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Identifying essential proteins based on sub-network partition and prioritization by integrating subcellular localization information

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Highlights

- Proposing essential protein prediction method SPP by integrating PPI network and subcellular localization. data
- SPP achieves higher prediction accuracy compared with existing computational methods on YDIP and YBioGRID network.
- Sub-network partition and prioritization can effectively reduce the effect of false positives in PPI networks.

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