Supporting information:

Table S1: amino acid sequences of peptides that mediate the oligomerization of STIL IDR as found in the peptide array screening

Residues	peptide sequence
367-381	FSKASKNFSIKRSSQ
376-390	IKRSSQKLSSGKMPI
382-396	KLSSGKMPIHDHDSG
406-420	PIPSPHPVSQKISKI
451-465	ENPPLINHLEHLKPL
457-471	NHLEHLKPLQPQLYD
487-501	GIPNQLNQDKPALLR
496-510	KPALLRHCKVRQPPA
502-516	HCKVRQPPAYKKGNP
511-525	YKKGNPHTRNSIKPS
517-531	HTRNSIKPSSHNGPS
547-561	QNEEYPIRPSTLNSR
571-585	PHDFVFSPHNSGRPM
592-606	PPLPSYCSTNVCRCC
601-615	NVCRCCQHHSHIQYS
607-621	QHHSHIQYSPLNSWQ
631-645	DVQSEALQKHSLFHP
652-666	YCNAFCSSSSPIALR

* Colored residues (His, Cys, Glu, Asp) are common residues for binding Zn^{2+} ions.

** The motif that was detected using the Block Maker alignment tool [1] is colored yellow.

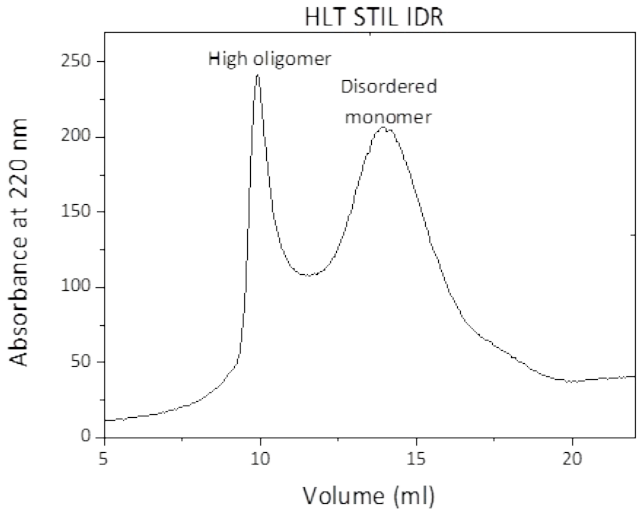

Figure S1: Analytical SEC of HLT STIL IDR: the protein exists as a mixture of monomer and high order oligomer.

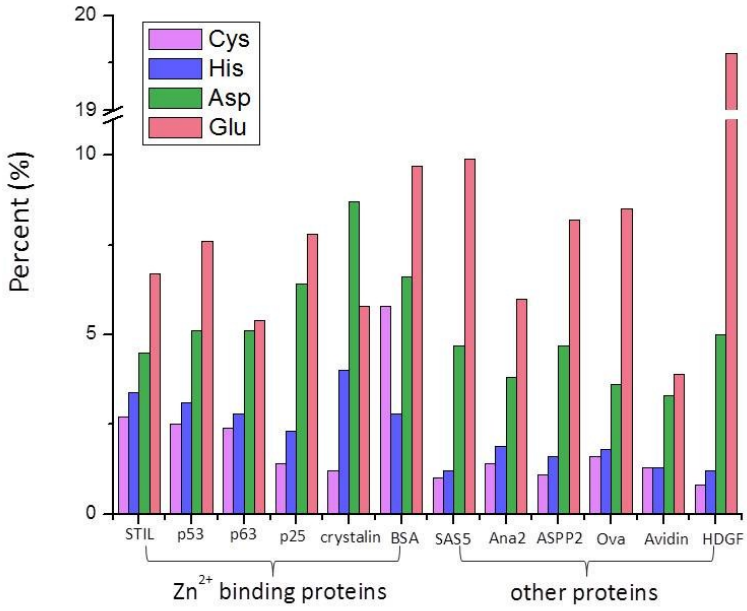

Figure S2: STIL is composed of a high portion of Cys and His residues. Shown is the amino acid composition of several Zn^{2+} and non-Zn^{2+} binding proteins, as was calculated by the Bioinformatics Resource Portal ProtParam tool [2].

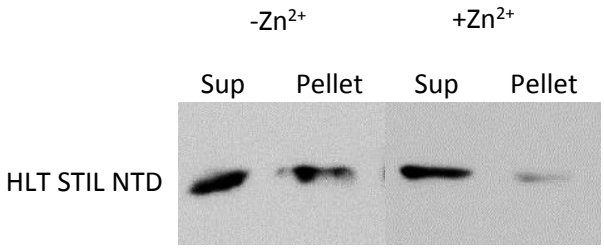

Figure S3: the presence of $ZnCl_2$ in the medium improved the expression of HLT STIL NTD. Western blot analysis of supernatant and pellet fractions from bacterial expression of HLT STIL NTD with or without addition of $ZnCl_2$ to the medium.

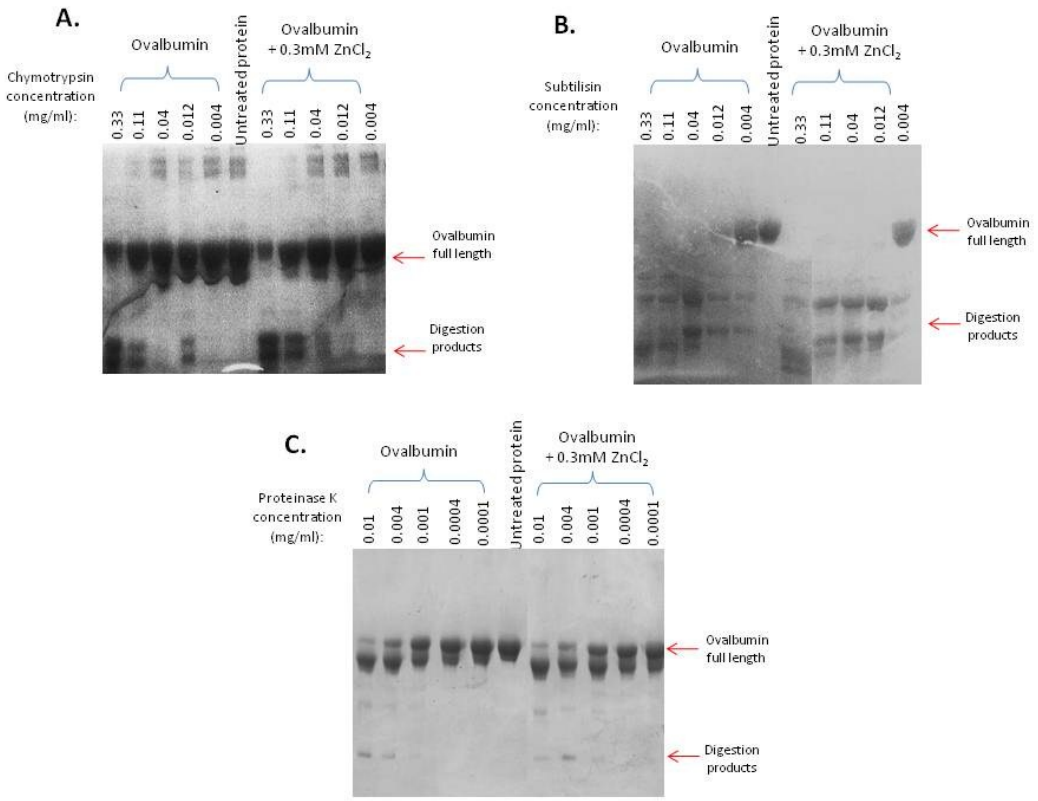

Figure S4: The presence of $ZnCl_2$ does not affect protease digestion of OvAlbumin. Shown is SDS-PAGE gel of OvAlbumin with and without $ZnCl_2$ at several concentrations of Chymotrypsin (A), Subtilisin (B) and Proteinase K (C).

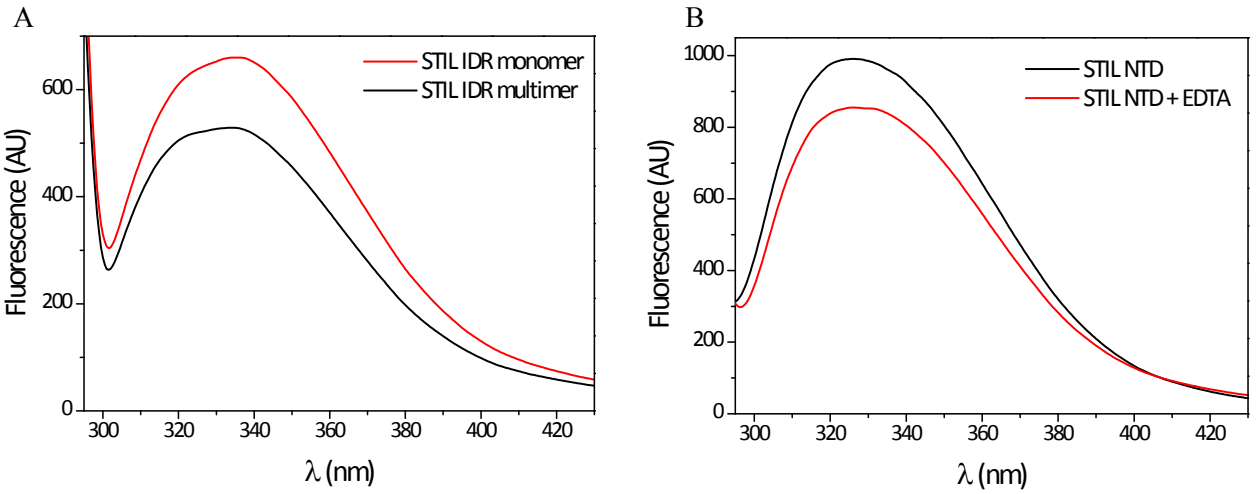

Figure S5: The presence of Zn^{2+} affects the structure of STIL IDR and NTD. A) Tryptophan fluorescence spectra of apo-STIL IDR (monomer - red) and holo-STIL IDR (multimer – black). B) Tryptophan fluorescence spectra of holo-STIL NTD (without EDTA addition – black) and apo-STIL NTD (with EDTA – red).

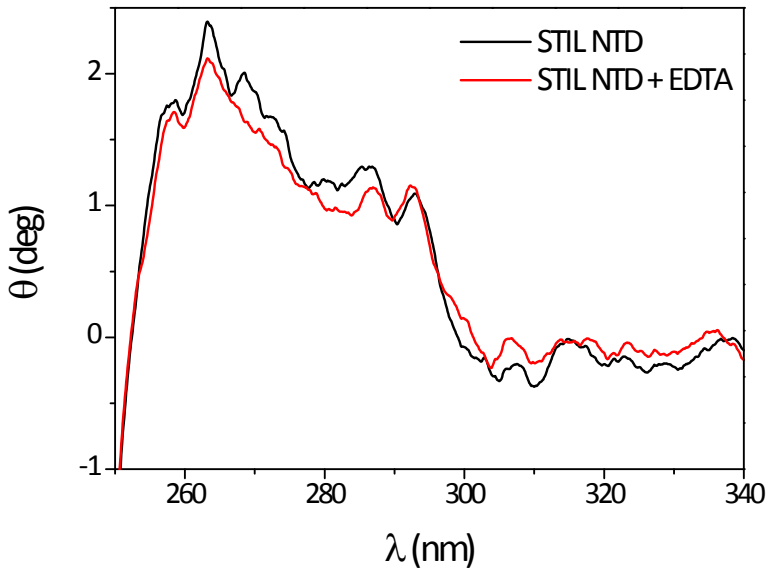

Figure S6: Near UV CD studies show that the structure of STIL NTD changes in presence of Zn^{2+}. Near UV CD spectra of Zn^{2+} pre-bound STIL NTD (black) and without Zn^{2+}, in the presence of EDTA (red).

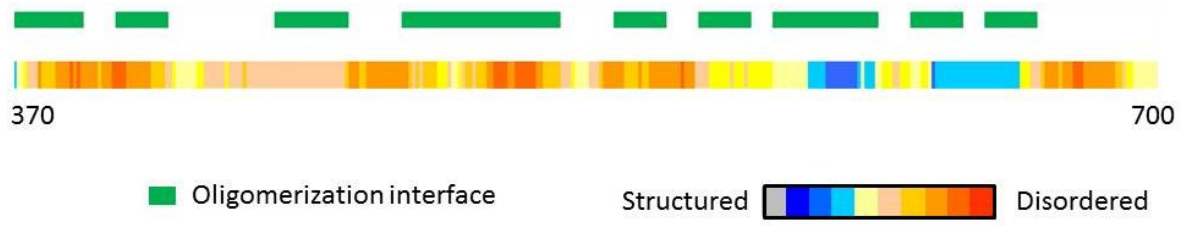

Figure S7: Oligomerization of the STIL IDR: The STIL IDR peptides that mediate its oligomerization were revealed by peptide array screening and are colored green on the STIL disordered region.

370

ASKNFSIKRSSQKLSSGKMPIHDHDSGVEDEDFSPRPIPSPHPVSQKISKIQPSVPEL

SLVLDGNFIESNPLPTPLEMVNNENPPLINHLEHLKPLQPQLYDEKHSPEVEAGE

PSLRGIPNQLNQDKPALLRHCKVRQPPAYKKGNPHTRNSIKPSSHNGPSHDIFEK

LQTVSAGNVQNEEYPIRPSTLNSRQSSLAPQSQPHDFVFSPHNSGRPMELQIPTP

PLPSYCSTNVCRCCQHHSHIQYSPLNSWQGANTVGSIQDVQSEALQKHSLFHP

700

SGCPALYCNAFCSSSSPIALRPQGDMGSCSPHSNIEPSPVARPPSHMDLCNPQPC

Figure S8: STIL oligomerization motifs on IDR sequence. The oligomerization motif SxKxS/SxHxS/SxLxS - colored orange and the Zn binding residues found in the oligomerization sites identified by peptide array screening: Cys residues - colored green and His residues -colored pink.

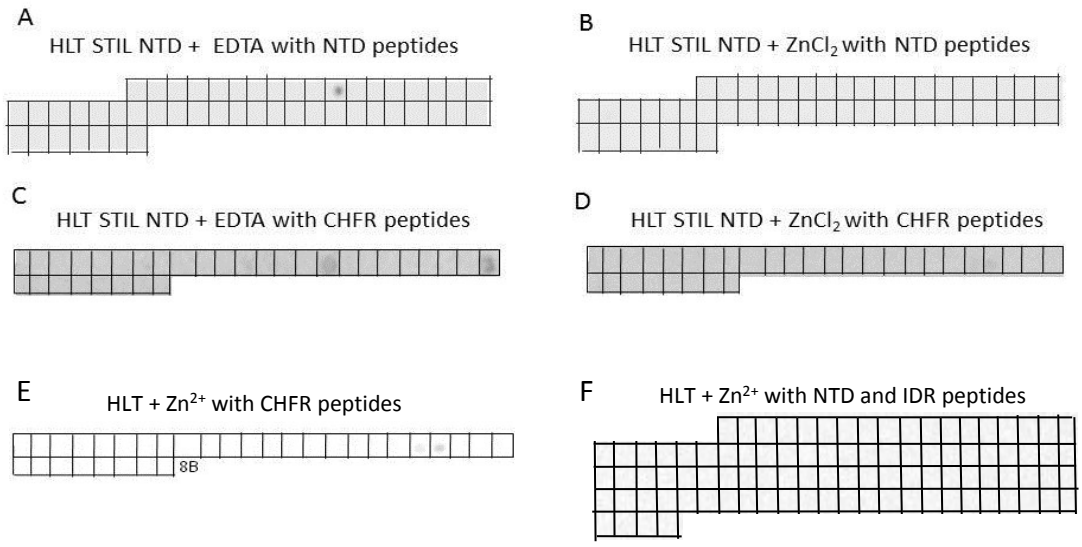

Figure S9: Testing the binding of STIL NTD and HLT to arrays of peptides derived from STIL and CHFR: Screening for binding of HLT STIL NTD to an array of peptides derived from STIL NTD derived peptides in the presence of EDTA (A) or $ZnCl_2$ (B), and to an array of CHFR derived peptides in the presence of EDTA (C) or $ZnCl_2$ (D). HLT was screened for binding CHFR derived peptide array (E) and STIL derived peptide array (F). Each black spot indicates binding between the protein and the corresponding peptide.

HHHHHHSGAFEFKLPDIGEGIHEGEIVKWFVKPGDEVNEDDVLCE

VQNDKAVVEIPSPVKGKVLEILVPEGTVATVGQTLITLDAPGYENM

TTGSDTGENLYFQG

A

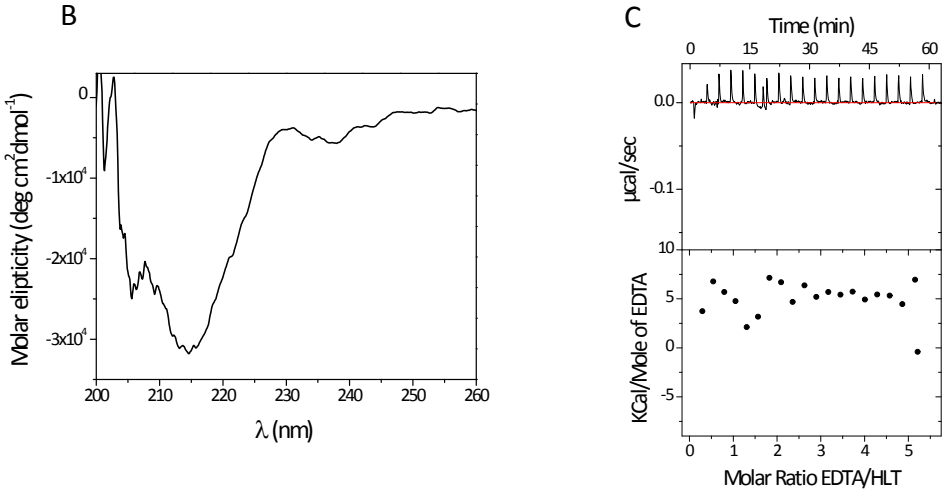

Figure S10: The HLT tag. (A) Primary sequence of HLT tag, composed of 6 His residues (pink), a Lipo-domain (blue) and a Tev cleavage site (red). (B) CD spectrum of HLT tag. (C) ITC control - titration of EDTA into a HLT.

References

1. S. Henikoff, S. Pietrokovski, and J. G. Henikoff, *Nucleic Acids Res.*, 1998, **26**, 309–312.

2. E. Gasteiger, A. Gattiker, C. Hoogland, I. Ivanyi, R. D. Appel, and A. Bairoch, *Nucleic Acids Res.*, 2003, **31**, 3784–3788.