Phyre^2

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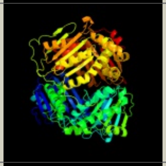
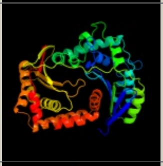
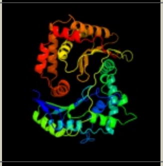
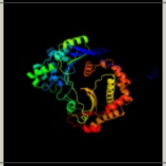
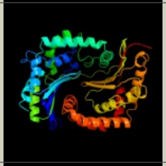
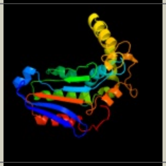
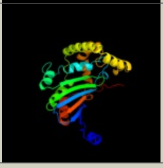
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1q2lA_	Alignment		100.0	100	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protease iii; **PDBTitle:** crystal structure of pitrilysin
2	c2jbuB_	Alignment		100.0	27	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**insulin-degrading enzyme; **PDBTitle:** crystal structure of human insulin degrading enzyme2 complexed with co-purified peptides.
3	c2wk3A_	Alignment		100.0	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**insulin degrading enzyme; **PDBTitle:** crystal structure of human insulin-degrading enzyme in2 complex with amyloid-beta (1-42)
4	c2fgeA_	Alignment		100.0	13	**PDB header:**hydrolase, plant protein **Chain:** A: **PDB Molecule:**zinc metalloprotease (insulinase family); **PDBTitle:** crystal structure of presequence protease prep from2 arabidopsis thaliana
5	c1hr9D_	Alignment		100.0	17	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**mitochondrial processing peptidase beta subunit; **PDBTitle:** yeast mitochondrial processing peptidase beta-e73q mutant2 complexed with malate dehydrogenase signal peptide
6	c1sqpA_	Alignment		100.0	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ubiquinol-cytochrome-c reductase complex core protein i, **PDBTitle:** crystal structure analysis of bovine bc1 with myxothiazol
7	c3eoqB_	Alignment		100.0	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative zinc protease; **PDBTitle:** the crystal structure of putative zinc protease beta-2 subunit from thermus thermophilus hb8
8	c3amiB_	Alignment		100.0	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**zinc peptidase; **PDBTitle:** the crystal structure of the m16b metallopeptidase subunit from2 sphingomonas sp. a1
9	c1nu1A_	Alignment		100.0	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ubiquinol-cytochrome c reductase complex core protein i, **PDBTitle:** crystal structure of mitochondrial cytochrome bc1 complexed with 2-2 nonyl-4-hydroxyquinoline n-oxide (nqno)
10	c3go9A_	Alignment		100.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**insulinase family protease; **PDBTitle:** predicted insulinase family protease from yersinia pestis
11	c1hr6C_	Alignment		100.0	12	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**mitochondrial processing peptidase alpha subunit; **PDBTitle:** yeast mitochondrial processing peptidase

12	c3hdiA_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**processing protease; **PDBTitle:** crystal structure of bacillus halodurans metallo peptidase
13	c1l0lB_	Alignment		100.0	11	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ubiquinol-cytochrome c reductase complex core protein 2; **PDBTitle:** structure of bovine mitochondrial cytochrome bc1 complex with a bound2 fungicide famoxadone
14	c3cx5L_	Alignment		100.0	15	**PDB header:**oxidoreductase **Chain:** L: **PDB Molecule:**cytochrome b-c1 complex subunit 1, mitochondrial; **PDBTitle:** structure of complex iii with bound cytochrome c in reduced2 state and definition of a minimal core interface for3 electron transfer.
15	c3gwbA_	Alignment		100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidase m16 inactive domain family protein; **PDBTitle:** crystal structure of peptidase m16 inactive domain from pseudomonas2 fluorescens. northeast structural genomics target plr293l
16	c3amjB_	Alignment		100.0	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**zinc peptidase inactive subunit; **PDBTitle:** the crystal structure of the heterodimer of m16b peptidase from2 sphingomonas sp. a1
17	c3d3yA_	Alignment		100.0	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a conserved protein from enterococcus faecalis2 v583
18	d1q2la4	Alignment		100.0	100	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
19	d2fgea4	Alignment		100.0	22	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
20	d1ppja1	Alignment		100.0	22	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
21	d1hr6b1	Alignment	not modelled	100.0	24	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
22	d1hr6a1	Alignment	not modelled	100.0	13	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
23	c3cxhM_	Alignment	not modelled	100.0	14	**PDB header:**oxidoreductase **Chain:** M: **PDB Molecule:**cytochrome b-c1 complex subunit 2, mitochondrial; **PDBTitle:** structure of yeast complex iii with isoform-2 cytochrome c2 bound and definition of a minimal core interface for3 electron transfer.
24	d1bcca1	Alignment	not modelled	100.0	22	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
25	d1q2la2	Alignment	not modelled	100.0	100	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
26	d1ppjb1	Alignment	not modelled	100.0	13	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
27	d1bccb1	Alignment	not modelled	100.0	13	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
28	d3cx5a1	Alignment	not modelled	100.0	15	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like

29	d3cx5b1	Alignment	not modelled	100.0	16	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
30	d1q2la3	Alignment	not modelled	100.0	100	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
31	d1q2la1	Alignment	not modelled	100.0	100	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
32	d1ppjb2	Alignment	not modelled	99.8	12	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
33	d1bcca2	Alignment	not modelled	99.8	7	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
34	d1hr6b2	Alignment	not modelled	99.8	7	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
35	d1hr6a2	Alignment	not modelled	99.8	11	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
36	d2fgea2	Alignment	not modelled	99.8	9	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
37	c3ivlA_	Alignment	not modelled	99.8	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative zinc protease; **PDBTitle:** the crystal structure of the inactive peptidase domain of a putative2 zinc protease from bordetella parapertussis to 2.2a
38	d1ppja2	Alignment	not modelled	99.8	6	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
39	d1bccb2	Alignment	not modelled	99.7	12	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
40	d3cx5a2	Alignment	not modelled	99.7	12	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
41	d2fgea3	Alignment	not modelled	99.6	12	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
42	d2fgea1	Alignment	not modelled	99.2	10	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
43	c3ffvA_	Alignment	not modelled	52.1	13	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**protein syd; **PDBTitle:** crystal structure analysis of syd
44	d1j96a_	Alignment	not modelled	37.5	31	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
45	d2rdea1	Alignment	not modelled	22.0	18	**Fold:**Split barrel-like **Superfamily:**PilZ domain-like **Family:**PilZ domain
46	c2rd9C_	Alignment	not modelled	20.5	14	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**bh0186 protein; **PDBTitle:** crystal structure of a putative yfit-like metal-dependent hydrolase2 (bh0186) from bacillus halodurans c-125 at 2.30 a resolution
47	c3hrmA_	Alignment	not modelled	18.2	26	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator sarz; **PDBTitle:** crystal structure of staphylococcus aureus protein sarz in sulfenic2 acid form
48	d1jgsa_	Alignment	not modelled	17.7	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
49	d1lb3a_	Alignment	not modelled	13.8	16	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ferritin
50	c3ostA_	Alignment	not modelled	12.9	10	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**serine/threonine-protein kinase kcc4; **PDBTitle:** structure of the kinase associated-1 (ka1) from kcc4p
51	c2kfvA_	Alignment	not modelled	12.9	25	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**fk506-binding protein 3; **PDBTitle:** structure of the amino-terminal domain of human fk506-2 binding protein 3 / northeast structural genomics3 consortium target ht99a
52	c2zkr9_	Alignment	not modelled	12.1	21	**PDB header:**ribosomal protein/rna **Chain:** 9: **PDB Molecule:**60s ribosomal protein l32; **PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
53	d1r03a_	Alignment	not modelled	11.9	18	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ferritin
54	d1xl7a1	Alignment	not modelled	10.9	15	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**Choline/Carnitine O-acyltransferase
55	c3l7vA_	Alignment	not modelled	10.1	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative uncharacterized protein smu.1377c;

						PDBTitle: crystal structure of a hypothetical protein smu.1377c from2 streptococcus mutans ua159
56	d3broa1	Alignment	not modelled	9.7	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
57	d1u1qa_	Alignment	not modelled	9.7	4	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
58	c1xgwA_	Alignment	not modelled	9.6	14	**PDB header:**endocytosis **Chain:** A: **PDB Molecule:**epsin 4; **PDBTitle:** the crystal structure of human enthoprotin n-terminal domain
59	c3g3zA_	Alignment	not modelled	9.4	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** the structure of nmb1585, a marr family regulator from neisseria2 meningitidis
60	d1qkia1	Alignment	not modelled	9.3	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
61	c3llkA_	Alignment	not modelled	8.9	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sulfhydryl oxidase 1; **PDBTitle:** sulfhydryl oxidase fragment of human qsox1
62	c2pbrB_	Alignment	not modelled	8.7	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**thymidylate kinase; **PDBTitle:** crystal structure of thymidylate kinase (aq_969) from aquifex aeolicus2 vf5
63	c2qm6C_	Alignment	not modelled	8.7	17	**PDB header:**transferase **Chain:** C: **PDB Molecule:**gamma-glutamyltranspeptidase; **PDBTitle:** crystal structure of helicobacter pylori gamma-glutamyltranspeptidase2 in complex with glutamate
64	d1p4xa1	Alignment	not modelled	8.5	7	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
65	c2uxsA_	Alignment	not modelled	8.4	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**inorganic pyrophosphatase; **PDBTitle:** 2.7a crystal structure of inorganic pyrophosphatase (rv3628)2 from mycobacterium tuberculosis at ph 7.5
66	c3onlB_	Alignment	not modelled	8.3	15	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**epsin-3; **PDBTitle:** yeast ent3_enth-vti1p_habc complex structure
67	d1y0ga_	Alignment	not modelled	8.1	19	**Fold:**Streptavidin-like **Superfamily:**YceI-like **Family:**YceI-like
68	d1r62a_	Alignment	not modelled	8.1	19	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**Histidine kinase
69	d1mfra_	Alignment	not modelled	8.0	15	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ferritin
70	d1eyha_	Alignment	not modelled	8.0	14	**Fold:**alpha-alpha superhelix **Superfamily:**ENTH/VHS domain **Family:**ENTH domain
71	d1z6om1	Alignment	not modelled	8.0	24	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ferritin
72	c3iz5h_	Alignment	not modelled	7.8	14	**PDB header:**ribosome **Chain:** H: **PDB Molecule:**60s ribosomal protein l7a (l7ae); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
73	d2fbha1	Alignment	not modelled	7.7	26	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
74	d3c7ba2	Alignment	not modelled	7.7	11	**Fold:**Ferredoxin-like **Superfamily:**Nitrite/Sulfite reductase N-terminal domain-like **Family:**DsrA/DsrB N-terminal-domain-like
75	c4a1cX_	Alignment	not modelled	7.7	18	**PDB header:**ribosome **Chain:** X: **PDB Molecule:**60s ribosomal protein l32; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 4.
76	d1udea_	Alignment	not modelled	7.6	9	**Fold:**OB-fold **Superfamily:**Inorganic pyrophosphatase **Family:**Inorganic pyrophosphatase
77	c3nnhA_	Alignment	not modelled	7.5	15	**PDB header:**rna binding protein/rna **Chain:** A: **PDB Molecule:**cugbp elav-like family member 1; **PDBTitle:** crystal structure of the cugbp1 rrm1 with guuguuuuguuu rna
78	c2adbA_	Alignment	not modelled	7.5	14	**PDB header:**rna binding protein/rna **Chain:** A: **PDB Molecule:**polypyrimidine tract-binding protein 1; **PDBTitle:** solution structure of polypyrimidine tract binding protein2 rbd2 complexed with cucucu rna
79	d1l3ka1	Alignment	not modelled	7.4	4	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
80	c2hvzA_	Alignment	not modelled	7.4	14	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**splicing factor, arginine/serine-rich 7; **PDBTitle:** solution structure of the rrm domain of sr rich factor 9g8
81	d2ceia1	Alignment	not modelled	7.4	19	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ferritin

82	d1zavz1	Alignment	not modelled	7.3	32	**Fold:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain **Superfamily:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain **Family:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain
83	c1zavZ_	Alignment	not modelled	7.3	32	**PDB header:**structural protein **Chain:** Z: **PDB Molecule:**50s ribosomal protein l7/l12; **PDBTitle:** ribosomal protein l10-l12(ntd) complex, space group p21
84	c1zawZ_	Alignment	not modelled	7.3	32	**PDB header:**structural protein **Chain:** Z: **PDB Molecule:**50s ribosomal protein l7/l12; **PDBTitle:** ribosomal protein l10-l12(ntd) complex, space group p212121,2 form a
85	c1zawX_	Alignment	not modelled	7.2	30	**PDB header:**structural protein **Chain:** X: **PDB Molecule:**50s ribosomal protein l7/l12; **PDBTitle:** ribosomal protein l10-l12(ntd) complex, space group p212121,2 form a
86	c1zawY_	Alignment	not modelled	7.2	30	**PDB header:**structural protein **Chain:** Y: **PDB Molecule:**50s ribosomal protein l7/l12; **PDBTitle:** ribosomal protein l10-l12(ntd) complex, space group p212121,2 form a
87	d2za7a1	Alignment	not modelled	7.2	16	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ferritin
88	c3ns5B_	Alignment	not modelled	7.2	26	**PDB header:**translation **Chain:** B: **PDB Molecule:**eukaryotic translation initiation factor 3 subunit b; **PDBTitle:** crystal structure of the rna recognition motif of yeast eif3b residues2 76-161
89	c1xl8B_	Alignment	not modelled	7.1	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**peroxisomal carnitine o-octanoyltransferase; **PDBTitle:** crystal structure of mouse carnitine octanoyltransferase in2 complex with octanoylcarnitine
90	d1whxa_	Alignment	not modelled	7.1	29	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
91	c2x3dC_	Alignment	not modelled	7.0	14	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**sso6206; **PDBTitle:** crystal structure of sso6206 from sulfolobus solfataricus p2
92	c3lv8A_	Alignment	not modelled	7.0	2	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thymidylate kinase; **PDBTitle:** 1.8 angstrom resolution crystal structure of a thymidylate kinase2 (tmk) from vibrio cholerae o1 biovar eltor str. n16961 in complex3 with tmp, thymidine-5'-diphosphate and adp
93	c2qy7A_	Alignment	not modelled	7.0	12	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**clathrin interactor 1; **PDBTitle:** crystal structure of human epsinr enth domain
94	d1lnwa_	Alignment	not modelled	7.0	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
95	c2rs2A_	Alignment	not modelled	6.9	9	**PDB header:**rna binding protein/rna **Chain:** A: **PDB Molecule:**rna-binding protein musashi homolog 1; **PDBTitle:** 1h, 13c, and 15n chemical shift assignments for musashi1 rbd1:r(guagu)2 complex
96	c2fa5B_	Alignment	not modelled	6.8	13	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator marr/emrr family; **PDBTitle:** the crystal structure of an unliganded multiple antibiotic-2 resistance repressor (marr) from xanthomonas campestris
97	c1ygaA_	Alignment	not modelled	6.7	10	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**hypothetical 37.9 kda protein in bio3-hxt17 **PDBTitle:** crystal structure of saccharomyces cerevisiae yn9a protein,2 new york structural genomics consortium
98	d1hsja1	Alignment	not modelled	6.6	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
99	c1qapA_	Alignment	not modelled	6.6	16	**PDB header:**glycosyltransferase **Chain:** A: **PDB Molecule:**quinolinic acid phosphoribosyltransferase; **PDBTitle:** quinolinic acid phosphoribosyltransferase with bound2 quinolinic acid