Phyre^2

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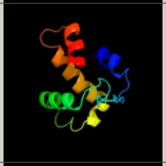
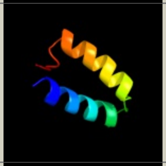
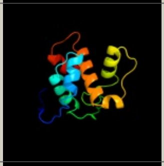
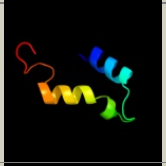
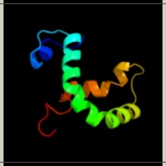
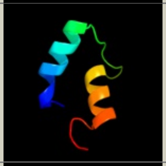
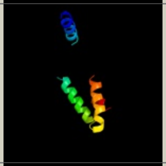
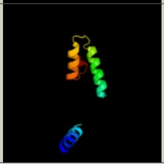
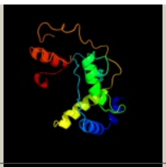
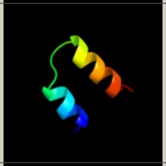
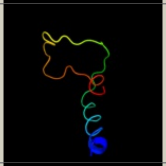
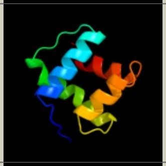
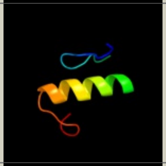
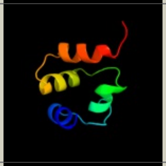
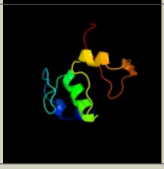
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1qsaa2	Alignment		93.0	25	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Bacterial muramidase, catalytic domain
2	c1slyA_	Alignment		82.0	31	**PDB header:**glycosyltransferase **Chain:** A: **PDB Molecule:**70-kda soluble lytic transglycosylase; **PDBTitle:** complex of the 70-kda soluble lytic transglycosylase with2 bulgecin a
3	c3ct5A_	Alignment		71.0	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**morphogenesis protein 1; **PDBTitle:** crystal and cryoem structural studies of a cell wall degrading enzyme2 in the bacteriophage phi29 tail
4	c2y8pA_	Alignment		70.1	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**endo-type membrane-bound lytic murein transglycosylase a; **PDBTitle:** crystal structure of an outer membrane-anchored endolytic2 peptidoglycan lytic transglycosylase (mlte) from3 escherichia coli
5	d1gbsa_	Alignment		70.0	11	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**G-type lysozyme
6	c3mgwA_	Alignment		69.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lysozyme g; **PDBTitle:** thermodynamics and structure of a salmon cold-active goose-type2 lysozyme
7	c3gxkB_	Alignment		65.6	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**goose-type lysozyme 1; **PDBTitle:** the crystal structure of g-type lysozyme from atlantic cod2 (gadus morhua l.) in complex with nag oligomers sheds new3 light on substrate binding and the catalytic mechanism.4 native structure to 1.9
8	c3csqC_	Alignment		54.9	24	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**morphogenesis protein 1; **PDBTitle:** crystal and cryoem structural studies of a cell wall2 degrading enzyme in the bacteriophage phi29 tail
9	d1kyqa2	Alignment		50.6	21	**Fold:**Siroheme synthase middle domains-like **Superfamily:**Siroheme synthase middle domains-like **Family:**Siroheme synthase middle domains-like
10	d2dt5a1	Alignment		43.6	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Transcriptional repressor Rex, N-terminal domain
11	c1kyqC_	Alignment		36.9	23	**PDB header:**oxidoreductase, lyase **Chain:** C: **PDB Molecule:**siroheme biosynthesis protein met8; **PDBTitle:** met8p: a bifunctional nad-dependent dehydrogenase and2 ferrochelatase involved in siroheme synthesis.

12	c1itkB_	Alignment		35.0	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**catalase-peroxidase; **PDBTitle:** crystal structure of catalase-peroxidase from haloarcula2 marismortui
13	c3bbzA_	Alignment		34.3	32	**PDB header:**viral protein, replication **Chain:** A: **PDB Molecule:**p protein; **PDBTitle:** structure of the nucleocapsid-binding domain from the mumps2 virus phosphoprotein
14	c2wscL_	Alignment		33.9	24	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**photosystem i reaction center subunit xi, **PDBTitle:** improved model of plant photosystem i
15	d1af7a1	Alignment		30.1	13	**Fold:**Chemotaxis receptor methyltransferase CheR, N-terminal domain **Superfamily:**Chemotaxis receptor methyltransferase CheR, N-terminal domain **Family:**Chemotaxis receptor methyltransferase CheR, N-terminal domain
16	c1ub2A_	Alignment		29.9	38	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**catalase-peroxidase; **PDBTitle:** crystal structure of catalase-peroxidase from synechococcus pcc 7942
17	d2eyqa6	Alignment		26.4	38	**Fold:**TRCF domain-like **Superfamily:**TRCF domain-like **Family:**TRCF domain
18	c3kxaD_	Alignment		26.3	25	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of ngo0477 from neisseria gonorrhoeae
19	d1tc3c_	Alignment		25.1	28	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
20	d2evra2	Alignment		24.9	25	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**NlpC/P60
21	d1pdnc_	Alignment	not modelled	24.7	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
22	c2dw3A_	Alignment	not modelled	22.6	46	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**intrinsic membrane protein pufx; **PDBTitle:** solution structure of the rhodobacter sphaeroides pufx2 membrane protein
23	c2qsrA_	Alignment	not modelled	22.5	10	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription-repair coupling factor; **PDBTitle:** crystal structure of c-terminal domain of transcription-repair2 coupling factor
24	c2ql2A_	Alignment	not modelled	21.5	27	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**transcription factor e2-alpha; **PDBTitle:** crystal structure of the basic-helix-loop-helix domains of2 the heterodimer e47/neurod1 bound to dna
25	c3h4zC_	Alignment	not modelled	20.8	12	**PDB header:**allergen **Chain:** C: **PDB Molecule:**maltose-binding periplasmic protein fused with allergen **PDBTitle:** crystal structure of an mbp-der p 7 fusion protein
26	c1n6dE_	Alignment	not modelled	19.8	10	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**tricorn protease; **PDBTitle:** tricorn protease in complex with tetrapeptide chloromethyl2 ketone derivative
27	c1k32E_	Alignment	not modelled	19.8	10	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**tricorn protease; **PDBTitle:** crystal structure of the tricorn protease
28	c6paxA_	Alignment	not modelled	19.6	17	**PDB header:**gene regulation/dna **Chain:** A: **PDB Molecule:**homeobox protein pax-6; **PDBTitle:** crystal structure of the human pax-6 paired domain-dna2 complex reveals a general model for pax protein-dna3 interactions
						Fold:alpha/beta knot

29	d2o3aa1	Alignment	not modelled	19.2	19	**Superfamily:**alpha/beta knot **Family:**AF0751-like
30	d1a6qa1	Alignment	not modelled	19.1	24	**Fold:**Another 3-helical bundle **Superfamily:**Protein serine/threonine phosphatase 2C, C-terminal domain **Family:**Protein serine/threonine phosphatase 2C, C-terminal domain
31	d1x2ma1	Alignment	not modelled	19.0	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
32	c1ee8A_	Alignment	not modelled	18.6	31	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**mutm (fpg) protein; **PDBTitle:** crystal structure of mutm (fpg) protein from thermus thermophilus hb8
33	c3g9wA_	Alignment	not modelled	17.7	12	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**talin-2; **PDBTitle:** crystal structure of talin2 f2-f3 in complex with the integrin beta1d2 cytoplasmic tail
34	c3dhiA_	Alignment	not modelled	17.1	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**toluene 4-monooxygenase hydroxylase alpha subunit; **PDBTitle:** crystal structure of reduced toluene 4-monoxygenase hydroxylase2 complexed with effector protein
35	d1txga1	Alignment	not modelled	17.0	31	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**Glycerol-3-phosphate dehydrogenase
36	d1rioa_	Alignment	not modelled	16.9	18	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
37	d1ul1x1	Alignment	not modelled	15.5	15	**Fold:**SAM domain-like **Superfamily:**5' to 3' exonuclease, C-terminal subdomain **Family:**5' to 3' exonuclease, C-terminal subdomain
38	c2dt5A_	Alignment	not modelled	15.4	19	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**at-rich dna-binding protein; **PDBTitle:** crystal structure of ttha1657 (at-rich dna-binding protein) from2 thermus thermophilus hb8
39	c3ketA_	Alignment	not modelled	15.1	31	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**redox-sensing transcriptional repressor rex; **PDBTitle:** crystal structure of a rex-family transcriptional regulatory protein2 from streptococcus agalactiae bound to a palindromic operator
40	c1go4F_	Alignment	not modelled	13.7	10	**PDB header:**cell cycle **Chain:** F: **PDB Molecule:**mad1 (mitotic arrest deficient)-like 1; **PDBTitle:** crystal structure of mad1-mad2 reveals a conserved mad22 binding motif in mad1 and cdc20.
41	d2cqxa1	Alignment	not modelled	13.5	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
42	d1llib_	Alignment	not modelled	13.3	16	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
43	d1s69a_	Alignment	not modelled	13.1	17	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Truncated hemoglobin
44	d1uhsa_	Alignment	not modelled	12.9	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
45	c2di7A_	Alignment	not modelled	12.6	22	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**bk158_1; **PDBTitle:** solution structure of the filamin domain from human bk158_12 protein
46	c2bmmA_	Alignment	not modelled	12.6	11	**PDB header:**oxygen storage/transport **Chain:** A: **PDB Molecule:**thermostable hemoglobin from thermobifida fusca; **PDBTitle:** x-ray structure of a novel thermostable hemoglobin from the2 actinobacterium thermobifida fusca
47	c3mmyF_	Alignment	not modelled	12.5	33	**PDB header:**nuclear protein **Chain:** F: **PDB Molecule:**nuclear pore complex protein nup98; **PDBTitle:** structural and functional analysis of the interaction between the2 nucleoporin nup98 and the mrna export factor rae1
48	c3f6wE_	Alignment	not modelled	11.6	12	**PDB header:**dna binding protein **Chain:** E: **PDB Molecule:**xre-family like protein; **PDBTitle:** xre-family like protein from pseudomonas syringae pv. tomato str.2 dc3000
49	d1vhna_	Alignment	not modelled	11.5	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
50	d1s95a_	Alignment	not modelled	11.2	18	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Protein serine/threonine phosphatase
51	c2k25A_	Alignment	not modelled	10.7	18	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**ubb; **PDBTitle:** automated nmr structure of the ubb by fapsy
52	d1k32a4	Alignment	not modelled	10.7	16	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Tail specific protease, catalytic domain
53	d1j5ya1	Alignment	not modelled	10.6	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Biotin repressor-like
54	c2fxhB_	Alignment	not modelled	10.2	29	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**catalase-peroxidase protein; **PDBTitle:** crystal structure of katg at ph 6.5

55	c2b2qB_	Alignment	not modelled	10.2	29	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**catalase-peroxidase; **PDBTitle:** crystal structure of native catalase-peroxidase katg at2 ph7.5
56	c2o01L_	Alignment	not modelled	10.1	24	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**photosystem i reaction center subunit xi, **PDBTitle:** the structure of a plant photosystem i supercomplex at 3.42 angstrom resolution
57	d1lmb3_	Alignment	not modelled	9.7	16	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
58	c1nnjA_	Alignment	not modelled	9.5	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**formamidopyrimidine-dna glycosylase; **PDBTitle:** crystal structure complex between the lactococcus lactis fpg and an2 abasic site containing dna
59	c2wusR_	Alignment	not modelled	9.3	19	**PDB header:**structural protein **Chain:** R: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** bacterial actin mreb assembles in complex with cell shape2 protein rodz
60	d1lkxa_	Alignment	not modelled	9.2	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Motor proteins
61	c2k1gA_	Alignment	not modelled	9.1	15	**PDB header:**lipoprotein **Chain:** A: **PDB Molecule:**lipoprotein spr; **PDBTitle:** solution nmr structure of lipoprotein spr from escherichia coli k12.2 northeast structural genomics target er541-37-162
62	d2ppxa1	Alignment	not modelled	9.0	22	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
63	c2ppxA_	Alignment	not modelled	9.0	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu1735; **PDBTitle:** crystal structure of a hth xre-family like protein from agrobacterium2 tumefaciens
64	d2b5ea2	Alignment	not modelled	8.9	53	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
65	c2kscA_	Alignment	not modelled	8.7	11	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**cyanoglobin; **PDBTitle:** solution structure of synechococcus sp. pcc 7002 hemoglobin
66	d3c5wc1	Alignment	not modelled	8.4	15	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Protein serine/threonine phosphatase
67	c1fuiB_	Alignment	not modelled	8.3	18	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**l-fucose isomerase; **PDBTitle:** l-fucose isomerase from escherichia coli
68	c2jf1A_	Alignment	not modelled	7.7	32	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**filamin-a; **PDBTitle:** crystal structure of the filamin a repeat 21 complexed with2 the integrin beta2 cytoplasmic tail peptide
69	d1l8qa2	Alignment	not modelled	7.7	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
70	d1u04a1	Alignment	not modelled	7.6	55	**Fold:**SH3-like barrel **Superfamily:**PAZ domain **Family:**PAZ domain
71	d1z3eb1	Alignment	not modelled	7.6	19	**Fold:**SAM domain-like **Superfamily:**C-terminal domain of RNA polymerase alpha subunit **Family:**C-terminal domain of RNA polymerase alpha subunit
72	c1th1C_	Alignment	not modelled	7.4	33	**PDB header:**cell adhesion/antitumor protein **Chain:** C: **PDB Molecule:**adenomatous polyposis coli protein; **PDBTitle:** beta-catenin in complex with a phosphorylated apc 20aa2 repeat fragment
73	d2hi3a1	Alignment	not modelled	7.2	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
74	d2b5aa1	Alignment	not modelled	7.2	18	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
75	d2ccaa2	Alignment	not modelled	7.2	23	**Fold:**Heme-dependent peroxidases **Superfamily:**Heme-dependent peroxidases **Family:**Catalase-peroxidase KatG
76	d2hddb_	Alignment	not modelled	7.2	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
77	d1xr4a2	Alignment	not modelled	7.1	17	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
78	c2vt2A_	Alignment	not modelled	6.8	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**redox-sensing transcriptional repressor rex; **PDBTitle:** structure and functional properties of the bacillus2 subtilis transcriptional repressor rex
79	c1dlyA_	Alignment	not modelled	6.7	19	**PDB header:**oxygen storage/transport **Chain:** A: **PDB Molecule:**hemoglobin; **PDBTitle:** x-ray crystal structure of hemoglobin from the green2 unicellular alga chlamydomonas eugametos
80	d1dlya_	Alignment	not modelled	6.7	19	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Truncated hemoglobin
						PDB header:transcription regulator/dna

81	c3clcC_	Alignment	not modelled	6.6	16	**Chain:** C: **PDB Molecule:**regulatory protein; **PDBTitle:** crystal structure of the restriction-modification controller protein2 c.esp1396i tetramer in complex with its natural 35 base-pair operator
82	d2b3na1	Alignment	not modelled	6.6	26	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like
83	c2ds4A_	Alignment	not modelled	6.3	32	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**tripartite motif protein 45; **PDBTitle:** solution structure of the filamin domain from human2 tripartite motif protein 45
84	c1htjF_	Alignment	not modelled	6.2	19	**PDB header:**signaling protein **Chain:** F: **PDB Molecule:**kiaa0380; **PDBTitle:** structure of the rgs-like domain from pdz-rhogef
85	d1htjf_	Alignment	not modelled	6.2	19	**Fold:**Regulator of G-protein signaling, RGS **Superfamily:**Regulator of G-protein signaling, RGS **Family:**Regulator of G-protein signaling, RGS
86	c1t73B_	Alignment	not modelled	6.2	100	**PDB header:**hormone/growth factor receptor **Chain:** B: **PDB Molecule:**fxxff motif peptide; **PDBTitle:** crystal structure of the androgen receptor ligand binding2 domain in complex with a fxxff motif
87	d1rfya_	Alignment	not modelled	6.1	29	**Fold:**Long alpha-hairpin **Superfamily:**Transcriptional repressor TraM **Family:**Transcriptional repressor TraM
88	d1cooa_	Alignment	not modelled	6.1	24	**Fold:**SAM domain-like **Superfamily:**C-terminal domain of RNA polymerase alpha subunit **Family:**C-terminal domain of RNA polymerase alpha subunit
89	d1ub2a1	Alignment	not modelled	6.1	30	**Fold:**Heme-dependent peroxidases **Superfamily:**Heme-dependent peroxidases **Family:**Catalase-peroxidase KatG
90	c2jxuA_	Alignment	not modelled	6.0	19	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**terb; **PDBTitle:** nmr solution structure of kp-terb, a tellurite resistance2 protein from klebsiella pneumoniae
91	c3s93B_	Alignment	not modelled	6.0	24	**PDB header:**transcription **Chain:** B: **PDB Molecule:**tudor domain-containing protein 5; **PDBTitle:** crystal structure of conserved motif in tdrd5
92	d1lb2b_	Alignment	not modelled	5.9	24	**Fold:**SAM domain-like **Superfamily:**C-terminal domain of RNA polymerase alpha subunit **Family:**C-terminal domain of RNA polymerase alpha subunit
93	d2di8a1	Alignment	not modelled	5.8	36	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
94	d1yqea1	Alignment	not modelled	5.8	13	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**AF0625-like **Family:**AF0625-like
95	d1xnya1	Alignment	not modelled	5.7	25	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
96	d2ozbb1	Alignment	not modelled	5.6	13	**Fold:**Nop domain **Superfamily:**Nop domain **Family:**Nop domain
97	c1wao4_	Alignment	not modelled	5.6	19	**PDB header:**hydrolase **Chain:** 4: **PDB Molecule:**serine/threonine protein phosphatase 5; **PDBTitle:** pp5 structure
98	d1k8rb_	Alignment	not modelled	5.6	15	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ras-binding domain, RBD
99	d1biaa1	Alignment	not modelled	5.6	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Biotin repressor-like