Phyre^2

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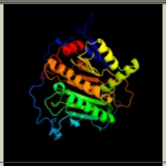
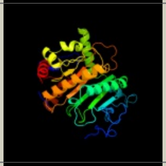
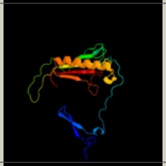
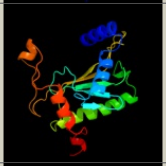
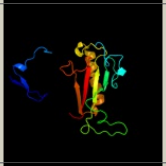
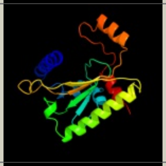
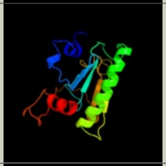
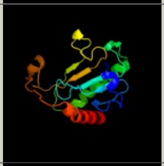
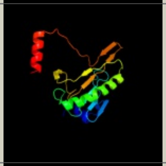
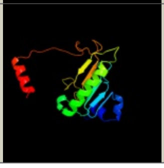
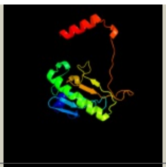
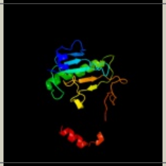
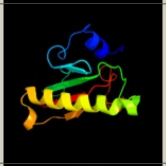
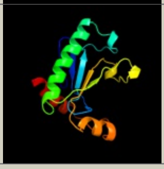
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1gupC_	Alignment		100.0	100	**PDB header:**nucleotidyltransferase **Chain:** C: **PDB Molecule:**galactose-1-phosphate uridylyltransferase; **PDBTitle:** structure of nucleotidyltransferase complexed with udp-2 galactose
2	c1zwjA_	Alignment		100.0	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative galactose-1-phosphate uridyl transferase; **PDBTitle:** x-ray structure of galt-like protein from arabidopsis thaliana2 at5g18200
3	d1guqa1	Alignment		100.0	99	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**Hexose-1-phosphate uridylyltransferase
4	d1guqa2	Alignment		100.0	100	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**Hexose-1-phosphate uridylyltransferase
5	d1z84a1	Alignment		100.0	25	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**Hexose-1-phosphate uridylyltransferase
6	d1z84a2	Alignment		100.0	24	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**Hexose-1-phosphate uridylyltransferase
7	c3lb5B_	Alignment		99.9	19	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**hit-like protein involved in cell-cycle regulation; **PDBTitle:** crystal structure of hit-like protein involved in cell-cycle2 regulation from bartonella henselae with unknown ligand
8	c3anoA_	Alignment		99.9	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ap-4-a phosphorylase; **PDBTitle:** crystal structure of a novel diadenosine 5',5'''-p1,p4-tetraphosphate2 phosphorylase from mycobacterium tuberculosis h37rv
9	c3o0mB_	Alignment		99.9	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hit family protein; **PDBTitle:** crystal structure of a zn-bound histidine triad family protein from2 mycobacterium smegmatis
10	c3l7xA_	Alignment		99.9	19	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**putative hit-like protein involved in cell-cycle **PDBTitle:** the crystal structure of smu.412c from streptococcus mutans ua159
11	c3ksvA_	Alignment		99.9	15	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** hypothetical protein from leishmania major

12	c3imiB_	Alignment		99.9	17	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hit family protein; **PDBTitle:** 2.01 angstrom resolution crystal structure of a hit family protein2 from bacillus anthracis str. 'ames ancestor'
13	c3p0tB_	Alignment		99.9	18	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an hit-like protein from mycobacterium2 paratuberculosis
14	d1y23a_	Alignment		99.9	18	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**HIT (HINT, histidine triad) family of protein kinase-interacting proteins
15	c2eo4A_	Alignment		99.9	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**150aa long hypothetical histidine triad nucleotide-binding **PDBTitle:** crystal structure of hypothetical histidine triad nucleotide-binding2 protein st2152 from sulfolobus tokodaii strain7
16	c3n1tE_	Alignment		99.9	13	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**hit-like protein hint; **PDBTitle:** crystal structure of the h101a mutant echint gmp complex
17	d1xqua_	Alignment		99.9	19	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**HIT (HINT, histidine triad) family of protein kinase-interacting proteins
18	c1xquA_	Alignment		99.9	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hit family hydrolase; **PDBTitle:** hit family hydrolase from clostridium thermocellum cth-393
19	d1rzya_	Alignment		99.9	19	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**HIT (HINT, histidine triad) family of protein kinase-interacting proteins
20	d1fita_	Alignment		99.9	21	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**HIT (HINT, histidine triad) family of protein kinase-interacting proteins
21	d1kpfa_	Alignment	not modelled	99.9	18	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**HIT (HINT, histidine triad) family of protein kinase-interacting proteins
22	d2oika1	Alignment	not modelled	99.9	16	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**HIT (HINT, histidine triad) family of protein kinase-interacting proteins
23	d1emsa1	Alignment	not modelled	99.9	20	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**HIT (HINT, histidine triad) family of protein kinase-interacting proteins
24	c3r6fA_	Alignment	not modelled	99.9	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hit family protein; **PDBTitle:** crystal structure of a zinc-containing hit family protein from2 encephalitozoon cuniculi
25	c3oj7A_	Alignment	not modelled	99.8	17	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**putative histidine triad family protein; **PDBTitle:** crystal structure of a histidine triad family protein from entamoeba2 histolytica, bound to sulfate
26	c1emsB_	Alignment	not modelled	99.8	19	**PDB header:**antitumor protein **Chain:** B: **PDB Molecule:**nit-fragile histidine triad fusion protein; **PDBTitle:** crystal structure of the c. elegans nitfhit protein
27	c3i24B_	Alignment	not modelled	99.6	15	**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
28	c3nrdB_	Alignment	not modelled	99.6	16	**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

29	c3i4sB_	Alignment	not modelled	99.6	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**histidine triad protein; **PDBTitle:** crystal structure of histidine triad protein blr8122 from2 bradyrhizobium japonicum
30	c3oheA_	Alignment	not modelled	99.6	17	**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
31	d3bl9a1	Alignment	not modelled	98.7	18	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**mRNA decapping enzyme DcpS C-terminal domain
32	c3bl9B_	Alignment	not modelled	98.6	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**scavenger mrna-decapping enzyme dcps; **PDBTitle:** synthetic gene encoded dcps bound to inhibitor dg157493
33	d1vlra1	Alignment	not modelled	98.4	21	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**mRNA decapping enzyme DcpS C-terminal domain
34	c1xmlA_	Alignment	not modelled	98.4	18	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**heat shock-like protein 1; **PDBTitle:** structure of human dcps
35	d2pofa1	Alignment	not modelled	85.2	14	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**CDH-like
36	c1m6vE_	Alignment	not modelled	34.9	13	**PDB header:**ligase **Chain:** E: **PDB Molecule:**carbamoyl phosphate synthetase large chain; **PDBTitle:** crystal structure of the g359f (small subunit) point mutant of2 carbamoyl phosphate synthetase
37	d1vpra1	Alignment	not modelled	22.3	60	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Dinoflagellate luciferase repeat
38	c3bddD_	Alignment	not modelled	22.3	27	**PDB header:**transcription **Chain:** D: **PDB Molecule:**regulatory protein marr; **PDBTitle:** crystal structure of a putative multiple antibiotic-resistance2 repressor (ssu05_1136) from streptococcus suis 89/1591 at 2.20 a3 resolution
39	c3g2bA_	Alignment	not modelled	19.5	28	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**coenzyme pqq synthesis protein d; **PDBTitle:** crystal structure of pqqd from xanthomonas campestris
40	c3ohmB_	Alignment	not modelled	18.2	25	**PDB header:**signaling protein / hydrolase **Chain:** B: **PDB Molecule:**1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase **PDBTitle:** crystal structure of activated g alpha q bound to its effector2 phospholipase c beta 3
41	d1zaka2	Alignment	not modelled	15.2	56	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain
42	d1ukfa_	Alignment	not modelled	14.7	19	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Avirulence protein Avrpph3
43	d1v58a1	Alignment	not modelled	14.0	50	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**DsbC/DsbG C-terminal domain-like
44	c1t3bA_	Alignment	not modelled	13.8	38	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbc; **PDBTitle:** x-ray structure of dsbc from haemophilus influenzae
45	d1qasa3	Alignment	not modelled	13.5	27	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLC-like phosphodiesterases **Family:**Mammalian PLC
46	c1v57A_	Alignment	not modelled	13.0	50	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbg; **PDBTitle:** crystal structure of the disulfide bond isomerase dsbg
47	c1jzdA_	Alignment	not modelled	12.4	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbc; **PDBTitle:** dsbc-dsbdalpha complex
48	d2nvna1	Alignment	not modelled	11.6	18	**Fold:**ssDNA-binding transcriptional regulator domain **Superfamily:**ssDNA-binding transcriptional regulator domain **Family:**PMN2A0962/syc2379c-like
49	c2rodB_	Alignment	not modelled	10.9	24	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**noxa; **PDBTitle:** solution structure of mcl-1 complexed with noxaa
50	d1rk4a2	Alignment	not modelled	10.7	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
51	d2psba1	Alignment	not modelled	10.6	33	**Fold:**YerB-like **Superfamily:**YerB-like **Family:**YerB-like
52	c2psbA_	Alignment	not modelled	10.6	33	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**yerb protein; **PDBTitle:** crystal structure of yerb protein from bacillus subtilis.2 northeast structural genomics target sr586
53	d1eeja1	Alignment	not modelled	10.6	38	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**DsbC/DsbG C-terminal domain-like
54	c1hyuA_	Alignment	not modelled	10.5	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**alkyl hydroperoxide reductase subunit f; **PDBTitle:** crystal structure of intact ahpf

55	c2hwtA_	Alignment	not modelled	10.4	19	**PDB header:**replication, hydrolase **Chain:** A: **PDB Molecule:**putative replicase-associated protein; **PDBTitle:** nmr solution structure of the master-rep protein nuclease2 domain (2-95) from the faba bean necrotic yellows virus
56	d1ji8a_	Alignment	not modelled	10.4	11	**Fold:**DsrC, the gamma subunit of dissimilatory sulfite reductase **Superfamily:**DsrC, the gamma subunit of dissimilatory sulfite reductase **Family:**DsrC, the gamma subunit of dissimilatory sulfite reductase
57	d2v4jc1	Alignment	not modelled	9.7	11	**Fold:**DsrC, the gamma subunit of dissimilatory sulfite reductase **Superfamily:**DsrC, the gamma subunit of dissimilatory sulfite reductase **Family:**DsrC, the gamma subunit of dissimilatory sulfite reductase
58	d2drpa2	Alignment	not modelled	9.6	50	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
59	c2elpA_	Alignment	not modelled	9.0	22	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein 406; **PDBTitle:** solution structure of the 13th c2h2 zinc finger of human2 zinc finger protein 406
60	d1t3ba1	Alignment	not modelled	8.4	38	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**DsbC/DsbG C-terminal domain-like
61	c3ghaA_	Alignment	not modelled	8.1	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**disulfide bond formation protein d; **PDBTitle:** crystal structure of etda-treated bdbd (reduced)
62	c3gv1A_	Alignment	not modelled	8.1	63	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**disulfide interchange protein; **PDBTitle:** crystal structure of disulfide interchange protein from neisseria2 gonorrhoeae
63	d1dqwa_	Alignment	not modelled	8.0	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Decarboxylase
64	d1ee8a1	Alignment	not modelled	7.9	21	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Middle domain of MutM-like DNA repair proteins
65	d1igna2	Alignment	not modelled	7.9	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**DNA-binding domain of rap1
66	d1k3sa_	Alignment	not modelled	7.7	20	**Fold:**Secretion chaperone-like **Superfamily:**Type III secretory system chaperone-like **Family:**Type III secretory system chaperone
67	c3c6cA_	Alignment	not modelled	7.7	42	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**3-keto-5-aminohexanoate cleavage enzyme; **PDBTitle:** crystal structure of a putative 3-keto-5-aminohexanoate cleavage2 enzyme (reut_c6226) from ralstonia eutropha jmp134 at 1.72 a3 resolution
68	c3lotC_	Alignment	not modelled	7.7	36	**PDB header:**structure genomics, unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of protein of unknown function (np_070038.1) from2 archaeoglobus fulgidus at 1.89 a resolution
69	c3e49A_	Alignment	not modelled	7.1	36	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein duf849 with a tim barrel fold; **PDBTitle:** crystal structure of a prokaryotic domain of unknown function (duf849)2 with a tim barrel fold (bxe_c0966) from burkholderia xenovorans lb4003 at 1.75 a resolution
70	c3e02A_	Alignment	not modelled	6.9	33	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein duf849; **PDBTitle:** crystal structure of a duf849 family protein (bxe_c0271) from2 burkholderia xenovorans lb400 at 1.90 a resolution
71	c3no5C_	Alignment	not modelled	6.8	27	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a pfam duf849 domain containing protein2 (reut_a1631) from ralstonia eutropha jmp134 at 1.90 a resolution
72	d2fbka1	Alignment	not modelled	6.2	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
73	c3chvA_	Alignment	not modelled	6.2	27	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**prokaryotic domain of unknown function (duf849) with a tim **PDBTitle:** crystal structure of a prokaryotic domain of unknown function (duf849)2 member (spoa0042) from silicibacter pomeroyi dss-3 at 1.45 a3 resolution
74	c3gn3B_	Alignment	not modelled	6.2	25	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative protein-disulfide isomerase; **PDBTitle:** crystal structure of a putative protein-disulfide isomerase from2 pseudomonas syringae to 2.5a resolution.
75	d1aisa1	Alignment	not modelled	6.1	15	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
76	c3nznA_	Alignment	not modelled	6.1	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin; **PDBTitle:** the crystal structure of the glutaredoxin from methanosarcina mazei2 go1
77	c2fd4A_	Alignment	not modelled	6.1	25	**PDB header:**ligase **Chain:** A: **PDB Molecule:**avirulence protein avrptob; **PDBTitle:** crystal structure of avrptob (436-553)
78	c3nqnB_	Alignment	not modelled	6.0	47	**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	c2ab3A_	Alignment	not modelled	5.9	45	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**znf29; **PDBTitle:** solution structures and characterization of hiv rre iib

						rna2 targeting zinc finger proteins
80	d1wika_	Alignment	not modelled	5.9	11	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
81	d2csta_	Alignment	not modelled	5.7	7	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
82	c3oopA_	Alignment	not modelled	5.7	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin2960 protein; **PDBTitle:** the structure of a protein with unknown function from listeria innocua2 clip11262
83	d2fiya1	Alignment	not modelled	5.6	22	**Fold:**FdhE-like **Superfamily:**FdhE-like **Family:**FdhE-like
84	c2y7eA_	Alignment	not modelled	5.6	27	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3-keto-5-aminohexanoate cleavage enzyme; **PDBTitle:** crystal structure of the 3-keto-5-aminohexanoate cleavage enzyme2 (kce) from candidatus cloacamonas acidaminovorans (tetragonal form)
85	d1dl0a_	Alignment	not modelled	5.5	50	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**omega toxin-like **Family:**Spider toxins
86	c1dl0A_	Alignment	not modelled	5.5	50	**PDB header:**toxin **Chain:** A: **PDB Molecule:**j-atracotoxin-hv1c; **PDBTitle:** solution structure of the insecticidal neurotoxin j-2 atracotoxin-hv1c
87	d1fm4a_	Alignment	not modelled	5.5	16	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**Pathogenesis-related protein 10 (PR10)-like
88	c2hw0A_	Alignment	not modelled	5.4	28	**PDB header:**hydrolase, replication **Chain:** A: **PDB Molecule:**replicase; **PDBTitle:** nmr solution structure of the nuclease domain from the2 replicator initiator protein from porcine circovirus pcv2
89	d1s6la1	Alignment	not modelled	5.4	26	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MerB N-terminal domain-like
90	d1qnaa1	Alignment	not modelled	5.4	12	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
91	c1zypB_	Alignment	not modelled	5.3	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**alkyl hydroperoxide reductase subunit f; **PDBTitle:** synchrotron reduced form of the n-terminal domain of2 salmonella typhimurium ahpf
92	d1egoa_	Alignment	not modelled	5.3	25	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
93	d1k0ma2	Alignment	not modelled	5.1	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
94	d1t3ca_	Alignment	not modelled	5.1	25	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Clostridium neurotoxins, catalytic domain
95	d1vr7a1	Alignment	not modelled	5.1	16	**Fold:**S-adenosylmethionine decarboxylase **Superfamily:**S-adenosylmethionine decarboxylase **Family:**Bacterial S-adenosylmethionine decarboxylase