

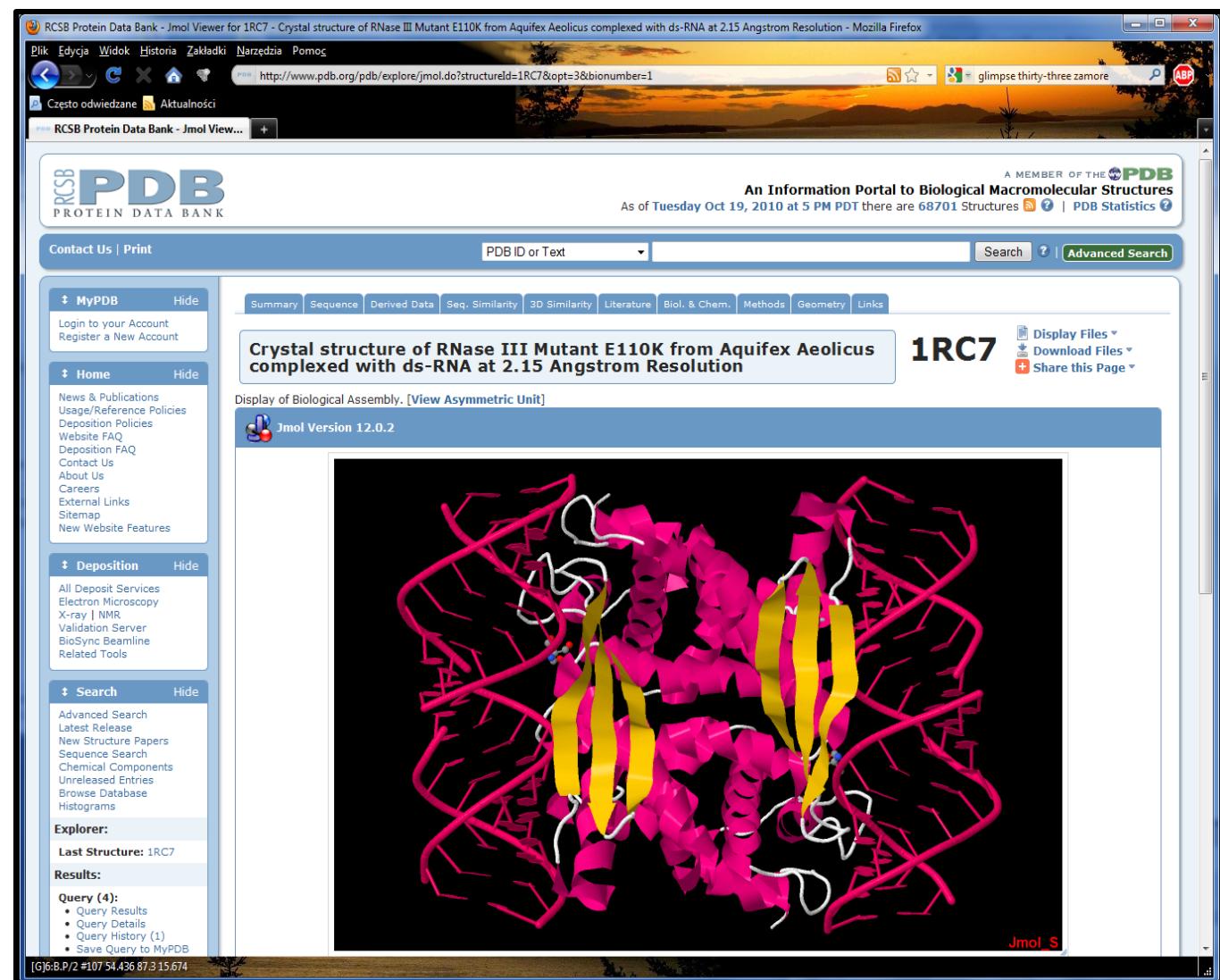


Ribonuclease III in Action: Catalytic Photographs of the Enzyme, Determined by X-ray Crystallography

Jarosław Błaszczyk

This “mini-review”
e-poster
presentation
is dedicated
to
Professor Wojciech J. Stec
on the occasion
of
His 75th Birthday

*Financial support
by the
Polish National Science Center,
grant No.
DEC-2012/05/B/ST4/00075
is gratefully acknowledged.*



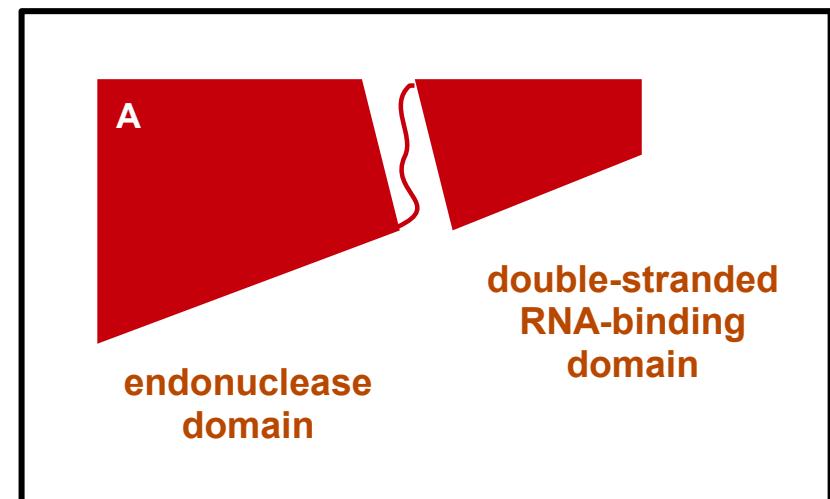
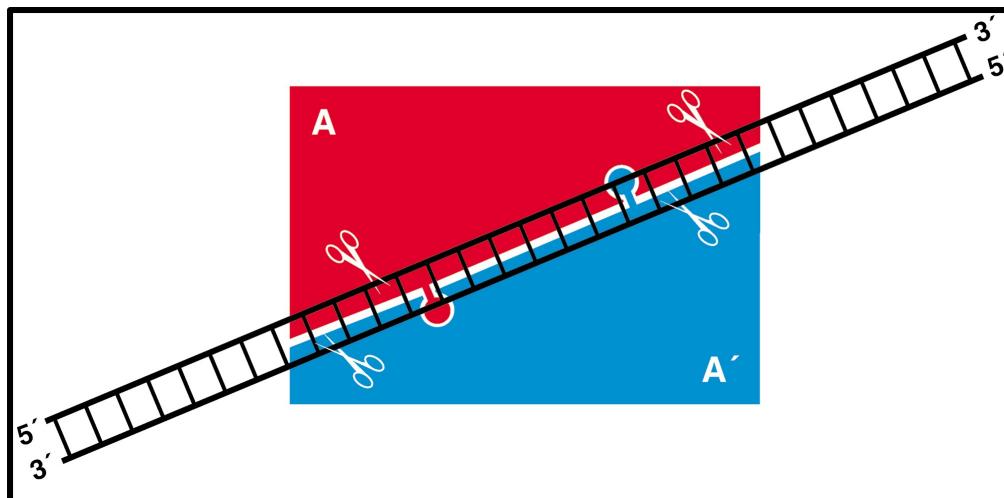
Ribonuclease III (RNase III)

an enzyme which catalyzes the cleavage of double-stranded RNA (dsRNA)

Ribonucleases (RNases) cleave RNA strands to shorter fragments or to single nucleotides by hydrolysis of the phosphodiester bonds.

Among ribonucleases, we can distinguish:

- **endoribonucleases**: they cleave RNA molecules inside the strands
- **exoribonucleases**: they detach nucleotides from RNA 3'- or 5'-ends.



Ribonuclease III is an endoribonuclease
that catalyzes a cleavage of
double-stranded RNA to short fragments

The RNase III monomer
contains two very loosely
connected domains

Very brief history of the struggle on determination of RNase III structure and function

1968: First time purified in *Escherichia coli*.

[1]. H.D. Robertson, R.E. Webster and N.D. Zinder, *J. Biol. Chem.* (1968), **243**, 82-91.
"Purification and properties of ribonuclease III from Escherichia coli."

1968-1993: Investigation of enzyme functions.

[2]. For example, see: H.L. Li, B.S. Chelladurai, K. Zhang, A.W. Nicholson, *Nucleic Acids Res.* (1993), **21**, 1919-1925. *"Ribonuclease III cleavage of a bacteriophage T7 processing signal. Divalent cation specificity, and specific anion effects."*

1995: First X-ray structure: The double-stranded RNA-binding domain, PDB 1di2.

[3.] A. Kharrat, J. Macias, T.J. Gibson, M. Nilges, A. Pastore, *EMBO J.* (1995), **14**, 3572-3584.
"Structure of the dsRNA binding domain of E. coli RNase III.
PDB 1di2, Xenopus laevis - frog.

double-stranded RNA-binding domain



1996-2004: The struggle to obtain pure protein and to get an X-ray structure of full-length RNase III

This includes my work in the National Cancer Institute at Frederick: in Macromolecular Crystallography Lab (Alex Wlodawer & Xinhua Ji; crystallization and structure determination), and in Gene Regulation and Chromosome Biology Lab (Don Court; where the expression and purification work I have done together with Daiguan Yu*)

Present: Daiguan Yu in his Lab in GIBH CAS in Guangzhou, China

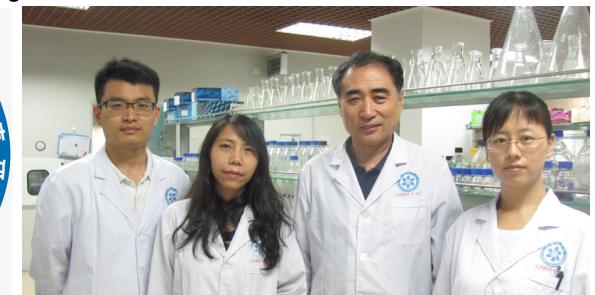
Donald Court



Daiguan Yu



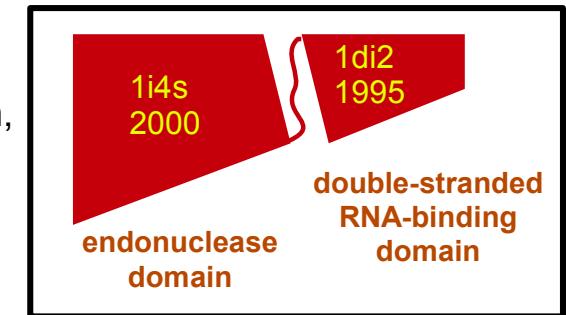
*Daiguan Yu is currently a Group Leader of the BioTherapeutics Core Technology Group at Guangzhou Institutes of Biomedicine and Health, Chinese Academy of Sciences



First X-ray structure which allowed to say something about the enzyme function

**2000: X-ray structure of endonuclease domain, 1i4s.
(not the full-length protein yet !)**

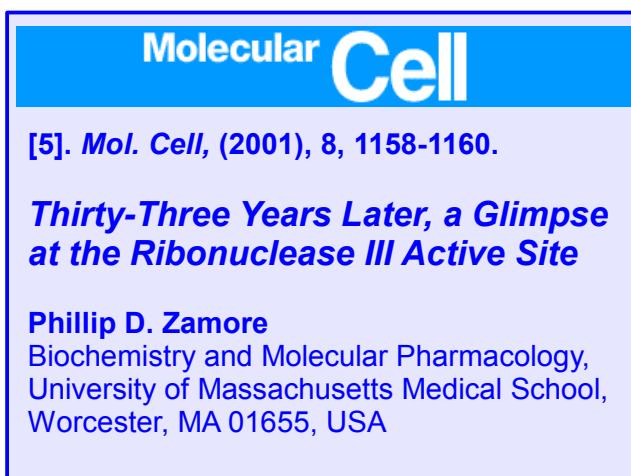
[4]. J. Blaszczyk, J.E. Tropea, M. Bubunenko, K.M. Routzahn, D.S. Waugh, D.L. Court, X. Ji, *Structure* (2001), **9**, 1225-1236. "Crystallographic and modeling studies of RNase III suggest a mechanism for double-stranded RNA cleavage." **PDB 1i4s, *Aquifex aeolicus*.**



Endonuclease domain (PDB 1i4s) is a functional domain.

Based on this structure, I proposed a model of RNase III with the cleavage product, 22bp ds-RNA, with 2bp overhang on each side.

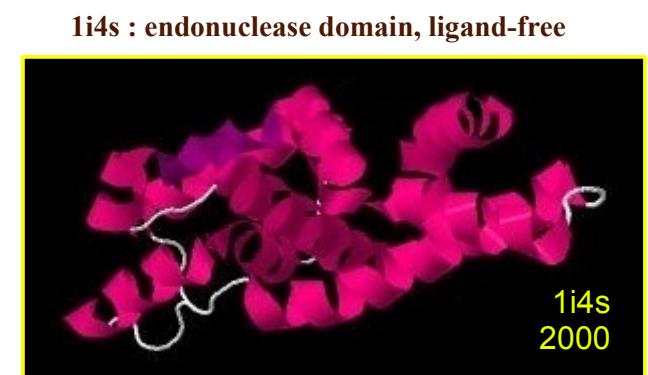
After years, my model was structurally proven: 2006, in entry 2ez6.



The paper which appreciates the impact of our work



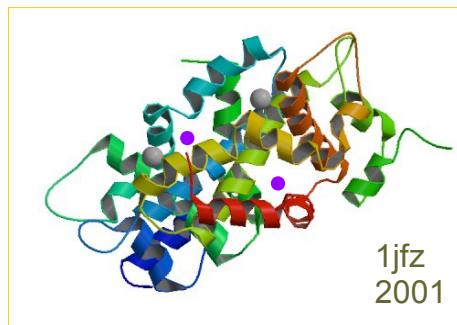
Our structure has been featured in December 2001 Issue cover



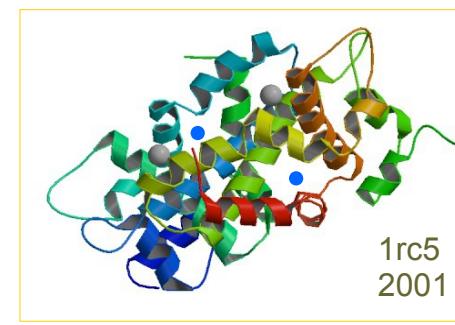
Our structure

First full-length RNase III structures

**2001: Probing the RNase III active center: Two X-ray structures of endonuclease domain in complex with metal ions
(1jfz: with Mn²⁺, 1rc5: with Mg²⁺) (still not the full-length protein!)**



1rc5 : endonuclease domain, Mg²⁺ complex

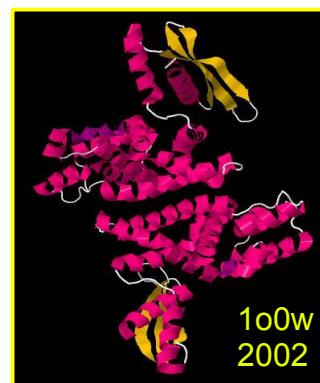


1jfz : endonuclease domain, Mn²⁺ complex

2002-2004: First structures of full-length RNase III (1o0w, 1rc7)

[6]. Joint Center for Structural Genomics (JCSG).
“Crystal structure of ribonuclease III (TM1102) from *Thermotoga maritima* at 2.0 Å resolution.”
PDB 1o0w. Apoenzyme, (2002), unpublished.

[7]. J. Blaszczyk, J. Gan, J.E. Tropea, D.L. Court, D.S. Waugh, X. Ji, *Structure* (2004), **12**, 457-466.
“Noncatalytic assembly of ribonuclease III with double-stranded RNA.”
PDB 1rc7. *Aquifex aeolicus*.



Full length, apo form (no RNA)



Full length, in complex with RNA

RNase III structural avalanche: the enzyme function disclosed in snapshots

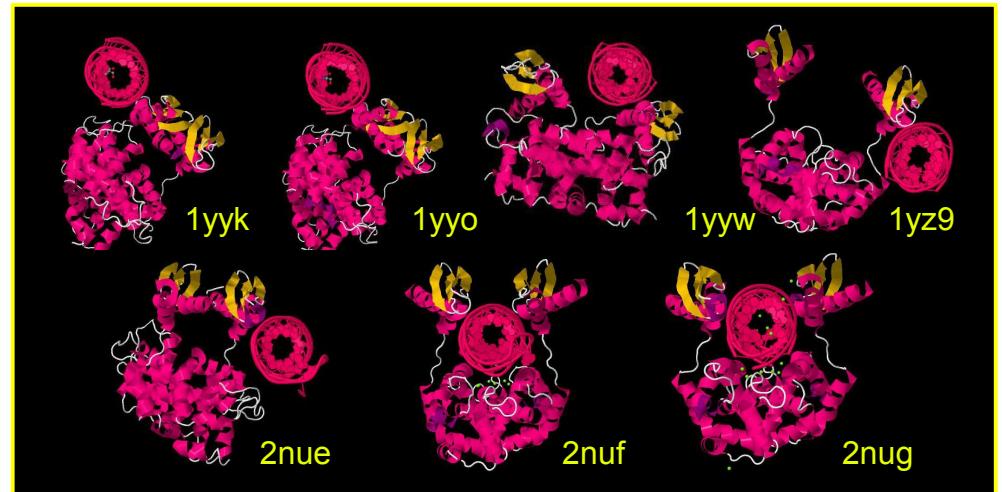
2005-2007: “Catalytic photographs” of RNase III in action

[8]. J. Gan, J.E. Tropea, B.P. Austin, D.L. Court, D.S. Waugh, X.Ji, *Structure* (2005), **13**, 1435-1442.
“Intermediate states of ribonuclease III in complex with double-stranded RNA.”

PDB 1yyk, 1yyo, 1yyw, 1yz9. *Aquifex aeolicus*.

[9]. J. Gan, G. Shaw, J.E. Tropea, D.S. Waugh, D.L. Court, X.Ji
Mol. Microbiol. (2007), **67**, 143-154.
“A stepwise model for double-stranded RNA processing by ribonuclease III.”

PDB 2nue, 2nuf, 2nug. *Aquifex aeolicus*.



2006: RNase III “Functional” complex with the product. Published in Cell !

[10]. J. Gan, J.E.Tropea, B.P. Austin, D.L. Court, D.S. Waugh, X.Ji, *Cell* (2006), **124**, 355-366.
“Structural insight into the mechanism of double-stranded RNA processing by ribonuclease III.”

PDB 2ez6. *Aquifex aeolicus*.



Cell 124, 355–366, January 27, 2006 ©2006 Elsevier Inc. Cell

Structural Insight into the Mechanism of Double-Stranded RNA Processing by Ribonuclease III

Jianhua Gan,¹ Joseph E. Tropea,¹ Brian P. Austin,¹ Donald L. Court,¹ David S. Waugh,¹ and Xinhua Ji^{1,*}

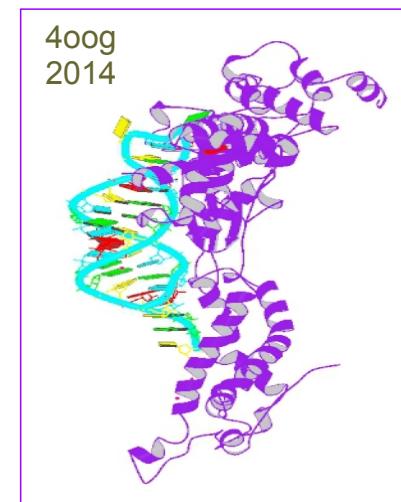
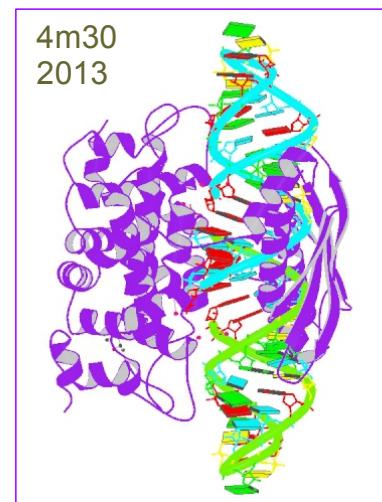
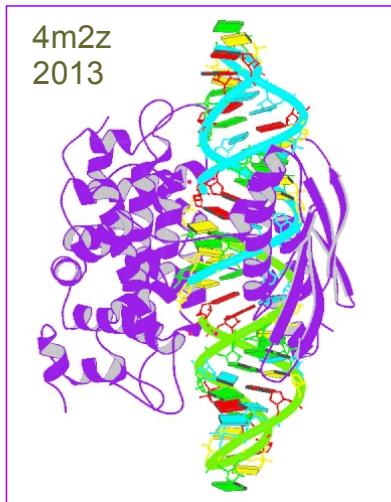
¹Center for Cancer Research, National Cancer Institute, National Institutes of Health, Frederick, MD 21702, USA

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 DOI 10.1016/j.cell.2005.11.034

RNase III structural avalanche: the enzyme function disclosed in snapshots (continued)

2008-2015: “Catalytic photographs” of RNase III in action (continued)

- [11]. D.L. Court, J. Gan, Y-H. Liang, G.X. Shaw, J.E. Tropea, N. Costantino, D.S. Waugh, X. Ji, *Annu. Rev. Genet.* (2013), **47**, 405-431. “RNase III: Genetics and Function; Structure and Mechanism.” **PDB 4m2z, 4m30. *Aquifex aeolicus*.**
- [12]. Y.H. Liang, M. Lavoie, M.A. Comeau, S. Abou Elela, X. Ji, *Mol. Cell* (2014), **54**, 431-444. “Structure of a eukaryotic RNase III postcleavage complex reveals a double-ruler mechanism for substrate selection.” **PDB 4oog. *Aquifex aeolicus*.**



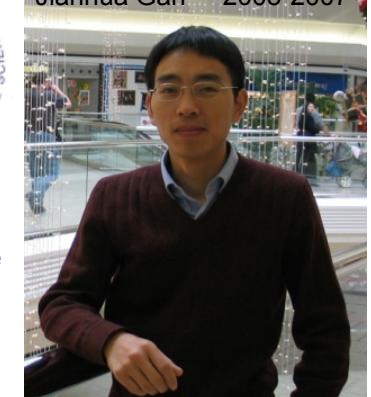
My (1996-2004) successors:

The two meanings of the word “successor”:

1. “The person who took charge of the project”
2. “The author of the success; the success holder”

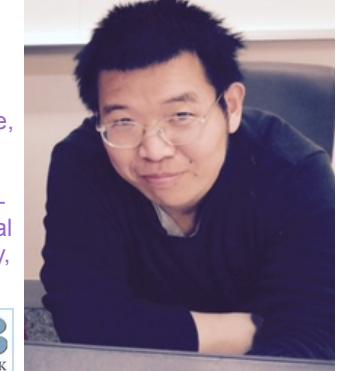


Jianhua Gan 2003-2007



Jianhua Gan is currently a Full-Time Professor at the Department of Physiology and Biophysics, School of Life Sciences, Fudan University, Shanghai, China

Yu-He Liang 2007-2011



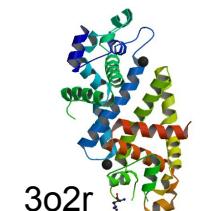
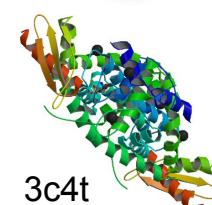
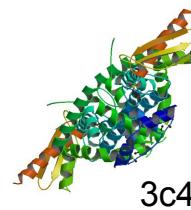
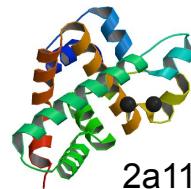
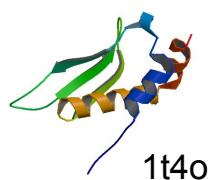
Yu-He Liang is currently a Research Associate, a PDB annotator at Rutgers University, Department of Chemistry and Chemical Biology, Piscataway, New Jersey, USA



The aftermath of our RNase III structural work

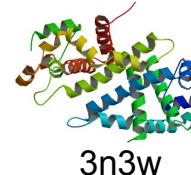
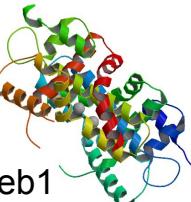
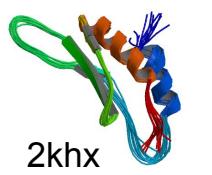
1t4o Rnt1p dsRNA-binding domain of RNase III

[13]. N. Leulliot, S. Quevillon-Cheruel, M. Graille, H. Van Tilbeurgh, T.C. Leeper, K.S. Godin, T.E. Edwards, S.T. Sigurdsson, N. Rozenkrants, R.J. Nagel, M. Ares, G. Varani, *Embo J.* (2004), **23**, 2468-2477. "A new alpha-helical extension promotes RNA binding by the dsRBD of Rnt1p RNase III."



2a11 Endonuclease Domain of RNase III from *Mycobacterium tuberculosis*

[14]. D.L. Akey, J.M. Berger, *Protein Sci.* (2005), **14**: 2744-2750.
"Structure of the nuclease domain of ribonuclease III from *M. tuberculosis* at 2.1 Å."



2khx Drosha double-stranded RNA binding motif

[15]. G.A. Mueller, M.T. Miller, E.F. Derose, M. Ghosh, R.E. London, T.M. Hall, *Silence* (2010), **1**:2. "Solution structure of the Drosha double-stranded RNA-binding domain."

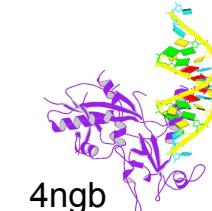
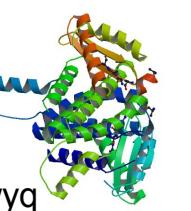
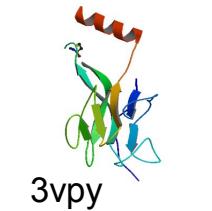
3c4b RNase IIIb and dsRNA binding domains of mouse Dicer (form 1)

3c4t RNase IIIb and dsRNA binding domains of mouse Dicer (form 2)

[16]. Z. Du, J.K. Lee, R. Tjhen, R.M. Stroud, T.L. James, *Proc.Natl.Acad.Sci.USA* (2008), **105**, 2391-2396. "Structural and biochemical insights into the dicing mechanism of mouse Dicer: a conserved lysine is critical for dsRNA cleavage."

2eb1 C-Terminal RNase III Domain of Human Dicer

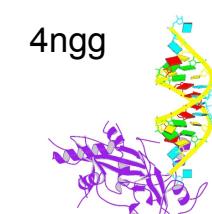
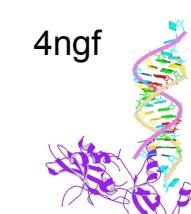
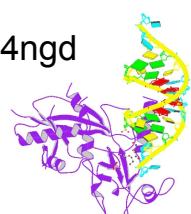
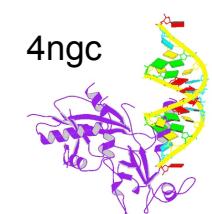
[17]. D. Takeshita, S. Zenno, W.C. Lee, K. Nagata, K. Saigo, M. Tanokura, *J.Mol.Biol.* (2007), **374**, 106-120. "Homodimeric structure and double-stranded RNA cleavage activity of the C-terminal RNase III domain of human dicer."



3n3w Nuclease Domain of RNase III from *Campylobacter jejuni* (form 1)

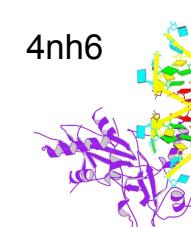
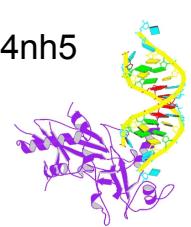
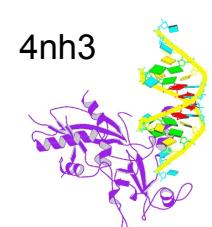
3o2r Nuclease Domain of RNase III from *Campylobacter jejuni* (form 2)

[18]. G. Minasov, A. Halavaty, L. Shuvalova, I. Dubrovska, J. Winsor, L. Papazisi, W.F. Anderson, *Center for Structural Genomics of Infectious Diseases* (2010). Unpublished.



3vpy Conserved phospho-threonine recognition cleft for dicer binding

[19]. S. Machida, Y.A. Yuan, *Mol Plant* (2013), **6**, 1290-1300. "Crystal structure of *Arabidopsis thaliana* Dawdle forkhead-associated domain reveals a conserved phospho-threonine recognition cleft for dicer-like 1 binding."



4wyq Dicer / tRNA-Binding Protein interface

[21]. R.C. Wilson, A. Tambe, M.A. Kidwell, C.L. Noland, C.P. Schneider, J.A. Doudna, *Mol.Cell.* (2015), **57**: 397-407. "Dicer-tRNA Binding Protein Complex Formation Ensures Accurate Mammalian MicroRNA Biogenesis."



A C K N O W L E D G E M E N T S

Jarosław Błaszczyk -
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Michigan State University
East Lansing, Michigan, USA, 2004-2006

- collected synchrotron data at:

National Synchrotron Light Source, X9B beamline
Brookhaven National Laboratory, Upton, New York, USA
Argonne National Laboratory, Advanced Photon Source
Argonne near Chicago, Illinois, USA

- and thanks to:

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