```
RFX2       .....SPIVSSAGAYLIHGG..MDSTRHSLAHTSRSSPATLEMAIENLQKSEGITSHKSGLLNSHLQWLLDNYETAEGVSLPRSSLYNHYLRHCQEHK.LDPVNAASFGK   102
RFX3       .VTGGQLISSSGGTYLIGNS..MENSGHSVTHTTRASPATIEMAIETLQKSDGLSTHRSSLLNSHLQWLLDNYETAEGVSLPRSTLYNHYLRHCQEHK.LDPVNAASFGK   106
RFX1       GSTGGG..GSGAGTYVIQGGYMLGSASQSYSHTTRASPAT.......................VQWLLDNYETAEGVSLPRSTLYCHYLLHCQEQK.LEPVNAASFGK    82
RFX4       ....RYSSHTSLGNVSNDEN...EEKENNRASKPHSTPAT.......................LQWLEENYEIAEGVCIPRSALYMHYLDFCEKND.TQPVNAASFGK    77
RFX5       ......SDNDKLYLYLQLPS...GPTTGDKSSEPSTLSNEE....................YMYAYRWIRNHLEEHTDTCLPKQSVYDAYRKYCESLACCRPLSTANFGK    81
consensus            **** ***     ** *  * **********                     **!*****!*******!****! *!***!** * **!***!*!!!


RFX2       LIRSVFMGLRTRRLGTRGNSKYHYYGIRLKPDSPLNRLQEDTQYMAM....   149
RFX3       LIRSIFMGLRTRRLGTRGNSKYHYYGIRVKPDSPLNRLQEDMQYMAMRQQP   157
RFX1       LIRSVFMGLRTRRLGTRGNSKYHYYGLRIKASSPLLRLMEDQQHMAMRG..   131
RFX4       IIRQQFPQLTTRRLGTRGQSKYHYYGIAVKESSQYYDVMYSKKGAAWVS..   126
RFX5       IIREIFPDIKARRLGGRGQSKYCYSGIRRKTLVSMPPLPGLDLKGSESPEM   132
consensus  *!!**!*****!!!!*!!*!!!*!*!***!   *** ** ** * ***
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