The 2.2-Angstrom resolution crystal structure of the carboxy-terminal region of ataxin-3

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Keywords
ataxia; ataxins; Huntington’s disease; polyglutamine; triplet repeat disorder

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An expansion of polyglutamine (polyQ) sequence in ataxin-3 protein causes spinocerebellar ataxia type 3, an inherited neurodegenerative disorder. The crystal structure of the polyQ-containing carboxy-terminal fragment of human ataxin-3 was solved at 2.2-Å resolution. The Atxn3 carboxy-terminal fragment including 14 glutamine residues adopts both random coil and α-helical conformations in the crystal structure. The polyQ sequence in α-helical structure is stabilized by intrahelical hydrogen bonds mediated by glutamine side chains. The intrahelical hydrogen-bond interactions between glutamine side chains along the axis of the polyQ α-helix stabilize the secondary structure. Analysis of this structure furthers our understanding of the polyQ-structural characteristics that likely underlie the pathogenesis of polyQ-expansion disorders.

Abbreviations
Htt, Huntingtin; JD, Josephin domain; MBP, maltose-binding protein; MJD/SCA3, Machado-Joseph Disease/Spinocerebellar Ataxia Type 3; polyQ, polyglutamine; UIM, ubiquitin-interacting motif.
our previous crystallographic studies of the Huntingtin (Htt) polyQ region [14,15].

Materials and methods

Crystallization and data collection

A fragment of human Atxn3 (amino acids 278–329) containing a 14-amino acid tract with 13 glutamines interrupted by a single lysine was amplified by polymerase chain reaction and cloned into NotI and PstI sites of the pMAL vector encoding the maltose-binding protein (MBP) with a modified carboxy-terminal tri-alanine linker [16]. A C-terminal tag of 19 amino acids (QSYQTAGKLGTGRRFTTS) was added to the MBP-Atxn3 fusion protein to facilitate crystallization [14,15]. Addition of the tag was essential in order to obtain diffracting crystals. The MBP-Atxn3-C fusion protein was expressed in Escherichia coli BL21(DE3) strain. A single colony carrying pMAL-Atxn3-C plasmid was inoculated into 10 mL of LB medium supplemented with ampicillin overnight at 37 °C with shaking. The culture was transferred into 1 L of LB containing ampicillin, and cells were cultivated until absorbance at 600 nm was 0.8. Protein synthesis was induced by the addition of IPTG (final concentration 0.3 mM) for 16 h at 16 °C with vigorous shaking. Then cells were harvested by centrifugation (5000 g, 10 min, 4 °C) and were resuspended in 50 mL of lysis buffer (25 mM Tris-HCl, pH 8.0, 200 mM NaCl, 1 mM DTT, 1 mM EDTA, 0.1% Triton X-100). Cells were disrupted by sonication (three cycles for 1 min on ice, 50 : 50 pulse mode, Branson Sonifier 450). Lysate was centrifuged (70 000 g, 1 h, 4 °C) and the supernatant was applied onto 3 mL of amylose resin (NEB) pre-equilibrated with equilibration buffer (25 mM Tris-HCl, pH 8.0, 200 mM NaCl,
1 mM DTT, 1 mM EDTA). After washing, protein was eluted with elution buffer (25 mM Tris-HCl, pH 8.0, 200 mM NaCl, 1 mM DTT, 1 mM EDTA, 15 mM maltose). MBP-Atxn3-C was concentrated and applied onto the gel-filtration column Superdex75 16/60 (GE Health Care, Piscataway, NJ, USA) pre-equilibrated with gel-filtration buffer (25 mM Tris-HCl, pH 8.0, 100 mM NaCl, 1 mM DTT, 0.5 mM EDTA, 0.02% NaN₃, 1 mM maltose) at 1 mL min⁻¹ flow rate. Fractions containing MBP-Atxn3-C fusion were pooled and concentrated to approximately 10 mg mL⁻¹ using Amicon centrifugal filters (Millipore Ltd, Cork, Ireland, 30000 Da MWCO). The resulting protein was at least 95% pure as shown by Coomassie staining of a SDS/PAGE. Purified MBP-Atxn3-C was crystallized using the hanging drop vapor diffusion technique without removing either MBP or the C-terminal tag. Single crystals were obtained in the following crystallization conditions: 25% polyethylene glycol monomethyl ether (5K), 1.0M sodium acetate, 0.1M zinc acetate (crystal C1) and 24% polyethylene glycol monomethyl ether (5K), 0.9M sodium acetate, 0.06M imidazole pH 8.0, 0.1M zinc acetate (crystal C2). No additional cryoprotection steps were undertaken due to the high polyethylene glycol concentration in the cryostate. These raw diffraction data were indexed and scaled using HKL-2000 software [17].

**Table 1. Data collection and refinement statistics.**

<table>
<thead>
<tr>
<th></th>
<th>C2 (PDB: 4WTH)</th>
<th>C1 (PDB: 4YS9)</th>
</tr>
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<tr>
<td>Wavelength (Å)</td>
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<tr>
<td>Temperature (K)</td>
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<tr>
<td>Detector</td>
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<td>a (Å)</td>
<td>49.01</td>
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<td>(2.05–2.00)</td>
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<td><strong>Refinement</strong></td>
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<td>37.65–2.00</td>
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<td>No. of reflections, working set</td>
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<tr>
<td>No. of reflections, test set</td>
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<td>Final R-work</td>
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<td>0.207 (0.221)</td>
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<tr>
<td>Final R-free</td>
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<tr>
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<td>2975</td>
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<tr>
<td>Ligand/ion</td>
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<td>4 (Zn), 23 (MAL)</td>
</tr>
<tr>
<td>Water</td>
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<td>Average B-factors (Å²)</td>
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<td>96.60</td>
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<td>Allowed (%)</td>
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<td>Outlier (%)</td>
<td>0.13</td>
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</table>

*Values in parentheses correspond to high-resolution shell.

**Structure determination**

Phasing was performed by the molecular replacement method in Phaser software [18] using 40 MBP PDB models from Protein Data Bank. The best solutions for datasets produced by Phaser with MBP structure (PDB ID 1ANF) were used for Atxn3-C structure model. Structure determination was performed separately for each crystal. Electron density in the region corresponding to MBP was well defined, whereas the initial map of the Atxn3-C region was of poor quality. The complete maps were obtained for MBP region, and partial maps were obtained for the Atxn3-C region. The map derived from the C1 crystal dataset allowed only limited determination of Atxn3-C structure due to intrinsic disorder of entire Atxn3-C region. Maps derived from C2 crystals were of better quality and enabled more extensive model building. In the process of the model building and refinement R/work, R/free improved and the electron density of the Atxn3-C region became clearer. The Cα backbone was built first, and side chains in the Atxn3-C region were assigned in the later stages of refinement. Crystallographic parameters for C1 and C2 crystals and final refinement statistics are listed in Table 1. Ramachadran statistics for C2 crystal are as follows: favored 98.12%, outliers 0.13% (Table 1). The models of MBP-Atxn3-C in the two crystals and for molecules within the unit cell were built separately but simultaneously using COOT software [19]. Refinement was performed using REFMAC5 program [20] and validation was performed using Molprobity software [21]. Molecular interfaces were analyzed with PISA software [22]. An OMIT map of the model and real-space correlation coefficients were...
used to validate the determined Atxn3-C structure (PHENIX, [23]). Hydrogen bonds were identified using HBOND server and secondary structure was assigned with DSSP algorithm [24,25].

Results and discussion

Crystal structures of Atxn3-C

To crystallize the carboxy-terminal fragment of Atxn3, we adopted the crystallization approach used successfully in our previous crystallographic studies of the polyQ region of Htt (Htt-Ex1) [14,15]. The sequence encoding human Atxn3 from S278 through D329 containing a 14-amino acid tract with 13 glutamines interrupted by a single lysine (K388) was cloned into MBP expression vector, pMAL (see Materials and methods section for details). This poly14Q tract sequence is the one most frequently observed in normal individuals [26–28]. The importance of the polyQ flanking sequences on polyQ structure, function, and toxicity have been addressed in many studies [8,29–34], thus we decided to express, purify, and crystallize the polyQ region of Atxn3 in its native context. The fragment we crystallized starts with S278; this residue is slightly upstream of the predicted boundary for the coiled-coil domain (L281-K291) [35]. The protein construct ends at position D329, which is located just in front of the third UIM (G331-T348). The structure of the UIM3 region was determined previously [13]. As in our studies of Htt-Ex1 [14,15], we added a 19-amino acid carboxy-terminal tag (indicated by yellow in Fig. 1A) to facilitate crystallization. Although the C-terminal tag was not resolved in the electron density map, only constructs having this C-tag yielded crystals. The MBP-Atxn3-C protein was expressed in bacteria, purified, and crystallized using the procedures reported previously [14,15] (see Methods for details). Crystals of MBP-Atxn3-C were obtained in two different shapes: a prism shape (C1, tetragonal) and a pyramid shape (C2, triclinic). Crystals in both shapes diffracted with up to 2 Å resolution but the unit cell parameters were different (Table 1). The C1 crystal contained one molecule of MBP-Atxn3-C in the asymmetric unit (Fig. 1B), whereas the C2 crystal contained two of the molecules (Fig. 1C).

Structures of MBP-Atxn3-C in C1 and C2 crystals were solved by molecular replacement with the MBP structure as a search model (see Materials and methods section for details). The structure of the Atxn3-C portion in the C1 crystal is illustrated on Fig. 2A. The region of Atxn3-C was exposed to solvent. Seven residues (S371-R377) were resolved, and these form two turns of α-helix (Fig. 2A). A model for remaining amino acids could not be built due to insufficient electron density (Fig. 2A). The similar lack of electron density was observed for some Htt polyQ region crystals [14,15].

In contrast to C1 crystals, the Atxn3-C regions in the C2 crystals are partially shielded from solvent by symmetry-related molecules of MBP (x-1, y, z) and (x-1, y, z-1) (Figs 1C and 2B). The amino acids from S371 to Q397 in both of the molecules of the Atxn3-C in the asymmetric units of the C2 crystals exist in α-helical conformation (Fig. 2B). The crystal structure of the Atxn3 α-helical region was solved at 2.2 Å resolution in the C2 crystals (refinement statistics in Table 1). The Atxn3-C α-helix forms several hydrophobic interactions with the fused MBP protein. These interactions are mediated by side chains of the N-terminal amino acids (Fig 2B,C; residues in green) and by the polyQ residues (Fig. 2B; orange). R377 and R378 form polar contacts with MBP residues E322, E308, and Y90; E379 and E383 are involved in coordination of a Zn$^{2+}$ ion, which bridges to H39 of MBP; and S371 and E372 form hydrogen bonds with Q335 of MBP via water molecules (Fig. 2C).

Structure of polyQ helix

The glutamine side chains of the polyQ α-helix in the C2 Atxn3-C structure form hydrogen bonds with various partners. In addition, several residues within the polyQ helix form polar contacts with MBP molecule. These interactions involve Q387, Q389, Q390, Q392, Q393, and Q394 residues and are almost exclusively with charged residues of MBP (Fig. 3): carboxy groups of aspartic or glutamic acid residues of MBP (Q387 (NE2)--E22(OE2), Q389(NE2)--D95(OD2), Q394 (NE2)--D236(OD2)) and amines of lysine (Q390 (OE2)--K295(NZ)). Interestingly, a proteomic study of polyQ-interacting proteins revealed enrichment in charged amino acids E, D, and K [36]. In addition, the glutamine side chain of residue Q392 pairs with the less polar hydroxyl group of residue Y176 of MBP (Q392(O)--Y176(0H)). Amine groups of glutamine also form hydrogen bonds with the carboxyl groups of the backbone in MBP (Q390(NE2)--D296(O)/K295 (O); Q393(NE2)--T237(O)). Several glutamine residues (Q391, Q392, Q385, Q386) form bonds with hydroxyl groups of the water molecules (Fig. 3).

The polyQ α-helix of Atxn3-C is also stabilized by interactions between glutamine residues. Eight of the 13 glutamines are involved in the formation of direct
intrahelical hydrogen bonds between residue i and residue i + 4 (in four cases) or between i and i + 3 (one case) (Table 2; Fig. 3). In addition to these direct glutamine-glutamine side chain interactions, Q385 interacts nonglutamine residues at i−4 (Y381) and i + 3 (K388) via a water-mediated bond (Table 2, Fig. 3). The polar moment of most glutamine side chains aligns in parallel with the α-helical axis and hydrogen bonds are formed parallel to the helical axis (Figs 3 and Fig. 4A). The hydrogens of the amines in glutamine side chains are the donors and that the carboxyl oxygens are acceptors; however, the exact orientation of the amide and carbonyl groups in the glutamines could not be determined and the orientation of Q–Q pair interaction can be flipped by rotating side chain by 180 degrees without affecting
the bonding pattern. Only Q392 is not involved in intrahelical interaction; it interacts with Y176 of MBP.

In the two molecules composing the asymmetric units of the C2 crystal, the glutamine side chains adopt slightly different conformations. The major difference is that in one the Q393--Q397 bond is present and in the other it is not. We calculated electron density maps with side chains omitted for both units and calculated a real-space correlation coefficient between the map and the model (Fig. 4B) and B-factors for main-chain and side-chain atoms (Fig. 4C). The modeled side chains show good quality of fit except at Q390 and Q394, which are resolved at lower resolution than the rest of the polyQ region.

To summarize, the α-helical structure of the Atxn3 polyQ region is stabilized by two kinds of hydrogen bonds, those mediated by main-chain atoms and those between by glutamine side chains. The polyQ α-helix is likely to be more thermodynamically stable due to the glutamine side chain-mediated hydrogen bonds. This observation agrees with the conclusions from the host-guest modeling study by Roy and Dannenberg [37].

**Comparison with other polyQ structures**

In our previous structural studies of Htt, we observed both α-helix and a random coil conformation of the polyQ region (PDB entries 3IOR, 3IOT, 3IOU, 3IOV,
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Table 2. Hydrogen bonding interaction within polyQ helix of Atxn3-C in C2 crystal.

<table>
<thead>
<tr>
<th>Hydrogen bonds within polyQ region</th>
<th>Residue 1 – Atxn3</th>
<th>Residue 2 – Atxn3</th>
<th>Interaction; Distance (Å)</th>
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</thead>
<tbody>
<tr>
<td>Y381 (OH)</td>
<td>Q385 (OE1)</td>
<td>Y381...HOH; 2.6</td>
<td></td>
</tr>
<tr>
<td>Q385 (NE2)</td>
<td>K388 (NZ)</td>
<td>Q385...HOH; 2.9</td>
<td></td>
</tr>
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<td>Q387 (NE2)</td>
<td>Q391 (OE1)</td>
<td>3.5</td>
<td></td>
</tr>
<tr>
<td>Q386 (NE2)</td>
<td>Q389 (OE1)</td>
<td>2.9</td>
<td></td>
</tr>
<tr>
<td>Q389 (NE2)</td>
<td>Q393 (OE1)</td>
<td>2.7</td>
<td></td>
</tr>
<tr>
<td>Q393 (NE2)</td>
<td>Q397 (OE1)</td>
<td>4.0</td>
<td></td>
</tr>
<tr>
<td>Q390 (NE2)</td>
<td>Q394 (OE1)</td>
<td>3.0</td>
<td></td>
</tr>
</tbody>
</table>

3IOW, 3IO4, 3IO6 and 4FE8, 4FEB, 4FEC, 4FED) [14,15]. The Htt-17Q and Htt-36Q structures were determined at 3.5 Å and 3.0 Å resolutions, respectively [14,15]. The side chains of the glutamine residues in the Htt-Ex1 structure were unresolved likely due to multiple conformations in the crystal. The conformational heterogeneity observed for the Htt-Ex1 structure was a single crystal was manifested in two different crystals for Atxn3-polyQ. Our hypothesis that the polyQ regions of Htt and Atxn3 exist in equilibrium between α-helical and random coil conformations is supported by structural studies of polyQ repeats in which structural flexibility was observed [30,35,38-44].

In our analysis of Atxn3-C, one cannot ignore the influence of MBP and crystallization effect. The stabilizing effect of MBP on the α-helix may be due to both solvation effects and molecular interactions. In the well-defined region from Q385 to Q394 in the C2 crystal MBP has a caging effect. MBP limits solvent access and favors intramolecular interactions between glutamines. Existing structural and biochemical data support the idea that polyQ itself is capable of forming an α-helix. For example, a similar helical structure was observed in the polyQ region of Htt-Ex1 without stabilizing interactions with other regions of the crystallized protein [14,15]. Circular dichroism studies, molecular modeling, and simulations also predict the presence of α-helix in polyQ repeats [38,41]. Glutamine has a high propensity for incorporation into helical motifs (e.g., see [45-50]). Glutamine can form side chain-side chain bonds [48,49]. A recent modeling study provides a direct evidence for Q–Q side chain stabilization along an α-helix [37]. Both α-helix and random coils formed by polyQ regions were also observed by circular dichroism and mutagenesis studies by Fiumara et al., Pelassa et al., and Kokona and colleagues supported the observation [35,44,50]. A ‘conformational stabilization’ was also observed in the high-resolution crystal structure of a 10Q peptide complexed with MW1 antibody [51]. In this structure, the 10Q peptide adopts an extended conformation and is tightly bound to the MW1 antibody (PDB entries 2OTTU, 2OTW). Structures of the apo-forms of other anti-polyQ antibodies also suggest that they recognize a similar extended polyQ conformation (4DCQ, 3S96, 4JJ5, 4ISV) [52]. Interactions between polyQ and MW1 involve both side- and main-chain atoms of the polyQ peptide. Nine of the glutamine side chains in 10Q are involved in interactions with the MW1 residues and backbones of each of the 10 glutamines contact MW1, indicating a very strong interaction between the peptide and the antibody [51]. We reason that the MW1 antibody likely selects one of the numerous potential conformations adopted by polyQ peptides. In contrast, the Atxn3-polyQ region forms only a few interactions with MBP cage (Figs 2B and 3), suggesting that the stabilization effect is not as stable in this crystal.

Intramolecular stabilization of a polyQ α-helix was previously proposed [53]. In this model, side chain-mediated stabilization involves i and i + 4 glutamine residues. This spacing of side-chain interactions was also discussed by Monoi and co-workers [54,55]. A crystal structure of glutamine-rich domain of HDAC4 revealed the importance of Q–Q interactions both on helical stability and helix bundle formation [56]. A more recent modeling study by Roy and Dannenberg is in the excellent agreement with our experimental findings [37]. In this host–guest modeling approach, regularly spaced (i, i + 4) glutamine residues were inserted into an otherwise alanine α-helix. These glutamine substitutions stabilize the α-helix structure, but the effect of water was not carefully examined. Our high-resolution structure (Fig. 3) suggests that glutamines can form hydrogen bonds within the α-helix with residues at either i + 4 or i + 3. The presence of both types of interaction leads to an interruption in the hydrogen-bonding network. This is contradictory to the predicted end-to-end hydrogen-bond array along the α-helix [53].

The mechanism of polyQ aggregation is not apparent from our findings because the current research was focused on the polyQ tract of nonpathogenic length. It has been proposed that the polyQ α-helix is involved in helix-helix interactions that lead to pathogenic fibril-aggregation in neurons [35,57]. Interestingly, in the article of Fiumara et al. the region of the Atxn3 sequence from L281 to K291 was predicted to be a part of an α-helix in agreement with our crystallographic data. In comparison to solution study on the synthetic polyQ peptides and native/pathogenic Htt exon I, the studies found the polyQ in solution exists in an equilib-
rium between random coil and alpha-helix (estimated helix content 40–75%) [35,44,50] meanwhile our study found both random coil and helical structures in each of two different crystals. Pelassa and colleagues proposed a model where random-coil polyQ adopts an α-helical structure upon a binding to its natural partners [44]. However, further studies are needed to confirm the correlation between the structural studies and biological functions.

In the MBP-Atxn3-C crystal structure, glutamine residues form multiple coordinated hydrogen bonds along the polyQ helix and limited interactions with MBP. Interestingly, Perutz initially proposed a model of polyQ known as a ‘polar zipper’ model [58] where Q–Q bonds stabilize a beta-sheet structure. The Atxn3-C structure and the polar zipper model both show that their secondary conformations could be stabilized by Q–Q interaction. This effect would likely be less pronounced in solution due to solvation by water molecules. However, when the solvent effect is diminished, such as when the local concentration of glutamine is high due to expansion of polyQ length or accumulation of proteasome-resistant polyQ fragments, the Q–Q stabilizing effect could lead to formation of aggregates. The exclusion of solvent could lead to self-association of glutamines, either inter- or intramolecurarily, further lowering the efficiency of proteasomal degradation of such oligomers and accelerating macro-aggregation of polyQ proteins.

**Conclusion**

Here, we observed that the polyQ regions of Atxn3 adopt random coil and α-helical conformations in two separate crystal structures. The presence of both random coil and α-helical conformations in the polyQ...
region is consistent with the result from our previous crystallographic studies of Htt-Ex1 [14]. The analysis of the polyQ α-helix in the MBP-Atxn3-C structure revealed intrahelical hydrogen bonds between glutamines along the helix axis. Such intramolecular Q-Q interactions were previously predicted to occur in both α-helix and β-sheet conformations of polyQ peptides. The information obtained from analysis of the polyQ domain of Atxn3 suggests that intrahelical hydrogen bonds between glutamines lead to the aggregation that is presumed to underlie the pathogenic mechanism of polyQ-expansion proteins.

Acknowledgements

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Author contributions

MWK designed the experiments. MWK performed the crystallization and data collection experiments. VZ and MWK processed and analyzed the data. VZ, MWK, AK, IB wrote the final manuscript. All authors read and approved the final manuscript.

References

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23 Adams PD, Afonine PV, Bunkoczi G, Chen VB, Davis
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20 Murshudov GN, Skub
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19 Emsley P, Lohkamp B, Scott WG and Cowtan K
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Crystal structure of ataxin-3 C-terminal fragment


