

Correction

BIOPHYSICS AND COMPUTATIONAL BIOLOGY

Correction for “Effect of charge, hydrophobicity, and sequence of nucleoporins on the translocation of model particles through the nuclear pore complex,” by Mario Tagliazucchi, Orit Peleg, Martin Kröger, Yitzhak Rabin, and Igal Szleifer, which appeared in issue 9, February 26, 2013, of *Proc Natl Acad Sci USA* (110:3363–3368; first published February 12, 2013; 10.1073/pnas.1212909110).

The authors note that Figs. 1 and 2 appeared incorrectly. Within these figures, the “Nuclear side” and “Cytoplasmic side” labels were swapped. As a result, the legend for Fig. 1 and some text appeared incorrectly.

On page 3365, right column, first full paragraph, line 4, “cytoplasmic” should instead appear as “nuclear.”

On page 3365, right column, first full paragraph, line 5, “nuclear” should instead appear as “cytoplasmic.”

On page 3365, right column, third full paragraph, line 4, “cytoplasmic” should instead appear as “nuclear.”

On page 3366, left column, first paragraph, line 4, “cytoplasmic” should instead appear as “nuclear.”

On page 3366, left column, first full paragraph, line 4, “cytoplasmic” should instead appear as “nuclear.”

On page 3366, left column, first full paragraph, line 7, “nuclear” should instead appear as “cytoplasmic.”

The corrected figures and the corrected legend for Fig. 1 appear below. This error does not affect the conclusions of the article.

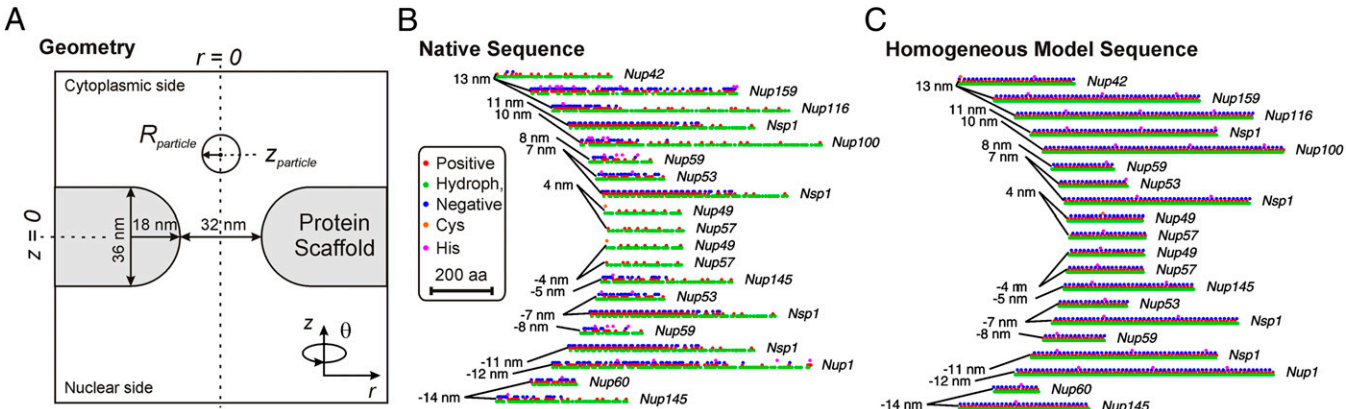


Fig. 1. (A) Geometry of the model NPC. The pore axis is defined as z , and the origin is set at the geometrical center of the pore, such that the cytoplasmic and nuclear bulk solutions are located at $z \rightarrow \infty$ and $z \rightarrow -\infty$, respectively. Schematic representations of the amino acid sequences of the FG-Nups for the native (28) (B) and homogeneous model (C) sequences. The FG-Nups in the homogeneous model sequence contain the same number and type of amino acids as those in the native sequence but in a regular order. The plot shows the different types of amino acids considered in the model: neutral hydrophobic (Hydroph; Ala, Ile, Leu, Phe, Trp, Tyr), Positive (Lys, Arg), Negative (Asp, Glu), Cys, and His (see Tables S1 and S2 and Fig. S1 for model and parameters). For simplicity in the graphical representation, neutral hydrophilic amino acids (Asn, Gln, Gly, Met, Pro, Ser, Thr, Val) are not shown. The figure shows the z -positions where the chains are anchored to the rigid protein scaffold.

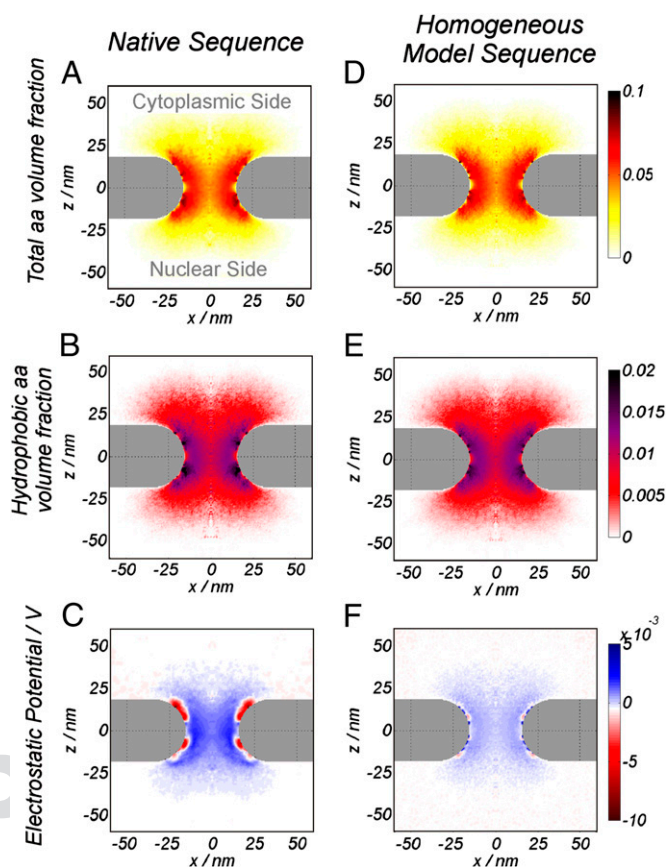


Fig. 2. Molecular organization of the yeast NPC. Total amino acid (aa) volume fraction (A and D), volume fraction of hydrophobic segments (B and E), and electrostatic potential (C and F) for the native and homogeneous model sequences (Fig. 1). The plots show that homogenizing the amino acid sequence affects the electrostatic potential but not the density of amino acids or the density of hydrophobic amino acids.

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AUTHOR QUERIES

AUTHOR PLEASE ANSWER ALL QUERIES

Q: 1_General question: It appears that the text in the original article is being corrected to match the original graphics, and the graphics in the original article are being corrected to match the original text. Typically, a Correction article will amend one or the other. Please confirm or change as needed.
