

Name	System	Type	Sequence	Length	e260 L/mol cm	MW, Da (Calculated)
DS_1XAV_FullC	promoter	artificial-G4-duplex flanked	CTATGTATACAAAAGAGGTGGGTAGGGTGGGTTTAATGCGGCACGC + GCGTGCCGCATTAATTTTTTTTTTTTTTTTTTTGTATACATAG	92	875400	28521

Table with descriptions of the two samples for Cryo-EM grid screening.

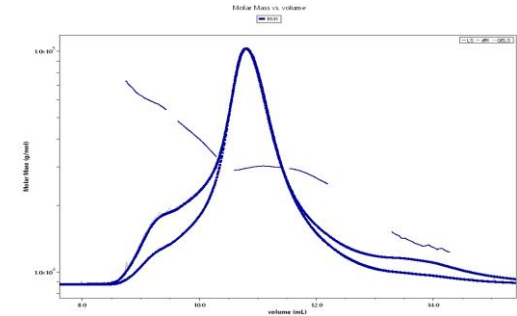


Fig 1. SEC-MALS analysis of DS\_1XAV\_FullC showing a main species of ~30 kDa (before purification).

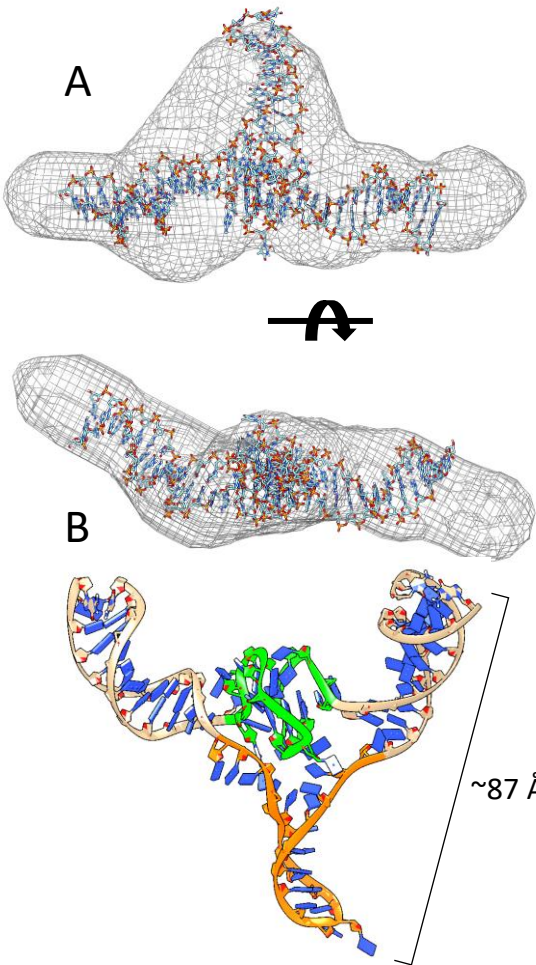


Fig 4. (A) Space filling SAXS envelope derived from scattering from main peak of Figure 1. The resolution is too poor to make out any fine details but there is a general shape agreement with an atomistic model built by hand. (B) Potential model of DS\_1XAV\_FullC built from an NMR solution structure of the G-quadruplex (green) and B-form duplexes (tan) with poly dT opposite strand in shown in orange.

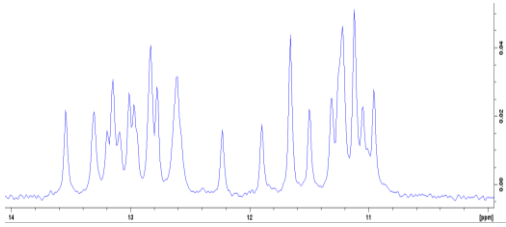


Fig 2. H-NMR analysis of Watson-Crick and Hoogsteen imino regions showing that both duplex and G-quadruplex features are formed.

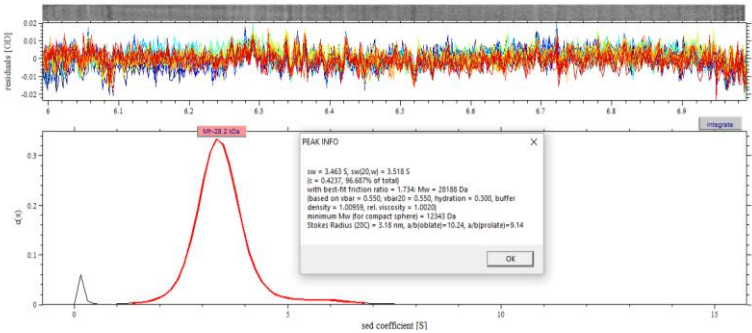


Fig 3. AUC sedimentation velocity analysis of pure fraction showing single major species of the correct MW (~28 kDa).

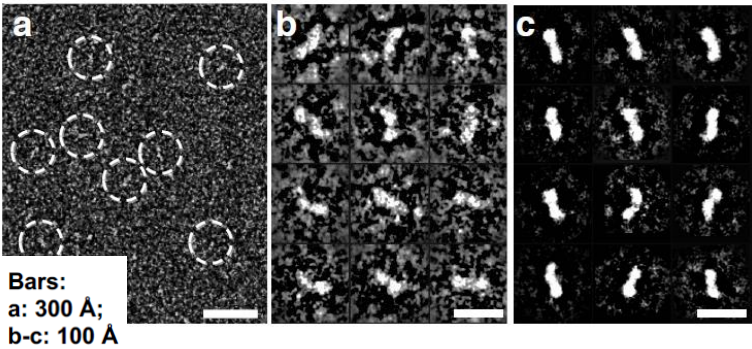


Fig 5. OpNS-EM images of the hTERT promoter G-quadruplex from a commercial service. Species of approximately the right size were identified but deviate from all solution conditions measured (AUC, SAXS, SEC, DLS). (a) survey micrograph, (b) particle selection, (c) reference-free and class-averaged images of selections in B.