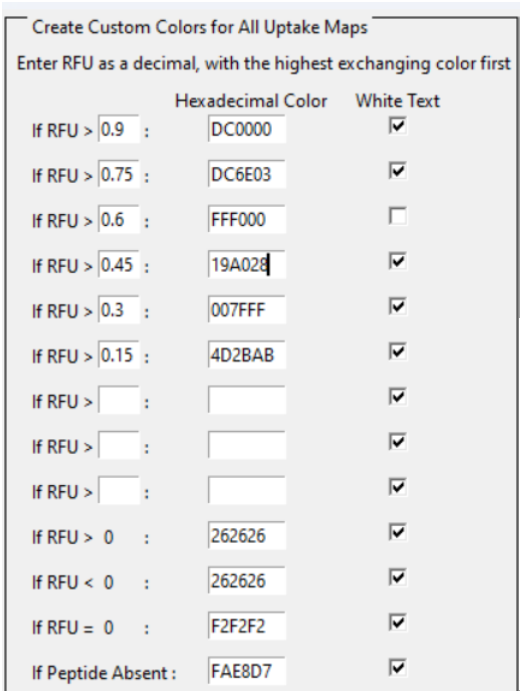
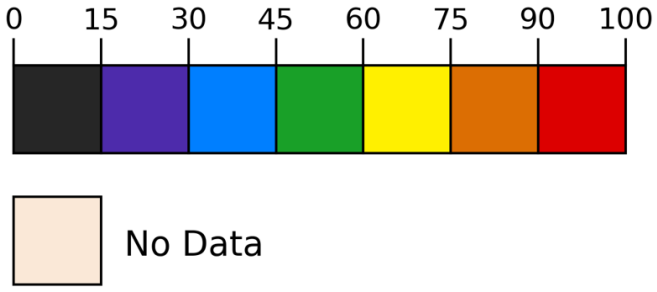
Creating Custom Color Schemes

By inputting the lower cutoff for a color to be applied to peptides, as well as the color, figure colors can be completely customizable. The text color of any text that appears over a peptide can also be modulated. Here are some examples of the inputs that generated the default coloring schemes, and the associated legend created dynamically by the software attached.

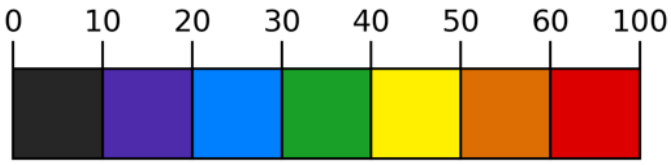
1)Default Corrected Uptake Colors - “corrected_df.json”

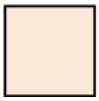




Note: Not all rows need to be filled. All text displayed on the yellow color here (FFF000) will appear as black for maximal visibility.

2)Default Uncorrected Uptake Colors – “uncorrected_df.json”





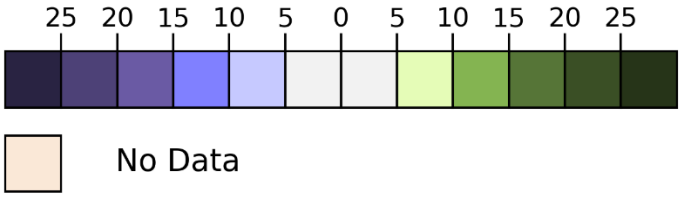
HDXWizard

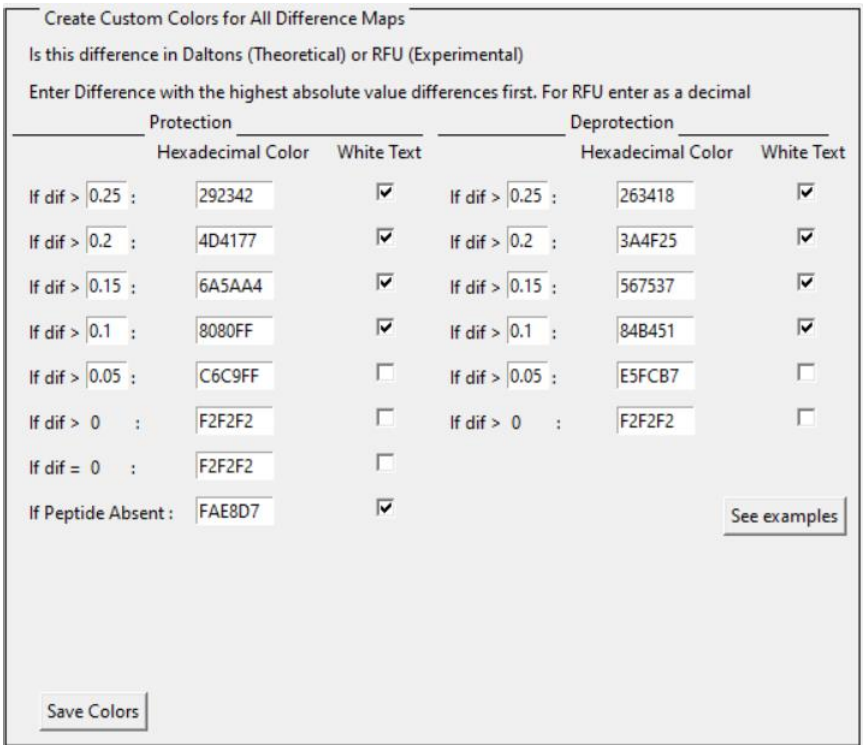
Create Custom Colors for All Uptake Maps

Enter RFU as a decimal, with the highest exchanging color first

	Hexadecimal Color	White Text
If RFU > 0.6 :	DC0000	☑
If RFU > 0.5 :	DC6E03	☑
If RFU > 0.4 :	FFF000	☐
If RFU > 0.3 :	19A028	☑
If RFU > 0.2 :	007FFF	☑
If RFU > 0.1 :	4D2BAB	☑
If RFU > :		☑
If RFU > :		☑
If RFU > :		☑
If RFU > 0 :	262626	☑
If RFU < 0 :	262626	☑
If RFU = 0 :	F2F2F2	☑
If Peptide Absent :	FAE8D7	☑

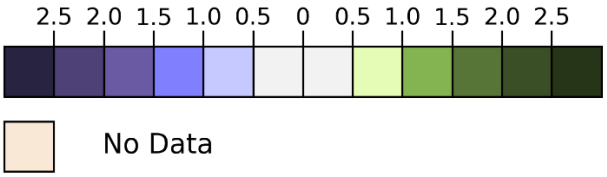
3)Default Experimental (maxD) Difference Colors – “RFU_green_blue.json”

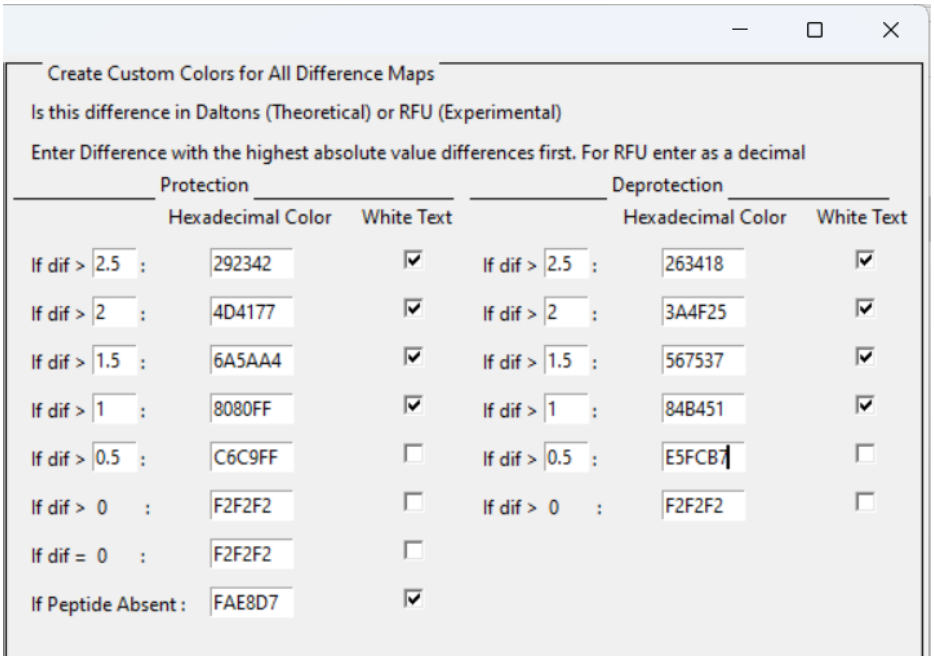




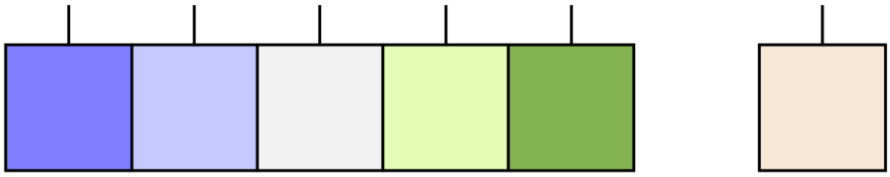
Note: Differences here are calculated by percent difference between maxD corrected RFUs.

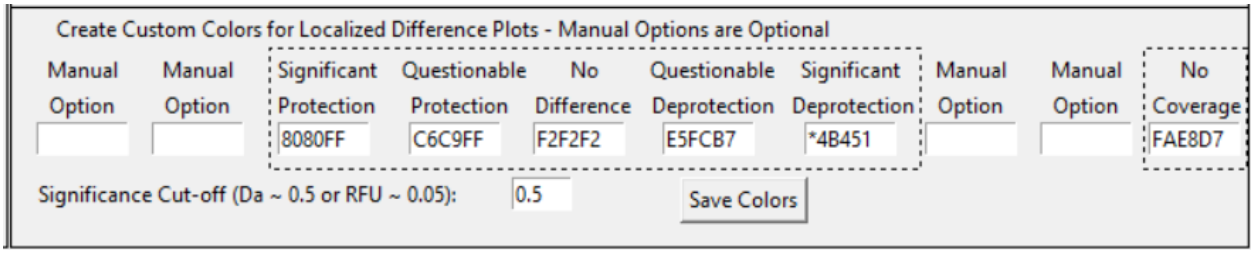
4)Default Theoretical (absolute difference) Difference Colors - “Da_green_blue.json”





5)Default Dalton 5 color difference – “5_Da_green_blue”





6)Default Dalton 9 color difference – “9_Da_green_blue”