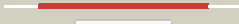



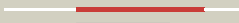
















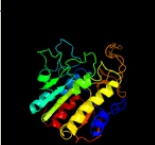


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2350c_plcB_2628791_2630329
Date	Mon Aug 5 13:25:50 BST 2019
Unique Job ID	04c26f7c4d13ee58

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2d1gB_	 Alignment		100.0	22	PDB header: hydrolase Chain: B: PDB Molecule: acid phosphatase; PDBTitle: structure of francisella tularensis acid phosphatase a (acpa) bound to2 orthovanadate
2	c6hr5A_	 Alignment		99.4	15	PDB header: hydrolase Chain: A: PDB Molecule: alpha-l-rhamnosidase/sulfatase (gh78); PDBTitle: structure of the s1_25 family sulfatase module of the rhamnosidase2 fa22250 from formosa agariphila
3	d1lauka_	 Alignment		99.4	18	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Arylsulfatase
4	c6b1vB_	 Alignment		99.4	16	PDB header: hydrolase Chain: B: PDB Molecule: iota-carrageenan sulfatase; PDBTitle: crystal structure of ps i-cgsb c78s in complex with i-neocarratetraose
5	c6j66B_	 Alignment		99.3	16	PDB header: hydrolase Chain: B: PDB Molecule: chondroitin sulfate/dermatan sulfate 4-o-endosulfatase PDBTitle: chondroitin sulfate/dermatan sulfate endolytic 4-o-sulfatase
6	c4fdia_	 Alignment		99.3	16	PDB header: hydrolase Chain: A: PDB Molecule: n-acetylgalactosamine-6-sulfatase; PDBTitle: the molecular basis of mucopolysaccharidosis iv a
7	c3lxqB_	 Alignment		99.2	10	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein vp1736; PDBTitle: the crystal structure of a protein in the alkaline phosphatase2 superfamily from vibrio parahaemolyticus to 1.95a
8	c5g2vA_	 Alignment		99.2	15	PDB header: hydrolase Chain: A: PDB Molecule: n-acetylglucosamine-6-sulfatase; PDBTitle: structure of bt4656 in complex with its substrate d-glucosamine-2-n,2 6-o-disulfate.
9	d1fsua_	 Alignment		99.1	19	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Arylsulfatase
10	c4mivB_	 Alignment		99.1	21	PDB header: hydrolase Chain: B: PDB Molecule: n-sulphoglucosamine sulphohydrolase; PDBTitle: crystal structure of sulfamidase, crystal form I
11	c3ed4A_	 Alignment		99.1	11	PDB header: transferase Chain: A: PDB Molecule: arylsulfatase; PDBTitle: crystal structure of putative arylsulfatase from escherichia coli

12	c5fqIA_	Alignment		99.1	17	PDB header: hydrolase Chain: A: PDB Molecule: iduronate-2-sulfatase; PDBTitle: insights into hunter syndrome from the structure of iduronate-2-2 sulfatase
13	d1p49a_	Alignment		99.1	17	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Arylsulfatase
14	c4upkC_	Alignment		99.1	16	PDB header: hydrolase Chain: C: PDB Molecule: phosphonate monoester hydrolase; PDBTitle: phosphonate monoester hydrolase sppmh from silicibacter pomeroyi
15	c6hbmA_	Alignment		99.1	12	PDB header: hydrolase Chain: A: PDB Molecule: arylsulfatase; PDBTitle: crystal structure of the family s1_7 ulvan-specific sulfatase fa220702 from formosa agariphila
16	c4ug4H_	Alignment		99.0	15	PDB header: hydrolase Chain: H: PDB Molecule: choline sulfatase; PDBTitle: crystal structure of a choline sulfatase from sinorhizobium2 melliloti
17	c2vqrA_	Alignment		99.0	15	PDB header: hydrolase Chain: A: PDB Molecule: putative sulfatase; PDBTitle: crystal structure of a phosphonate monoester hydrolase from rhizobium2 leguminosarum: a new member of the alkaline phosphatase superfamily
18	c4uopB_	Alignment		99.0	13	PDB header: transferase Chain: B: PDB Molecule: lipoteichoic acid primase; PDBTitle: crystal structure of the lipoteichoic acid synthase ltap from listeria2 monocytogenes
19	c4uplC_	Alignment		99.0	14	PDB header: hydrolase Chain: C: PDB Molecule: sulfatase family protein; PDBTitle: dimeric sulfatase spas2 from silicibacter pomeroyi
20	c2w8dB_	Alignment		99.0	12	PDB header: transferase Chain: B: PDB Molecule: processed glycerol phosphate lipoteichoic acid synthase 2; PDBTitle: distinct and essential morphogenic functions for wall-and2 lipo-teichoic acids in bacillus subtilis
21	c4uphA_	Alignment	not modelled	99.0	17	PDB header: hydrolase Chain: A: PDB Molecule: sulfatase (sulfuric ester hydrolase) protein; PDBTitle: crystal structure of phosphonate monoester hydrolase of agrobacterium2 radiobacter
22	c2qzuA_	Alignment	not modelled	99.0	11	PDB header: hydrolase Chain: A: PDB Molecule: putative sulfatase yidj; PDBTitle: crystal structure of the putative sulfatase yidj from bacteroides2 fragilis. northeast structural genomics consortium target bfr123
23	c4uorK_	Alignment	not modelled	99.0	12	PDB header: transferase Chain: K: PDB Molecule: lipoteichoic acid synthase; PDBTitle: structure of lipoteichoic acid synthase ltas from listeria2 monocytogenes in complex with glycerol phosphate
24	c4upiA_	Alignment	not modelled	99.0	13	PDB header: hydrolase Chain: A: PDB Molecule: sulfatase family protein; PDBTitle: dimeric sulfatase spas1 from silicibacter pomeroyi
25	d1hdha_	Alignment	not modelled	98.9	19	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Arylsulfatase
26	c3b5qB_	Alignment	not modelled	98.9	15	PDB header: hydrolase Chain: B: PDB Molecule: putative sulfatase yidj; PDBTitle: crystal structure of a putative sulfatase (np_810509.1) from2 bacteroides thetaiotaomicron vpi-5482 at 2.40 a resolution
27	c5i5fA_	Alignment	not modelled	98.8	11	PDB header: membrane protein Chain: A: PDB Molecule: inner membrane protein yejm; PDBTitle: salmonella global domain 191
28	c4kayA_	Alignment	not modelled	98.7	13	PDB header: transferase Chain: A: PDB Molecule: yhbxb/yhjw/yjpb family protein; PDBTitle: structure of the soluble domain of lipooligosaccharide2 phosphoethanolamine transferase a from neisseria meningitidis -3

						complex with zn PDB header: transferase Chain: A: PDB Molecule: phosphoethanolamine transferase; PDBTitle: crystal structure of the intrinsic colistin resistance enzyme icr(mc)2 from moraxella catarrhalis, catalytic domain, phosphate-bound complex
29	c6bneA	Alignment	not modelled	98.7	12	PDB header: transferase Chain: A: PDB Molecule: phosphoethanolamine transferase eptc; PDBTitle: crystal structure of the c-terminal periplasmic domain of eceptc from2 escherichia coli
30	c6a82A	Alignment	not modelled	98.7	13	PDB header: transferase Chain: A: PDB Molecule: processed glycerol phosphate lipoteichoic acid PDBTitle: structure-based mechanism of lipoteichoic acid synthesis by2 staphylococcus aureus ltas.
31	c2w5tA	Alignment	not modelled	98.7	14	PDB header: transferase Chain: A: PDB Molecule: probable phosphatidylethanolamine transferase mcr-1; PDBTitle: catalytic domain of mcr-1 phosphoethanolamine transferase
32	c5k4pA	Alignment	not modelled	98.6	13	PDB header: transferase Chain: C: PDB Molecule: upf0141 protein yjdb; PDBTitle: crystal structure of the c-terminal periplasmic domain of2 phosphoethanolamine transferase eptc from campylobacter jejuni
33	c4tn0C	Alignment	not modelled	98.4	15	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: 2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, catalytic domain
34	d1o98a2	Alignment	not modelled	98.4	12	PDB header: hydrolase Chain: A: PDB Molecule: ectonucleotide pyrophosphatase/phosphodiesterase family PDBTitle: human ectonucleotide pyrophosphatase / phosphodiesterase 5 (enpp5,2 npp5)
35	c5vemA	Alignment	not modelled	98.3	11	PDB header: hydrolase Chain: D: PDB Molecule: ectonucleotide pyrophosphatase/phosphodiesterase family PDBTitle: structure of enpp6, a choline-specific glycerophosphodiester-2 phosphodiesterase
36	c5egeD	Alignment	not modelled	98.1	15	PDB header: hydrolase Chain: A: PDB Molecule: ectonucleotide pyrophosphatase/phosphodiesterase family PDBTitle: human alkaline sphingomyelinase (alk-smase, enpp7, npp7)
37	c5udyA	Alignment	not modelled	97.9	12	PDB header: transferase,hydrolase Chain: A: PDB Molecule: lipooligosaccharide phosphoethanolamine transferase a; PDBTitle: integral membrane protein lipooligosaccharide phosphoethanolamine2 transferase a (epta) from neisseria meningitidis
38	c5fgnA	Alignment	not modelled	97.8	12	PDB header: hydrolase Chain: A: PDB Molecule: bis(5'-adenosyl)-triphosphatase enpp4; PDBTitle: crystal structure of human enpp4 with amp
39	c4lqyA	Alignment	not modelled	97.8	12	PDB header: transferase Chain: B: PDB Molecule: phosphoglycerol transferase; PDBTitle: phosphoglycerol transferase gach from streptococcus pyogenes
40	c5u9zB	Alignment	not modelled	97.7	11	PDB header: hydrolase Chain: B: PDB Molecule: phosphodiesterase-nucleotide pyrophosphatase; PDBTitle: structure of xac nucleotide pyrophosphatase/phosphodiesterase in2 complex with vanadate
41	c2gsoB	Alignment	not modelled	97.7	16	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: DeoB catalytic domain-like
42	d2i09a1	Alignment	not modelled	97.7	14	PDB header: isomerase Chain: C: PDB Molecule: phosphopentomutase; PDBTitle: phosphopentomutase from bacillus cereus after glucose-1,6-bisphosphate2 activation
43	c3m8yC	Alignment	not modelled	97.4	22	PDB header: hydrolase Chain: A: PDB Molecule: alkaline phosphatase; PDBTitle: crystal structure of spap: an novel alkaline phosphatase from2 bacterium sphingomonas sp. strain bsar-1
44	c3q3qA	Alignment	not modelled	97.4	18	PDB header: hydrolase Chain: A: PDB Molecule: ectonucleotide pyrophosphatase/phosphodiesterase family PDBTitle: structure of ectonucleotide pyrophosphatase-phosphodiesterase-12 (npp1)
45	c4b56A	Alignment	not modelled	97.0	15	PDB header: hydrolase Chain: A: PDB Molecule: snake venom phosphodiesterase (pde); PDBTitle: crystal structure of snake venom phosphodiesterase (pde) from taiwan2 cobra (naja atra atra)
46	c5gz4A	Alignment	not modelled	96.9	12	PDB header: hydrolase Chain: A: PDB Molecule: snake venom phosphodiesterase (pde); PDBTitle: crystal structure of snake venom phosphodiesterase (pde) from taiwan2 cobra (naja atra atra) in complex with amp
47	c5gz5A	Alignment	not modelled	96.9	12	PDB header: isomerase Chain: A: PDB Molecule: phosphopentomutase; PDBTitle: crystal structure of putative phosphopentomutase from streptococcus2 mutans
48	c2i09A	Alignment	not modelled	96.7	17	PDB header: isomerase Chain: B: PDB Molecule: 2,3-bisphosphoglycerate-independent phosphoglycerate PDBTitle: structure of ph0037 protein from pyrococcus horikoshii
49	c2zktB	Alignment	not modelled	96.7	16	PDB header: hydrolase Chain: B: PDB Molecule: ectonucleotide pyrophosphatase/phosphodiesterase family PDBTitle: human ectonucleotide pyrophosphatase / phosphodiesterase 3 (enpp3,2 npp3, cd203c), inactive (t205a), n594s, with alpha.beta-methylene-atp3 (ampcpp)
50	c6c02B	Alignment	not modelled	95.7	12	PDB header: hydrolase Chain: A: PDB Molecule: ectonucleotide

51	c2xrgA_	Alignment	not modelled	95.2	14	pyrophosphatase/phosphodiesterase family PDBTitle: crystal structure of autotaxin (enpp2) in complex with the2 ha155 boronic acid inhibitor PDB header: hydrolase
52	c2xr9A_	Alignment	not modelled	95.2	14	Chain: A: PDB Molecule: ectonucleotide pyrophosphatase/phosphodiesterase family PDBTitle: crystal structure of autotaxin (enpp2) PDB header: isomerase
53	c5kgmA_	Alignment	not modelled	95.1	14	Chain: A: PDB Molecule: 2,3-bisphosphoglycerate-independent phosphoglycerate PDBTitle: 2.95a resolution structure of apo independent phosphoglycerate mutase2 from c. elegans (monoclinic form) PDB header: hydrolase
54	c5tj3A_	Alignment	not modelled	94.5	9	Chain: A: PDB Molecule: alkaline phosphatase pafa; PDBTitle: crystal structure of wild type alkaline phosphatase pafa to 1.7a2 resolution PDB header: photosynthesis
55	c2e76D_	Alignment	not modelled	94.1	22	Chain: D: PDB Molecule: cytochrome b6-f complex iron-sulfur subunit; PDBTitle: crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus PDB header: isomerase
56	c3igzB_	Alignment	not modelled	90.9	14	Chain: B: PDB Molecule: cofactor-independent phosphoglycerate mutase; PDBTitle: crystal structures of leishmania mexicana phosphoglycerate2 mutase at low cobalt concentration PDB header: oxidoreductase
57	c2fynO_	Alignment	not modelled	89.9	28	Chain: O: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur PDBTitle: crystal structure analysis of the double mutant rhodobacter2 sphaeroides bc1 complex PDB header: isomerase
58	c1o98A_	Alignment	not modelled	89.1	16	Chain: A: PDB Molecule: 2,3-bisphosphoglycerate-independent PDBTitle: 1.4a crystal structure of phosphoglycerate mutase from2 bacillus stearothermophilus complexed with3 2-phosphoglycerate PDB header: isomerase
59	c5vpuA_	Alignment	not modelled	86.6	14	Chain: A: PDB Molecule: 2,3-bisphosphoglycerate-independent phosphoglycerate PDBTitle: crystal structure of 2,3-bisphosphoglycerate-independent2 phosphoglycerate mutase bound to 3-phosphoglycerate, from3 acinetobacter baumannii
60	d1ei6a_	Alignment	not modelled	86.4	12	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Phosphonoacetate hydrolase PDB header: isomerase
61	c4my4A_	Alignment	not modelled	79.2	19	Chain: A: PDB Molecule: 2,3-bisphosphoglycerate-independent phosphoglycerate PDBTitle: crystal structure of phosphoglycerate mutase from staphylococcus2 aureus. PDB header: oxidoreductase
62	c2fyuE_	Alignment	not modelled	79.1	23	Chain: E: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur subunit, PDBTitle: crystal structure of bovine heart mitochondrial bc1 with jg1442 inhibitor PDB header: hydrolase
63	c3szzA_	Alignment	not modelled	79.0	19	Chain: A: PDB Molecule: phosphonoacetate hydrolase; PDBTitle: crystal structure of phosphonoacetate hydrolase from sinorhizobium2 meliloti 1021 in complex with acetate PDB header: chaperone/oxidoreductase
64	c2pq4B_	Alignment	not modelled	76.0	37	Chain: B: PDB Molecule: periplasmic nitrate reductase precursor; PDBTitle: nmr solution structure of napd in complex with napa1-352 signal peptide PDB header: oxidoreductase
65	c1p84E_	Alignment	not modelled	75.0	7	Chain: E: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur subunit; PDBTitle: hdbt inhibited yeast cytochrome bc1 complex PDB header: membrane protein
66	c6fo2R_	Alignment	not modelled	67.4	25	Chain: R: PDB Molecule: cytochrome b-c1 complex subunit rieske, mitochondrial; PDBTitle: cryoem structure of bovine cytochrome bc1 with no ligand bound
67	d1y6va1	Alignment	not modelled	65.3	17	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Alkaline phosphatase
68	c2w0yB_	Alignment	not modelled	52.0	31	PDB header: hydrolase Chain: B: PDB Molecule: alkaline phosphatase; PDBTitle: h.salinarum alkaline phosphatase
69	c6dq3B_	Alignment	not modelled	40.8	20	PDB header: hydrolase Chain: B: PDB Molecule: polysaccharide deacetylase; PDBTitle: streptococcus pyogenes deacetylase pdi in complex with acetate
70	c2iucB_	Alignment	not modelled	39.6	16	PDB header: hydrolase Chain: B: PDB Molecule: alkaline phosphatase; PDBTitle: structure of alkaline phosphatase from the antarctic bacterium tab5
71	d1okta2	Alignment	not modelled	32.8	21	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
72	d2e74d2	Alignment	not modelled	32.8	33	Fold: Single transmembrane helix Superfamily: ISP transmembrane anchor Family: ISP transmembrane anchor
73	d1k0ma2	Alignment	not modelled	29.3	20	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
74	c6jcnB_	Alignment	not modelled	27.6	11	PDB header: transferase Chain: B: PDB Molecule: dehydrodolichyl diphosphate synthase complex subunit nus1; PDBTitle: yeast dehydrodolichyl diphosphate synthase complex subunit nus1

75	c2x98A	Alignment	not modelled	25.2	29	PDB header: hydrolase Chain: A: PDB Molecule: alkaline phosphatase; PDBTitle: h.salinarum alkaline phosphatase
76	c6acsA	Alignment	not modelled	24.5	27	PDB header: transferase Chain: A: PDB Molecule: ditrans,polycis-undecaprenyl-diphosphate synthase ((2e,6e)- PDBTitle: poly-cis-prenyltransferase
77	d2p02a2	Alignment	not modelled	23.5	31	Fold: S-adenosylmethionine synthetase Superfamily: S-adenosylmethionine synthetase Family: S-adenosylmethionine synthetase
78	c2d2rA	Alignment	not modelled	20.2	19	PDB header: transferase Chain: A: PDB Molecule: undecaprenyl pyrophosphate synthase; PDBTitle: crystal structure of helicobacter pylori undecaprenyl pyrophosphate2 synthase
79	c3couA	Alignment	not modelled	20.1	25	PDB header: hydrolase Chain: A: PDB Molecule: nucleoside diphosphate-linked moiety x motif 16; PDBTitle: crystal structure of human nudix motif 16 (nudd16)
80	c3e2dB	Alignment	not modelled	18.9	30	PDB header: hydrolase Chain: B: PDB Molecule: alkaline phosphatase; PDBTitle: the 1.4 a crystal structure of the large and cold-active vibrio sp.2 alkaline phosphatase
81	d2gsra2	Alignment	not modelled	18.1	21	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
82	c5j43F	Alignment	not modelled	18.0	56	PDB header: toxin Chain: F: PDB Molecule: trna nuclease cdiA; PDBTitle: cdiA-ct from uropathogenic escherichia coli in complex with cysk
83	c4nv4A	Alignment	not modelled	17.9	33	PDB header: hydrolase Chain: A: PDB Molecule: signal peptidase i; PDBTitle: 1.8 angstrom crystal structure of signal peptidase i from bacillus2 anthracis.
84	c6hwhB	Alignment	not modelled	17.7	11	PDB header: electron transport Chain: B: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur subunit; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
85	d1m0ua2	Alignment	not modelled	17.3	15	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
86	c4ke3D	Alignment	not modelled	17.3	23	PDB header: transferase Chain: D: PDB Molecule: glutathione s-transferase domain; PDBTitle: crystal structure of a glutathione transferase family member from2 burkholderia graminis, target efi-507264, no gsh, disordered domains,3 space group p21, form(2)
87	c4q9mA	Alignment	not modelled	17.1	31	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: isoprenyl transferase; PDBTitle: crystal structure of upps in complex with fpp and an allosteric2 inhibitor
88	d1qm4a2	Alignment	not modelled	17.0	25	Fold: S-adenosylmethionine synthetase Superfamily: S-adenosylmethionine synthetase Family: S-adenosylmethionine synthetase
89	c4h8eA	Alignment	not modelled	16.9	38	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: undecaprenyl pyrophosphate synthase; PDBTitle: structure of s. aureus undecaprenyl diphosphate synthase in complex2 with fpp and sulfate
90	c3wbhB	Alignment	not modelled	16.6	24	PDB header: hydrolase Chain: B: PDB Molecule: alkaline phosphatase; PDBTitle: structural characteristics of alkaline phosphatase from a moderately2 halophilic bacteria halomonas sp.593
91	c5ec0A	Alignment	not modelled	16.4	45	PDB header: structural protein Chain: A: PDB Molecule: alp7a; PDBTitle: crystal structure of actin-like protein alp7a
92	c2odiA	Alignment	not modelled	15.3	26	PDB header: hydrolase/dna Chain: A: PDB Molecule: r.bcni; PDBTitle: restriction endonuclease bcni-cognate dna substrate complex
93	d1f75a	Alignment	not modelled	15.0	31	Fold: Undecaprenyl diphosphate synthase Superfamily: Undecaprenyl diphosphate synthase Family: Undecaprenyl diphosphate synthase
94	d1txka2	Alignment	not modelled	14.9	36	Fold: Supersandwich Superfamily: Galactose mutarotase-like Family: MdoG-like
95	c5nkmE	Alignment	not modelled	14.1	13	PDB header: rna binding protein Chain: E: PDB Molecule: protein smg-8; PDBTitle: smg8-smg9 complex
96	d1v2aa2	Alignment	not modelled	14.0	15	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
97	c1txkA	Alignment	not modelled	13.9	36	PDB header: biosynthetic protein Chain: A: PDB Molecule: glucans biosynthesis protein g; PDBTitle: crystal structure of escherichia coli oppg
98	c5bu6B	Alignment	not modelled	13.2	4	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
99	c4k8wA	Alignment	not modelled	13.0	28	PDB header: cell adhesion Chain: A: PDB Molecule: lepa; PDBTitle: an arm-swapped dimer of the s. pyogenes pilin specific assembly factor2 sipa