### Table S1. Characteristic parameters of the proteins used in this study.

Nine IDPs and four globular proteins (cf. Table 1) have been used in this study. Their sequences have been analyzed by the ProtParam tool of the ExPaSy server ([https://web.expasy.org/protparam/](https://web.expasy.org/protparam/)), and a variety of features are given in this table, such as: length, pI, number of negative and positive residues, net charge, % content of hydrophobic amino acids (Ala + Ile + Leu + Val + Trp + Tyr + Phe), proline content and the Grand average of hydropathicity (GRAVY) value as calculated from the sum of hydropathy of all residues of the sequence.

| Protein                                      | UniProt # | FL/fragment | length | pI  | Negative | positive | net charge | hydrophobic amino acids (%) | proline (%) | GRAVY |
|----------------------------------------------|-----------|-------------|--------|-----|----------|----------|------------|------------------------------|-------------|-------|
| **Intrinsically disordered proteins**        |           |             |        |     |          |          |            |                              |             |       |
| AF1 (activation function 1 of androgen receptor) | P10275    | 150-485     | 336    | 4.57| 35       | 18       | -17        | 32.2                         | 9.2         | -0.319|
| EM (*T. aestivum* (wheat) Em protein)        | P04568    | FL          | 93     | 5.56| 17       | 16       | -1         | 17.4                         | 1.1         | -1.375|
| ERD10 (*A. thaliana* early response to dehydration 10) | P42759    | FL          | 260    | 5.11| 65       | 45       | -20        | 20.9                         | 7.3         | -1.348|

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**Note:** The values for GRAVY are calculated from the sum of hydropathy of all residues of the sequence.
| Protein Description                                                                 | Accession | Start | End   | Width | Height | Log2 Fold Change | p-Value |
|------------------------------------------------------------------------------------|-----------|-------|-------|-------|--------|------------------|---------|
| ERD14 (A. thaliana early response to dehydration 14)                                | P42763    | 185   | 46    | 37    | -9     | 23.3             | 8.6     | -1.265           |
| hCSD1 (human calpastatin domain 1)                                                  | P20810    | 140   | 17    | 13    | -4     | 27.9             | 10.3    | -0.735           |
| ID1 (of CREB-binding protein)                                                       | Q92793    | 331   | 15    | 14    | -1     | 27.2             | 9.1     | -0.398           |
| ID5 (of CREB-binding protein)                                                       | Q92793    | 319   | 9     | 12    | 3      | 20               | 13.2    | -0.936           |
| α-synuclein                                                                        | P37840    | 140   | 4     | 15    | -9     | 35.8             | 3.6     | -0.403           |
| β-casein                                                                           | P02666    | 224   | 5.26  | 23    | -7     | 36.6             | 15.6    | -0.154           |
| DBD (DNA-binding domain of androgen receptor)                                      | P10275_3  | 94    | 9     | 19    | 10     | 29.8             | 3.2     | -0.604           |
| BSA (bovine serum albumin)                                                          | P02769    | 607   | 99    | 86    | -13    | 36.3             | 4.6     | -0.429           |
| **Globular proteins**                                                               |           |       |       |       |        |                  |         |                  |
| **DBD (DNA-binding domain of androgen receptor)**                                   |           |       |       |       |        |                  |         |                  |
| **BSA (bovine serum albumin)**                                                      |           |       |       |       |        |                  |         |                  |
|                  | P01966 | P02070 | FL  | 227  | 7.39 | 25  | 25  | 0   | 46  | 3.5 | 0.073 |
|------------------|--------|--------|-----|------|------|-----|-----|-----|-----|-----|-------|
| Hint1 (human     | P49773 | FL     | 26  | 6.43 | 16   | 14  | -2  | 37.2| 5.6 | -0.175 | Histidine triad nucleotide-binding protein 1) |