Phyre^2

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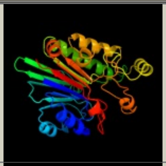
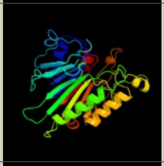
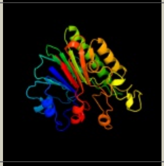
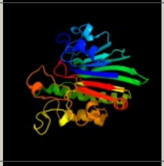
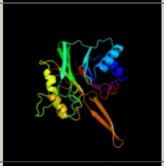
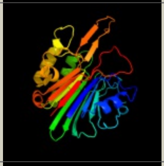
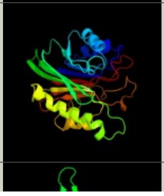
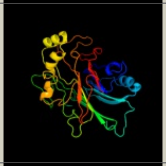
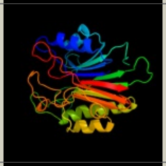
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1akoa_	Alignment		100.0	100	**Fold:**DNase I-like **Superfamily:**DNase I-like **Family:**DNase I-like
2	c2voaB_	Alignment		100.0	31	**PDB header:**lyase **Chain:** B: **PDB Molecule:**exodeoxyribonuclease iii; **PDBTitle:** structure of an ap endonuclease from archaeoglobus fulgidus
3	c2jc4A_	Alignment		100.0	36	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exodeoxyribonuclease iii; **PDBTitle:** 3'-5' exonuclease (nexo) from neisseria meningitidis
4	c2j63B_	Alignment		100.0	23	**PDB header:**lyase **Chain:** B: **PDB Molecule:**ap-endonuclease; **PDBTitle:** crystal structure of ap endonuclease lmap from leishmania2 major
5	c3g0rA_	Alignment		100.0	28	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**exodeoxyribonuclease; **PDBTitle:** complex of mth0212 and an 8bp dsdna with distorted ends
6	c2jc5A_	Alignment		100.0	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exodeoxyribonuclease; **PDBTitle:** apurinic apyrimidinic (ap) endonuclease (nape) from2 neisseria meningitidis
7	c1e9nB_	Alignment		100.0	24	**PDB header:**dna repair **Chain:** B: **PDB Molecule:**dna-(apurinic or apyrimidinic site) lyase; **PDBTitle:** a second divalent metal ion in the active site of a new2 crystal form of human apurinic/apyrimidinic endonuclease,3 ape1, and its implications for the catalytic mechanism
8	c3tebA_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endonuclease/exonuclease/phosphatase; **PDBTitle:** endonuclease/exonuclease/phosphatase family protein from leptotrichia2 buccalis c-1013-b
9	d1vyba_	Alignment		100.0	24	**Fold:**DNase I-like **Superfamily:**DNase I-like **Family:**DNase I-like
10	d1hd7a_	Alignment		100.0	25	**Fold:**DNase I-like **Superfamily:**DNase I-like **Family:**DNase I-like
11	c3g6sA_	Alignment		100.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative endonuclease/exonuclease/phosphatase **PDBTitle:** crystal structure of the2 endonuclease/exonuclease/phosphatase (bvu_0621) from3 bacteroides vulgatus. northeast structural genomics4 consortium target bvr56d
						

12	c3ngoA_	Alignment		100.0	16	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**ccr4-not transcription complex subunit 6-like; **PDBTitle:** crystal structure of the human cnot6l nuclease domain in complex with2 poly(a) dna
13	c3mprB_	Alignment		100.0	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative endonuclease/exonuclease/phosphatase family **PDBTitle:** crystal structure of endonuclease/exonuclease/phosphatase family2 protein from bacteroides thetaiotaomicron, northeast structural3 genomics consortium target btr318a
14	d2imqx1	Alignment		100.0	13	**Fold:**DNase I-like **Superfamily:**DNase I-like **Family:**Inositol polyphosphate 5-phosphatase (IPP5)
15	d1zwxa1	Alignment		100.0	14	**Fold:**DNase I-like **Superfamily:**DNase I-like **Family:**Sphingomyelin phosphodiesterase-like
16	c3i46B_	Alignment		99.9	17	**PDB header:**toxin **Chain:** B: **PDB Molecule:**beta-hemolysin; **PDBTitle:** crystal structure of beta toxin from staphylococcus aureus f277a,2 p278a mutant with bound calcium ions
17	c3mtcA_	Alignment		99.9	14	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**type ii inositol-1,4,5-trisphosphate 5-phosphatase; **PDBTitle:** crystal structure of inpp5b in complex with phosphatidylinositol 4-2 phosphate
18	c3l1wE_	Alignment		99.9	16	**PDB header:**structural genomics, unknown function **Chain:** E: **PDB Molecule:**uncharacterized protein; **PDBTitle:** the crystal structure of a functionally unknown conserved2 protein from enterococcus faecalis v583
19	d2ddra1	Alignment		99.9	20	**Fold:**DNase I-like **Superfamily:**DNase I-like **Family:**Sphingomyelin phosphodiesterase-like
20	c3nr8A_	Alignment		99.9	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphatidylinositol-3,4,5-trisphosphate 5-phosphatase 2; **PDBTitle:** crystal structure of human ship2
21	d1wdua_	Alignment	not modelled	99.9	15	**Fold:**DNase I-like **Superfamily:**DNase I-like **Family:**DNase I-like
22	d1sr4b_	Alignment	not modelled	99.9	16	**Fold:**DNase I-like **Superfamily:**DNase I-like **Family:**DNase I-like
23	d2f1na1	Alignment	not modelled	99.9	20	**Fold:**DNase I-like **Superfamily:**DNase I-like **Family:**DNase I-like
24	c2ei9A_	Alignment	not modelled	99.9	14	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**non-ltr retrotransposon r1bmks orf2 protein; **PDBTitle:** crystal structure of r1bm endonuclease domain
25	d2a40b1	Alignment	not modelled	99.9	16	**Fold:**DNase I-like **Superfamily:**DNase I-like **Family:**DNase I-like
26	c2xswB_	Alignment	not modelled	99.8	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**72 kda inositol polyphosphate 5-phosphatase; **PDBTitle:** crystal structure of human inpp5e
27	d1i9za_	Alignment	not modelled	99.8	16	**Fold:**DNase I-like **Superfamily:**DNase I-like **Family:**Inositol polyphosphate 5-phosphatase (IPP5)
28	d3bula2	Alignment	not modelled	46.3	22	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
29	c2vhiG_	Alignment	not modelled	43.2	8	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**cg3027-pa; **PDBTitle:** crystal structure of a pyrimidine degrading enzyme from2 drosophila melanogaster

30	c2i2xD_	Alignment	not modelled	24.3	22	**PDB header:**transferase **Chain:** D: **PDB Molecule:**methyltransferase 1; **PDBTitle:** crystal structure of methanol:cobalamin methyltransferase complex2 mtabc from methanosarcina barkeri
31	d1xrsb1	Alignment	not modelled	23.4	13	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
32	d1f89a_	Alignment	not modelled	19.9	15	**Fold:**Carbon-nitrogen hydrolase **Superfamily:**Carbon-nitrogen hydrolase **Family:**Nitrilase
33	d1emsa2	Alignment	not modelled	19.5	6	**Fold:**Carbon-nitrogen hydrolase **Superfamily:**Carbon-nitrogen hydrolase **Family:**Nitrilase
34	c1xrsB_	Alignment	not modelled	17.3	13	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**d-lysine 5,6-aminomutase beta subunit; **PDBTitle:** crystal structure of lysine 5,6-aminomutase in complex with plp,2 cobalamin, and 5'-deoxyadenosine
35	c2yxbA_	Alignment	not modelled	16.9	37	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**coenzyme b12-dependent mutase; **PDBTitle:** crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
36	c1y80A_	Alignment	not modelled	16.6	35	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**predicted cobalamin binding protein; **PDBTitle:** structure of a corrinoid (factor iiim)-binding protein from2 moorella thermoacetica
37	d1ccwa_	Alignment	not modelled	16.1	13	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
38	c1bmtB_	Alignment	not modelled	15.7	22	**PDB header:**methyltransferase **Chain:** B: **PDB Molecule:**methionine synthase; **PDBTitle:** how a protein binds b12: a 3.o angstrom x-ray structure of2 the b12-binding domains of methionine synthase
39	c2gm2A_	Alignment	not modelled	14.0	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** nmr structure of xanthomonas campestris xcc1710: northeast2 structural genomics consortium target xcr35
40	c1k98A_	Alignment	not modelled	13.8	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methionine synthase; **PDBTitle:** adomet complex of meth c-terminal fragment
41	c3jvvA_	Alignment	not modelled	12.5	15	**PDB header:**atp binding protein **Chain:** A: **PDB Molecule:**twitching mobility protein; **PDBTitle:** crystal structure of p. aeruginosa pilt with bound amp-pcp
42	d1g6oa_	Alignment	not modelled	11.5	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
43	c2w1vA_	Alignment	not modelled	10.8	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nitrilase homolog 2; **PDBTitle:** crystal structure of mouse nitrilase-2 at 1.4a resolution
44	d1uf5a_	Alignment	not modelled	10.2	14	**Fold:**Carbon-nitrogen hydrolase **Superfamily:**Carbon-nitrogen hydrolase **Family:**Carbamilase
45	c3ezxA_	Alignment	not modelled	9.8	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**monomethylamine corrinoid protein 1; **PDBTitle:** structure of methanosarcina barkeri monomethylamine2 corrinoid protein
46	c3hkxA_	Alignment	not modelled	9.6	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**amidase; **PDBTitle:** crystal structure analysis of an amidase from nesterenkonia sp.
47	c3nrbD_	Alignment	not modelled	9.4	41	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (puru,2 pp_1943) from pseudomonas putida kt2440 at 2.05 a resolution
48	c3n0vD_	Alignment	not modelled	9.3	12	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (pp_0327)2 from pseudomonas putida kt2440 at 2.25 a resolution
49	c2eyuA_	Alignment	not modelled	8.9	16	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**twitching motility protein pilt; **PDBTitle:** the crystal structure of the c-terminal domain of aquifex2 aeolicus pilt
50	c3n05B_	Alignment	not modelled	8.7	6	**PDB header:**ligase **Chain:** B: **PDB Molecule:**nh(3)-dependent nad(+) synthetase; **PDBTitle:** crystal structure of nh3-dependent nad+ synthetase from streptomyces2 avermitilis
51	c2p10D_	Alignment	not modelled	8.5	15	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**mll9387 protein; **PDBTitle:** crystal structure of a putative phosphonopyruvate hydrolase (mll9387)2 from mesorhizobium loti maff303099 at 2.15 a resolution
52	c3o1lB_	Alignment	not modelled	8.1	35	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (pspto_4314)2 from pseudomonas syringae pv. tomato str. dc3000 at 2.20 a resolution
53	c3obiC_	Alignment	not modelled	8.1	18	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (np_949368)2 from rhodopseudomonas palustris cga009 at 1.95 a resolution
54	c2gzaB_	Alignment	not modelled	8.1	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**type iv secretion system protein virb11; **PDBTitle:** crystal structure of the virb11 atpase from the brucella suis type iv2 secretion system in complex with sulphate
						PDB header:hydrolase

55	c3louB_	Alignment	not modelled	7.9	18	**Chain:** B: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of formyltetrahydrofolate deformylase (yp_105254.1)2 from burkholderia mallei atcc 23344 at 1.90 a resolution
56	d1p9ra_	Alignment	not modelled	7.5	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
57	c1emsB_	Alignment	not modelled	7.3	9	**PDB header:**antitumor protein **Chain:** B: **PDB Molecule:**nit-fragile histidine triad fusion protein; **PDBTitle:** crystal structure of the c. elegans nitfhit protein
58	c2dclB_	Alignment	not modelled	7.1	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical upf0166 protein ph1503; **PDBTitle:** structure of ph1503 protein from pyrococcus horikoshii ot3
59	d1j31a_	Alignment	not modelled	6.9	18	**Fold:**Carbon-nitrogen hydrolase **Superfamily:**Carbon-nitrogen hydrolase **Family:**Carbamilase
60	c3p9xB_	Alignment	not modelled	6.9	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphoribosylglycinamide formyltransferase; **PDBTitle:** crystal structure of phosphoribosylglycinamide formyltransferase from2 bacillus halodurans
61	c3q9cF_	Alignment	not modelled	6.8	7	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**acetylpolyamine amidohydrolase; **PDBTitle:** crystal structure of h159a apah complexed with n8-acetylspermidine
62	d2odka1	Alignment	not modelled	6.6	12	**Fold:**YefM-like **Superfamily:**YefM-like **Family:**YefM-like
63	d3bzka5	Alignment	not modelled	6.4	33	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Tex RuvX-like domain-like
64	c3kxyB_	Alignment	not modelled	6.4	13	**PDB header:**chaperone/transcription inhibitor **Chain:** B: **PDB Molecule:**exoenzyme s synthesis protein c; **PDBTitle:** crystal structure of the exsc-exse complex
65	d1fmfa_	Alignment	not modelled	6.3	13	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
66	d2fvta1	Alignment	not modelled	6.3	6	**Fold:**MTH938-like **Superfamily:**MTH938-like **Family:**MTH938-like
67	d2eg6a1	Alignment	not modelled	6.2	50	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Dihydroorotase
68	d1zgha2	Alignment	not modelled	6.0	15	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
69	c2odkD_	Alignment	not modelled	5.9	11	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**hypothetical protein; **PDBTitle:** putative prevent-host-death protein from nitrosomonas europaea
70	d1noya_	Alignment	not modelled	5.9	12	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
71	d1ih7a1	Alignment	not modelled	5.9	6	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
72	d1o51a_	Alignment	not modelled	5.7	8	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**DUF190/COG1993
73	c3jzeC_	Alignment	not modelled	5.6	50	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**dihydroorotase; **PDBTitle:** 1.8 angstrom resolution crystal structure of dihydroorotase (pyrc)2 from salmonella enterica subsp. enterica serovar typhimurium str. lt2
74	c2gszE_	Alignment	not modelled	5.5	21	**PDB header:**protein transport **Chain:** E: **PDB Molecule:**twitching motility protein pilt; **PDBTitle:** structure of a. aeolicus pilt with 6 monomers per2 asymmetric unit
75	c3pnuA_	Alignment	not modelled	5.4	67	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dihydroorotase; **PDBTitle:** 2.4 angstrom crystal structure of dihydroorotase (pyrc) from2 campylobacter jejuni.
76	d1jkxa_	Alignment	not modelled	5.2	29	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
77	d1uf3a_	Alignment	not modelled	5.2	17	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**TT1561-like