```
MSBa       24   CREFQRNK-CSRQDTECKFAH
TTP        109  CRTFSESGRCRYGAK-CQFAH
PIE-1      104  CDAFRREGYCPYNDN-CTYAH
U2AF35kD   17   CSFYFKIGACRHGDR-CSRLH
RTMORF1    155  CRFDAGMNGCRNSSQDCKFIH
```

Figure B: Multiple sequence alignment of several CCCH zinc finger motifs from several proteins. Protein accession numbers, MSBa (Muscleblind A) *Drosophila*, AAC47757; TTP: homo sapiens AAC37600; PIE-1, *Caenorhabditis elegans* S71796; U2AF35kD: homo sapiens NP_006749.