNA pseudouridine synthase TruD
56	d1wh0a_	Alignment	not modelled	14.6	12	**Fold:**HSP20-like chaperones **Superfamily:**HSP20-like chaperones **Family:**GS domain
57	c3ggeA_	Alignment	not modelled	14.5	14	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**pdz domain-containing protein gipc2; **PDBTitle:** crystal structure of the pdz domain of pdz domain-containing protein2 gipc2
58	c3n4dF_	Alignment	not modelled	13.8	11	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**putative tautomerase; **PDBTitle:** crystal structure of cg10062 inactivated by(r)-oxirane-2-carboxylate
59	c2flzC_	Alignment	not modelled	13.7	11	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**cis-3-chloroacrylic acid dehalogenase; **PDBTitle:** the x-ray structure of cis-3-chloroacrylic acid dehalogenase (cis-2 caad) with a sulfate ion bound in the active site
60	d2bgxa2	Alignment	not modelled	11.5	24	**Fold:**N-acetylmuramoyl-L-alanine amidase-like **Superfamily:**N-acetylmuramoyl-L-alanine amidase-like **Family:**N-acetylmuramoyl-L-alanine amidase-like
61	c2l9fA_	Alignment	not modelled	11.3	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cale8; **PDBTitle:** nmr solution structure of meacp
62	d1vlba4	Alignment	not modelled	10.9	11	**Fold:**Molybdenum cofactor-binding domain **Superfamily:**Molybdenum cofactor-binding domain **Family:**Molybdenum cofactor-binding domain
63	d1w55a2	Alignment	not modelled	10.9	3	**Fold:**Bacillus chorismate mutase-like **Superfamily:**IpsF-like **Family:**IpsF-like
64	c2pmpA_	Alignment	not modelled	10.8	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**2-c-methyl-d-erythritol 2,4-cyclodiphosphate synthase; **PDBTitle:** structure of 2c-methyl-d-erythritol 2,4-cyclodiphosphate synthase from2 the isoprenoid biosynthetic pathway of arabidopsis thaliana
65	d1o57a1	Alignment	not modelled	10.3	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**N-terminal domain of Bacillus PurR
66	d1jmxa1	Alignment	not modelled	10.3	25	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
67	c2oghA_	Alignment	not modelled	10.2	20	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic translation initiation factor eif-1; **PDBTitle:** solution structure of yeast eif1
68	c3re3B_	Alignment	not modelled	10.0	18	**PDB header:**lyase **Chain:** B: **PDB Molecule:**2-c-methyl-d-erythritol 2,4-cyclodiphosphate synthase; **PDBTitle:** crystal structure of 2-c-methyl-d-erythritol 2,4-cyclodiphosphate2 synthase from francisella tularensis
69	c3b6nA_	Alignment	not modelled	9.9	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**2-c-methyl-d-erythritol 2,4-cyclodiphosphate **PDBTitle:** crystal structure of 2c-methyl-d-erythritol 2,4-2 cyclodiphosphate synthase pv003920 from plasmodium vivax
70	d1ee0a2	Alignment	not modelled	9.8	0	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
71	d1v2da_	Alignment	not modelled	9.5	28	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
72	d1gx1a_	Alignment	not modelled	9.4	10	**Fold:**Bacillus chorismate mutase-like **Superfamily:**IpsF-like **Family:**IpsF-like
73	d1iv3a_	Alignment	not modelled	9.3	15	**Fold:**Bacillus chorismate mutase-like **Superfamily:**IpsF-like **Family:**IpsF-like
74	d1kwaa_	Alignment	not modelled	9.1	19	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
75	d1vh8a_	Alignment	not modelled	8.9	10	**Fold:**Bacillus chorismate mutase-like **Superfamily:**IpsF-like **Family:**IpsF-like
76	c3n0kA_	Alignment	not modelled	8.7	23	**PDB header:**hydrolase inhibitor **Chain:** A: **PDB Molecule:**serine protease inhibitor 1; **PDBTitle:** proteinase inhibitor from coprinopsis cinerea
77	c3f0gA_	Alignment	not modelled	8.6	8	**PDB header:**lyase **Chain:** A: **PDB Molecule:**2-c-methyl-d-erythritol 2,4-cyclodiphosphate synthase; **PDBTitle:** co-crystal structure of 2c-methyl-d-erythritol 2,4-cyclodiphosphate2 synthase with cmp
						Fold:PHP14-like

78	d2o8ra2	Alignment	not modelled	8.6	7	**Superfamily:**PHP14-like **Family:**PPK middle domain-like
79	d1pbya1	Alignment	not modelled	8.5	8	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
80	c2gzvA_	Alignment	not modelled	8.5	10	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**prkca-binding protein; **PDBTitle:** the cystal structure of the pdz domain of human pick1 (casp target)
81	c3r1fO_	Alignment	not modelled	8.5	20	**PDB header:**transcription **Chain:** O: **PDB Molecule:**esx-1 secretion-associated regulator espr; **PDBTitle:** crystal structure of a key regulator of virulence in mycobacterium2 tuberculosis
82	d1p1da2	Alignment	not modelled	8.4	17	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
83	c3hdoB_	Alignment	not modelled	8.4	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**histidinol-phosphate aminotransferase; **PDBTitle:** crystal structure of a histidinol-phosphate aminotransferase from2 geobacter metallireducens
84	d1v5ma_	Alignment	not modelled	8.2	26	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Pleckstrin-homology domain (PH domain)
85	c1vlbA_	Alignment	not modelled	8.1	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldehyde oxidoreductase; **PDBTitle:** structure refinement of the aldehyde oxidoreductase from2 desulfovibrio gigas at 1.28 a
86	d1wh5a_	Alignment	not modelled	8.1	5	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
87	d1u2ca2	Alignment	not modelled	8.0	8	**Fold:**Dystroglycan, domain 2 **Superfamily:**Dystroglycan, domain 2 **Family:**Dystroglycan, domain 2
88	c3i0oA_	Alignment	not modelled	7.9	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**spectinomycin phosphotransferase; **PDBTitle:** crystal structure of spectinomycin phosphotransferase,2 aph(9)-ia, in complex with adp and spectinomcyin
89	d1okta2	Alignment	not modelled	7.9	25	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
90	d1fg7a_	Alignment	not modelled	7.9	16	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
91	c3cbfA_	Alignment	not modelled	7.8	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**alpha-aminodipate aminotransferase; **PDBTitle:** crystal structure of lysn, alpha-aminoadipate2 aminotransferase, from thermus thermophilus hb27
92	c3ftbA_	Alignment	not modelled	7.8	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histidinol-phosphate aminotransferase; **PDBTitle:** the crystal structure of the histidinol-phosphate2 aminotransferase from clostridium acetobutylicum
93	c2eeiA_	Alignment	not modelled	7.7	17	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**pdz domain-containing protein 1; **PDBTitle:** solution structure of second pdz domain of pdz domain2 containing protein 1
94	d1dgja4	Alignment	not modelled	7.7	4	**Fold:**Molybdenum cofactor-binding domain **Superfamily:**Molybdenum cofactor-binding domain **Family:**Molybdenum cofactor-binding domain
95	c2d92A_	Alignment	not modelled	7.6	16	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**inad-like protein; **PDBTitle:** solution structure of the fifth pdz domain of inad-like2 protein
96	d1duga2	Alignment	not modelled	7.6	0	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
97	c2y0fD_	Alignment	not modelled	7.6	15	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; **PDBTitle:** structure of gcpe (ispg) from thermus thermophilus hb27
98	d1glqa2	Alignment	not modelled	7.5	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
99	c1qysA_	Alignment	not modelled	7.5	13	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**top7; **PDBTitle:** crystal structure of top7: a computationally designed2 protein with a novel fold