

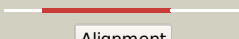

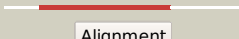

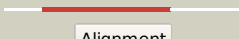

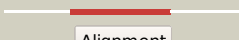
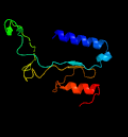



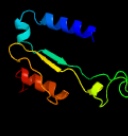






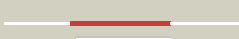



Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1755c_plcD_1986861_1987682
 Date Fri Aug 2 13:30:36 BST 2019
 Unique Job ID 95c2e7892fb87a9b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2d1gB_	 Alignment		100.0	24	PDB header: hydrolase Chain: B: PDB Molecule: acid phosphatase; PDBTitle: structure of francisella tularensis acid phosphatase a (acpa) bound to2 orthovanadate
2	c6hr5A_	 Alignment		98.5	18	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		98.4	18	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Arylsulfatase
4	c6b1vB_	 Alignment		98.3	17	PDB header: hydrolase Chain: B: PDB Molecule: iota-carrageenan sulfatase; PDBTitle: crystal structure of ps i-cgsb c78s in complex with i-neocarratetraose
5	d1p49a_	 Alignment		98.2	17	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Arylsulfatase
6	c4upkC_	 Alignment		98.2	16	PDB header: hydrolase Chain: C: PDB Molecule: phosphonate monoester hydrolase; PDBTitle: phosphonate monoester hydrolase sppmh from silicibacter pomeroyi
7	c6j66B_	 Alignment		98.2	14	PDB header: hydrolase Chain: B: PDB Molecule: chondroitin sulfate/dermatan sulfate 4-o-endosulfatase PDBTitle: chondroitin sulfate/dermatan sulfate endolytic 4-o-sulfatase
8	c3lxqB_	 Alignment		98.2	17	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
9	c4uopB_	 Alignment		98.2	16	PDB header: transferase Chain: B: PDB Molecule: lipoteichoic acid primase; PDBTitle: crystal structure of the lipoteichoic acid synthase ltap from listeria2 monocytogenes
10	c4fdiA_	 Alignment		98.0	16	PDB header: hydrolase Chain: A: PDB Molecule: n-acetylgalactosamine-6-sulfatase; PDBTitle: the molecular basis of mucopolysaccharidosis iv a
11	d1fsua_	 Alignment		98.0	20	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Arylsulfatase

12	c4ug4H_	Alignment		97.9	11	PDB header: hydrolase Chain: H: PDB Molecule: choline sulfatase; PDBTitle: crystal structure of a choline sulfatase from sinorhizobium2 melliloti
13	c6hbmA_	Alignment		97.9	16	PDB header: hydrolase Chain: A: PDB Molecule: arylsulfatase; PDBTitle: crystal structure of the family s1_7 ulvan-specific sulfatase fa220702 from formosa agariphila
14	c5g2vA_	Alignment		97.9	17	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.
15	c4uplC_	Alignment		97.9	12	PDB header: hydrolase Chain: C: PDB Molecule: sulfatase family protein; PDBTitle: dimeric sulfatase spas2 from silicibacter pomeroyi
16	c5fqIA_	Alignment		97.9	20	PDB header: hydrolase Chain: A: PDB Molecule: iduronate-2-sulfatase; PDBTitle: insights into hunter syndrome from the structure of iduronate-2-2 sulfatase
17	c4mivB_	Alignment		97.8	20	PDB header: hydrolase Chain: B: PDB Molecule: n-sulphoglucosamine sulphohydrolase; PDBTitle: crystal structure of sulfamidase, crystal form I
18	c3ed4A_	Alignment		97.8	15	PDB header: transferase Chain: A: PDB Molecule: arylsulfatase; PDBTitle: crystal structure of putative arylsulfatase from escherichia coli
19	c2qzuA_	Alignment		97.8	15	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
20	c5i5fA_	Alignment		97.8	17	PDB header: membrane protein Chain: A: PDB Molecule: inner membrane protein yejm; PDBTitle: salmonella global domain 191
21	d1hdha_	Alignment	not modelled	97.8	16	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Arylsulfatase
22	c2vqrA_	Alignment	not modelled	97.7	16	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
23	c4uorK_	Alignment	not modelled	97.7	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
24	c4upiA_	Alignment	not modelled	97.7	12	PDB header: hydrolase Chain: A: PDB Molecule: sulfatase family protein; PDBTitle: dimeric sulfatase spas1 from silicibacter pomeroyi
25	c2w8dB_	Alignment	not modelled	97.6	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
26	c2w5tA_	Alignment	not modelled	97.6	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	c5k4pA_	Alignment	not modelled	97.6	13	PDB header: transferase Chain: A: PDB Molecule: probable phosphatidylethanolamine transferase mcr-1; PDBTitle: catalytic domain of mcr-1 phosphoethanolamine transferase PDB header: transferase

28	c4tn0C_	Alignment	not modelled	97.5	8	Chain: C: PDB Molecule: upf0141 protein yjdb; PDBTitle: crystal structure of the c-terminal periplasmic domain of2 phosphoethanolamine transferase eptc from campylobacter jejuni
29	c3b5qB_	Alignment	not modelled	97.5	19	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
30	c4uphA_	Alignment	not modelled	97.5	22	PDB header: hydrolase Chain: A: PDB Molecule: sulfatase (sulfuric ester hydrolase) protein; PDBTitle: crystal structure of phosphonate monoester hydrolase of agrobacterium2 radiobacter
31	c6a82A_	Alignment	not modelled	97.4	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
32	c6bneA_	Alignment	not modelled	97.1	14	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
33	c3m8yC_	Alignment	not modelled	97.0	26	PDB header: isomerase Chain: C: PDB Molecule: phosphopentomutase; PDBTitle: phosphopentomutase from bacillus cereus after glucose-1,6-bisphosphate2 activation
34	d2i09a1	Alignment	not modelled	96.5	16	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: DeoB catalytic domain-like
35	c4kayA_	Alignment	not modelled	96.4	8	PDB header: transferase Chain: A: PDB Molecule: yhbxx/yhjw/yjip/yjdb family protein; PDBTitle: structure of the soluble domain of lipooligosaccharide2 phosphoethanolamine transferase a from neisseria meningitidis -3 complex with zn
36	d1o98a2	Alignment	not modelled	96.3	14	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: 2,3-bisphosphoglycerate-independent phosphoglycerate mutase, catalytic domain
37	c5u9zB_	Alignment	not modelled	96.1	12	PDB header: transferase Chain: B: PDB Molecule: phosphoglycerol transferase; PDBTitle: phosphoglycerol transferase gach from streptococcus pyogenes
38	c2zktB_	Alignment	not modelled	95.5	14	PDB header: isomerase Chain: B: PDB Molecule: 2,3-bisphosphoglycerate-independent phosphoglycerate PDBTitle: structure of ph0037 protein from pyrococcus horikoshii
39	c2i09A_	Alignment	not modelled	95.5	16	PDB header: isomerase Chain: A: PDB Molecule: phosphopentomutase; PDBTitle: crystal structure of putative phosphopentomutase from streptococcus2 mutans
40	c5fgnA_	Alignment	not modelled	93.9	8	PDB header: transferase,hydrolase Chain: A: PDB Molecule: lipooligosaccharide phosphoethanolamine transferase a; PDBTitle: integral membrane protein lipooligosaccharide phosphoethanolamine2 transferase a (epta) from neisseria meningitidis
41	c5udyA_	Alignment	not modelled	92.8	16	PDB header: hydrolase Chain: A: PDB Molecule: ectonucleotide pyrophosphatase/phosphodiesterase family PDBTitle: human alkaline sphingomyelinase (alk-smase, enpp7, npp7)
42	c5kgmA_	Alignment	not modelled	91.4	26	PDB header: isomerase Chain: A: PDB Molecule: 2,3-bisphosphoglycerate-independent phosphoglycerate PDBTitle: 2.95Å resolution structure of apo independent phosphoglycerate mutase2 from c. elegans (monoclinic form)
43	c1o98A_	Alignment	not modelled	81.5	20	PDB header: isomerase Chain: A: PDB Molecule: 2,3-bisphosphoglycerate-independent PDBTitle: 1.4Å crystal structure of phosphoglycerate mutase from2 bacillus stearothermophilus complexed with3 2-phosphoglycerate
44	c3iqzB_	Alignment	not modelled	81.3	14	PDB header: isomerase Chain: B: PDB Molecule: cofactor-independent phosphoglycerate mutase; PDBTitle: crystal structures of leishmania mexicana phosphoglycerate2 mutase at low cobalt concentration
45	c5egeD_	Alignment	not modelled	80.7	14	PDB header: hydrolase Chain: D: PDB Molecule: ectonucleotide pyrophosphatase/phosphodiesterase family PDBTitle: structure of enpp6, a choline-specific glycerophosphodiester-2 phosphodiesterase
46	c4lqyA_	Alignment	not modelled	78.5	10	PDB header: hydrolase Chain: A: PDB Molecule: bis(5'-adenosyl)-triphosphatase enpp4; PDBTitle: crystal structure of human enpp4 with amp
47	c5tj3A_	Alignment	not modelled	76.8	10	PDB header: hydrolase Chain: A: PDB Molecule: alkaline phosphatase pafa; PDBTitle: crystal structure of wild type alkaline phosphatase pafa to 1.7Å2 resolution
48	c5vemA_	Alignment	not modelled	73.8	11	PDB header: hydrolase Chain: A: PDB Molecule: ectonucleotide pyrophosphatase/phosphodiesterase family PDBTitle: human ectonucleotide pyrophosphatase / phosphodiesterase 5 (enpp5,2 npp5)
49	c2gsoB_	Alignment	not modelled	73.1	13	PDB header: hydrolase Chain: B: PDB Molecule: phosphodiesterase-nucleotide pyrophosphatase; PDBTitle: structure of xac nucleotide pyrophosphatase/phosphodiesterase in2 complex with vanadate
50	c5vpuA_	Alignment	not modelled	69.7	16	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
						PDB header: isomerase

51	c4my4A	Alignment	not modelled	55.4	23	Chain: A: PDB Molecule: 2,3-bisphosphoglycerate-independent phosphoglycerate PDBTitle: crystal structure of phosphoglycerate mutase from staphylococcus2 aureus.
52	c5bu6B	Alignment	not modelled	50.9	10	PDB header: hydrolase Chain: B: PDB Molecule: bpsb (pgab), poly-beta-1,6-n-acetyl-d-glucosamine n- PDBTitle: structure of bpsb deaceylase domain from bordetella bronchiseptica
53	c4f9dA	Alignment	not modelled	45.5	17	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
54	d1okta2	Alignment	not modelled	40.9	21	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
55	c4u10B	Alignment	not modelled	40.8	17	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
56	d1y6va1	Alignment	not modelled	38.8	16	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Alkaline phosphatase
57	d1k0ma2	Alignment	not modelled	37.8	22	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
58	c6dq3B	Alignment	not modelled	36.8	20	PDB header: hydrolase Chain: B: PDB Molecule: polysaccharide deacetylase; PDBTitle: streptococcus pyogenes deacetylase pdi in complex with acetate
59	d1ei6a	Alignment	not modelled	34.5	12	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Phosphonoacetate hydrolase
60	c2w0yB	Alignment	not modelled	29.5	29	PDB header: hydrolase Chain: B: PDB Molecule: alkaline phosphatase; PDBTitle: h.salinarum alkaline phosphatase
61	c5j43F	Alignment	not modelled	27.0	56	PDB header: toxin Chain: F: PDB Molecule: trna nuclease cdia; PDBTitle: cdia-ct from uropathogenic escherichia coli in complex with cysk
62	c2x98A	Alignment	not modelled	26.3	29	PDB header: hydrolase Chain: A: PDB Molecule: alkaline phosphatase; PDBTitle: h.salinarum alkaline phosphatase
63	c3q3qA	Alignment	not modelled	25.2	15	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
64	c4ke3D	Alignment	not modelled	23.9	33	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)
65	c1x5eA	Alignment	not modelled	22.7	4	PDB header: electron transport Chain: A: PDB Molecule: thioredoxin domain containing protein 1; PDBTitle: the solution structure of the thioredoxin-like domain of2 human thioredoxin-related transmembrane protein
66	d2gsra2	Alignment	not modelled	22.1	30	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
67	d1m0ua2	Alignment	not modelled	21.3	19	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
68	d1v2aa2	Alignment	not modelled	20.5	15	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
69	c2iucB	Alignment	not modelled	18.4	14	PDB header: hydrolase Chain: B: PDB Molecule: alkaline phosphatase; PDBTitle: structure of alkaline phosphatase from the antarctic bacterium tab5
70	d2gsqa2	Alignment	not modelled	17.0	23	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
71	c3e2dB	Alignment	not modelled	16.2	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
72	c2kwlA	Alignment	not modelled	15.6	29	PDB header: lipid binding protein Chain: A: PDB Molecule: acyl carrier protein; PDBTitle: solution structure of acyl carrier protein from borrelia burgdorferi
73	d1pn9a2	Alignment	not modelled	15.3	13	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
74	c2odiA	Alignment	not modelled	14.9	32	PDB header: hydrolase/dna Chain: A: PDB Molecule: r.bcni; PDBTitle: restriction endonuclease bcni-cognate dna substrate complex
75	d2g8oa1	Alignment	not modelled	14.9	20	Fold: Thymidylate synthase/dCMP hydroxymethylase Superfamily: Thymidylate synthase/dCMP hydroxymethylase Family: Thymidylate synthase/dCMP hydroxymethylase
76	d1rk4a2	Alianment	not modelled	14.8	21	Fold: Thioredoxin fold Superfamily: Thioredoxin-like

						Family: Glutathione S-transferase (GST), N-terminal domain
77	d1b5ea_	Alignment	not modelled	14.5	17	Fold: Thymidylate synthase/dCMP hydroxymethylase Superfamily: Thymidylate synthase/dCMP hydroxymethylase Family: Thymidylate synthase/dCMP hydroxymethylase
78	c5vodA_	Alignment	not modelled	14.0	27	PDB header: viral protein/immune system Chain: A: PDB Molecule: envelope glycoprotein h; PDBTitle: crystal structure of hcmv pentamer in complex with neutralizing2 antibody 9i6
79	c5a63A_	Alignment	not modelled	13.9	19	PDB header: hydrolase Chain: A: PDB Molecule: nicastrin; PDBTitle: cryo-em structure of the human gamma-secretase complex at 3.4 angstrom2 resolution.
80	d1tu7a2	Alignment	not modelled	13.7	22	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
81	d1g57a_	Alignment	not modelled	13.6	29	Fold: YrdC/RibB Superfamily: YrdC/RibB Family: 3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
82	d1tw9a2	Alignment	not modelled	13.5	26	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
83	c3wbhB_	Alignment	not modelled	13.5	24	PDB header: hydrolase Chain: B: PDB Molecule: alkaline phosphatase; PDBTitle: structural characteristics of alkaline phosphatase from a moderately2 halophilic bacteria halomonas sp.593
84	c3ogmW_	Alignment	not modelled	13.3	50	PDB header: protein binding Chain: W: PDB Molecule: jaz1 degron peptide; PDBTitle: structure of coi1-ask1 in complex with coronatine and the jaz1 degron
85	c3ogmX_	Alignment	not modelled	13.3	50	PDB header: protein binding Chain: X: PDB Molecule: jaz1 degron peptide; PDBTitle: structure of coi1-ask1 in complex with coronatine and the jaz1 degron
86	c3ogmU_	Alignment	not modelled	13.3	50	PDB header: protein binding Chain: U: PDB Molecule: jaz1 degron peptide; PDBTitle: structure of coi1-ask1 in complex with coronatine and the jaz1 degron
87	c3ogmS_	Alignment	not modelled	13.3	50	PDB header: protein binding Chain: S: PDB Molecule: jaz1 degron peptide; PDBTitle: structure of coi1-ask1 in complex with coronatine and the jaz1 degron
88	c3oglU_	Alignment	not modelled	13.3	50	PDB header: protein binding Chain: U: PDB Molecule: jaz1 incomplete degron peptide; PDBTitle: structure of coi1-ask1 in complex with ja-isoleucine and the jaz12 degron
89	c3oglS_	Alignment	not modelled	13.3	50	PDB header: protein binding Chain: S: PDB Molecule: jaz1 incomplete degron peptide; PDBTitle: structure of coi1-ask1 in complex with ja-isoleucine and the jaz12 degron
90	c3ogmQ_	Alignment	not modelled	13.3	50	PDB header: protein binding Chain: Q: PDB Molecule: jaz1 degron peptide; PDBTitle: structure of coi1-ask1 in complex with coronatine and the jaz1 degron
91	c3oglW_	Alignment	not modelled	13.3	50	PDB header: protein binding Chain: W: PDB Molecule: jaz1 incomplete degron peptide; PDBTitle: structure of coi1-ask1 in complex with ja-isoleucine and the jaz12 degron
92	c3oglR_	Alignment	not modelled	13.3	50	PDB header: protein binding Chain: R: PDB Molecule: jaz1 incomplete degron peptide; PDBTitle: structure of coi1-ask1 in complex with ja-isoleucine and the jaz12 degron
93	c3ogmV_	Alignment	not modelled	13.3	50	PDB header: protein binding Chain: V: PDB Molecule: jaz1 degron peptide; PDBTitle: structure of coi1-ask1 in complex with coronatine and the jaz1 degron
94	c3oglQ_	Alignment	not modelled	13.3	50	PDB header: protein binding Chain: Q: PDB Molecule: jaz1 incomplete degron peptide; PDBTitle: structure of coi1-ask1 in complex with ja-isoleucine and the jaz12 degron
95	c3oglV_	Alignment	not modelled	13.3	50	PDB header: protein binding Chain: V: PDB Molecule: jaz1 incomplete degron peptide; PDBTitle: structure of coi1-ask1 in complex with ja-isoleucine and the jaz12 degron
96	c3ogmR_	Alignment	not modelled	13.3	50	PDB header: protein binding Chain: R: PDB Molecule: jaz1 degron peptide; PDBTitle: structure of coi1-ask1 in complex with coronatine and the jaz1 degron
97	c3oglX_	Alignment	not modelled	13.3	50	PDB header: protein binding Chain: X: PDB Molecule: jaz1 incomplete degron peptide; PDBTitle: structure of coi1-ask1 in complex with ja-isoleucine and the jaz12 degron
98	c2qnwA_	Alignment	not modelled	13.0	26	PDB header: signaling protein Chain: A: PDB Molecule: acyl carrier protein; PDBTitle: toxoplasma gondii apicoplast-targeted acyl carrier protein
99	c1q7tA_	Alignment	not modelled	12.8	21	PDB header: hydrolase Chain: A: PDB Molecule: hypothetical protein rv1170; PDBTitle: rv1170 (mshb) from mycobacterium tuberculosis