

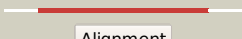





















Phyre2

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Description	RVBD3031 (-) _3389933_3391513
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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3n92A_	 Alignment		100.0	31	PDB header: transferase Chain: A; PDB Molecule: alpha-amylase, gh57 family; PDBTitle: crystal structure of tk1436, a gh57 branching enzyme from 2 hyperthermophilic archaeon thermococcus kodakaraensis, in complex3 with glucose
2	c5wu7A_	 Alignment		100.0	31	PDB header: hydrolase Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of gh57-type branching enzyme from hyperthermophilic2 archaeon pyrococcus horikoshii
3	c2b5dX_	 Alignment		100.0	26	PDB header: hydrolase Chain: X; PDB Molecule: alpha-amylase; PDBTitle: crystal structure of the novel alpha-amylase amyc from thermotoga2 maritima
4	c1ufaA_	 Alignment		100.0	33	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: tt1467 protein; PDBTitle: crystal structure of tt1467 from thermus thermophilus hb8
5	d2b5dx2	 Alignment		100.0	26	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: AmyC N-terminal domain-like
6	d1ufaa2	 Alignment		100.0	34	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: AmyC N-terminal domain-like
7	c1k1yA_	 Alignment		100.0	22	PDB header: transferase Chain: A; PDB Molecule: 4-alpha-glucanotransferase; PDBTitle: crystal structure of thermococcus litoralis 4-alpha-glucanotransferase2 complexed with acarbose
8	d1k1xa3	 Alignment		100.0	22	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: 4-alpha-glucanotransferase, N-terminal domain
9	d2b5dx1	 Alignment		100.0	23	Fold: immunoglobulin/albumin-binding domain-like Superfamily: Families 57/38 glycoside transferase middle domain Family: AmyC C-terminal domain-like
10	d1ufaa1	 Alignment		100.0	28	Fold: immunoglobulin/albumin-binding domain-like Superfamily: Families 57/38 glycoside transferase middle domain Family: AmyC C-terminal domain-like
11	c1htyA_	 Alignment		99.9	16	PDB header: hydrolase Chain: A; PDB Molecule: alpha-mannosidase ii; PDBTitle: golgi alpha-mannosidase ii

12	c2ow7A_	Alignment		99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: alpha-mannosidase 2; PDBTitle: golgi alpha-mannosidase ii complex with (1r,6s,7r,8s)-1-2 thioniabicyclo[4.3.0]nonan-7,8-diol chloride
13	c2wyhA_	Alignment		99.9	13	PDB header: hydrolase Chain: A: PDB Molecule: alpha-mannosidase; PDBTitle: structure of the streptococcus pyogenes family gh38 alpha-2 mannosidase
14	c6b9pA_	Alignment		99.9	14	PDB header: hydrolase Chain: A: PDB Molecule: alpha-mannosidase from canavalia ensiformis (jack bean); PDBTitle: structure of gh 38 jack bean alpha-mannosidase in complex with a 36-2 valent iminosugar cluster inhibitor
15	c5jm0A_	Alignment		99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: alpha-mannosidase,alpha-mannosidase,alpha-mannosidase; PDBTitle: structure of the s. cerevisiae alpha-mannosidase 1
16	c3lvtA_	Alignment		99.8	15	PDB header: hydrolase Chain: A: PDB Molecule: glycosyl hydrolase, family 38; PDBTitle: the crystal structure of a protein in the glycosyl hydrolase family 382 from enterococcus faecalis to 2.55a
17	d3bvua3	Alignment		99.7	15	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: alpha-mannosidase
18	c1o7dA_	Alignment		99.4	20	PDB header: hydrolase Chain: A: PDB Molecule: lysosomal alpha-mannosidase; PDBTitle: the structure of the bovine lysosomal a-mannosidase suggests a novel2 mechanism for low ph activation
19	c4cmrB_	Alignment		99.2	22	PDB header: hydrolase Chain: B: PDB Molecule: glycosyl hydrolase/deacetylase family protein; PDBTitle: the crystal structure of novel exo-type maltose-forming2 amylase(py04_0872) from pyrococcus sp. st04
20	c3qbuD_	Alignment		99.0	13	PDB header: hydrolase Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of putative peptidoglycan deactylase (hp0310) from2 helicobacter pylori
21	c3rxzA_	Alignment	not modelled	98.9	18	PDB header: hydrolase Chain: A: PDB Molecule: polysaccharide deacetylase; PDBTitle: crystal structure of putative polysaccharide deacetylase from2 mycobacterium smegmatis
22	c3s6oD_	Alignment	not modelled	98.6	16	PDB header: hydrolase Chain: D: PDB Molecule: polysaccharide deacetylase family protein; PDBTitle: crystal structure of a polysaccharide deacetylase family protein from2 burkholderia pseudomallei
23	d1z7aa1	Alignment	not modelled	98.5	12	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: PA1517-like
24	c1w17A_	Alignment	not modelled	98.4	12	PDB header: hydrolase Chain: A: PDB Molecule: probable polysaccharide deacetylase pdaa; PDBTitle: structure of bacillus subtilis pdaa, a family 4 carbohydrate esterase.
25	c2y8uA_	Alignment	not modelled	98.4	20	PDB header: hydrolase Chain: A: PDB Molecule: chitin deacetylase; PDBTitle: a. nidulans chitin deacetylase
26	c4m1bA_	Alignment	not modelled	98.3	20	PDB header: hydrolase Chain: A: PDB Molecule: polysaccharide deacetylase; PDBTitle: structural determination of ba0150, a polysaccharide deacetylase from2 bacillus anthracis
27	d2j13a1	Alignment	not modelled	98.3	16	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: NodB-like polysaccharide deacetylase
28	c2vyoA_	Alignment	not modelled	98.2	14	PDB header: hydrolase Chain: A: PDB Molecule: polysaccharide deacetylase domain-containing protein PDBTitle: chitin deacetylase family member from encephalitozoon

						cuniculi
29	d2c1ia1	Alignment	not modelled	98.2	14	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: NodB-like polysaccharide deacetylase
30	d2iw0a1	Alignment	not modelled	98.2	17	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: NodB-like polysaccharide deacetylase
31	d1ny1a_	Alignment	not modelled	98.2	12	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: NodB-like polysaccharide deacetylase
32	c4l1gB_	Alignment	not modelled	98.2	14	PDB header: hydrolase Chain: B: PDB Molecule: peptidoglycan n-acetylglucosamine deacetylase; PDBTitle: crystal structure of the bc1960 peptidoglycan n-acetylglucosamine2 deacetylase from bacillus cereus
33	c2iw0A_	Alignment	not modelled	98.1	18	PDB header: hydrolase Chain: A: PDB Molecule: chitin deacetylase; PDBTitle: structure of the chitin deacetylase from the fungal2 pathogen colletotrichum lindemuthianum
34	c2c1ia_	Alignment	not modelled	98.0	17	PDB header: hydrolase Chain: A: PDB Molecule: peptidoglycan glcnac deacetylase; PDBTitle: structure of streptococcus pneumoniae peptidoglycan deacetylase2 (sppgda) d 275 n mutant.
35	c4wcjA_	Alignment	not modelled	97.9	14	PDB header: hydrolase Chain: A: PDB Molecule: polysaccharide deacetylase; PDBTitle: structure of icab from ammonifex degensii
36	c5lqcA_	Alignment	not modelled	97.9	18	PDB header: hydrolase Chain: A: PDB Molecule: arce4a; PDBTitle: t48 deacetylase with substrate
37	c6dq3B_	Alignment	not modelled	97.9	12	PDB header: hydrolase Chain: B: PDB Molecule: polysaccharide deacetylase; PDBTitle: streptococcus pyogenes deacetylase pdi in complex with acetate
38	d2cc0a1	Alignment	not modelled	97.8	16	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: NodB-like polysaccharide deacetylase
39	c4f9dA_	Alignment	not modelled	97.8	16	PDB header: hydrolase Chain: A: PDB Molecule: poly-beta-1,6-n-acetyl-d-glucosamine n-deacetylase; PDBTitle: structure of escherichia coli pgab 42-655 in complex with nickel
40	d3bvua1	Alignment	not modelled	97.7	13	Fold: immunoglobulin/albumin-binding domain-like Superfamily: Families 57/38 glycoside transferase middle domain Family: alpha-mannosidase, domain 2
41	d2c71a1	Alignment	not modelled	97.7	18	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: NodB-like polysaccharide deacetylase
42	c5bu6B_	Alignment	not modelled	97.6	20	PDB header: hydrolase Chain: B: PDB Molecule: bpsb (pgab), poly-beta-1,6-n-acetyl-d-glucosamine n- PDBTitle: structure of bpsb deacetylase domain from bordetella bronchiseptica
43	c6go1A_	Alignment	not modelled	97.6	9	PDB header: hydrolase Chain: A: PDB Molecule: polysaccharide deacetylase-like protein; PDBTitle: crystal structure of a bacillus anthracis peptidoglycan deacetylase
44	c4u10B_	Alignment	not modelled	97.5	15	PDB header: hydrolase Chain: B: PDB Molecule: poly-beta-1,6-n-acetyl-d-glucosamine n-deacetylase; PDBTitle: probing the structure and mechanism of de-n-acetylase from2 aggregatibacter actinomycetemcomitans
45	c5ncdA_	Alignment	not modelled	97.3	13	PDB header: hydrolase Chain: A: PDB Molecule: peptidoglycan n-acetylglucosamine deacetylase; PDBTitle: crystal structure of the polysaccharide deacetylase bc1974 from2 bacillus cereus in complex with (2s)-2-amino-5-3 (diaminomethylideneamino)-n-hydroxypentanamide
46	c4hd5A_	Alignment	not modelled	97.2	10	PDB header: hydrolase Chain: A: PDB Molecule: polysaccharide deacetylase; PDBTitle: crystal structure of bc0361, a polysaccharide deacetylase from2 bacillus cereus
47	c5znsA_	Alignment	not modelled	96.6	14	PDB header: hydrolase Chain: A: PDB Molecule: chitin deacetylase; PDBTitle: insect chitin deacetylase
48	c5z34A_	Alignment	not modelled	96.6	13	PDB header: hydrolase Chain: A: PDB Molecule: chitin deacetylase; PDBTitle: the structure of a chitin deacetylase from bombyx mori provide the2 first insight into insect chitin deacetylation mechanism
49	c5jp6A_	Alignment	not modelled	95.0	12	PDB header: hydrolase Chain: A: PDB Molecule: putative polysaccharide deacetylase; PDBTitle: bdellovibrio bacteriovorus peptidoglycan deacetylase bd3279
50	d1k1xa1	Alignment	not modelled	94.6	15	Fold: immunoglobulin/albumin-binding domain-like Superfamily: Families 57/38 glycoside transferase middle domain Family: 4-alpha-glucanotransferase, domain 2
51	c2w3zA_	Alignment	not modelled	94.6	14	PDB header: hydrolase Chain: A: PDB Molecule: putative deacetylase; PDBTitle: structure of a streptococcus mutans ce4 esterase
52	c4nz3A_	Alignment	not modelled	92.3	13	PDB header: hydrolase Chain: A: PDB Molecule: deacetylase da1; PDBTitle: structure of vibrio cholerae chitin de-n-acetylase in complex with2 di(n-acetyl-d-glucosamine) (cbs) in p 21 21 21
53	d2nlva1	Alignment	not modelled	91.3	13	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: Divergent polysaccharide deacetylase

54	c2vldA	Alignment	not modelled	81.7	10	PDB header: hydrolase Chain: A: PDB Molecule: endonuclease nucs; PDBTitle: crystal structure of a repair endonuclease from <i>pyrococcus abyssii</i>
55	c5gkeB	Alignment	not modelled	70.7	10	PDB header: hydrolase/dna Chain: B: PDB Molecule: endonuclease endoms; PDBTitle: structure of endoms-dsdna1 complex
56	c1o7dB	Alignment	not modelled	69.7	10	PDB header: hydrolase Chain: B: PDB Molecule: lysosomal alpha-mannosidase; PDBTitle: the structure of the bovine lysosomal a-mannosidase suggests a novel2 mechanism for low ph activation
57	c2vwtA	Alignment	not modelled	69.4	24	PDB header: lyase Chain: A: PDB Molecule: yfau, 2-keto-3-deoxy sugar aldolase; PDBTitle: crystal structure of yfau, a metal ion dependent class ii2 aldolase from <i>escherichia coli</i> k12 - mg-pyruvate product3 complex
58	c2v5jB	Alignment	not modelled	62.2	21	PDB header: lyase Chain: B: PDB Molecule: 2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase; PDBTitle: apo class ii aldolase hpch
59	d1dxea	Alignment	not modelled	61.1	21	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Hpch/Hpal aldolase
60	d1wuua1	Alignment	not modelled	60.4	14	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: GHMP Kinase, N-terminal domain
61	c6r62A	Alignment	not modelled	57.7	9	PDB header: lyase Chain: A: PDB Molecule: hpch/hpai aldolase; PDBTitle: crystal structure of a class ii pyruvate aldolase from <i>sphingomonas2 wittichii</i> rw1 in complex with hydroxypyruvate
62	c4zrxA	Alignment	not modelled	54.1	11	PDB header: hydrolase Chain: A: PDB Molecule: f5/8 type c domain protein; PDBTitle: crystal structure of a putative alpha-l-fucosidase (<i>bacova_04357</i>) from <i>2 bacteroides ovatus</i> atcc 8483 at 1.59 a resolution
63	c5gtxA	Alignment	not modelled	47.3	17	PDB header: oxidoreductase Chain: A: PDB Molecule: buckwheat glutaredoxin; PDBTitle: crystal structure of mutated buckwheat glutaredoxin
64	c4tv6A	Alignment	not modelled	45.7	23	PDB header: lyase Chain: A: PDB Molecule: 2-dehydro-3-deoxyglucarate aldolase; PDBTitle: crystal structure of citrate synthase variant sbng e151q
65	c4f5yA	Alignment	not modelled	44.4	12	PDB header: immune system Chain: A: PDB Molecule: transmembrane protein 173; PDBTitle: crystal structure of human sting ctd complex with c-di-gmp
66	c3ff4A	Alignment	not modelled	44.3	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein chu_1412
67	d1izca	Alignment	not modelled	43.4	16	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Hpch/Hpal aldolase
68	c1izcA	Alignment	not modelled	43.4	16	PDB header: lyase Chain: A: PDB Molecule: macrophomate synthase intermolecular diels-alderase; PDBTitle: crystal structure analysis of macrophomate synthase
69	c4b5sB	Alignment	not modelled	41.3	19	PDB header: lyase Chain: B: PDB Molecule: 4-hydroxy-2-oxo-heptane-1,7-dioate aldolase; PDBTitle: crystal structures of divalent metal dependent pyruvate aldolase,2 hpai, in complex with pyruvate
70	c2ztbB	Alignment	not modelled	37.2	18	PDB header: toxin Chain: B: PDB Molecule: crystal protein; PDBTitle: crystal structure of the parasporin-2 <i>bacillus thuringiensis</i> toxin2 that recognizes cancer cells
71	c4mf4F	Alignment	not modelled	36.8	21	PDB header: lyase Chain: F: PDB Molecule: hpch/hpai aldolase/citrate lyase family protein; PDBTitle: crystal structure of a hpch/hpal aldolase/citrate lyase family protein2 from <i>burkholderia cenocepacia</i> j2315
72	d1r7ha	Alignment	not modelled	35.3	22	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
73	c4rl6A	Alignment	not modelled	35.2	14	PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine dehydrogenase; PDBTitle: crystal structure of the q04103_strp2 protein from <i>streptococcus2 pneumoniae</i> . northeast structural genomics consortium target spr105
74	c1uasA	Alignment	not modelled	34.2	26	PDB header: hydrolase Chain: A: PDB Molecule: alpha-galactosidase; PDBTitle: crystal structure of rice alpha-galactosidase
75	c2mxnA	Alignment	not modelled	31.6	29	PDB header: protein binding Chain: A: PDB Molecule: mono-cysteine glutaredoxin; PDBTitle: nmr structure of the mature form of <i>trypanosoma brucei</i> 1cgrx1
76	c3zywB	Alignment	not modelled	29.9	12	PDB header: metal binding protein Chain: B: PDB Molecule: glutaredoxin-3; PDBTitle: crystal structure of the first glutaredoxin domain of human2 glutaredoxin 3 (glrx3)
77	d1r46a2	Alignment	not modelled	29.4	29	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
78	c4mfkA	Alignment	not modelled	28.8	13	PDB header: transferase Chain: A: PDB Molecule: putative uncharacterized protein tcp24; PDBTitle: the crystal structure of acyltransferase in complex with decanoyl-coa
						PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine dehydrogenase;

79	c4inaA_	Alignment	not modelled	28.6	12	PDBTitle: crystal structure of the q7mss8_wolsu protein from wolinella2 succinogenes. northeast structural genomics consortium target wsr35
80	c3qz6A_	Alignment	not modelled	26.6	29	PDB header: lyase Chain: A: PDB Molecule: hpch/hpai aldolase; PDBTitle: the crystal structure of hpch/hpai aldolase from desulfitobacterium2 hafniense dcb-2
81	c1ykaA_	Alignment	not modelled	25.9	21	PDB header: electron transport Chain: A: PDB Molecule: monothiol glutaredoxin ydhd; PDBTitle: solution structure of grx4, a monothiol glutaredoxin from2 e. coli.
82	c5zv1B_	Alignment	not modelled	25.9	19	PDB header: oxidoreductase Chain: B: PDB Molecule: glutaredoxin; PDBTitle: crystal structure of wheat glutarredoxin
83	c2e7pC_	Alignment	not modelled	25.2	19	PDB header: electron transport Chain: C: PDB Molecule: glutaredoxin; PDBTitle: crystal structure of the holo form of glutaredoxin c1 from populus2 tremula x tremuloides
84	c4tr1A_	Alignment	not modelled	23.4	22	PDB header: oxidoreductase Chain: A: PDB Molecule: glutaredoxin 3; PDBTitle: crystal structure of gsh-bound cgrx2/c15s
85	c3mo4B_	Alignment	not modelled	23.3	12	PDB header: hydrolase Chain: B: PDB Molecule: alpha-1,3/4-fucosidase; PDBTitle: the crystal structure of an alpha-(1-3,4)-fucosidase from2 bifidobacterium longum subsp. infantis atcc 15697
86	d2d59a1	Alignment	not modelled	22.9	12	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
87	c3qmxA_	Alignment	not modelled	22.3	11	PDB header: electron transport Chain: A: PDB Molecule: glutaredoxin a; PDBTitle: x-ray crystal structure of synechocystis sp. pcc 6803 glutaredoxin a
88	c5lnfA_	Alignment	not modelled	21.2	15	PDB header: chaperone Chain: A: PDB Molecule: peroxisomal biogenesis factor 19; PDBTitle: solution nmr structure of farnesylated pex19, c-terminal domain
89	c2lqoA_	Alignment	not modelled	21.2	15	PDB header: oxidoreductase Chain: A: PDB Molecule: putative glutaredoxin rv3198.1/mt3292; PDBTitle: mrx1 reduced
90	d1iuka_	Alignment	not modelled	20.3	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
91	c5y4uA_	Alignment	not modelled	19.4	13	PDB header: oxidoreductase Chain: A: PDB Molecule: monothiol glutaredoxin-3; PDBTitle: crystal structure of grx domain of grx3 from saccharomyces cerevisiae
92	c1o7dC_	Alignment	not modelled	19.3	5	PDB header: hydrolase Chain: C: PDB Molecule: lysosomal alpha-mannosidase; PDBTitle: the structure of the bovine lysosomal a-mannosidase suggests a novel2 mechanism for low ph activation
93	d1rbli_	Alignment	not modelled	19.2	13	Fold: RuBisCO, small subunit Superfamily: RuBisCO, small subunit Family: RuBisCO, small subunit
94	c3z1jA_	Alignment	not modelled	18.9	15	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: crystal structure of the thioredoxin-like protein bc3987
95	c2ybvN_	Alignment	not modelled	18.0	9	PDB header: lyase Chain: N: PDB Molecule: ribulose bisphosphate carboxylase small subunit; PDBTitle: structure of rubisco from thermosynechococcus elongatus
96	d1wdds_	Alignment	not modelled	17.6	14	Fold: RuBisCO, small subunit Superfamily: RuBisCO, small subunit Family: RuBisCO, small subunit
97	c5bq9B_	Alignment	not modelled	17.5	36	PDB header: unknown function, structural genomics Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein lpg1496 legionella2 pneumophila subsp. pneumophila
98	c2duwA_	Alignment	not modelled	17.3	23	PDB header: ligand binding protein Chain: A: PDB Molecule: putative coa-binding protein; PDBTitle: solution structure of putative coa-binding protein of2 klebsiella pneumoniae
99	c2y48B_	Alignment	not modelled	17.3	30	PDB header: oxidoreductase Chain: B: PDB Molecule: rest corepressor 1; PDBTitle: crystal structure of lsd1-corest in complex with a n-2 terminal snail peptide