

CLUSTAL W (1.83) multiple sequence alignment

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RFX3-IVT      TLQWLLDNYETAEGVSLPRSTLYNHYLRHCQEHKLDPVNAASFGKLIRSSIFMGLRTRRLG 60
RFX3-purified HLQWLLDNYETAEGVSLPRSTLYNHYLRHCQEHKLDPVNAASFGKLIRSSIFMGLRTRRLG 60
hRFX1        TVQWLLDNYETAEGVSLPRSTLYCHYLLHCQEQKLEPVNAASFGKLIRSSIFMGLRTRRLG 60
RFX4-IVT     TLQWLEENYEIAEGVCIPRSALYMHYLDFCEKNDTQPVNAASFGKIIRQQFPQLTTRRLG 60
RFXDC2-purified AFSWIRNTLEEHPETSLPKQEVYDEYKSYCDNLGYHPLSAADFGKIMKNVFPNMKARRLG 60
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RFX3-IVT      TRGNSKYHYYGIRVKPDSPLNR 82
RFX3-purified TRGNSKYHYYGIRVKPDSPLN- 81
hRFX1        TRGNSKYHYYGLRIKASSPLLR 82
RFX4-IVT     TRGQSKYHYYGIAVKESSQYY- 81
RFXDC2-purified TRGKSKYCYSGLRKKAFVHMP- 81
              ***:*** * *: *

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Figure S12. RFX family protein-DNA recognition positions. It is likely that RFX3, RFX4, and RFXDC2 all use the same mechanism of alternative modes of DNA recognition as RFX1 (Gajiwala *et al.*, *Nature*, 2000), because seven out of nine residues involved in direct or water-mediated DNA contacts (highlighted in red) are identical among these proteins, while the other two residues have conservative substitutions.