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Carlos A Elena-Real, Amin Sagar, Annika Urbanek, Matija Popovic, Anna Morató, et al.. The structure of pathogenic huntingtin exon-1 defines the bases of its aggregation propensity. 2022. hal-03846359

HAL Id: hal-03846359

<https://hal.science/hal-03846359>

Preprint submitted on 10 Nov 2022

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The structure of pathogenic huntingtin exon-1 defines the bases of its aggregation propensity

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24

25 **Abstract**

26 Huntington's Disease is a neurodegenerative disorder caused by a CAG expansion of the first exon
 27 of the *HTT* gene, resulting in an extended poly-glutamine (poly-Q) tract in the N-terminus of the
 28 protein huntingtin (httex1). The structural changes occurring to the poly-Q when increasing its
 29 length remain poorly understood mainly due to its intrinsic flexibility and the strong compositional
 30 bias of the protein. The systematic application of site-specific isotopic labeling has enabled residue-
 31 specific NMR investigations of the poly-Q tract of pathogenic httex1 variants with 46 and 66
 32 consecutive glutamines. The integrative analysis of the data reveals that the poly-Q tract adopts
 33 long α -helical conformations stabilized by glutamine side-chain to backbone hydrogen bonds. ^{19}F -
 34 NMR of site-specifically incorporated fluoro-glutamines and molecular dynamics simulations
 35 demonstrate that the mechanism propagating α -helical conformations towards the poly-Q from the
 36 upstream N17 domain is independent of the poly-Q track length. Aggregation and atomic force
 37 microscopy experiments show that the presence of long and persistent α -helices in the poly-Q tract
 38 is a stronger signature in defining the aggregation kinetics and the structure of the resulting fibrils
 39 than the number of glutamines. The ensemble of our observations provides a structural perspective
 40 of the pathogenicity of expanded httex1 and paves the way to a deeper understanding of poly-Q
 41 related diseases.

42

Introduction

Among the nine neurodegenerative disorders caused by expansions of polyglutamine (poly-Q) tracts, Huntington's Disease (HD) stands out due to its prevalence and devastating effects¹. HD is triggered by an abnormal expansion of the poly-Q tract located in exon1 (httex1) of the 348-kDa huntingtin, a ubiquitous protein involved in multiple pathways^{2,3}. In its non-pathogenic form, the httex1 poly-Q tract is comprised of 17-20 glutamines⁴; however, when the number of consecutive glutamines exceeds the pathogenic threshold of 35, it results in aggregation-prone mutants. Indeed, fragments of mutant httex1 can be found forming large cytoplasmic and nuclear aggregates within neurons of the striatum, a well-known hallmark of HD^{5,6}. The presence of such aggregates, the neuronal degeneration, the age of onset and disease severity, all correlate with the length of the expanded poly-Q tract⁷. Notably, the mutant httex1 fragment alone suffices to reproduce HD symptoms in mice⁸. Unfortunately, no effective treatment is currently available, mainly because of the lack of knowledge regarding the molecular mechanisms underlying the disease⁹.

Amyloidogenic aggregates were initially proposed to be the toxic species in HD, acting by sequestering essential cellular proteins and components¹⁰. However, they have also been related to neuronal survival in certain cell types, suggesting that aggregates may be protective¹¹⁻¹⁴. It has also been proposed that toxicity is caused by soluble species of httex1, which are characterized by a high polymorphism comprising monomers, dimers, tetramers and small oligomers^{15,16}. It has been shown that N17, the 17 residue-long fragment preceding poly-Q (Fig. 1a), is the pivotal element triggering httex1 self-recognition and enhancing aggregation¹⁷⁻¹⁹. However, the structural mechanism by which N17 propagates aggregation and cytotoxicity of expanded httex1 remains to be defined.

Two models have been suggested to connect the pathological threshold and toxicity, the 'toxic structure' and the 'linear lattice' models²⁰. While the 'toxic structure' model proposes the appearance of a distinct toxic conformation when the poly-Q tract is expanded beyond the pathological threshold^{21,22}; the 'linear lattice' model suggests that poly-Q tracts are inherently toxic and that their toxicity systematically increases with the homorepeat length^{23,24}. Intriguingly, both models have been supported by antibody recognition experiments in different studies. Furthermore, the absence of sharp changes in single-molecule Förster resonance energy transfer (smFRET), circular dichroism and electron paramagnetic resonance (EPR) experiments around the pathological threshold has been argued to substantiate the 'linear lattice' model²⁵⁻²⁷. High-resolution structures of non-pathogenic and pathogenic httex1 variants are required to evaluate the changes occurring upon poly-Q expansion, discriminate between both models and finally define the bases of httex1 cytotoxicity.

Until recently, the detailed high-resolution structural characterization of soluble httex1, especially of those with pathogenic poly-Q length, has been hampered by the intrinsic properties of the protein, namely the highly flexible nature, its aggregation propensity and the strong compositional bias. X-ray diffraction or electron microscopy, normally used to study folded proteins, cannot be applied to probe disordered proteins such as httex1. Furthermore, the presence of low complexity regions, such as the long glutamine and proline homorepeats, results in important signal overlap when nuclear magnetic resonance (NMR) is used, hampering the collection of high-resolution information²⁸. Despite these difficulties, several high-resolution NMR studies of non-pathogenic httex1 and N-terminal fragments have been reported^{19,26,27,29,30}. However, due to the severe overlap, only assignments of the first and last glutamines of the poly-Q tract could be achieved.

To circumvent the NMR signal overlap, our lab recently developed a site-specific isotopic labeling (SSIL) strategy that combines cell-free protein expression and non-sense suppression, enabling the investigation of homorepeats in a residue-specific manner^{31,32}. When applying this methodology to a non-pathogenic version of httex1 containing a 16-residue-long poly-Q tract (H16), it was shown that the protein was enriched in helical conformations whose length and stability were defined by flanking regions³³. While the helical propensity was propagated from N17 to the poly-Q through a hydrogen-bond network, it was blocked by the helix-breaking effect caused by the proline-rich region (PRR) that follows the poly-Q tract (Fig. 1a). The structural effects imposed by N17 and PRR may explain the positive and negative regulation of httex1 aggregation by both poly-Q flanking regions, respectively^{34,35}. Whether these structural mechanisms also govern the conformational landscape of pathogenic httex1 remains to be discerned.

In the present study, we applied SSIL to a pathogenic form of httex1 containing a 46 residue-long poly-Q tract (H46) to unambiguously assign sixteen of these glutamines spread along the tract and probed the structure and dynamics of the homorepeat. The integration of the NMR information and small-angle X-ray scattering (SAXS) data provided the structural description of H46 as an ensemble of elongated, partially helical conformations, whose propagation and stability mechanisms were deciphered by ¹⁹F-NMR and molecular dynamics (MD) simulations. All together, our observations provides a detailed structural perspective of the ‘linear lattice’ toxicity model, demonstrating that the presence of long, persistent, aggregation-prone α -helices is concomitant to the expansion of the poly-Q tract beyond the pathological threshold.

110 Results

111 Pathogenic and non-pathogenic httex1 forms present similar structural features

112 In order to study a pathogenic form of httex1, a construct comprising the N17 domain, a 46-residue-
113 long poly-Q tract and the PRR was fused to superfolder GFP (sfGFP) (Fig. 1a). A fully ^{15}N -labeled
114 H46 sample was prepared and a ^{15}N -HSQC NMR spectrum was recorded in order to evaluate its
115 general spectroscopic features. Similarly to H16³³, the spectrum revealed that while peaks from N17
116 and the PRR were well dispersed, the peaks corresponding to glutamine residues remained in a
117 large poorly resolved density (Fig. 1b). As expected, the increased molecular weight led to a
118 general peak broadening, which was particularly striking in the region of the expanded poly-Q tract.

119 The reduced stability of H46 at high concentration precluded the use of traditional 3D-NMR
120 experiments for the frequency assignment. Thus, to confirm the similarities found between the
121 pathogenic and non-pathogenic httex1 constructs, selectively labeled samples of H46 were prepared
122 (^{15}N -Ala and ^{15}N -Lys; ^{15}N -Gly, ^{15}N -Ser and ^{15}N -Arg; ^{15}N -Leu and ^{15}N -Glu; and ^{15}N -Phe), therefore
123 reducing the overlap of some N17 and PRR signals (Fig. S1a). The selective labeling showed that
124 the vast majority of peaks corresponding to N17 and PRR residues nicely overlap for both H46 and
125 H16. Interestingly, F17 peaks in H16 and H46 displayed different chemical shifts. Altogether, our
126 observations suggest that both httex1 forms share similar structural features outside of the poly-Q
127 tract, although some perturbations in the N17/poly-Q boundary are induced upon the extension of
128 the homorepeat.

129 In order to obtain high-resolution information on the poly-Q tract of H46, the SSIL approach using
130 previously optimized protocols³⁶ was used to specifically study 16 of the 46 glutamines of the H46
131 poly-Q tract, as well as two glutamines within the PRR (Fig. 1a). ^{15}N -HSQC spectra of these
132 samples revealed that the glutamines adjacent to N17 (Q18, Q20 and Q21) adopted the lowest
133 chemical shift values of the poly-Q region without any specific trend, while the following
134 glutamines (Q24-Q56) exhibited steadily increasing ^1H and ^{15}N chemical shifts. This last
135 observation points towards a gradual structural change along the homorepeat (Fig. 1c, upper
136 panels). Finally, the last glutamines of the tract (Q61-Q63) were found at the highest chemical
137 shifts, with Q63, affected by the adjacent poly-P tract, displaying an isolated peak outside of the
138 poly-Q density. The signals corresponding to Q75 and Q91 in the PRR did not show any specific
139 trend. The same features were observed when monitoring the Ca - Ha correlations of the same SSIL
140 samples (Fig. 1c, lower panels). Notably, the Q21 SSIL sample presented two Ca peaks with
141 similar intensity, suggesting the presence of two slowly interconverting conformations. While one
142 of the peaks appeared close to these of Q18 and Q20, the second one was shifted to the same
143 spectral region of the central glutamines of the homorepeat.

glutamines of the tract (Q30-Q33 in H16 and Q60-Q63 in H46) showed the same conformational trends, this similarity was reduced for more distant glutamines, such as Q56. Notice that this residue is closer to the helix-promoting N17 in H16 (Q26) than in H46.

H66 substantiates the persistence of long α -helical conformations in long poly-Q tracts

The above results suggest that the distance to the PRR is the only parameter defining the length of α -helical conformations in httex1 and that helical conformations encompass larger sections of the homorepeat when the length of the poly-Q tract is increased. In order to validate this hypothesis, we studied an httex1 construct with 66 consecutive glutamines (H66). The ^{15}N -HSQC of H66 produced by cell-free expression nicely overlapped with that of H46, indicating that no structural changes occur in httex1 upon incorporating twenty additional glutamines (Fig. S2a). The glutamine region of H66 and H46 spectra displayed the same elongated shape and their maximum intensities were centered at the same proton and nitrogen frequencies. Then, using our standard protocols, we applied the SSIL strategy to two glutamines (Q56 and Q76) of H66 to probe their helical content. Note that these two residues are located at equivalent positions to residue Q56 in H46 when aligning both sequences from the N- and C-termini, respectively (Fig. 2a). The NH peak of H66-Q76 appeared in a position equivalent to H46-Q56, whereas H66-Q56 had a lower chemical shift, suggesting that this glutamine adopted a more helical structure than the other two residues (Fig. 2b). This observation was further confirmed by monitoring the $\text{C}\alpha$ - $\text{H}\alpha$ correlations for the three residues (Fig. 2c). Indeed, while the $\text{C}\alpha$ - $\text{H}\alpha$ peaks for H46-Q56 and H66-Q76 overlapped, H66-Q56 was shifted towards more helical conformations. The helical propensity of these residues was quantified with the SCS analysis, indicating an enhanced helicity for H66-Q56 (1.18 ppm) when compared with H66-Q76 (0.50 ppm) and H46-Q56 (0.53 ppm) (Fig. 3c). Interestingly, the SCS value for H66-Q56 was very similar to those observed for the plateau in H46, indicating that the additional twenty glutamines in H66 adopt helical conformations (Fig. S2b). These results evidenced that the extent of the α -helix-breaking capacity of the PRR is the same in all httex1 forms, allowing the α -helical propensity to be propagated through a larger number of glutamines when the length of the homorepeat is increased.

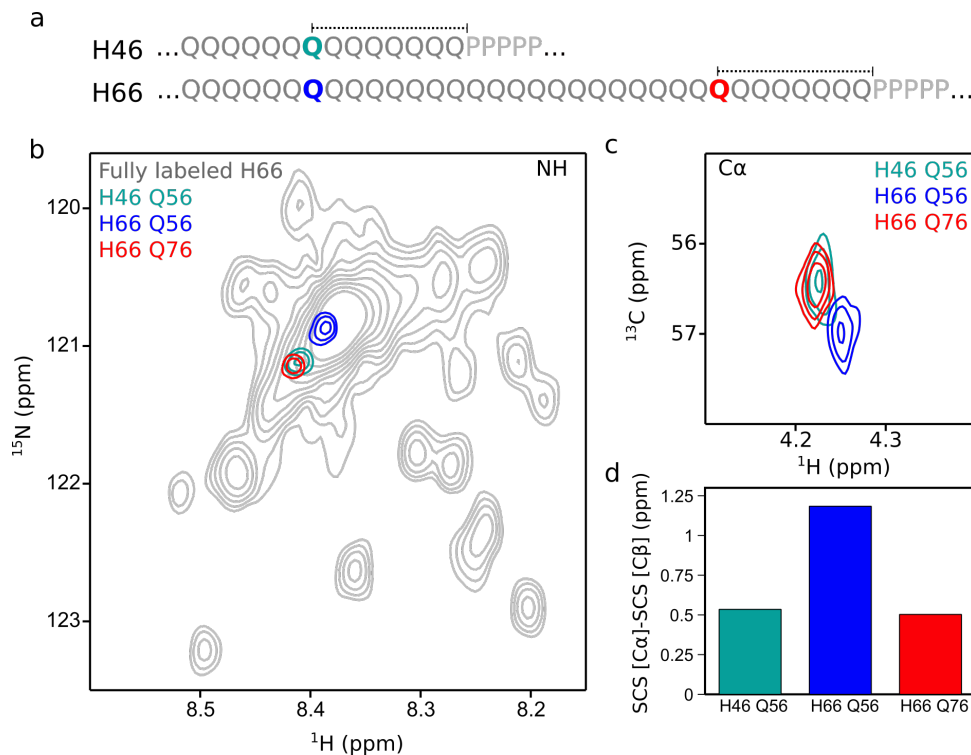


Figure 2. NMR analyses of H66 and comparison with H46. (a) Partial sequences of H46 and H66 indicating the positions of Q56 in H66 (green) and H46 (blue), and Q76 in H66 (red). This color code identifies the individual glutamines throughout the figure. Dashed lines highlight the equal distance of Q56 in H46 and Q76 in H66 to the PRR. Zoom of the ¹⁵N-HSQC (b) and ¹³C-HSQC (c) with individually superimposed colored SSIL spectra showing the poly-Q NH and Cα regions, respectively. (d) Secondary chemical shift (SCS) analysis of H66-Q56, H66-Q76 and H46-Q56, using experimental Cα and Cβ chemical shifts and a neighbor-corrected random-coil library.

SAXS indicates that H46 is an elongated particle in solution with a large degree of flexibility

Small angle X-ray scattering (SAXS) was applied to derive the overall size of H46 in solution. To this end, we applied size-exclusion chromatography (SEC) coupled with SAXS, which allowed us to isolate the H46 peak from potential aggregates and partially digested sfGFP (Fig. S3). The analysis of the resulting profile (Fig. 3a and Table S2) indicates that H46 is a monomeric particle with a radius of gyration, R_g , of 41.5 ± 0.5 Å according to Guinier analysis and a maximum dimension, D_{max} , of 148 Å, calculated using pair-wise distance distribution, $p(r)$, analysis (Fig. S3c). Although the Kratky representation displayed a peak indicating the presence of a folded protein, which was attributed to the sfGFP, the intensity did not completely return to base line, suggesting that the httex1 part of H46 exhibited a high level of flexibility (Fig. 3b). The smooth decrease of the $p(r)$ when approaching the D_{max} value and the departure in the maximum of the Kratky plot from the standard values of a globular protein substantiate the flexibility and the overall extendedness of the protein.

To further confirm that the overall extendedness is inherent to httex1, we performed an equivalent SAXS analysis for H16 (FigS. 3a, S3 and Table S2). Not surprisingly, the resulting SAXS profile of H16 indicated that the protein is a smaller particle ($R_g=32.9 \pm 0.2$ Å and $D_{max} = 126$ Å) in solution

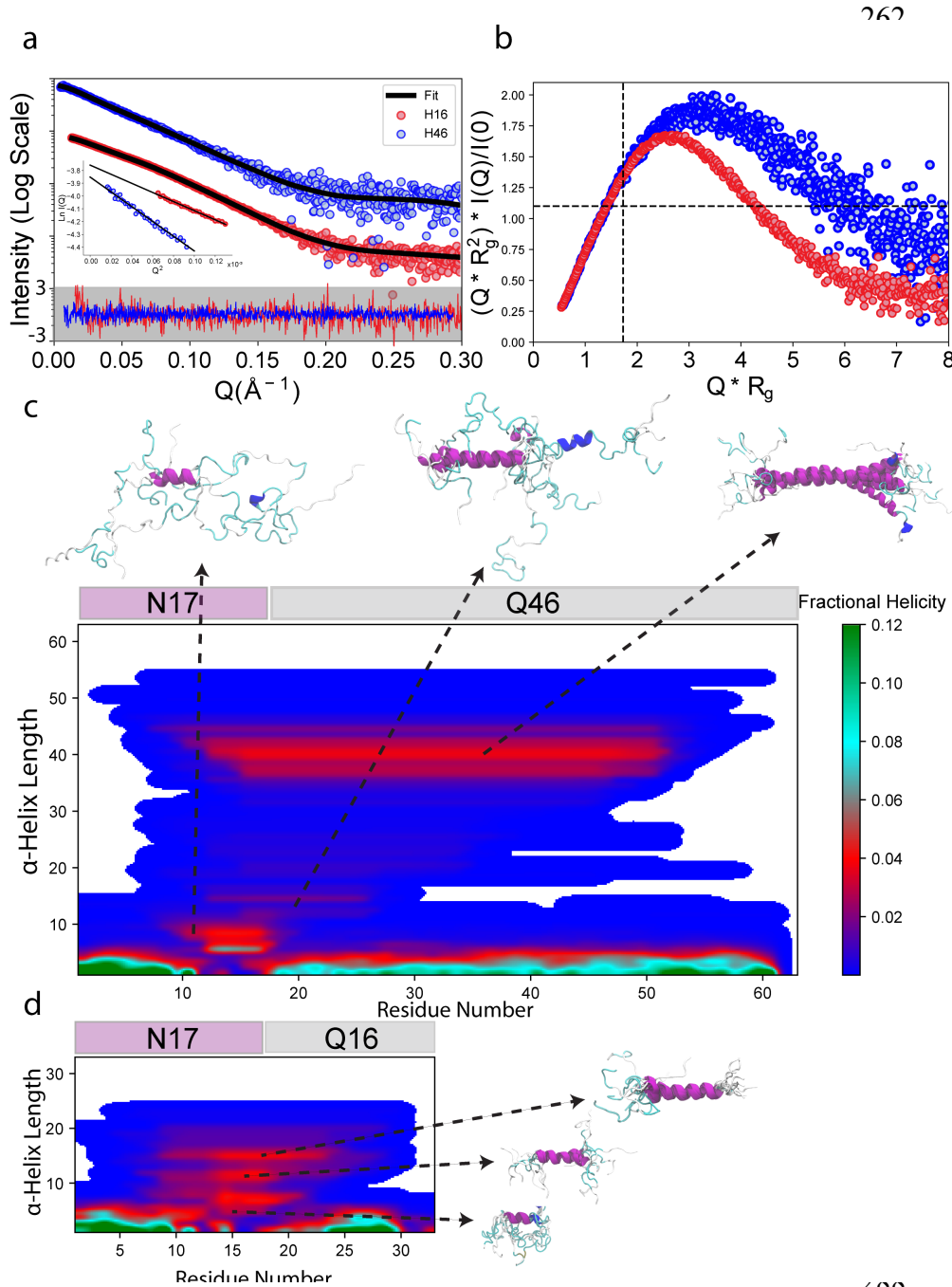
than H46 (Table S2). Importantly, H16 retained SAXS features corresponding to an extended and flexible particle observed for H46.

H46 consists of a mixture of α -helical conformations of different lengths

The $C\alpha$ chemical shifts and the SAXS data measured for H46 were integrated to derive a structural model of the protein. Similar to our previous study of the non-pathogenic H16, two families of ensembles were generated to capture the conformational influence of both flanking regions using a conformational sampling method for intrinsically disordered proteins (see Methods section for details)³⁸. For the first family (N \rightarrow C ensembles), starting with the ¹⁰AFESLKS¹⁶ region of N17 as partially structured, multiple ensembles of 5,000 conformations were built by successively including F17 and an increasing number of glutamines in the poly-Q tract (from Q18 to Q63) as partially structured, while the rest of the chain was considered to be fully disordered. An equivalent strategy was followed for the second family of ensembles (N \leftarrow C ensembles) for which glutamines (from Q63 to Q18) were successively considered as partially structured starting from the poly-P tract. Note that using this building strategy, secondary structural propensities are naturally propagated due to the neighboring effects. For the resulting ensembles of each family and after building the side chains with the program SCWRL4³⁹, averaged $C\alpha$ chemical shifts were computed with SPARTA+⁴⁰. For each family, the relative populations of these ensembles were optimized using the experimental $C\alpha$ chemical shifts with Q55 as the boundary position (Fig. S4). Then, an NMR-compatible ensemble was built by randomly taking conformation from the selected ensembles with the appropriate populations (see Methods for details). This ensemble was further refined by integrating the SAXS data with the ensemble optimization method (EOM)^{41,42}. For this, we included the crystallographic structure of sfGFP (PDBID: 3LVA) and the C-terminal His-tag to the individual conformations of the NMR-optimized ensemble to generate the pool of conformations used by EOM (see Methods). It must be noted that the H46 ensemble had an overall size ($R_g = 42.7$ Å) very similar to the experimentally determined one ($R_g = 41.5 \pm 0.5$ Å), highlighting the quality of our starting model despite using local NMR information for the refinement. Sub-ensembles selected with EOM yielded an excellent fit to the experimental profile ($\chi^2 = 0.2$) (Fig. 3a). The resulting R_g distribution was quite broad and very similar to that of the initial ensemble, indicating that H46 is a highly flexible particle in solution and slightly more extended than the ensemble derived only using chemical shifts (Fig. S4).

The structural analysis of the NMR and SAXS compatible ensemble was performed with SS-map⁴³, which displays the length, the residues involved and the population of the α -helices present in the ensemble in a comprehensible manner. This analysis substantiated the presence of a mixture of multiple helical conformations encompassing different sections of the H46 poly-Q tract (Fig. 3c).

258 These α -helices were initiated in the last residues of the N17 domain ($^{14}\text{LKSF}^{17}$) and propagated
 259 along the tract. Interestingly, an enrichment of long α -helices encompassing around 40 residues and
 260 reaching up to Q52 was observed. The presence of these long stable helical conformations explains
 261 the steady plateau observed in the SCS analysis (Fig. 1d).



289 **Figure 3. A structural model of pathogenic and non-pathogenic httex1 from the synergistic integration of NMR**
 290 **and SAXS data. (a)** The SAXS intensity profiles for H16 (red) and H46 (blue) along with the theoretical profiles of
 291 EOM selected sub-ensembles (black lines). The residuals from EOM fitting are shown at the bottom. The inset shows
 292 the Guinier plots with linear fits as black lines. **(b)** The normalized Kratky plots for H16 (red) and H46 (blue)
 293 displaying a shift from the values expected for globular proteins (shown as black dashed lines) on both X and Y axes.
 294 **(c)** SS-maps calculated from the conformations selected during 100 cycles of EOM for H46 (top) and H16 (bottom).
 295 The population of the different α -helix lengths is shown according to the color code on the right. Some representative
 296 conformations with different lengths of helices are also shown.
 297

A similar structural refinement was performed for H16, using the previously reported NMR-refined ensemble³³ and the SAXS data (Fig. 3a). The EOM fit yielded an excellent agreement with the experimental curve ($\chi^2 = 1.12$) and, as in the case of H46, the resulting sub-ensemble was slightly more elongated than that obtained using only the NMR information. We observed that H16 also consisted of a mixture of α -helical structures of different lengths, with prevalence for these encompassing a large fraction of the homorepeat (Fig. 3d).

Side chain to backbone hydrogen bonds trigger and stabilize helical conformations in H46

It has been shown in non-pathogenic H16 and the androgen receptor that a network of hydrogen bonds involving backbone and side chains is at the origin of the helical propagation from the N-flanking region to the poly-Q tract^{33,44}. Here, we investigated whether this effect is conserved in pathogenic httex1. To this end, we monitored the C β , H β , C γ , H γ and NH ϵ chemical shifts, which could be unambiguously assigned through SSIL samples (Fig. 4a and S5). The two diastereotopic H β glutamine protons displayed resolved responses, with the difference in their chemical shifts increasing along the sequence. The maximum difference was observed for the last glutamines of the tract (Q62 and Q63) and those within the PRR (Q75 and Q91), while Q18 displayed the smallest one, featuring virtually degenerate H β chemical shifts (Fig. 4a, Fig. S5a). These observations indicate a correlation between the chemical shift difference and the level of disorder. Interestingly, Q21 exhibited three peaks that we attributed to the equilibrium between two conformations in slow exchange at the NMR timescale. One of the two conformations of Q21 displayed the spectroscopic features observed for Q18 (degenerate H β chemical shifts) and the other one those observed for the rest of the glutamines (distinct H β chemical shifts). This observation is in agreement with the two C α peaks observed for Q21 (Fig. 1c), which were attributed to two conformations with different helical content.

The H γ signals followed an inverse trend than that observed for H β . The last glutamines of the tract and those located in the PRR presented a single correlation, corresponding to degenerate diastereotopic H γ chemical shifts, as expected for a flexible glutamine side chain (Fig. 4a and S5b). Conversely, the majority of glutamines of the homorepeat (up to Q48) displayed a small but measurable difference between the H γ chemical shifts, suggesting a transient rigidification of the side chain. Again, in line with the H β signals, Q18, Q20 and Q21 were exceptions to this behavior. While Q18 exhibited a single C γ -H γ peak in the ¹³C-HSQC, Q21 displayed three peaks, substantiating the equilibrium between the two previously eluded conformational states. Although Q20 only exhibited two C γ -H γ peaks, their difference in intensity suggested a similar situation as

for Q21, but with the C γ -H γ peak of the conformational state with degenerate H γ chemical shifts overlapping with one of the C γ -H γ peaks of the other state.

These results confirm previous observations for a non-pathological version of httex1 and the androgen receptor^{33,44}, demonstrating the presence of $i \rightarrow i+4$ bifurcated hydrogen bonds structurally connecting the first residues of the poly-Q tract with the upstream flanking region (Fig. 4b). Furthermore, our data indicate that these hydrogen bonds are present, although to a lower extent, along the homorepeat, incorporating an additional mechanism for structural stabilization.

2S,4R-Fluoroglutamine (4F-Gln) as a new probe to study the structure and dynamics of httex1

In order to confirm the different conformational behavior of glutamine side chains along the poly-Q tract and benefiting from the SSIL methodology, a fluorinated glutamine was site-specifically incorporated at different positions of H46 (Fig. 1a). Consequently, we synthesized with high yield and stereospecificity 2S,4R-fluoroglutamine (4F-Gln), in which a fluorine atom replaced a hydrogen atom on C γ (Fig. S6)⁴⁵. This 4F-Gln was successfully loaded onto the tRNA_{CUA} using the yeast glutaminyl-tRNA synthetase with similar yields as for canonical glutamine (Fig. S7), suggesting that the fluorine atom is not changing the structural and electronic properties of glutamine, enabling the recognition by the enzyme³¹.

4F-Gln was used in two sets of experiments. First, we used 4F-Gln to substantiate the participation of Q20 and Q21 in the hydrogen bond network that propagates helicity in the homorepeat. To this end, we incorporated 4F-Gln in positions Q20 or Q21 in two H46 samples that were also isotopically labeled with ¹⁵N-Ser or ¹⁵N-Phe, respectively (Fig. 4c left panels and Fig. S8). When comparing their ¹⁵N-HSQC spectra with those of non-fluorinated H46 (Fig. 4c, left panels), substantial changes could be observed in S16 and F17 upon Q20 or Q21 fluorination, respectively. The presence of a fluorinated glutamine in position 20 produced a slight chemical shift change of S16, while fluorination of Q21 induced a stronger effect on F17, leading to the appearance of a second peak. Furthermore, no chemical shift changes were observed for the other serines and phenylalanines of H46, highlighting the specificity of the interaction. Importantly, similar observations were made when 4F-Gln was incorporated in the same positions in H16, in samples simultaneously labeled with ¹⁵N-Ser and ¹⁵N-Phe (Fig. 4c right panels and Fig. S8). Indeed, when Q20 was fluorinated in the non-pathogenic form, not only S16 was affected, but F17 was also perturbed (Fig. S8). Fluorination of Q21 again resulted in the appearance of a second F17 signal and slightly affected S16. These data underline the structural coupling between Q20 and S16 as well as Q21 and F17, in both pathogenic and non-pathogenic forms of httex1.

In a second set of experiments, we incorporated 4F-Gln in four H46 positions strategically located at the beginning (Q20 and Q21), the middle (Q40) and the end (Q60) of the poly-Q tract to be monitored by 1D ^{19}F -NMR (Fig. 1a). Note that the ^{19}F chemical shift is exquisitely sensitive to small differences in the electronic surroundings of the fluorine nucleus, and thus an excellent reporter on biomolecular structure and dynamics^{46,47}. Strong differences in ^{19}F chemical shifts were observed for the four positions despite the homogeneity of the amino acid sequence (Fig. 4b). This demonstrates important structural changes along the poly-Q tract, most likely linked to the amount of helical content. The chemical shift of Q21 was particularly high, most probably due to its proximity to the ring currents exerted by F17 in the hydrogen-bonded form (Fig 4b and 4d).

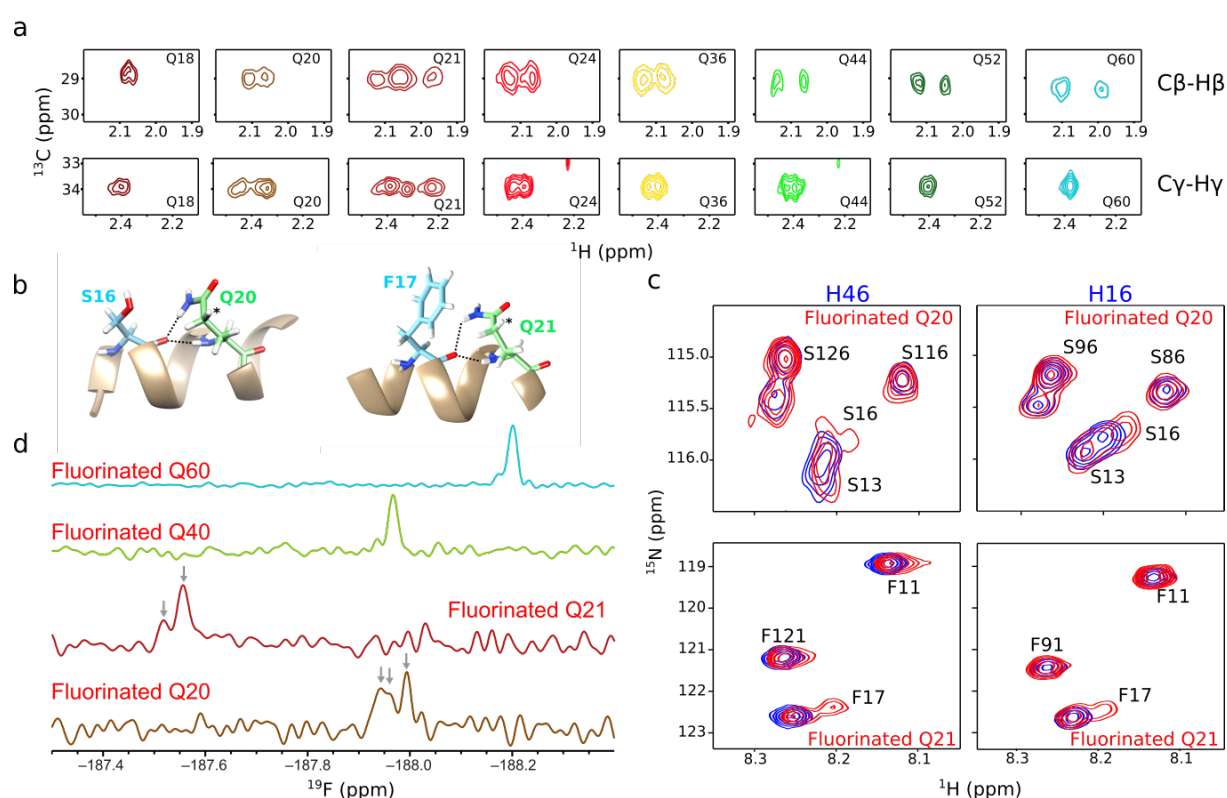


Figure 4. NMR analysis of H46 side chains. (a) Cβ-Hβ and Cγ-Hγ regions of the ^{13}C -HSQC spectra of selected glutamines within the poly-Q. The spectra of Q60 display the standard behavior of disordered glutamines with non-degenerate and degenerate diastereotopic protons for Cβ-Hβ and Cγ-Hγ, respectively. (b) Structural model of the N17-poly-Q coupling showing bifurcated H-bonds between S16 and Q20 (left) and F17 and Q21 (right). The asterisk indicates the proton substituted with a fluorine atom when 4F-Gln was incorporated. (c) Zoom of ^1H - ^{15}N HSQC spectra of H46 (left panels) and H16 (right panels) samples labeled with either ^{15}N -Ser or ^{15}N -Phe. In red, spectra of samples with fluorinated glutamine at position Q20 (upper panels) or Q21 (lower panels). Non-fluorinated samples are colored in blue. (d) 1D ^{19}F spectra of H46 samples with fluorinated glutamines at positions Q20, Q21, Q40 or Q60.

Interestingly, multiple ^{19}F -NMR resonances were observed for Q20 and Q21. For Q20, three distinct responses were measured, including two signals with very close chemical shifts that could only just be resolved. In line with the Cγ-Hγ peaks, it can be concluded that the Q20 side chain adopts at least two different conformations in a slow exchange regime. Given the sensitivity of the

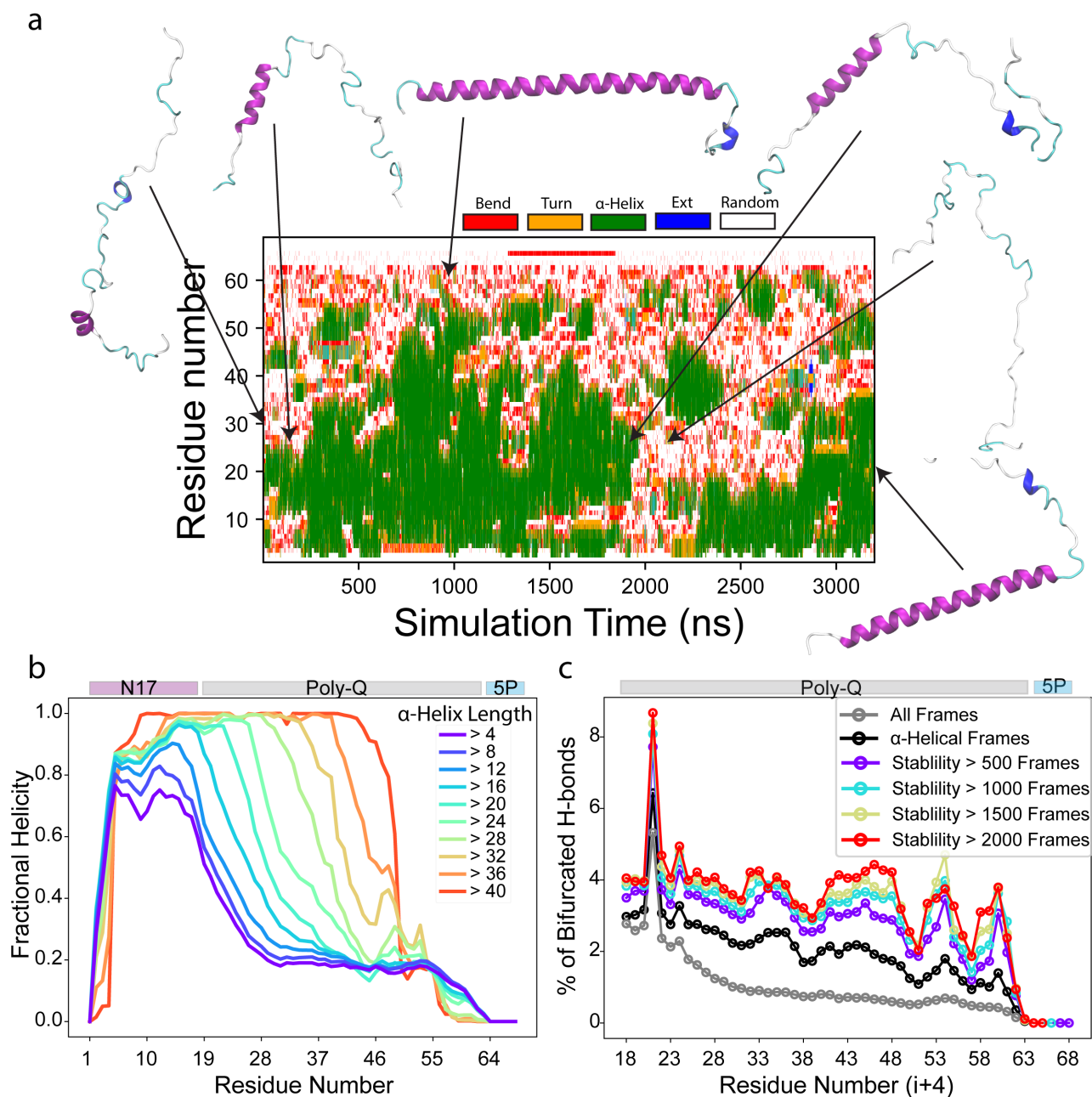
¹⁹F chemical shift, the two closely resonating signals can be explained by the fluorine sensing the different conformational states of neighboring glutamines. For Q21, a weak second ¹⁹F signal could be detected, in agreement with the two populations previously identified in the C α -H α , C β -H β and C γ -H γ correlations. Altogether, the site-specific incorporation of 4F-Gln substantiates the structural link of N17 with the poly-Q tract, the distinct glutamine side-chain conformational preference along the poly-Q tract, and the presence of multiple conformations in the homorepeat.

Molecular dynamics simulations provides insights into the helix propagation and stabilization mechanisms in httex1

We performed Gaussian accelerated molecular dynamics (GaMD)⁴⁸ simulations to understand the secondary structure propensities of httex1 and get further insights into the role of N17 in inducing helicity. Previous MD studies of httex1 have yielded vastly different results ranging from completely α -helical to highly β -strand rich structures, most likely due to the use of non-adapted force-fields⁴⁹. To simulate a httex1 fragment encompassing N17, the polyQ tract and five prolines, we used the recently developed ff99SBws-STQ force-field, which has been refined to describe the secondary structure propensities of low-complexity proteins⁵⁰. In all the 8 independent MD simulations, with an aggregated time of $\approx 20 \mu s$, we observed that the poly-Q tract sampled a wide conformational landscape and mainly adopted α -helical and disordered conformations, while N17 presented a higher helical propensity (Fig. 5a and S9a). Interestingly, several helical folding and melting events could be observed along these trajectories. For some of the simulations, we observed the formation of long α -helices that spanned almost the whole length of N17 and poly-Q tract and were only absent in the residues close to the poly-P region (Fig. 5a). In line with the directionality observed experimentally, the process of α -helix melting systematically occurred from C to N, as observed in the 1600-1800 ns period in Fig. 5a, while α -helices in httex1 preferentially grew from N to C (Fig. S10). The spontaneous formation of short α -helical conformations unconnected with N17 was also observed along the trajectories (*e.g.*, frames 2000-2300 in Fig. 5a), although they dissolved relatively fast. This suggests a small inherent α -helical propensity of poly-Q tracts.

The weighted average per-residue fractional helicity of all the simulations indicated that the poly-Q tract adopted higher α -helical propensity when closer to N17 (Fig. S9b). Moving further from N17, the helicity decreased until Q30 from where it remained flat until Q55 to finally decrease when approaching the poly-P. Importantly, this behavior was qualitatively very similar to the experimentally determined α -helix propensity of httex1 (Fig. 1d and 1e). This suggests that our simulations captured the structural mechanisms present in httex1, although the relative population of α -helix in the poly-Q tract was underestimated. When analyzing the frames with α -helices with

422 increasing length (from 4 to 40), we observed a gradual increase in fractional helicity from N- to C-
423 terminus, substantiating the structural propagation from N17 towards the poly-Q (Fig. 5b).



424 **Figure 5. Insights into the conformational landscape of httex1 with MD simulations.** (a) The per-residue secondary
425 structure plot for one of the GaMD trajectories showing a transition from an almost completely random-coil
426 conformation to a long α -helix and back to random coil. (b) The reweighted fractional helicity calculated using frames
427 with increasing minimum α -helix length ranging from 4 to 40. (c) The percentage of frames with bifurcated hydrogen
428 bonds for each residue of the poly-Q tract using all frames (gray), only the frames where the fragment ($i \rightarrow i+4$) was in
429 helical conformation (black) and the segments of the trajectory where the fragment ($i \rightarrow i+4$) formed a stable α -helix
430 for an increasing number of frames ranging from 500 to 2000.

432
433 We analyzed the trajectories for the existence of $i \rightarrow i+4$ bifurcated hydrogen bonds. Interestingly,
434 they were found throughout the poly-Q, although they were more abundant in the beginning of the

tract where the hydrogen bonds were formed with the residues of N17 region and their number slowly decreased along the tract (Fig. 5c). Residue Q21 presented the highest propensity to form bifurcated hydrogen bonds with F17. Taken together, the trend of bifurcated hydrogen bonds agrees with the results of the appearance of doublets in C γ -H γ correlations and the results from specifically fluorinated glutamines probing the initial residues of the poly-Q (Fig. 4). Then, we analyzed the correlation between bifurcate hydrogen bonds and α -helix stability. Not surprisingly, the percentage of these hydrogen bonds was higher in frames where the segment ($i \rightarrow i+4$) adopted a helical conformation. Importantly, the population consistently increased with the stability of the helix, suggesting that bifurcated hydrogen bonds stabilize α -helical conformations in httex1 (Fig. 5c).

The structure of the poly-Q governs aggregation kinetics and fibril structure of httex1

The hydrogen bond network connecting N17 and the poly-Q tract enabled the design of point mutants in H16 altering the level of structure in the homorepeat while preserving its length³³. Its application to H46 allowed the interrogation of the relative relevance of the helical content and the poly-Q tract length for the aggregation propensity in a pathogenic variant of httex1. With this aim, two N17 mutants of H46 were produced (Fig. 1a). First, by substituting ¹⁶SF¹⁷ by ¹⁶GG¹⁷ (LKGG-H46), we hamper the H-bond network connecting both domains. Second, when ¹⁵KS¹⁶ were replaced by ¹⁵LL¹⁶ (LLLH-H46), the hydrogen bond network was strengthened by incorporating two additional large hydrophobic residues. Uniformly labeled and SSIL samples of these mutants were produced and analyzed by NMR. On one hand, LKGG-H46 glutamine ¹⁵N-HSQC signals collapsed in a broad, high-intensity, downfield-shifted peak, proving a substantial loss of helicity in comparison with the wild-type H46 (Fig. 6a). Interestingly, this broad peak did not overlap with the positions corresponding to fully unstructured glutamines, which were shifted further downfield. This indicates that poly-Q, even when disconnected from the flanking region, contains a small intrinsic propensity for helical conformations, in agreement with our MD simulations and previous studies³⁵. On the other hand, the ¹⁵N-HSQC spectrum of fully labeled LLLH-H46 displayed a more dispersed density of glutamine peaks and an additional upfield density, pointing to a helicity increase of the poly-Q tract (Fig. 6b). The detailed analysis of NH, N ϵ H₂ and C α signals of Q18, Q20 and Q21 SSIL samples from both mutants confirmed the decrease in structuration of LKGG-H46 and the increase in helicity in LLLH-H46, in comparison with the wild-type form (H46) (Fig 6a,b and Fig. S11). Importantly, Q21 in LLLH-H46 displayed signatures of two conformations as also observed for the wild-type. Interestingly, this residue exhibited two NH ϵ correlation peaks, suggesting the formation of a stronger bifurcated hydrogen bond than in the wild-type.

468 Unfortunately, a single Ca peak, corresponding to the less helical conformation, was observed for
469 Q21 in this mutant, suggesting an unfavorable exchange regime for the NMR detection.

470 Once the structural features of the H46 mutants were confirmed, their propensities to aggregate
471 were measured. For this, 15 μ M samples of H46, LKGG-H46 and LLLF-H46 were incubated at
472 37°C and the soluble fractions of the proteins were analyzed by SDS-PAGE over a period of 48 h
473 (Fig. 6c and Fig. S12). Several essays were performed to better sample the monitored period. H46
474 presented a moderate aggregation propensity, with a systematic decrease of the soluble fraction
475 from the first hours of incubation that almost disappeared after 48 h. When the soluble fraction was
476 fitted to a reverse sigmoid function an aggregation half-time, $t_{1/2}$, of 19 h was obtained. A much
477 stronger aggregation propensity was observed for the LLLF-H46 mutant, for which a $t_{1/2}$ of only 1.4
478 h was derived. These observations indicate that increasing the α -helical stability strongly enhances
479 the aggregation propensity of httex1. When the same experiment was performed with the LKGG-
480 H46 mutant, which has a more disordered poly-Q tract similar to pure poly-Q peptides⁵¹, the first
481 signs of aggregation occur after 20 h of incubation and a $t_{1/2}$ of 29 h was obtained. The presence of
482 sfGFP fused to the C-terminus of the httex1 variants, which certainly slows down aggregation,
483 makes the quantitative comparison with previous studies difficult⁵². However, the relative
484 aggregation propensity of the three httex1 forms can be unambiguously obtained.

485 The morphology of the aggregates for H46 and the two mutants after 48 and 120 h were
486 investigated by correlative atomic force microscopy (AFM) – total internal reflection fluorescence
487 (TIRF) (Fig. 6d,e and S13a,b). The intrinsic fluorescence of the proteins allowed the easier
488 localization of the aggregates on the silica surface and indicated that no proteolytic activity
489 preceded the aggregation process of the samples. The inspection of H46 micrographs measured
490 after 48 h of incubation revealed the presence of typical amyloid structures with interconnected
491 fibrils, often presenting a length larger than 1 μ m (Fig. 6d, upper panels, left row). Those fibrils
492 exhibited a heterogeneous morphology, with notable variations in width and height, similarly to
493 those recently described^{53,54}. Interestingly, LLLF-H46 aggregates displayed similar features,
494 although the presence of fibrils was substantially more abundant (Fig. 6d, middle panels). Indeed,
495 large aggregates containing long fibrils were easily found in the sample (Fig S13a). Again, width
496 variations were often observed along the fibrils. The analysis of LKGG-H46 preparation revealed a
497 different behavior. Considerably larger and more heterogeneous aggregates, presenting often well-
498 defined limits, were observed for this mutant. Images indicated the presence of very short fibrils,
499 although relatively long isolated fibrils with a similar morphology than the wild-type and the LLLF-
500 H46 were found in the boundaries of the heterogeneous aggregates.

To verify whether the morphology was maintained after longer maturation times, 5-day-old fibrils were also imaged (Fig. 6e and Fig. S13b). Long fibrils were found in wild-type and LLLF-H46 preparations and, interestingly, elongated bundle structures involving several paired filaments were observed. However, these coiled structures were seldom found in LKGG-H46 aggregates and, when observed, they were less ordered (Fig. 6e). Indeed, fibrils around LKGG-H46 bundles were fragmented and small aggregates could be detected along the whole sample, suggesting reduced fibril stability. Altogether, aggregation and AFM experiments demonstrate that the structural properties of httex1 exert a stronger influence on the aggregation propensity and the final form of the fibrils than the poly-Q tract length.

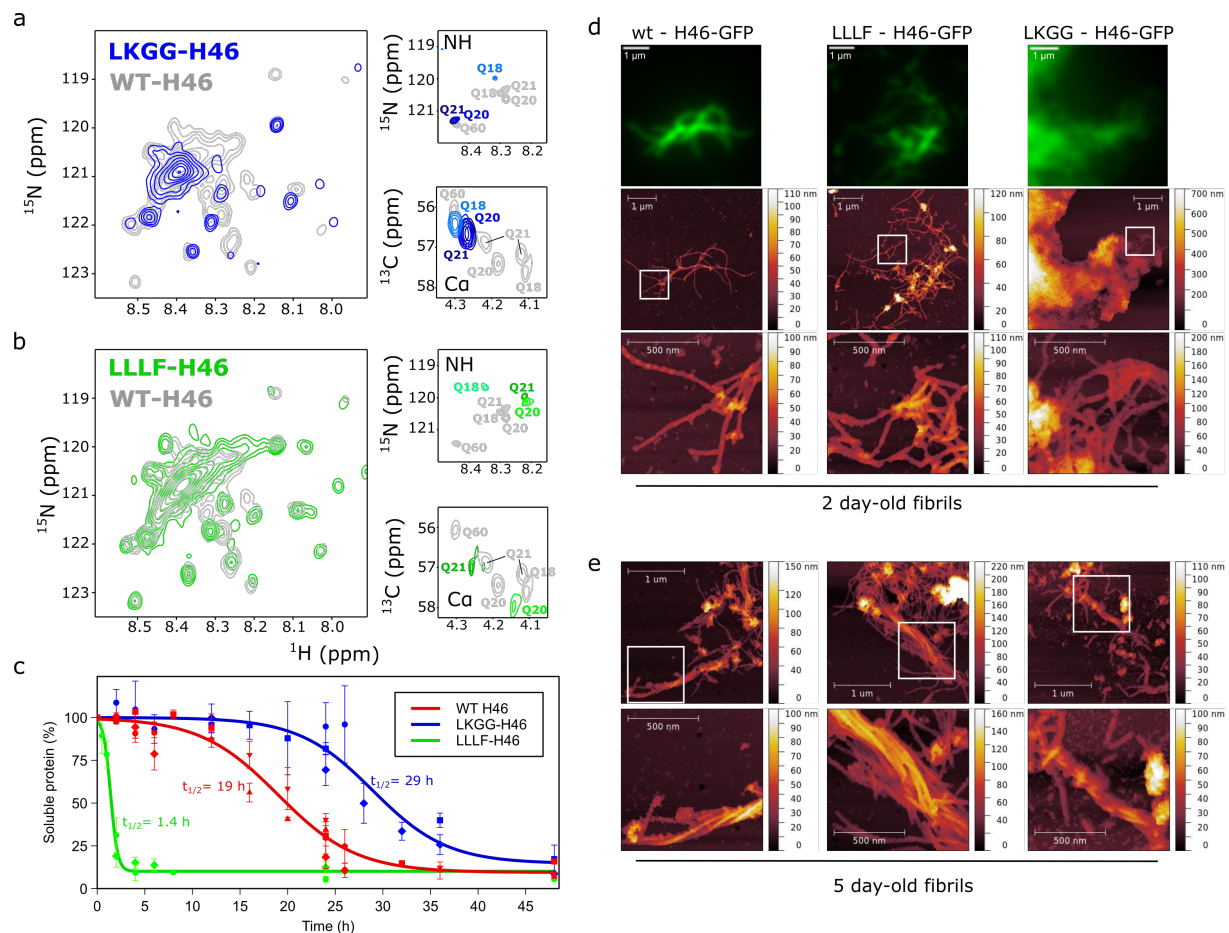


Figure 6. Structural and fibrillation analyses of H46 N17 mutants. (a, b) Overlay of the glutamine region of the ¹⁵N-HSQC of fully labeled H46 (gray) with the N17 mutants LKGG-H46 (blue) and LLLF-H46 (green), as well as zooms of the NH and Ca regions of the corresponding Q18, Q20 and Q21 SSIL samples. (c) Time course of aggregation for wild-type, LKGG- and LLLF-H46 (15 μ M) at 37 $^{\circ}$ C. Each data point corresponds to the mean and associated standard deviation calculated from three replicates. Symbols represent different independent experiments. Half-time ($t_{1/2}$) values calculated for each H46 species are indicated according to the color code shown in the legend. (d) Fluorescence microscopy (upper panels) and AFM (middle and lower panels) images of 2-day-old fibrils of wild-type, LLLF- and LKGG-H46. Each fluorescence image corresponds to the average of 150 pictures. (e) AFM images of 5-day-old fibrils of three H46 species. White squares indicate the zoom region displayed in the panels below.

Discussion

Huntington's disease is the most notorious example of the poly-Q-related diseases and findings connecting structure and disease unveiled for huntingtin are most probably applicable to the whole family of pathologies¹. In this study, we have characterized at high resolution a pathogenic form of httex1 containing 46 consecutive glutamines, a system that is out of the reach for traditional structural biology approaches. We demonstrate that SSIL can be systematically applied to highly repetitive sequences, such as H66, and the only limitations arise from the capacity to purify the protein and preserve its stability in solution.

The systematic application of SSIL to H46 demonstrates that this protein retains the α -helical conformation previously observed for non-pathogenic versions of httex1^{26,29,33}. Using circular dichroism, α -helical propensity in pathogenic httex1 had been previously identified for httex1 with up to 55 glutamines²⁷. Moreover, it was shown that the helical content increased concomitantly with the length of the tract. However, the low-resolution of circular dichroism hampered the analysis of the extent and stability of helical conformations. One of the most striking observations of our study is the fairly flat plateau of measured secondary chemical shifts along a large fraction of the poly-Q tract (Fig. 1d). These chemical shifts are consistent with the coexistence of multiple partially formed α -helices of different lengths, spanning almost the complete poly-Q tract. However, these helices are not equally populated and long α -helices are prevalent according to our synergistic analysis of NMR and SAXS data (Fig. 3). This behavior evidences that the helices, which are formed through a nucleation process triggered by the interaction between the N17 and the first glutamines of the tract, are cooperatively propagated along the homorepeat. A faster decrease in the SCS values would be expected if all helical lengths would display a similar thermodynamic stability. The comparison of the NMR observables for H16 with those of H46 also substantiates the helical stabilization with the poly-Q length. For instance, despite both proteins having the same sequence context, NH, α and $N\epsilon H_2$ chemical shifts for initial glutamines of the tract are systematically shifted towards more helical conformations in H46 than in H16 (Fig. S1). Moreover, experiments performed on H66 demonstrate that α -helical conformations are maintained for long poly-Q tracts and the distance of individual glutamines to the PRR defines their helical propensity (Fig. 2).

From a structural perspective, the α -helical stability found in httex1 could arise from the formation of bifurcate hydrogen bonds all along the homorepeat. Indeed, up to Q48, the diastereotopic H_γ protons have non-degenerate chemical shifts, although the chemical shift difference decreases along the repeat (Fig. S5). An opposite trend is observed for the diastereotopic H_β protons, which present increasing chemical shift differences when reaching the less structured glutamines of H46. These

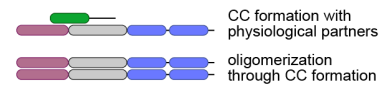
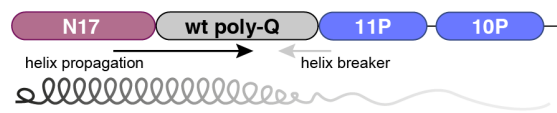
spectroscopic features have been associated with the formation of bifurcated hydrogen bonds and the concomitant rigidification of glutamine side chains^{33,44}. Our MD simulations indicated that the percentage of bifurcated hydrogen bonds is correlated with the stability of α -helical conformations. The ensemble of these observations suggests that glutamine side chains are actively involved in the stabilization of the helical conformation of the poly-Q tract and that the strength of this mechanism declines when approaching the PRR.

Partial structuration in the poly-Q implies that individual glutamines co-exist in (at least) two different conformational states. A similar conclusion was reached by EPR experiments after incorporating stable radicals in several positions of a pathogenic httex1²⁷. In that study, two dynamic regimes were identified in N17 and poly-Q tract residues, but not in glutamines in the PRR. However, structural details of this conformational fluctuation could not be unveiled. Several NMR signatures collected for H46 using SSIL samples, which can be rationalized through the MD simulations, define the structural bases of this conformational equilibrium. These include, among others, the two C α -H α peaks for Q21 (Fig. 1c), the two sets of C β -H β and C γ -H γ peaks for Q20 and Q21 (Fig. 4a), and the multiple ¹⁹F-NMR frequencies also detected for these two residues. Remarkably, the co-existence of a conformational equilibrium is also manifested in most of the other glutamines of the tract, which exhibit the previously eluded non-degenerate C γ -H γ peaks. Our observations demonstrate that httex1 fluctuates between a rigid α -helical conformation, which is stabilized with bifurcate hydrogen bonds, and a more disordered state. Furthermore, our data suggest that the dynamic regime also changes in conjunction with the stability of the helical conformation. While the first glutamines of the tract, which have the highest helical propensity, exhibit a slow exchange on the NMR frequency timescale, a fast exchange regime is observed for the other helical glutamines. This asymmetric behavior suggests that helix unwinding is initiated in the proximity of the PRR and progresses towards the N-terminus, substantiating the previously proposed protective role exerted by the PRR^{34,35,55,56}.

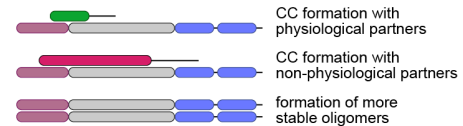
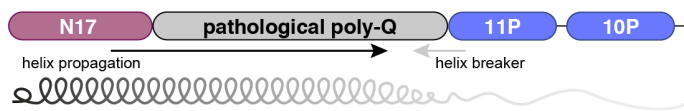
The synergistic combination of NMR and SAXS data has enabled the elucidation of an ensemble model of H46⁵⁷, showing that the presence of long α -helices determines the overall shape of httex1. The refined ensemble indicates that H46 is a flexible elongated particle in solution and that the overall size is correlated with the length of the poly-Q tract (Fig. 3c). Importantly, our structural model is in contradiction to previously reported compact models of httex1^{25,26,49,58}. In these models, compactness is driven by extensive fuzzy contacts between N17 and the poly-Q, a situation that is not compatible with our data. Despite the overall extendedness of the httex1 structure derived here, our ensemble description requires that a large fraction of the protein ensemble remains disordered. This disorder explains the fluorescence transfer efficiency observed in smFRET measurements²⁵

591 and the lack of permanent hydrogen bonds observed in NMR hydrogen deuterium exchange (HDX)
592 experiments²⁶.
593

non-pathological httex1



pathological httex1



594
595 **Figure 7. Scheme illustrating the structural influences within non-pathogenic and pathogenic httex1 and their**
596 **respective modes of interaction. (Top, non-pathogenic httex1)** The poly-Q tract of non-pathogenic httex1
597 experiences opposing structural effects from the N17 (α -helix propagation; black arrow) and the PRR (helix breaking;
598 gray arrow). The gradually shaded helix represents the decrease in helical propensity. Due to its helical conformation,
599 non-pathogenic httex1 can form coiled coil (CCs) with physiological partners or with other httex1 molecules, resulting
600 in oligomers. **(Bottom, pathogenic httex1)** Pathogenic httex1 experiences the same structural effects, however, helix
601 propagation outweighs the helix-breaking effect coming from the PRR and enhances the formation of CCs. Pathogenic
602 httex1 can still interact with its physiological partners *via* CC formation, but it can also interact with non-physiological
603 partners and form more stable oligomers, which eventually drive to fibrils.

604
605 The similarity of the mechanisms defining the structure of non-pathogenic and pathogenic forms of
606 httex1 validates ‘linear lattice’ as the model accounting for the existence of the pathological
607 threshold^{20,22–24}. According to this model, the expansion of the poly-Q induces a systematic increase
608 of the toxicity of httex1 and, beyond the pathological threshold, triggers cytotoxicity and neuronal
609 aggregation. Importantly, our study provides a structural perspective for this model. Our results
610 demonstrate that the poly-Q extension is associated with an increase in the length and stability of
611 the coexisting helical conformations. This is relevant as our aggregation experiments
612 unambiguously show that the α -helical content and not the homorepeat length is the key factor
613 promoting aggregation. Although N17 has been demonstrated to be the aggregation-triggering
614 domain^{18,30,34}, httex1 becomes aggregation-prone when N17 is structurally coupled to the poly-Q
615 tract. This suggests that when structurally uncoupled, such as in the LKGG-H46 mutant, partially
616 helical N17 is still able to oligomerize, but the resulting oligomers are less stable and aggregation
617 propensity is notably reduced. Conversely, strengthening the structural coupling between both
618 domains stabilizes the helical content of the protein and accelerates aggregation, as observed for
619 LLLF-H46. In line with these observations, previous aggregation experiments with httex1
620 analogues modifying the poly-Q tract structure highlighted the relevance of the homorepeat
621 conformational preferences in defining the aggregation propensity^{15,59}. In addition to modified
622 aggregation kinetics, we have observed that mutations in the flanking regions also result in fibers

with distinct morphologies, with the LKGG-H46 mutant forming shorter amyloids and exhibiting less capacity to associate to form bundles. Polymorphism in httex1 aggregates has been previously observed *in vivo* and *in vitro* when modifying the experimental conditions or when deleting flanking regions^{15,52,60-62}. This polymorphism has been associated to the contribution of N17 and the PRR to the fibril packaging^{62,63}. Conversely, the amyloid core is consistently formed by antiparallel poly-Q stretches forming β -sheet monolayers connected through interdigitated glutamine side chains^{63,64}.

In light of our observations, we can speculate about the structural bases of the mechanisms leading to the pathology (Fig. 7). The helical propensity in the poly-Q tract may facilitate intermolecular assemblies through coiled coil (CC) interactions. Indeed, more than 60% of the described httex1 partners have, or are predicted to have, CCs⁶⁵. Furthermore, CC formation has also been suggested to be an important step for the oligomerization and subsequent aggregation of httex1^{17,19}. In the non-pathological scenario, the short length and relatively low stability of the poly-Q helical conformations precisely define the selectivity of partners recognized by httex1. Moreover, resulting httex1 oligomers exhibit reduced stability. When the number of glutamines exceeds the pathological threshold, there is a concomitant population increase of long α -helical conformations. These long poly-Q helices could still interact with their physiological partners, although most probably with different thermodynamic properties compared to the non-pathological scenario. However, they could also associate with other non-physiological partners, sequester them and perturb crucial signaling and metabolic pathways, inducing the symptoms associated to HD². In terms of the fibrillation capacity, longer helices can form more stable oligomers through CC interactions. These oligomers can eventually nucleate the formation of the amyloidogenic fibrils^{17,66} or being the source of cytotoxicity by sequestering crucial cellular components⁶⁷.

Altogether, this study shows that the expansion of the poly-Q tract in pathogenic httex1 is associated with an increase in the length and stability of α -helical conformations, which are the main driving force for the enhanced aggregation propensity. Our results provide a high-resolution structural perspective of the pathological threshold in HD that goes beyond the length of the poly-Q tract by underlining the associated conformational preferences. The generalization of these observations to the other poly-Q related diseases remains to be unveiled. However, the possibility to explore their associated proteins at the residue level and independently of the length of the homorepeat paves the way to a detailed structural understanding of the origin of these pathologies.

654 **Materials and Methods**

655 **Huntingtin exon1 constructs**

656 All plasmids were prepared as previously described³³. Synthetic genes of wild-type huntingtin
 657 exon1 with 16, 46 and 66 consecutive glutamines (H16, H46 and H66 respectively) or H46 and H66
 658 carrying the amber codon (TAG) instead of the glutamine codon, *e.g.* Q18 (H46Q18), were ordered
 659 from GeneArt. Following this strategy, 16 amber mutants for H46 and two for H66 were purchased:
 660 Q18, Q20, Q21, etc. Synthetic genes of the structural H46 mutants (LKGG-H46 and LLLF-H46)
 661 and their corresponding amber codon mutants (Q18, Q20, Q21) were also ordered from GeneArt.
 662 All genes were cloned into pIVEX 2.3d, giving rise to pIVEX-httex1-3C-sfGFP-His₆ and mutants.
 663 The sequence of all plasmids was confirmed by sequencing by GENEWIZ.

665 **Synthesis of 2S,4R-fluoroglutamine**

666 The synthesis of the 2S,4R-fluoroglutamine ((2S, 4R)-2,5-Diamino-4-fluoro-5-oxopentanoic acid),
 667 4F-Gln, was performed as detailed by Qu *et al.*⁴⁵. The purity and the enantiomeric excess (98%)
 668 were evaluated by ¹H- and ¹⁹F-NMR (see Fig. S6 in Supplementary information).

670 **Preparation and aminoacylation of suppressor tRNA_{CUA}**

671 A tRNA_{CUA}/tRNA synthetase pair based on the Gln2 tRNA and glutamine ligase GLN4 from
 672 *Saccharomyces cerevisiae* was prepared in house as previously described³². Briefly, the artificial
 673 suppressor tRNA_{CUA} was transcribed *in vitro* and purified by phenol-chloroform extraction. Prior to
 674 use, the suppressor tRNA_{CUA} was refolded in 100 mM HEPES-KOH pH 7.5, 10 mM KCl at 70°C
 675 for 5 min and a final concentration of 5 mM MgCl₂ was added just before the reaction was placed
 676 on ice. The refolded tRNA_{CUA} was then aminoacylated with [¹⁵N, ¹³C]-glutamine (CortecNet) in a
 677 standard aminoacylation reaction: 20 μM tRNA_{CUA}, 0.5 μM GLN4, 0.1 mM [¹⁵N, ¹³C]-Gln (or 0.5
 678 mM of 4F-Gln) in 100 mM HEPES-KOH pH 7.5, 10 mM KCl, 20 mM MgCl₂, 1 mM DTT and
 679 10 mM ATP³⁷. After incubation at 37°C for 1 hour GLN4 was removed by addition of glutathione
 680 beads and loaded suppressor tRNA_{CUA} was precipitated with 300 mM sodium acetate pH 5.2 and
 681 2.5 volumes of 96% EtOH at -80°C and stored as dry pellets at -20°C. Successful loading was
 682 confirmed by urea-PAGE (6.5% acrylamide 19:1, 8 M urea, 100 mM sodium acetate pH 5.2).

684 **Standard cell-free expression conditions**

685 Lysate was prepared as previously described³³ and based on the *Escherichia coli* strain BL21 Star
 686 (DE3)::RF1-CBD₃, a gift from Gottfried Otting (Australian National University, Canberra,
 687 Australia)⁶⁸. Cell-free protein expression was performed in batch mode as described by Apponyi *et*
 688 *al.*⁶⁹. The standard reaction mixture consisted of the following components: 55 mM HEPES-KOH

(pH 7.5), 1.2 mM ATP, 0.8 mM each of CTP, GTP and UTP, 1.7 mM DTT, 0.175 mg/mL *E. coli* total tRNA mixture (from strain MRE600), 0.64 mM cAMP, 27.5 mM ammonium acetate, 68 μ M 1-5-formyl-5,6,7,8-tetrahydrofolic acid (folinic acid), 1 mM of each of the 20 amino acids, 80 mM creatine phosphate (CP), 250 μ g/mL creatine kinase (CK), plasmid (16 μ g/mL) and 22.5% (v/v) S30 extract. The concentrations of magnesium acetate (5-20 mM) and potassium glutamate (60-200 mM) were adjusted for each new batch of S30 extract. A titration of both compounds was performed to obtain the maximum yield.

Preparation of NMR samples

Samples for NMR studies were produced in cell-free at 5-15 mL scale and incubated at 23°C and 450 rpm in a thermomixer for 4 h. Uniformly labeled NMR samples were obtained by substituting the standard amino acid mix with 3 mg/mL [^{15}N , ^{13}C]-labeled ISOGRO⁴⁰ (an algal extract lacking four amino acids: Asn, Cys, Gln and Trp) and additionally supplying [^{15}N , ^{13}C]-labeled Asn, Cys and Trp (1 mM each) and 4 mM Gln. H46 samples in which only certain amino acids were selectively labeled (Ala and Lys; Gly, Ser and Arg; Leu and Glu; and Phe) were prepared by substituting the respective amino acids for the [^{15}N , ^{13}C]-labeled ones. To enable the labeling of glutamates, potassium glutamate was substituted with potassium acetate, which was optimized by testing a range of concentrations³⁶. To produce site-specifically labeled samples, the standard reaction mixture was slightly modified. Instead of adding 1 mM of each amino acid, proline and glutamine were substituted by deuterated versions (Eurisotop) and used at 2 or 4 mM, respectively. 10 μ M of [^{15}N , ^{13}C]-Gln or 4F-Gln suppressor tRNA_{CUA} were added for suppressed samples. The same procedures were used for the preparation of H66 samples.

Expression of H16 in *E. coli*

Escherichia coli BL21 (DE3) transformed with H16 construct was grown in LB medium supplemented with 50 μ g/mL kanamycin at 37°C under stirring. When an OD_{600nm} 0.7 was reached, the culture was induced using 1 mM IPTG and grown for 24 hours at 23°C. The cell pellet was collected by centrifugation at 5,000 x g for 15 minutes at 4°C and resuspended in 10 mL buffer A (50 mM Tris, 1000 mM NaCl, pH 8.5), supplemented with cComplete EDTA free protease inhibitor tablet (Roche), per 1 L of expression volume. Cells were lysed by sonication at 35% for 2 minutes with on-off cycles and cell debris was pelleted by centrifugation at 20,000 xg for 30 minutes at 4°C. *E. coli* H16 was used for SAXS experiments.

Protein purification

The cell-free reactions were diluted 5-10 fold with buffer A (50 mM Tris-HCl pH 7.5, 500 mM NaCl, 5 mM imidazole) before incubating it 1 h with 1.5 mL of Ni-resin (cOmplete™ His-Tag Purification Resin). The matrix was packed by gravity-flow and washed with buffer B (50 mM Tris-HCl pH 7.5, 1000 mM NaCl, 5 mM imidazole) and the target protein was eluted with buffer C (50 mM Tris-HCl pH 7.5, 150 mM NaCl, 250 mM imidazole). For SAXS measurements, this affinity chromatography step was carried out in an AKTA pure System (GE Healthcare) with a 5 mL Histrap® Excel column. Elution fractions were checked under UV light and fluorescent fractions were pooled, protease inhibitors were added (cOmplete EDTA-free protease inhibitor cocktail, Sigma Aldrich) and the sample was dialyzed against NMR buffer (20 mM BisTris-HCl pH 6.5, 150 mM NaCl) at 4°C using SpectraPor 4 MWCO 12-14 kDa dialysis tubing (Spectrum Labs). Dialyzed protein was then concentrated with 10 kDa MWCO Vivaspinn centrifugal concentrators (3,500 xg, 4°C) (Sartorius). Protein concentrations were determined by means of fluorescence using an sfGFP calibration curve. Final NMR sample concentrations ranged from 4 to 15 μM. Protein integrity was analyzed by SDS-PAGE.

For both aggregation and SAXS experiments, an additional size-exclusion chromatography step, using a Superdex S200 10/300 column, was carried out. For aggregation measurements, this step was performed in aggregation buffer (50 mM sodium phosphate, pH 7.5, 150 mM NaCl) and for SAXS measurements in NMR buffer.

NMR experiments and data analysis

All NMR samples contained final concentrations of 10% D₂O and 0.5 mM 4,4-dimethyl-4-silapentane-1-sulfonic acid (DSS). ¹⁵N and ¹³C-HSQC experiments, in order to determine amide (¹H_N and ¹⁵N) and aliphatic (¹H_{aliphatic} and ¹³C_{aliphatic}) chemical shifts, were performed at 293 K on a Bruker Avance III spectrometer equipped with a cryogenic triple resonance probe and Z gradient coil, operating at a ¹H frequency of 700 MHz or 800 MHz. Spectra acquisition parameters were set up depending on the sample concentration and the magnet strength. All spectra were processed with TopSpin v3.5 (Bruker Biospin) and analyzed using CCPN-Analysis software⁷⁰. Chemical shifts were referenced with respect to the H₂O signal relative to DSS using the ¹H/X frequency ratio of the zero point according to Markley *et al.*⁷¹.

Random coil chemical shifts were predicted using POTENCI, a pH, temperature and neighbor corrected IDP library (<http://nmr.chem.rug.nl/potenci/>)³⁷. Secondary chemical shifts (SCS) were obtained by subtracting the predicted value from the experimental one (SCS=δ_{exp}-δ_{pred}). For better reliability of the results regarding possible referencing errors, we used the combined C_α and C_β secondary chemical shifts (SCS(C_α)-SCS(C_β)).

¹⁹F-NMR experiments

All NMR samples were first concentrated up to a ca. 200 µl volume using Vivaspin centrifugal concentrators (Sartorius) with a 5 kDa cutoff at 4°C. 0.1 µl of a trimethylsilylpropanoic acid (TMSP) solution for chemical shift referencing and 10 µl of D₂O were added before NMR measurement. All ¹⁹F NMR experiments were performed on a Bruker Avance III HD spectrometer operating at a ¹H and ¹⁹F frequencies of 600.13 MHz and 564.69 MHz, respectively, equipped with a CP-QCI-F cryoprobe with ¹⁹F cryo-detection. All ¹⁹F 1D experiments were performed at 293.0 K with ¹H decoupling during acquisition using waltz16 composite pulse decoupling. An acquisition time of 0.58 s, spectral width of 100.6 s and relaxation delay of 1.0 s was used for all samples, except for the sample fluorinated at Q20, where an acquisition time of 0.29 s and a relaxation delay of 0.5 s was used. Concatenated 1D ¹⁹F spectra of 128 transients each were acquired in order to monitor any spectral changes over time. Signal averaging was then performed up to a time point before significant spectral changes over time could be detected. Final number of transients varied were 77824, 49152, 39680 and 53760 for samples fluorinated at Q20, Q21, Q40 and Q60, respectively. ¹⁹F spectra were referenced to the ¹H signal of TMSP using the unified chemical shift scale.

Model building and chemical shift ensemble optimization

Ensemble models for the two families capturing the conformational influences of the flanking regions, N→C and N←C, were constructed with the algorithm described in reference³⁸, which uses a curated database of three-residue fragments extracted from high-resolution protein structures. The model building strategy consecutively appends residues, which are considered to be either fully disordered or partially structured. For fully disordered residues, amino acid specific φ/ψ angles defining the residue conformation are randomly selected from the database, disregarding their sequence context. For partially structured residues, the nature and the conformation of the flanking residues are taken into account when selecting the conformation of the incorporated residue. Steric clashes are tested at each step, and a backtracking strategy is applied to solve possible conflicts (see detailed explanation of the algorithm in reference³⁸).

Two families of ensembles were built. For the first family (N→C ensembles), starting with the ¹⁰AFESLKS¹⁶ region of N17 as partially structured, multiple ensembles of 5,000 conformations were built by successively including an increasing number of glutamines in the poly-Q tract (from F17 to Q63) as partially structured, while the rest of the chain was considered to be fully disordered. An equivalent strategy was followed for the second family of ensembles (N←C ensembles) for which glutamines were considered successively as partially structured from the poly-P tract (from Q63 to Q18). Note that in the partially structured building strategy secondary structural elements

are propagated due to the conformational influence of neighboring residues. Two tripeptide databases were used to generate the conformational ensemble models. Both were constructed from the protein domains in the SCOP (Structural Classification of Proteins)^{72,73} repository filtered to 95% sequence identity. An “unfiltered” tripeptide database was built disregarding secondary structure content, and “coil” database included tripeptides not participating in α -helices or β -strands. For the N \rightarrow C ensembles, the best results were obtained when using the “unfiltered” and “coil” databases to sample the partially-structured and the fully disordered sections, respectively. For the N \leftarrow C ensembles, the “coil” database yielded the best results. For the resulting 47 ensembles of each family, and after building the side chains with the program SCWRL4³⁹, averaged C α chemical shifts were computed with SPARTA+⁴⁰, and used for the optimization. The optimized ensemble model of H46 was built by reweighting the populations of the pre-computed ensembles, minimizing the error with respect to the experimental C α CSs. In order to capture the influence of the flanking regions, glutamines within the tract were divided into two groups: those influenced by N17 and those influenced by the poly-P tract, whose chemical shifts were fitted with the N \rightarrow C and N \leftarrow C ensembles, respectively. The limit between both families was systematically explored by computing the agreement between the experimental and optimized CSs through a χ^2 value. An optimal description of the complete CS profile was obtained when Q55 was chosen as the last residue structurally connected with N17. Finally, an ensemble of 11,000 conformations was built using the optimized weights and it was used to derive secondary structure population using SS-map⁴³ and to analyze the SAXS data.

SAXS data measurement and analysis

The SAXS data for H16 were collected at the SWING beamline at the SOLEIL synchrotron, France, equipped with an Eiger 4M detector with a sample-to-detector distance of 1.5 m⁷⁴. The data for H46 were collected at EMBL-bioSAXS-P12 beamline at PETRAIII, Hamburg, Germany equipped with a Pilatus 6M detector with a sample-to-detector distance of 3 m⁷⁵. The parameters used for SAXS data collection are given in Table S2. All the data were collected in SEC-SAXS mode with an in-line Superdex 200 Increase 10/300 GL column (GE Healthcare). Both proteins were concentrated to 8 mg/mL and centrifuged at 20,000 x g immediately before injecting the protein onto the column. 80 μ L of the sample were injected into the column and the flow rate was maintained at 0.5 mL/min. The initial data processing steps including masking and azimuthal averaging were performed using the program FOXTROT⁷⁶ for H16 and SASFLOW pipeline⁷⁵ for H46. The resulting 1D profiles were analyzed using CHROMIXS⁷⁷ from ATSAS suite to select the frames corresponding to sample and buffer and perform buffer subtraction. The final buffer subtracted and averaged SAXS profiles were analyzed using ATSAS 2.8 software package⁷⁸,

including AUTORG for calculating the radius of gyration and calculation of extrapolated value of radius of gyration (R_g), GNOM⁷⁹ for calculation of pairwise distance distribution profiles and DATBAYES⁸⁰ for calculation of molecular weight by Bayesian estimate from four approaches. The ensemble optimization approach (EOM) was used to select sub-ensembles that collectively describe the SAXS data. The program RanCH was first used to join each of the conformations of H16 and H46 (generated as described above) to the modelled structure of sfGFP and the hexahistidine tag used for purification. GAJOE was then used to find a sub-ensemble from this pool which collectively describes the SAXS data^{41,42}. The graphical representations were generated using the program VMD⁸¹.

Molecular dynamics simulations

We performed Gaussian Accelerated Molecular Dynamics (GaMD)⁴⁸ simulations to explore the conformational landscape and the secondary structure propensities of a fragment of httex1 consisting of N17, 46 glutamines and 5 prolines. We used ff03ws-STQ⁵⁰ force field, which is adapted to proteins with low-complexity sequences (obtained from https://bitbucket.org/jeetain/all-atom_ff_refinements/src/master/). We chose an extended conformation built using the protocol described earlier in the model building section as the starting structure and prepared the simulation system using tools available with GROMACS 2020.5. This included addition of hydrogens, solvation and addition of ions (Na^+ and Cl^-) to neutralize the system and set the final salt concentration to 0.15 M. Thereafter, the system was converted to AMBER format using ParmEd tool in AMBER20. At this stage, hydrogen mass repartitioning was also done to allow a time step of 4 fs. We used periodic boundary conditions and restrained the bonds containing hydrogen atoms using SHAKE algorithm. Particle Mesh Ewald summation (PME) was used to calculate electrostatic interaction with a cut-off of 9 Å on the long-range interactions. The system was energy minimized for 5000 steps. This was followed by an NVT (constant number, volume and temperature) equilibration for 5 ns and further equilibration in NPT (constant number, pressure and temperature) for 10ns. For all the simulations, the temperature was maintained at 293 K and for NPT simulations the pressure was maintained at 1 atm. This was followed by a GaMD equilibration stage which consisted of a classical MD simulation of 40 ns during which the potential statistics to calculate GaMD parameters were collected followed by a 120 ns long equilibration during which the boost was added and updated. Finally, 8 independent simulations with an aggregate simulation time of ~ 20 μs were launched using the boost parameters obtained in the equilibration stage. The simulations were run in “dual-boost” mode and the reference energy was set to the lower bound ($E=V_{\text{max}}$). The average and standard deviation of the potential energy were calculated every 2ns (number of steps $\approx 4 \times \text{system size}$).

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864 **Aggregation experiments**

865 Time-dependent aggregation of H46 variants was followed with SDS-PAGE analysis as previously
 866 described, with minor modifications⁵². 15 μ M wild-type-, LKGG- and LLLF-H46 samples,
 867 prepared in aggregation buffer (50 mM sodium phosphate, pH 7.5, 150 mM NaCl), were incubated
 868 at 37°C for 48 h, without shaking. 10 μ L-aliquots were extracted at different time intervals,
 869 immediately mixed with denaturing buffer (125 mM Tris-HCl, pH 6.8, 20% glycerol, 4% SDS, 200
 870 mM dithiothreitol, 0.05% bromophenol blue), incubated for 10 min at 95°C, and frozen at -20 °C
 871 until analysis on Bolt™ 4–12% Bis-Tris Plus gels (Invitrogen). The gels were washed in water,
 872 stained with Instant Blue Coomassie Protein Stain (Abcam), and visualized using a Gel Doc™ Ez
 873 Imager (Bio-Rad). The amount of SDS-soluble species trapped in the stacking gel was quantified
 874 using the Image Lab 5.1 software. The percentages of soluble protein were referenced to time 0
 875 values, and plotted against time. The plots were fitted using GraphPad Prism Software. For each
 876 protein variant, at least two independent experiments, with three replicates at each time point, were
 877 recorded.

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879 **Atomic force microscopy (AFM) and total internal reflection fluorescence (TIRF)**

880 Correlative AFM-TIRF microscopy was developed in-house⁸². AFM images were acquired using a
 881 Nanowizard 4 (JPK Instruments, Bruker) mounted on a Zeiss inverted optical microscope and
 882 equipped with a Vortis-SPM control unit. A custom-made TIRF microscope was coupled to the
 883 AFM using a LX 488-50 OBIS laser source (Coherent). We used an oil immersion objective with a
 884 1.4 numerical aperture (Plan-Apochromat 100x, Zeiss). Fluorescence was collected with an
 885 EmCCD iXon Ultra897 (Andor) camera. The setup includes a 1.5x telescope to obtain a final
 886 imaging magnification of 150-fold, corresponding to a camera pixel size of 81.3 nm. An ET800sp
 887 short pass filter (Chroma) was used in the emission optical path to filter out the light source of the
 888 AFM optical beam deflection system. The excitation laser wavelength was centered at 488 nm and
 889 the power was measured before the objective with a PM100 energy meter (purchased from
 890 Thorlabs) and was optimized in all the experiments in the range of 1-5 μ W. Fluorescence images
 891 were acquired using an ET525/50 nm (Chroma) emission filter and an acousto-optic tuneable filter
 892 (AOTFnc-400.650-TN, AA opto-electronics) to modulate the laser intensity. Fluorescence images
 893 were obtained by averaging 150 individual images, each acquired over 50 ms as exposure time.

894 AFM images were collected in liquid environment (Dulbecco's PBS named D-PBS) using the
 895 quantitative-imaging (QI) mode. Each image was acquired with 256x256 lines/pixels and the
 896 following scan size: 5 μ m \times 5 μ m, 2.5 μ m \times 2.5 μ m and 1 μ m \times 1 μ m. Typical force *versus* distance
 897 curves were recorded with a tip approach speed ranging from 10 μ m/s to 30 μ m/s and an oscillation

amplitude (Z length) of 100 nm or 150 nm, adjusted depending on the height of the aggregates. The maximal force exerted in each pixel was set to 100-150 pN and optimized during the image acquisition. We used MSNL-D and MSNL-E (Bruker) AFM probes with resonances in liquid of ≈ 2 kHz and 10 kHz, respectively, and nominal spring constants of 0.03 N/m and 0.1 N/m. MSNL cantilevers have a sharp tip radius (≈ 2 nm), which is ideal for high-resolution imaging. The inverse optical lever sensitivity was calibrated with the acquisition of a force *versus* distance curve on the glass coverslip whereas the cantilever stiffness was calibrated using thermal method⁸³.

Samples for correlative AFM and TIRF were prepared on circular glass coverslips (2.5 cm, 165 μ m thick, purchased from Marienfeld). Coverslips were cleaned with a 15 min cycle of sonication with ultrasounds in 1M KOH, rinsed 20 times with deionized water and finally with a second cycle of sonication in deionized water. Fibrils were then deposited on the clean glass coverslips and let dry before being immersed in D-PBS for AFM imaging.

Acknowledgements

The authors thank Gottfried Otting for providing the BL21 (DE3) Star::RF1-CBD3 strain. This work was supported by the European Research Council under the European Union's H2020 Framework Programme (2014-2020) / ERC Grant agreement n° [648030] awarded to PB, ANR-17-CE11-0022-01 awarded to NS, and Labex EpiGenMed, an « Investissements d'avenir » program (ANR-10-LABX-12-01). The CBS is a member of France-BioImaging (FBI) and the French Infrastructure for Integrated Structural Biology (FRISBI), 2 national infrastructures supported by the French National Research Agency (ANR-10-INBS-04-01 and ANR-10-INBS-05, respectively). AU is supported by a grant from the Fondation pour la Recherche Médicale (SPF20150934061). DS acknowledge a grant from the Métropole Européenne de Lille (PUSHUP). Géraldine Levy, Université de Lille, is thanked for help with sample preparation and the ¹⁹F-NMR experiments. This work benefited from the HPC resources of the CALMIP supercomputing center under the allocations 2016-P16032 and 2021-P21043. The 600 MHz spectrometer for ¹⁹F NMR measurements is funded by the Nord Region Council, CNRS, Institut Pasteur de Lille, the European Community (ERDF), the French Ministry of Research and the Université de Lille and by the CTRL CPER cofunded by the European Union with the European Regional Development Fund (ERDF), by the Hauts-de-France Regional Council (contract n°17003781), Métropole Européenne de Lille (contract n°2016_ESR_05), and French State (contract n°2017-R3-CTRL-Phase1). The authors thank the SWING beamline at SOLEIL synchrotron, Saint-Aubin, France (proposal 20181386) and P12 beamline at PETRAIII, Hamburg, Germany for beamtime allocation to the project and assistance during data collection.

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Author Contributions

P.B. conceived the project. C.A.E.R, A.U., A.S., A.B., D.S., N.S. and P.B. designed experiments. C.A.E.R, A.U., A.S., M.P., A.M., A.E., A.F., X.L.L., Z.D.S., L.C., A.T., F.A. and D.S. performed experiments. R.E.S., P.E.M., A.B., J.C., N.S. and P.B. supervised experiments. C.A.E.R., A.U., A.S. and P.B. wrote the manuscript with the help of all the co-authors.

Competing Interest

The authors declare no competing interests

Data Availability Statement

The datasets generated during and/or analysed during the current study are available from the corresponding author on reasonable request.

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