Phyre2

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Description	P42592
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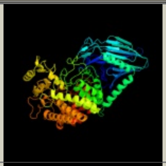
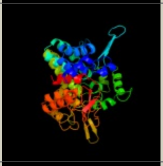
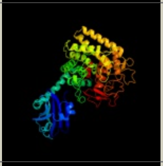
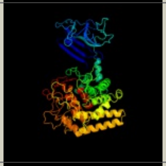
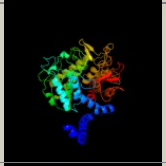
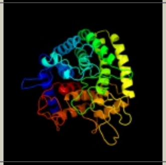
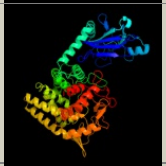
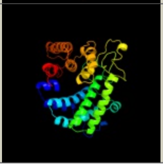
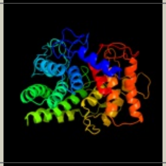
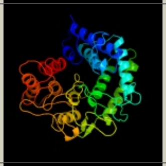
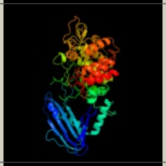
Unique Job ID	34cc4bd31f07a4dc

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3c67B_	Alignment		100.0	100	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**uncharacterized protein ygjk; **PDBTitle:** escherichia coli k12 ygjk in a complexed with glucose
2	d2jg0a1	Alignment		100.0	16	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Trehalase-like
3	c2jg0A_	Alignment		100.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**periplasmic trehalase; **PDBTitle:** family 37 trehalase from escherichia coli in complex with 1-2 thiatrehazolin
4	c2z07A_	Alignment		100.0	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein ttha0978; **PDBTitle:** crystal structure of uncharacterized conserved protein from2 thermus thermophilus hb8
5	c1v7wA_	Alignment		100.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**chitobiose phosphorylase; **PDBTitle:** crystal structure of vibrio proteolyticus chitobiose phosphorylase in2 complex with glcnac
6	c2cqtA_	Alignment		100.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cellobiose phosphorylase; **PDBTitle:** crystal structure of cellvibrio gilvus cellobiose phosphorylase2 crystallized from sodium/potassium phosphate
7	d1v7wa1	Alignment		100.0	16	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Glycosyltransferase family 36 C-terminal domain
8	d1lf6a1	Alignment		100.0	16	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Bacterial glucoamylase C-terminal domain-like
9	c2okxB_	Alignment		99.9	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**rhamnosidase b; **PDBTitle:** crystal structure of gh78 family rhamnosidase of bacillus sp. gl1 at2 1.9 a
10	c1lf6A_	Alignment		99.9	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glucoamylase; **PDBTitle:** crystal structure of bacterial glucoamylase
11	c3cihA_	Alignment		99.9	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative alpha-rhamnosidase; **PDBTitle:** crystal structure of a putative alpha-rhamnosidase from2 bacteroides thetaiotaomicron

12	d1ulva1	Alignment		99.8	16	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Bacterial glucoamylase C-terminal domain-like
13	d1gaia_	Alignment		99.7	18	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Glucoamylase
14	c1ug9A_	Alignment		99.7	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glucodextranase; **PDBTitle:** crystal structure of glucodextranase from arthrobacter globiformis i42
15	d2fbaa1	Alignment		99.7	17	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Glucoamylase
16	c2vn4A_	Alignment		99.6	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glucoamylase; **PDBTitle:** glycoside hydrolase family 15 glucoamylase from hypocrea2 jecorina
17	c3qspB_	Alignment		98.9	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** analysis of a new family of widely distributed metal-independent alpha2 mannosidases provides unique insight into the processing of n-linked3 glycans, streptococcus pneumoniae sp_2144 non-productive substrate4 complex with alpha-1,6-mannobiose
18	c2eacB_	Alignment		98.9	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-fucosidase; **PDBTitle:** crystal structure of 1,2-a-l-fucosidase from2 bifidobacterium bifidum in complex with3 deoxyfuconojirimycin
19	c2ww1B_	Alignment		98.7	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative alpha-1,2-mannosidase; **PDBTitle:** structure of the family gh92 inverting mannosidase bt39902 from bacteroides thetaiotaomicron vpi-5482 in complex with3 thiomannobioside
20	d2nvpa1	Alignment		98.7	15	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**CPF0428-like
21	d1h54a1	Alignment	not modelled	98.7	13	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Glycosyltransferase family 36 C-terminal domain
22	c2wvyA_	Alignment	not modelled	98.6	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-1,2-mannosidase; **PDBTitle:** structure of the family gh92 inverting mannosidase bt21992 from bacteroides thetaiotaomicron vpi-5482
23	c2p0vA_	Alignment	not modelled	98.6	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein bt3781; **PDBTitle:** crystal structure of bt3781 protein from bacteroides2 thetaiotaomicron, northeast structural genomics target3 btr58
24	d2p0va1	Alignment	not modelled	98.6	19	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**CPF0428-like
25	c1h54B_	Alignment	not modelled	98.2	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**maltose phosphorylase; **PDBTitle:** maltose phosphorylase from lactobacillus brevis
26	c2rdyB_	Alignment	not modelled	98.2	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**bh0842 protein; **PDBTitle:** crystal structure of a putative glycoside hydrolase family2 protein from bacillus halodurans
27	c3gt5A_	Alignment	not modelled	96.3	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**n-acetylglucosamine 2-epimerase; **PDBTitle:** crystal structure of an n-acetylglucosamine 2-epimerase family protein2 from xylella fastidiosa
28	d2afaa1	Alignment	not modelled	95.1	15	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**N-acylglucosamine (NAG) epimerase
						Fold:alpha/alpha toroid

29	d1fp3a_	Alignment	not modelled	94.1	16	**Superfamily:**Six-hairpin glycosidases **Family:**N-acylglucosamine (NAG) epimerase
30	d2d5ja1	Alignment	not modelled	91.1	16	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Glycosyl Hydrolase Family 88
31	c2zzrA_	Alignment	not modelled	87.7	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**unsaturated glucuronyl hydrolase; **PDBTitle:** crystal structure of unsaturated glucuronyl hydrolase from2 streptcoccus agalactiae
32	c1ut9A_	Alignment	not modelled	70.3	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cellulose 1,4-beta-cellobiosidase; **PDBTitle:** structural basis for the exocellulase activity of the2 cellobiohydrolase cbha from c. thermocellum
33	c3k11A_	Alignment	not modelled	70.1	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative glycosyl hydrolase; **PDBTitle:** crystal structure of putative glycosyl hydrolase (np_813087.1) from2 bacteroides thetaiotaomicron vpi-5482 at 1.80 a resolution
34	d1ut9a1	Alignment	not modelled	65.6	14	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Cellulases catalytic domain
35	d1nc5a_	Alignment	not modelled	62.2	11	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Hypothetical protein YteR
36	c1ga2A_	Alignment	not modelled	61.2	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoglucanase 9g; **PDBTitle:** the crystal structure of endoglucanase 9g from clostridium2 cellulolyticum complexed with cellobiose
37	d1ia6a_	Alignment	not modelled	60.6	14	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Cellulases catalytic domain
38	c1clcA_	Alignment	not modelled	55.5	15	**PDB header:**glycosyl hydrolase **Chain:** A: **PDB Molecule:**endoglucanase celd; ec: 3.2.1.4; **PDBTitle:** three-dimensional structure of endoglucanase d at 1.92 angstroms resolution
39	c3pmmA_	Alignment	not modelled	54.7	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative cytoplasmic protein; **PDBTitle:** the crystal structure of a possible member of gh105 family from2 klebsiella pneumoniae subsp. pneumoniae mgh 78578
40	d1clca1	Alignment	not modelled	52.7	12	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Cellulases catalytic domain
41	d1g87a1	Alignment	not modelled	50.1	19	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Cellulases catalytic domain
42	c2xfgA_	Alignment	not modelled	43.6	14	**PDB header:**hydrolase/sugar binding protein **Chain:** A: **PDB Molecule:**endoglucanase 1; **PDBTitle:** reassembly and co-crystallization of a family 9 processive2 endoglucanase from separately expressed gh9 and cbm3c3 modules
43	c3gzkA_	Alignment	not modelled	40.5	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cellulase; **PDBTitle:** structure of a. acidocaldarius cellulase cela
44	c3nrdB_	Alignment	not modelled	30.5	22	**PDB header:**nucleotide binding protein **Chain:** B: **PDB Molecule:**histidine triad (hit) protein; **PDBTitle:** crystal structure of a histidine triad (hit) protein (smc02904) from2 sinorhizobium meliloti 1021 at 2.06 a resolution
45	d1tf4a1	Alignment	not modelled	29.2	12	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Cellulases catalytic domain
46	d1ks8a_	Alignment	not modelled	27.4	10	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Cellulases catalytic domain
47	c1x9dA_	Alignment	not modelled	25.3	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoplasmic reticulum mannosyl-oligosaccharide 1, **PDBTitle:** crystal structure of human class i alpha-1,2-mannosidase in2 complex with thio-disaccharide substrate analogue
48	d1x9da1	Alignment	not modelled	25.3	17	**Fold:**alpha/alpha toroid **Superfamily:**Seven-hairpin glycosidases **Family:**Class I alpha-1;2-mannosidase, catalytic domain
49	d1of5b_	Alignment	not modelled	22.0	19	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**NTF2-like
50	d2h8pc1	Alignment	not modelled	17.6	7	**Fold:**Voltage-gated potassium channels **Superfamily:**Voltage-gated potassium channels **Family:**Voltage-gated potassium channels
51	d2pifa1	Alignment	not modelled	16.3	15	**Fold:**PSTPO5379-like **Superfamily:**PSTPO5379-like **Family:**PSTPO5379-like
52	c3oheA_	Alignment	not modelled	16.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**histidine triad (hit) protein; **PDBTitle:** crystal structure of a histidine triad protein (maqu_1709) from2 marinobacter aquaeolei vt8 at 1.20 a resolution
53	c3k7xA_	Alignment	not modelled	15.4	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin0763 protein; **PDBTitle:** crystal structure of the lin0763 protein from listeria2 innocua. northeast structural genomics consortium target3 lkr23.
54	c2lbbA_	Alignment	not modelled	12.7	27	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**acyl coa binding protein; **PDBTitle:** solution structure of acyl coa binding protein from babesia bovis t2bo

55	c1xc0A_	Alignment	not modelled	12.4	41	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**pardaxin p-4; **PDBTitle:** twenty lowest energy structures of pa4 by solution nmr
56	d1nzpa_	Alignment	not modelled	12.3	15	**Fold:**SAM domain-like **Superfamily:**DNA polymerase beta, N-terminal domain-like **Family:**DNA polymerase beta, N-terminal domain-like
57	c3sohB_	Alignment	not modelled	11.2	20	**PDB header:**motor protein **Chain:** B: **PDB Molecule:**flagellar motor switch protein flig; **PDBTitle:** architecture of the flagellar rotor
58	d1i39a_	Alignment	not modelled	11.1	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Ribonuclease H
59	c1i3aA_	Alignment	not modelled	11.1	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ribonuclease hii; **PDBTitle:** rnase hii from archaeoglobus fulgidus with cobalt hexammine2 chloride
60	d1gwya_	Alignment	not modelled	10.9	11	**Fold:**Cytolysin/lectin **Superfamily:**Cytolysin/lectin **Family:**Anemone pore-forming cytolysin
61	c2xtdB_	Alignment	not modelled	10.6	8	**PDB header:**transcription **Chain:** B: **PDB Molecule:**tbl1 f-box-like/wd repeat-containing protein tbl1x; **PDBTitle:** structure of the tbl1 tetramerisation domain
62	c3db3A_	Alignment	not modelled	10.2	43	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase uhrf1; **PDBTitle:** crystal structure of the tandem tudor domains of the e3 ubiquitin-2 protein ligase uhrf1 in complex with trimethylated histone h3-k93 peptide
63	c2xteH_	Alignment	not modelled	9.8	8	**PDB header:**transcription **Chain:** H: **PDB Molecule:**f-box-like/wd repeat-containing protein tbl1x; **PDBTitle:** structure of the tbl1 tetramerisation domain
64	c2r7aC_	Alignment	not modelled	9.5	13	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**bacterial heme binding protein; **PDBTitle:** crystal structure of a periplasmic heme binding protein2 from shigella dysenteriae
65	c3kioA_	Alignment	not modelled	9.4	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ribonuclease h2 subunit a; **PDBTitle:** mouse rnase h2 complex
66	c2axtc_	Alignment	not modelled	9.0	16	**PDB header:**electron transport **Chain:** C: **PDB Molecule:**photosystem ii cp43 protein; **PDBTitle:** crystal structure of photosystem ii from thermosynechococcus elongatus
67	d2axtc1	Alignment	not modelled	9.0	16	**Fold:**Photosystem II antenna protein-like **Superfamily:**Photosystem II antenna protein-like **Family:**Photosystem II antenna protein-like
68	d1iwpa_	Alignment	not modelled	8.9	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Cobalamin (vitamin B12)-dependent enzymes **Family:**Diol dehydratase, alpha subunit
69	d1jmsa1	Alignment	not modelled	8.9	10	**Fold:**SAM domain-like **Superfamily:**DNA polymerase beta, N-terminal domain-like **Family:**DNA polymerase beta, N-terminal domain-like
70	c2jw1A_	Alignment	not modelled	8.8	21	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**lipoprotein mxim; **PDBTitle:** structural characterization of the type iii pilotin-2 secretin interaction in shigella flexneri by nmr3 spectroscopy
71	c3i4sB_	Alignment	not modelled	8.8	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**histidine triad protein; **PDBTitle:** crystal structure of histidine triad protein blr8122 from2 bradyrhizobium japonicum
72	d3boja1	Alignment	not modelled	8.6	20	**Fold:**CdCA1 repeat-like **Superfamily:**CdCA1 repeat-like **Family:**CdCA1 repeat-like
73	d1ekea_	Alignment	not modelled	8.5	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Ribonuclease H
74	c2qx5B_	Alignment	not modelled	8.4	21	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**nucleoporin nic96; **PDBTitle:** structure of nucleoporin nic96
75	d1uaxa_	Alignment	not modelled	8.4	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Ribonuclease H
76	c2vixB_	Alignment	not modelled	8.3	14	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**protein mxic; **PDBTitle:** methylated shigella flexneri mxic
77	c2d0bA_	Alignment	not modelled	8.2	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ribonuclease hiii; **PDBTitle:** crystal structure of bst-rnase hiii in complex with mg2+
78	d3boea1	Alignment	not modelled	8.2	23	**Fold:**CdCA1 repeat-like **Superfamily:**CdCA1 repeat-like **Family:**CdCA1 repeat-like
79	c3i24B_	Alignment	not modelled	8.1	43	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hit family hydrolase; **PDBTitle:** crystal structure of a hit family hydrolase protein from2 vibrio fischeri. northeast structural genomics consortium3 target id vfr176
80	d1w8ia_	Alignment	not modelled	8.0	16	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**PIN domain
81	d2pbea2	Alignment	not modelled	7.9	26	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase

						Family: AadK N-terminal domain-like
82	c2r2vB_	Alignment	not modelled	7.6	36	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**gcn4 leucine zipper; **PDBTitle:** sequence determinants of the topology of the lac repressor2 tetrameric coiled coil
83	d1io2a_	Alignment	not modelled	7.6	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Ribonuclease H
84	c1ichA_	Alignment	not modelled	7.3	0	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**tumor necrosis factor receptor-1; **PDBTitle:** solution structure of the tumor necrosis factor receptor-12 death domain
85	d1icha_	Alignment	not modelled	7.3	0	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**DEATH domain, DD
86	d1h2vc2	Alignment	not modelled	7.2	14	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**MIF4G domain-like
87	c3igmA_	Alignment	not modelled	7.0	16	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**pf14_0633 protein; **PDBTitle:** a 2.2a crystal structure of the ap2 domain of pf14_0633 from p.2 falciparum, bound as a domain-swapped dimer to its cognate dna
88	d2bcqa1	Alignment	not modelled	7.0	17	**Fold:**SAM domain-like **Superfamily:**DNA polymerase beta, N-terminal domain-like **Family:**DNA polymerase beta, N-terminal domain-like
89	c3fgrB_	Alignment	not modelled	6.8	32	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative phospholipase b-like 2 40 kda form; **PDBTitle:** two chain form of the 66.3 kda protein at 1.8 angstroem
90	c2fqzC_	Alignment	not modelled	6.7	13	**PDB header:**hydrolase/dna **Chain:** C: **PDB Molecule:**r.ecl18ki; **PDBTitle:** metal-depleted ecl18ki in complex with uncleaved dna
91	c3hwjA_	Alignment	not modelled	6.7	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase mycbp2; **PDBTitle:** crystal structure of the second phr domain of mouse myc-2 binding protein 2 (mycbp-2)
92	d2d5ua1	Alignment	not modelled	6.6	10	**Fold:**PUG domain-like **Superfamily:**PUG domain-like **Family:**PUG domain
93	c2bldD_	Alignment	not modelled	6.5	17	**PDB header:**virus **Chain:** D: **PDB Molecule:**penton protein; **PDBTitle:** the quasi-atomic model of human adenovirus type 52 capsid (part 1)
94	c3renB_	Alignment	not modelled	6.5	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glycosyl hydrolase, family 8; **PDBTitle:** cpf_2247, a novel alpha-amylase from clostridium perfringens
95	d1su3a1	Alignment	not modelled	6.4	17	**Fold:**PGBD-like **Superfamily:**PGBD-like **Family:**MMP N-terminal domain
96	d2etja1	Alignment	not modelled	6.4	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Ribonuclease H
97	c2etjA_	Alignment	not modelled	6.4	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ribonuclease hii; **PDBTitle:** crystal structure of ribonuclease hii (ec 3.1.26.4) (rnase hii)2 (tm0915) from thermotoga maritima at 1.74 a resolution
98	d3pmga4	Alignment	not modelled	6.3	20	**Fold:**TBP-like **Superfamily:**Phosphoglucomutase, C-terminal domain **Family:**Phosphoglucomutase, C-terminal domain
99	c3no8A_	Alignment	not modelled	6.3	25	**PDB header:**isomerase regulator **Chain:** A: **PDB Molecule:**btb/poz domain-containing protein 2; **PDBTitle:** crystal structure of the phr domain from human btbd2 protein