






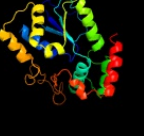







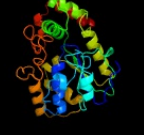









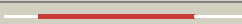



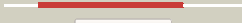
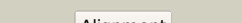




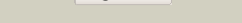


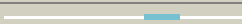
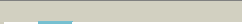



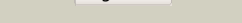





Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1373_(-)_1546018_1546998
Date	Wed Jul 31 22:05:47 BST 2019
Unique Job ID	b0ea83868c388fb2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5mekA_	 Alignment		100.0	20	PDB header: transferase Chain: A: PDB Molecule: cytosolic sulfotransferase 18; PDBTitle: sulphotransferase-18 from arabidopsis thaliana in complex with 3'-2 phosphoadenosine 5'-phosphate (pap)
2	d1fmja_	 Alignment		100.0	28	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: PAPS sulfotransferase
3	d1g3ma_	 Alignment		100.0	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: PAPS sulfotransferase
4	c2h8kA_	 Alignment		100.0	23	PDB header: transferase Chain: A: PDB Molecule: sult1c3 splice variant d; PDBTitle: human sulfotranferase sult1c3 in complex with pap
5	c3u3oA_	 Alignment		100.0	23	PDB header: transferase Chain: A: PDB Molecule: sulfotransferase 1a1; PDBTitle: crystal structure of human sult1a1 bound to pap and two 3-cyano-7-2 hydroxycoumarin
6	d1ls6a_	 Alignment		100.0	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: PAPS sulfotransferase
7	c2zvpX_	 Alignment		100.0	22	PDB header: transferase Chain: X: PDB Molecule: tyrosine-ester sulfotransferase; PDBTitle: crystal structure of mouse cytosolic sulfotransferase msult1d1 complex2 with pap and p-nitrophenol
8	d1xv1a_	 Alignment		100.0	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: PAPS sulfotransferase
9	d1q20a_	 Alignment		100.0	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: PAPS sulfotransferase
10	d1j99a_	 Alignment		100.0	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: PAPS sulfotransferase
11	d2a3ra1	 Alignment		100.0	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: PAPS sulfotransferase

12	d1aqua_	Alignment		100.0	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: PAPS sulfotransferase
13	c5x2bK_	Alignment		100.0	21	PDB header: transferase Chain: K: PDB Molecule: sulfotransferase; PDBTitle: crystal structure of mouse sulfotransferase sult7a1 complexed with pap
14	d1q44a_	Alignment		100.0	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: PAPS sulfotransferase
15	c2gwhA_	Alignment		100.0	24	PDB header: transferase Chain: A: PDB Molecule: sulfotransferase 1c2; PDBTitle: human sulfotransferase sult1c2 in complex with pap and2 pentachlorophenol
16	c1q1qA_	Alignment		100.0	25	PDB header: transferase Chain: A: PDB Molecule: sulfotransferase family, cytosolic, 2b, member 1 isoform a; PDBTitle: crystal structure of human pregnenolone sulfotransferase (sult2b1a) in2 the presence of pap
17	d3bfxa1	Alignment		100.0	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: PAPS sulfotransferase
18	c1zd1B_	Alignment		100.0	24	PDB header: transferase Chain: B: PDB Molecule: sulfotransferase 4a1; PDBTitle: human sulfotransferase sult4a1
19	c3mgbA_	Alignment		100.0	16	PDB header: transferase/antibiotic Chain: A: PDB Molecule: teg12; PDBTitle: teg 12 ternary structure complexed with pap and the teicoplanin2 aglycone
20	c3mg9A_	Alignment		100.0	16	PDB header: transferase/antibiotic Chain: A: PDB Molecule: teg12; PDBTitle: teg 12 binary structure complexed with the teicoplanin aglycone
21	c2ovfA_	Alignment	not modelled	100.0	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: stal; PDBTitle: crystal structure of stal-pap complex
22	c3ap3A_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: A: PDB Molecule: protein-tyrosine sulfotransferase 2; PDBTitle: crystal structure of human tyrosylprotein sulfotransferase-2 complexed2 with pap
23	d1t8ta_	Alignment	not modelled	100.0	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: PAPS sulfotransferase
24	c4goxA_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: A: PDB Molecule: polyketide synthase; PDBTitle: sulfotransferase domain from the synechococcus pcc 7002 olefin2 synthase
25	c4gbmA_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: A: PDB Molecule: curm sulfotransferase; PDBTitle: sulfotransferase domain from the curacin biosynthetic pathway
26	d1nsta_	Alignment	not modelled	100.0	10	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: PAPS sulfotransferase
27	c1nsta_	Alignment	not modelled	100.0	10	PDB header: sulfotransferase Chain: A: PDB Molecule: heparan sulfate n-deacetylase/n-sulfotransferase; PDBTitle: the sulfotransferase domain of human haparin sulfate n-deacetylase/n-2 sulfotransferase
28	d1vkja_	Alignment	not modelled	99.9	11	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: PAPS sulfotransferase

29	c1vkjA_	 Alignment	not modelled	99.9	11	PDB header: transferase Chain: A: PDB Molecule: heparan sulfate (glucosamine) 3-o-sulfotransferase 1; PDBTitle: crystal structure of heparan sulfate 3-o-sulfotransferase isoform 1 in2 the presence of pap
30	c3rnIA_	 Alignment	not modelled	99.9	16	PDB header: transferase Chain: A: PDB Molecule: sulfotransferase; PDBTitle: crystal structure of sulfotransferase from alicyclobacillus2 acidocaldarius
31	c3bd9A_	 Alignment	not modelled	99.9	10	PDB header: transferase Chain: A: PDB Molecule: heparan sulfate glucosamine 3-o-sulfotransferase PDBTitle: human 3-o-sulfotransferase isoform 5 with bound pap
32	c2z6vA_	 Alignment	not modelled	99.9	17	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of sulfotransferase stf9 from2 mycobacterium avium
33	c2zq5A_	 Alignment	not modelled	99.9	17	PDB header: transferase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of sulfotransferase stf1 from2 mycobacterium tuberculosis h37rv (type1 form)
34	d1texa_	 Alignment	not modelled	99.8	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: PAPS sulfotransferase
35	c5tizA_	 Alignment	not modelled	99.5	13	PDB header: transferase Chain: A: PDB Molecule: sulfotransferase; PDBTitle: schistosoma japonicum (blood fluke) sulfotransferase
36	c4mubA_	 Alignment	not modelled	98.9	10	PDB header: transferase Chain: A: PDB Molecule: sulfotransferase; PDBTitle: schistosoma mansoni (blood fluke) sulfotransferase/oxamniquine complex
37	c5t0aB_	 Alignment	not modelled	97.6	13	PDB header: transferase Chain: B: PDB Molecule: maltose binding protein - heparan sulfate 6-o- PDBTitle: crystal structure of heparan sulfate 6-o-sulfotransferase with bound2 pap and heptasaccharide substrate
38	c3f5fA_	 Alignment	not modelled	97.3	19	PDB header: transport, transferase Chain: A: PDB Molecule: maltose-binding periplasmic protein, heparan sulfate 2-o- PDBTitle: crystal structure of heparan sulfate 2-o-sulfotransferase from gallus2 gallus as a maltose binding protein fusion.
39	d1j09a2	 Alignment	not modelled	68.2	15	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
40	c4xrpA_	 Alignment	not modelled	50.4	19	PDB header: protein binding Chain: A: PDB Molecule: pnkp1; PDBTitle: structure of the pnkp1/rnl/hen1 rna repair complex
41	d1nzza_	 Alignment	not modelled	48.9	19	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
42	d1xjca_	 Alignment	not modelled	48.4	26	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
43	c4g6zA_	 Alignment	not modelled	39.0	19	PDB header: ligase Chain: A: PDB Molecule: glutamate-trna ligase; PDBTitle: crystal structure of a glutamyl-trna synthetase glurs from2 burkholderia thailandensis bound to l-glutamate
44	c2f1rA_	 Alignment	not modelled	38.1	32	PDB header: biosynthetic protein Chain: A: PDB Molecule: molybdopterin-guanine dinucleotide biosynthesis PDBTitle: crystal structure of molybdopterin-guanine biosynthesis2 protein b (mobb)
45	c4nkrB_	 Alignment	not modelled	35.3	20	PDB header: unknown function Chain: B: PDB Molecule: molybdopterin-guanine dinucleotide biosynthesis protein b; PDBTitle: the crystal structure of bacillus subtilis mobb
46	c4clvB_	 Alignment	not modelled	33.2	5	PDB header: metal binding protein Chain: B: PDB Molecule: nickel-cobalt-cadmium resistance protein nccx; PDBTitle: crystal structure of dodecylphosphocholine-solubilized nccx2 from cupriavidus metallidurans 31a
47	d1vj5a2	 Alignment	not modelled	31.7	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
48	c6mzml_	 Alignment	not modelled	30.3	10	PDB header: transcription/dna Chain: I: PDB Molecule: transcription initiation factor tfiid subunit 6; PDBTitle: human tfiid bound to promoter dna and tfiia
49	c3aiiA_	 Alignment	not modelled	26.3	14	PDB header: ligase Chain: A: PDB Molecule: glutamyl-trna synthetase; PDBTitle: archaeal non-discriminating glutamyl-trna synthetase from2 methanothermobacter thermautotrophicus
50	c2hw2A_	 Alignment	not modelled	25.9	17	PDB header: transferase Chain: A: PDB Molecule: rifampin adp-ribosyl transferase; PDBTitle: crystal structure of rifampin adp-ribosyl transferase in complex with2 rifampin
51	d2iela1	 Alignment	not modelled	25.0	17	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
52	c6f3tK_	 Alignment	not modelled	24.6	13	PDB header: transcription Chain: K: PDB Molecule: transcription initiation factor tfiid subunit 6; PDBTitle: crystal structure of the human taf5-taf6-taf9 complex
53	c3epvB_	 Alignment	not modelled	24.0	5	PDB header: metal binding protein Chain: B: PDB Molecule: nickel and cobalt resistance protein cnrr; PDBTitle: x-ray structure of the metal-sensor cnrx in both the apo- and copper-2 bound forms PDB header: transferase

54	c1yj5B_	Alignment	not modelled	22.5	17	Chain: B: PDB Molecule: 5' polynucleotide kinase-3' phosphatase catalytic domain; PDBTitle: molecular architecture of mammalian polynucleotide kinase, a dna2 repair enzyme
55	c4fczB_	Alignment	not modelled	22.4	11	PDB header: transport protein Chain: B: PDB Molecule: toluene-tolerance protein; PDBTitle: crystal structure of toluene-tolerance protein from pseudomonas putida2 (strain kt2440), northeast structural genomics consortium (nesg)3 target ppr99
56	d2if6a1	Alignment	not modelled	20.2	32	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: YiiX-like
57	c3r3pB_	Alignment	not modelled	20.0	8	PDB header: hydrolase Chain: B: PDB Molecule: mobile intron protein; PDBTitle: homing endonuclease i-bth0305i catalytic domain
58	c1nija_	Alignment	not modelled	19.4	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein yjia; PDBTitle: yjia protein
59	c1pznG_	Alignment	not modelled	18.0	12	PDB header: recombination Chain: G: PDB Molecule: dna repair and recombination protein rad51; PDBTitle: rad51 (rada)
60	d1cr2a_	Alignment	not modelled	16.9	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
61	c4me8A_	Alignment	not modelled	16.3	24	PDB header: hydrolase Chain: A: PDB Molecule: signal peptidase i; PDBTitle: crystal structure of a signal peptidase i (ef3073) from enterococcus2 faecalis v583 at 2.27 a resolution
62	d1nija1	Alignment	not modelled	15.1	11	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
63	c2d58A_	Alignment	not modelled	14.7	22	PDB header: metal binding protein Chain: A: PDB Molecule: allograft inflammatory factor 1; PDBTitle: human microglia-specific protein iba1
64	c3j20G_	Alignment	not modelled	14.4	27	PDB header: ribosome Chain: G: PDB Molecule: 30s ribosomal protein s6e; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
65	c6hqaE_	Alignment	not modelled	14.3	15	PDB header: transcription Chain: E: PDB Molecule: subunit (60 kda) of tfiid and saga complexes; PDBTitle: molecular structure of promoter-bound yeast tfiid
66	c3o39A_	Alignment	not modelled	14.1	5	PDB header: chaperone Chain: A: PDB Molecule: periplasmic protein related to spheroblast formation; PDBTitle: crystal structure of spy
67	c4zc0A_	Alignment	not modelled	13.3	24	PDB header: hydrolase Chain: A: PDB Molecule: replicative dna helicase; PDBTitle: structure of a dodecameric bacterial helicase
68	c4gp6A_	Alignment	not modelled	13.0	18	PDB header: transferase Chain: A: PDB Molecule: metallophosphoesterase; PDBTitle: polynucleotide kinase
69	c4kblA_	Alignment	not modelled	11.9	13	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase arih1; PDBTitle: structure of hhari, a ring-ibr-ring ubiquitin ligase: autoinhibition2 of an ariadne-family e3 and insights into ligation mechanism
70	d1qtra2	Alignment	not modelled	11.5	8	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
71	c3t76A_	Alignment	not modelled	10.4	17	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator vanug; PDBTitle: crystal structure of transcriptional regulator vanug, form ii
72	c3zey3_	Alignment	not modelled	10.2	18	PDB header: ribosome Chain: 3: PDB Molecule: 40s ribosomal protein s6; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
73	c4yyca_	Alignment	not modelled	10.2	15	PDB header: transferase Chain: A: PDB Molecule: putative trimethylamine methyltransferase; PDBTitle: crystal structure of trimethylamine methyltransferase from2 sinorhizobium melloti in complex with unknown ligand
74	c5xxuG_	Alignment	not modelled	10.1	18	PDB header: ribosome Chain: G: PDB Molecule: ribosomal protein es6; PDBTitle: small subunit of toxoplasma gondii ribosome
75	c5j9wA_	Alignment	not modelled	10.1	28	PDB header: ligase Chain: A: PDB Molecule: acetophenone carboxylase delta subunit; PDBTitle: crystal structure of the apc core complex
76	c5i34B_	Alignment	not modelled	10.0	12	PDB header: ligase Chain: B: PDB Molecule: adenylosuccinate synthetase; PDBTitle: adenylosuccinate synthetase from cryptococcus neoformans complexed2 with gdp and imp
77	c5bnzA_	Alignment	not modelled	9.6	7	PDB header: ligase Chain: A: PDB Molecule: glutamine--trna ligase; PDBTitle: crystal structure of glutamine-trna ligase /glutaminyl-trna synthetase2 (glnrs) from pseudomonas aeruginosa
78	d1iwea_	Alignment	not modelled	9.6	12	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
						PDB header: ribosome Chain: G: PDB Molecule: 40s ribosomal protein s6-a;

79	c3u5cG_	Alignment	not modelled	9.6	9	PDBTitle: the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 40s subunit, ribosome a
80	c3r7tA_	Alignment	not modelled	9.6	12	PDB header: ligase Chain: A: PDB Molecule: adenylosuccinate synthetase; PDBTitle: crystal structure of adenylosuccinate synthetase from campylobacter2 jejuni
81	c2p1nD_	Alignment	not modelled	9.4	12	PDB header: signaling protein Chain: D: PDB Molecule: skp1-like protein 1a; PDBTitle: mechanism of auxin perception by the tir1 ubiquitin ligase
82	d1tafb_	Alignment	not modelled	9.3	23	Fold: Histone-fold Superfamily: Histone-fold Family: TBP-associated factors, TAFs
83	c3j38G_	Alignment	not modelled	9.3	9	PDB header: ribosome Chain: G: PDB Molecule: 40s ribosomal protein s6; PDBTitle: structure of the d. melanogaster 40s ribosomal proteins
84	c1iweB_	Alignment	not modelled	9.2	12	PDB header: ligase Chain: B: PDB Molecule: adenylosuccinate synthetase; PDBTitle: imp complex of the recombinant mouse-muscle adenylosuccinate2 synthetase
85	d1v5wa_	Alignment	not modelled	9.2	11	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
86	d1dj3a_	Alignment	not modelled	9.0	12	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
87	c1w1zD_	Alignment	not modelled	8.9	11	PDB header: unknown function Chain: D: PDB Molecule: cap-binding protein complex interacting protein PDBTitle: crystal structure of djbp fragment which was obtained by2 limited proteolysis
88	d1wlza1	Alignment	not modelled	8.9	11	Fold: EF Hand-like Superfamily: EF-hand Family: EF-hand modules in multidomain proteins
89	d1g7sa4	Alignment	not modelled	8.8	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
90	c1q57G_	Alignment	not modelled	8.7	11	PDB header: transferase Chain: G: PDB Molecule: dna primase/helicase; PDBTitle: the crystal structure of the bifunctional primase-helicase of2 bacteriophage t7
91	d1pzna2	Alignment	not modelled	8.7	12	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
92	c2xznY_	Alignment	not modelled	8.7	9	PDB header: ribosome Chain: Y: PDB Molecule: rps6e; PDBTitle: crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
93	c4m0gB_	Alignment	not modelled	8.6	12	PDB header: ligase Chain: B: PDB Molecule: adenylosuccinate synthetase; PDBTitle: the crystal structure of an adenylosuccinate synthetase from bacillus2 anthracis str. ames ancestor.
94	c5ymxB_	Alignment	not modelled	8.5	25	PDB header: signaling protein, hydrolase Chain: B: PDB Molecule: mutual gliding-motility protein mgla; PDBTitle: myxococcus xanthus mgla in gdp bound conformation
95	c5d4zF_	Alignment	not modelled	8.5	23	PDB header: dna binding protein Chain: F: PDB Molecule: repressor; PDBTitle: crystal structure of repressor from salmonella-temperate phage
96	c3b7hA_	Alignment	not modelled	8.5	19	PDB header: structural protein Chain: A: PDB Molecule: prophage lp1 protein 11; PDBTitle: crystal structure of the prophage lp1 protein 11
97	c2kpiA_	Alignment	not modelled	8.5	19	PDB header: transcription regulator Chain: A: PDB Molecule: sos-response transcriptional repressor, lexa; PDBTitle: solution structure of protein sos-response transcriptional2 repressor, lexa from eubacterium rectale. northeast3 structural genomics consortium target err9a
98	c4p2bA_	Alignment	not modelled	8.5	13	PDB header: ligase Chain: A: PDB Molecule: glutamine aminoacyl-trna synthetase; PDBTitle: crystal structure of the apo form of the glutaminyl-trna synthetase2 catalytic domain from toxoplasma gondii.
99	c2hz7A_	Alignment	not modelled	8.4	14	PDB header: ligase Chain: A: PDB Molecule: glutaminyl-trna synthetase; PDBTitle: crystal structure of the glutaminyl-trna synthetase from deinococcus2 radiodurans