Phyre2

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Description	P0AGL5
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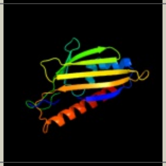
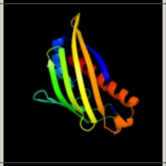
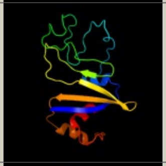
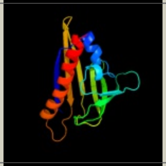
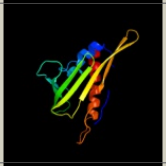
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1t17a_	Alignment		100.0	31	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**oligoketide cyclase/dehydrase-like
2	d2d4ra1	Alignment		99.9	16	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**oligoketide cyclase/dehydrase-like
3	c3tfzB_	Alignment		99.9	21	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**cyclase; **PDBTitle:** crystal structure of zhui aromatase/cyclase from streptomcyes sp.2 r1128
4	c2kf2A_	Alignment		99.9	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative polyketide cyclase; **PDBTitle:** solution nmr structure of of streptomyces coelicolor2 polyketide cyclase sco5315. northeast structural genomics3 consortium target rr365
5	c2le1A_	Alignment		99.9	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of tfu_2981 from thermobifida fusca, northeast2 structural genomics consortium target tfr85a
6	c3p9vA_	Alignment		99.9	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** high resolution crystal structure of protein maqu_3174 from2 marinobacter aquaeolei, northeast structural genomics consortium3 target mqr197
7	d2pcsa1	Alignment		99.9	10	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**CoxG-like
8	d2rera1	Alignment		99.9	11	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**oligoketide cyclase/dehydrase-like
9	d2ns9a1	Alignment		99.9	12	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**CoxG-like
10	d2b79a1	Alignment		99.8	9	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**Smu440-like
11	d3cnwa1	Alignment		99.8	14	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**Atu1531-like

12	c3p51A_	Alignment		99.8	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** three-dimensional structure of protein q2y8n9_nitmu from nitrosospira2 multiformis, northeast structural genomics consortium target nmr118
13	c2kczA_	Alignment		99.7	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein dr_a0006; **PDBTitle:** solution nmr structure of the c-terminal domain of protein2 dr_a0006 from deinococcus radiodurans. northeast3 structural genomics consortium target drr147d
14	c3oquB_	Alignment		99.6	11	**PDB header:**hormone receptor **Chain:** B: **PDB Molecule:**abscisic acid receptor pyl9; **PDBTitle:** crystal structure of native abscisic acid receptor pyl9 with aba
15	c3qtjA_	Alignment		99.6	6	**PDB header:**hormone receptor **Chain:** A: **PDB Molecule:**abscisic acid receptor pyl10; **PDBTitle:** crystal strcuture of aba receptor pyl10 (apo)
16	c3k90C_	Alignment		99.6	12	**PDB header:**hormone receptor, hydrolase regulator **Chain:** C: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** the abscisic acid receptor pyr1 in complex with abscisic acid
17	d2qpva1	Alignment		99.6	10	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**Atu1531-like
18	c2vq5B_	Alignment		99.5	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**s-norcoclaurine synthase; **PDBTitle:** x-ray structure of norcoclaurine synthase from thalictrum2 flavum in complex with dopamine and hydroxybenzaldehyde
19	c3oh8A_	Alignment		99.5	8	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**nucleoside-diphosphate sugar epimerase (sula family); **PDBTitle:** crystal structure of the nucleoside-diphosphate sugar epimerase from2 corynebacterium glutamicum. northeast structural genomics consortium3 target cgr91
20	c3qszB_	Alignment		99.4	12	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**star-related lipid transfer protein; **PDBTitle:** crystal structure of the star-related lipid transfer protein (fragment2 25-204) from xanthomonas axonopodis at the resolution 2.4a, northeast3 structural genomics consortium target xar342
21	d1ifva_	Alignment	not modelled	99.4	13	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**Pathogenesis-related protein 10 (PR10)-like
22	c3klxB_	Alignment	not modelled	99.4	9	**PDB header:**hormone receptor **Chain:** B: **PDB Molecule:**f3n23.20 protein; **PDBTitle:** crystal structure of native abscisic acid receptor pyl3
23	d1xfsa_	Alignment	not modelled	99.3	9	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**AHSA1 domain
24	d1icxa_	Alignment	not modelled	99.3	12	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**Pathogenesis-related protein 10 (PR10)-like
25	c2lf2A_	Alignment	not modelled	99.3	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of the ahsa1-like protein chu_1110 from2 cytophaga hutchinsonii, northeast structural genomics consortium3 target chr152
26	c3uidA_	Alignment	not modelled	99.3	12	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of protein ms6760 from mycobacterium smegmatis
27	c3c0vC_	Alignment	not modelled	99.3	9	**PDB header:**plant protein **Chain:** C: **PDB Molecule:**cytokinin-specific binding protein; **PDBTitle:** crystal structure of cytokinin-specific binding protein in complex2 with cytokinin and ta6br12
28	d1xuva_	Alignment	not modelled	99.3	12	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**AHSA1 domain
						PDB header:structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein;

29	c2ldkA_	Alignment	not modelled	99.3	10	**PDBTitle:** solution nmr structure of protein aaur_3427 from arthrobacter2 aurescens, northeast structural genomics consortium target aar96
30	c3pu2G_	Alignment	not modelled	99.3	7	**PDB header:**structure genomics, unknown function **Chain:** G: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the q3j4m4_rhos4 protein from rhodobacter2 sphaeroides. northeast structural genomics consortium target rhr263.
31	c2l9pA_	Alignment	not modelled	99.3	7	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of q5hli9 from staphylococcus epidermidis,2 northeast structural genomics consortium target ser147
32	c3kdiA_	Alignment	not modelled	99.3	11	**PDB header:**hormone receptor **Chain:** A: **PDB Molecule:**putative uncharacterized protein at2g26040; **PDBTitle:** structure of (+)-aba bound pyl2
33	d2bk0a1	Alignment	not modelled	99.3	16	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**Pathogenesis-related protein 10 (PR10)-like
34	c2leqA_	Alignment	not modelled	99.3	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** chemical shift assignment and solution structure of chr145 from2 cytophaga hutchinsonii, northeast structural genomics consortium3 target chr145
35	c3q64A_	Alignment	not modelled	99.3	7	**PDB header:**structure genomics, unknown function **Chain:** A: **PDB Molecule:**mll3774 protein; **PDBTitle:** x-ray crystal structure of protein mll3774 from mesorhizobium loti,2 northeast structural genomics consortium target mlr405.
36	c2lghA_	Alignment	not modelled	99.3	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of the ahsa1-like protein aha_2358 from2 aeromonas hydrophila refined with nh rdcs, northeast structural3 genomics consortium target ahr99.
37	c2lcgA_	Alignment	not modelled	99.2	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of protein rmet_5065 from ralstonia2 metallidurans, northeast structural genomics consortium target crr115
38	c2r55B_	Alignment	not modelled	99.2	15	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**star-related lipid transfer protein 5; **PDBTitle:** human star-related lipid transfer protein 5
39	c2k7hA_	Alignment	not modelled	99.2	14	**PDB header:**allergen **Chain:** A: **PDB Molecule:**stress-induced protein sam22; **PDBTitle:** nmr solution structure of soybean allergen gly m 4
40	c3rd6A_	Alignment	not modelled	99.2	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**mll3558 protein; **PDBTitle:** crystal structure of mll3558 protein from rhizobium loti. northeast2 structural genomics consortium target id mlr403
41	c3p0lC_	Alignment	not modelled	99.2	12	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**steroidogenic acute regulatory protein, mitochondrial; **PDBTitle:** human steroidogenic acute regulatory protein
42	d1qmra_	Alignment	not modelled	99.2	12	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**Pathogenesis-related protein 10 (PR10)-like
43	d1z94a1	Alignment	not modelled	99.2	11	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**AHSA1 domain
44	d1e09a_	Alignment	not modelled	99.1	16	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**Pathogenesis-related protein 10 (PR10)-like
45	d1fm4a_	Alignment	not modelled	99.1	15	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**Pathogenesis-related protein 10 (PR10)-like
46	c3otlA_	Alignment	not modelled	99.1	7	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** three-dimensional structure of the putative uncharacterized protein2 from rhizobium leguminosarum at the resolution 1.9a, northeast3 structural genomics consortium target rlr261
47	d2il5a1	Alignment	not modelled	99.1	8	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**AHSA1 domain
48	c3q63F_	Alignment	not modelled	99.1	5	**PDB header:**structure genomics, unknown function **Chain:** F: **PDB Molecule:**mll2253 protein; **PDBTitle:** x-ray crystal structure of protein mll2253 from mesorhizobium loti,2 northeast structural genomics consortium target mlr404.
49	c2l8oA_	Alignment	not modelled	99.1	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of chr148 from cytophaga hutchinsonii, northeast2 structural genomics consortium target chr148
50	d1xdfa1	Alignment	not modelled	99.1	15	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**Pathogenesis-related protein 10 (PR10)-like
51	c2i9yA_	Alignment	not modelled	99.1	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**major latex protein-like protein 28 or mlp-like **PDBTitle:** solution structure of arabidopsis thaliana protein2 at1g70830, a member of the major latex protein family
52	d1em2a_	Alignment	not modelled	99.1	16	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**STAR domain

53	d1xn6a_	Alignment	not modelled	99.1	6	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**AHSA1 domain
54	d1txca1	Alignment	not modelled	99.0	15	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**Pathogenesis-related protein 10 (PR10)-like
55	d1ln1a_	Alignment	not modelled	99.0	6	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**STAR domain
56	c1jssB_	Alignment	not modelled	99.0	9	**PDB header:**lipid binding protein **Chain:** B: **PDB Molecule:**cholesterol-regulated start protein 4; **PDBTitle:** crystal structure of the mus musculus cholesterol-regulated2 start protein 4 (stard4).
57	d1jssa_	Alignment	not modelled	99.0	9	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**STAR domain
58	c2kewA_	Alignment	not modelled	99.0	5	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein yndb; **PDBTitle:** the solution structure of bacillus subtilis sr211 start domain by nmr2 spectroscopy
59	d1xn5a_	Alignment	not modelled	98.9	5	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**AHSA1 domain
60	d1zxfa1	Alignment	not modelled	98.9	11	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**AHSA1 domain
61	c2lakA_	Alignment	not modelled	98.9	11	**PDB header:**structure genomics, unknown function **Chain:** A: **PDB Molecule:**ahsa1-like protein rhe_ch02687; **PDBTitle:** solution nmr structure of the ahsa1-like protein rhe_ch02687 (1-152)2 from rhizobium etli, northeast structural genomics consortium target3 rer242
62	c2nn5A_	Alignment	not modelled	98.9	7	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ef_2215; **PDBTitle:** structure of conserved protein of unknown function ef2215 from2 enterococcus faecalis
63	c3ie5A_	Alignment	not modelled	98.9	11	**PDB header:**plant protein, biosynthetic protein **Chain:** A: **PDB Molecule:**phenolic oxidative coupling protein hyp-1; **PDBTitle:** crystal structure of hyp-1 protein from hypericum perforatum2 (st john's wort) involved in hypericin biosynthesis
64	c3q6aH_	Alignment	not modelled	98.8	15	**PDB header:**structure genomics, unknown function **Chain:** H: **PDB Molecule:**uncharacterized protein; **PDBTitle:** x-ray crystal structure of the protein ssp2350 from staphylococcus2 saprophyticus, northeast structural genomics consortium target syr116
65	d2nn5a1	Alignment	not modelled	98.8	6	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**AHSA1 domain
66	d3elia1	Alignment	not modelled	98.8	11	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**AHSA1 domain
67	c2e3rB_	Alignment	not modelled	98.7	12	**PDB header:**lipid transport **Chain:** B: **PDB Molecule:**lipid-transfer protein cert; **PDBTitle:** crystal structure of cert start domain in complex with c18-2 ceramide (p1)
68	c3fo5A_	Alignment	not modelled	98.7	12	**PDB header:**lipid transport **Chain:** A: **PDB Molecule:**thioesterase, adipose associated, isoform bfit2; **PDBTitle:** human start domain of acyl-coenzyme a thioesterase 11 (acot11)
69	d2k5ga1	Alignment	not modelled	98.6	11	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**AHSA1 domain
70	c3ni8A_	Alignment	not modelled	98.5	9	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**pfc0360w protein; **PDBTitle:** crystal structure of pfc0360w, an hsp90 activator from plasmodium2 falciparum
71	d1x53a1	Alignment	not modelled	98.3	15	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**AHSA1 domain
72	d2psoa1	Alignment	not modelled	98.2	9	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**STAR domain
73	c2psoC_	Alignment	not modelled	97.0	12	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**star-related lipid transfer protein 13; **PDBTitle:** human stard13 (dlc2) lipid transfer and protein localization domain
74	d2ffsa1	Alignment	not modelled	96.4	12	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**PA1206-like
75	d1vjha_	Alignment	not modelled	94.8	12	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**Pathogenesis-related protein 10 (PR10)-like
76	c2lioA_	Alignment	not modelled	75.8	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of bfr322 from bacteroides fragilis, northeast2 structural genomics consortium target bfr322
77	c2ejxA_	Alignment	not modelled	48.2	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**st0812; **PDBTitle:** crystal structure of the hypothetical protein st0812 from2 sulfolobus tokodaii
78	c3nqnB_	Alignment	not modelled	43.5	7	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a protein with unknown function.

						(dr_2006) from2 deinococcus radiodurans at 1.88 a resolution
79	c2lafA_	Alignment	not modelled	25.6	9	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**lipoprotein 34; **PDBTitle:** nmr solution structure of the n-terminal domain of the e. coli2 lipoprotein bamc
80	d1hg7a_	Alignment	not modelled	7.1	26	**Fold:**beta-clip **Superfamily:**AFP III-like domain **Family:**AFP III-like domain
81	c2dezA_	Alignment	not modelled	5.6	18	**PDB header:**neuropeptide **Chain:** A: **PDB Molecule:**peptide yy; **PDBTitle:** structure of human pyy
82	c1tz5A_	Alignment	not modelled	5.5	24	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**chimera of pancreatic hormone and neuropeptide y; **PDBTitle:** [pnpy19-23]-hpp bound to dpc micelles
83	d1j27a_	Alignment	not modelled	5.5	20	**Fold:**Ferredoxin-like **Superfamily:**Hypothetical protein TT1725 **Family:**Hypothetical protein TT1725
84	d1ucsa_	Alignment	not modelled	5.1	19	**Fold:**beta-clip **Superfamily:**AFP III-like domain **Family:**AFP III-like domain