Phyre^2

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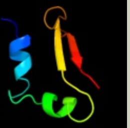
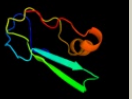
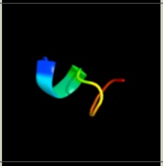
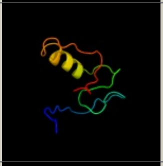
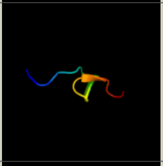
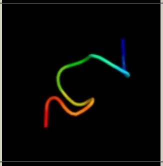
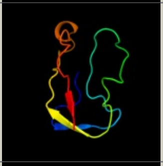
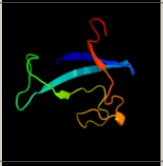
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2qzbB_	Alignment		100.0	99	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein yfey; **PDBTitle:** crystal structure of the uncharacterized protein yfey from escherichia2 coli
2	d1jnya1	Alignment		60.4	16	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Elongation factors
3	c3cihA_	Alignment		46.5	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative alpha-rhamnosidase; **PDBTitle:** crystal structure of a putative alpha-rhamnosidase from2 bacteroides thetaiotaomicron
4	c2jnvA_	Alignment		40.0	26	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**nifu-like protein 1, chloroplast; **PDBTitle:** solution structure of c-terminal domain of nifu-like2 protein from oryza sativa
5	c3ib5A_	Alignment		34.6	16	**PDB header:**hormone **Chain:** A: **PDB Molecule:**sex pheromone precursor; **PDBTitle:** crystal structure of sex pheromone precursor (yp_536235.1)2 from lactobacillus salivarius subsp. salivarius ucc118 at3 1.35 a resolution
6	c2ejgD_	Alignment		29.7	28	**PDB header:**ligase **Chain:** D: **PDB Molecule:**149aa long hypothetical methylmalonyl-coa decarboxylase **PDBTitle:** crystal structure of the biotin protein ligase (mutation r48a) and2 biotin carboxyl carrier protein complex from pyrococcus horikoshii3 ot3
7	c3e1yG_	Alignment		26.8	15	**PDB header:**translation **Chain:** G: **PDB Molecule:**eukaryotic peptide chain release factor gtp-binding subunit **PDBTitle:** crystal structure of human erf1/erf3 complex
8	d2i5nh1	Alignment		25.4	13	**Fold:**PRC-barrel domain **Superfamily:**PRC-barrel domain **Family:**Photosynthetic reaction centre, H-chain, cytoplasmic domain
9	c2ejmA_	Alignment		24.6	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**methylcrotonoyl-coa carboxylase subunit alpha; **PDBTitle:** solution structure of ruh-072, an apo-biotnyl domain form2 human acetyl coenzyme a carboxylase
10	c2qx2A_	Alignment		16.2	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**sex pheromone staph-cam373; **PDBTitle:** structure of the c-terminal domain of sex pheromone staph-cam3732 precursor from staphylococcus aureus
11	c1javA_	Alignment		16.1	63	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**transmembrane glycoprotein (gp41); **PDBTitle:** average nmr solution structure of the trp-rich peptide of2 hiv gp41 bound to dpc micelles

12	d1dcza_	Alignment		15.9	21	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
13	c2pv6A_	Alignment		15.6	56	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**envelope glycoprotein; **PDBTitle:** hiv-1 gp41 membrane proximal ectodomain region peptide in2 dpc micelle
14	c3cxmA_	Alignment		15.5	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uracil-dna glycosylase; **PDBTitle:** leishmania naiffi uracil-dna glycosylase in complex with 5-bromouracil
15	c2wcyA_	Alignment		15.0	27	**PDB header:**immune system **Chain:** A: **PDB Molecule:**complement component c7; **PDBTitle:** nmr solution structure of factor i-like modules of2 complement c7.
16	c1jauA_	Alignment		14.7	56	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**transmembrane glycoprotein (gp41); **PDBTitle:** nmr solution structure of the trp-rich peptide of hiv gp412 bound to dpc micelles
17	d1o78a_	Alignment		14.5	21	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
18	c2b8gA_	Alignment		13.9	20	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**biotin/lipoyl attachment protein; **PDBTitle:** solution structure of bacillus subtilis blap biotinylated-2 form (energy minimized mean structure)
19	d1f60a1	Alignment		13.6	12	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Elongation factors
20	c3rleA_	Alignment		13.3	10	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**golgi reassembly-stacking protein 2; **PDBTitle:** crystal structure of grasp55 grasp domain (residues 7-208)
21	c1s1hI_	Alignment	not modelled	12.9	33	**PDB header:**ribosome **Chain:** I: **PDB Molecule:**40s ribosomal protein s16; **PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1h,4 contains 40s subunit. the 60s ribosomal subunit is in file5 1s1i.
22	c3h00A_	Alignment	not modelled	12.9	56	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**envelope glycoprotein gp160; **PDBTitle:** structure of the c-terminal domain of a putative hiv-1 gp412 fusion intermediate
23	d1nsja_	Alignment	not modelled	12.7	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
24	d1laue_	Alignment	not modelled	11.9	23	**Fold:**Uracil-DNA glycosylase-like **Superfamily:**Uracil-DNA glycosylase-like **Family:**Uracil-DNA glycosylase
25	c2z51A_	Alignment	not modelled	11.0	32	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**nifu-like protein 2, chloroplast; **PDBTitle:** crystal structure of arabidopsis cnfu involved in iron-2 sulfur cluster biosynthesis
26	c2dn8A_	Alignment	not modelled	10.7	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**acetyl-coa carboxylase 2; **PDBTitle:** solution structure of rsgi ruh-053, an apo-biotin carboxy2 carrier protein from human transcarboxylase
27	d1kzyc2	Alignment	not modelled	10.5	26	**Fold:**BRCT domain **Superfamily:**BRCT domain **Family:**53BP1
28	c2v1xB_	Alignment	not modelled	9.5	27	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**atp-dependent dna helicase q1; **PDBTitle:** crystal structure of human recq-like dna helicase

29	c3efyB_	Alignment	not modelled	8.9	24	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**cif (cell cycle inhibiting factor); **PDBTitle:** structure of the cyclomodulin cif from pathogenic2 escherichia coli
30	c2q8iB_	Alignment	not modelled	8.9	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dihydrolipoyllysine-residue acetyltransferase component of **PDBTitle:** pyruvate dehydrogenase kinase isoform 3 in complex with antitumor drug2 radicicol
31	c2booA_	Alignment	not modelled	8.8	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uracil-dna glycosylase; **PDBTitle:** the crystal structure of uracil-dna n-glycosylase (ung)2 from deinococcus radiodurans.
32	d1bdoa_	Alignment	not modelled	8.1	23	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
33	d1tt2a_	Alignment	not modelled	8.0	16	**Fold:**OB-fold **Superfamily:**Staphylococcal nuclease **Family:**Staphylococcal nuclease
34	c3dzmB_	Alignment	not modelled	7.7	26	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hypothetical conserved protein; **PDBTitle:** crystal structure of a major outer membrane protein from thermus2 thermophilus hb27
35	d1xhja_	Alignment	not modelled	7.7	20	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Fe-S cluster assembly (FSCA) domain-like **Family:**NifU C-terminal domain-like
36	c3g9rF_	Alignment	not modelled	7.5	56	**PDB header:**viral protein **Chain:** F: **PDB Molecule:**fusion complex of hiv-1 envelope glycoprotein **PDBTitle:** structure of the hiv-1 gp41 membrane-proximal ectodomain2 region in a putative prefusion conformation
37	c3nahC_	Alignment	not modelled	7.3	8	**PDB header:**transferase **Chain:** C: **PDB Molecule:**rna dependent rna polymerase; **PDBTitle:** crystal structures and functional analysis of murine norovirus rna-2 dependent rna polymerase
38	d2vv5a1	Alignment	not modelled	7.0	15	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Mechanosensitive channel protein MscS (YggB), middle domain
39	d1kjqa1	Alignment	not modelled	7.0	22	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**BC C-terminal domain-like
40	c1y8oA_	Alignment	not modelled	6.8	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**[pyruvate dehydrogenase [lipoamide]] kinase isozyme 3; **PDBTitle:** crystal structure of the pdk3-l2 complex
41	d1zunb1	Alignment	not modelled	6.7	14	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Elongation factors
42	d1oywa2	Alignment	not modelled	6.7	30	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
43	c3cxjB_	Alignment	not modelled	6.7	21	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an uncharacterized protein from2 methanothermobacter thermautotrophicus
44	d1m0sa2	Alignment	not modelled	6.7	48	**Fold:**Ferredoxin-like **Superfamily:**D-ribose-5-phosphate isomerase (RpiA), lid domain **Family:**D-ribose-5-phosphate isomerase (RpiA), lid domain
45	d1hv8a1	Alignment	not modelled	6.6	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
46	c2c2aA_	Alignment	not modelled	6.5	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor histidine kinase; **PDBTitle:** structure of the entire cytoplasmic portion of a sensor2 histidine kinase protein
47	c2zhxG_	Alignment	not modelled	6.4	13	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** G: **PDB Molecule:**uracil-dna glycosylase; **PDBTitle:** crystal structure of uracil-dna glycosylase from mycobacterium2 tuberculosis in complex with a proteinaceous inhibitor
48	d2zgwa1	Alignment	not modelled	6.4	27	**Fold:**SH3-like barrel **Superfamily:**C-terminal domain of transcriptional repressors **Family:**Biotin repressor (BirA)
49	c3i5yA_	Alignment	not modelled	6.3	32	**PDB header:**hydrolase/rna **Chain:** A: **PDB Molecule:**atp-dependent rna helicase mss116; **PDBTitle:** structure of mss116p bound to ssrna containing a single 5-bru and amp-2 pnp
50	c1hv8B_	Alignment	not modelled	6.3	21	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**putative atp-dependent rna helicase mj0669; **PDBTitle:** crystal structure of a dead box protein from the2 hyperthermophile methanococcus jannaschii
51	d1czda2	Alignment	not modelled	6.2	21	**Fold:**DNA clamp **Superfamily:**DNA clamp **Family:**DNA polymerase processivity factor
52	c3owvA_	Alignment	not modelled	6.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dna-entry nuclease; **PDBTitle:** structural insights into catalytic and substrate binding mechanisms of2 the strategic enda nuclease from streptococcus pneumoniae
53	c2k8fB_	Alignment	not modelled	6.0	33	**PDB header:**transferase/transcription **Chain:** B: **PDB Molecule:**cellular tumor antigen p53; **PDBTitle:** structural basis for the regulation of p53 function by p300

54	d2igsa1	Alignment	not modelled	5.7	25	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**PA2222-like
55	c3eqnB_	Alignment	not modelled	5.7	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glucan 1,3-beta-glucosidase; **PDBTitle:** crystal structure of beta-1,3-glucanase from phanerochaete2 chrysosporium (lam55a)
56	d2a9da2	Alignment	not modelled	5.5	27	**Fold:**Oxidoreductase molybdopterin-binding domain **Superfamily:**Oxidoreductase molybdopterin-binding domain **Family:**Oxidoreductase molybdopterin-binding domain
57	c3k9aA_	Alignment	not modelled	5.4	56	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**hiv glycoprotein gp41; **PDBTitle:** crystal structure of hiv gp41 with mper
58	d1sr9a3	Alignment	not modelled	5.4	24	**Fold:**2-isopropylmalate synthase LeuA, allosteric (dimerisation) domain **Superfamily:**2-isopropylmalate synthase LeuA, allosteric (dimerisation) domain **Family:**2-isopropylmalate synthase LeuA, allosteric (dimerisation) domain
59	c2vsxA_	Alignment	not modelled	5.4	20	**PDB header:**translation/hydrolase **Chain:** A: **PDB Molecule:**atp-dependent rna helicase eif4a; **PDBTitle:** crystal structure of a translation initiation complex
60	d1ogpa2	Alignment	not modelled	5.3	19	**Fold:**Oxidoreductase molybdopterin-binding domain **Superfamily:**Oxidoreductase molybdopterin-binding domain **Family:**Oxidoreductase molybdopterin-binding domain
61	d1okba_	Alignment	not modelled	5.3	13	**Fold:**Uracil-DNA glycosylase-like **Superfamily:**Uracil-DNA glycosylase-like **Family:**Uracil-DNA glycosylase
62	d1y8ob1	Alignment	not modelled	5.3	16	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
63	c2l5tA_	Alignment	not modelled	5.3	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lipoamide acyltransferase; **PDBTitle:** solution nmr structure of e2 lipoyl domain from thermoplasma2 acidophilum
64	c1oywA_	Alignment	not modelled	5.3	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent dna helicase; **PDBTitle:** structure of the recq catalytic core
65	d2j8xa1	Alignment	not modelled	5.1	9	**Fold:**Uracil-DNA glycosylase-like **Superfamily:**Uracil-DNA glycosylase-like **Family:**Uracil-DNA glycosylase