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Re: cfg_rRequest_2950

Core H [coreh@emory.edu]

To: Islam Hussein

Attachments: (4) Download all attachments

H3N2-HA_16687_v5.1_RESULTS.xls (265 KB) [Open as Web Page]; H3N2-HA-precomplex_16706_v~1.xls (266 KB) [Open as Web Page]; H3N8-HA_16686_v5.1_RESULTS.xls (265 KB) [Open as Web Page]; H3N8-HA-precomplex_16705_v~1.xls (266 KB) [Open as Web Page]

Friday, January 10, 2014 11:06 AM

- You replied on 1/12/2014 9:17 PM.

Dear Islam,

We apologize for the delay in sending your data. We tested your samples by two methods, one where we added the sample, anti-His, and anti-mouse in sequential steps to the slide, and another where we pre-complexed the reagents in a tube before adding to the slide. The precomplex method has shown improved binding for some samples in the past. In this case, it increased our signals a bit, but the data look very similar.

We have attached 4 Excel files that we obtained from the screening of your glycan binding proteins. Version 5.1 of the printed array consists of 610 glycans in replicates of 6. This version of the array has 1 less glycan than v5.0. Glycan #56 on v5.0 was exhausted and is not present on v5.1. Glycan #56 (Neu5Aca2-6Galb1-4GlcNAcb1-2Mana1-6(Neu5Aca2-6Galb1-4GlcNAcb1-2Mana1-3)Manb1-4GlcNAcb1-4GlcNAcb-Sp13) is a biantennary N-glycan that is found on v5.1 as glycan #55 and #57 with different linkers. To compare v5.0 and v5.1 data, simply eliminate #56 from v5.0 data and change the glycan ID values on v5.0, accordingly. The Excel spread sheet presents in columns A-E, respectively, the Glycan number, the structure or name, the average RFU value from the replicates, the standard deviation, and %CV (%CV=100 X Std. Dev / Mean). Column F contains the graph of glycan number vs. Average RFU with standard error of the mean (SEM) plotted in the error bars (standard deviation/2 = SEM), and Columns G-K is the data from A-E sorted by RFU (high to low) to provide a list of the Glycans bound with highest intensity. The highest and lowest point from each set of six replicates has been removed so the average is of 4 values rather than 6. This eliminates some of the false hits that contain a single very high or low point. Thus, points with high %CV should be considered suspect. Please analyze your data with regard to what glycan structures your sample binds, as well as what related structures it DOES NOT bind. This comparison provides information on binding specificity. You can search for structures using the search function of Excel. The scanner response is linear to a maximum RFU value of about 50,000.

Please review the data and let us know your thoughts and questions. If we do not hear from