

PUBLICATIONS

Peer Reviewed Journals

1. Shi H., Yan K.K., **Ding L.**, Qian C., Chi H., Yu J. Network Approaches for Dissecting the Immune System. *iScience* 23 (8).
2. Silveira A.B., Kasper L.H., Fan Y., Jin H., Wu G., Shaw T.I., Zhu X., Larson J.D., Easton J., Shao Y., Yergeau D.A., Rosencrance C., Boggs K., Rusch M.C., **Ding L.**, Zhang J., Finkelstein D., Noyes R.M., Russell B.L., Xu B., Broniscer A., Wetmore C., Pounds S.B., Ellison D.W., Zhang J., Baker S.J. H3.3 K27M depletion increases differentiation and extends latency of diffuse intrinsic pontine glioma growth in vivo. *Acta Neuropathol.* 2019 Apr;137(4):637-655. doi: 10.1007/s00401-019-01975-4.
3. Kohei K., **Ding L.**, Michael N.E., Stephen V.R., Scott N., John E., Juncheng D., Soheil M., Rhonda E.R., Michael R., Jinghui Z. RNAIndel: discovering somatic coding indels from tumor RNA-Seq data. *Bioinformatics*, btz753, <https://doi.org/10.1093/bioinformatics/btz753>.
4. Silveira A.B., Kasper L.H., Fan Y., Jin H., Wu G., Shaw T., Zhu X., Larson J.D., Easton J., Shao Y., Yergeau D.A., Rosencrance C., Boggs K., Rusch M.C., **Ding L.**, Zhang J., Finkelstein D., Noyes R.M., Russell B.L., Xu B., Broniscer A., Wetmore C., Pounds S.B., Ellison D.W., Zhang J., Baker S.J.. (2019) H3.3 K27M depletion increases differentiation and extends latency of diffuse intrinsic pontine glioma growth in vivo. *Acta Neuropathologica*. 137(4):637-655. doi: 10.1007/s00401-019-01975-4.
5. Hagiwara K., **Ding L.**, Edmonson, M.N., Rice, S.V., Newman, S., Meshinchi, S., Ries, R.E., Rusch, M., Zhang, J. (2019) RNAIndel: a machine-learning framework for discovery of somatic coding indels using tumor RNA-Seq data. *bioRxiv* 512749; doi: <https://doi.org/10.1101/512749>.
6. Xu K., **Ding L.**, Chang T.C., Shao Y., Chiang J., Mulder H., Wang S., Shaw T.I., Wen J., Hover L., McLeod C., Wang Y.D., Easton J., Rusch M., Dalton J., Downing J.R., Ellison D.W., Zhang J., Baker S.J., Wu G.. (2018) Structure and evolution of double minutes in diagnosis and relapse brain tumors. *Acta Neuropathologica*. 137(1):123-137. doi: 10.1007/s00401-018-1912-1.
7. Alexander T.B., Gu Z., Iacobucci I., Dickerson K., Choi J.K., Xu B., Payne-Turner D., Yoshihara H., Loh M.L., Horan J., Buldini B., Basso G., Elitzur S., de Haas V., Zwaan C.M., Yeoh A., Reinhardt D., Tomizawa D., Kiyokawa N., Lammens T., De Moerloose B., Catchpoole D., Hori H., Moorman A., Moore A.S., Hrusak O., Meshinchi S., Orgel E., Devidas M., Borowitz M., Wood B., Heerema N.A., Carrol A., Yang Y., Smith M.A., Davidsen T.M., Hermida L.C., Gesuwan P., Marra M.A., Ma Y., Mungall A.J., Moore R.A., Jones S.J.M., Valentine M., Janke L.J., Rubnitz J.E., Pui C., **Ding L.**, Liu Y., Zhang J., Nichols K.E., Downing J.R., Cao X., Shi L., Pounds S., Newman S., Pei D., Guidry Auvil J.M., Gerhard D.S., Hunger S.P., Inaba H., Mullighan C.G.. The genetic basis and cell of origin of mixed phenotype acute leukaemia. (2018) *Nature*, 562(7727):373-379.
8. Mohebbi, M, **Ding, L.**, Malmberg, R.L., Momany, C, Rasheed, K, Cai, L. (2018) Accurate prediction of human miRNA targets via graph modeling of miRNA-target duplex. *Journal of Bioinformatics and Computational Biology*, 7:1850013.
9. **Ding, L.**, Xue, X., LaMarca, S., Mohebbi, M., Samad, A., Malmberg, R.L., Cai, L. (2015) Accurate Prediction of RNA Nucleotide Interactions with Backbone k-Tree Model", *Bioinformatics*, 31(16): 2660-2667.

Conference Proceedings

1. **Ding, L.**, Xue, X., LaMarca, S., Mohebbi M., Samad, A., Malmberg, R., and Cai, L. (2014) Abinitio prediction of RNA nucleotide interactions with backbone k-tree model”, Proceedings of ECCB’14 Workshop on Computational Methods for Structural RNAs, Strasbourg France, 25-42.
2. **Ding, L.**, Samad, A., Xue, X., Huang, X., Malmberg, R., and Cai, L. (2014) Stochastic k-tree grammar and its application in bimolecular structure modeling”, International Conference on Language and Automata Theory and Applications (LATA 2014) Vol 8370, 308-322.
3. **Ding, L.**, Robertson, J., Malmberg, R., and Cai, L. (2013) Protein closed loop prediction from contact probabilities”, International Symposium on Bioinformatics Research and Applications (ISBRA 2013), 199-210.
4. **Ding, L.**, Fu, B., and Zhu, B. (2011) Minimum Interval Cover and Its Application to Genome Sequencing”. International Conference on Combinatorial Optimization and Applications (COCOA 2011), 287- 298.
5. **Ding, L.**, Fu, B., and Fu, Y. (2010) Improved Sublinear Time Algorithm for Width- bounded Separators”. International Workshop on Frontiers in Algorithmics, 101-112.
6. **Ding, L.**, Fu, B., Fu, Y., Lu, Z., and Zhao, Z. (2010) $O((\log n)^2)$ Time Online Approximation Schemes for Bin Packing and Subset Sum Problem”. International Workshop on Frontiers in Algorithmics, 250-261.

Book Chapters

1. Cai, L., **Ding, L.**, Huang, X., Malmberg, RL, and Xue, X. (2014) Stochastic grammar systems for biomolecular structure modeling, Integrative Bioinformatics for Biomedical Research: A No Boundary Thinking Approach”, Huang and Moore ed. Cambridge Press, to appear.
2. **Ding, L.**, Fu, B. (2013) Algebrization and Randomization Methods”. Handbook of Combinatorial Optimization, Springer, pp 171-220.
3. **Ding, L.**, Fu, B., Fu, Y., Wan, Y. (2012) Application of Width-Bounded Separators to Protein Side-Chain Packing Problem”, Sequence and Genome Analysis: Methods and Applications, iConcep Press.

Preprints

1. Michael R., **Liang D.**, Sasi A., Andrew T., Hongjian J., Michael M., Lawryn K., Andre S., Michael A.D., Suzanne J.B., Jinghui Z. XenoCP: Cloud-based BAM cleansing tool for RNA and DNA from Xenograft. bioRxiv 843250; doi: <https://doi.org/10.1101/843250>.
2. **Ding, L.**, Chang, Di., Malmberg, R., Martinez, A., Robinson, D., Wicker, M., Yan, H., Cai, L. (2018) Efficient Learning of Optimal Markov Network Topology with k-Tree Modeling. arXiv preprint arXiv:1801.06900.
3. **Ding. L.**, Samad, A., Xue, X., Huang, X., Cai, L. (2013) Polynomial kernels collapse the W-hierarchy. arXiv preprint arXiv:1308.3613.