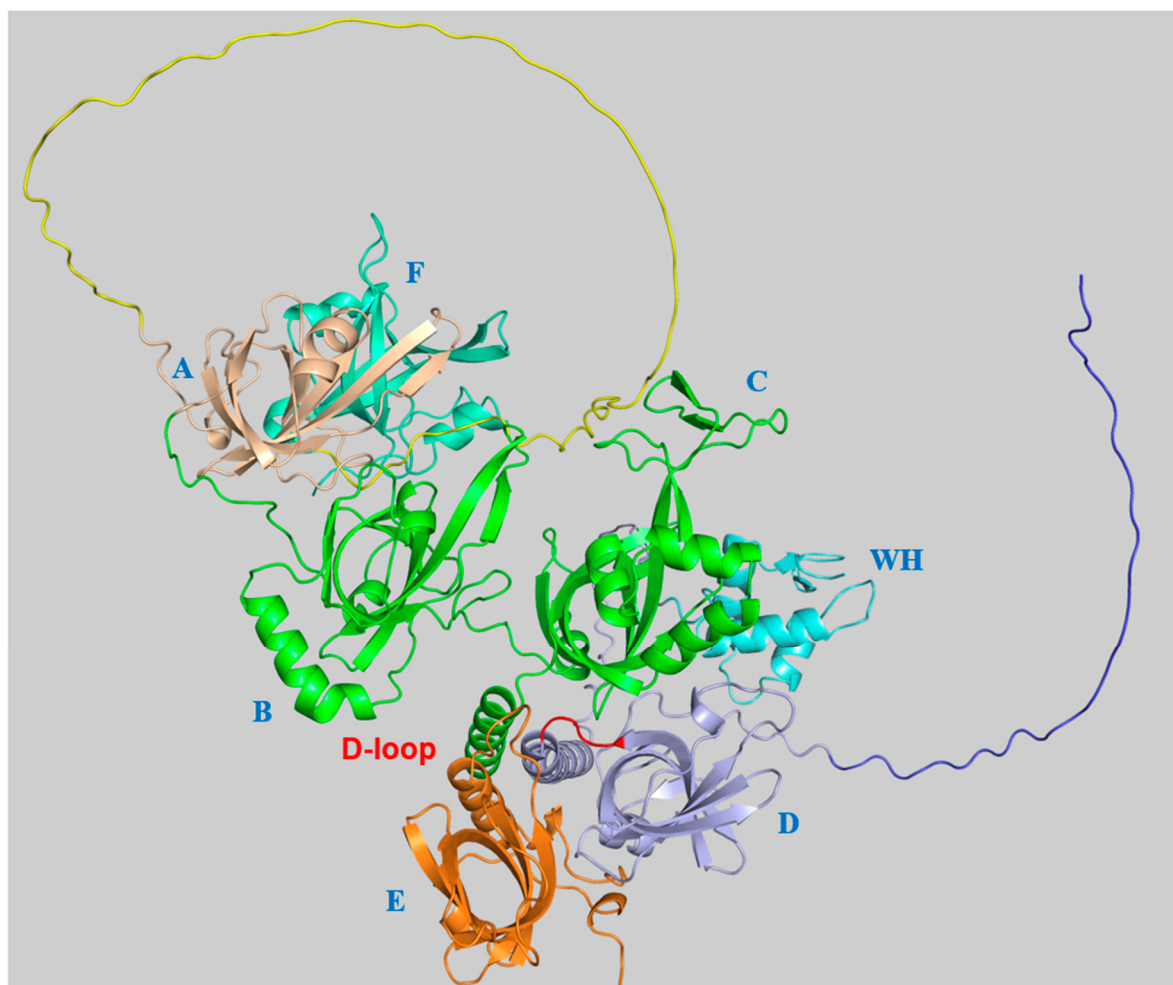
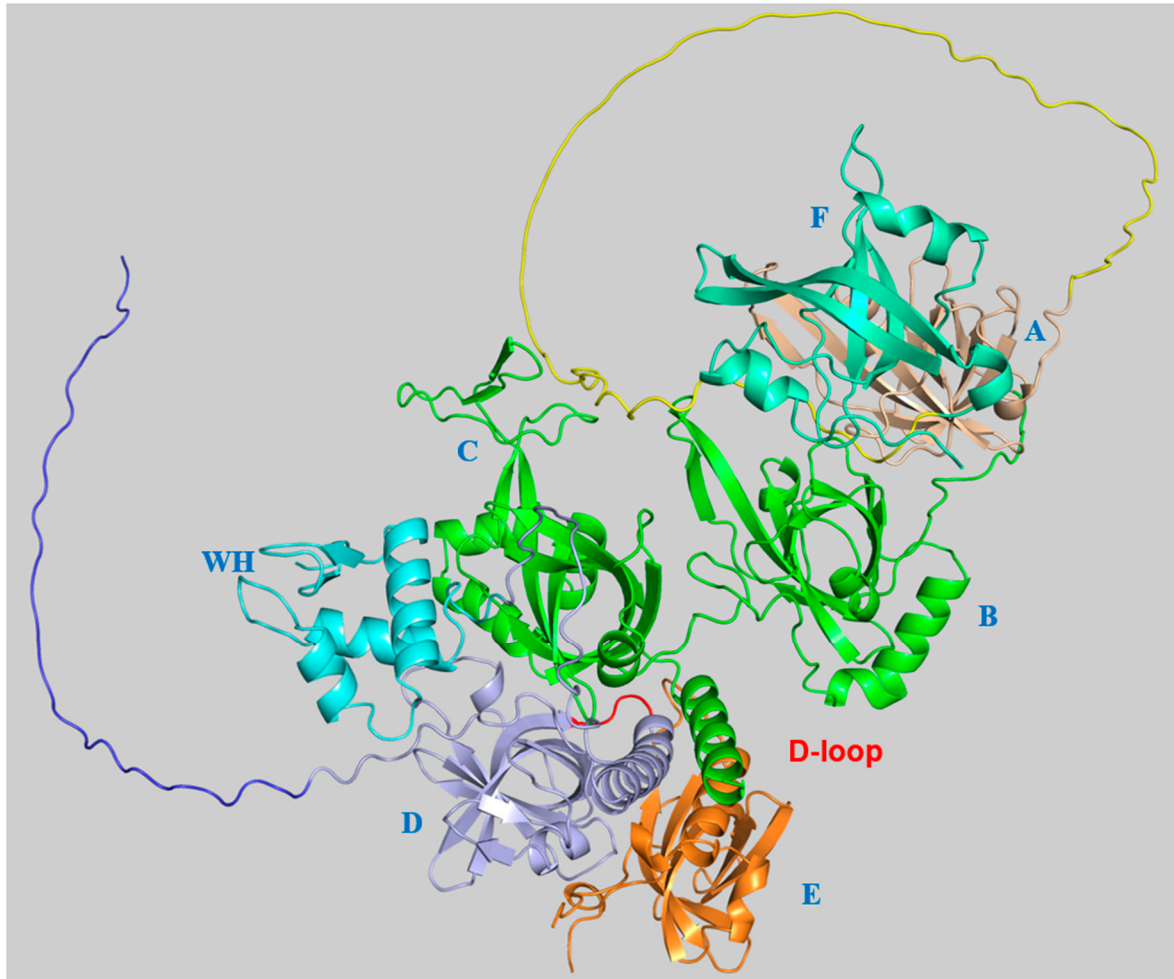


Supplemental Information:

**A**



**B**

**Supplemental Figure S1. The Predicted Structure of Human RPA.** Panels **A** and **B** present images of the RPA trimer predicted by AlphaFold [25] and visualized using the PyMOL 2.5.5 program (Schroedinger Inc. (USA)). The light green and light brown colours represent the DNA binding domains of RPA70 DBD-F and DBD-A, respectively. The linker between these two domains is shown in yellow. DBD-B, DBD-C and the short linker between the two domains are presented in green. The RPA32 phosphorylation sequence is in dark blue [23], whereas WH domain of RPA32 is in cyan. DBD-D and the aa connecting DBD-D and WH are shown in light blue. In DBD-D the loop containing the conserved aa D151 is called D loop (see also figure 1) and shown in red. It is important to note that the linker regions of RPA70 and RPA32 plus the N-terminal phosphorylation sequences of RPA32 are predicted with a very low per-residue model confidence score (pLDDT) suggesting they are unstructured without ligands or modifications. Panel **B** is the same predicted AlphaFold structure as in **A**, but with its atomic coordinates of atoms being rotated (arguments of rotation: y-axis and 180 degrees) using PyMol. The predicted structure suggests that DBD-F (light green) and WH domain (cyan), which are both important for RPA-protein interactions, are on the same site of the RPA molecule. It is important to note that the linker regions of RPA70 and RPA32 plus the N-terminal phosphorylation sequences of RPA32 have a very low per-residue model confidence score (pLDDT) and might be unstructured. Due to very low pLDDT scores and the N-linker sequence of RPA70 other arrangements for DBD-F within the RPA complex are also possible. However, published, experimental RPA structures including the *Ustilago maydis* RPA structure (PDB 4gop [13] see also figure 1, panels B and C) have not yet included DBD-F, the N-terminal linker sequence of RPA70, the WH domain, and the N-terminus of RPA32 in a structure of the heterotrimeric RPA complex. Therefore, the presented structure is very helpful for further discussion of RPA functions. The RPA domains are marked with blue letters, A to F (DBD-A to F) and WH.

|        |                                                                                                     |                         |
|--------|-----------------------------------------------------------------------------------------------------|-------------------------|
| hSTN1  | -----MQPGSSR-CEETPSLLWGLDPVFLAF <del>AKL</del>                                                      | 29                      |
| hRPA32 | MWNSGFESYGSS---SYGGAGGYTQSPGGFGSPAP-SQAEEKSRARA-----QHIVPC                                          | 49                      |
| uRPA32 | MFNNGFGGESNPYAQNYSTGGG--ASGGGFLANGSQNDSPSGKKAGN-----NTLRPV                                          | 51                      |
|        | . . . :                                                                                             | :                       |
| hSTN1  | YIRDILDMKESRVPGVF <del>LYNGHPIKQVDVLGT</del> VIGVRERDAFYSYGVDDST-GVINCIC                            | 88                      |
| hRPA32 | TISQLLSA-T-LVDEVFRIGNVEISQVTIVGIIRHAEKAPTNI <del>VYKIDMTAAPMDVRQ</del>                              | 106                     |
| uRPA32 | TIRQILNA-EQPHPDAEFILDGAELGQLTFVAVRNISR <del>NATNVAYSVEDGT-QQIEVRQ</del>                             | 109                     |
|        | * ::* . * .. : *: .:: : : : * ::* * . ::                                                            |                         |
| hSTN1  | WKKLNTESVSAA <del>P</del> SAAARELSLTSQLKKLQETIEQKT <del>K</del> IEIGDTIRVRGSIRTYREEREIH             | 148                     |
| hRPA32 | WVDTTDDT-SS <del>EN</del> -----TVVPPE <del>T</del> YVKVAGHLRSFQNK <del>KSLV</del>                   | 142                     |
| uRPA32 | WLDSSSD <del>DSSKA</del> -----SEIRNNVVYRVLGTLKS <del>FQNR</del> RSIS                                | 146                     |
|        | * . . *                                                                                             | : : : : * * : : : : : : |
| hSTN1  | ATTYYKV <del>DDP</del> VWNIIQIARMLELPT---IYRKVYDQPFHSSALEKEEALSNPGALDLPLST                          | 205                     |
| hRPA32 | AFKIMPLE <del>DM</del> --NEFTTHILEVINAHMVL <del>SKANSQPSAGR</del> APISNPGMSEAGNF <del>GGS</del> NFM | 200                     |
| uRPA32 | SGHMRPVI <del>DY</del> --NEVMFHRLEAVHAHLQATRGP <del>TASAL-KGAT</del> STALFNQAGGLE <del>SN</del> DMN | 203                     |
|        | : : * * : ** : : : : : *                                                                            |                         |
| hSTN1  | SLNSEKAKEFLMENRVQS <del>F</del> YQQELEMVESLLSLANQPVIHSASSDQVNFKK--DTTSKAI                           | 263                     |
| hRPA32 | PANG-----LT---VAQNQVLNL--IKA--CPRPEGLNFQDLKNQ <del>LKHMS</del>                                      | 238                     |
| uRPA32 | AYS <del>G</del> SKK-----QDVNDLYKNLGE <del>LPQQIMSIV</del> TRES--QNHPDG <del>VHVSLIAR</del> LLNGVD  | 255                     |
|        | . : : : : : : .                                                                                     |                         |
| hSTN1  | HSIFKNAIQLLQEKG <del>LVFQKDDGFD</del> NLYYTREDKDLHRKI <del>HRIIQQCQKPNHMEKGC</del> H                | 323                     |
| hRPA32 | VSSI <del>KQAVDF</del> LSNEGHIYSTVDD-----DHFKSTD-----AE----                                         | 270                     |
| uRPA32 | VNDVKS <del>AVEDLSSDG</del> YLTAADD-----NHVLPTA-----                                                | 285                     |
|        | . *.*: : *...* : : *                                                                                | . . . .                 |
| hSTN1  | FLHILACARLSIRPGLSEAVLQ <del>QVLELLEDQSD</del> IVSTM <del>EHHYTAF</del>                              | 368                     |
| hRPA32 | -----                                                                                               | 270                     |
| uRPA32 | -----                                                                                               | 285                     |