華中農業大學
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The Architecture of Trypanosoma brucei editosomes

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BackGround

- RNA编辑：RNA编辑是指在mRNA水平上改变遗传信息的过程。

- 目前对RNA编辑机制研究最清楚的是锥虫动质体中 U 的插入与删除编辑，其他编辑方式的机制还不是很清楚

- 锥虫RNA编辑多由U的插入与删除完成，由20s编辑执行，并与其他多种复合体协调完成，称为编辑体

Methods

- CXMS：化学交联质谱法，

  它利用化学交联剂处理蛋白质样品，将空间距离足够接近、可以与交联剂反应的两个氨基酸以共价键连接起来，鉴定彼此空间接近的赖氨酸和N末端残基对，揭示了潜在区域相互作用，在整体结构上理解蛋白网络。

- TAP标记法：

  将单独的某一个蛋白的复合物提取出，从单个蛋白情况下理解相互作用蛋白网络。

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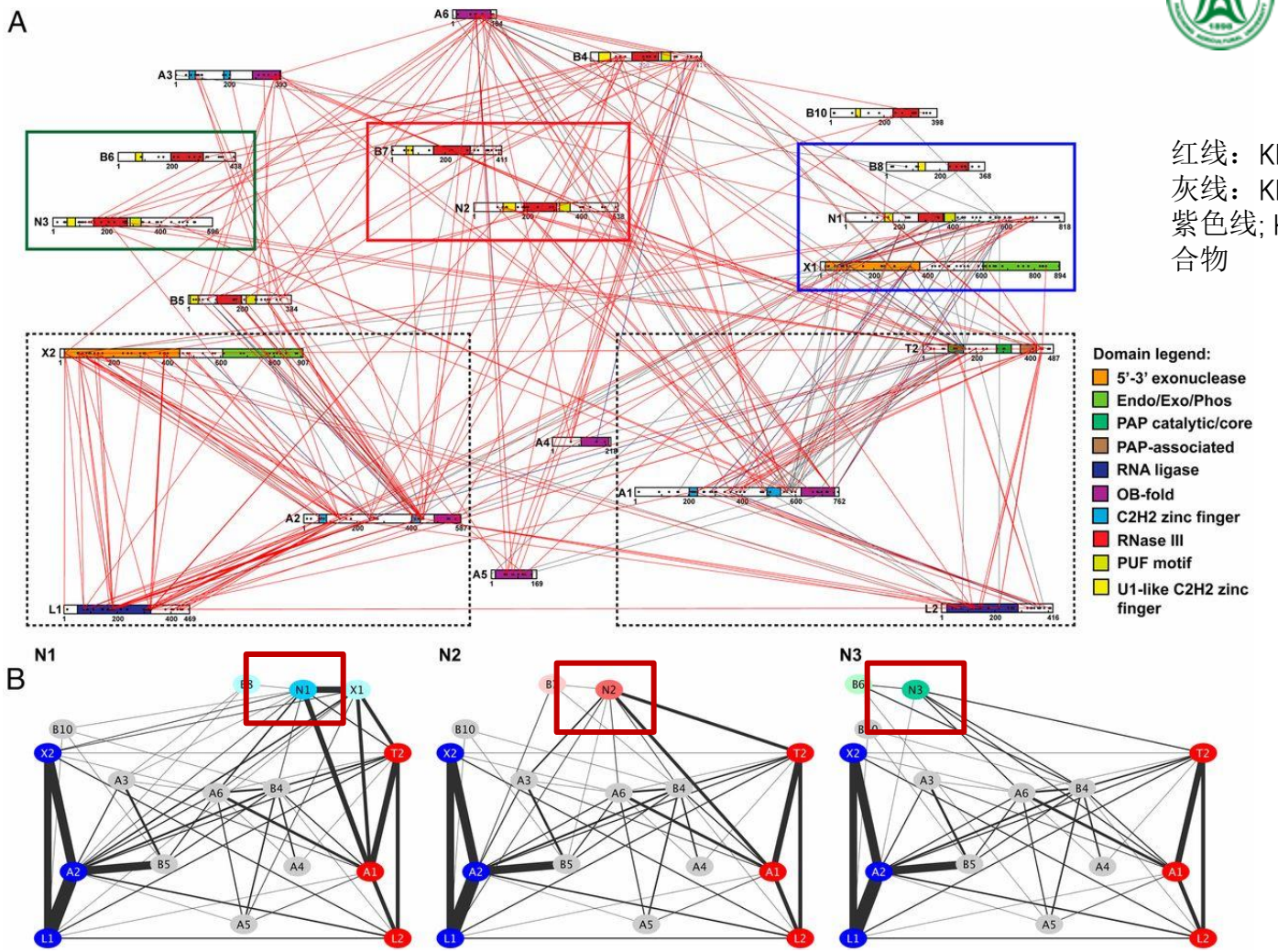
Result 1

1.CXMS of Editosomes.

(A) BS3 interprotein cross-linking map of editosome complexes.



红线：KREPB5-TAP复合物
灰线：KREN1-TAP复合物
紫色线; KREPB5-TAP和KREN1-TAP复合物

与CXMS结果相同：
B5：278个连接，68个蛋白对
N1：81个连接，30个蛋白对
一共：345个连接，77个蛋白对

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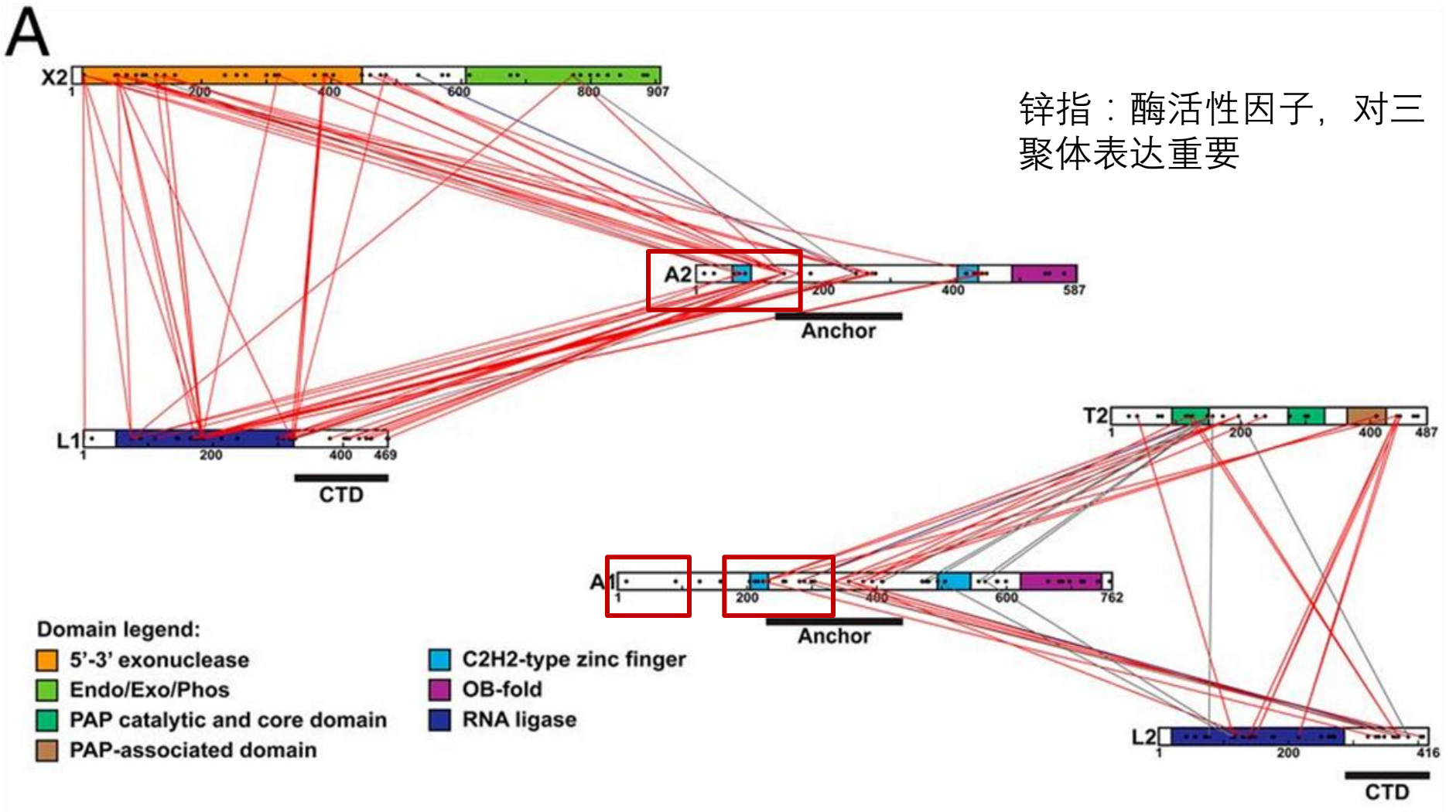
Result 2

2.Architecture of the Heterotrimeric Insertion and Deletion Dubcomplexes

3.“A” Protein Network That Links the Insertion and Deletion Subcomplexes

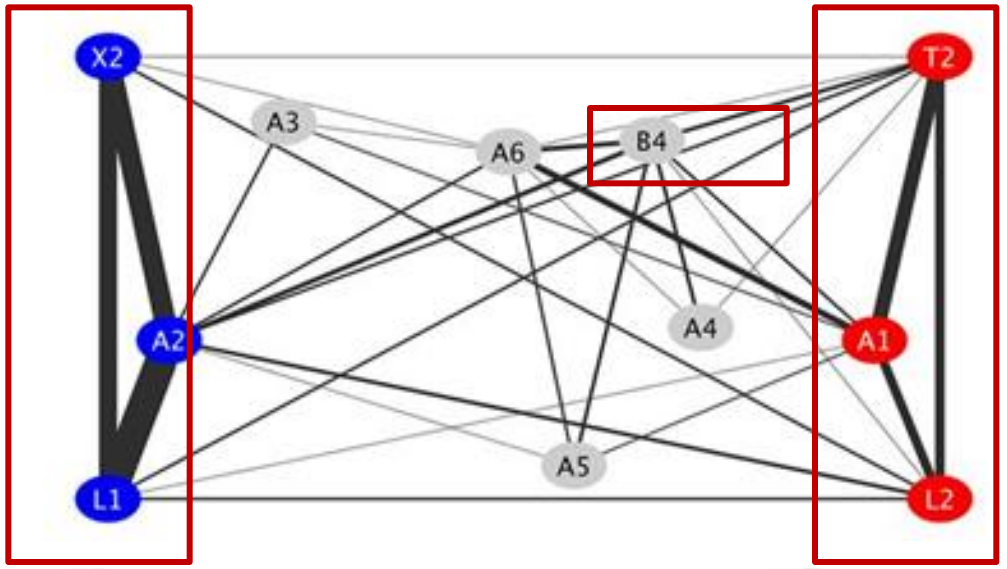
CXMS results for heterotrimeric insertion and deletion subcomplexes in editosomes.



锌指：酶活性因子，对三聚体表达重要

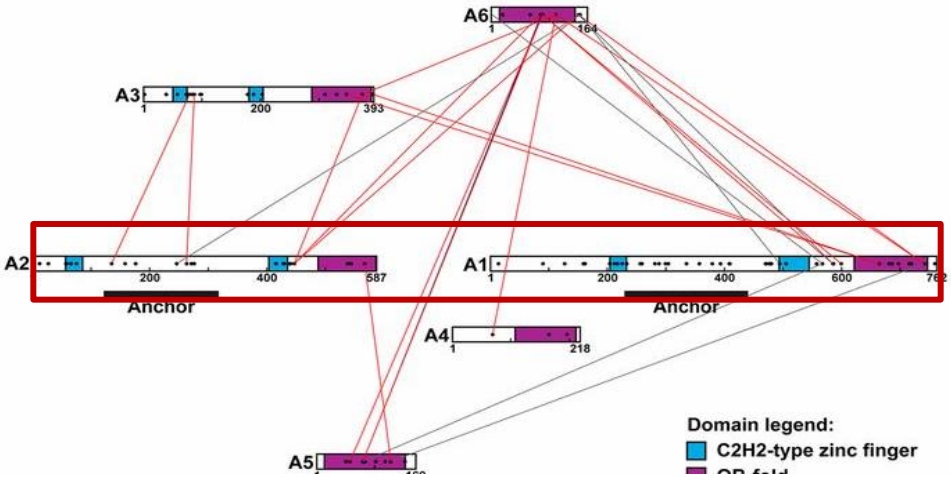
“A” Protein Network That Links the Insertion and Deletion

B



结论：B4与“A”蛋白网络交联多，B4与网络强相关

C



结论：A1,A2无交联，锌指序列无同源性

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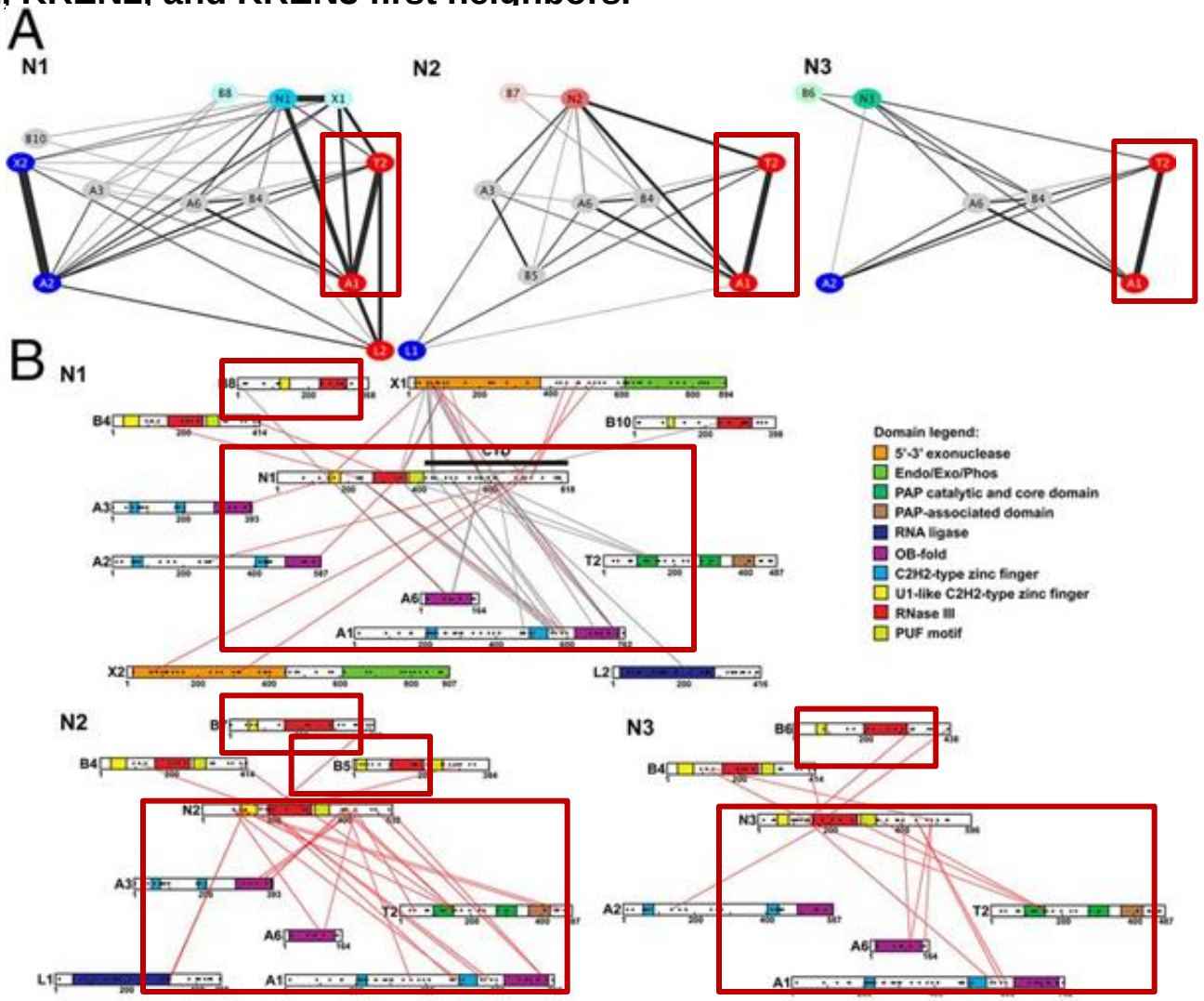
Result 3

4、Endonuclease Association with Other Editosome Proteins

5、Endonuclease Association with KREPB6, -B7, -B8, and KREX1

(A) Network diagrams and (B) interprotein cross-linking maps of KREN1, KREN2, and KREN3 first neighbors.



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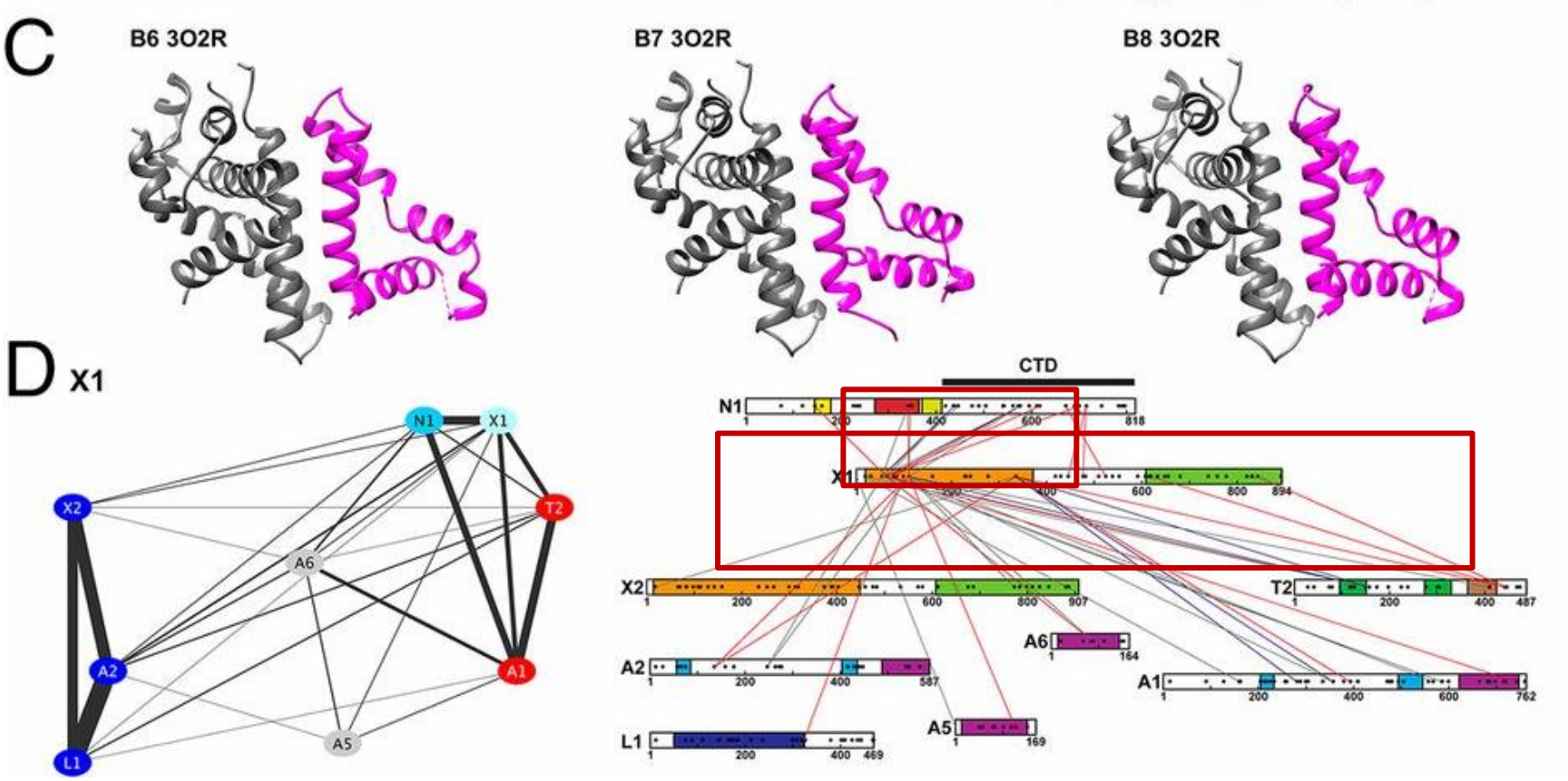
Endonuclease Association with KREPB6, -B7, -B8, and KREX1



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Result 4

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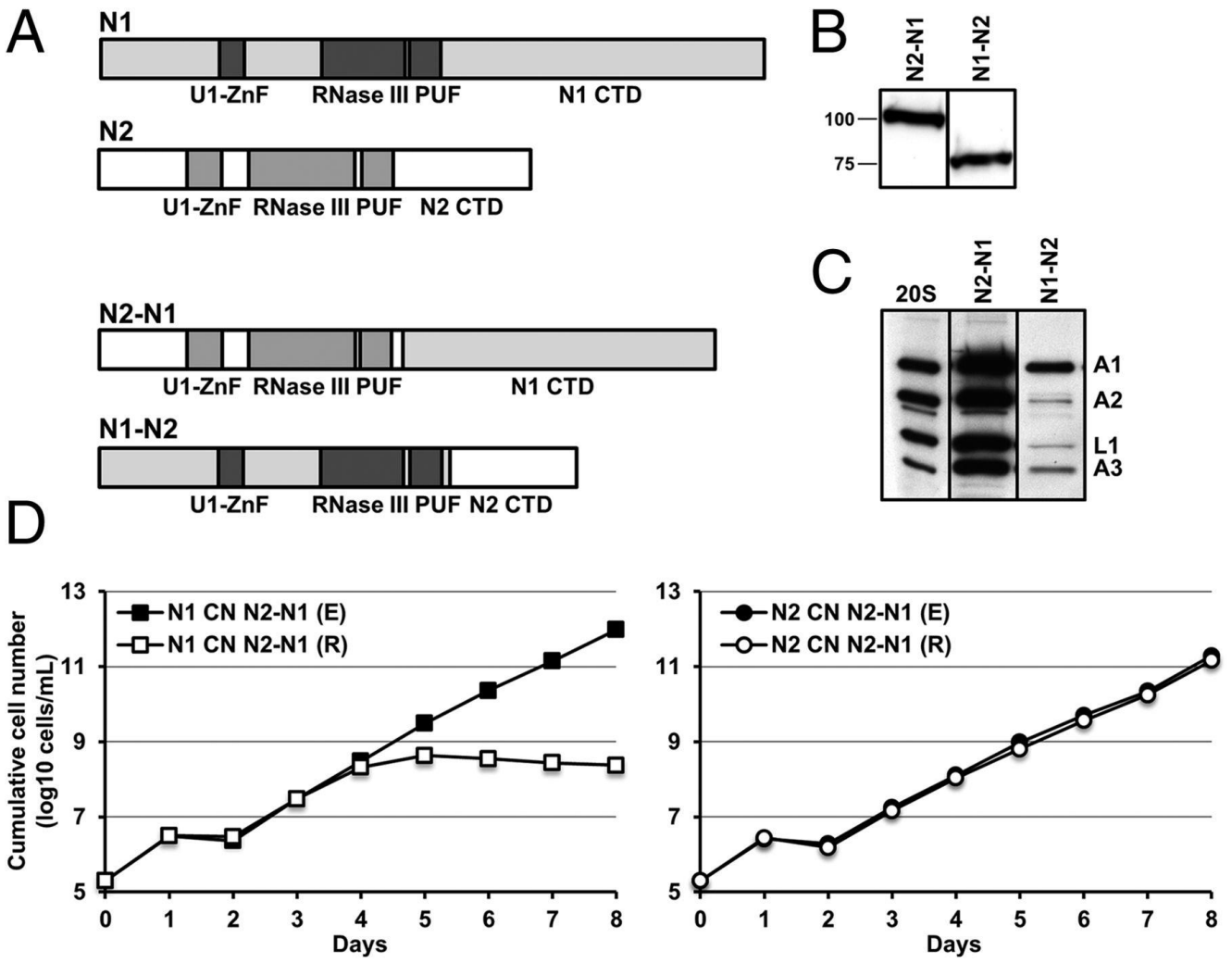
6.Experimental Validation of Endonuclease Protein Proximities Identified by CXMS

(A) Diagram showing U1-like zinc finger, RNase III, and PUF motifs of KREN1 and KREN2 and the C-terminal regions exchanged in the chimeric KREN1-N2 and KREN2-N1 proteins.



N2表达补偿

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Result 5

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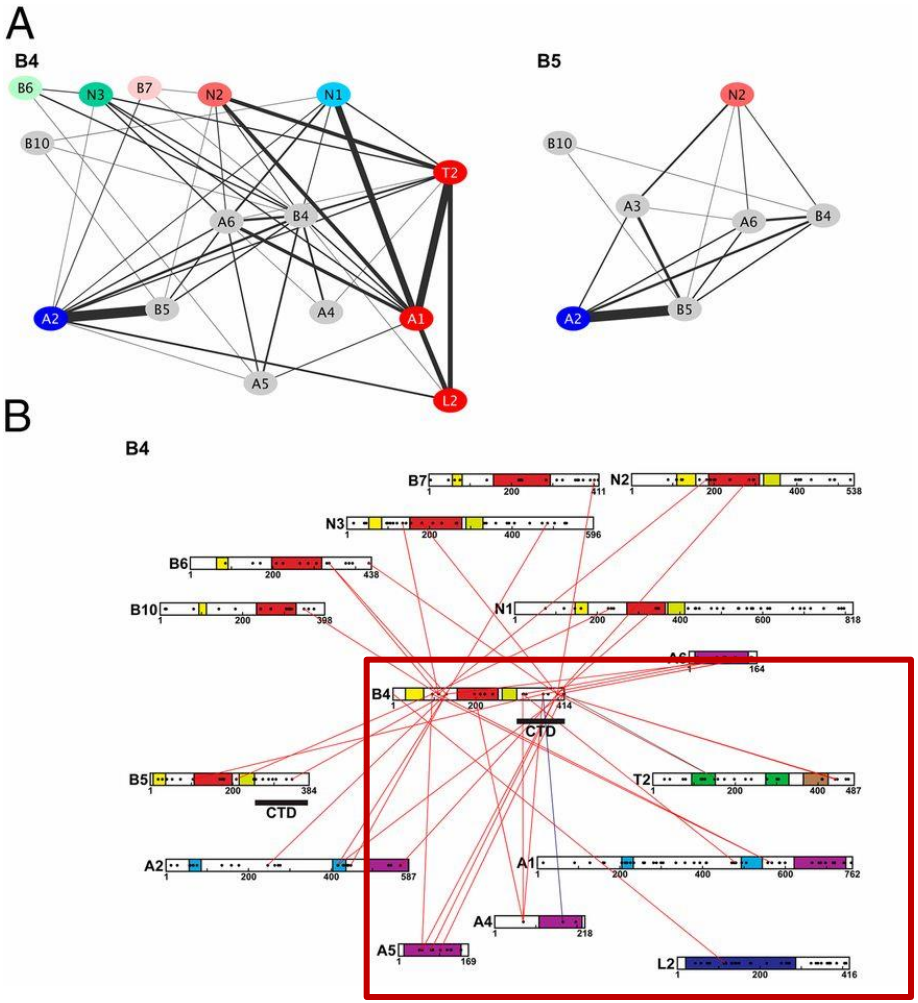
7.Differential Association of KREPB4 and KREPB5 with Endonuclease

8.Partner Proteins and Other Editosome Proteins

(A) Network diagrams and (B) interprotein cross-linking maps of KREPB4 and KREPB5 first neighbors.



结论：N1,N2,N3都有和N2不同，说明不同蛋白附近连接不同

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Result 6

9.Experimental Validation of KREPB5 Protein Proximities

Identified by CXMS

(A) Diagram showing the U1-like zinc finger, RNase III, and PUF motifs, and the C-terminal domain of KREPB5.

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总结

- 本文研究了编辑体的精细网络图，对RNA编辑做了一个整体的研究，属结果创新。

- 文章对我的启发：通过对网络的各部分理解，下一次遇见蛋白网络图时理解会更加深刻。

- 文章的不足：我认为他在进行这些包括每一部分是编辑体的网络时，如B4、B5在蛋白网络中存在差异，但他也得出结论。可以做一些生物体实验去验证，这样文章会更有说服力。

THANKS！