






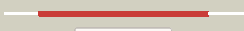














Phyre2

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 Description RVBD0427c_xthA_516020_516895
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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2jc4A_	 Alignment		100.0	38	PDB header: hydrolase Chain: A; PDB Molecule: exodeoxyribonuclease iii; PDBTitle: 3'-5' exonuclease (nexo) from neisseria meningitidis
2	d1akoa_	 Alignment		100.0	28	Fold: DNase I-like Superfamily: DNase I-like Family: DNase I-like
3	c2j63B_	 Alignment		100.0	20	PDB header: lyase Chain: B; PDB Molecule: ap-endonuclease; PDBTitle: crystal structure of ap endonuclease lmap from leishmania major
4	c2voaB_	 Alignment		100.0	36	PDB header: lyase Chain: B; PDB Molecule: exodeoxyribonuclease iii; PDBTitle: structure of an ap endonuclease from archaeoglobus fulgidus
5	c3g0rA_	 Alignment		100.0	23	PDB header: hydrolase/dna Chain: A; PDB Molecule: exodeoxyribonuclease; PDBTitle: complex of mth0212 and an 8bp dsdna with distorted ends
6	c5j8nA_	 Alignment		100.0	23	PDB header: hydrolase Chain: A; PDB Molecule: exodeoxyribonuclease iii; PDBTitle: exonuclease iii homologue mm3148 from methanosarcina mazei
7	c1e9nB_	 Alignment		100.0	28	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 new crystal form2 of human apurinic/apyrimidinic endonuclease, ape1, and its3 implications for the catalytic mechanism
8	c4ruwA_	 Alignment		100.0	21	PDB header: hydrolase Chain: A; PDB Molecule: endonuclease/exonuclease/phosphatase; PDBTitle: the crystal structure of endonuclease/exonuclease/phosphatase from2 beutenbergia cavernae dsm 12333
9	c2jc5A_	 Alignment		100.0	25	PDB header: hydrolase Chain: A; PDB Molecule: exodeoxyribonuclease; PDBTitle: apurinic apyrimidinic (ap) endonuclease (nape) from neisseria2 meningitidis
10	c5ewtA_	 Alignment		100.0	23	PDB header: hydrolase Chain: A; PDB Molecule: exodeoxyribonuclease iii xth; PDBTitle: crystal structure of exoiii endonuclease from sulfobolus islandicus
11	c4f1rA_	 Alignment		100.0	22	PDB header: transcription regulator Chain: A; PDB Molecule: catabolite repression control protein; PDBTitle: structure analysis of the global metabolic regulator crc from2 pseudomonas aeruginos

12	c4f1iA_	Alignment		100.0	16	PDB header: hydrolase Chain: A; PDB Molecule: 5'-tyrosyl-dna phosphodiesterase; PDBTitle: crystal structure of smet tdp2 from caenorhabditis elegans
13	c5cfeA_	Alignment		100.0	28	PDB header: hydrolase Chain: A; PDB Molecule: exodeoxyribonuclease; PDBTitle: bacillus subtilis ap endonuclease exoa
14	d1hd7a_	Alignment		100.0	28	Fold: DNase I-like Superfamily: DNase I-like Family: DNase I-like
15	c4fvaD_	Alignment		100.0	17	PDB header: hydrolase Chain: D; PDB Molecule: 5'-tyrosyl-dna phosphodiesterase; PDBTitle: crystal structure of truncated caenorhabditis elegans tdp2
16	c3tebA_	Alignment		100.0	17	PDB header: hydrolase Chain: A; PDB Molecule: endonuclease/exonuclease/phosphatase; PDBTitle: endonuclease/exonuclease/phosphatase family protein from leptotrichia2 buccalis c-1013-b
17	c4zkfA_	Alignment		100.0	15	PDB header: hydrolase Chain: A; PDB Molecule: 2',5'-phosphodiesterase 12; PDBTitle: crystal structure of human phosphodiesterase 12
18	d1vyba_	Alignment		100.0	21	Fold: DNase I-like Superfamily: DNase I-like Family: DNase I-like
19	c4gz1B_	Alignment		100.0	15	PDB header: hydrolase/dna Chain: B; PDB Molecule: tyrosyl-dna phosphodiesterase 2; PDBTitle: mus musculus tdp2 reaction product (5'-phosphorylated dna)-mg2+2 complex at 1.5 angstroms resolution
20	c4f1hA_	Alignment		100.0	16	PDB header: hydrolase/dna Chain: A; PDB Molecule: tyrosyl-dna phosphodiesterase 2; PDBTitle: crystal structure of tdp2 from danio rerio complexed with a single2 strand dna
21	c3ngoA_	Alignment	not modelled	100.0	15	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
22	d2imqx1	Alignment	not modelled	100.0	13	Fold: DNase I-like Superfamily: DNase I-like Family: Inositol polyphosphate 5-phosphatase (IPP5)
23	c3mprB_	Alignment	not modelled	100.0	18	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
24	c3g6sA_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A; PDB Molecule: putative endonuclease/exonuclease/phosphatase family PDBTitle: crystal structure of the endonuclease/exonuclease/phosphatase2 (bv0_0621) from bacteroides vulgatus. northeast structural genomics3 consortium target bvr56d
25	c6bt2B_	Alignment	not modelled	100.0	16	PDB header: hydrolase, rna binding protein Chain: B; PDB Molecule: nocturnin; PDBTitle: structure of the human nocturnin catalytic domain with bound sulfate2 anion
26	c3l1wE_	Alignment	not modelled	100.0	17	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
						PDB header: toxin

27	c3i46B_	Alignment	not modelled	100.0	14	Chain: B; PDB Molecule: beta-nemolysin; PDBTitle: crystal structure of beta toxin from staphylococcus aureus f277a,2 p278a mutant with bound calcium ions
28	d1wdua_	Alignment	not modelled	100.0	14	Fold: DNase I-like Superfamily: DNase I-like Family: DNase I-like
29	d1zwxal	Alignment	not modelled	100.0	13	Fold: DNase I-like Superfamily: DNase I-like Family: Sphingomyelin phosphodiesterase-like
30	c5uvqA_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A; PDB Molecule: sphingomyelin phosphodiesterase 3,sphingomyelin PDBTitle: crystal structure of the human neutral sphingomyelinase 2 (nsmase2)2 catalytic domain with insertion deleted and calcium bound
31	c3wcaA_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A; PDB Molecule: sphingomyelinase c; PDBTitle: crystal structure of sphingomyelinase c from streptomyces2 griseocarneus
32	d2ddra1	Alignment	not modelled	100.0	16	Fold: DNase I-like Superfamily: DNase I-like Family: Sphingomyelin phosphodiesterase-like
33	c3mtcA_	Alignment	not modelled	100.0	13	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
34	c2ei9A_	Alignment	not modelled	100.0	13	PDB header: gene regulation Chain: A; PDB Molecule: non-ltr retrotransposon r1bmks orf2 protein; PDBTitle: crystal structure of r1bm endonuclease domain
35	c3nr8A_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: A; PDB Molecule: phosphatidylinositol-3,4,5-trisphosphate 5-phosphatase 2; PDBTitle: crystal structure of human ship2
36	c4k6fF_	Alignment	not modelled	99.9	21	PDB header: toxin Chain: F; PDB Molecule: cytolethal distending toxin subunit b homolog; PDBTitle: structure of typhoid toxin
37	d2a40b1	Alignment	not modelled	99.9	16	Fold: DNase I-like Superfamily: DNase I-like Family: DNase I-like
38	d2f1na1	Alignment	not modelled	99.9	23	Fold: DNase I-like Superfamily: DNase I-like Family: DNase I-like
39	d1sr4b_	Alignment	not modelled	99.9	19	Fold: DNase I-like Superfamily: DNase I-like Family: DNase I-like
40	c2xswB_	Alignment	not modelled	99.8	12	PDB header: hydrolase Chain: B; PDB Molecule: 72 kda inositol polyphosphate 5-phosphatase; PDBTitle: crystal structure of human inpp5e
41	c6ibdA_	Alignment	not modelled	99.8	12	PDB header: hydrolase Chain: A; PDB Molecule: phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 1; PDBTitle: the phosphatase and c2 domains of human ship1
42	c4cmnA_	Alignment	not modelled	99.8	13	PDB header: hydrolase Chain: A; PDB Molecule: inositol polyphosphate 5-phosphatase ocr1-1; PDBTitle: crystal structure of ocr1 in complex with a phosphate ion
43	c5okmA_	Alignment	not modelled	99.8	15	PDB header: hydrolase Chain: A; PDB Molecule: phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 2; PDBTitle: crystal structure of human ship2 phosphatase-c2
44	d1i9za_	Alignment	not modelled	99.8	16	Fold: DNase I-like Superfamily: DNase I-like Family: Inositol polyphosphate 5-phosphatase (IPP5)
45	c6a42A_	Alignment	not modelled	99.7	14	PDB header: dna binding protein Chain: A; PDB Molecule: rna-directed dna polymerase homolog (r1),polyubiquitin-c; PDBTitle: r1en(5-223)-ubiquitin fusion
46	d1f89a_	Alignment	not modelled	53.7	19	Fold: Carbon-nitrogen hydrolase Superfamily: Carbon-nitrogen hydrolase Family: Nitrilase
47	d1emsa2	Alignment	not modelled	35.7	10	Fold: Carbon-nitrogen hydrolase Superfamily: Carbon-nitrogen hydrolase Family: Nitrilase
48	c2vhhA_	Alignment	not modelled	34.8	12	PDB header: hydrolase Chain: A; PDB Molecule: cg3027-pa; PDBTitle: crystal structure of a pyrimidine degrading enzyme from2 drosophila melanogaster
49	c6ftqA_	Alignment	not modelled	33.6	16	PDB header: hydrolase Chain: A; PDB Molecule: beta-ureidopropionase; PDBTitle: crystal structure of human beta-ureidopropionase (beta-alanine2 synthase) - mutant t299c
50	c2vhiG_	Alignment	not modelled	31.6	12	PDB header: hydrolase Chain: G; PDB Molecule: cg3027-pa; PDBTitle: crystal structure of a pyrimidine degrading enzyme from2 drosophila melanogaster
51	c4hh3C_	Alignment	not modelled	31.0	11	PDB header: flavoprotein/transcription Chain: C; PDB Molecule: appa protein; PDBTitle: structure of the appa-pps2 core complex from rb. sphaeroides
52	c5zfqA_	Alignment	not modelled	30.5	26	PDB header: transport protein Chain: A; PDB Molecule: twitching motility pilus retraction protein; PDBTitle: crystal structure of pilt-4, a retraction atpase motor of type iv2 pilus , from geobacter sulfurreducens

53	c3hkxA	Alignment	not modelled	29.6	15	PDB header: hydrolase Chain: A: PDB Molecule: amidase; PDBTitle: crystal structure analysis of an amidase from nesterenkonkia sp.
54	d3bula2	Alignment	not modelled	29.2	7	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
55	c5h8IM	Alignment	not modelled	27.6	16	PDB header: hydrolase Chain: M: PDB Molecule: n-carbamoylputrescine amidohydrolase; PDBTitle: crystal structure of medicago truncatula n-carbamoylputrescine2 amidohydrolase (mtcpa) c158s mutant in complex with putrescine
56	d1g6oa	Alignment	not modelled	25.5	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
57	d1uf5a	Alignment	not modelled	24.8	19	Fold: Carbon-nitrogen hydrolase Superfamily: Carbon-nitrogen hydrolase Family: Carbamilase
58	c5ul4A	Alignment	not modelled	21.7	16	PDB header: metal binding protein Chain: A: PDB Molecule: oxsb protein; PDBTitle: structure of cobalamin-dependent s-adenosylmethionine radical enzyme2 oxsb with aqua-cobalamin and s-adenosylmethionine bound
59	c2gzaB	Alignment	not modelled	21.2	9	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
60	c3ilvA	Alignment	not modelled	19.3	19	PDB header: ligase Chain: A: PDB Molecule: glutamine-dependent nad(+) synthetase; PDBTitle: crystal structure of a glutamine-dependent nad(+) synthetase2 from cytophaga hutchinsonii
61	c3jvVA	Alignment	not modelled	19.2	20	PDB header: atp binding protein Chain: A: PDB Molecule: twitching mobility protein; PDBTitle: crystal structure of p. aeruginosa pilt with bound amp-ppc
62	c4kssC	Alignment	not modelled	18.7	23	PDB header: protein transport Chain: C: PDB Molecule: type ii secretion system protein e, hemolysin-coregulated PDBTitle: crystal structure of vibrio cholerae atpase gspse hexamer
63	c2w1vA	Alignment	not modelled	17.6	16	PDB header: hydrolase Chain: A: PDB Molecule: nitrilase homolog 2; PDBTitle: crystal structure of mouse nitrilase-2 at 1.4a resolution
64	c1y80A	Alignment	not modelled	16.5	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: predicted cobalamin binding protein; PDBTitle: structure of a corrinoid (factor iim)-binding protein from moorella2 thermoacetica
65	c3wuyA	Alignment	not modelled	16.5	14	PDB header: hydrolase Chain: A: PDB Molecule: nitrilase; PDBTitle: crystal structure of nit6803
66	c6gebK	Alignment	not modelled	16.1	10	PDB header: hydrolase Chain: K: PDB Molecule: dotb; PDBTitle: x-ray structure of the legionella pneumophila atpase dotb
67	c2i2xD	Alignment	not modelled	15.3	19	PDB header: transferase Chain: D: PDB Molecule: methyltransferase 1; PDBTitle: crystal structure of methanol:cobalamin methyltransferase complex2 mtabc from methanosarcina barkeri
68	d1p9ra	Alignment	not modelled	13.1	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
69	c4phtC	Alignment	not modelled	13.0	23	PDB header: protein transport Chain: C: PDB Molecule: general secretory pathway protein e; PDBTitle: atpase gspe in complex with the cytoplasmic domain of gspl from the2 vibrio vulnificus type ii secretion system
70	c3n05B	Alignment	not modelled	12.9	22	PDB header: ligase Chain: B: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: crystal structure of nh3-dependent nad+ synthetase from streptomyces2 avermitilis
71	d1xrsb1	Alignment	not modelled	12.5	13	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
72	c4hcwC	Alignment	not modelled	12.2	19	PDB header: transferase Chain: C: PDB Molecule: thiaminase-i; PDBTitle: structure of a eukaryotic thiaminase-i
73	c2yxbA	Alignment	not modelled	11.3	26	PDB header: isomerase Chain: A: PDB Molecule: coenzyme b12-dependent mutase; PDBTitle: crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
74	c1bmtB	Alignment	not modelled	10.9	7	PDB header: methyltransferase Chain: B: PDB Molecule: methionine synthase; PDBTitle: how a protein binds b12: a 3.0 angstrom x-ray structure of2 the b12-binding domains of methionine synthase
75	c5it5B	Alignment	not modelled	10.5	21	PDB header: transport protein Chain: B: PDB Molecule: atp binding motif-containing protein pilf; PDBTitle: thermus thermophilus pilb core atpase region
76	c4ryaA	Alignment	not modelled	10.5	24	PDB header: transport protein Chain: A: PDB Molecule: abc transporter substrate binding protein (sorbitol); PDBTitle: crystal structure of abc transporter solute binding protein avi_35672 from agrobacterium vitis s4, target efi-510645, with bound d-mannitol
77	d2yvta1	Alignment	not modelled	10.3	12	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: TT1561-like
78	c5fl3A	Alignment	not modelled	10.2	23	PDB header: transport protein Chain: A: PDB Molecule: pili retraction protein pilt;

						PDBTitle: pilt2 from thermus thermophilus
79	c4hg3C_	Alignment	not modelled	10.2	23	PDB header: hydrolase Chain: C: PDB Molecule: probable hydrolase nit2; PDBTitle: structural insights into yeast nit2: wild-type yeast nit2 in complex2 with alpha-ketoglutarate
80	c3ezxA_	Alignment	not modelled	9.8	4	PDB header: transferase Chain: A: PDB Molecule: monomethylamine corrinoid protein 1; PDBTitle: structure of methanosarcina barkeri monomethylamine2 corrinoid protein
81	c5fyoA_	Alignment	not modelled	9.6	27	PDB header: hydrolase Chain: A: PDB Molecule: phosphoinositol-specific phospholipase c; PDBTitle: calcium-dependent phosphoinositol-specific phospholipase c from a2 gram-negative bacterium, pseudomonas sp, apo form, crystal form 1
82	c2gszE_	Alignment	not modelled	9.0	26	PDB header: protein transport Chain: E: PDB Molecule: twitching motility protein pilt; PDBTitle: structure of a. aeolicus pilt with 6 monomers per asymmetric unit
83	c1xrsB_	Alignment	not modelled	8.6	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
84	c4jgiB_	Alignment	not modelled	8.6	11	PDB header: protein binding Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: 1.5 angstrom crystal structure of a novel cobalamin-binding protein2 from desulfitobacterium hafniense dcb-2
85	c5tshF_	Alignment	not modelled	8.4	19	PDB header: atp-binding protein Chain: F: PDB Molecule: type iv pilus biogenesis atpase pilb; PDBTitle: pilb from geobacter metallireducens bound to amp-pnp
86	c2eyuA_	Alignment	not modelled	8.2	19	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
87	c3nrbD_	Alignment	not modelled	8.0	6	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
88	c6gefB_	Alignment	not modelled	7.8	11	PDB header: hydrolase Chain: B: PDB Molecule: type iv secretion system protein dotb; PDBTitle: x-ray structure of the yersinia pseudotuberculosis atpase dotb
89	c3w7bB_	Alignment	not modelled	7.7	24	PDB header: hydrolase Chain: B: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of formyltetrahydrofolate deformylase from thermus2 thermophilus hb8
90	c3n0vD_	Alignment	not modelled	7.6	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
91	d1ccwa_	Alignment	not modelled	7.2	9	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
92	d3thia_	Alignment	not modelled	7.1	27	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
93	c4ii7D_	Alignment	not modelled	7.0	13	PDB header: hydrolase Chain: D: PDB Molecule: flai atpase; PDBTitle: archaeum assembly atpase flai
94	c3obiC_	Alignment	not modelled	6.7	6	PDB header: hydrolase Chain: C: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (np_949368)2 from rhodospseudomonas palustris cga009 at 1.95 a resolution
95	d1xm7a_	Alignment	not modelled	6.6	6	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Hypothetical protein aq 1666
96	c1k98A_	Alignment	not modelled	6.6	9	PDB header: transferase Chain: A: PDB Molecule: methionine synthase; PDBTitle: adomet complex of meth c-terminal fragment
97	c3o1lB_	Alignment	not modelled	6.5	24	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
98	c5ji5A_	Alignment	not modelled	6.4	17	PDB header: hydrolase Chain: A: PDB Molecule: bupha.10154.a.b1; PDBTitle: crystal structure of a histone deacetylase superfamily protein from2 burkholderia phymatumphymatum
99	c3louB_	Alignment	not modelled	6.3	12	PDB header: hydrolase 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