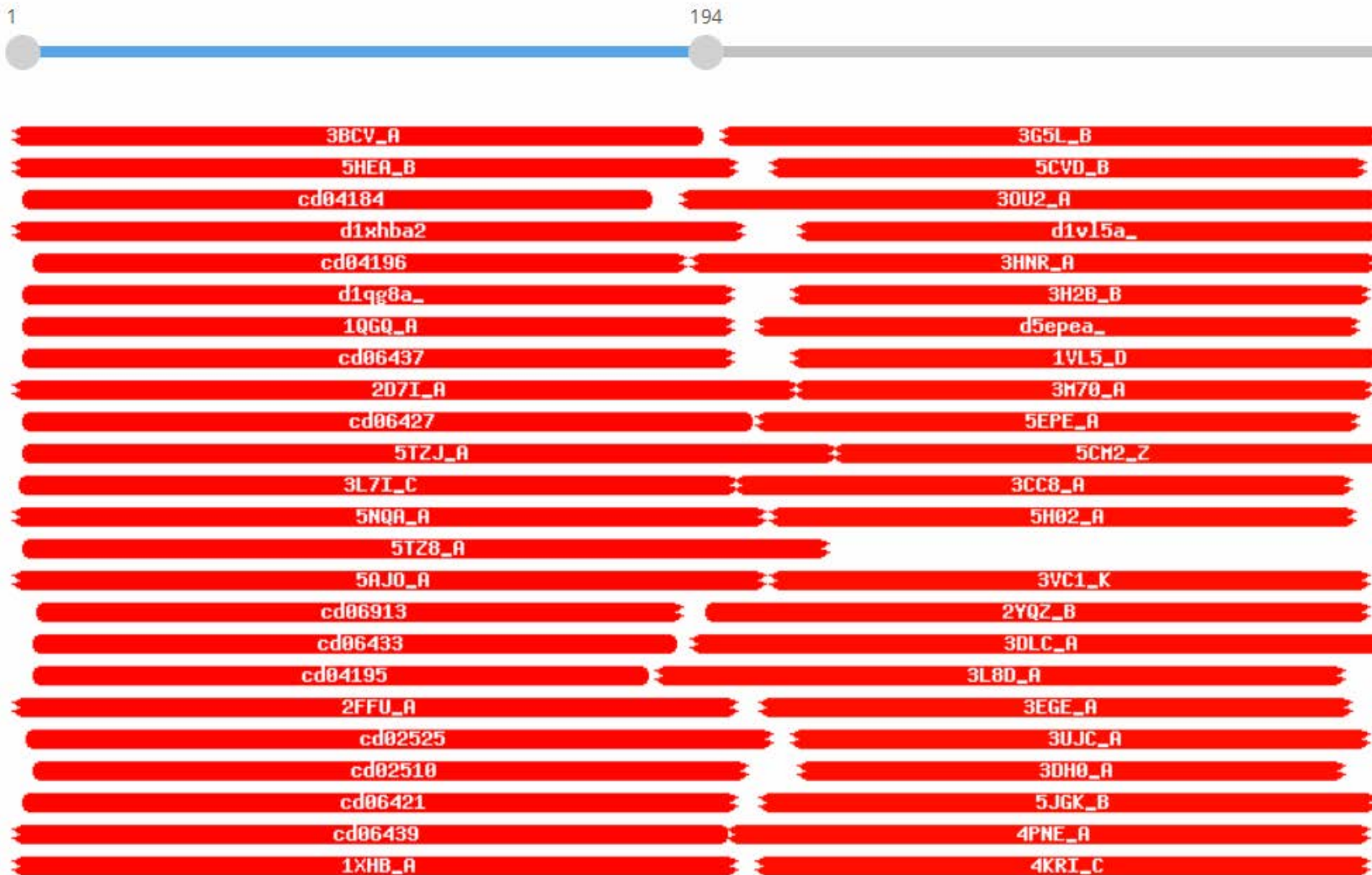


Sequence of ThetaBob_107, in pham 3147 on 7Jul2018:

MNPDL SILIC SVA ERHDNFAIKIQRQIYDQIAKLDDPSRVEVLVLTDRSMSIGTKRNHLVRMASGRYTVFVDDDDDEVADNYVSALLDATNSGAD
VLTFFPLEYRLNGVKRWTVKQSIHYTDDHRRKLN SPRHTSAVRRDIALALPFVESSYGEDADWAQRLRTVAETDHVINDTLYFYCDVPATSVARQY
AAEHSPNAYRQWLESQPKQDYNLGRRLGRDMTSTLQHALSLNPTGTALEFGVGTGKTLRMIAEQMPVIGFDSFQGLPEKWRDGFDKGMFAC
EPPDVPNATLIPGWFEDELPGFEFPELIGLVHIDCDLYSSTKTVLNHLQPHLRPGCILVFDEWHGFPGA AENAHEQKAFREFVTQTGWTWTVLG
HGPEQWSIRLT



Show 25 entries

Search:

Nr	Hit	Name	Probability	E-value	SS	Cols	Target Length
<input type="checkbox"/> 1	3BCV_A	Putative glycosyltransferase protein; Glycosyltransferase, Protein Structure Initiative II; HET: MSE; 2.35A {Bacteroides fragilis}	99.66	2.1e-17	17.5	189	240
<input type="checkbox"/> 2	5HEA_B	Putative glycosyltransferase (GalT1); Glycosyltransferase, helix binding domain, TRANSFERASE; 2.003A {Streptococcus parasanguinis FW213}	99.64	6.6e-17	19	197	296
<input type="checkbox"/> 3	cd04184	GT2_RfbC_Mx_like; Myxococcus xanthus RfbC like proteins are required for O-antigen biosynthesis. The rfbC gene encodes a predicted protein of 1,276 amino acids, which is required for O-antigen biosynthesis in Myxococcus xanthus.	99.59	3e-16	16.1	174	202
<input type="checkbox"/> 4	d1xhba2	c.68.1.17 (A:95-422) Polypeptide N-acetylgalactosaminyltransferase 1, N-terminal domain {Mouse (Mus musculus) [TaxId: 10090]}	99.57	1.1e-15	18.9	202	328
<input type="checkbox"/> 5	cd04196	GT_2_like_d; Subfamily of Glycosyltransferase Family GT2 of unknown function. GT-2 includes diverse families of glycosyltransferases with a common GT-A type structural fold, which has two tightly associated beta/alpha/beta domains that tend to form a continuous central sheet of at least eight beta-strands.	99.57	1.1e-15	17.8	180	214
<input type="checkbox"/> 6	d1qg8a_	c.68.1.1 (A:) Spore coat polysaccharide biosynthesis protein SpsA {Bacillus subtilis [TaxId: 1423]}	99.56	1.5e-15	18.7	193	255

<input checked="" type="checkbox"/>	66	3G5L_B	Putative S-adenosylmethionine dependent methyltransferase; STRUCTURAL GENOMICS, METHYLTRANSFERASE, PSI-2, PROTEIN; 2.35A {Listeria monocytogenes str. 4b F2365}	99.08	5e-12	10	174	253
<input type="checkbox"/>	67	3HNR_A	probable methyltransferase BT9727_4108 (E.C.2.1.1.-); methyltransferase BT9727_4108, Structural Genomics, PSI-2; 2.8A {Bacillus thuringiensis serovar konkukian}	99.07	1.3e-11	11.7	181	220
<input checked="" type="checkbox"/>	68	d1fo8a_	c.68.1.10 (A:) N-acetylglucosaminyltransferase I {Rabbit (Oryctolagus cuniculus) [TaxId: 9986]}	99.05	3e-11	13.5	230	343
<input type="checkbox"/>	69	PF13506.5	; Glyco_transf_21 ; Glycosyl transferase family 21	99.04	1e-11	9.4	137	163
<input checked="" type="checkbox"/>	70	cd04179	DPM_DPG-synthase_like; DPM_DPG-synthase_like is a member of the Glycosyltransferase 2 superfamily. DPM1 is the catalytic subunit of eukaryotic dolichol-phosphate mannose (DPM) synthase.	99.04	2.9e-12	6.3	151	185
<input type="checkbox"/>	71	1FO8_A	N-ACETYLGLUCOSAMINYLTRANSFERASE I; methylmercury derivative, ALPHA-1, 3-MANNOSYL-GLYCOPROTEIN BETA-1; 1.4A {Oryctolagus cuniculus} SCOP: c.68.1.10	99.04	3.9e-11	13.8	230	343
<input checked="" type="checkbox"/>	72	cd04187	DPM1_like_bac; Bacterial DPM1_like enzymes are related to eukaryotic DPM1. A family of bacterial enzymes related to eukaryotic DPM1.	99.02	5.4e-12	6.9	151	181
<input type="checkbox"/>	73	3L8D_A	Methyltransferase; STRUCTURAL GENOMICS, PSI, NYSGRG, METHYLTRANSFERASE; HET: MSE; 1.7A {Bacillus thuringiensis}	99.01	2.6e-11	11.1	177	242