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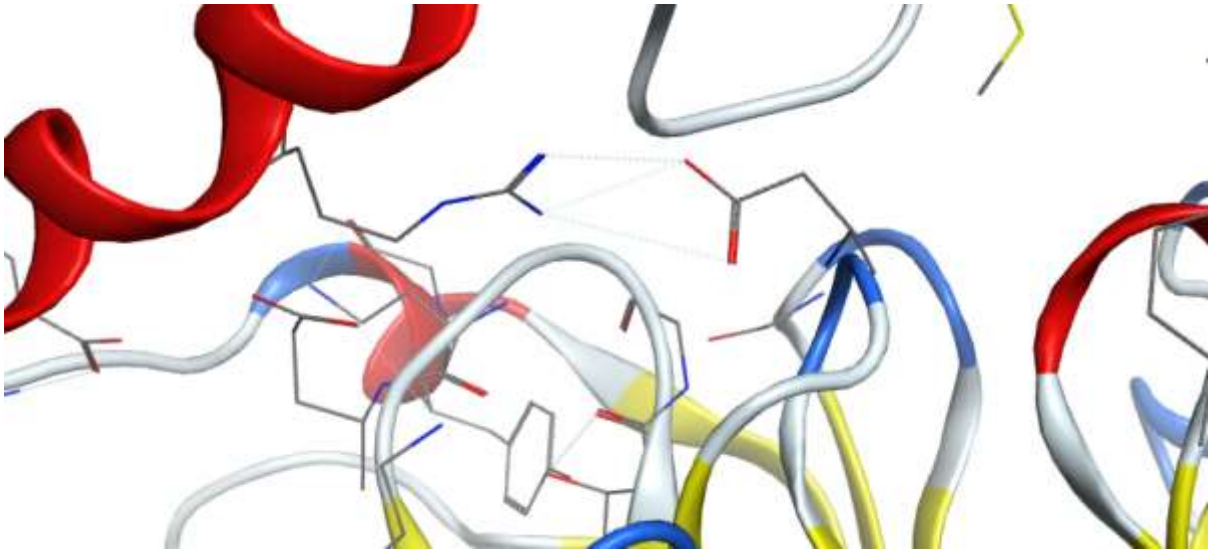
Supplementary Table 1. PCR primers used in this study.

Primer name	**Sequence (5′-> 3′)**	**Location**
Exon 32-33 Forward	ACCATCATAAACGAGAGCCTTAATTTC	In exon 31
Exon 33 Reverse	TGCCCTTAGGGTGTTTTGGACAACCTT	In exon 34
Exon 36 Reverse	CCATTCTTCCATGAGAGAATCAATG	In exon 37
In Exon 39 Forward	TGATGGCAGTTTTGGATCAGTTTA	In exon 39
Exon 43 Reverse	TTTAGGTAATAAAATGCGTCTCGTCAG	In exon 44
In Exon 45 Reverse	TTGCAATACAAACAAGTGACAGAAT	In exon 45
Exon 48 Forward	TGTGGGGAGGATGTGGCACAAAGA	In exon 47
Exon 50 Reverse	GAAGATTGATGTCCCAAACGGTC	In exon 51

Supplementary Figure 1. Interactions established between the modelled WD40 domain of LRRK2 and the adjacent a-helix that was co-crystallized in the template structure. A series of specific hydrogen bonds, water-mediated bridges and hydrophobic interactions secure the association between the two proteins.



Supplementary Figure 2. Surface representation of the WD40 to the C-terminal a-helix of eIF3b/PRT1 interaction. The WD40 model is shown in magenta ribbon, while the sliced structure is shown in red ribbon. The C-terminal a-helix of eIF3b/PRT1 is shown in ball and stick representation in a calculated electrostatic surface. WD40's interaction domain is the one that gets removed (red ribbon) and therefore, we propose that this splicing event is a protein-protein interaction control mechanism.