

Supplementary material

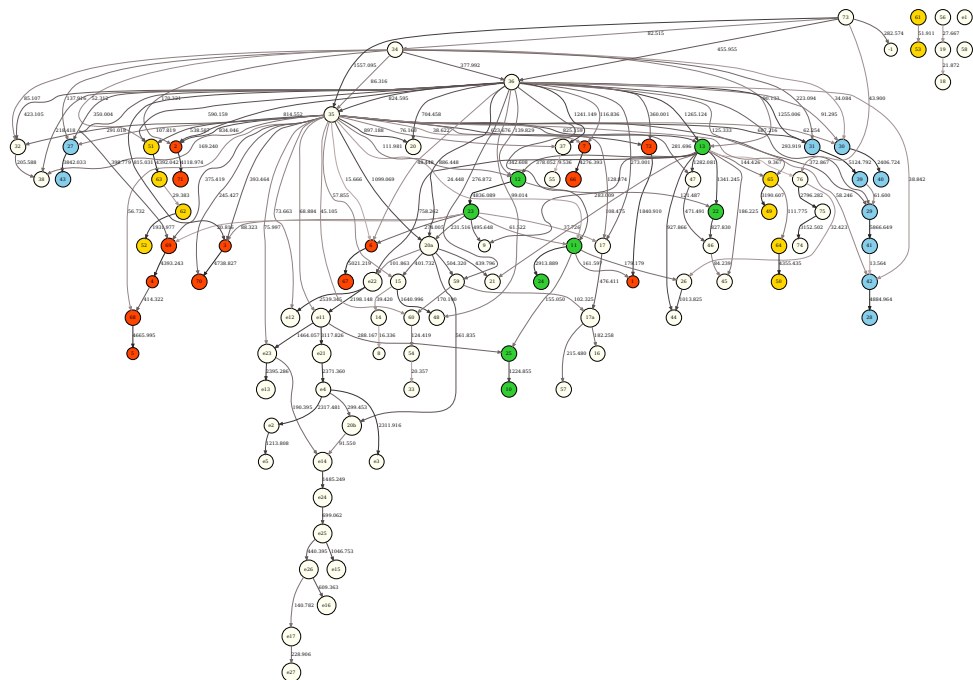


Fig. S1: BN scored with MDL against a random subsample of 4689 tRNAs (50 percent of the full sample). See Figure 6 legend for further details.

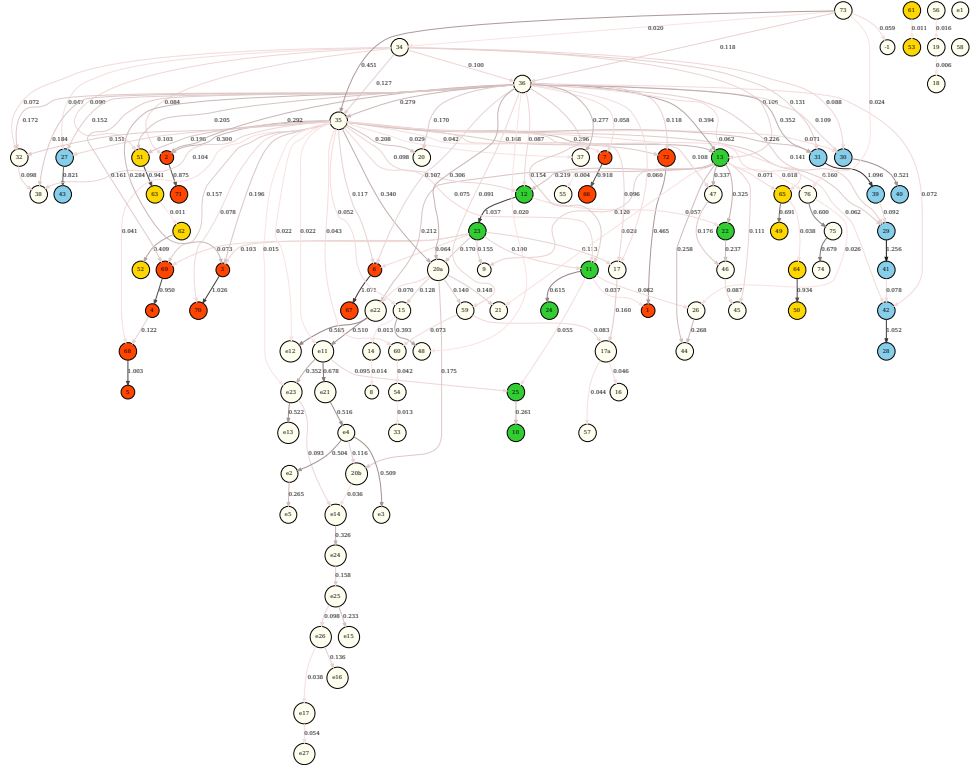


Fig. S2: BN scored with the MU criterion against the full sample (9378 tRNAs). See Figure 6 legend for further details.

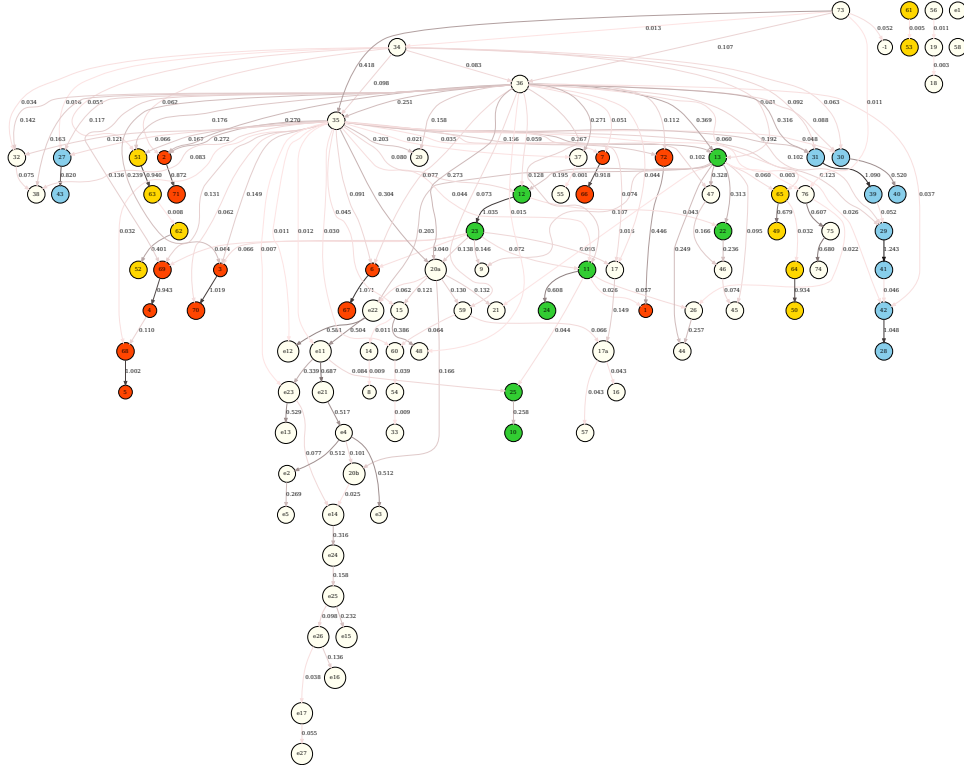


Fig. S3: BN scored with the MU criterion against a random subsample of 4689 tRNAs (50 percent of the full sample). See Figure 6 legend for further details.

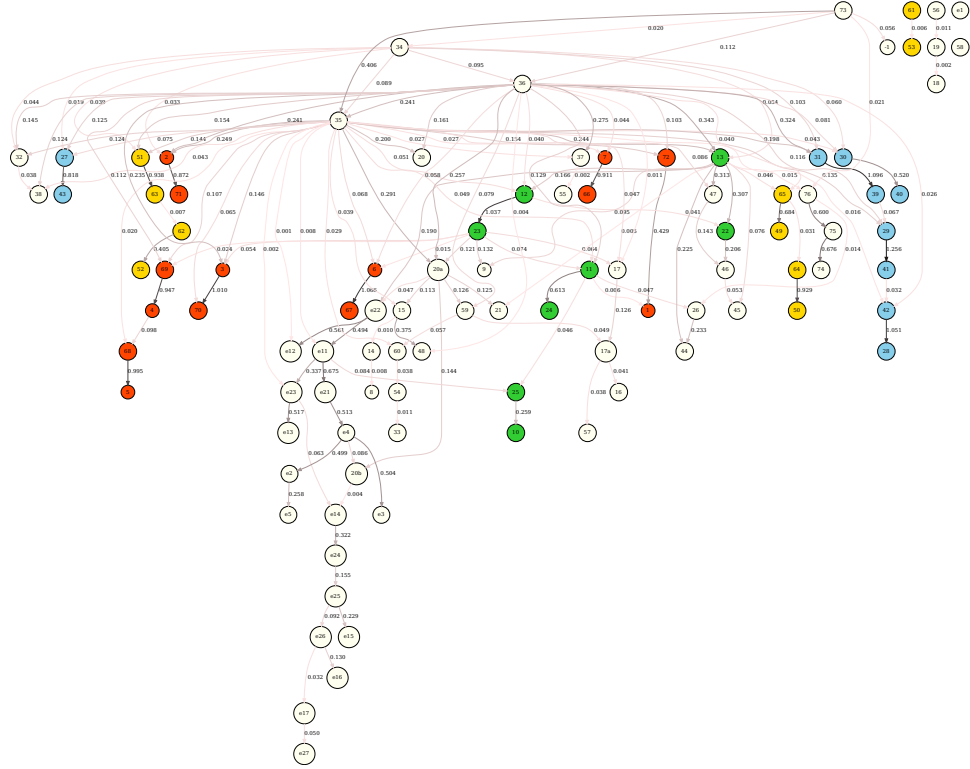


Fig. S4: BN scored with the MDL criterion scaled by $1/N$ against the full sample (9378 tRNAs). See Figure 6 legend for further details.

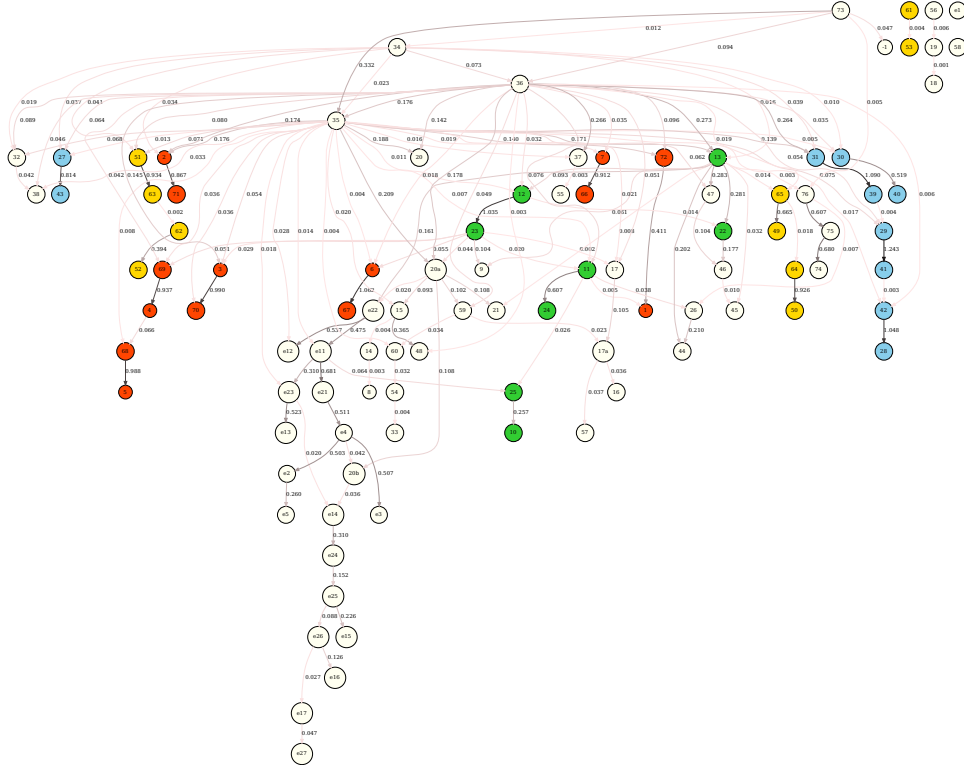
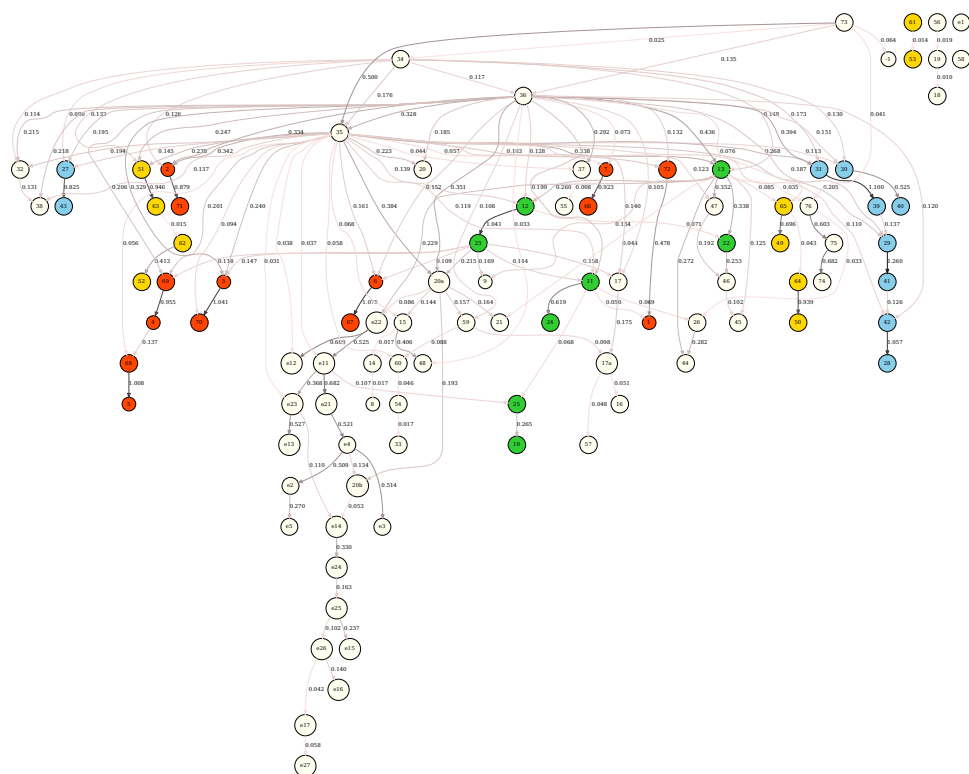


Fig. S5: BN scored with the MDL criterion scaled by $1/N$ against a random subsample of 4689 tRNAs (50 percent of the full sample). See Figure 6 legend for further details.



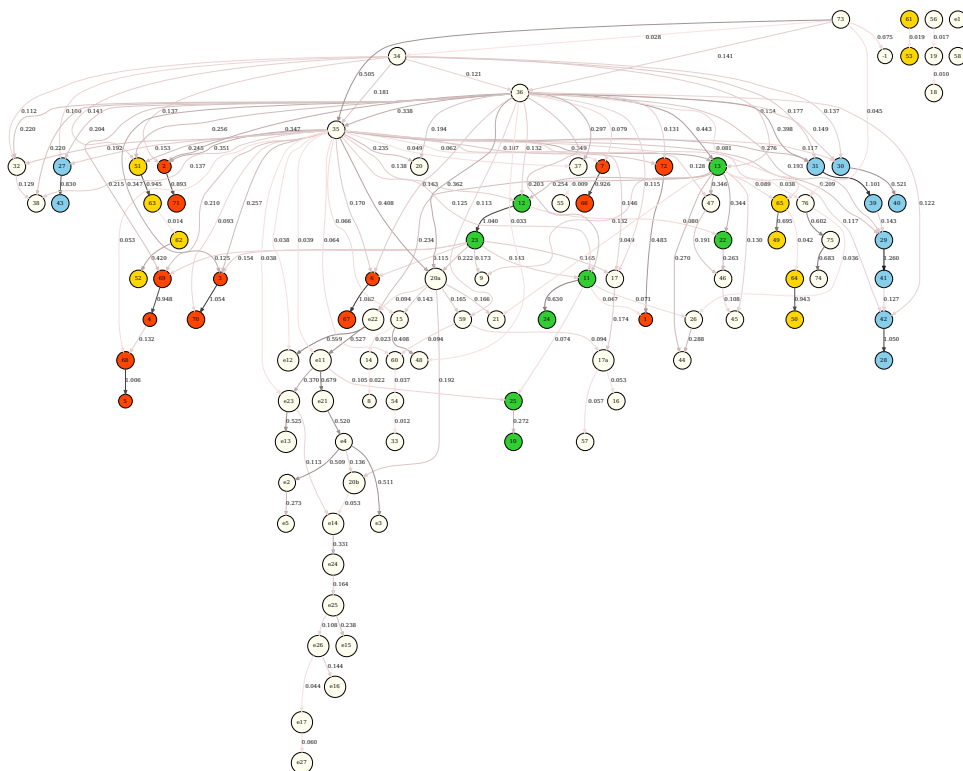


Fig. S7: BN scored without penalty, with ΔH alone, against a random subsample of 4689 tRNAs (50 percent of the full sample). See Figure 6 legend for further details.