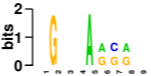
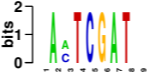
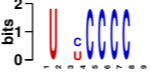
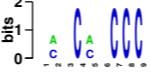




| optimized motif   | location | MI (bits) | z-score | robustness | position bias | orientation bias | conservation index | seed    | motif name                 | protein array |
|---|----------|-----------|---------|------------|---------------|------------------|--------------------|---------|----------------------------|---------------|
|    | 3'UTR    | 0.007     | 38.7    | 10/10      | Y             | ↔                | 1.00               | GAAAACA | -                          | -             |
|    | 5'       | 0.004     | 25.2    | 10/10      | -             | ↔                | 1.00               | AATCGAT | CEH-28, CEH_28, CEH-38 ... | -             |
|    | 3'UTR    | 0.004     | 23.8    | 10/10      | -             | →                | 0.99               | UUUGCCC | -                          | -             |
|   | 5'       | 0.004     | 21.8    | 10/10      | Y             | →                | 1.00               | CTCGCC  | KLF_1                      | -             |
|  | 5'       | 0.003     | 18.4    | 10/10      | -             | ↔                | 0.29               | ATAGTAA | DAF_19, PIE_1              | -             |
|  | 5'       | 0.002     | 11.5    | 7/10       | -             | -                | 0.51               | CAGTGCA | LIN_15B, PIE_1             | -             |