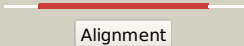

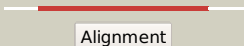

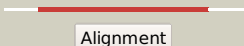







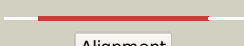











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0296c_(-)_359758_361155
Date	Tue Jul 23 14:50:36 BST 2019
Unique Job ID	19e4207588d88f1b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4uplC_	 Alignment		100.0	28	PDB header: hydrolase Chain: C: PDB Molecule: sulfatase family protein; PDBTitle: dimeric sulfatase spas2 from silicibacter pomeroyi
2	c4upiA_	 Alignment		100.0	28	PDB header: hydrolase Chain: A: PDB Molecule: sulfatase family protein; PDBTitle: dimeric sulfatase spas1 from silicibacter pomeroyi
3	c4mivB_	 Alignment		100.0	29	PDB header: hydrolase Chain: B: PDB Molecule: n-sulphoglucosamine sulphohydrolase; PDBTitle: crystal structure of sulfamidase, crystal form I
4	c4ug4H_	 Alignment		100.0	28	PDB header: hydrolase Chain: H: PDB Molecule: choline sulfatase; PDBTitle: crystal structure of a choline sulfatase from sinorhizobium2 melliloti
5	c4upkC_	 Alignment		100.0	28	PDB header: hydrolase Chain: C: PDB Molecule: phosphonate monoester hydrolase; PDBTitle: phosphonate monoester hydrolase sppmh from silicibacter pomeroyi
6	c6hhmA_	 Alignment		100.0	24	PDB header: hydrolase Chain: A: PDB Molecule: arylsulfatase; PDBTitle: crystal structure of the family s1_7 ulvan-specific sulfatase fa220702 from formosa agariphila
7	c4uphA_	 Alignment		100.0	26	PDB header: hydrolase Chain: A: PDB Molecule: sulfatase (sulfuric ester hydrolase) protein; PDBTitle: crystal structure of phosphonate monoester hydrolase of agrobacterium2 radiobacter
8	c3b5qB_	 Alignment		100.0	26	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 Å resolution
9	c2vqrA_	 Alignment		100.0	30	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
10	c3ed4A_	 Alignment		100.0	29	PDB header: transferase Chain: A: PDB Molecule: arylsulfatase; PDBTitle: crystal structure of putative arylsulfatase from escherichia coli
11	c5g2vA_	 Alignment		100.0	28	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.

12	c2qzuA_	Alignment		100.0	24	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
13	c6b1vB_	Alignment		100.0	24	PDB header: hydrolase Chain: B; PDB Molecule: iota-carrageenan sulfatase; PDBTitle: crystal structure of ps i-cgsb c78s in complex with i-neocarratetraose
14	d1fsua_	Alignment		100.0	25	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Arylsulfatase
15	d1hdha_	Alignment		100.0	26	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Arylsulfatase
16	d1lauka_	Alignment		100.0	30	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Arylsulfatase
17	c5fqIA_	Alignment		100.0	27	PDB header: hydrolase Chain: A; PDB Molecule: iduronate-2-sulfatase; PDBTitle: insights into hunter syndrome from the structure of iduronate-2-2 sulfatase
18	d1p49a_	Alignment		100.0	22	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Arylsulfatase
19	c6j66B_	Alignment		100.0	28	PDB header: hydrolase Chain: B; PDB Molecule: chondroitin sulfate/dermatan sulfate 4-o-endosulfatase PDBTitle: chondroitin sulfate/dermatan sulfate endolytic 4-o-sulfatase
20	c4fdiA_	Alignment		100.0	25	PDB header: hydrolase Chain: A; PDB Molecule: n-acetylgalactosamine-6-sulfatase; PDBTitle: the molecular basis of mucopolysaccharidosis iv a
21	c6hr5A_	Alignment	not modelled	100.0	24	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
22	c3lxqB_	Alignment	not modelled	100.0	21	PDB header: structure 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
23	c4uopB_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: B; PDB Molecule: lipoteichoic acid primase; PDBTitle: crystal structure of the lipoteichoic acid synthase ltap from listeria2 monocytogenes
24	c2w8dB_	Alignment	not modelled	100.0	18	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
25	c5i5fA_	Alignment	not modelled	100.0	19	PDB header: membrane protein Chain: A; PDB Molecule: inner membrane protein yejm; PDBTitle: salmonella global domain 191
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	c4uorK_	Alignment	not modelled	100.0	18	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
28	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
29	c6bneA	Alignment	not modelled	100.0	16	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
30	c6a82A	Alignment	not modelled	100.0	14	PDB header: transferase Chain: A: PDB Molecule: phosphoethanolamine transferase eptc; PDBTitle: crystal structure of the c-terminal periplasmic domain of eceptc from2 escherichia coli
31	c4tn0C	Alignment	not modelled	100.0	10	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
32	c4kayA	Alignment	not modelled	100.0	14	PDB header: transferase Chain: A: PDB Molecule: yhbxyjhwyjip/yjdb family protein; PDBTitle: structure of the soluble domain of lipooligosaccharide2 phosphoethanolamine transferase a from neisseria meningitidis -3 complex with zn
33	c2zktB	Alignment	not modelled	100.0	20	PDB header: isomerase Chain: B: PDB Molecule: 2,3-bisphosphoglycerate-independent phosphoglycerate PDBTitle: structure of ph0037 protein from pyrococcus horikoshii
34	c5tj3A	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: alkaline phosphatase pafa; PDBTitle: crystal structure of wild type alkaline phosphatase pafa to 1.7a2 resolution
35	c4lqvA	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: bis(5'-adenosyl)-triphosphatase enpp4; PDBTitle: crystal structure of human enpp4 with amp
36	c3q3qA	Alignment	not modelled	100.0	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
37	c3m8yC	Alignment	not modelled	100.0	15	PDB header: isomerase Chain: C: PDB Molecule: phosphopentomutase; PDBTitle: phosphopentomutase from bacillus cereus after glucose-1,6-bisphosphate2 activation
38	c5udyA	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: ectonucleotide pyrophosphatase/phosphodiesterase family PDBTitle: human alkaline sphingomyelinase (alk-smase, enpp7, npp7)
39	c5u9zB	Alignment	not modelled	100.0	11	PDB header: transferase Chain: B: PDB Molecule: phosphoglycerol transferase; PDBTitle: phosphoglycerol transferase gach from streptococcus pyogenes
40	c2qsoB	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: B: PDB Molecule: phosphodiesterase-nucleotide pyrophosphatase; PDBTitle: structure of xac nucleotide pyrophosphatase/phosphodiesterase in2 complex with vanadate
41	c5fgnA	Alignment	not modelled	100.0	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
42	c5vemA	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: ectonucleotide pyrophosphatase/phosphodiesterase family PDBTitle: human ectonucleotide pyrophosphatase / phosphodiesterase 5 (enpp5,2 npp5)
43	d1o98a2	Alignment	not modelled	100.0	18	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: 2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, catalytic domain
44	c5egeD	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: D: PDB Molecule: ectonucleotide pyrophosphatase/phosphodiesterase family PDBTitle: structure of enpp6, a choline-specific glycerophosphodiester-2 phosphodiesterase
45	d2i09a1	Alignment	not modelled	100.0	16	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: DeoB catalytic domain-like
46	c2i09A	Alignment	not modelled	100.0	14	PDB header: isomerase Chain: A: PDB Molecule: phosphopentomutase; PDBTitle: crystal structure of putative phosphopentomutase from streptococcus2 mutans
47	c6c02B	Alignment	not modelled	100.0	21	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)
48	c5gz4A	Alignment	not modelled	100.0	18	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)
49	c4b56A	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: ectonucleotide pyrophosphatase/phosphodiesterase family PDBTitle: structure of ectonucleotide pyrophosphatase-phosphodiesterase-12 (npp1)
50	c5gz5A	Alignment	not modelled	100.0	18	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
51	c2xrgA	Alignment	not modelled	100.0	24	PDB header: hydrolase Chain: A: PDB Molecule: ectonucleotide pyrophosphatase/phosphodiesterase family PDBTitle: crystal structure of autotaxin (enpp2) in complex with

						the2 ha155 boronic acid inhibitor
52	c2xr9A_	Alignment	not modelled	100.0	25	PDB header: hydrolase Chain: A: PDB Molecule: ectonucleotide pyrophosphatase/phosphodiesterase family PDBTitle: crystal structure of autotaxin (enpp2)
53	c3szzA_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: phosphonoacetate hydrolase; PDBTitle: crystal structure of phosphonoacetate hydrolase from sinorhizobium2 meliloti 1021 in complex with acetate
54	d1ei6a_	Alignment	not modelled	100.0	20	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Phosphonoacetate hydrolase
55	c1o98A_	Alignment	not modelled	99.8	23	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
56	c5kgmA_	Alignment	not modelled	99.8	21	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)
57	c4my4A_	Alignment	not modelled	99.8	25	PDB header: isomerase Chain: A: PDB Molecule: 2,3-bisphosphoglycerate-independent phosphoglycerate PDBTitle: crystal structure of phosphoglycerate mutase from staphylococcus2 aureus.
58	c2d1gB_	Alignment	not modelled	99.8	15	PDB header: hydrolase Chain: B: PDB Molecule: acid phosphatase; PDBTitle: structure of francisella tularensis acid phosphatase a (acpa) bound to2 orthovanadate
59	c5vpuA_	Alignment	not modelled	99.8	20	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
60	c3igzB_	Alignment	not modelled	99.8	17	PDB header: isomerase Chain: B: PDB Molecule: cofactor-independent phosphoglycerate mutase; PDBTitle: crystal structures of leishmania mexicana phosphoglycerate2 mutase at low cobalt concentration
61	c2iucB_	Alignment	not modelled	99.6	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	99.5	19	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Alkaline phosphatase
63	c2w0yB_	Alignment	not modelled	99.4	20	PDB header: hydrolase Chain: B: PDB Molecule: alkaline phosphatase; PDBTitle: h.salinarum alkaline phosphatase
64	d1zeda1	Alignment	not modelled	99.3	17	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Alkaline phosphatase
65	c1ew2A_	Alignment	not modelled	99.3	14	PDB header: hydrolase Chain: A: PDB Molecule: phosphatase; PDBTitle: crystal structure of a human phosphatase
66	c2x98A_	Alignment	not modelled	99.3	20	PDB header: hydrolase Chain: A: PDB Molecule: alkaline phosphatase; PDBTitle: h.salinarum alkaline phosphatase
67	c3a52A_	Alignment	not modelled	99.2	17	PDB header: hydrolase Chain: A: PDB Molecule: cold-active alkaline phosphatase; PDBTitle: crystal structure of cold-active alkailne phosphatase from2 psychrophile shewanella sp.
68	d1k7ha_	Alignment	not modelled	99.2	17	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Alkaline phosphatase
69	c3e2dB_	Alignment	not modelled	99.1	18	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	98.9	20	PDB header: hydrolase Chain: B: PDB Molecule: alkaline phosphatase; PDBTitle: structural characteristics of alkaline phosphatase from a moderately2 halophilic bacteria halomonas sp.593
71	c5oltA_	Alignment	not modelled	98.4	14	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
72	c3iddA_	Alignment	not modelled	96.2	19	PDB header: isomerase Chain: A: PDB Molecule: 2,3-bisphosphoglycerate-independent PDBTitle: cofactor-independent phosphoglycerate mutase from2 thermoplasma acidophilum dsm 1728
73	d1b4ub_	Alignment	not modelled	73.1	14	Fold: Phosphorylase/hydrolase-like Superfamily: LigB-like Family: LigB-like
74	c5xq0B_	Alignment	not modelled	60.8	13	PDB header: signaling protein Chain: B: PDB Molecule: fermitin family homolog 2,integrin beta-1; PDBTitle: structural basis of kindlin-mediated integrin recognition and2 activation
75	d3cu0a1	Alignment	not modelled	56.2	28	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: 1,3-glucuronyltransferase
76	c2d0jD_	Alignment	not modelled	40.9	24	PDB header: transferase Chain: D: PDB Molecule: galactosylgalactosylxylosylprotein 3-beta- PDBTitle: crystal structure of human glcat-s apo form

77	c3oaaO_	Alignment	not modelled	40.5	20	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
78	d1v82a_	Alignment	not modelled	34.2	28	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: 1,3-glucuronyltransferase
79	d1xo1a2	Alignment	not modelled	31.3	15	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
80	c5mq9A_	Alignment	not modelled	29.4	31	PDB header: translation Chain: A: PDB Molecule: uncharacterized protein yacp; PDBTitle: crystal structure of rae1 (yacp) from bacillus subtilis (w164l mutant)
81	c4awaA_	Alignment	not modelled	28.8	33	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
82	c5zwlG_	Alignment	not modelled	28.1	14	PDB header: hydrolase Chain: G: PDB Molecule: atp synthase gamma chain; PDBTitle: crystal structure of the gamma - epsilon complex of photosynthetic2 cyanobacterial f1-atpase
83	c5zbiB_	Alignment	not modelled	23.1	13	PDB header: plant protein Chain: B: PDB Molecule: peptide asparaginyl ligase; PDBTitle: crystal structure of asparaginyl endopeptidases from viola canadensis
84	c6f5dG_	Alignment	not modelled	23.1	13	PDB header: hydrolase Chain: G: PDB Molecule: atp synthase gamma subunit; PDBTitle: trypanosoma brucei f1-atpase
85	c3wrbb_	Alignment	not modelled	21.2	16	PDB header: oxidoreductase Chain: B: PDB Molecule: gallate dioxygenase; PDBTitle: crystal structure of the anaerobic h124f desb-gallate complex
86	c2w6hG_	Alignment	not modelled	18.4	11	PDB header: hydrolase Chain: G: PDB Molecule: atp synthase subunit gamma, mitochondrial; PDBTitle: low resolution structures of bovine mitochondrial f1-atpase during2 controlled dehydration: hydration state 4a.
87	c5h0ib_	Alignment	not modelled	18.0	11	PDB header: hydrolase Chain: B: PDB Molecule: asparaginyl endopeptidase; PDBTitle: name to be released when published
88	d1tfra2	Alignment	not modelled	17.5	19	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
89	c4f6oA_	Alignment	not modelled	16.5	14	PDB header: hydrolase Chain: A: PDB Molecule: metacaspase-1; PDBTitle: crystal structure of the yeast metacaspase yca1
90	c6fkig_	Alignment	not modelled	16.4	16	PDB header: membrane protein Chain: G: PDB Molecule: atp synthase subunit c, chloroplastic; PDBTitle: chloroplast f1fo conformation 3
91	c6idvb_	Alignment	not modelled	16.2	10	PDB header: ligase Chain: B: PDB Molecule: peptide asparaginyl ligases; PDBTitle: peptide asparaginyl ligases from viola yedoensis
92	d1okga1	Alignment	not modelled	15.0	18	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
93	c4fquB_	Alignment	not modelled	15.0	8	PDB header: hydrolase Chain: B: PDB Molecule: legumain; PDBTitle: crystal structure of prolegumain
94	c6q45G_	Alignment	not modelled	14.7	12	PDB header: hydrolase Chain: G: PDB Molecule: atp synthase gamma chain; PDBTitle: f1-atpase from fusobacterium nucleatum
95	c5nijB_	Alignment	not modelled	14.4	13	PDB header: ligase Chain: B: PDB Molecule: vacuolar-processing enzyme gamma-isozyme; PDBTitle: crystal structure of arabidopsis thaliana legumain isoform gamma in2 two-chain activation state
96	c4hdnB_	Alignment	not modelled	14.0	14	PDB header: transferase Chain: B: PDB Molecule: arsb; PDBTitle: crystal structure of arsb in the substrate-free state.
97	d1l5oa_	Alignment	not modelled	13.9	40	Fold: Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) Superfamily: Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) Family: Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT)
98	d1ntha_	Alignment	not modelled	13.5	18	Fold: TIM beta/alpha-barrel Superfamily: Monomethylamine methyltransferase MtmB Family: Monomethylamine methyltransferase MtmB
99	c2r1fB_	Alignment	not modelled	12.7	17	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: predicted aminodeoxychorismate lyase; PDBTitle: crystal structure of predicted aminodeoxychorismate lyase from2 escherichia coli