Phyre2

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Description	P06282
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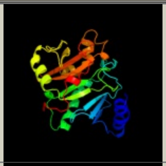
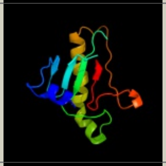
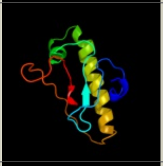
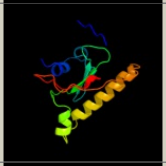
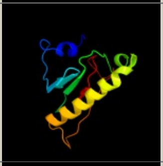
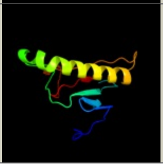
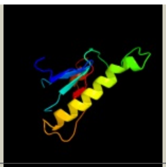
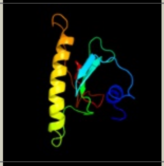
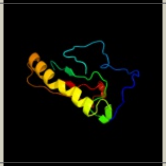
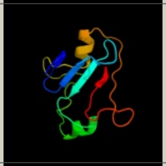
Unique Job ID	fd597bf2b1001f8f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2pofa1	Alignment		100.0	96	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**CDH-like
2	c3n1tE_	Alignment		96.2	12	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**hit-like protein hint; **PDBTitle:** crystal structure of the h101a mutant echint gmp complex
3	c1xquA_	Alignment		95.9	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hit family hydrolase; **PDBTitle:** hit family hydrolase from clostridium thermocellum cth-393
4	d1xqua_	Alignment		95.9	16	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**HIT (HINT, histidine triad) family of protein kinase-interacting proteins
5	c1emsB_	Alignment		95.9	17	**PDB header:**antitumor protein **Chain:** B: **PDB Molecule:**nit-fragile histidine triad fusion protein; **PDBTitle:** crystal structure of the c. elegans nitfhit protein
6	d1emsa1	Alignment		95.8	15	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**HIT (HINT, histidine triad) family of protein kinase-interacting proteins
7	c3anoA_	Alignment		95.7	14	**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
8	d1rzya_	Alignment		95.5	12	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**HIT (HINT, histidine triad) family of protein kinase-interacting proteins
9	c3lb5B_	Alignment		95.4	13	**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
10	d1kpfa_	Alignment		95.4	14	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**HIT (HINT, histidine triad) family of protein kinase-interacting proteins
11	c3oj7A_	Alignment		95.1	24	**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

12	d1fita_	Alignment		94.9	15	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**HIT (HINT, histidine triad) family of protein kinase-interacting proteins
13	c3ksvA_	Alignment		94.3	17	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** hypothetical protein from leishmania major
14	d1vlra1	Alignment		93.8	22	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**mRNA decapping enzyme DcpS C-terminal domain
15	c2eo4A_	Alignment		93.7	17	**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	c3l7xA_	Alignment		93.7	16	**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
17	c3r6fA_	Alignment		93.5	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hit family protein; **PDBTitle:** crystal structure of a zinc-containing hit family protein from2 encephalitozoon cuniculi
18	d1z84a2	Alignment		93.5	11	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**Hexose-1-phosphate uridylyltransferase
19	d3bl9a1	Alignment		93.1	19	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**mRNA decapping enzyme DcpS C-terminal domain
20	c3bl9B_	Alignment		92.7	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**scavenger mrna-decapping enzyme dcps; **PDBTitle:** synthetic gene encoded dcps bound to inhibitor dg157493
21	c3o0mB_	Alignment	not modelled	92.2	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hit family protein; **PDBTitle:** crystal structure of a zn-bound histidine triad family protein from2 mycobacterium smegmatis
22	c1xmlA_	Alignment	not modelled	91.5	20	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**heat shock-like protein 1; **PDBTitle:** structure of human dcps
23	c3imiB_	Alignment	not modelled	90.4	19	**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'
24	d1y23a_	Alignment	not modelled	89.0	17	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**HIT (HINT, histidine triad) family of protein kinase-interacting proteins
25	d1guqa2	Alignment	not modelled	88.4	15	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**Hexose-1-phosphate uridylyltransferase
26	c3p0tB_	Alignment	not modelled	88.1	17	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an hit-like protein from mycobacterium2 paratuberculosis
27	c3i24B_	Alignment	not modelled	85.1	11	**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	d2oika1	Alignment	not modelled	84.6	17	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**HIT (HINT, histidine triad) family of protein kinase-interacting proteins

29	c1zwjA_	Alignment	not modelled	80.5	11	**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
30	c3nrdB_	Alignment	not modelled	74.4	13	**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
31	c3i4sB_	Alignment	not modelled	71.9	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**histidine triad protein; **PDBTitle:** crystal structure of histidine triad protein blr8122 from2 bradyrhizobium japonicum
32	c3oheA_	Alignment	not modelled	68.4	13	**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
33	c1gupC_	Alignment	not modelled	61.7	15	**PDB header:**nucleotidyltransferase **Chain:** C: **PDB Molecule:**galactose-1-phosphate uridylyltransferase; **PDBTitle:** structure of nucleotidyltransferase complexed with udp-2 galactose
34	d1z84a1	Alignment	not modelled	43.8	11	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**Hexose-1-phosphate uridylyltransferase
35	d2soba_	Alignment	not modelled	36.0	19	**Fold:**OB-fold **Superfamily:**Staphylococcal nuclease **Family:**Staphylococcal nuclease
36	c3bdlA_	Alignment	not modelled	35.7	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**staphylococcal nuclease domain-containing **PDBTitle:** crystal structure of a truncated human tudor-sn
37	d1rkna_	Alignment	not modelled	30.0	22	**Fold:**OB-fold **Superfamily:**Staphylococcal nuclease **Family:**Staphylococcal nuclease
38	c2jvaA_	Alignment	not modelled	22.5	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidyl-trna hydrolase domain protein; **PDBTitle:** nmr solution structure of peptidyl-trna hydrolase domain protein from2 pseudomonas syringae pv. tomato. northeast structural genomics3 consortium target psr211
39	c3ngbI_	Alignment	not modelled	21.8	44	**PDB header:**viral protein/immune system **Chain:** I: **PDB Molecule:**envelope glycoprotein gp160; **PDBTitle:** crystal structure of broadly and potently neutralizing antibody vrc012 in complex with hiv-1 gp120
40	d1vdla_	Alignment	not modelled	20.6	18	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
41	d1qpma_	Alignment	not modelled	19.2	13	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Excisionase-like
42	d1tnsa_	Alignment	not modelled	19.0	9	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Excisionase-like
43	d2amxa1	Alignment	not modelled	17.8	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Adenosine/AMP deaminase
44	c3gwhB_	Alignment	not modelled	15.1	18	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional antiterminator (bglg family); **PDBTitle:** crystallographic ab initio protein solution far below atomic2 resolution
45	c3dnlB_	Alignment	not modelled	14.8	29	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**hiv-1 envelope glycoprotein gp120; **PDBTitle:** molecular structure for the hiv-1 gp120 trimer in the b12-2 bound state
46	c1ql1A_	Alignment	not modelled	12.9	32	**PDB header:**virus **Chain:** A: **PDB Molecule:**pf1 bacteriophage coat protein b; **PDBTitle:** inovirus (filamentous bacteriophage) strain pf1 major coat2 protein assembly
47	d1tafa_	Alignment	not modelled	12.8	15	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**TBP-associated factors, TAFs
48	c3jwdA_	Alignment	not modelled	12.3	40	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**hiv-1 gp120 envelope glycoprotein; **PDBTitle:** structure of hiv-1 gp120 with gp41-interactive region: layered2 architecture and basis of conformational mobility
49	d1jz8a1	Alignment	not modelled	12.0	38	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**beta-Galactosidase/glucuronidase domain **Family:**beta-Galactosidase/glucuronidase domain
50	d1snoa_	Alignment	not modelled	11.7	22	**Fold:**OB-fold **Superfamily:**Staphylococcal nuclease **Family:**Staphylococcal nuclease
51	c2i45C_	Alignment	not modelled	11.5	22	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of protein nmb1881 from neisseria meningitidis
52	d1yq2a2	Alignment	not modelled	11.1	15	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**beta-Galactosidase/glucuronidase domain **Family:**beta-Galactosidase/glucuronidase domain
53	d1mr0a_	Alignment	not modelled	11.1	21	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Agouti-related protein **Family:**Agouti-related protein
54	d1k8kd2	Alignment	not modelled	10.2	18	**Fold:**Secretion chaperone-like **Superfamily:**Arp2/3 complex subunits

						Family: Arp2/3 complex subunits
55	c2i34B_	Alignment	not modelled	9.7	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**acid phosphatase; **PDBTitle:** the crystal structure of class c acid phosphatase from bacillus2 anthracis with tungstate bound
56	c3dwlI_	Alignment	not modelled	9.6	18	**PDB header:**structural protein **Chain:** I: **PDB Molecule:**actin-related protein 2/3 complex subunit 2; **PDBTitle:** crystal structure of fission yeast arp2/3 complex lacking the arp22 subunit
57	d2fnaa1	Alignment	not modelled	9.5	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Helicase DNA-binding domain
58	c2k21A_	Alignment	not modelled	9.3	20	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**potassium voltage-gated channel subfamily e **PDBTitle:** nmr structure of human kcne1 in lmpg micelles at ph 6.0 and2 40 degree c
59	d1es6a2	Alignment	not modelled	9.0	43	**Fold:**EV matrix protein **Superfamily:**EV matrix protein **Family:**EV matrix protein
60	c2rrlA_	Alignment	not modelled	8.8	20	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**flagellar hook-length control protein; **PDBTitle:** solution structure of the c-terminal domain of the flik
61	c3u1dA_	Alignment	not modelled	8.3	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** the structure of a protein with a gntr superfamily winged-helix-turn-2 helix domain from halomicrobium mukohataei.
62	c2k2wA_	Alignment	not modelled	8.2	25	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**recombination and dna repair protein; **PDBTitle:** second brct domain of nbs1
63	c3hx6A_	Alignment	not modelled	7.4	28	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**type 4 fimbrial biogenesis protein pily1; **PDBTitle:** crystal structure of pseudomonas aeruginosa pily1 c-terminal2 domain
64	d2glia1	Alignment	not modelled	7.2	30	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
65	d2b1xa1	Alignment	not modelled	7.0	15	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Ring hydroxylating alpha subunit ISP domain
66	d1a4ma_	Alignment	not modelled	6.9	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Adenosine/AMP deaminase
67	d1j26a_	Alignment	not modelled	6.6	16	**Fold:**dsRBD-like **Superfamily:**Peptidyl-tRNA hydrolase domain-like **Family:**Peptidyl-tRNA hydrolase domain
68	d2nxya1	Alignment	not modelled	6.3	29	**Fold:**gp120 core **Superfamily:**gp120 core **Family:**gp120 core
69	c2p9lD_	Alignment	not modelled	6.3	18	**PDB header:**structural protein **Chain:** D: **PDB Molecule:**actin-related protein 2/3 complex subunit 2; **PDBTitle:** crystal structure of bovine arp2/3 complex
70	c2iirJ_	Alignment	not modelled	6.2	26	**PDB header:**transferase **Chain:** J: **PDB Molecule:**acetate kinase; **PDBTitle:** acetate kinase from a hypothermophile thermotoga maritima
71	c3rysA_	Alignment	not modelled	6.2	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adenosine deaminase 1; **PDBTitle:** the crystal structure of adenine deaminase (aaur1117) from2 arthrobacter aurescens
72	d1hqia_	Alignment	not modelled	6.2	11	**Fold:**Monooxygenase (hydroxylase) regulatory protein **Superfamily:**Monooxygenase (hydroxylase) regulatory protein **Family:**Monooxygenase (hydroxylase) regulatory protein
73	d2b7ea1	Alignment	not modelled	6.1	45	**Fold:**Another 3-helical bundle **Superfamily:**FF domain **Family:**FF domain
74	d2ihoa2	Alignment	not modelled	6.1	14	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**MOA C-terminal domain-like
75	d1t0ga_	Alignment	not modelled	6.0	19	**Fold:**Cytochrome b5-like heme/steroid binding domain **Superfamily:**Cytochrome b5-like heme/steroid binding domain **Family:**Steroid-binding domain
76	d1vfla1	Alignment	not modelled	6.0	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Adenosine/AMP deaminase
77	d1iufa1	Alignment	not modelled	6.0	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Centromere-binding
78	d1d2za_	Alignment	not modelled	5.9	30	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**DEATH domain, DD
79	c2l1nA_	Alignment	not modelled	5.9	27	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of the protein yp_399305.1
80	d2bf2a1	Alignment	not modelled	5.6	19	**Fold:**Monooxygenase (hydroxylase) regulatory protein **Superfamily:**Monooxygenase (hydroxylase) regulatory protein **Family:**Monooxygenase (hydroxylase) regulatory protein
						Fold: Arp2/3 complex 21 kDa subunit ARPC3

81	d1k8ke_	Alignment	not modelled	5.6	27	**Superfamily:**Arp2/3 complex 21 kDa subunit ARPC3 **Family:**Arp2/3 complex 21 kDa subunit ARPC3
82	d2bf5a1	Alignment	not modelled	5.5	19	**Fold:**Monooxygenase (hydroxylase) regulatory protein **Superfamily:**Monooxygenase (hydroxylase) regulatory protein **Family:**Monooxygenase (hydroxylase) regulatory protein
83	c2e5nA_	Alignment	not modelled	5.5	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**rna polymerase ii elongation factor ell2; **PDBTitle:** solution structure of the ell_n2 domain of target of rna2 polymerase ii elongation factor ell2
84	c1bmv2_	Alignment	not modelled	5.4	21	**PDB header:**virus/rna **Chain:** 2: **PDB Molecule:**protein (icosahedral virus - b and c domain); **PDBTitle:** protein-rna interactions in an icosahedral virus at 3.02 angstroms resolution
85	c1es6A_	Alignment	not modelled	5.4	43	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**matrix protein vp40; **PDBTitle:** crystal structure of the matrix protein of ebola virus
86	d1nexa2	Alignment	not modelled	5.3	20	**Fold:**POZ domain **Superfamily:**POZ domain **Family:**BTB/POZ domain
87	c2bfuL_	Alignment	not modelled	5.3	18	**PDB header:**virus **Chain:** L: **PDB Molecule:**cowpea mosaic virus, large (l) subunit; **PDBTitle:** x-ray structure of cpmv top component