

Publications

PUBLICATIONS: (* as corresponding author)

Research Papers

1. Xu X, Li Y, Bharath SR, Ozturk MB, Bowler MW, Loo BZL, Tergaonkar V, Song H* (2018)
Structural basis for reactivating the mutant TERT promoter by cooperative binding of p52 and ETS1.

Nature Commun. 9, 3183.

2. Na Z, Yeo SP, Bharath SR, Bowler MW, Balıkçı E, Wang C, Song H* (2017)
Structural basis of blocking PD-1 mediated immune response by therapeutic antibody pembrolizumab.

Cell Res. 27, 147-150

3. Kaan HYK1, Sim AYL, Tan SKJ1, Verma C, Song H* (2017)
Targeting YAP/TAZ-TEAD protein-protein interactions using fragment-based and computational modeling approaches.

PLoS One 12:e0178381

4. Kaan HYK, Chan SW, Tan SKJ, Guo F, Lim CJ, Hong W, Song H* (2017)
Crystal structure of TAZ-TEAD complex reveals a distinct interaction mode from that of YAP-TEAD complex.

Sci Rep. 7:2035

5. Tang X, Bharath SR, Piao S, Tan VQ, Bowler MW, Song H* (2016)
Structural basis for specific recognition of pre-snRNA by Gemin5.

Cell Res. 26, 1353-1356

6. Tang X, Zhu Y, Baker SL, Bowler MW, Chen BJ, Chen C, Hogg JR, Goff SP, Song H*(2016)
Structural basis of suppression of host translation termination by Moloney Murine Leukemia Virus

Nature Commun. 7, 12070.

7. Zhou X, Ren W, Bharath SR, Tang X, He Y, Chen C, Liu Z, Li D, Song H*. (2016)
Structural and Functional Insights into the Unwinding Mechanism of Bacteroides sp Pif1.

Cell Rep. 14, 2030-2039

8. Wu D, Kaan HY, Zheng X, Tang X, He Y, Vanessa Tan Q, Zhang N, Song H*. (2015)
Structural basis of Ornithine Decarboxylase inactivation and accelerated degradation by polyamine sensor Antizyme1.

Sci Rep. 5,14738

9. Ngeow J, Yu W, Yehia L, Niazi F, Chen J, Tang X, Heald B, Lei J, Romigh T, Tucker-Kellogg L, Lim KH, Song H, Eng C. (2015) Exome Sequencing Reveals Germline SMAD9 Mutation That Reduces Phosphatase and Tensin Homolog Expression and Is Associated With Hamartomatous Polyposis and Gastrointestinal Ganglioneuromas.

Gastroenterology 149, 886-889.

10. Ren W, Chen H, Sun Q, Tang X, Lim SC, Huang J, Song H* (2014)
Structural Basis of SOSS1 Complex Assembly and Recognition of ssDNA.

Cell Rep. 6, 982-91.

11. Wu D, Muhlrads D, Bowler MW, Liu Z, Parker R, Song H* (2014)
Lsm2 and Lsm3 bridge the interaction of the Lsm1-7 complex with Pat1 for decapping activation.
Cell Res. 24, 233-46.
12. Cottenie E, Kochanski A, Jordanova A, Bansagi B, Zimon M, Horga A, Jaunmuktane Z, Saveri P, Rasic VM, Baets J, Bartsakoulia M, Ploski R, Teterycz P, Nikolic M, Quinlivan R, Laura M, Sweeney MG, Taroni F, Lunn MP, Moroni I, Gonzalez M, Hanna MG, Bettencourt C, Chabrol E, Franke A, von Au K, Schilhabel M, Kabzińska D, Hausmanowa-Petrusewicz I, Brandner S, Lim SC, Song H, Choi BO, Horvath R, Chung KW, Zuchner S, Pareyson D, Harms M, Reilly MM, Houlden H. (2014).
Truncating and missense mutations in IGHMBP2 cause Charcot-Marie Tooth disease type 2.
Am J Hum Genet. 95, 590-601
13. Wang Y, Li D, Huan X, Zhang L, Song H* (2014)
Crystallization and preliminary X-ray crystallographic analysis of a putative nonribosomal peptide synthase AmbB from *Pseudomonas aeruginosa*.
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14. Fan H, Dong Y, Wu D, Bowler MW, Zhang L, Song H* (2013)
QslA disrupts LasR dimerization in antiactivation of bacterial quorum sensing.
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15. Lai T, Cho H, Liu Z, Bowler MW, Piao S, Parker R, Kim YK, Song H* (2012)
Structural Basis of the PNRC2-Mediated Link between mRNA Surveillance and Decapping
Structure 20, 2025-37.
16. Lim SC, Bowler MW, Lai TF, Song H* (2012).
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17. Deng Y, Schmid N, Wang C, Wang J, Pessi G, Wu D, Lee J, Aguilar C, Ahrens CH, Chang C, Song H, Eberl L, Zhang LH. (2012).
Cis-2-dodecenoic acid receptor RpfR links quorum-sensing signal perception with regulation of virulence through cyclic dimeric guanosine monophosphate turnover.
Proc Natl Acad Sci U S A. 109, 15479-84.
18. Pobbati AV, Chan SW, Lee I, Song H, Hong W. (2012)
Structural and functional similarity between the Vgll1-TEAD and the YAP-TEAD complexes.
Structure 20, 1135-40
19. Wu D, Lim SC, Dong Y, Wu J, Tao F, Zhou L, Zhang LH, Song H* (2012)
Structural Basis of Substrate Binding Specificity Revealed by the Crystal Structures of Polyamine Receptors SpuD and SpuE from *Pseudomonas aeruginosa*.
J Mol Biol. 416, 697-712.
20. Wu D, Jiang S, Bowler MW, Song H* (2012)
Crystal structures of Lsm3, Lsm4 and Lsm5/6/7 from *Schizosaccharomyces pombe*.
PLoS One. 7, e36768.
21. Chen L, Muhlrads D, Hauryliuk V, Cheng Z, Lim MK, Shyp V, Parker R and Song H* (2010)
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22. Nissan T, Rajyaguru P, She M, Song H, Parker R. (2010).
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23. Cheng Z, He YW, Lim SC, Qamra R, Walsh MA, Zhang LH, Song H.* (2010)
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Biosynthesis. Structure, 18, 199-209.

24. Chen L, Chan SW, Zhang X, Walsh M, Lim CJ, Hong W and Song H* (2010)
Structural basis of YAP recognition by TEAD4 in the Hippo pathway
Genes & Development, 24, 290-300.

25. Henriksson N, Nilsson P, Wu M, Song H and Anders Virtanen A. (2010). Recognition of
adenosine residues by the active site of poly(a)-specific ribonuclease.
J Biol. Chem. 285, 163-70.

26. Fan, JS, Cheng Z, Zhang J, Noble C, Zhou Z, Song H* and Yang D (2009).
Solution and crystal structures of mRNA exporter Dbp5p and its interaction with nucleotide.
J Mol. Biol. 388, 1-10.

27. Cheng Z, Saito K, Pisarev AV, Wada M, Pisareva VP, Pestova TV, Gajda M, Round A,
Kong C, Lim M, Nakamura Y, Svergun DI, Ito K, Song H.* (2009).
Structural insights into eRF3 and stop codon recognition by eRF1.
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33. She M, Decker CJ, Svergun DI, Round A, Chen N, Muhlrud D, Parker R, Song H.*
(2008).

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Mol. Cell 29, 337-349.

34. Noble CG, Song H.* (2007).
MLN51 stimulates the RNA-helicase activity of eIF4AIII.
PLoS One, 2:e303.

35. Gao, H., Zhou, Z., Rawat, U., Huang, C., Bouakaz, L., Wang, C., Cheng, Z., Liu, Y., Zaviyalov, A., Gursky, R., Sanyal, S., Ehrenberg, M., Frank, J. and Song H.* (2007).
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36. Cheng, Z., Muhlrad, D., Lim, M. K., Parker R. and Song H.* (2007).
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Crystal structure and functional analysis of Dcp2p from *Schizosaccharomyces pombe*.
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EMBO J. 24, 1491-1501.

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Structural insight into poly(A) binding and catalytic mechanism of human PARN.
EMBO J. 24, 4082-4093.

42. Chen N, Walsh MA, Liu Y, Parker R, Song H. * (2005).
Crystal structures of human DcpS in ligand-free and m7GDP-bound forms suggest a dynamic mechanism for scavenger mRNA decapping.
J Mol. Biol. 347, 707-18.

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Nat. Struct. & Mol. Biol. 11, 249-56.

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Structural basis for recruitment of GRIP domain golgin-245 by small GTPase Arl1.
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Crystal Structure and Functional Analysis of the Eukaryotic Class II Release Factor eRF3 from *S. pombe*.

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Pharmacol Ther. 93, 113-24.

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The Crystal Structure of Human Eukaryotic Release Factor eRF1-

Mechanism of Stop Codon Recognition and Peptidyl-tRNA Hydrolysis.

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Crystal Structure of intact Elongation Factor Tu from *Escherichia coli* in GDP conformation at 2.0Å Resolution.

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Review Articles

1. Tang X, Lim SC, Song H* (2014)
RNase AS versus RNase T: similar yet different.
Structure. 22, 663-4.

2. Arribas-Layton M, Wu D, Lykke-Andersen J and Song H* (2013).
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3. Chan SW, Lim CJ, Chen L, Chong YF, Huang C, Song H, Hong W (2011)
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4. Ling SH, Qamra R, Song H* (2011)
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Book Chapters

1. Portia Gloria Loh and Haiwei Song* (2010) Superfamily 1 RNA helicases: Biology & Mechanism.
In RNA helicases for the Biomolecular Sciences, edited by Eckhard Jankowsky (The Royal Society of Chemistry).
ISBN: 978-1-84973-221-5; DOI:10.1039/9781849732215-00189