Phyre^2

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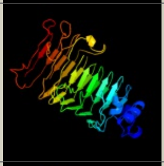
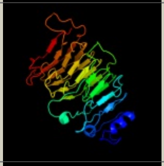
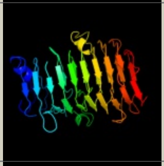
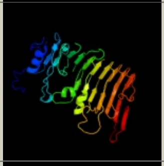
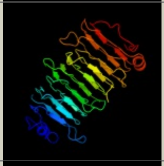
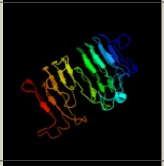
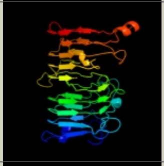
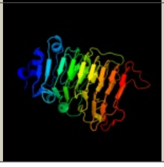
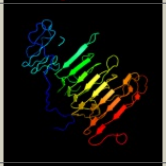
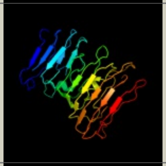
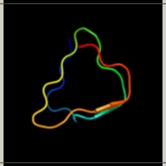
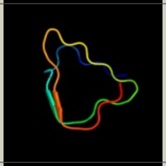
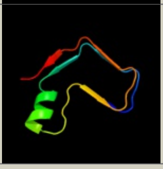
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3jurA_	Alignment		98.5	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exo-poly-alpha-d-galacturonosidase; **PDBTitle:** the crystal structure of a hyperthermoactive exopolygalacturonase from2 thermotoga maritima
2	c2uveA_	Alignment		98.1	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exopolygalacturonase; **PDBTitle:** structure of yersinia enterocolitica family 282 exopolygalacturonase
3	d1bhea_	Alignment		97.8	17	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**Galacturonase
4	d1rmga_	Alignment		97.1	16	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**Galacturonase
5	c3gqnA_	Alignment		96.5	19	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**preneck appendage protein; **PDBTitle:** crystal structure of the pre-mature bacteriophage phi29 gene product2 12
6	d1k5ca_	Alignment		96.3	17	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**Galacturonase
7	c3eqnB_	Alignment		95.9	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glucan 1,3-beta-glucosidase; **PDBTitle:** crystal structure of beta-1,3-glucanase from phanerochaete2 chrysosporium (lam55a)
8	c2iq7D_	Alignment		95.8	18	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**endopolygalacturonase; **PDBTitle:** crystal structure of the polygalacturonase from colletotrichum lupini2 and its implications for the interaction with polygalacturonase-3 inhibiting proteins
9	c1czfB_	Alignment		95.6	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**polygalacturonase ii; **PDBTitle:** endo-polygalacturonase ii from aspergillus niger
10	d1czfa_	Alignment		95.6	21	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**Galacturonase
11	c3gq8A_	Alignment		95.6	24	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**preneck appendage protein; **PDBTitle:** crystal structure of the bacteriophage phi29 gene product2 12 n-terminal fragment in complex with 2-(n-3 cyclohexylamino)ethane sulfonic acid (ches)

12	d1ia5a_	Alignment		95.5	21	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**Galacturonase
13	c2z8gB_	Alignment		91.7	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**isopullulanase; **PDBTitle:** aspergillus niger atcc9642 isopullulanase complexed with isopanose
14	d1nhca_	Alignment		81.0	18	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**Galacturonase
15	d1hg8a_	Alignment		79.0	21	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**Galacturonase
16	d1ogmx2	Alignment		71.6	19	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**Dextranase, catalytic domain
17	d1hf2a1	Alignment		55.1	41	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Cell-division inhibitor MinC, C-terminal domain **Family:**Cell-division inhibitor MinC, C-terminal domain
18	c1hf2A_	Alignment		53.4	41	**PDB header:**cell division protein **Chain:** A: **PDB Molecule:**septum site-determining protein minc; **PDBTitle:** crystal structure of the bacterial cell-division inhibitor2 minc from t. maritima
19	c1dbgA_	Alignment		52.2	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**chondroitinase b; **PDBTitle:** crystal structure of chondroitinase b
20	d1o88a_	Alignment		51.5	17	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**Pectate lyase-like
21	d1pcla_	Alignment	not modelled	46.7	12	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**Pectate lyase-like
22	d1xqma_	Alignment	not modelled	46.5	30	**Fold:**GFP-like **Superfamily:**GFP-like **Family:**Fluorescent proteins
23	c1ogoX_	Alignment	not modelled	44.9	20	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**dextranase; **PDBTitle:** dex49a from penicillium minioluteum complex with isomaltose
24	c3mezA_	Alignment	not modelled	44.5	20	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**mannose-specific lectin 3 chain 1; **PDBTitle:** x-ray structural analysis of a mannose specific lectin from dutch2 crocus (crocus vernus)
25	c2xvsA_	Alignment	not modelled	43.6	19	**PDB header:**antitumor protein **Chain:** A: **PDB Molecule:**tetratricopeptide repeat protein 5; **PDBTitle:** crystal structure of human ttc5 (strap) c-terminal ob2 domain
26	d2f2ha1	Alignment	not modelled	38.8	28	**Fold:**Putative glucosidase YicI, C-terminal domain **Superfamily:**Putative glucosidase YicI, C-terminal domain **Family:**Putative glucosidase YicI, C-terminal domain
27	d1bn8a_	Alignment	not modelled	38.6	22	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**Pectate lyase-like
28	c2pyhB_	Alignment	not modelled	37.8	19	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**poly(beta-d-mannuronate) c5 epimerase 4; **PDBTitle:** azotobacter vinelandii mannuronan c-5 epimerase alge4 a-module2 complexed with mannuronan trisaccharide

29	d1j3pa_	Alignment	not modelled	33.3	22	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Glucose-6-phosphate isomerase, GPI
30	c1nkgA_	Alignment	not modelled	30.2	30	**PDB header:**lyase **Chain:** A: **PDB Molecule:**rhamnogalacturonase b; **PDBTitle:** rhamnogalacturonan lyase from aspergillus aculeatus
31	d1idka_	Alignment	not modelled	29.8	21	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**Pectin lyase
32	c2dd9C_	Alignment	not modelled	29.2	20	**PDB header:**luminescent protein **Chain:** C: **PDB Molecule:**green fluorescent protein; **PDBTitle:** a mutant of gfp-like protein from chiridius poppei
33	d2qqra1	Alignment	not modelled	28.6	37	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**Tudor domain
34	c1vblA_	Alignment	not modelled	26.2	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**pectate lyase 47; **PDBTitle:** structure of the thermostable pectate lyase pl 47
35	c2qy1B_	Alignment	not modelled	26.1	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**pectate lyase ii; **PDBTitle:** pectate lyase a31g/r236f from xanthomonas campestris
36	c2dpfB_	Alignment	not modelled	25.6	25	**PDB header:**plant protein **Chain:** B: **PDB Molecule:**curculin; **PDBTitle:** crystal structure of curculin1 homodimer
37	c3rrrB_	Alignment	not modelled	25.3	32	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**fusion glycoprotein f0; **PDBTitle:** structure of the rsv f protein in the post-fusion conformation
38	d1bwud_	Alignment	not modelled	25.0	13	**Fold:**beta-Prism II **Superfamily:**alpha-D-mannose-specific plant lectins **Family:**alpha-D-mannose-specific plant lectins
39	c3jyvT_	Alignment	not modelled	24.8	23	**PDB header:**ribosome **Chain:** T: **PDB Molecule:**s19e protein; **PDBTitle:** structure of the 40s rrna and proteins and p/e trna for eukaryotic2 ribosome based on cryo-em map of thermomyces lanuginosus ribosome at3 8.9a resolution
40	d1x82a_	Alignment	not modelled	24.7	23	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Glucose-6-phosphate isomerase, GPI
41	c3r0eC_	Alignment	not modelled	23.3	33	**PDB header:**sugar binding protein **Chain:** C: **PDB Molecule:**lectin; **PDBTitle:** structure of remusatia vivipara lectin
42	d1s0ua2	Alignment	not modelled	21.3	78	**Fold:**Elongation factor/aminomethyltransferase common domain **Superfamily:**EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain **Family:**EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain
43	c3rkiB_	Alignment	not modelled	21.0	32	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**fusion glycoprotein f0; **PDBTitle:** structural basis for immunization with post-fusion rsv f to elicit2 high neutralizing antibody titers
44	c3u5ga_	Alignment	not modelled	19.6	33	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**40s ribosomal protein s0-a; **PDBTitle:** the structure of the eukaryotic ribosome at 3.0 a resolution
45	c3cfhB_	Alignment	not modelled	19.5	31	**PDB header:**fluorescent protein **Chain:** B: **PDB Molecule:**gfp-like photoswitchable fluorescent protein; **PDBTitle:** photoswitchable red fluorescent protein psrfp, off-state
46	d1jpca_	Alignment	not modelled	19.5	23	**Fold:**beta-Prism II **Superfamily:**alpha-D-mannose-specific plant lectins **Family:**alpha-D-mannose-specific plant lectins
47	d1npla_	Alignment	not modelled	19.0	28	**Fold:**beta-Prism II **Superfamily:**alpha-D-mannose-specific plant lectins **Family:**alpha-D-mannose-specific plant lectins
48	d1pxza_	Alignment	not modelled	18.7	12	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**Pectate lyase-like
49	c2xzn5_	Alignment	not modelled	17.9	28	**PDB header:**ribosome **Chain:** 5: **PDB Molecule:**ribosomal protein s26e containing protein; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
50	c3lasA_	Alignment	not modelled	17.2	31	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative carbonic anhydrase; **PDBTitle:** crystal structure of carbonic anhydrase from streptococcus mutans to2 1.4 angstrom resolution
51	c3nezB_	Alignment	not modelled	16.8	23	**PDB header:**fluorescent protein **Chain:** B: **PDB Molecule:**mrojoa; **PDBTitle:** mrojoa
52	c3kv4A_	Alignment	not modelled	16.6	42	**PDB header:**h3k4me3 binding protein, transferase **Chain:** A: **PDB Molecule:**phd finger protein 8; **PDBTitle:** structure of phf8 in complex with histone h3
53	c1z8rA_	Alignment	not modelled	15.8	50	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**coxsackievirus b4 polyprotein; **PDBTitle:** 2a cysteine proteinase from human coxsackievirus b4 (strain2 jvb / benschoten / new york / 51)
54	d1xd5a_	Alignment	not modelled	15.7	25	**Fold:**beta-Prism II **Superfamily:**alpha-D-mannose-specific plant lectins **Family:**alpha-D-mannose-specific plant lectins
55	c3iz6S_	Alignment	not modelled	15.6	16	**PDB header:**ribosome **Chain:** S: **PDB Molecule:**40s ribosomal protein s19 (s19e);

[illegible]	[illegible]	Alignment	not modelled	[illegible]	[illegible]	**PDBTitle:** localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
56	c3mezB_	Alignment	not modelled	15.1	10	**PDB header:**sugar binding protein **Chain:** B: **PDB Molecule:**mannose-specific lectin 3 chain 2; **PDBTitle:** x-ray structural analysis of a mannose specific lectin from dutch2 crocus (crocus vernus)
57	d1o12a1	Alignment	not modelled	15.1	17	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**N-acetylglucosamine-6-phosphate deacetylase, NagA
58	d2hv2a1	Alignment	not modelled	14.6	19	**Fold:**SCP-like **Superfamily:**SCP-like **Family:**EF1021 C-terminal domain-like
59	d2hrva_	Alignment	not modelled	14.4	33	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral cysteine protease of trypsin fold
60	c2nlwA_	Alignment	not modelled	14.4	16	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic translation initiation factor 3 **PDBTitle:** solution structure of the rrm domain of human eukaryotic2 initiation factor 3b
61	d2c5lc1	Alignment	not modelled	13.9	43	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ras-binding domain, RBD
62	c2wulB_	Alignment	not modelled	13.9	27	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glutaredoxin related protein 5; **PDBTitle:** crystal structure of the human glutaredoxin 5 with bound2 glutathione in an fes cluster
63	c3a0cA_	Alignment	not modelled	13.8	19	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**mannose/sialic acid-binding lectin; **PDBTitle:** crystal structure of an anti-hiv mannose-binding lectin from2 polygonatum cyrtonema hua
64	c3grhA_	Alignment	not modelled	13.6	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**acyl-coa thioester hydrolase ybgc; **PDBTitle:** crystal structure of escherichia coli ybhc
65	d2v7fa1	Alignment	not modelled	13.2	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Rps19E-like
66	c3b08H_	Alignment	not modelled	13.1	43	**PDB header:**signaling protein/metal binding protein **Chain:** H: **PDB Molecule:**ranbp-type and c3hc4-type zinc finger-containing protein 1; **PDBTitle:** crystal structure of the mouse hoil1-l-nzf in complex with linear di-2 ubiquitin
67	c3ipzA_	Alignment	not modelled	12.9	40	**PDB header:**electron transport, oxidoreductase **Chain:** A: **PDB Molecule:**monothiol glutaredoxin-s14, chloroplastic; **PDBTitle:** crystal structure of arabidopsis monothiol glutaredoxin atgrxcp
68	c2e7pC_	Alignment	not modelled	12.7	47	**PDB header:**electron transport **Chain:** C: **PDB Molecule:**glutaredoxin; **PDBTitle:** crystal structure of the holo form of glutaredoxin c1 from populus2 tremula x tremuloides
69	d1jnya2	Alignment	not modelled	12.6	19	**Fold:**Elongation factor/aminomethyltransferase common domain **Superfamily:**EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain **Family:**EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain
70	c3hz7A_	Alignment	not modelled	12.5	50	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the sira-like protein (dsy4693) from2 desulfitobacterium hafniense, northeast structural genomics3 consortium target dhr2a
71	c2z6zA_	Alignment	not modelled	12.4	26	**PDB header:**fluorescent protein **Chain:** A: **PDB Molecule:**fluorescent protein dronpa; **PDBTitle:** crystal structure of a photoswitchable gfp-like protein2 dronpa in the bright-state
72	c3l4nA_	Alignment	not modelled	12.4	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**monothiol glutaredoxin-6; **PDBTitle:** crystal structure of yeast monothiol glutaredoxin grx6
73	c2jacA_	Alignment	not modelled	11.7	47	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**glutaredoxin-1; **PDBTitle:** glutaredoxin grx1p c30s mutant from yeast
74	c3c1sA_	Alignment	not modelled	10.9	50	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin-1; **PDBTitle:** crystal structure of grx1 in glutathionylated form
75	d1moua_	Alignment	not modelled	10.9	23	**Fold:**GFP-like **Superfamily:**GFP-like **Family:**Fluorescent proteins
76	d1jhba_	Alignment	not modelled	10.7	27	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
77	d1kj1d_	Alignment	not modelled	10.6	14	**Fold:**beta-Prism II **Superfamily:**alpha-D-mannose-specific plant lectins **Family:**alpha-D-mannose-specific plant lectins
78	c3r0eD_	Alignment	not modelled	10.6	20	**PDB header:**sugar binding protein **Chain:** D: **PDB Molecule:**lectin; **PDBTitle:** structure of remusatia vivipara lectin
79	d1nkga3	Alignment	not modelled	10.1	20	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**Rhamnogalacturonase B, RhgB, N-terminal domain
80	c3pu3A_	Alignment	not modelled	9.9	45	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**phd finger protein 2; **PDBTitle:** phf2 jumonji domain-nog complex
81	c3k3nA_	Alignment	not modelled	9.8	50	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**phd finger protein 8; **PDBTitle:** crystal structure of the catalytic core domain of human

						phf8
82	d1ggxa_	Alignment	not modelled	9.8	27	**Fold:**GFP-like **Superfamily:**GFP-like **Family:**Fluorescent proteins
83	c2gw4D_	Alignment	not modelled	9.8	23	**PDB header:**luminescent protein **Chain:** D: **PDB Molecule:**kaede; **PDBTitle:** crystal structure of stony coral fluorescent protein kaede, red form
84	c2w3nA_	Alignment	not modelled	9.7	31	**PDB header:**lyase **Chain:** A: **PDB Molecule:**carbonic anhydrase 2; **PDBTitle:** structure and inhibition of the co2-sensing carbonic2 anhydrase can2 from the pathogenic fungus cryptococcus3 neoformans
85	d1ktea_	Alignment	not modelled	9.7	27	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
86	d2rkya1	Alignment	not modelled	9.7	57	**Fold:**FnI-like domain **Superfamily:**FnI-like domain **Family:**Fibronectin type I module
87	d1bwua_	Alignment	not modelled	9.6	17	**Fold:**beta-Prism II **Superfamily:**alpha-D-mannose-specific plant lectins **Family:**alpha-D-mannose-specific plant lectins
88	d1jdqa_	Alignment	not modelled	9.4	50	**Fold:**IF3-like **Superfamily:**SirA-like **Family:**SirA-like
89	c3gztF_	Alignment	not modelled	9.3	86	**PDB header:**virus **Chain:** F: **PDB Molecule:**outer capsid glycoprotein vp7; **PDBTitle:** vp7 recoated rotavirus dlp
90	d2naca2	Alignment	not modelled	9.3	20	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**Formate/glycerate dehydrogenases, substrate-binding domain
91	d1lbqa_	Alignment	not modelled	9.3	29	**Fold:**Chelatase-like **Superfamily:**Chelatase **Family:**Ferrochelatase
92	d1xd6a_	Alignment	not modelled	9.2	30	**Fold:**beta-Prism II **Superfamily:**alpha-D-mannose-specific plant lectins **Family:**alpha-D-mannose-specific plant lectins
93	c1ylkA_	Alignment	not modelled	9.2	25	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical protein rv1284/mt1322; **PDBTitle:** crystal structure of rv1284 from mycobacterium tuberculosis in complex2 with thiocyanate
94	d2cg7a1	Alignment	not modelled	9.1	57	**Fold:**FnI-like domain **Superfamily:**FnI-like domain **Family:**Fibronectin type I module
95	c2zo7A_	Alignment	not modelled	9.0	24	**PDB header:**luminescent protein **Chain:** A: **PDB Molecule:**cyan/green-emitting gfp-like protein, kusabira-cyan mutant **PDBTitle:** crystal structure of a kusabira-cyan mutant (kcy-r1), a cyan/green-2 emitting gfp-like protein
96	c2hzfA_	Alignment	not modelled	8.9	27	**PDB header:**electron transport, oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin-1; **PDBTitle:** crystal structures of a poxviral glutaredoxin in the oxidized and2 reduced states show redox-correlated structural changes
97	d2rkya2	Alignment	not modelled	8.9	71	**Fold:**FnI-like domain **Superfamily:**FnI-like domain **Family:**Fibronectin type I module
98	c2eceA_	Alignment	not modelled	8.7	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**462aa long hypothetical selenium-binding protein; **PDBTitle:** x-ray structure of hypothetical selenium-binding protein2 from sulfolobus tokodaii, st0059
99	c2ddcA_	Alignment	not modelled	8.6	34	**PDB header:**luminescent protein **Chain:** A: **PDB Molecule:**photoconvertible fluorescent protein; **PDBTitle:** unique behavior of a histidine responsible for an2 engineered green-to-red photoconversion process