Phyre2

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Description	P31129
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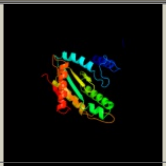
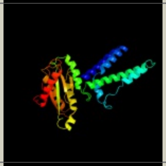
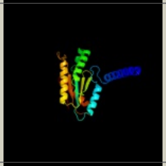
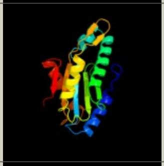
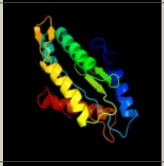
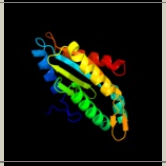
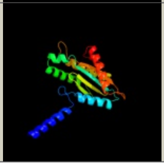
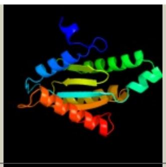
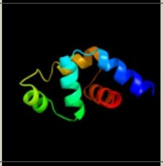
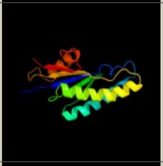
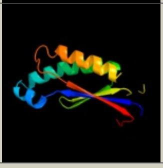
Unique Job ID	d61215a7ed87826a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1w25B_	Alignment		100.0	31	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**stalked-cell differentiation controlling protein; **PDBTitle:** response regulator pled in complex with c-digmp
2	c3ezuA_	Alignment		100.0	20	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ggdef domain protein; **PDBTitle:** crystal structure of multidomain protein of unknown function with2 ggdef-domain (np_951600.1) from geobacter sulfurreducens at 1.95 a3 resolution
3	c3breA_	Alignment		100.0	30	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**probable two-component response regulator; **PDBTitle:** crystal structure of p.aeruginosa pa3702
4	c3iclA_	Alignment		100.0	31	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**eal/ggdef domain protein; **PDBTitle:** x-ray structure of protein (eal/ggdef domain protein) from2 m.capsulatus, northeast structural genomics consortium3 target mcr174c
5	c3ignA_	Alignment		100.0	35	**PDB header:**transferase **Chain:** A: **PDB Molecule:**diguanylate cyclase; **PDBTitle:** crystal structure of the ggdef domain from marinobacter2 aquaeolei diguanylate cyclase complexed with c-di-gmp -3 northeast structural genomics consortium target mqr89a
6	c3i5bA_	Alignment		100.0	32	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**wspr response regulator; **PDBTitle:** crystal structure of the isolated ggdef domain of wpsr from2 pseudomonas aeruginosa
7	c3hvaA_	Alignment		100.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein fimx; **PDBTitle:** crystal structure of fimx ggdef domain from pseudomonas2 aeruginosa
8	c3mtkA_	Alignment		100.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**diguanylate cyclase/phosphodiesterase; **PDBTitle:** x-ray structure of diguanylate cyclase/phosphodiesterase from2 caldicellulosiruptor saccharolyticus, northeast structural genomics3 consortium target clr27c
9	d1w25a3	Alignment		100.0	36	**Fold:**Ferredoxin-like **Superfamily:**Nucleotide cyclase **Family:**GGDEF domain
10	c3i5aA_	Alignment		100.0	30	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator/ggdef domain protein; **PDBTitle:** crystal structure of full-length wpsr from pseudomonas syringae
11	c3i5cA_	Alignment		100.0	30	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**fusion of general control protein gcn4 and wspr response **PDBTitle:** crystal structure of a fusion protein containing the leucine zipper of2 gcn4 and the ggdef domain of wspr from pseudomonas aeruginosa

12	c3qyyB_	Alignment		100.0	32	**PDB header:**signaling protein/inhibitor **Chain:** B: **PDB Molecule:**response regulator; **PDBTitle:** a novel interaction mode between a microbial ggdef domain and the bis-2 (3, 5)-cyclic di-gmp
13	c3pjwA_	Alignment		100.0	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**cyclic dimeric gmp binding protein; **PDBTitle:** structure of pseudomonas fluorescence lapd ggdef-eal dual domain, i23
14	c3hvwA_	Alignment		99.9	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**diguanylate-cyclase (dgc); **PDBTitle:** crystal structure of the ggdef domain of the pa2567 protein2 from pseudomonas aeruginosa, northeast structural genomics3 consortium target par365c
15	c3gfzB_	Alignment		99.5	11	**PDB header:**hydrolase, signaling protein **Chain:** B: **PDB Molecule:**klebsiella pneumoniae blrp1; **PDBTitle:** klebsiella pneumoniae blrp1 ph 6 manganese/cy-digmp complex
16	c3p7nB_	Alignment		98.3	13	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**sensor histidine kinase; **PDBTitle:** crystal structure of light activated transcription factor el222 from2 erythrobacter litoralis
17	c2qv6D_	Alignment		97.0	15	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**gtp cyclohydrolase iii; **PDBTitle:** gtp cyclohydrolase iii from m. jannaschii (mj0145)2 complexed with gtp and metal ions
18	c3mr7B_	Alignment		94.0	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**adenylate/guanylate cyclase/hydrolase, alpha/beta fold **PDBTitle:** crystal structure of adenylate/guanylate cyclase/hydrolase from2 silicibacter pomeroyi
19	d1wc1a_	Alignment		88.8	13	**Fold:**Ferredoxin-like **Superfamily:**Nucleotide cyclase **Family:**Adenylyl and guanylyl cyclase catalytic domain
20	c1cjkA_	Alignment		87.2	9	**PDB header:**lyase/lyase/signaling protein **Chain:** A: **PDB Molecule:**adenylate cyclase, type v; **PDBTitle:** complex of gs-alpha with the catalytic domains of mammalian adenylyl2 cyclase: complex with adenosine 5'-(alpha thio)-triphosphate (rp),3 mg, and mn
21	c3uvjC_	Alignment	not modelled	85.7	12	**PDB header:**lyase **Chain:** C: **PDB Molecule:**guanylate cyclase soluble subunit alpha-3; **PDBTitle:** crystal structure of the catalytic domain of the heterodimeric human2 soluble guanylate cyclase 1.
22	d1fx2a_	Alignment	not modelled	85.1	21	**Fold:**Ferredoxin-like **Superfamily:**Nucleotide cyclase **Family:**Adenylyl and guanylyl cyclase catalytic domain
23	c1ybuA_	Alignment	not modelled	84.7	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lipj; **PDBTitle:** mycobacterium tuberculosis adenylyl cyclase rv1900c chd, in complex2 with a substrate analog.
24	c3et6A_	Alignment	not modelled	83.7	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**soluble guanylyl cyclase beta; **PDBTitle:** the crystal structure of the catalytic domain of a eukaryotic2 guanylate cyclase
25	d1azsa_	Alignment	not modelled	82.9	9	**Fold:**Ferredoxin-like **Superfamily:**Nucleotide cyclase **Family:**Adenylyl and guanylyl cyclase catalytic domain
26	c3r5gB_	Alignment	not modelled	82.5	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**cyab; **PDBTitle:** crystal structure of the adenylyl cyclase cyab from p. aeruginosa
27	c1y10C_	Alignment	not modelled	80.4	10	**PDB header:**lyase **Chain:** C: **PDB Molecule:**hypothetical protein rv1264/mt1302; **PDBTitle:** mycobacterial adenylyl cyclase rv1264, holoenzyme, inhibited state
28	c1wc6B_	Alignment	not modelled	77.0	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**adenylate cyclase; **PDBTitle:** soluble adenylyl cyclase cyac from s. platensis in complex2 with rp-atpalphas in presence of bicarbonate

29	c2aq4A_	Alignment	not modelled	74.4	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna repair protein rev1; **PDBTitle:** ternary complex of the catalytic core of rev1 with dna and dctp.
30	c3gqcB_	Alignment	not modelled	74.3	19	**PDB header:**transferase/dna **Chain:** B: **PDB Molecule:**dna repair protein rev1; **PDBTitle:** structure of human rev1-dna-dntp ternary complex
31	c2wz1B_	Alignment	not modelled	73.7	10	**PDB header:**lyase **Chain:** B: **PDB Molecule:**guanylate cyclase soluble subunit beta-1; **PDBTitle:** structure of the catalytic domain of human soluble2 guanylate cyclase 1 beta 3.
32	d1fx4a_	Alignment	not modelled	67.0	22	**Fold:**Ferredoxin-like **Superfamily:**Nucleotide cyclase **Family:**Adenylyl and guanylyl cyclase catalytic domain
33	c1s97D_	Alignment	not modelled	59.3	22	**PDB header:**transferase/dna **Chain:** D: **PDB Molecule:**dna polymerase iv; **PDBTitle:** dpo4 with gt mismatch
34	d1azsb_	Alignment	not modelled	59.1	9	**Fold:**Ferredoxin-like **Superfamily:**Nucleotide cyclase **Family:**Adenylyl and guanylyl cyclase catalytic domain
35	c2w01C_	Alignment	not modelled	53.9	14	**PDB header:**lyase **Chain:** C: **PDB Molecule:**adenylate cyclase; **PDBTitle:** crystal structure of the guanylyl cyclase cya2
36	c1k1qA_	Alignment	not modelled	52.4	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dbh protein; **PDBTitle:** crystal structure of a dinb family error prone dna2 polymerase from sulfolobus solfataricus
37	c3onqB_	Alignment	not modelled	47.4	7	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**regulator of polyketide synthase expression; **PDBTitle:** crystal structure of regulator of polyketide synthase expression2 bad_0249 from bifidobacterium adolescentis
38	d1im4a_	Alignment	not modelled	44.3	20	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Lesion bypass DNA polymerase (Y-family), catalytic domain
39	c1yk9A_	Alignment	not modelled	38.1	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**adenylate cyclase; **PDBTitle:** crystal structure of a mutant form of the mycobacterial2 adenylyl cyclase rv1625c
40	c3mr2A_	Alignment	not modelled	26.3	18	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**dna polymerase eta; **PDBTitle:** human dna polymerase eta in complex with normal dna and incoming2 nucleotide (nrm)
41	c2oh2B_	Alignment	not modelled	24.5	17	**PDB header:**transferase/dna **Chain:** B: **PDB Molecule:**dna polymerase kappa; **PDBTitle:** ternary complex of human dna polymerase
42	d1jx4a2	Alignment	not modelled	23.1	22	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Lesion bypass DNA polymerase (Y-family), catalytic domain
43	c1xaxA_	Alignment	not modelled	14.5	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical upf0054 protein hi0004; **PDBTitle:** nmr structure of hi0004, a putative essential gene product2 from haemophilus influenzae
44	c3lfhF_	Alignment	not modelled	13.6	13	**PDB header:**transferase **Chain:** F: **PDB Molecule:**phosphotransferase system, mannose/fructose-specific **PDBTitle:** crystal structure of manxa from thermoanaerobacter tengcongensis
45	c2vg2C_	Alignment	not modelled	11.5	19	**PDB header:**transferase **Chain:** C: **PDB Molecule:**undecaprenyl pyrophosphate synthetase; **PDBTitle:** rv2361 with ipp
46	c2r8kB_	Alignment	not modelled	10.3	20	**PDB header:**replication, transferase/dna **Chain:** B: **PDB Molecule:**dna polymerase eta; **PDBTitle:** structure of the eukaryotic dna polymerase eta in complex with 1,2-d(gpg)-cisplatin containing dna
47	c1jihA_	Alignment	not modelled	10.2	20	**PDB header:**translation **Chain:** A: **PDB Molecule:**dna polymerase eta; **PDBTitle:** yeast dna polymerase eta
48	d1zbfa1	Alignment	not modelled	10.0	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Ribonuclease H
49	c3l0oB_	Alignment	not modelled	9.9	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**transcription termination factor rho; **PDBTitle:** structure of rna-free rho transcription termination factor from2 thermotoga maritima
50	d2o5aa1	Alignment	not modelled	9.8	8	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Iojap/YbeB-like
51	d1jiha2	Alignment	not modelled	8.9	20	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Lesion bypass DNA polymerase (Y-family), catalytic domain
52	c2d4vD_	Alignment	not modelled	8.5	7	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**isocitrate dehydrogenase; **PDBTitle:** crystal structure of nad dependent isocitrate dehydrogenase2 from acidithiobacillus thiooxidans
53	d1k1sa2	Alignment	not modelled	8.4	18	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Lesion bypass DNA polymerase (Y-family), catalytic domain
54	c2kq2A_	Alignment	not modelled	8.2	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ribonuclease h-related protein; **PDBTitle:** solution nmr structure of the apo form of a ribonuclease h2 domain of protein dsy1790 from desulfitobacterium3 hafniense,

						northeast structural genomics target dhr1a
55	c2e0cA_	Alignment	not modelled	7.2	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**409aa long hypothetical nadp-dependent isocitrate **PDBTitle:** crystal structure of isocitrate dehydrogenase from sulfolobus tokodaii2 strain7 at 2.0 a resolution
56	c2jroA_	Alignment	not modelled	7.0	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of so0334 from shewanella oneidensis. northeast2 structural genomics target sor75
57	d2ox6a1	Alignment	not modelled	7.0	21	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**YdiL-like
58	c1qgeE_	Alignment	not modelled	6.9	23	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**protein (triacylglycerol hydrolase); **PDBTitle:** new crystal form of pseudomonas glumae (formerly chromobacterium2 viscosum atcc 6918) lipase
59	d1tgoa2	Alignment	not modelled	6.5	14	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**DNA polymerase I
60	c2bblA_	Alignment	not modelled	6.0	67	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**genome linked protein vpg; **PDBTitle:** nmr structures of the peptide linked to the genome (vpg) of2 poliovirus in a stabilizing solvent
61	d1vtmp_	Alignment	not modelled	5.9	20	**Fold:**Four-helical up-and-down bundle **Superfamily:**TMV-like viral coat proteins **Family:**TMV-like viral coat proteins
62	c3kmlB_	Alignment	not modelled	5.8	33	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**coat protein; **PDBTitle:** circular permutant of the tobacco mosaic virus
63	c3blxM_	Alignment	not modelled	5.7	17	**PDB header:**oxidoreductase **Chain:** M: **PDB Molecule:**isocitrate dehydrogenase [nad] subunit 1; **PDBTitle:** yeast isocitrate dehydrogenase (apo form)
64	d2id1a1	Alignment	not modelled	5.7	3	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Iojap/YbeB-like
65	c3upsA_	Alignment	not modelled	5.6	8	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**iojap-like protein; **PDBTitle:** crystal structure of iojap-like protein from zymomonas mobilis
66	d1wjoa_	Alignment	not modelled	5.6	14	**Fold:**CH domain-like **Superfamily:**Calponin-homology domain, CH-domain **Family:**Calponin-homology domain, CH-domain
67	d1pb1a_	Alignment	not modelled	5.5	9	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
68	d1ei7a_	Alignment	not modelled	5.5	31	**Fold:**Four-helical up-and-down bundle **Superfamily:**TMV-like viral coat proteins **Family:**TMV-like viral coat proteins
69	c2kygC_	Alignment	not modelled	5.5	22	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**protein cbfa2t1; **PDBTitle:** structure of the aml1-eto nervy domain - pka(riia) complex and its2 contribution to aml1-eto activity
70	d1wdia_	Alignment	not modelled	5.3	13	**Fold:**QueA-like **Superfamily:**QueA-like **Family:**QueA-like
71	c1x0lB_	Alignment	not modelled	5.2	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**homoisocitrate dehydrogenase; **PDBTitle:** crystal structure of tetrameric homoisocitrate dehydrogenase from an2 extreme thermophile, thermus thermophilus
72	c2zqeA_	Alignment	not modelled	5.2	13	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**muts2 protein; **PDBTitle:** crystal structure of the smr domain of thermus thermophilus muts2