|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Protein | Unfolding force (pN)a | Force-loading rate (pN/s) | Molecular weight (kDa) | Methodb |
| LZ26 zipper1 | 15c | 125 | 11.3 | OT |
| Barnase2 | 20c | 4.1 | 12.4 | OT |
| UCH-L13 | 37c | 70 | 24.5 | OT |
| vWF multimer4  vWF (A1A2A3)3 | 22.8, 40.0  23.1 | 90  22 | 250  210 | OT |
| cSc5 | 8.5, 8.9, 9.8  11.3, 11.4 | 1.5, 3.2, 5.5  8.6, 15.1 | 24.2 | OT |
| HIV-1-PR6 | 23.0, 24.2, 40.5 | 5 | 10.7 | OT |
| T4L (16, 61)7  T4L (16, 159) | 51.8  47.9 | 4.5  13.5 | 5.0  16.2 | OT |
| MJ03368 | 19.5c | 10 | 10.0 | OT |
| Calmodulin9 | 21c | 5.5 | 16.8 | OT |
| ACBP (1, 86)10  ACBP (46, 86) | 10.7, 10.9  18 | 15, 45  11 | 9.9  4.8 | OT |
| PrP11 | 10 | 37.5 | 16.2 | OT |
| Apo-Mb (1, 153)12  Apo-Mb (53, 153) | 12.5  12.0 | 5 | 17.2  11.2 | OT |
| RNase H13 | 19 | 13,53 | 17.5 | OT |
| NCS114 | 10.6 (N-domain)  13.8 (C-domain) | 5 | 21.4 | OT |
| Apo-SOD115 | 10c | 91 | 15.8 | OT |
| MBP16 | 25c | 5 | 40.7 | OT |
| Luciferase17 | 40c | 8.5 | 60.7 | OT |
| CBD-A18 | 9c | 5 | 15.2 | OT |
| Hsp9019 | 14.1 (N-domain)  17.6 (M-domain)  9.2 (C-domain) | 4 | 81.3 | OT |
| EF-G (full)20  EF-G (G-II-III) | 36c  38c | 10 | 77.6  53.8 | OT |
| DHFR21 | 26c | 6 | 21.5 | OT |
| PKA22 | 10.5, 13.6 (CNB-A)  5.2, 9.1 (CNB-B) | 5.6 | 28.9 | OT |
| pARC23 | 9.0 | 7.5 | 11.7 | OT |
| Arc-L1-Arc (unknotted)23  Arc-L1-Arc (knotted) | 8.2  14.7 | 7.5 | 13.2 | OT |
| ROSS24 | 17 | 100 | 12.4 | OT |
| NuG225 | 34c | 2.55 | 6.2 | OT |
| RTX (1529, 1664)26  RTX (1529, 1681) | 12.7  14.2 | 8.5 | 16.0 | OT |
| Top727 | 42 | 7.5 | 10.6 | OT |
| Vim2B-N28  Vim2B-C | 8c  10c | 137.5 | 20.8  20.7 | OT |
| FLNa2029 | 15 | 55 | 29.6 | OT |
| FL domain30 | 5c | 40, 200 | 9.7 | OT |
| PADC31 | 15 | 8.5 | 17.6 | OT |
| AFV3-10932 | 10 | 5 | 12.3 | OT |
| GFP33 | 40c | 210 | 26.6 | OT |
| Syt1 C2AB34  E-Syt2 C2AB  E-Syt2 C2C | 12c, 28c  16c, 32c  27c | 1.5 | 37.2  35.0  17.0 | OT |
| SNARE complex (Vn)35  SNARE complex (Vc) | 16.7c  18.5c | 0.6 | 41.7 | OT |
| SNARE complex36 | 14.4 | 1 | 42.8 | MT |
| Spectrin37 | 10.8, 15.7,  26.1, 30.0, 33.2 | 0.05, 0.1,  0.5, 1.0, 2.0 | 61.0 | MT |
| scTMHC238 | 18c | 0.5d | 17.8 | MT |
| GlpG39,40 | 22.5c, 25c | 1, 0.5d | 21.3 | MT |
| β2AR40 | 14.2c | 1 | 39.6 | MT |
| ClC41 | 46c | 0.5d | 47.5 | MT |

Figure 4–source data 1. Protein unfolding forces measured by single-molecule tweezers. a The unfolding forces indicate the most probable unfolding forces except the items with the superscript c. b OT and MT indicate optical tweezers and magnetic tweezers, respectively. c The unfolding force is an approximate or averaged value. d The force-loading rate is an averaged value over the force scanning of 1–50 pN.

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