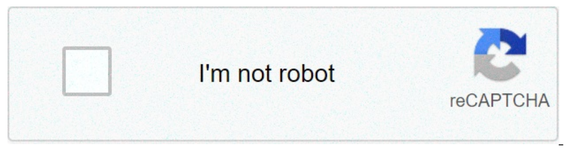


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# To different extents

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Source: r / opts.r The opt_table_lines () Function Set the table lines in one of three ways: (1) All possible chart drawn lines ( "All"), (2) No rows table ( "None" ), and (3) to restore the default line styles ( "default"). This is great if you want to start with many lines and subtract some with tab_options () or tab_style (). Or, use it to start with a completely online with no table, by adding the individual lines according to necessity. opt_table_lines (data extension = c ( "All", "none", "default")) Given a table object created using the GT () function. extension of the measure in which the lines will be visible in the table. The options are "all", "none" or "default". An object of GT_TBL class. Figure 9-5 Function ID # Use examples See also "Esclibbly" to create a table # GT with a number of parts of added table; Then, use # "Opt_table_lines ()" function "function to # Haves lines everywhere can possibly be # Tab_1 lines % gt (rowname_col =" row ", groupname_col =" Group ")%>% Sommario_rows (Groups = Groups = "GRP_A" columns = C (num, currency), fns = list (min = ~ min (., na.rm = true), max = ~ max (., na.rm = true)))%> grand_summary_rows% (Columns = Currency, FNS = List (total sum = ~ (., na.rm = true)))%>% tab_source_note (source_note = "This is a known source.")%>% tab_footnote (note note = "This is a note at the page footers." Locations = cells_body (columns = 1, rows = 1))%>% tab_header (title = "the title of the table", sottotitle = "the subtitle of the table ")%>% opt_table_lines () JVI Volume 74, Number May 1015 200000abstractmateriali and metodiRESUSLsDiscussIonaChowledGessReFerenCestro They clarify the role of phosphorylation of key protein-rna nell'incapsidazione of pregenomic of hepatitis and human um duck (DHBV and HBV, respectively), we examined the states of phosphorylation of different forms of intracellular proteins â â HBV lar HBV core and the phenotypic effects of the mutations in the protein phosphorylation sites â â HBV and DHBV core. We show that the HBV core protein is phosphorylated for similar extensions in the form of dimers of protein â â and after a further assembly into capsids pregenomiche containing RNA. The single and most alanine substitutions and aspartic acid for serine phosphorylation sites in the HBV core protein have resulted in site-specific effects and synergistic RNA sull'incapsidazione, ranging from improving to 2 times to more than 10 times inhibition. The main â â protein variants with mutations in all phosphorylation sites showed dominant-negative effects sull'incapsidazione RNA by proteins â â wild type. The results suggest that the presence of phosphoserine in position 162 of the HBV core protein is required for the encapsidation pregenomica-RNA, while the phosphoserine at position 170 optimizes the process and serine may be preferable in position 155. Examination of the ability to pregenomico encapsidation of the RNA-protein â â the variants of the DHBV core, in which four phosphorylation sites have been mutated jointly or aspartic acid Alanine, suggests that phosphorylation of the DHBV core protein in these sites can optimize the encapsidation pregenomica-RNA, but its impact is much shallower than in the case of HBV. The possible mechanisms by which RNA encapsidation can be modulated by phosphorylation of proteins â â core is discussed in the context of the observed differences between the two viruses. The genome of the hepadnaviruses DNA is replicated by reverse transcription of an RNA intermediate, the RNA pregenomico (reviewed in reference amount4). Replication begins with the RNA encapsidation pregenomica, a process that takes two proteins â â viral proteins (Capside) and polymerase; However, polymerase enzyme activities are not essential. The sequential synthesis of a minus-strand DNA from the reverse transcription and the synthesis of the second wire of DNA are performed by the polymerase within the nucleocapsid.core protein is a phosphorotein (9, 11, 14, 15, 17). Three phosphorylation sites have been identified in the main protein of the human hepatitis B (HBV) virus, located in the in the C-terminal protein domain (S155, S162 and S170 in AYW subtype, equivalent to S157, S164 and S172 in ADW2 subtype) (10). The main hepatitis B virus (DHBV) duck protein has four phosphorylation sites within the 12 amino acid terminal sequence (T239, S245, S257 and S259) and is also phosphorylated elsewhere (20). The function (s) of protein phosphorylation â €

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