SUPPLEMENTARY ONLINE DATA

A study of the ultrastructure of Fragile-X-related proteins

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Figure S1 Multiple sequence alignment of FXR proteins

The sequences are shaded according to the positional conservation. The positions of the putative PEST motifs are underlined.

Figure S2 Gel of the three stable constructs discussed in the main text to exemplify the degree of purity

The molecular mass in kDa is indicated on the left-hand side.
Table S1 Potential PEST sequences which could promote degradation of FXR proteins

The predictions were made using PESTFind.

| Protein   | Potential PEST sequences (amino acid residues) | Poor PEST sequences (amino acid residues) |
|-----------|-----------------------------------------------|------------------------------------------|
| FMRP      | 484–505; 507–522                               | 24–40; 158–179; 246–263; 276–343; 324–344 |
| FXR1P     | 391–415; 470–497                               | 24–40; 162–179; 246–263; 328–341; 578–593 |
| FXR2P     | 437–459; 512–544; 557–581                       | 1–19; 162–189; 256–273; 266–300; 338–351; 606–617 |

Figure S3 SAXS data

(A) Distance distribution functions from FXR1P Nt-KH1 (12 μM), FXR1P Nt-KH2 (12 μM) and FMRP Nt-KH1 (18 μM). (B) Ab initio bead model of FXR1P Nt-KH2 calculated with DAMMIN (grey semi-transparent spheres). The right-hand view is rotated counter-clockwise around the vertical axis. (C) Rg distributions from EOM for FXR1P Nt-KH1 (12 μM): initial random pool (solid line) and selected ensembles averaged over 50 independent EOM runs (broken line). The wide width of these distributions supports the flexibility of the HLH region.