

Peer-reviewed journal papers

1. Dinanath Sulakhe, Sandhya Balasubramanian, BingqingXie, Bo Feng, Andrew Taylor, Sheng Wang, Eduardo Berrocal, Paul Dave, **Jinbo Xu**, Daniela Bornigen, Conrad Gilliam and Natalia Maltsev. *Lynx: a database and knowledge extraction engine for integrative medicine*. Nucleic Acids Research, 2013 Nov 21. [Epub ahead of print]
2. Sheng Wang, Jian Peng, Jianzhu Ma and **Jinbo Xu***. *Protein structure alignment beyond spatial proximity*. (Nature Publishing Group) Scientific Reports, 2013; 3:1448.
3. Raghavendra Hosur, Jian Peng, Arunachalam Vinayagam, Ulrich Stelzl, **Jinbo Xu**, Norbert Perrimon, Jadwiga Bienkowska and Bonnie Berger. *Coev2Net: a computational framework for boosting confidence in high-throughput protein-protein interaction dataset*. Genome Biology 2012, **13**:R76.
4. Feng Zhao and **Jinbo Xu***. *A position-specific distance dependent statistical potential for protein structure and functional study*. (Cell) STRUCTURE, volume 20, Issue 6, 1118-1126, 17 May 2012.
5. Morten Kallerg, Haipeng Wang, Jian Peng, Sheng Wang, Zhiyong Wang, Hui Lu and **Jinbo Xu***. *Template-based protein modeling using the RaptorX web server*. Nature Protocols, 2012 Jul 19; 7(8):1511-22.
6. Jian Peng and **Jinbo Xu***. *A multiple-template approach to protein threading*. PROTEINS, [Volume 79, Issue 6](#), pages 1930–1939, June 2011.
7. Jian Peng and **Jinbo Xu***. *RaptorX: exploiting structure information for protein alignment by statistical inference*. PROTEINS, Volume 79, Issue S10, pages 161–171, 2011 (**invited paper to CASP9**).
8. Sheng Wang, Jian Peng and **Jinbo Xu***. *Alignment of distantly-related protein structures: algorithm, bound and implications to homology modeling*. Bioinformatics, 2011 Sep 15;27(18):2537-45.
9. Raghavendra Hosur, **Jinbo Xu**, Jadwiga Bienkowska, and Bonnie Berger. *iWRAP: An interface threading approach with application to prediction of cancer related protein-protein interactions*. Journal of Molecular Biology, 2011 Feb 4; 405(5):1295-310.
10. Rohit Singh, Daniel Park, **Jinbo Xu**, Raghavendra Hosur and Bonnie Berger. *Struct2Net: a Web-Service to Predict Protein-Protein Interactions Using a Structure-based Approach*. Nucleic acids research, Vol. 38, No. Web Server issue. (July 2010), pp. W508-15. (**The first three authors equally contribute to this paper.**)
11. Feng Zhao, Jian Peng, Joe DeBartolo, Karl F. Freed, Tobin R. Sosnick and **Jinbo Xu***. *A probabilistic and continuous model of protein conformational space for template-free modeling*. Journal of Computational Biology, 2010 Jun; 17(6):783-98.
12. Zhiyong Wang, Jian Peng, Feng Zhao and **Jinbo Xu***. *Protein 8-class secondary structure prediction using Conditional Neural Fields*. Proteomics, 2011 Oct; 11(19):3786-92. Early version appears in the Proceedings of IEEE BIBM 2010.
13. Xin Gao, Dongbo Bu, **Jinbo Xu** and Ming Li. *Improving consensus contact prediction via server correlation reduction*. BMC Structural Biology 2009, 9:28
14. **Jinbo Xu***, Jian Peng and Feng Zhao. *Template-based and free modeling by RAPTOR++ in CASP8*. PROTEINS, 2009; 77(Suppl 9): 133–137. (**invited paper**)

15. Shuaicheng Li, Dongbo Bu, **Jinbo Xu*** and Ming Li. *Fragment-HMM: A new approach to protein structure prediction*. Protein Science, 2008 Nov; 17(11):1925-34.
16. Feng Zhao, ShuaiCheng Li, Beckett W. Sterner and **Jinbo Xu***. *Discriminative learning for protein conformation sampling*. PROTEINS, 2008 Oct; 73(1):228-40.
17. Rohit Singh, **Jinbo Xu** and Bonnie Berger. *Global Alignment of Multiple Protein-Protein Interaction Networks*. PNAS, 2008 Sep 2;105(35):12763-8.
18. Ben Boyerinas, Sun-Mi Park, Noam Shomron, Cydney B. Nielsen, Christine Feig, **Jinbo Xu**, Christopher B. Burge and Marcus E. Peter. *Identification of let-7-regulated Oncofetal Genes for Human Cancer*. Cancer Research, 2008 Apr 15; 68(8):2587-91.
19. **Jinbo Xu**, Daniel Brown, Ming Li and Bin Ma. *Optimizing multiple spaced seeds for homology search*. Journal of Computational Biology, 13(7):1355-1368, 2006.
20. **Jinbo Xu**, Ying Xu, Dongsup Kim and Ming Li. *RAPTOR: Optimal Protein Threading by Linear Programming*. Journal of Bioinformatics and Computational Biology, 1(1):95-118, 2003. (**invited paper**)
21. **Jinbo Xu*** and Ming Li. *Assessment of RAPTOR's linear programming approach in CAFASP3*. PROTEINS 2003, 53 Suppl 6:579-84. (**invited paper**)
22. **Jinbo Xu***, Bonnie Berger. *Fast and Accurate Algorithms for Protein Side-Chain Packing*. The Journal of the ACM, 53(4):1-25, 2006. (**invited paper. JACM provides coverage of the most significant work in computer science.**)
23. **Jinbo Xu**. *Protein Fold Recognition by Predicted Alignment Accuracy*. IEEE/ACM Trans. on Computational Biology and Bioinformatics. 2(2):157-165, 2005.
24. **Jinbo Xu**, Ying Xu and Ming Li. *Protein Threading by Linear Programming: Theoretical Analysis and Computational Results*. Journal of Combinatorial Optimization, 8(4):403-418, 2004.
25. Zhi-Zhong Chen, Tao Jiang, Guo-Hui Lin, Jianjun Wen, Dong Xu, **Jinbo Xu** and Ying Xu. *Approximation Algorithms for NMR Spectral Peak Assignment*. Theoretical Computer Science, 299:211-229, 2003. (**authors ranked alphabetically**)