Phyre2

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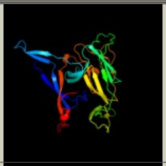
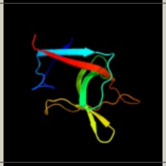
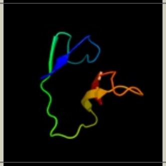
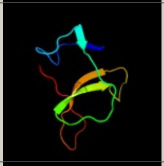
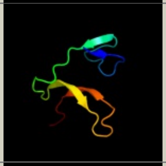
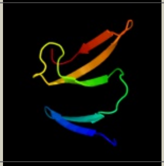
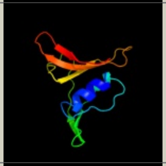
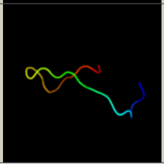
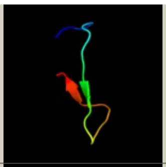
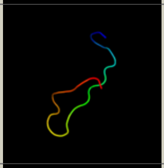
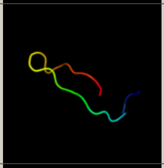
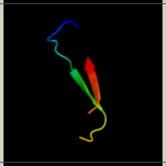
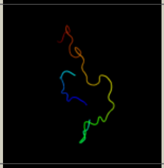
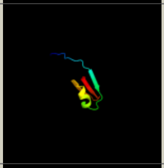
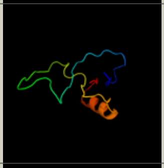
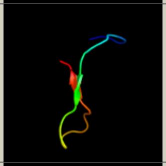
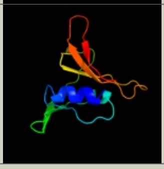
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1b12a_	Alignment		100.0	100	**Fold:**LexA/Signal peptidase **Superfamily:**LexA/Signal peptidase **Family:**Type 1 signal peptidase
2	d1f39a_	Alignment		97.4	29	**Fold:**LexA/Signal peptidase **Superfamily:**LexA/Signal peptidase **Family:**LexA-related
3	d1umua_	Alignment		97.0	20	**Fold:**LexA/Signal peptidase **Superfamily:**LexA/Signal peptidase **Family:**LexA-related
4	c1jhhB_	Alignment		96.7	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**lexa repressor; **PDBTitle:** lexa s119a mutant
5	d1jhfa2	Alignment		96.6	31	**Fold:**LexA/Signal peptidase **Superfamily:**LexA/Signal peptidase **Family:**LexA-related
6	c3k2zA_	Alignment		96.6	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lexa repressor; **PDBTitle:** crystal structure of a lexa protein from thermotoga maritima
7	c2hnfA_	Alignment		96.4	19	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**repressor protein ci101-229dm-k192a; **PDBTitle:** structure of a hyper-cleavable monomeric fragment of phage2 lambda repressor containing the cleavage site region
8	c3bdnB_	Alignment		94.9	23	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**lambda repressor; **PDBTitle:** crystal structure of the lambda repressor
9	c2fjrB_	Alignment		93.7	13	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**repressor protein ci; **PDBTitle:** crystal structure of bacteriophage 186
10	d2io8a2	Alignment		72.1	13	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**CHAP domain
11	d1hr0w_	Alignment		65.1	55	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like

12	c3i4oA_	Alignment		57.8	45	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation initiation factor if-1; **PDBTitle:** crystal structure of translation initiation factor 1 from2 mycobacterium tuberculosis
13	d1ah9a_	Alignment		53.6	45	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
14	c2oqkA_	Alignment		51.5	32	**PDB header:**translation **Chain:** A: **PDB Molecule:**putative translation initiation factor eif-1a; **PDBTitle:** crystal structure of putative cryptosporidium parvum translation2 initiation factor eif-1a
15	d1jt8a_	Alignment		44.8	23	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
16	c2nqqA_	Alignment		39.0	17	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**molybdopterin biosynthesis protein moea; **PDBTitle:** moea r137q
17	d1zvpa1	Alignment		38.5	21	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**VC0802-like
18	d1g2oa_	Alignment		34.1	19	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
19	c2dgyA_	Alignment		31.5	43	**PDB header:**translation **Chain:** A: **PDB Molecule:**mgc11102 protein; **PDBTitle:** solution structure of the eukaryotic initiation factor 1a2 in mgc11102 protein
20	c2ioaA_	Alignment		30.3	14	**PDB header:**ligase, hydrolase **Chain:** A: **PDB Molecule:**bifunctional glutathionylspermidine **PDBTitle:** e. coli bifunctional glutathionylspermidine2 synthetase/amidase incomplex with mg2+ and adp and3 phosphinate inhibitor
21	d1wu2a2	Alignment	not modelled	29.8	22	**Fold:**MoeA N-terminal region -like **Superfamily:**MoeA N-terminal region -like **Family:**MoeA N-terminal region -like
22	c2k3aA_	Alignment	not modelled	28.4	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chap domain protein; **PDBTitle:** nmr solution structure of staphylococcus saprophyticus chap2 (cysteine, histidine-dependent amidohydrolases/peptidases)3 domain protein. northeast structural genomics consortium4 target syr11
23	d2nqra2	Alignment	not modelled	27.4	17	**Fold:**MoeA N-terminal region -like **Superfamily:**MoeA N-terminal region -like **Family:**MoeA N-terminal region -like
24	c1wu2B_	Alignment	not modelled	26.6	22	**PDB header:**structural genomics,biosynthetic protein **Chain:** B: **PDB Molecule:**molybdopterin biosynthesis moea protein; **PDBTitle:** crystal structure of molybdopterin biosynthesis moea2 protein from pyrococcus horikoshii ot3
25	c3qpbB_	Alignment	not modelled	24.7	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**uridine phosphorylase; **PDBTitle:** crystal structure of streptococcus pyogenes uridine phosphorylase2 reveals a subclass of the np-i superfamily
26	c3up6A_	Alignment	not modelled	24.1	36	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**hypothetical protein bacova_04078; **PDBTitle:** crystal structure of a hypothetical protein bacova_04078 [bacteroides2 ovatus atcc 8483] (zp_02067074.1, sp17169a, jcsg 417104) from3 bacteroides ovatus atcc 8483 at 2.80 a resolution
27	d1je0a_	Alignment	not modelled	23.8	27	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
						PDB header:hydrolase

28	c3khsB_	Alignment	not modelled	23.3	30	**Chain:** B: **PDB Molecule:**purine nucleoside phosphorylase; **PDBTitle:** crystal structure of grouper iridovirus purine nucleoside2 phosphorylase
29	c2k8iA_	Alignment	not modelled	23.3	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase; **PDBTitle:** solution structure of e.coli slyd
30	d1d7qa_	Alignment	not modelled	23.0	24	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
31	d1rxya_	Alignment	not modelled	22.9	19	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
32	d1gvha2	Alignment	not modelled	22.8	14	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
33	c2pmzQ_	Alignment	not modelled	22.7	36	**PDB header:**translation, transferase **Chain:** Q: **PDB Molecule:**dna-directed rna polymerase subunit a; **PDBTitle:** archaeal rna polymerase from sulfolobus solfataricus
34	d1uz5a2	Alignment	not modelled	22.4	22	**Fold:**MoeA N-terminal region -like **Superfamily:**MoeA N-terminal region -like **Family:**MoeA N-terminal region -like
35	d2ftxa1	Alignment	not modelled	22.3	80	**Fold:**Kinetochore globular domain-like **Superfamily:**Kinetochore globular domain **Family:**Spc25-like
36	c1tcvB_	Alignment	not modelled	21.5	30	**PDB header:**transferase **Chain:** B: **PDB Molecule:**purine-nucleoside phosphorylase; **PDBTitle:** crystal structure of the purine nucleoside phosphorylase2 from schistosoma mansoni in complex with non-detergent3 sulfobetaine 195 and acetate
37	d1jnpa_	Alignment	not modelled	20.7	26	**Fold:**Oncogene products **Superfamily:**Oncogene products **Family:**Oncogene products
38	d1k9sa_	Alignment	not modelled	20.6	14	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
39	d1qe5a_	Alignment	not modelled	20.4	20	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
40	c1ar1B_	Alignment	not modelled	20.4	21	**PDB header:**complex (oxidoreductase/antibody) **Chain:** B: **PDB Molecule:**cytochrome c oxidase; **PDBTitle:** structure at 2.7 angstrom resolution of the paracoccus2 denitrificans two-subunit cytochrome c oxidase complexed3 with an antibody fv fragment
41	c1qleB_	Alignment	not modelled	20.4	21	**PDB header:**oxidoreductase/immune system **Chain:** B: **PDB Molecule:**cytochrome c oxidase polypeptide ii; **PDBTitle:** cryo-structure of the paracoccus denitrificans four-subunit2 cytochrome c oxidase in the completely oxidized state3 complexed with an antibody fv fragment
42	c1m57H_	Alignment	not modelled	20.2	16	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**cytochrome c oxidase; **PDBTitle:** structure of cytochrome c oxidase from rhodobacter2 sphaeroides (eq(i-286) mutant))
43	c3tl6B_	Alignment	not modelled	19.9	24	**PDB header:**transferase **Chain:** B: **PDB Molecule:**purine nucleoside phosphorylase; **PDBTitle:** crystal structure of purine nucleoside phosphorylase from entamoeba2 histolytica
44	c1qcrD_	Alignment	not modelled	19.7	10	**PDB header:** **PDB COMPND:**
45	c3ggsA_	Alignment	not modelled	19.1	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**purine nucleoside phosphorylase; **PDBTitle:** human purine nucleoside phosphorylase double mutant e201q,n243d2 complexed with 2-fluoro-2'-deoxyadenosine
46	d1jsga_	Alignment	not modelled	19.0	28	**Fold:**Oncogene products **Superfamily:**Oncogene products **Family:**Oncogene products
47	d1ub4a_	Alignment	not modelled	18.9	23	**Fold:**SH3-like barrel **Superfamily:**Cell growth inhibitor/plasmid maintenance toxic component **Family:**Kid/PemK
48	d1a1xa_	Alignment	not modelled	18.9	17	**Fold:**Oncogene products **Superfamily:**Oncogene products **Family:**Oncogene products
49	d3bgsa1	Alignment	not modelled	18.7	19	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
50	c3cgnA_	Alignment	not modelled	18.0	22	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase; **PDBTitle:** crystal structure of thermophilic slyd
51	d1aono_	Alignment	not modelled	17.8	23	**Fold:**GroES-like **Superfamily:**GroES-like **Family:**GroES
52	d1njjb1	Alignment	not modelled	17.5	31	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
53	d1cb0a_	Alignment	not modelled	17.0	28	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
54	c2p4sA	Alignment	not modelled	17.0	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**purine nucleoside phosphorylase;

54	c2p4sA_	Alignment	not modelled	17.0	25	**PDBTitle:** structure of purine nucleoside phosphorylase from anopheles gambiae in2 complex with dadme-immh
55	d1t8sa_	Alignment	not modelled	16.5	31	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
56	c1wtaA_	Alignment	not modelled	16.0	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**5'-methylthioadenosine phosphorylase; **PDBTitle:** crystal structure of 5'-deoxy-5'-methylthioadenosine from aeropyrum2 pernix (r32 form)
57	c3ozbF_	Alignment	not modelled	16.0	10	**PDB header:**transferase **Chain:** F: **PDB Molecule:**methylthioadenosine phosphorylase; **PDBTitle:** crystal structure of 5'-methylthioinosine phosphorylase from2 psedomonas aeruginosa in complex with hypoxanthine
58	c3nx6A_	Alignment	not modelled	15.7	25	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**10kda chaperonin; **PDBTitle:** crystal structure of co-chaperonin, groes (xoo4289) from xanthomonas2 oryzae pv. oryzae kacc10331
59	d3btaa2	Alignment	not modelled	15.4	24	**Fold:**beta-Trefoil **Superfamily:**STI-like **Family:**Clostridium neurotoxins, C-terminal domain
60	c1z34A_	Alignment	not modelled	15.3	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**purine nucleoside phosphorylase; **PDBTitle:** crystal structure of trichomonas vaginalis purine nucleoside2 phosphorylase complexed with 2-fluoro-2'-deoxyadenosine
61	d2qmma1	Alignment	not modelled	15.1	21	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**AF1056-like
62	d1knwa1	Alignment	not modelled	14.8	25	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
63	d1uwva1	Alignment	not modelled	14.7	20	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**TRAM domain
64	d3pnpa_	Alignment	not modelled	14.4	26	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
65	d1ybfa_	Alignment	not modelled	14.0	22	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
66	c2k1gA_	Alignment	not modelled	13.7	25	**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
67	d3dtub2	Alignment	not modelled	13.2	16	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region
68	c2uwqA_	Alignment	not modelled	13.0	67	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**apoptosis-stimulating of p53 protein 2; **PDBTitle:** solution structure of aspp2 n-terminus
69	c1uz5A_	Alignment	not modelled	12.9	22	**PDB header:**molybdopterin biosynthesis **Chain:** A: **PDB Molecule:**402aa long hypothetical molybdopterin **PDBTitle:** the crystal structure of molybdopterin biosynthesis moea2 protein from pyrococcus horikosii
70	c3mb8A_	Alignment	not modelled	12.6	32	**PDB header:**transferase **Chain:** A: **PDB Molecule:**purine nucleoside phosphorylase; **PDBTitle:** crystal structure of purine nucleoside phosphorylase from toxoplasma2 gondii in complex with immucillin-h
71	c2vpmB_	Alignment	not modelled	12.6	12	**PDB header:**ligase **Chain:** B: **PDB Molecule:**trypanothione synthetase; **PDBTitle:** trypanothione synthetase
72	d2bgwa2	Alignment	not modelled	12.5	21	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**XPF/Rad1/Mus81 nuclease
73	d1xpna_	Alignment	not modelled	12.2	7	**Fold:**Prealbumin-like **Superfamily:**Hypothetical protein PA1324 **Family:**Hypothetical protein PA1324
74	d3ehbb2	Alignment	not modelled	12.1	21	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region
75	c1yr3A_	Alignment	not modelled	12.1	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**xanthosine phosphorylase; **PDBTitle:** escherichia coli purine nucleoside phosphorylase ii, the2 product of the xapa gene
76	d1vhwa_	Alignment	not modelled	12.1	10	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
77	d1qcsa1	Alignment	not modelled	11.9	17	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Cdc48 N-terminal domain-like
78	d1kt0a2	Alignment	not modelled	11.8	29	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
79	d1j23a_	Alignment	not modelled	11.8	50	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**XPF/Rad1/Mus81 nuclease
						Fold: Reductase/isomerase/elongation factor common domain

80	d2cnda1	Alignment	not modelled	11.8	18	**Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
81	d1vnba_	Alignment	not modelled	11.8	38	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Scorpion toxin-like **Family:**Long-chain scorpion toxins
82	d2gyci1	Alignment	not modelled	11.6	13	**Fold:**Ribosomal protein L14 **Superfamily:**Ribosomal protein L14 **Family:**Ribosomal protein L14
83	d2nn6g1	Alignment	not modelled	11.6	25	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
84	d1fftb2	Alignment	not modelled	11.5	13	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region
85	d1yeza1	Alignment	not modelled	10.8	30	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**TRAM domain
86	d7odca1	Alignment	not modelled	10.6	31	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
87	c3lhnB_	Alignment	not modelled	10.6	41	**PDB header:**lipid binding protein **Chain:** B: **PDB Molecule:**lipoprotein; **PDBTitle:** crystal structure of putative lipoprotein (np_718719.1) from2 shewanella oneidensis at 1.42 a resolution
88	c2kieA_	Alignment	not modelled	10.5	58	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**inositol polyphosphate 5-phosphatase ocrl-1; **PDBTitle:** a ph domain within ocrl bridges clathrin mediated membrane2 trafficking to phosphoinositide metabolis
89	d2cr9a1	Alignment	not modelled	10.5	29	**Fold:**WGR domain-like **Superfamily:**WGR domain-like **Family:**WGR domain
90	d1odka_	Alignment	not modelled	10.4	19	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
91	d2ja9a1	Alignment	not modelled	10.4	38	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
92	d1vmka_	Alignment	not modelled	10.3	23	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
93	c3dinD_	Alignment	not modelled	10.2	23	**PDB header:**membrane protein, protein transport **Chain:** D: **PDB Molecule:**preprotein translocase subunit sece; **PDBTitle:** crystal structure of the protein-translocation complex formed by the2 secy channel and the seca atpase
94	c2e6zA_	Alignment	not modelled	10.2	31	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor spt5; **PDBTitle:** solution structure of the second kow motif of human2 transcription elongation factor spt5
95	d1yvca1	Alignment	not modelled	10.1	10	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**TRAM domain
96	d2ac7a1	Alignment	not modelled	10.1	14	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
97	c2eocA_	Alignment	not modelled	10.0	43	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly [adp-ribose] polymerase 3; **PDBTitle:** solution structure of the wgr domain from human poly [adp-2 ribose] polymerase-3
98	d1jzaa_	Alignment	not modelled	9.7	35	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Scorpion toxin-like **Family:**Long-chain scorpion toxins
99	d1p3ha_	Alignment	not modelled	9.7	20	**Fold:**GroES-like **Superfamily:**GroES-like **Family:**GroES