

CORRECTION

Correction: A disordered encounter complex is central to the yeast Abp1p SH3 domain binding pathway

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[S1 Fig](#) is incorrect. Please see the correct [S1 Fig](#) below.

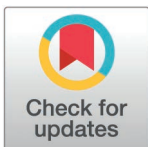
Supporting information

S1 Fig. Pairwise distances used in the determination of whether the encounter simulation has reached the bound state. The distances K(3)-Y10, P(2)-V55, P(0)-Y54, and K(-3)-K38 were used in the seg1 simulations and all seven distances were used in the ArkA simulations. The pairwise distance in the NMR ranges from 8.73 to 8.99 Å.

(PNG)

Reference

1. Gerlach GJ, Carrock R, Stix R, Stollar EJ, Ball KA. A disordered encounter complex is central to the yeast Abp1p SH3 domain binding pathway. PLoS Comput Biol. 2020;16(9):e1007815. <https://doi.org/10.1371/journal.pcbi.1007815> PMID: [32925900](https://pubmed.ncbi.nlm.nih.gov/32925900/)



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