
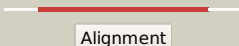

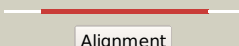

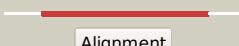




















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3310_(-)_3697369_3698268
Date	Thu Aug 8 16:20:52 BST 2019
Unique Job ID	56c20990dddd4ba0

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4uplC_	 Alignment		100.0	18	PDB header: hydrolase Chain: C: PDB Molecule: sulfatase family protein; PDBTitle: dimeric sulfatase spas2 from silicibacter pomeroyi
2	c4upiA_	 Alignment		100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: sulfatase family protein; PDBTitle: dimeric sulfatase spas1 from silicibacter pomeroyi
3	c4ug4H_	 Alignment		100.0	15	PDB header: hydrolase Chain: H: PDB Molecule: choline sulfatase; PDBTitle: crystal structure of a choline sulfatase from sinorhizobium2 melliloti
4	d1auka_	 Alignment		100.0	15	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Arylsulfatase
5	c4fdiA_	 Alignment		100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: n-acetylgalactosamine-6-sulfatase; PDBTitle: the molecular basis of mucopolysaccharidosis iv a
6	c2qzuA_	 Alignment		100.0	21	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
7	d1p49a_	 Alignment		100.0	18	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Arylsulfatase
8	c4upkC_	 Alignment		100.0	15	PDB header: hydrolase Chain: C: PDB Molecule: phosphonate monoester hydrolase; PDBTitle: phosphonate monoester hydrolase sppmh from silicibacter pomeroyi
9	c4mivB_	 Alignment		100.0	15	PDB header: hydrolase Chain: B: PDB Molecule: n-sulphoglucosamine sulphohydrolase; PDBTitle: crystal structure of sulfamidase, crystal form I
10	c5fqIA_	 Alignment		100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: iduronate-2-sulfatase; PDBTitle: insights into hunter syndrome from the structure of iduronate-2-2 sulfatase
11	c6b1vB_	 Alignment		100.0	18	PDB header: hydrolase Chain: B: PDB Molecule: iota-carrageenan sulfatase; PDBTitle: crystal structure of ps i-cgsb c78s in complex with i-neocarratetraose

12	d1hdha_	Alignment		100.0	18	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Arylsulfatase
13	c4uphA_	Alignment		100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: sulfatase (sulfuric ester hydrolase) protein; PDBTitle: crystal structure of phosphonate monoester hydrolase of agrobacterium2 radiobacter
14	c3ed4A_	Alignment		100.0	17	PDB header: transferase Chain: A: PDB Molecule: arylsulfatase; PDBTitle: crystal structure of putative arylsulfatase from escherichia coli
15	c6j66B_	Alignment		100.0	18	PDB header: hydrolase Chain: B: PDB Molecule: chondroitin sulfate/dermatan sulfate 4-o-endosulfatase PDBTitle: chondroitin sulfate/dermatan sulfate endolytic 4-o-sulfatase
16	c3b5qB_	Alignment		100.0	17	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
17	c6hhmA_	Alignment		100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: arylsulfatase; PDBTitle: crystal structure of the family s1_7 ulvan-specific sulfatase fa220702 from formosa agariphila
18	d1fsua_	Alignment		100.0	16	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Arylsulfatase
19	c2vqrA_	Alignment		100.0	18	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
20	c3lxqB_	Alignment		100.0	14	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
21	c5g2vA_	Alignment	not modelled	100.0	12	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.
22	c2w8dB_	Alignment	not modelled	100.0	16	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
23	c6hr5A_	Alignment	not modelled	100.0	13	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
24	c4uorK_	Alignment	not modelled	100.0	15	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
25	c4uopB_	Alignment	not modelled	100.0	12	PDB header: transferase Chain: B: PDB Molecule: lipoteichoic acid primase; PDBTitle: crystal structure of the lipoteichoic acid synthase ltap from listeria2 monocytogenes
26	c2w5tA_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: A: PDB Molecule: processed glycerol phosphate lipoteichoic acid PDBTitle: structure-based mechanism of lipoteichoic acid synthesis by2 staphylococcus aureus ltas.
27	c5i5fA_	Alignment	not modelled	100.0	16	PDB header: membrane protein Chain: A: PDB Molecule: inner membrane protein yejm; PDBTitle: salmonella global domain 191
28	c2d1qB_	Alignment	not modelled	100.0	26	PDB header: hydrolase Chain: B: PDB Molecule: acid phosphatase; PDBTitle: structure of francisella tularensis acid phosphatase a

						(acpa) bound to 2 orthovanadate
29	c4kayA	Alignment	not modelled	100.0	15	PDB header: transferase Chain: A: PDB Molecule: yhbxyjhwyjyp/yjdb family protein; PDBTitle: structure of the soluble domain of lipooligosaccharide2 phosphoethanolamine transferase a from neisseria meningitidis-3 complex with zn
30	c6bneA	Alignment	not modelled	100.0	13	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
31	c6a82A	Alignment	not modelled	100.0	13	PDB header: transferase Chain: A: PDB Molecule: phosphoethanolamine transferase eptc; PDBTitle: crystal structure of the c-terminal periplasmic domain of eceptc from 2 escherichia coli
32	c5k4pA	Alignment	not modelled	100.0	12	PDB header: transferase Chain: A: PDB Molecule: probable phosphatidylethanolamine transferase mcr-1; PDBTitle: catalytic domain of mcr-1 phosphoethanolamine transferase
33	c2zktB	Alignment	not modelled	100.0	13	PDB header: isomerase Chain: B: PDB Molecule: 2,3-bisphosphoglycerate-independent phosphoglycerate PDBTitle: structure of ph0037 protein from pyrococcus horikoshii
34	c3q3qA	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: alkaline phosphatase; PDBTitle: crystal structure of spap: an novel alkaline phosphatase from 2 bacterium sphingomonas sp. strain bsar-1
35	c4lqyA	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: bis(5'-adenosyl)-triphosphatase enpp4; PDBTitle: crystal structure of human enpp4 with amp
36	c5vemA	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: ectonucleotide pyrophosphatase/phosphodiesterase family PDBTitle: human ectonucleotide pyrophosphatase / phosphodiesterase 5 (enpp5,2 npp5)
37	c4tn0C	Alignment	not modelled	100.0	14	PDB header: transferase Chain: C: PDB Molecule: upf0141 protein yjdb; PDBTitle: crystal structure of the c-terminal periplasmic domain of 2 phosphoethanolamine transferase eptc from campylobacter jejuni
38	c5tj3A	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: alkaline phosphatase pafa; PDBTitle: crystal structure of wild type alkaline phosphatase pafa to 1.7a2 resolution
39	c5udyA	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: A: PDB Molecule: ectonucleotide pyrophosphatase/phosphodiesterase family PDBTitle: human alkaline sphingomyelinase (alk-smase, enpp7, npp7)
40	c3m8yC	Alignment	not modelled	100.0	18	PDB header: isomerase Chain: C: PDB Molecule: phosphopentomutase; PDBTitle: phosphopentomutase from bacillus cereus after glucose-1,6-bisphosphate2 activation
41	d1o98a2	Alignment	not modelled	100.0	9	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: 2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, catalytic domain
42	c2gsoB	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: B: PDB Molecule: phosphodiesterase-nucleotide pyrophosphatase; PDBTitle: structure of xac nucleotide pyrophosphatase/phosphodiesterase in 2 complex with vanadate
43	c5fgnA	Alignment	not modelled	100.0	16	PDB header: transferase,hydrolase Chain: A: PDB Molecule: lipooligosaccharide phosphoethanolamine transferase a; PDBTitle: integral membrane protein lipooligosaccharide phosphoethanolamine2 transferase a (epta) from neisseria meningitidis
44	c5egeD	Alignment	not modelled	100.0	12	PDB header: hydrolase Chain: D: PDB Molecule: ectonucleotide pyrophosphatase/phosphodiesterase family PDBTitle: structure of enpp6, a choline-specific glycerophosphodiester-2 phosphodiesterase
45	c5u9zB	Alignment	not modelled	100.0	10	PDB header: transferase Chain: B: PDB Molecule: phosphoglycerol transferase; PDBTitle: phosphoglycerol transferase gach from streptococcus pyogenes
46	c5gz5A	Alignment	not modelled	100.0	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) in complex with amp
47	c5gz4A	Alignment	not modelled	100.0	14	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)
48	c6c02B	Alignment	not modelled	100.0	14	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)
49	c2xrgA	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: ectonucleotide pyrophosphatase/phosphodiesterase family PDBTitle: crystal structure of autotaxin (enpp2) in complex with the 2 ha155 boronic acid inhibitor
50	c4b56A	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: A: PDB Molecule: ectonucleotide pyrophosphatase/phosphodiesterase family PDBTitle: structure of ectonucleotide pyrophosphatase-phosphodiesterase-12 (npp1)
						Fold: Alkaline phosphatase-like

51	d2i09a1	Alignment	not modelled	100.0	14	Superfamily: Alkaline phosphatase-like Family: DeoB catalytic domain-like
52	c2xr9A	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: ectonucleotide pyrophosphatase/phosphodiesterase family PDBTitle: crystal structure of autotaxin (enpp2)
53	c3szzA	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: phosphonoacetate hydrolase; PDBTitle: crystal structure of phosphonoacetate hydrolase from sinorhizobium2 meliloti 1021 in complex with acetate
54	c2i09A	Alignment	not modelled	100.0	13	PDB header: isomerase Chain: A: PDB Molecule: phosphopentomutase; PDBTitle: crystal structure of putative phosphopentomutase from streptococcus2 mutans
55	d1ei6a	Alignment	not modelled	100.0	18	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Phosphonoacetate hydrolase
56	c1o98A	Alignment	not modelled	99.8	14	PDB header: isomerase Chain: A: PDB Molecule: 2,3-bisphosphoglycerate-independent PDBTitle: 1.4a crystal structure of phosphoglycerate mutase from2 bacillus stearothermophilus complexed with3 2-phosphoglycerate
57	c5kgmA	Alignment	not modelled	99.7	16	PDB header: isomerase Chain: A: PDB Molecule: 2,3-bisphosphoglycerate-independent phosphoglycerate PDBTitle: 2.95a resolution structure of apo independent phosphoglycerate mutase2 from c. elegans (monoclinic form)
58	c4my4A	Alignment	not modelled	99.7	13	PDB header: isomerase Chain: A: PDB Molecule: 2,3-bisphosphoglycerate-independent phosphoglycerate PDBTitle: crystal structure of phosphoglycerate mutase from staphylococcus2 aureus.
59	c3igzB	Alignment	not modelled	99.7	18	PDB header: isomerase Chain: B: PDB Molecule: cofactor-independent phosphoglycerate mutase; PDBTitle: crystal structures of leishmania mexicana phosphoglycerate2 mutase at low cobalt concentration
60	c5vpuA	Alignment	not modelled	99.6	18	PDB header: isomerase 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
61	c2iucB	Alignment	not modelled	99.5	15	PDB header: hydrolase Chain: B: PDB Molecule: alkaline phosphatase; PDBTitle: structure of alkaline phosphatase from the antarctic bacterium tab5
62	d1y6va1	Alignment	not modelled	99.4	19	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Alkaline phosphatase
63	c1ew2A	Alignment	not modelled	99.3	16	PDB header: hydrolase Chain: A: PDB Molecule: phosphatase; PDBTitle: crystal structure of a human phosphatase
64	d1zeda1	Alignment	not modelled	99.3	16	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Alkaline phosphatase
65	c3a52A	Alignment	not modelled	99.2	18	PDB header: hydrolase Chain: A: PDB Molecule: cold-active alkaline phosphatase; PDBTitle: crystal structure of cold-active alkaline phosphatase from2 psychrophile shewanella sp.
66	c2w0yB	Alignment	not modelled	99.1	21	PDB header: hydrolase Chain: B: PDB Molecule: alkaline phosphatase; PDBTitle: h.salinarum alkaline phosphatase
67	c2x98A	Alignment	not modelled	99.1	21	PDB header: hydrolase Chain: A: PDB Molecule: alkaline phosphatase; PDBTitle: h.salinarum alkaline phosphatase
68	d1k7ha	Alignment	not modelled	99.0	13	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Alkaline phosphatase
69	c3e2dB	Alignment	not modelled	98.9	16	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
70	c3wbhB	Alignment	not modelled	98.8	15	PDB header: hydrolase Chain: B: PDB Molecule: alkaline phosphatase; PDBTitle: structural characteristics of alkaline phosphatase from a moderately2 halophilic bacteria halomonas sp.593
71	c3iddA	Alignment	not modelled	98.3	20	PDB header: isomerase Chain: A: PDB Molecule: 2,3-bisphosphoglycerate-independent PDBTitle: cofactor-independent phosphoglycerate mutase from2 thermoplasma acidophilum dsm 1728
72	c5oltA	Alignment	not modelled	97.5	12	PDB header: transferase Chain: A: PDB Molecule: cellulose biosynthesis protein bcsG; PDBTitle: crystal structure of the extramembrane domain of the cellulose2 biosynthetic protein bcsG from salmonella typhimurium
73	c4f9dA	Alignment	not modelled	72.0	11	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
74	d1b4ub	Alignment	not modelled	64.7	14	Fold: Phosphorylase/hydrolase-like Superfamily: LigB-like Family: LigB-like
75	d1xo1a2	Alignment	not modelled	36.0	8	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
						PDB header: hydrolase

76	c2c61A_	Alignment	not modelled	35.0	13	Chain: A: PDB Molecule: a-type atp synthase non-catalytic subunit b; PDBTitle: crystal structure of the non-catalytic b subunit of a-type2 atpase from m. mazei go1
77	c5mq9A_	Alignment	not modelled	32.3	23	PDB header: translation Chain: A: PDB Molecule: uncharacterized protein yacp; PDBTitle: crystal structure of rae1 (yacp) from bacillus subtilis (w164l mutant)
78	c5ujdB_	Alignment	not modelled	27.0	17	PDB header: gene regulation Chain: B: PDB Molecule: siderophore biosynthesis protein sbni; PDBTitle: sbni from staphylococcus pseudintermedius
79	d1tfra2	Alignment	not modelled	23.0	12	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
80	c2ihnA_	Alignment	not modelled	19.4	8	PDB header: hydrolase/dna Chain: A: PDB Molecule: ribonuclease h; PDBTitle: co-crystal of bacteriophage t4 rnase h with a fork dna2 substrate
81	d1okga1	Alignment	not modelled	19.3	6	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
82	c3wrB_	Alignment	not modelled	17.6	19	PDB header: oxidoreductase Chain: B: PDB Molecule: gallate dioxygenase; PDBTitle: crystal structure of the anaerobic h124f desb-gallate complex
83	c4awaA_	Alignment	not modelled	17.0	14	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: legumain; PDBTitle: crystal structure of active legumain in complex with yvad-cmk2 at ph 5.0
84	d1skyb3	Alignment	not modelled	16.1	8	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
85	d1fx0a3	Alignment	not modelled	16.0	5	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
86	c30aaO_	Alignment	not modelled	15.7	11	PDB header: hydrolase/transport protein Chain: O: PDB Molecule: atp synthase gamma chain; PDBTitle: structure of the e.coli f1-atp synthase inhibited by subunit epsilon
87	c5ujeA_	Alignment	not modelled	15.0	12	PDB header: gene regulation Chain: A: PDB Molecule: sbni protein; PDBTitle: sbni with c-terminal truncation from staphylococcus aureus
88	c1okgA_	Alignment	not modelled	15.0	6	PDB header: transferase Chain: A: PDB Molecule: possible 3-mercaptopyruvate sulfurtransferase; PDBTitle: 3-mercaptopyruvate sulfurtransferase from leishmania major
89	c4f6oA_	Alignment	not modelled	14.1	19	PDB header: hydrolase Chain: A: PDB Molecule: metacaspase-1; PDBTitle: crystal structure of the yeast metacaspase yca1
90	c5bo5B_	Alignment	not modelled	14.1	10	PDB header: hydrolase Chain: B: PDB Molecule: neq263; PDBTitle: structure of a unique atp synthase subunit neqb from nanoarchaeum2 equitans
91	c3k1tA_	Alignment	not modelled	13.8	12	PDB header: ligase Chain: A: PDB Molecule: glutamate--cysteine ligase gsha; PDBTitle: crystal structure of putative gamma-glutamylcysteine synthetase2 (yp_546622.1) from methylobacillus flagellatus kt at 1.90 a3 resolution
92	c6re1S_	Alignment	not modelled	13.0	17	PDB header: proton transport Chain: S: PDB Molecule: atp synthase gamma chain, mitochondrial; PDBTitle: cryo-em structure of polytomella f-atp synthase, rotary substate 2a,2 focussed refinement of f1 head and rotor
93	d2ffea1	Alignment	not modelled	11.5	14	Fold: CofD-like Superfamily: CofD-like Family: CofD-like
94	c2v6zM_	Alignment	not modelled	11.0	14	PDB header: transferase Chain: M: PDB Molecule: dna polymerase epsilon subunit 2; PDBTitle: solution structure of amino-terminal domain of human dna polymerase2 epsilon subunit b
95	d1iowa1	Alignment	not modelled	10.8	35	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: D-Alanine ligase N-terminal domain
96	c6q45C_	Alignment	not modelled	10.5	7	PDB header: hydrolase Chain: C: PDB Molecule: atp synthase subunit alpha; PDBTitle: f1-atpase from fusobacterium nucleatum
97	d2cz4a1	Alignment	not modelled	10.4	7	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Prokaryotic signal transducing protein
98	c2r9vA_	Alignment	not modelled	9.9	15	PDB header: hydrolase Chain: A: PDB Molecule: atp synthase subunit alpha; PDBTitle: crystal structure of atp synthase subunit alpha (tm1612) from2 thermotoga maritima at 2.10 a resolution
99	c4ng4B_	Alignment	not modelled	9.5	15	PDB header: transferase Chain: B: PDB Molecule: phosphoglycerate kinase; PDBTitle: structure of phosphoglycerate kinase (cbu_1782) from coxiella burnetii