Supplemental information

Employing non-targeted interactomics approach

and subcellular fractionation to increase our

understanding of the ghost proteome

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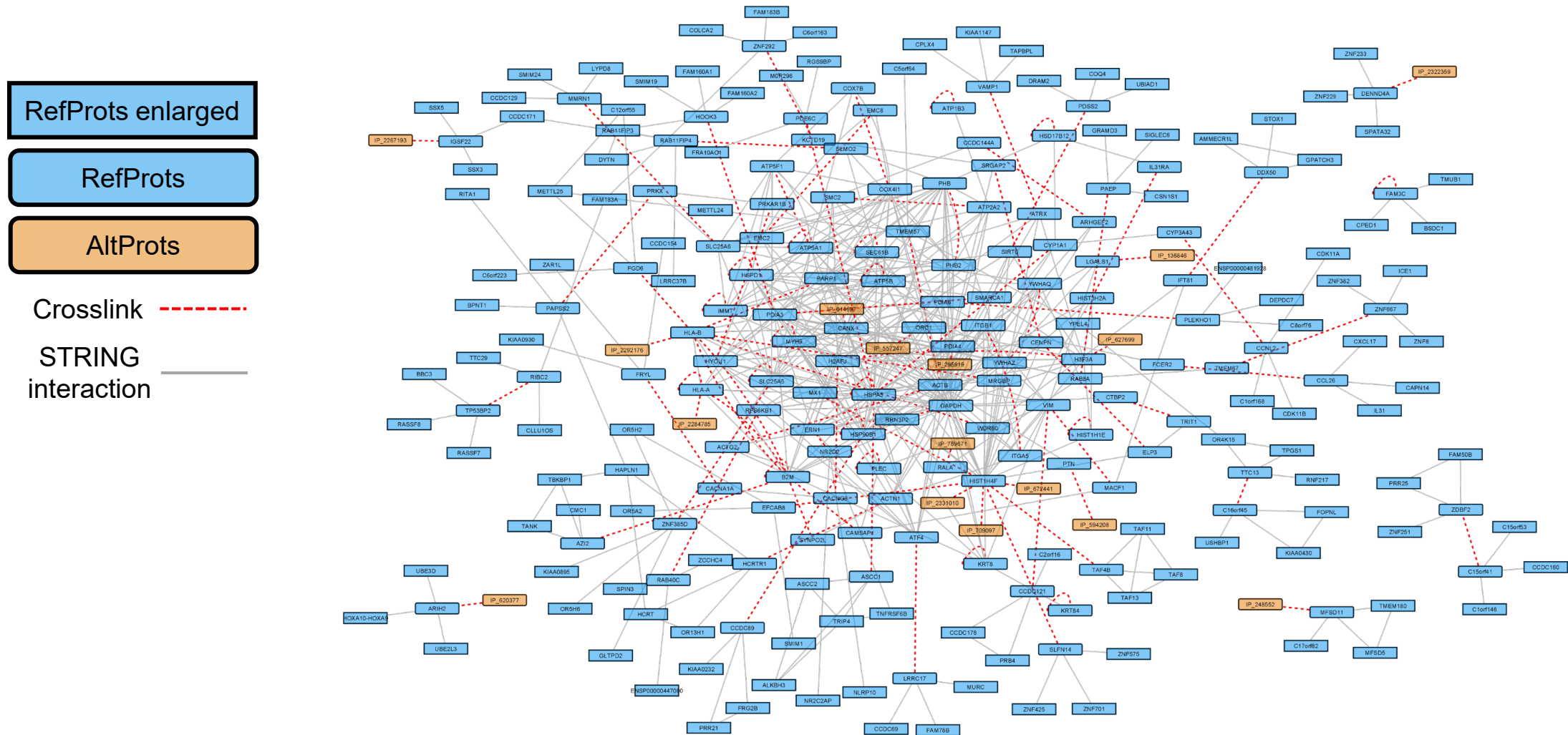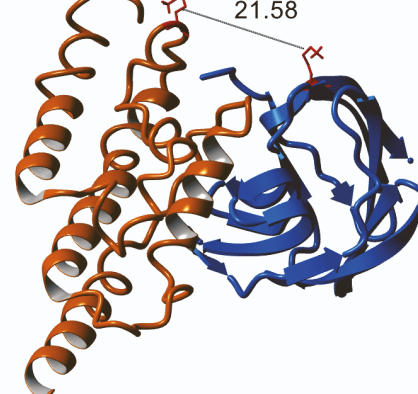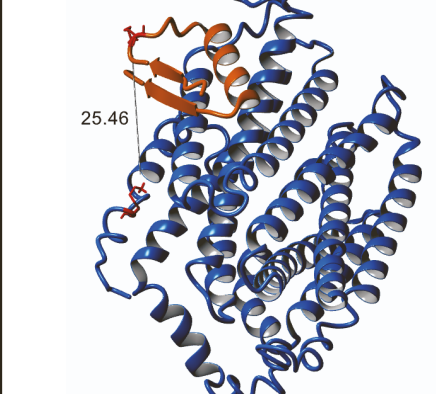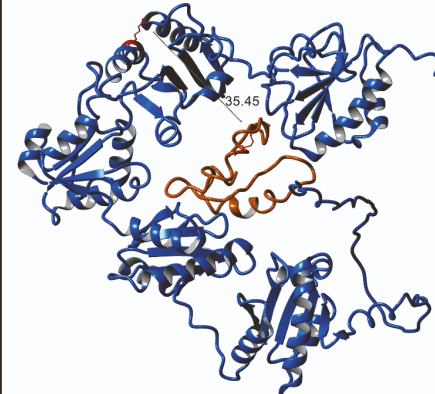
Supplemental Figures
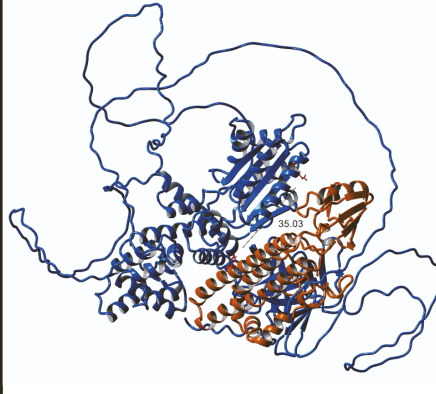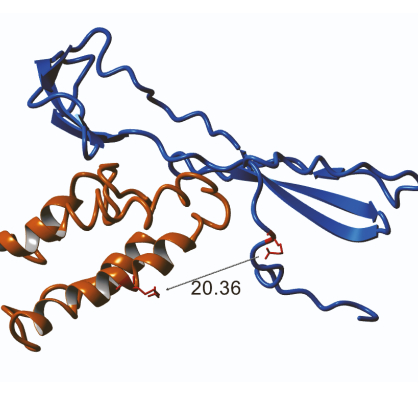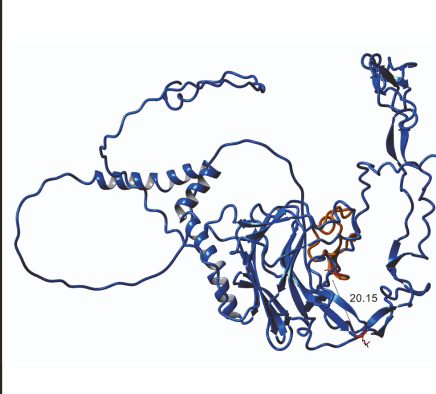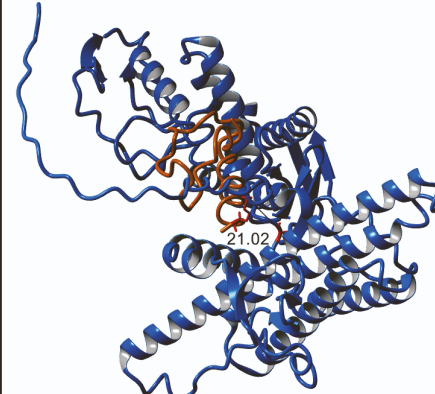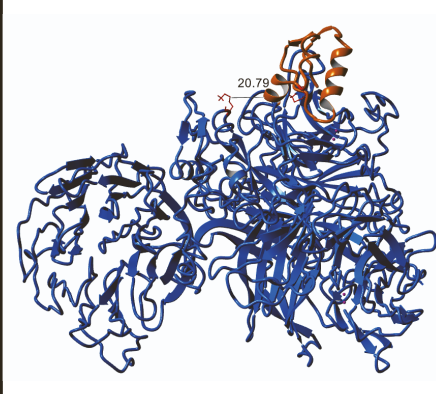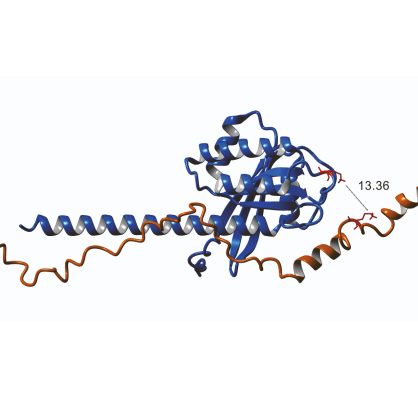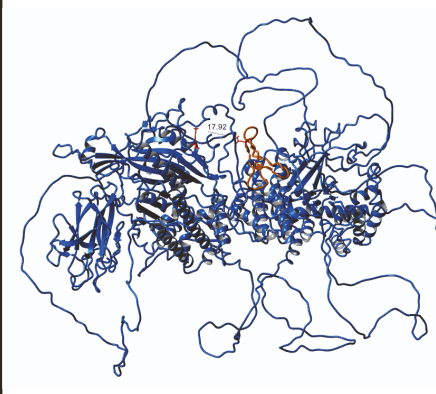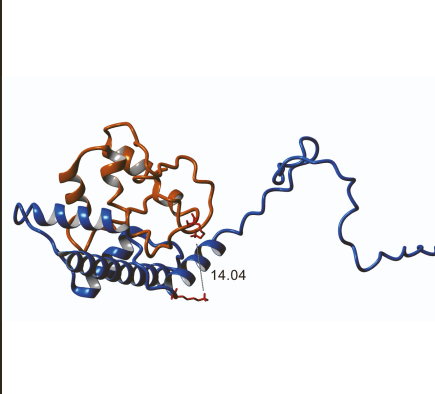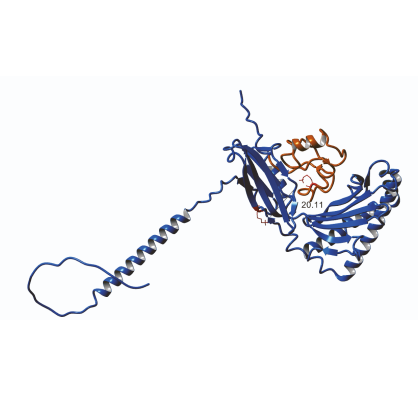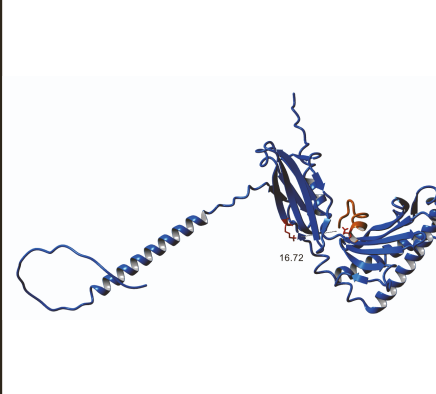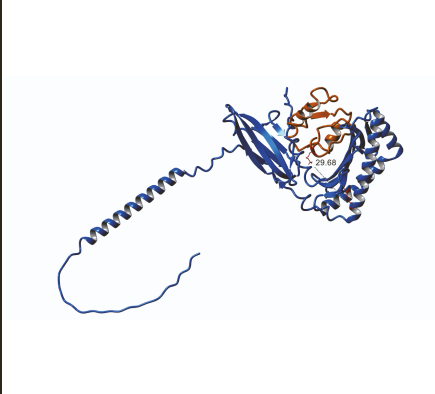
Figure S1. Crosslinked network enriched by the STRING interactions (gray lines) retrieved between these crosslinked (red dash lines) RefProts. Related to Figure 5. For the RefProts that did not present referenced STRING interaction, an enrichment has been performed to expand the network.

IP_136846-LGALS1
crosslink position = 21.58Å
center energy = -487.3

IP_248552-MFSD11
crosslink position = 25.46Å
center energy = -908.5

IP_295919-PDIA4
crosslink position = 35.45Å
center energy = -825.2

IP_557247-ORC1
crosslink position = 35.03Å
center energy = -951.6

IP_594208-PTN
crosslink position = 20.36Å
center energy = -569.2

IP_614697-CANX
crosslink position = 20.15Å
center energy = -664.4

IP_620377-ARIH2
crosslink position = 21.02Å
center energy = -622

IP_2267193-IGSF22
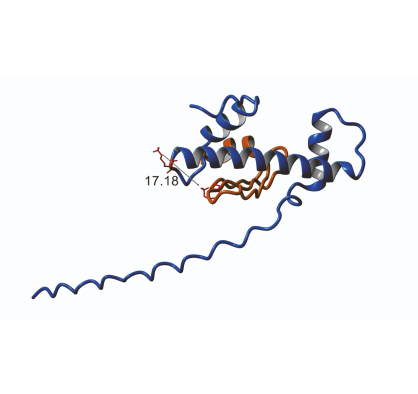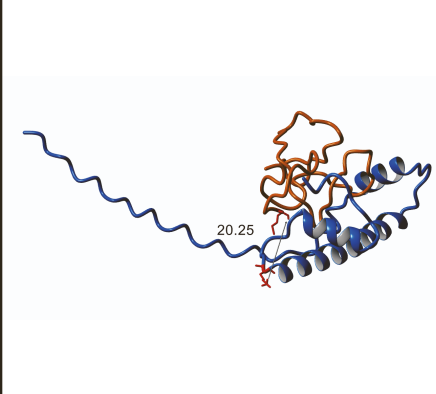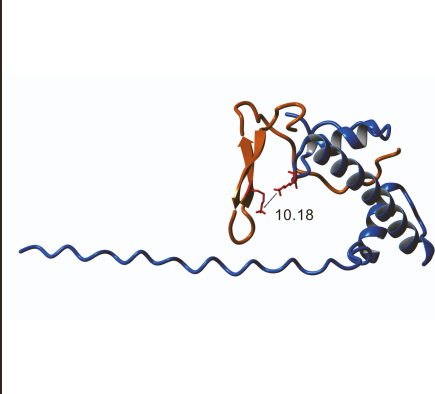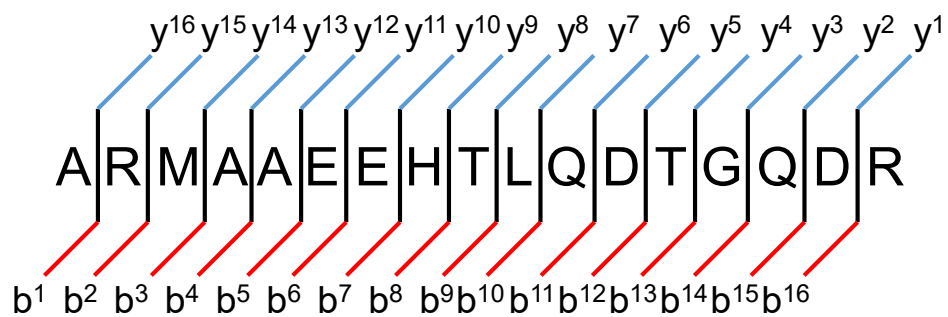crosslink position = 20.79Å
center energy = -858.1

IP_789671-RALA
crosslink position = 13.36Å
center energy = -732.2

IP_2322359-DENND4A
crosslink position = 17.92Å
center energy = -977.7

IP_627699-H3F3A
crosslink position = 14.04Å
center energy = -860.9

Figure S2. Predicted interaction models docked in ClusPro for the RefProts (blue) and AltProts (orange). Related to Figures 6 and 7. The distance between the residues crosslinked is displayed for each interaction.

IP_2292176-HLA-B
crosslink position = 20.11Å
center energy = -847.7

[PEP]IP_2292176-HLA-B
crosslink position = 16.72Å
center energy = -587.1

IP_2284785-HLA-A
crosslink position = 29.68Å
center energy = -761.2

IP_2331010-H4C1
crosslink position = 17.18Å
center energy = -914.1

IP_709097-H4C1
crosslink position = 20.25Å
center energy = -629.5

IP_672441-H4C1
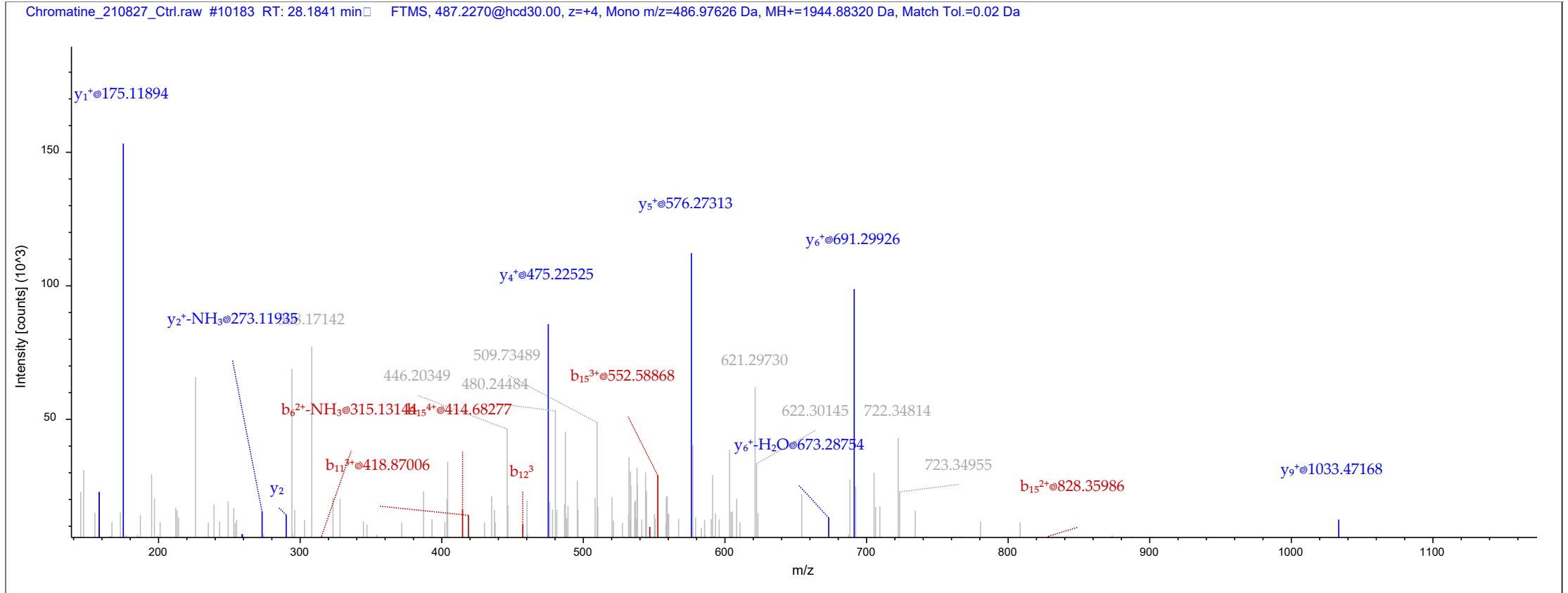crosslink position = 10.18Å
center energy = -858.8

Figure S3. Tandem mass spectrum for the peptide ARMAAEEHTLQDT GQDRGRTCKT which was unique for the AltProt IP_756980. Related to STAR Methods. In red (b ions) and in blue (y ions) are observed in the spectra. No significant similarity was found for this AltProt in protein BLAST. Additionally, the peptide was not identified at NextProt Peptide uniqueness checker.
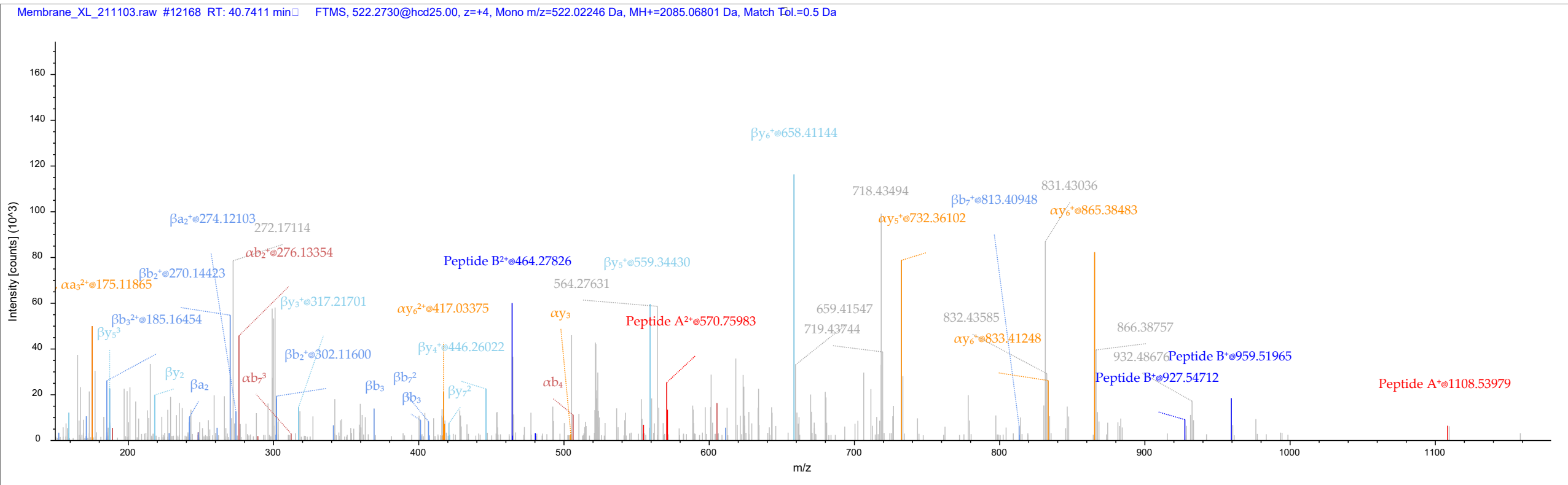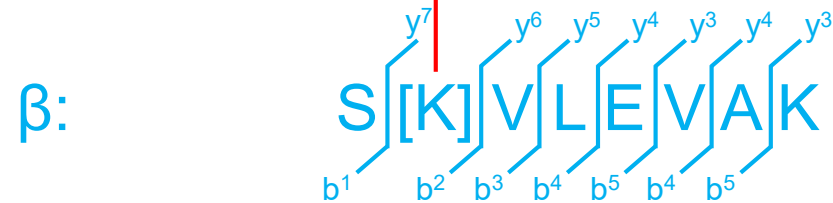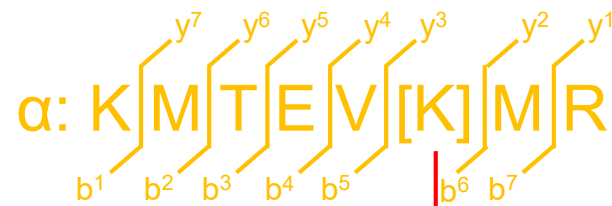
Figure S4. Crosslinking tandem mass spectrum which identified the interaction between IP_295919 (orange) and PDIA4 (blue). Related to STAR Methods. The b and y ions for the individual and crosslink,ing peptides are observed. The unique peptide of IP_295919 was not identified at NextProt.
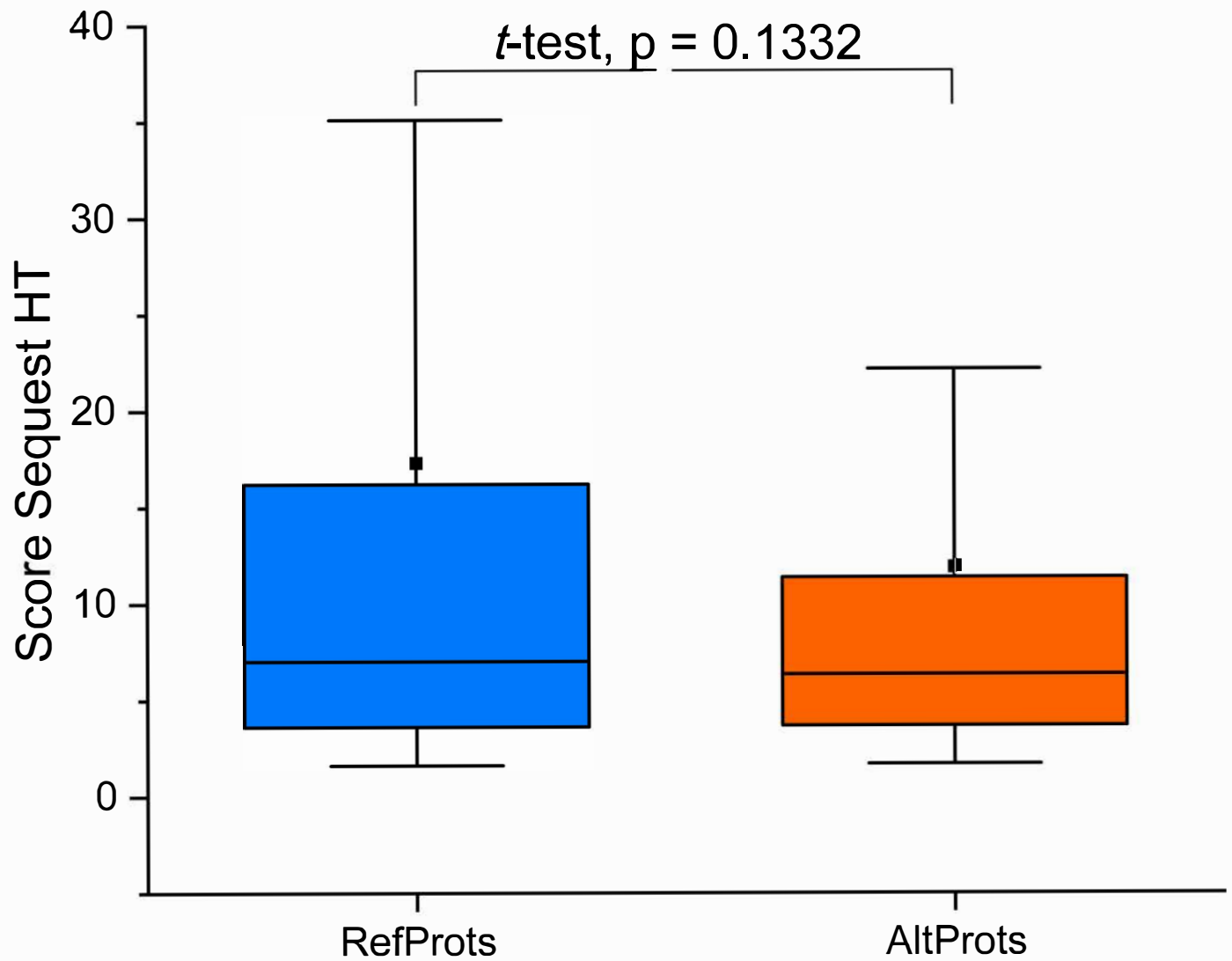
Figure S5. Boxplot of the Sequest HT Scores from the RefProts (blue) and AltProts (orange) identified using at least one peptide and OpenProt from the nuclear fraction. Related to STAR Methods. The Sequest HT Scores are not significantly different between RefProts (n=5764) and AltProts (n=151) (t-test, average Sequest HT Score 17.29 vs 11.91, p = 0.1332).