

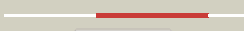


























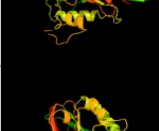



Phyre2

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Description	RVBD0888 (-) _987236_988708
Date	Fri Jul 26 01:50:48 BST 2019
Unique Job ID	049fe7a8a3398a1a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5uvga_	 Alignment		100.0	17	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
2	c4ruwA_	 Alignment		99.9	19	PDB header: hydrolase Chain: A: PDB Molecule: endonuclease/exonuclease/phosphatase; PDBTitle: the crystal structure of endonuclease/exonuclease/phosphatase from2 beutenbergia cavernae dsm 12333
3	c4f1iA_	 Alignment		99.9	19	PDB header: hydrolase Chain: A: PDB Molecule: 5'-tyrosyl-dna phosphodiesterase; PDBTitle: crystal structure of semet tdp2 from caenorhabditis elegans
4	d1zwx1	 Alignment		99.9	16	Fold: DNase I-like Superfamily: DNase I-like Family: Sphingomyelin phosphodiesterase-like
5	c3wca_	 Alignment		99.9	20	PDB header: hydrolase Chain: A: PDB Molecule: sphingomyelinase c; PDBTitle: crystal structure of sphingomyelinase c from streptomyces2 griseocarneus
6	c4f1hA_	 Alignment		99.9	19	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
7	d2imqx1	 Alignment		99.9	17	Fold: DNase I-like Superfamily: DNase I-like Family: Inositol polyphosphate 5-phosphatase (IPP5)
8	c3tebA_	 Alignment		99.9	18	PDB header: hydrolase Chain: A: PDB Molecule: endonuclease/exonuclease/phosphatase; PDBTitle: endonuclease/exonuclease/phosphatase family protein from leptotrichia2 buccalis c-1013-b
9	d2ddra1	 Alignment		99.9	16	Fold: DNase I-like Superfamily: DNase I-like Family: Sphingomyelin phosphodiesterase-like
10	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
11	c3mprB_	 Alignment		99.9	14	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

12	c3mtcA	Alignment		99.9	19	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
13	c4fvaD	Alignment		99.9	18	PDB header: hydrolase Chain: D: PDB Molecule: 5'-tyrosyl-dna phosphodiesterase; PDBTitle: crystal structure of truncated caenorhabditis elegans tdp2
14	c4gz1B	Alignment		99.9	18	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
15	c6bt2B	Alignment		99.9	17	PDB header: hydrolase, rna binding protein Chain: B: PDB Molecule: nocturnin; PDBTitle: structure of the human nocturnin catalytic domain with bound sulfate2 anion
16	c3g6sA	Alignment		99.9	16	PDB header: hydrolase Chain: A: PDB Molecule: putative endonuclease/exonuclease/phosphatase family PDBTitle: crystal structure of the endonuclease/exonuclease/phosphatase2 (bvu_0621) from bacteroides vulgatus. northeast structural genomics3 consortium target bvr56d
17	c3nr8A	Alignment		99.9	17	PDB header: hydrolase Chain: A: PDB Molecule: phosphatidylinositol-3,4,5-trisphosphate 5-phosphatase 2; PDBTitle: crystal structure of human ship2
18	c3ngoA	Alignment		99.9	13	PDB header: hydrolase/dna Chain: A: PDB Molecule: ccc4-not transcription complex subunit 6-like; PDBTitle: crystal structure of the human cnot6l nuclease domain in complex with2 poly(a) dna
19	c3j1wE	Alignment		99.9	15	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
20	d1sr4b	Alignment		99.9	15	Fold: DNase I-like Superfamily: DNase I-like Family: DNase I-like
21	c2j63B	Alignment	not modelled	99.9	17	PDB header: lyase Chain: B: PDB Molecule: ap-endonuclease; PDBTitle: crystal structure of ap endonuclease lmap from leishmania major
22	c4zkfA	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: A: PDB Molecule: 2',5'-phosphodiesterase 12; PDBTitle: crystal structure of human phosphodiesterase 12
23	d2f1na1	Alignment	not modelled	99.9	17	Fold: DNase I-like Superfamily: DNase I-like Family: DNase I-like
24	d2a40b1	Alignment	not modelled	99.9	16	Fold: DNase I-like Superfamily: DNase I-like Family: DNase I-like
25	c5j8nA	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: A: PDB Molecule: exodeoxyribonuclease iii; PDBTitle: exonuclease iii homologue mm3148 from methanosarcina mazei
26	c4k6fF	Alignment	not modelled	99.8	18	PDB header: toxin Chain: F: PDB Molecule: cytolethal distending toxin subunit b homolog; PDBTitle: structure of typhoid toxin
27	c2jc5A	Alignment	not modelled	99.8	19	PDB header: hydrolase Chain: A: PDB Molecule: exodeoxyribonuclease; PDBTitle: apurinic apyrimidinic (ap) endonuclease (nape) from neisseria2 meningitidis
28	d1akoa	Alignment	not modelled	99.8	18	Fold: DNase I-like Superfamily: DNase I-like Family: DNase I-like
29	c5ewtA	Alignment	not modelled	99.8	17	PDB header: hydrolase Chain: A: PDB Molecule: exodeoxyribonuclease iii xth; PDBTitle: crystal structure of exoiii endonuclease from sulfobolus

						islandicus
30	c1e9nB	Alignment	not modelled	99.8	15	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
31	c2jc4A	Alignment	not modelled	99.8	18	PDB header: hydrolase Chain: A: PDB Molecule: exodeoxyribonuclease iii; PDBTitle: 3'-5' exonuclease (nexo) from neisseria meningitidis
32	c4f1rA	Alignment	not modelled	99.8	15	PDB header: transcription regulator Chain: A: PDB Molecule: catabolite repression control protein; PDBTitle: structure analysis of the global metabolic regulator crc from2 pseudomonas aeruginos
33	c2xswB	Alignment	not modelled	99.8	18	PDB header: hydrolase Chain: B: PDB Molecule: 72 kda inositol polyphosphate 5-phosphatase; PDBTitle: crystal structure of human inpp5e
34	c2voaB	Alignment	not modelled	99.8	15	PDB header: lyase Chain: B: PDB Molecule: exodeoxyribonuclease iii; PDBTitle: structure of an ap endonuclease from archaeoglobus fulgidus
35	d1vyba	Alignment	not modelled	99.7	18	Fold: DNase I-like Superfamily: DNase I-like Family: DNase I-like
36	c3g0rA	Alignment	not modelled	99.7	16	PDB header: hydrolase/dna Chain: A: PDB Molecule: exodeoxyribonuclease; PDBTitle: complex of mth0212 and an 8bp dsdna with distorted ends
37	c5cfeA	Alignment	not modelled	99.7	15	PDB header: hydrolase Chain: A: PDB Molecule: exodeoxyribonuclease; PDBTitle: bacillus subtilis ap endonuclease exoa
38	d1hd7a	Alignment	not modelled	99.7	16	Fold: DNase I-like Superfamily: DNase I-like Family: DNase I-like
39	c4cmnA	Alignment	not modelled	99.6	17	PDB header: hydrolase Chain: A: PDB Molecule: inositol polyphosphate 5-phosphatase ocr1; PDBTitle: crystal structure of ocr1 in complex with a phosphate ion
40	d1wdua	Alignment	not modelled	99.5	12	Fold: DNase I-like Superfamily: DNase I-like Family: DNase I-like
41	c2ei9A	Alignment	not modelled	99.5	17	PDB header: gene regulation Chain: A: PDB Molecule: non-itr retrotransposon r1bmks orf2 protein; PDBTitle: crystal structure of r1bm endonuclease domain
42	c6ibdA	Alignment	not modelled	99.5	21	PDB header: hydrolase Chain: A: PDB Molecule: phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 1; PDBTitle: the phosphatase and c2 domains of human ship1
43	d1i9za	Alignment	not modelled	99.5	18	Fold: DNase I-like Superfamily: DNase I-like Family: Inositol polyphosphate 5-phosphatase (IPP5)
44	c5okmA	Alignment	not modelled	99.5	18	PDB header: hydrolase Chain: A: PDB Molecule: phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 2; PDBTitle: crystal structure of human ship2 phosphatase-c2
45	c6a42A	Alignment	not modelled	98.5	19	PDB header: dna binding protein Chain: A: PDB Molecule: rna-directed dna polymerase homolog (r1),polyubiquitin-c; PDBTitle: r1en(5-223)-ubiquitin fusion
46	c2yhgA	Alignment	not modelled	82.5	19	PDB header: hydrolase Chain: A: PDB Molecule: cellulose-binding protein; PDBTitle: ab initio phasing of a nucleoside hydrolase-related hypothetical2 protein from saccharophagus degradans that is associated with3 carbohydrate metabolism
47	c6ihbR	Alignment	not modelled	73.9	21	PDB header: virus Chain: R: PDB Molecule: dyslexia-associated protein kiaa0319-like protein; PDBTitle: adeno-associated virus 2 in complex with aavr
48	c2q8uA	Alignment	not modelled	70.4	15	PDB header: hydrolase Chain: A: PDB Molecule: exonuclease, putative; PDBTitle: crystal structure of mre11 from thermotoga maritima msb8 (tm1635) at2 2.20 a resolution
49	c3av0A	Alignment	not modelled	64.7	14	PDB header: recombination Chain: A: PDB Molecule: dna double-strand break repair protein mre11; PDBTitle: crystal structure of mre11-rad50 bound to atp s
50	c5iryB	Alignment	not modelled	62.6	14	PDB header: cell adhesion Chain: B: PDB Molecule: desmocollin-1; PDBTitle: crystal structure of human desmocollin-1 ectodomain
51	c3ib7A	Alignment	not modelled	62.2	18	PDB header: hydrolase Chain: A: PDB Molecule: icc protein; PDBTitle: crystal structure of full length rv0805
52	c3mbfA	Alignment	not modelled	57.2	42	PDB header: lyase Chain: A: PDB Molecule: fructose-bisphosphate aldolase; PDBTitle: crystal structure of fructose bisphosphate aldolase from2 encephalitozoon cuniculi, bound to fructose 1,6-bisphosphate
53	d2hy1a1	Alignment	not modelled	55.2	18	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: GpdQ-like
54	c2hy1A	Alignment	not modelled	55.2	18	PDB header: hydrolase Chain: A: PDB Molecule: rv0805; PDBTitle: crystal structure of rv0805
55	c5wlyA	Alignment	not modelled	54.0	23	PDB header: hydrolase Chain: A: PDB Molecule: udp-2,3-diacetylglucosamine hydrolase; PDBTitle: e. coli lpxh- 8 mutations

56	c5erdB_	Alignment	not modelled	52.4	16	PDB header: cell adhesion Chain: B: PDB Molecule: desmoglein-2; PDBTitle: crystal structure of human desmoglein-2 ectodomain
57	d1ozha1	Alignment	not modelled	52.2	21	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
58	d1jifa_	Alignment	not modelled	47.3	26	Fold: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Superfamily: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Family: Antibiotic resistance proteins
59	c5d8mA_	Alignment	not modelled	45.0	13	PDB header: hydrolase Chain: A: PDB Molecule: metagenomic carboxyl esterase mgs0156; PDBTitle: crystal structure of the metagenomic carboxyl esterase mgs0156
60	c5k8kA_	Alignment	not modelled	44.9	16	PDB header: hydrolase Chain: A: PDB Molecule: udp-2,3-diacetylglucosamine hydrolase; PDBTitle: structure of the haemophilus influenzae lpxh-lipid x complex
61	c6nvoA_	Alignment	not modelled	44.7	22	PDB header: dna binding protein Chain: A: PDB Molecule: nuclease mpe; PDBTitle: crystal structure of pseudomonas putida nuclease mpe
62	c6dnsA_	Alignment	not modelled	44.3	27	PDB header: hydrolase Chain: A: PDB Molecule: alpha-1,4-endofucoidanase; PDBTitle: endo-fucoidan hydrolase mffcna9 from glycoside hydrolase family 107
63	c4n04B_	Alignment	not modelled	43.0	33	PDB header: oxidoreductase Chain: B: PDB Molecule: glyoxalase/bleomycin resistance protein/dioxygenase; PDBTitle: the crystal structure of glyoxalase / bleomycin resistance protein2 from catenulispora acidiphila dsm 44928
64	c3auzA_	Alignment	not modelled	40.4	14	PDB header: recombination Chain: A: PDB Molecule: dna double-strand break repair protein mre11; PDBTitle: crystal structure of mre11 with manganese
65	c3qfnA_	Alignment	not modelled	40.2	17	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of streptococcal asymmetric ap4a hydrolase and2 phosphodiesterase spr1479/saph in complex with inorganic phosphate
66	c6a4xA_	Alignment	not modelled	39.1	33	PDB header: biosynthetic protein Chain: A: PDB Molecule: bleomycin resistance protein; PDBTitle: oxidase chap-h2
67	c4tvvA_	Alignment	not modelled	38.8	17	PDB header: hydrolase Chain: A: PDB Molecule: tyrosine phosphatase ii superfamily protein; PDBTitle: crystal structure of lppa from legionella pneumophila
68	c4fcxB_	Alignment	not modelled	38.8	12	PDB header: hydrolase Chain: B: PDB Molecule: dna repair protein rad32; PDBTitle: s.pombe mre11 apoenzym
69	c3cf4G_	Alignment	not modelled	38.5	17	PDB header: oxidoreductase Chain: G: PDB Molecule: acetyl-coa decarboxylase/synthase epsilon subunit; PDBTitle: structure of the codh component of the m. barkeri acids complex
70	c3kx6C_	Alignment	not modelled	37.6	47	PDB header: lyase Chain: C: PDB Molecule: fructose-bisphosphate aldolase; PDBTitle: crystal structure of fructose-1,6-bisphosphate aldolase from babesia2 bovis at 2.1a resolution
71	d1twua_	Alignment	not modelled	37.0	47	Fold: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Superfamily: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Family: Hypothetical protein YycE
72	d1zpdA1	Alignment	not modelled	36.6	16	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
73	c1l3wA_	Alignment	not modelled	35.6	15	PDB header: cell adhesion, metal binding protein Chain: A: PDB Molecule: ep-cadherin; PDBTitle: c-cadherin ectodomain
74	d2ji7a1	Alignment	not modelled	35.1	26	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
75	c4m02A_	Alignment	not modelled	35.0	20	PDB header: calcium binding protein Chain: A: PDB Molecule: serine-rich adhesin for platelets; PDBTitle: middle fragment(residues 494-663) of the binding region of srap
76	d2yvta1	Alignment	not modelled	32.7	9	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: TT1561-like
77	d1ii7a_	Alignment	not modelled	32.7	10	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: DNA double-strand break repair nuclease
78	c6a4zA_	Alignment	not modelled	30.9	31	PDB header: biosynthetic protein Chain: A: PDB Molecule: chap protein; PDBTitle: oxidase chap
79	c5kinC_	Alignment	not modelled	30.2	5	PDB header: lyase Chain: C: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha beta complex from2 streptococcus pneumoniae
80	c3ff7B_	Alignment	not modelled	29.6	13	PDB header: cell adhesion/immune system Chain: B: PDB Molecule: epithelial cadherin; PDBTitle: structure of nk cell receptor klrp1 bound to e-cadherin
						Fold: DHS-like NAD/FAD-binding domain

81	d1pvdal	Alignment	not modelled	28.9	8	Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
82	c4ltyD	Alignment	not modelled	28.4	18	PDB header: hydrolase Chain: D: PDB Molecule: exonuclease subunit sbcd; PDBTitle: crystal structure of e.coli sbcd at 1.8 a resolution
83	c3t1iC	Alignment	not modelled	27.8	15	PDB header: hydrolase Chain: C: PDB Molecule: double-strand break repair protein mre11a; PDBTitle: crystal structure of human mre11: understanding tumorigenic mutations
84	c4k6iC	Alignment	not modelled	27.5	14	PDB header: toxin Chain: C: PDB Molecule: putative pertussis-like toxin subunit; PDBTitle: structure of typhoid toxin
85	c2yopB	Alignment	not modelled	25.8	12	PDB header: apoptosis Chain: B: PDB Molecule: protein fam3b; PDBTitle: long wavelength s-sad structure of fam3b pander
86	d2ihtal	Alignment	not modelled	25.4	23	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
87	c5svan	Alignment	not modelled	25.3	32	PDB header: transcription, transferase/dna Chain: N: PDB Molecule: mediator of rna polymerase ii transcription subunit 8; PDBTitle: mediator-rna polymerase ii pre-initiation complex
88	d1ovma1	Alignment	not modelled	24.8	11	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
89	c4ykeA	Alignment	not modelled	23.9	10	PDB header: hydrolase Chain: A: PDB Molecule: mre11; PDBTitle: crystal structure of eukaryotic mre11 catalytic domain from chaetomium2 thermophilum
90	d1a5ca	Alignment	not modelled	23.4	75	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
91	c4fbkB	Alignment	not modelled	23.0	12	PDB header: hydrolase, protein binding Chain: B: PDB Molecule: dna repair and telomere maintenance protein nbs1,dna repair PDBTitle: crystal structure of a covalently fused nbs1-mre11 complex with one2 manganese ion per active site
92	c2zw7A	Alignment	not modelled	22.5	28	PDB header: transferase Chain: A: PDB Molecule: bleomycin acetyltransferase; PDBTitle: crystal structure of bleomycin n-acetyltransferase complexed2 with bleomycin a2 and coenzyme a
93	d1zaia1	Alignment	not modelled	22.5	75	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
94	d1qo5b	Alignment	not modelled	22.4	88	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
95	d1fdja	Alignment	not modelled	22.4	88	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
96	d2qapa1	Alignment	not modelled	21.8	75	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
97	c2qapC	Alignment	not modelled	21.7	75	PDB header: lyase Chain: C: PDB Molecule: fructose-1,6-bisphosphate aldolase; PDBTitle: fructose-1,6-bisphosphate aldolase from leishmania mexicana
98	d1fbaa	Alignment	not modelled	21.4	50	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
99	c3qg5D	Alignment	not modelled	21.2	16	PDB header: hydrolase Chain: D: PDB Molecule: mre11; PDBTitle: the mre11:rad50 complex forms an atp dependent molecular clamp in dna2 double-strand break repair
100	c5b4bB	Alignment	not modelled	21.1	16	PDB header: hydrolase Chain: B: PDB Molecule: udp-2,3-diacetylglucosamine hydrolase; PDBTitle: crystal structure of lpxh with lipid x in spacegroup c2
101	d1t9ba1	Alignment	not modelled	20.4	21	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
102	d3d03a1	Alignment	not modelled	20.2	19	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: GpdQ-like
103	c2iqtA	Alignment	not modelled	20.1	75	PDB header: lyase Chain: A: PDB Molecule: fructose-bisphosphate aldolase class 1; PDBTitle: crystal structure of fructose-bisphosphate aldolase, class i from2 porphyromonas gingivalis