Epigenetics & Chromatin

CORRECTION

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Correction to: N^6-Adenosine methylation on mRNA is recognized by YTH2 domain protein of human malaria parasite *Plasmodium falciparum*

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The original version of this article [1], unfortunately contained a mistake. The presentation of Fig. 2 has been published incorrectly. The correct Fig. 2 is provided.

The original article has been corrected.

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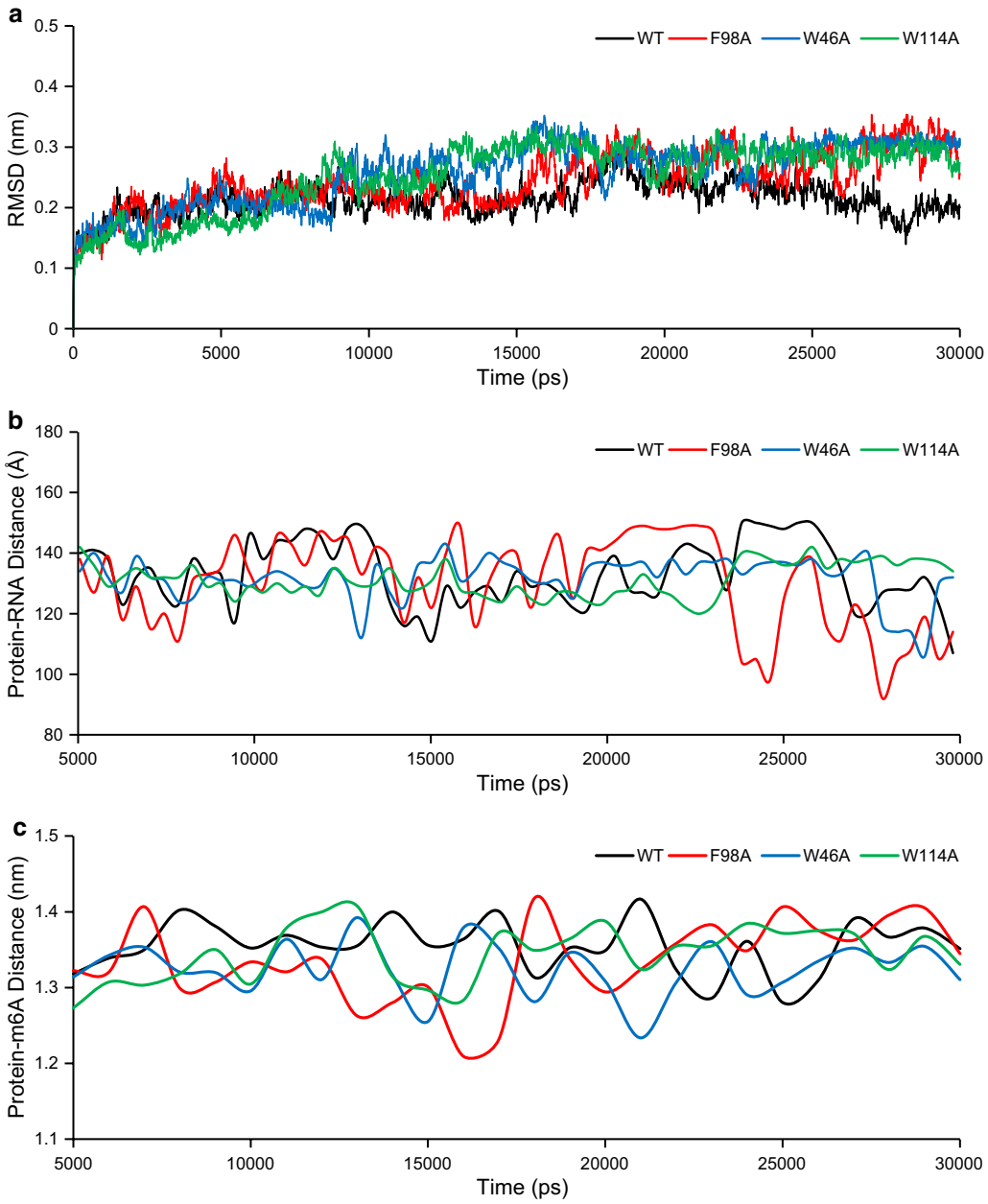

d

Protein	Average energy (kJ/mol)	Error (kJ/mol)	RMSD(Å)	Total Drift (kJ/mol)
Wild type (WT)	– 429818	24	722.1	– 60.51
W46A	– 434987	8.2	718.72	– 37.35
F98A	– 425498	24	713.73	– 122.34
W114A	– 443210	6.9	725.87	– 0.9

Fig. 2 Molecular dynamics simulation analysis of wild type and mutant PfYTH2 proteins in complex with RNA. **a** Backbone Root Mean Square Deviation (RMSD) profiles of PfYTH2 over molecular dynamics simulations time scale (picoseconds). **b** Spatial distance fluctuations (Angstroms), monitored over the MD simulations timescale (picoseconds) for Wild type and mutant PfYTH proteins in complex with RNA. **c** Distance drifts computed between PfYTH wild type and mutant proteins with m6A residue from RNA (nanometers), monitored over the MD simulations timescale (picoseconds). **d** The table presents the calculated PfYTH (wild type and mutants)–RNA complex potential energy values over the molecular dynamics simulation time scale

Reference

1. Govindaraju G, Kadumuri RV, Sethumadhavan DV, Jabeena CA, Chavali S, Rajavelu A. N6-Adenosine methylation on mRNA is recognized by YTH2 domain protein of human malaria parasite Plasmodium falciparum. Epigenetics Chromatin. 2020;13:33. https://doi.org/10.1186/s13072-020-00355-7.

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