

The Dot/Icm Type IV secretion system and effector proteins: essential players in *Legionella* infection.

Hiroki Nagai

RIMD, Osaka University, JAPAN

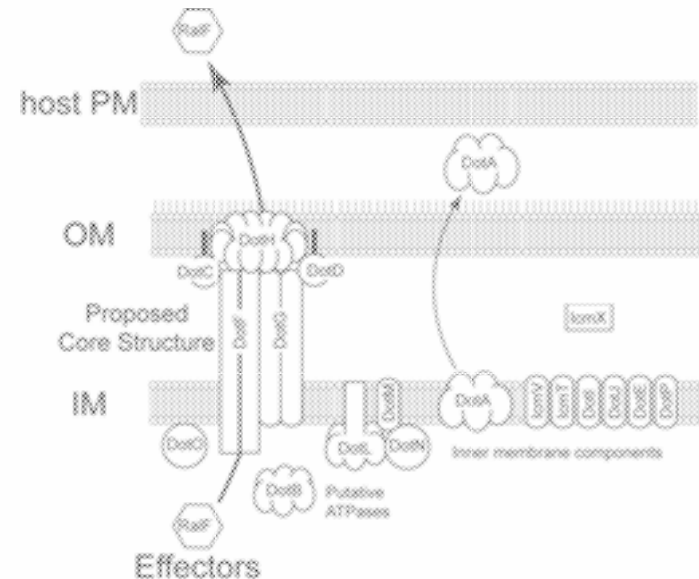


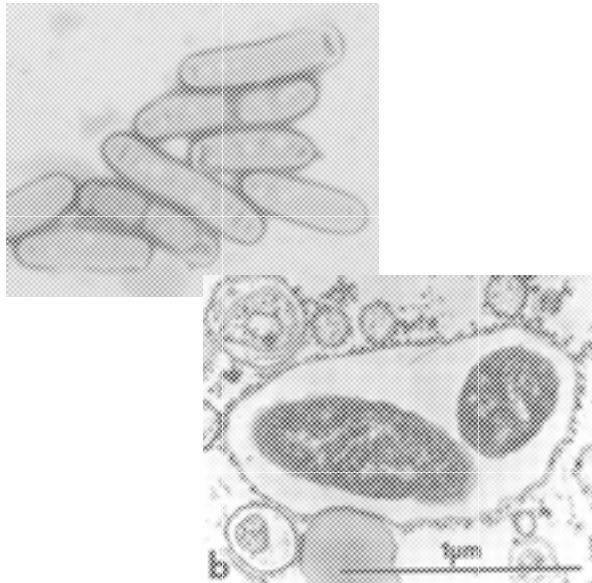
Legionella pneumophila

- Gram negative bacilli ubiquitously found in soil and freshwater environment.
- Replicate within a niche originated from phagosomes - **vacuolar pathogen**
- Natural hosts are unicellular protozoa such as freshwater amoeba - **accidental pathogen**

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- The functions of most of Dot/Icm substrates remain to be clarified.



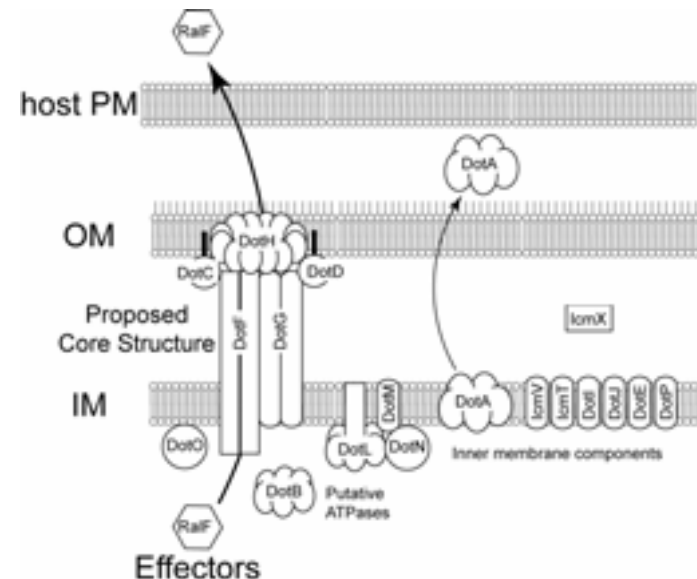


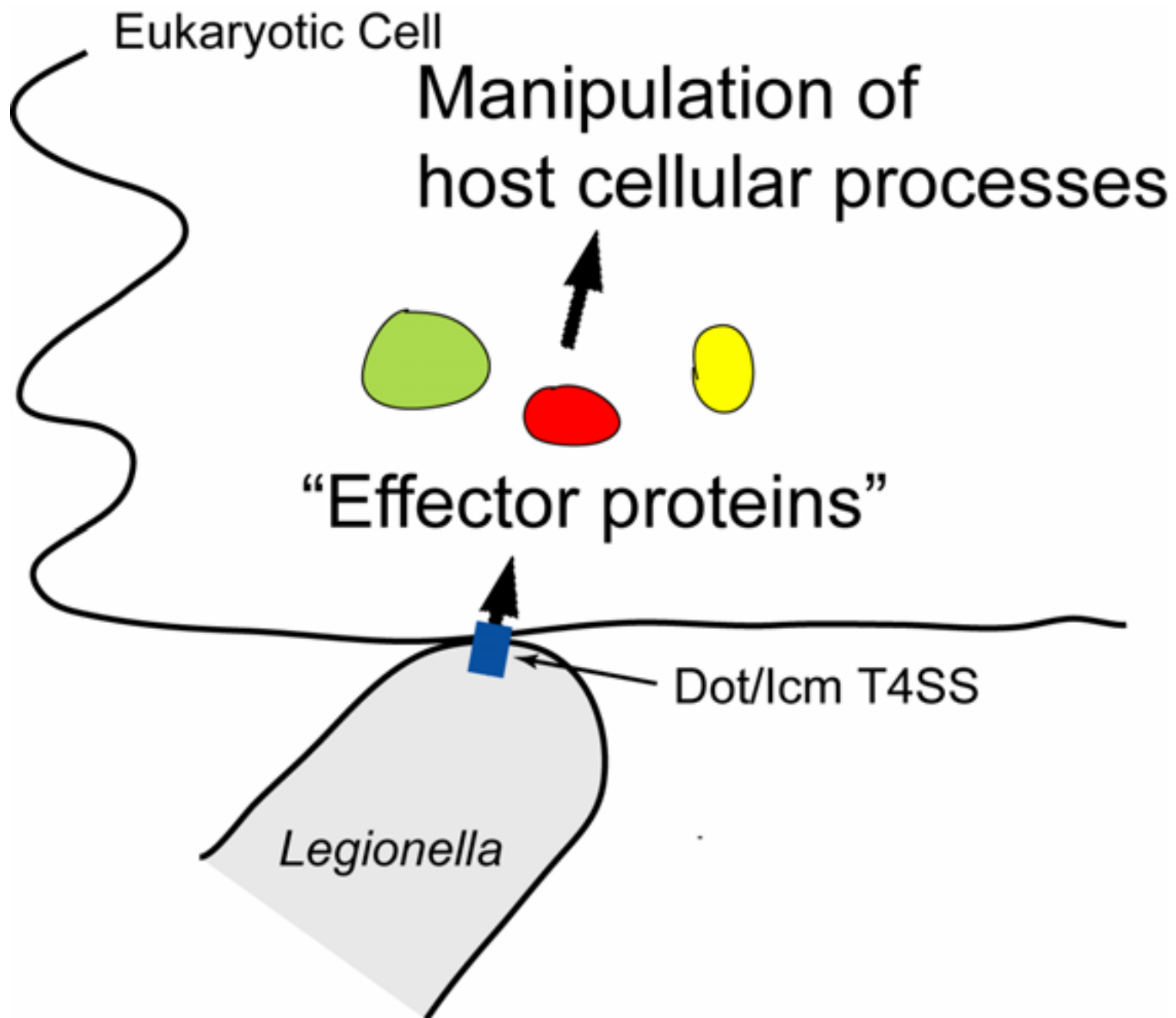
Legionella pneumophila

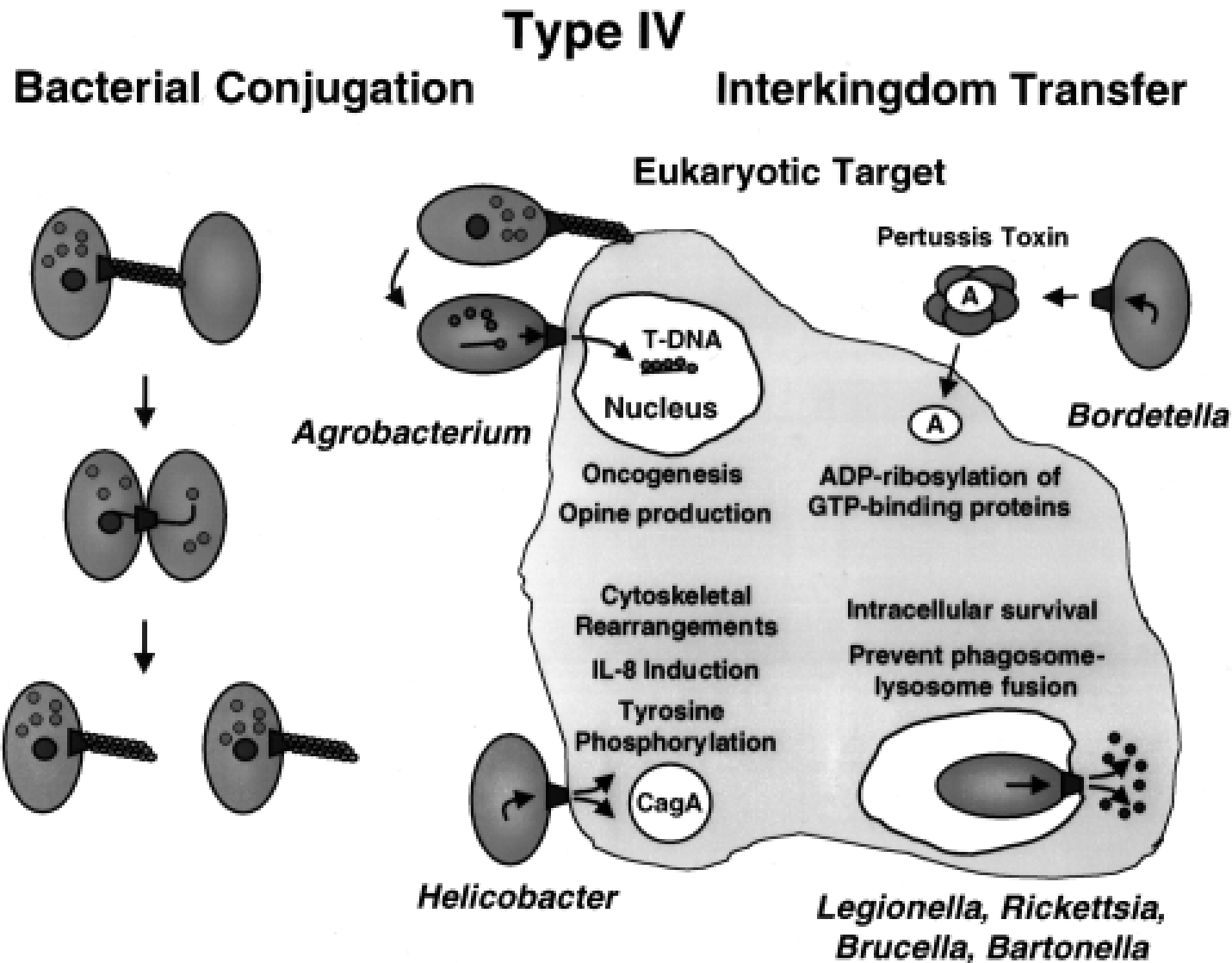
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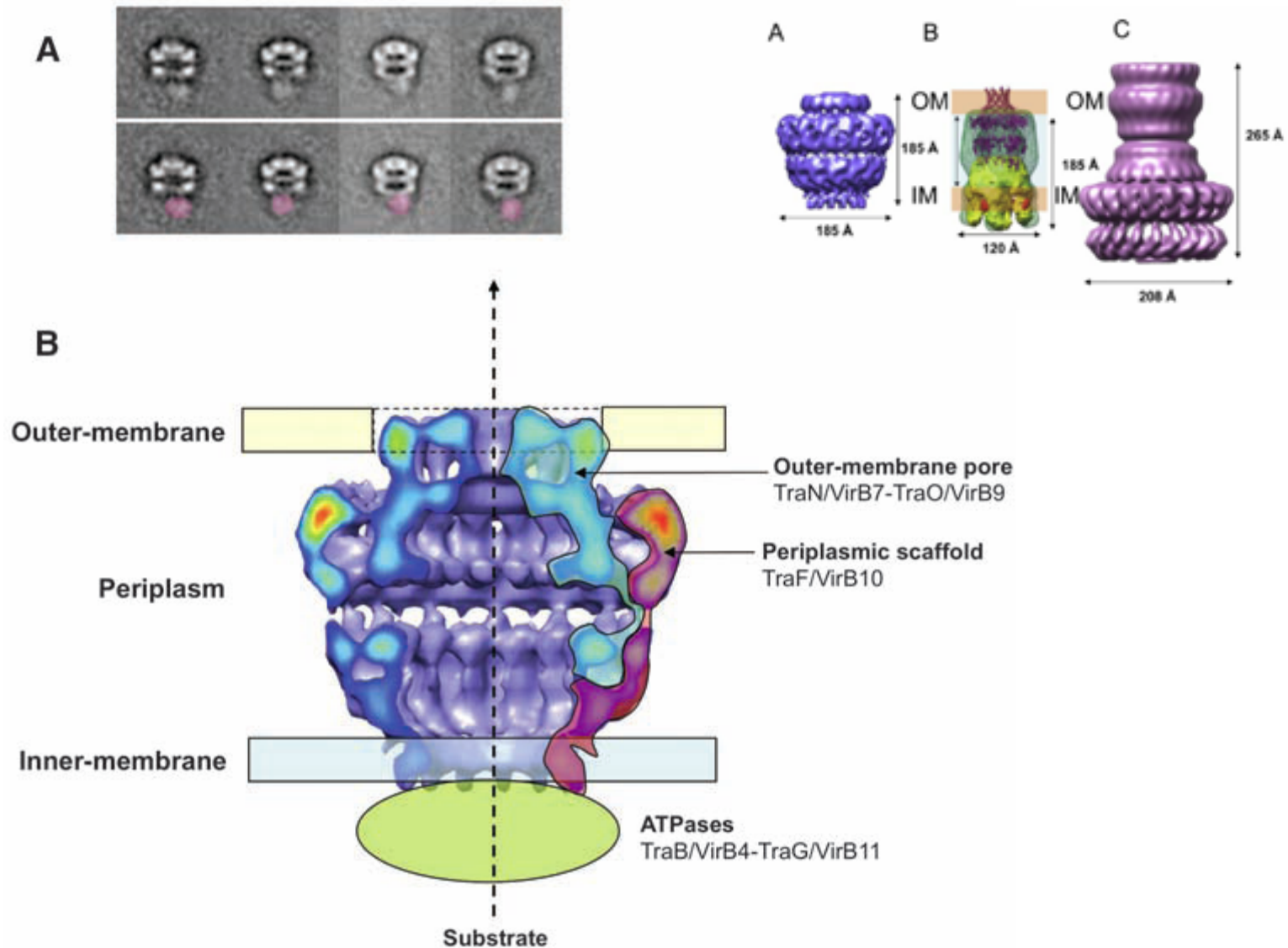






Christie, P. (2001) Mol. Microbiol. **40** (2), 294-305.

The core complex of the pKM101 T4SS



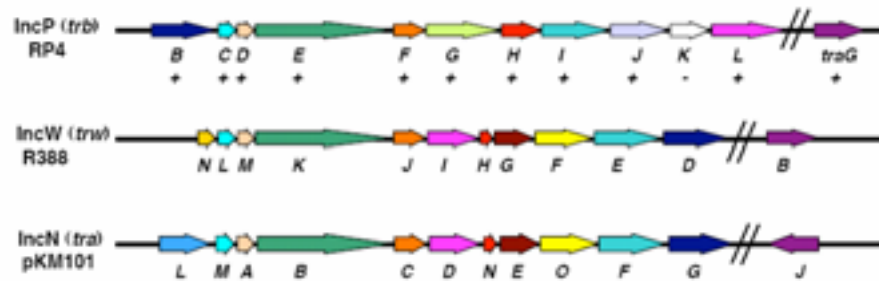
Type IVA

pKM101 plasmid

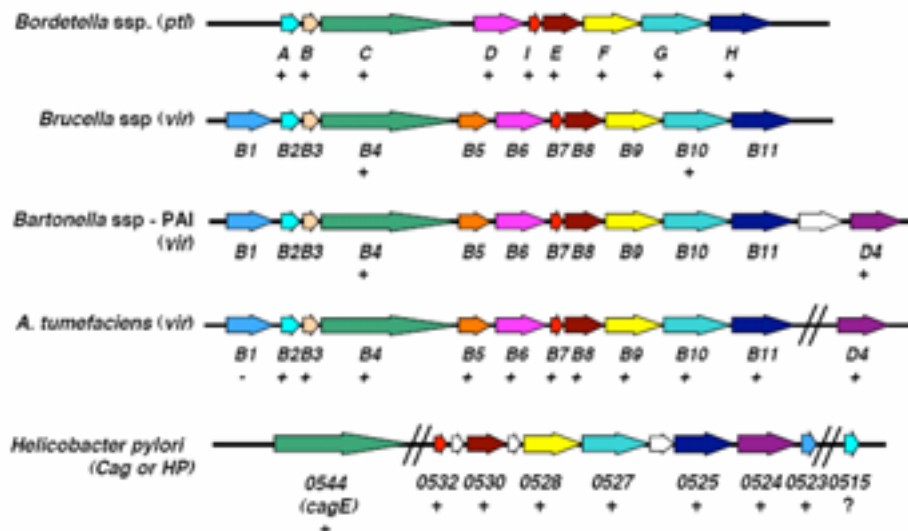
Agrobacterium tumefaciens

Helicobacter pylori

Conjugation systems



Type IVA secretion systems



Type IVB

Col1b plasmid

Legionella pneumophila

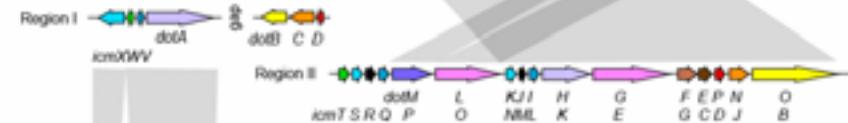
Coxiella burnetii

IncIプラスミド接合伝達系



IVB型分泌系

レジオネラ

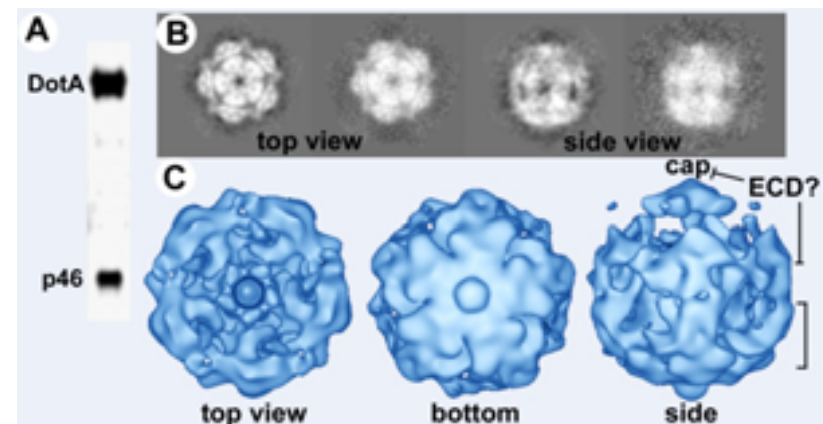
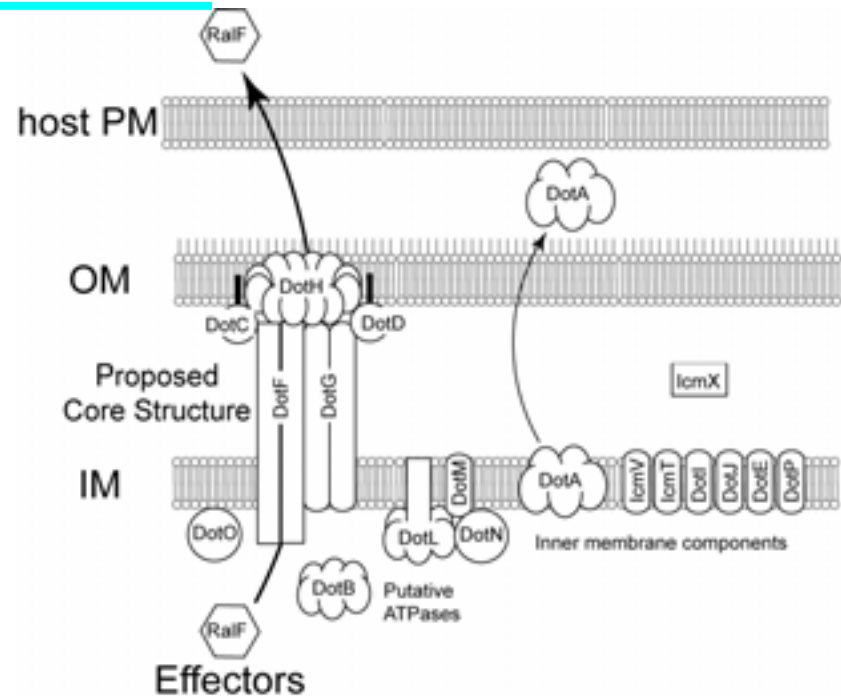


コクシエラ

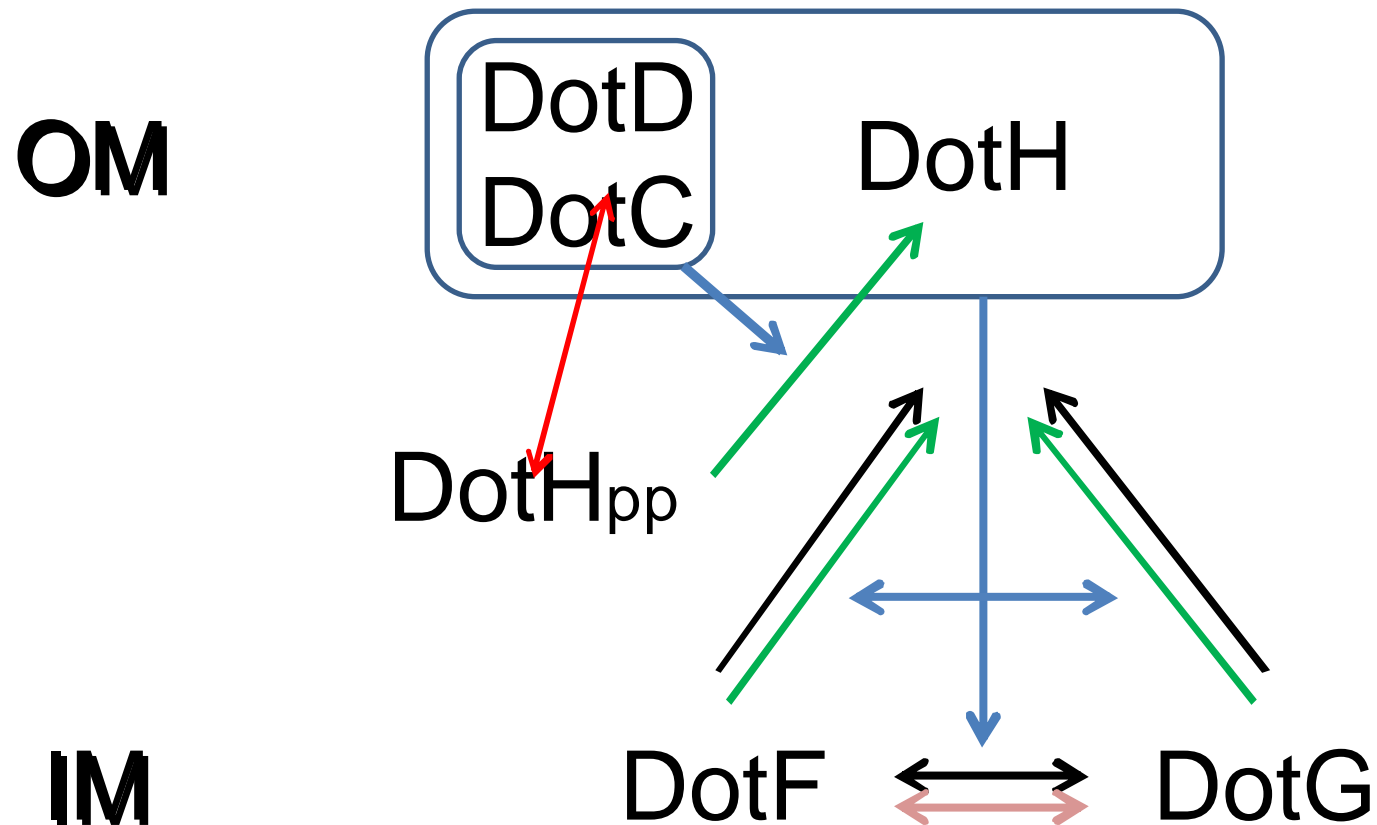


The *Legionella* Dot/Icm type IV secretion system

- Putative core components
 - DotH forms channel in OM?
 - DotC required for DotH sorting
 - DotD required for DotH sorting
 - DotG forms channel in IM?
 - DotF required for efficient core assembly?
- Inner membrane components
 - DotO/DotP/DotI/DotJ/DotE/IcmT ?
 - DotL/DotM/DotN coupling factor and associates
- Periplasmic component
 - IcmX ?
- Cytosolic components
 - DotB ATPase
 - IcmS/IcmW global chaperone?
 - IcmQ/IcmR ?
- Inner membrane / extracellular
 - DotA forms ring-like structure



Lines of evidence suggest a complex containing DotC/DotD/DotF/DotG/DotH.

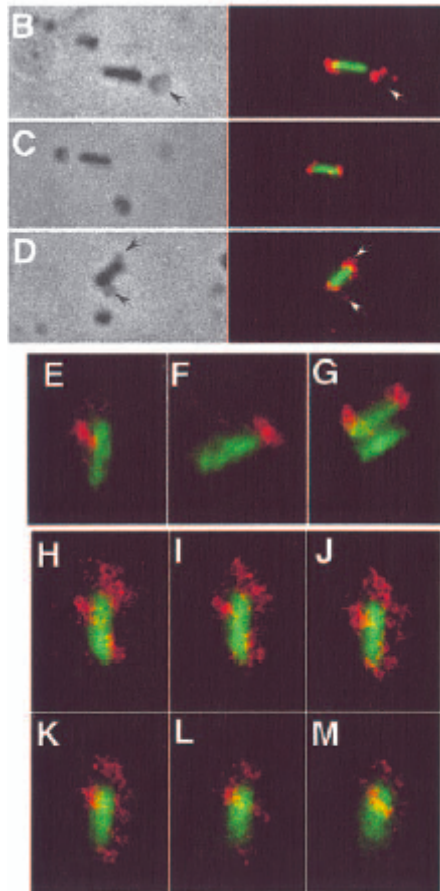


ColIP B2H Localization Functional analysis Biochemistry

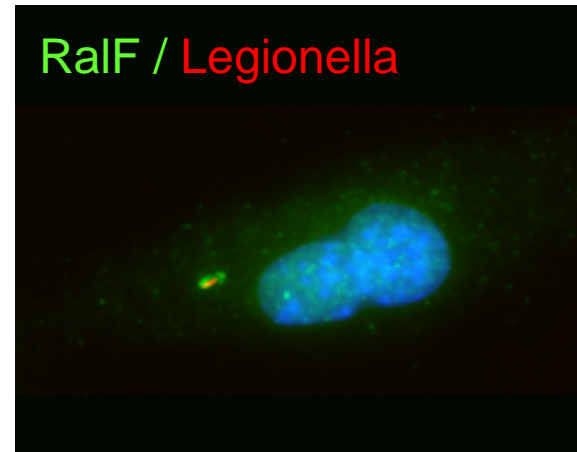
Does the Dot/Icm T4SS localize to cell poles?

Legionella effectors were found in the vicinity of the bacterial cell poles

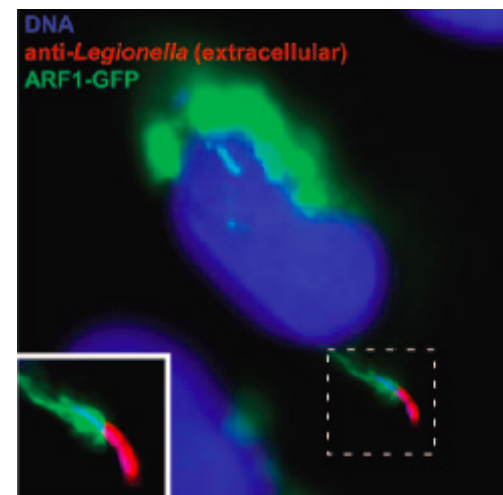
LidA on isolated *Legionella*-containing vacuole



Conover et al. *Mol. Microbiol.* 2003

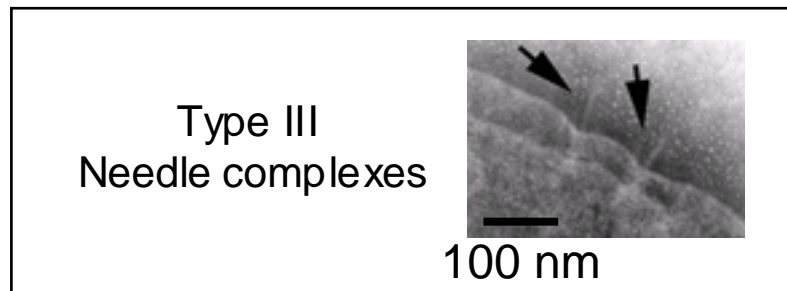
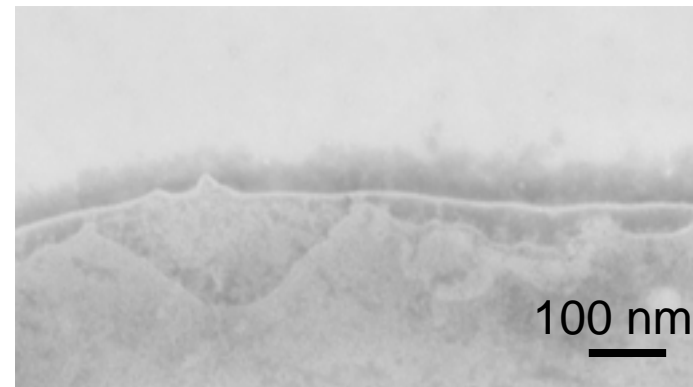
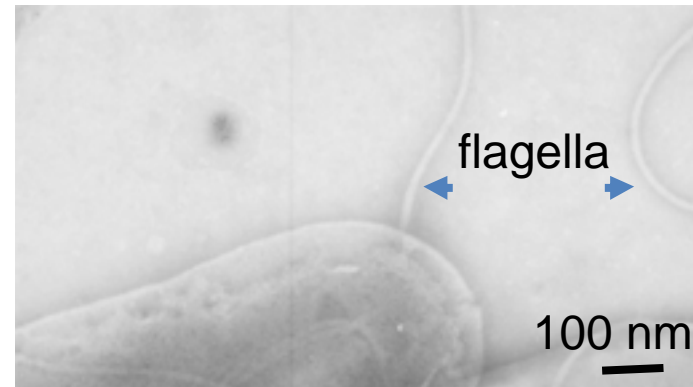
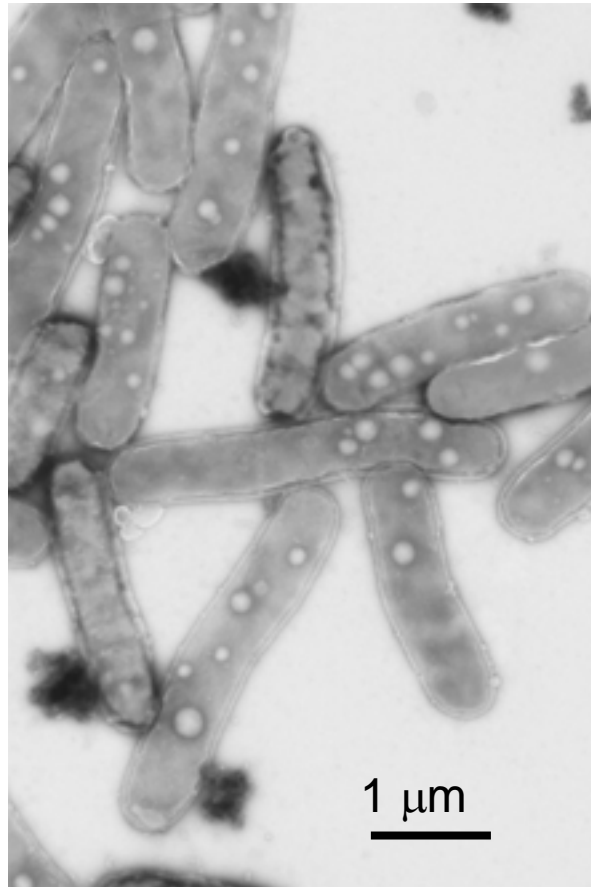


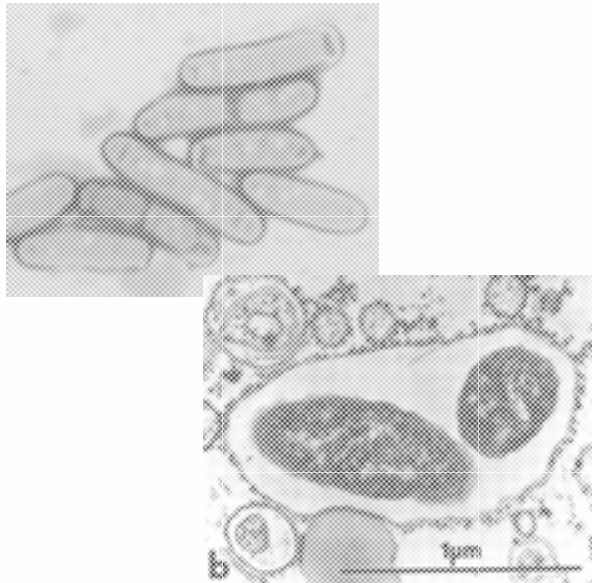
By H. Nagai
unpublished



By Jon Kagan
Nagai et al. *PNAS* 2005

No needle-like structure was found on *L. pneumophila* cell surface



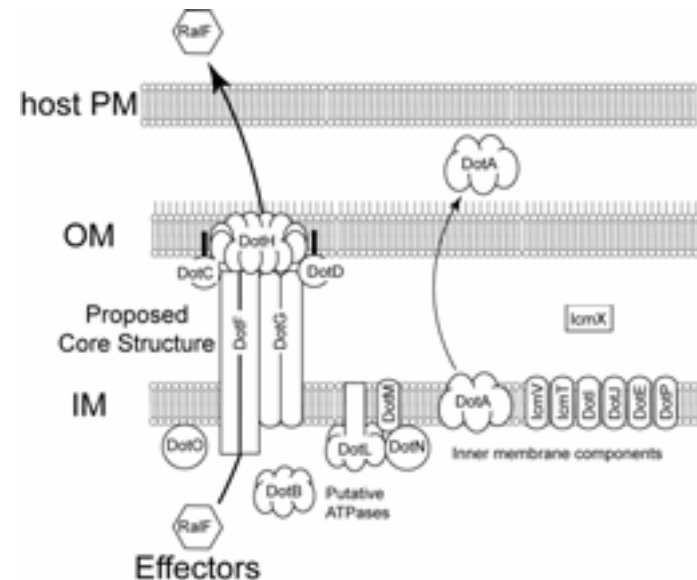


Legionella pneumophila

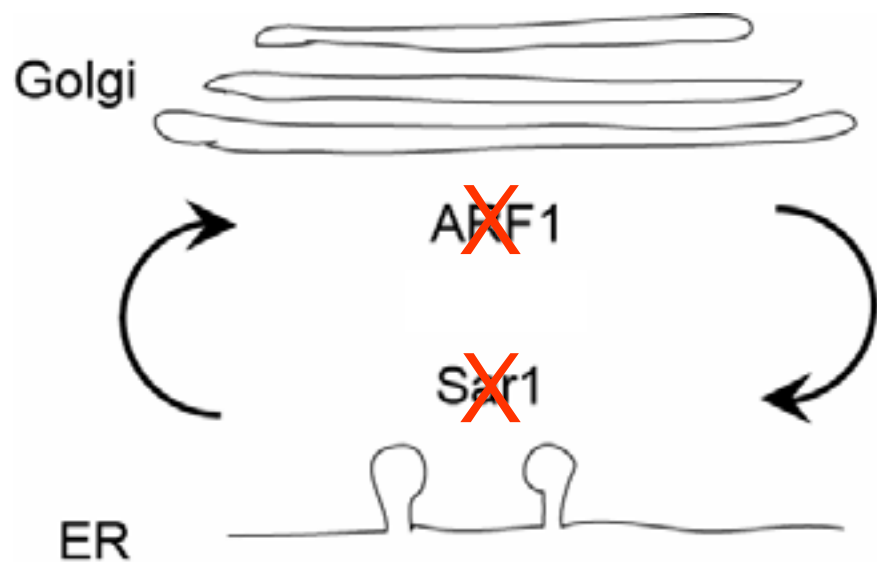
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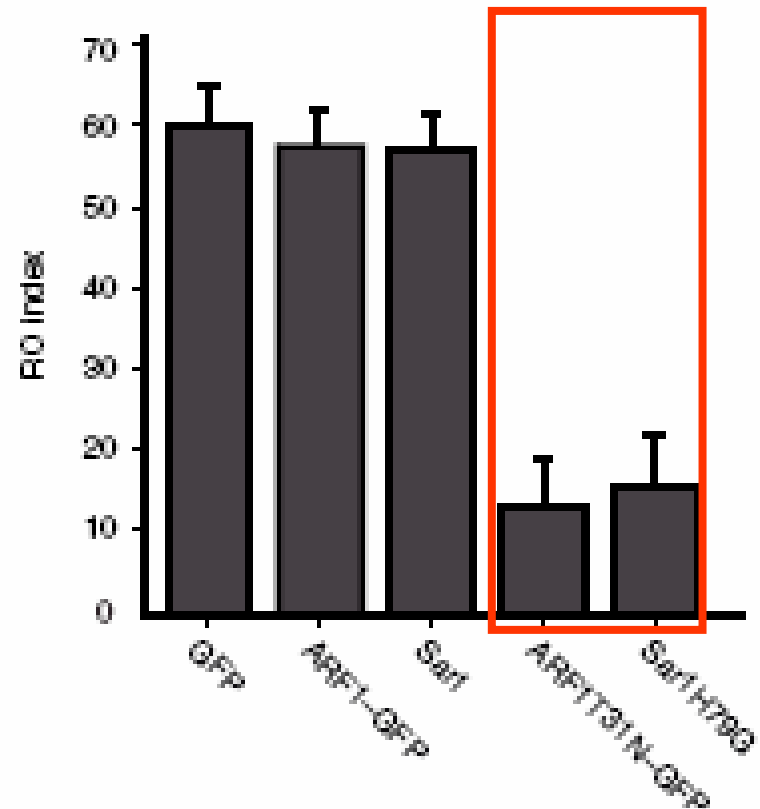
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Inhibition of Sar1 or ARF1 by d/n alleles, by knock-down or by ARF inhibitor BFA severely restrict intracellular growth of *Legionella*



b

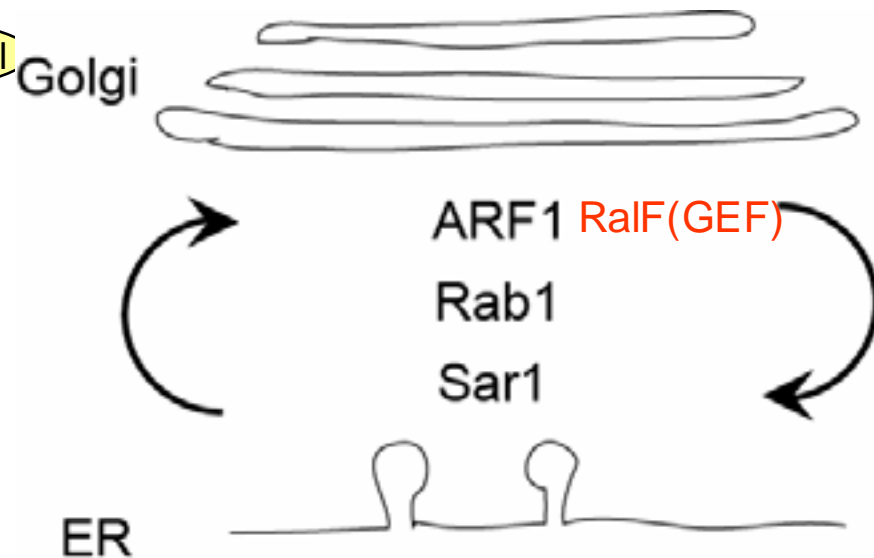
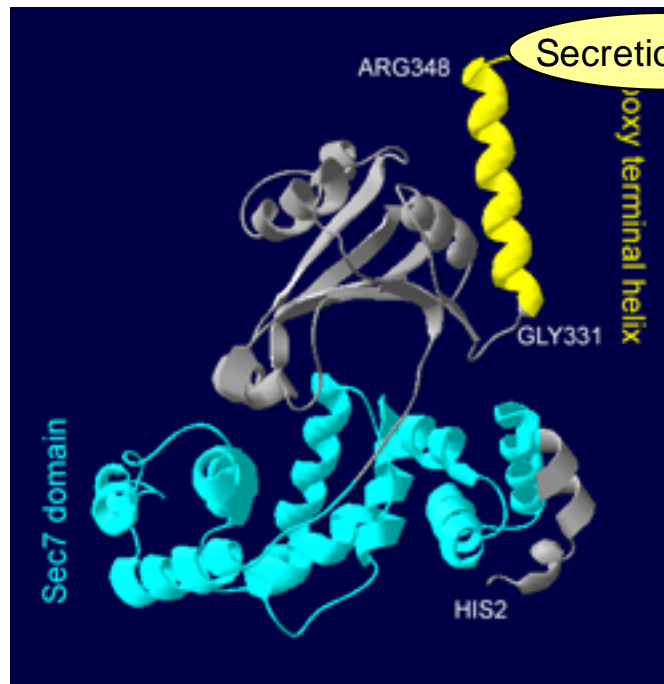


Jon Kagan and Craig Roy
Nat. Cell Biol. 2002

Legionella effector proteins and membrane traffic between ER-Golgi

RaIF

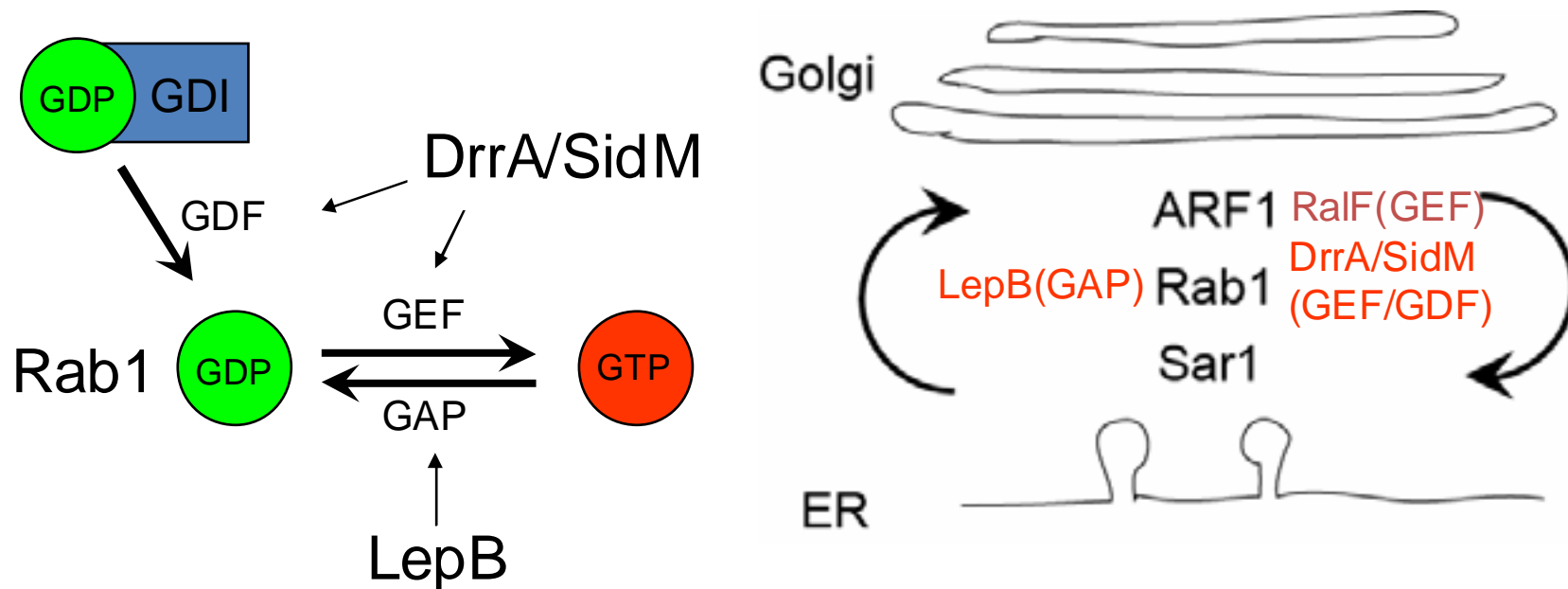
GEF for ARF1



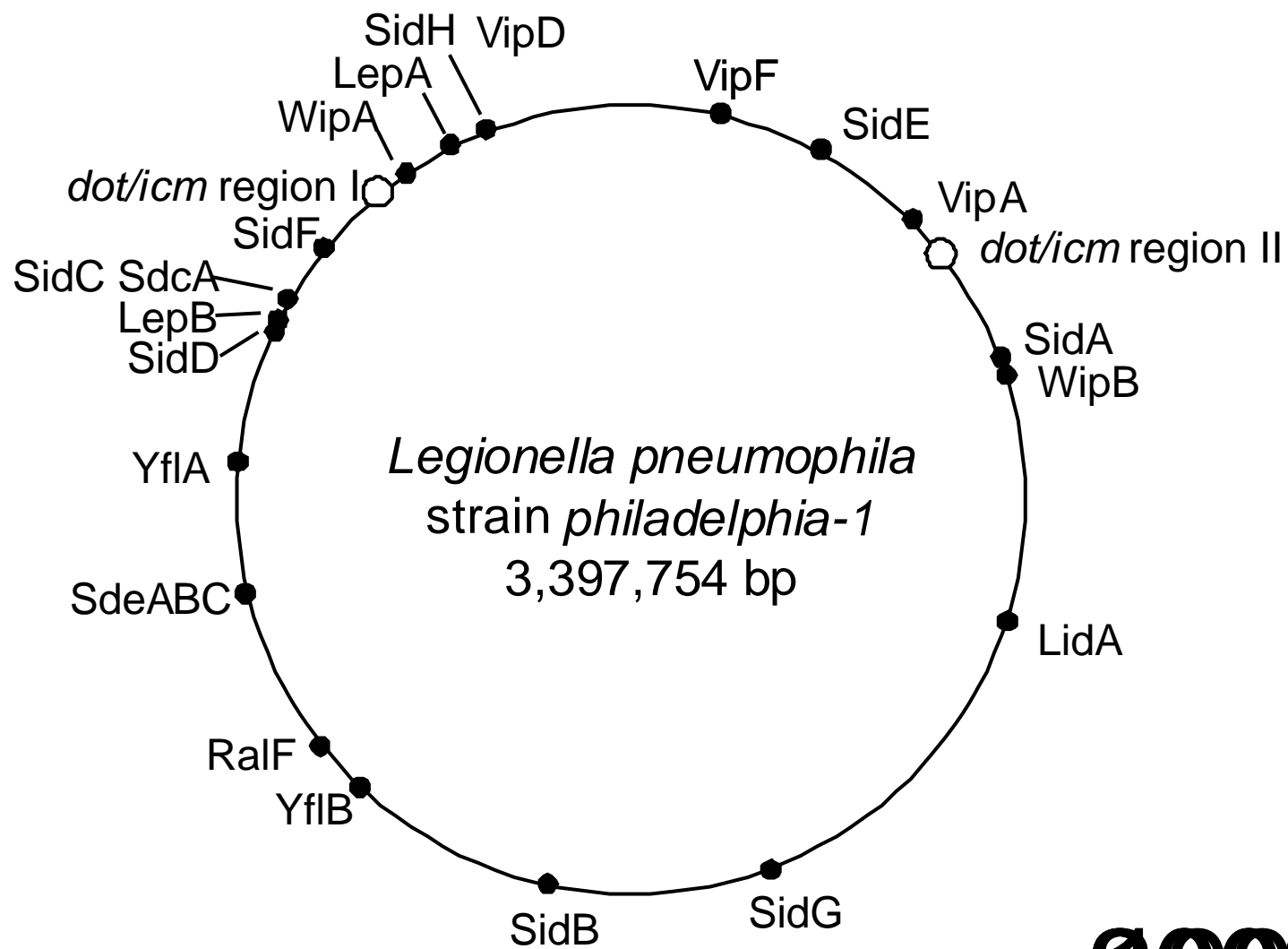
Nagai et al. Science 2002
Amor et al. J. Biol. Chem. 2005
Nagai et al. PNAS 2005

Legionella effector proteins and membrane traffick between ER-Golgi

DrrA/SidM and LepB
modulate Rab1 activity.



Murata et al. Nat. Cell Biol. 2006
Machner et al. Dev. Cell 2006
Ingmundson et al. Nature 2007
Machner et al. Science 2007

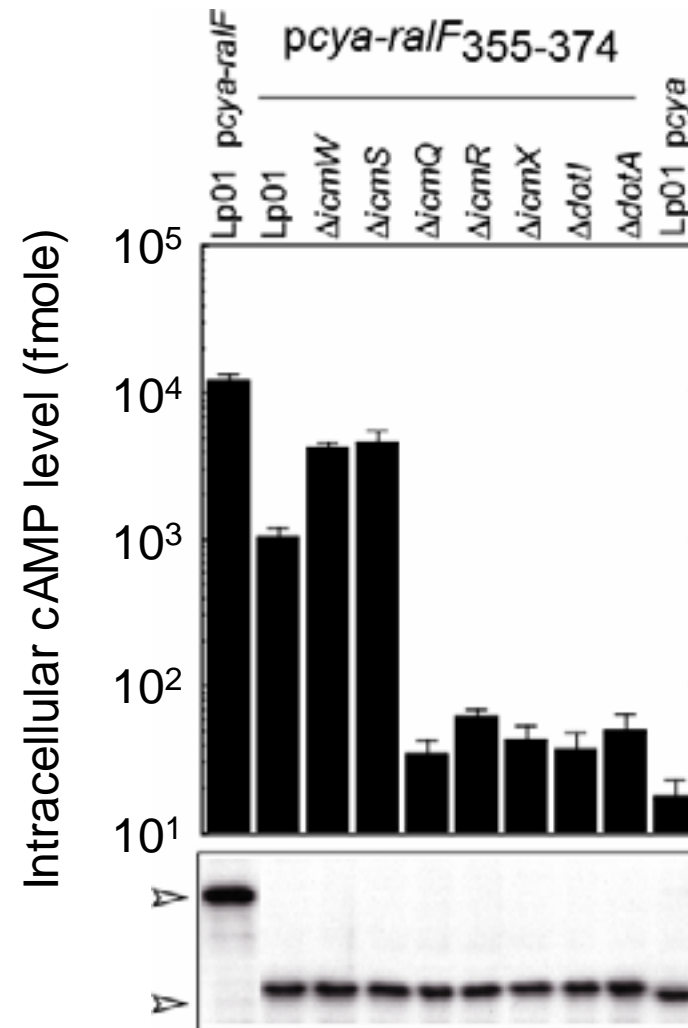


~2004

Towards high-throughput systematic screening of effector proteins.

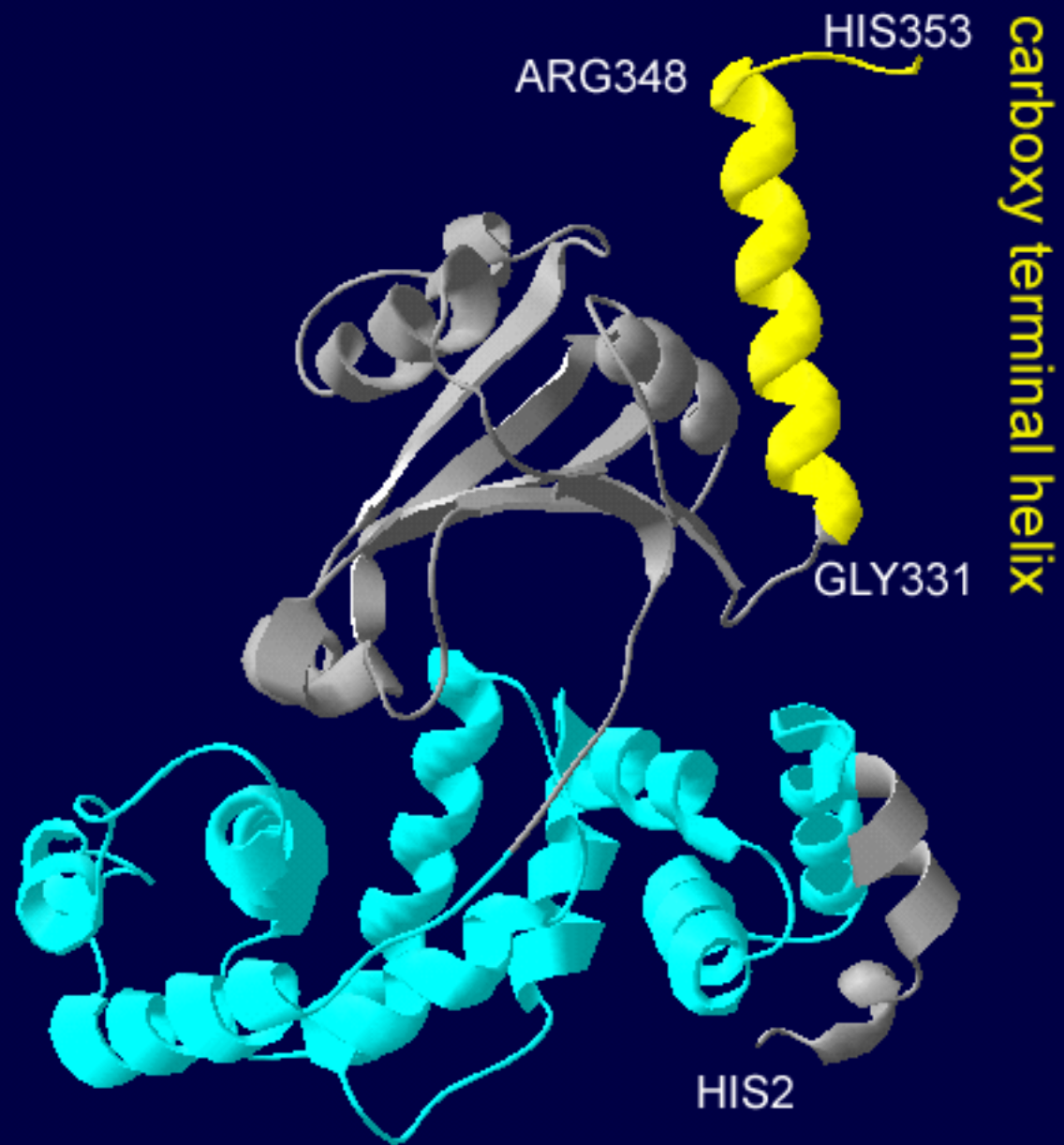
- Establish a reporter system to detect protein translocation to host cell cytoplasm.
 - Unavailability of such a system was a bottle-neck of the *Legionella* research.
- Analyses of secretion signals of known effector proteins.
 - Together with genome sequence completed 2004, the outcome will help *in silico* screening of putative effector proteins.

Carboxy terminal 20 amino acid region of RalF is sufficient for translocation by the Dot/Icm TFSS.



Nagai *et al.* PNAS 2005.

Sec7 domain



Amor et al. *J. Biol. Chem.* 2005.

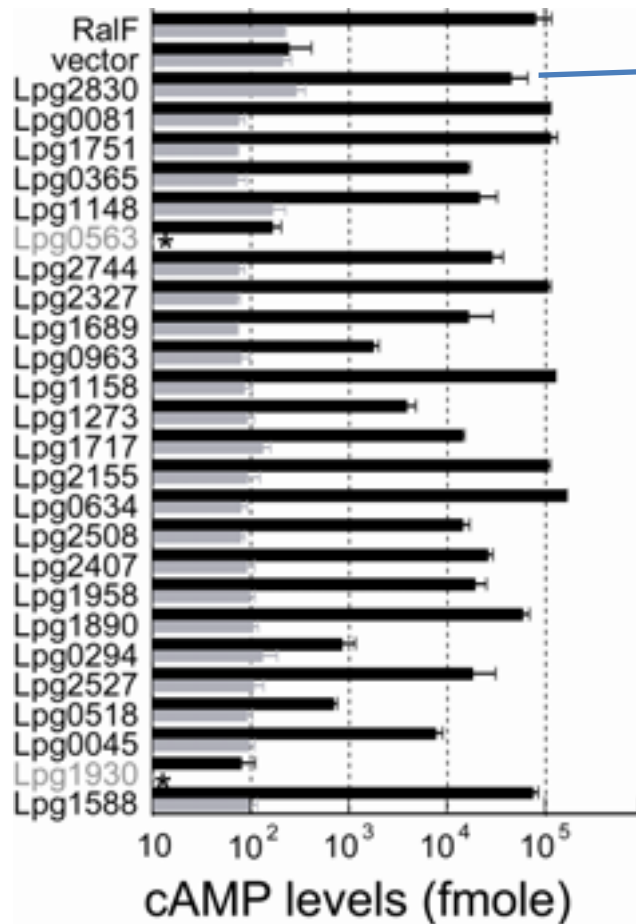
Hydrophobicity of the third last residue appeared to be important for **RalF** translocation by the *Legionella* Dot/Icm secretion system.

% Translocation

RalF	TIERNLALKEGVPKDPDAEMQKEKGRQ L KF	100
1-373	TIERNLALKEGVPKDPDAEMQKEKGRQ L K	24
1-372	TIERNLALKEGVPKDPDAEMQKEKGRQ L	0.5
1-371	TIERNLALKEGVPKDPDAEMQKEKGRQ	0
L372F	TIERNLALKEGVPKDPDAEMQKEKGRQ F KF	99
L372P	TIERNLALKEGVPKDPDAEMQKEKGRQ P KF	89
L372V	TIERNLALKEGVPKDPDAEMQKEKGRQ V KF	20
L372A	TIERNLALKEGVPKDPDAEMQKEKGRQ A KF	18
L372S	TIERNLALKEGVPKDPDAEMQKEKGRQ S KF	2.7
L372T	TIERNLALKEGVPKDPDAEMQKEKGRQ T KF	0.3
K373A	TIERNLALKEGVPKDPDAEMQKEKGRQ L AF	81
K373E	TIERNLALKEGVPKDPDAEMQKEKGRQ L E F	93
K373R	TIERNLALKEGVPKDPDAEMQKEKGRQ L R F	125

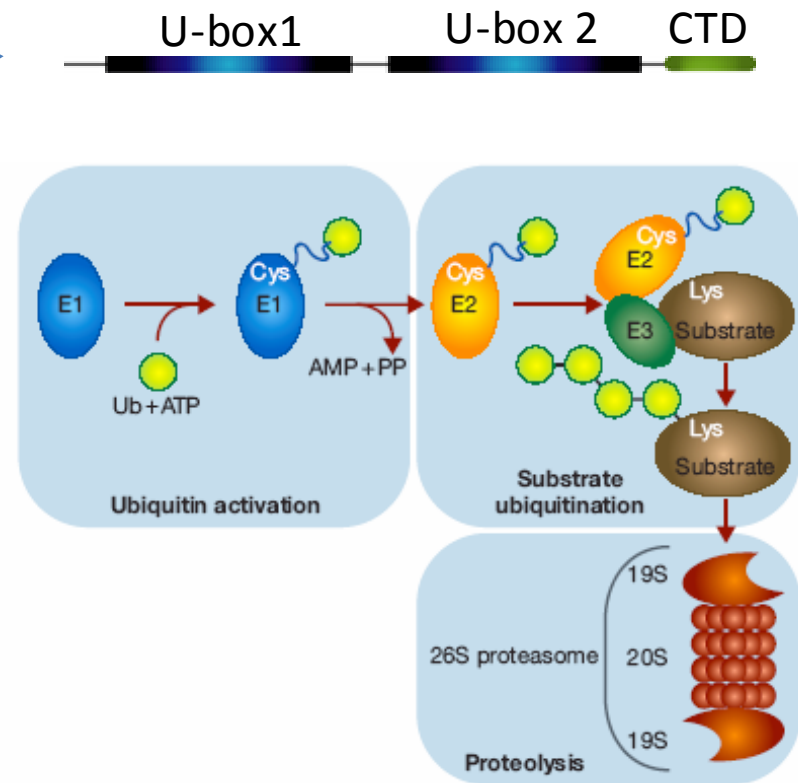
Nagai et al. PNAS 2005.

Dot/Icm substrate proteins identified in our lab.



LubX:

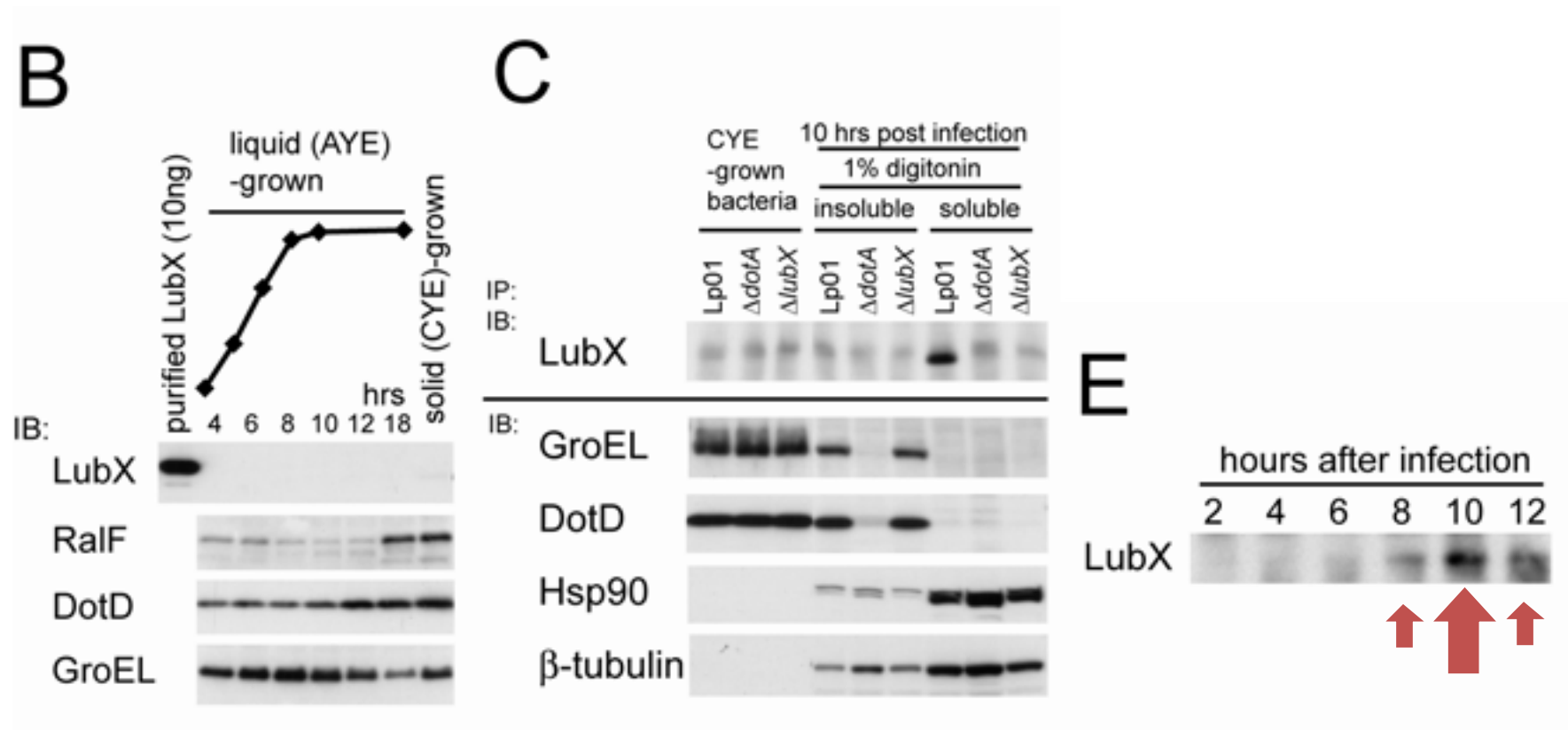
Legionella U-box-containing protein



Question:

Is LubX an E3 ubiquitin ligase?

Expression of LubX is induced upon infection, and LubX level within the host cells peaks at a late stage of infection.

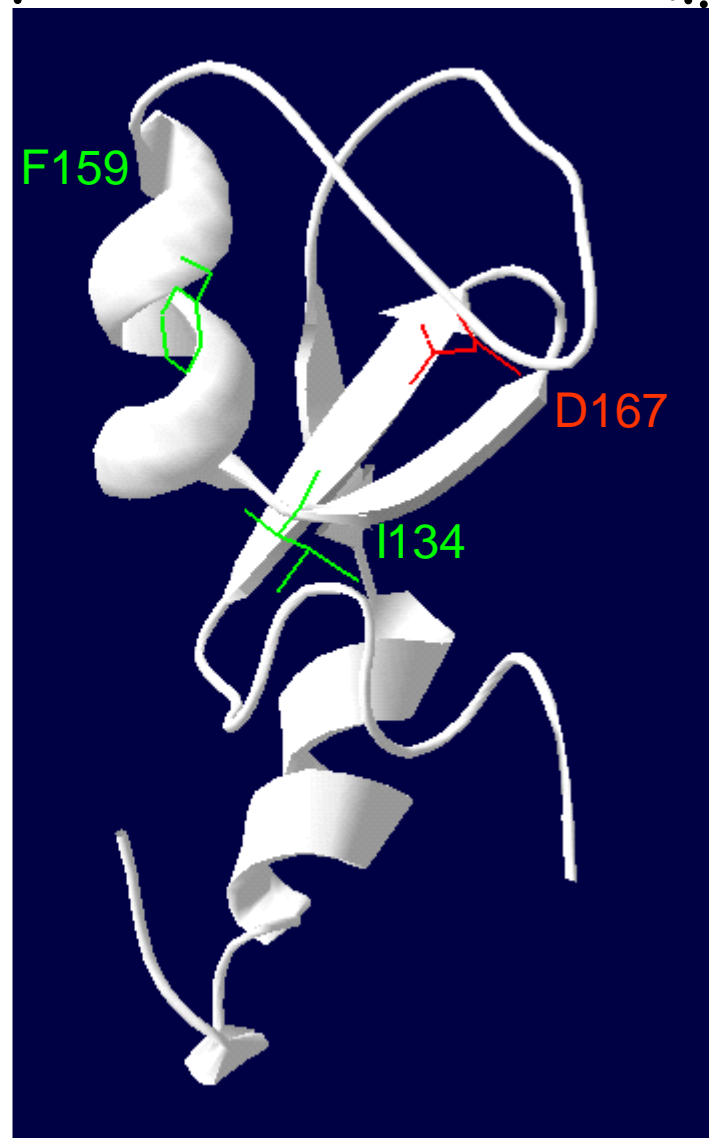
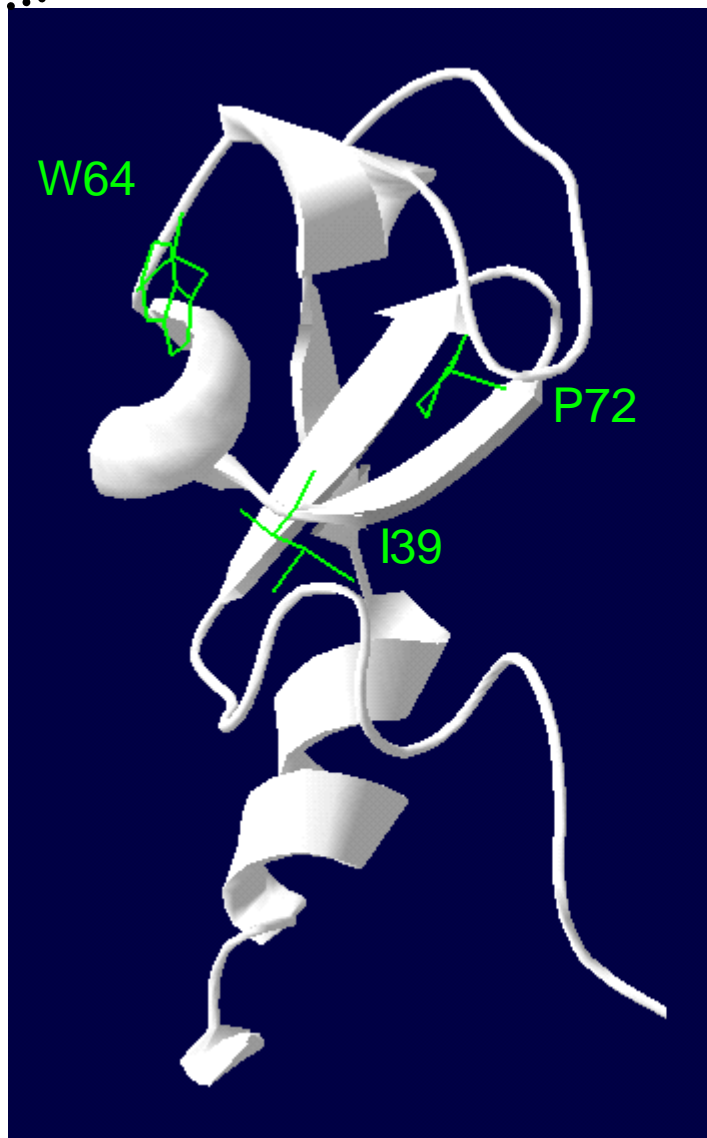


LubX

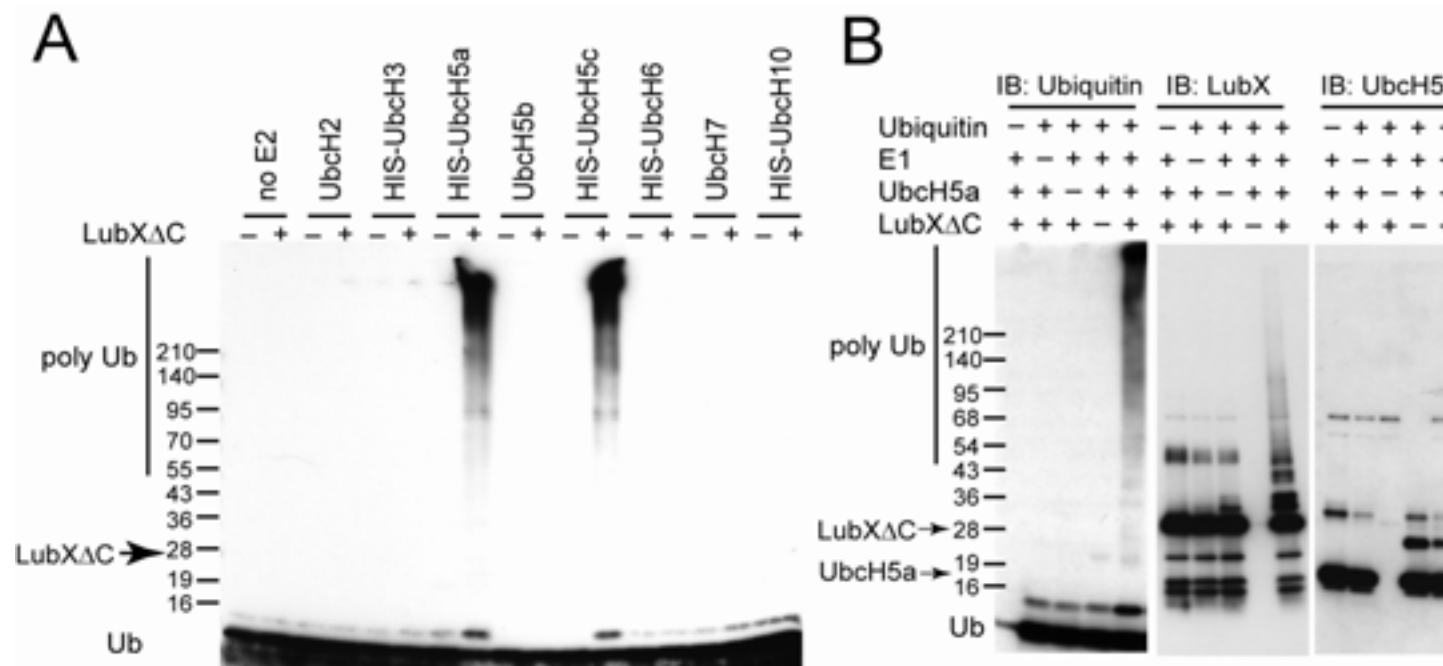
U-box 1

U-box 2

CTD



LubX functions as an E3 Ubiquitin ligase in conjunction with the E2 enzymes UbcH5a or UbcH5c.

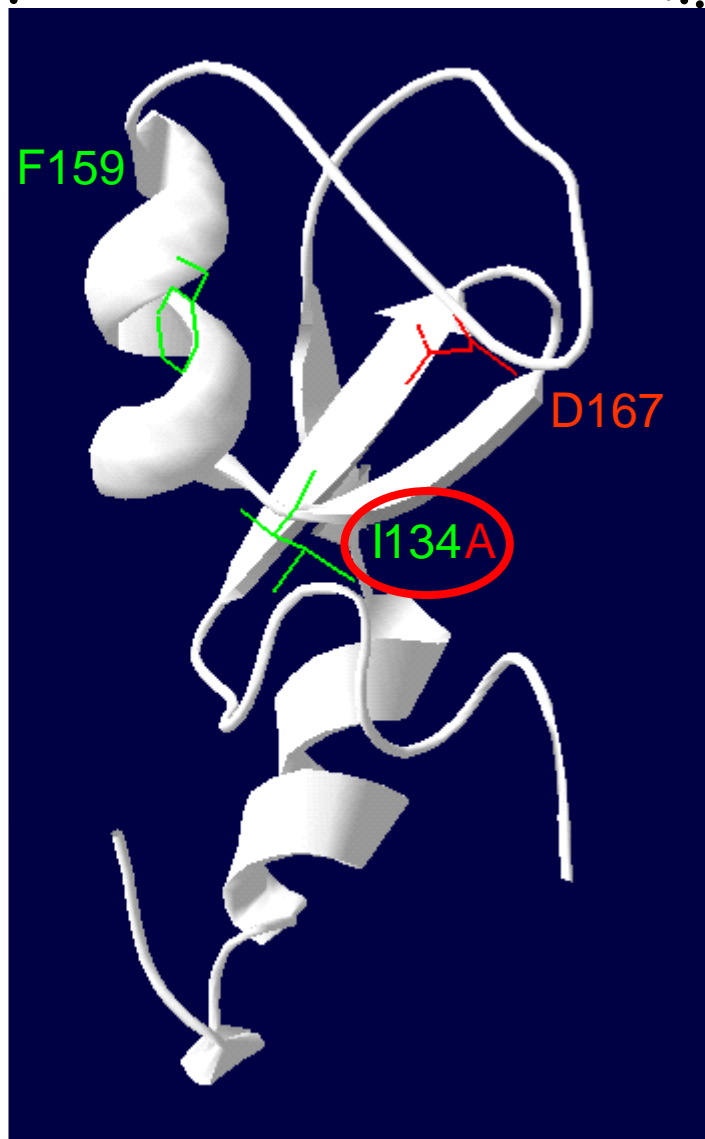
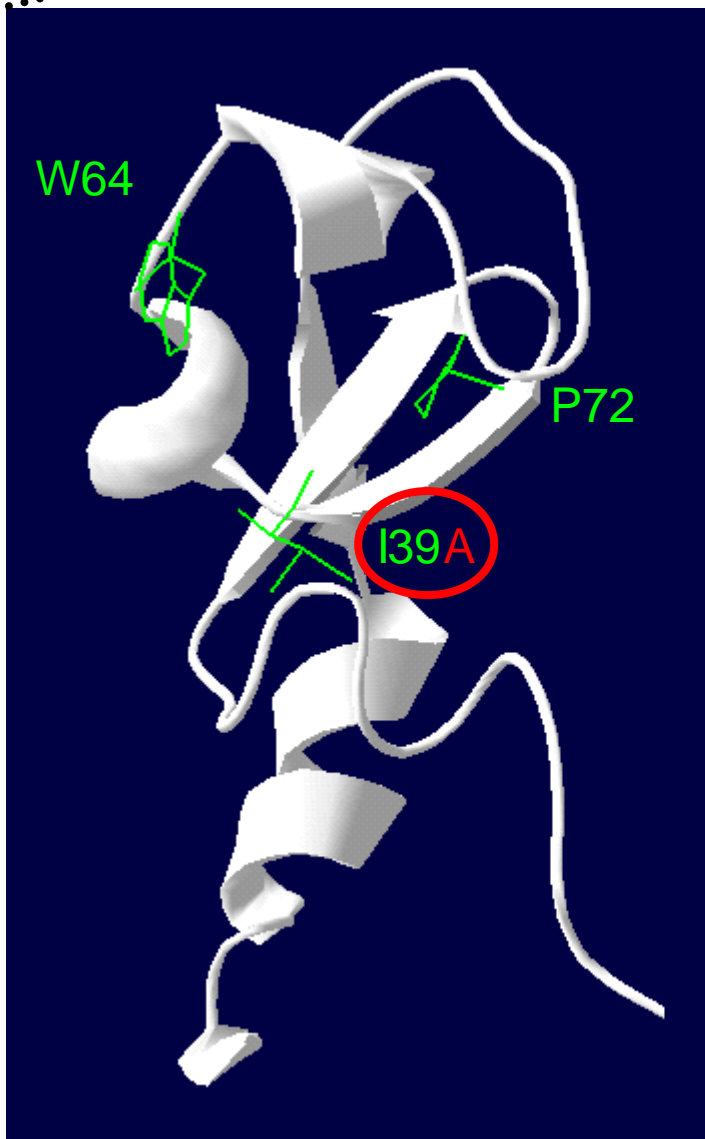


LubX

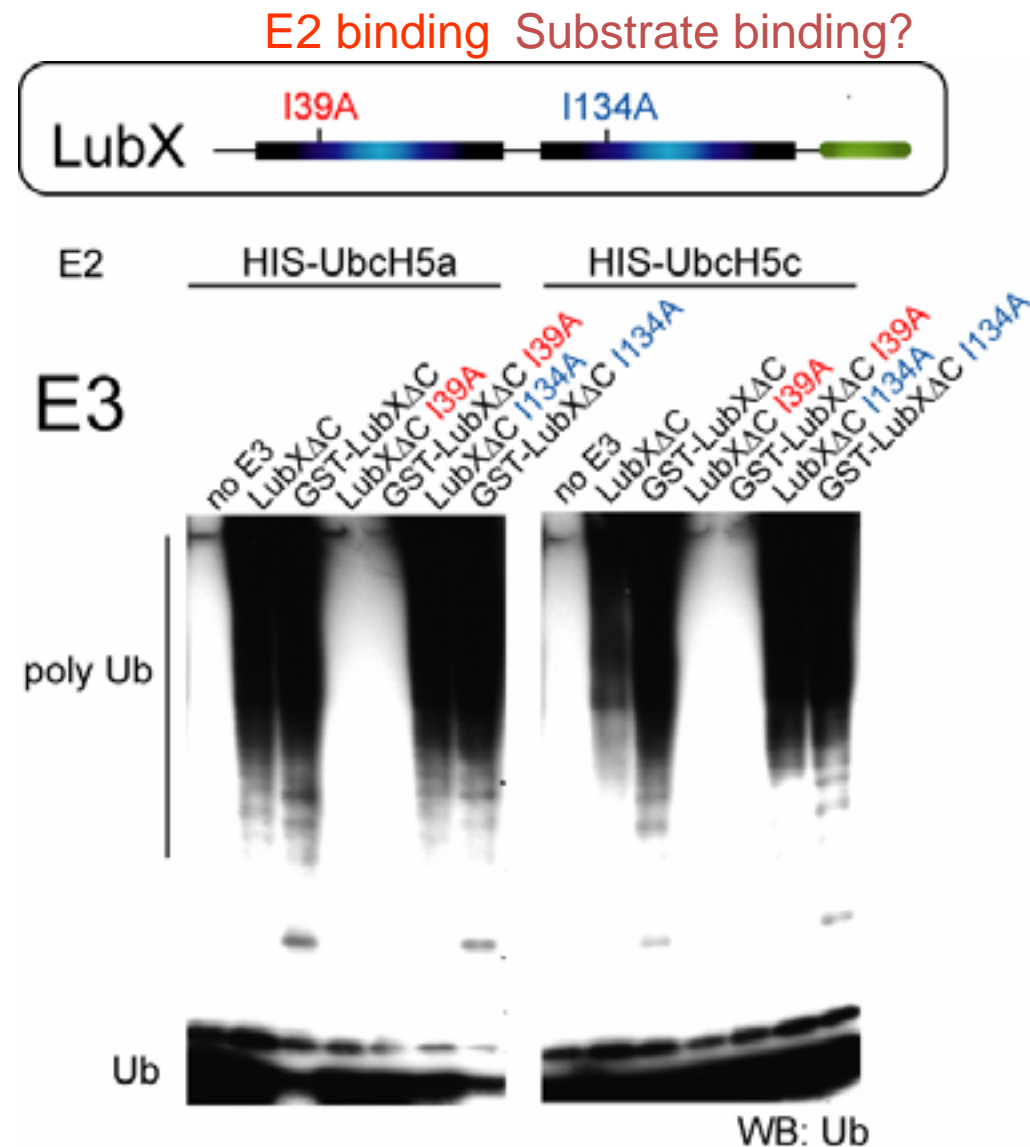
U-box 1

U-box 2

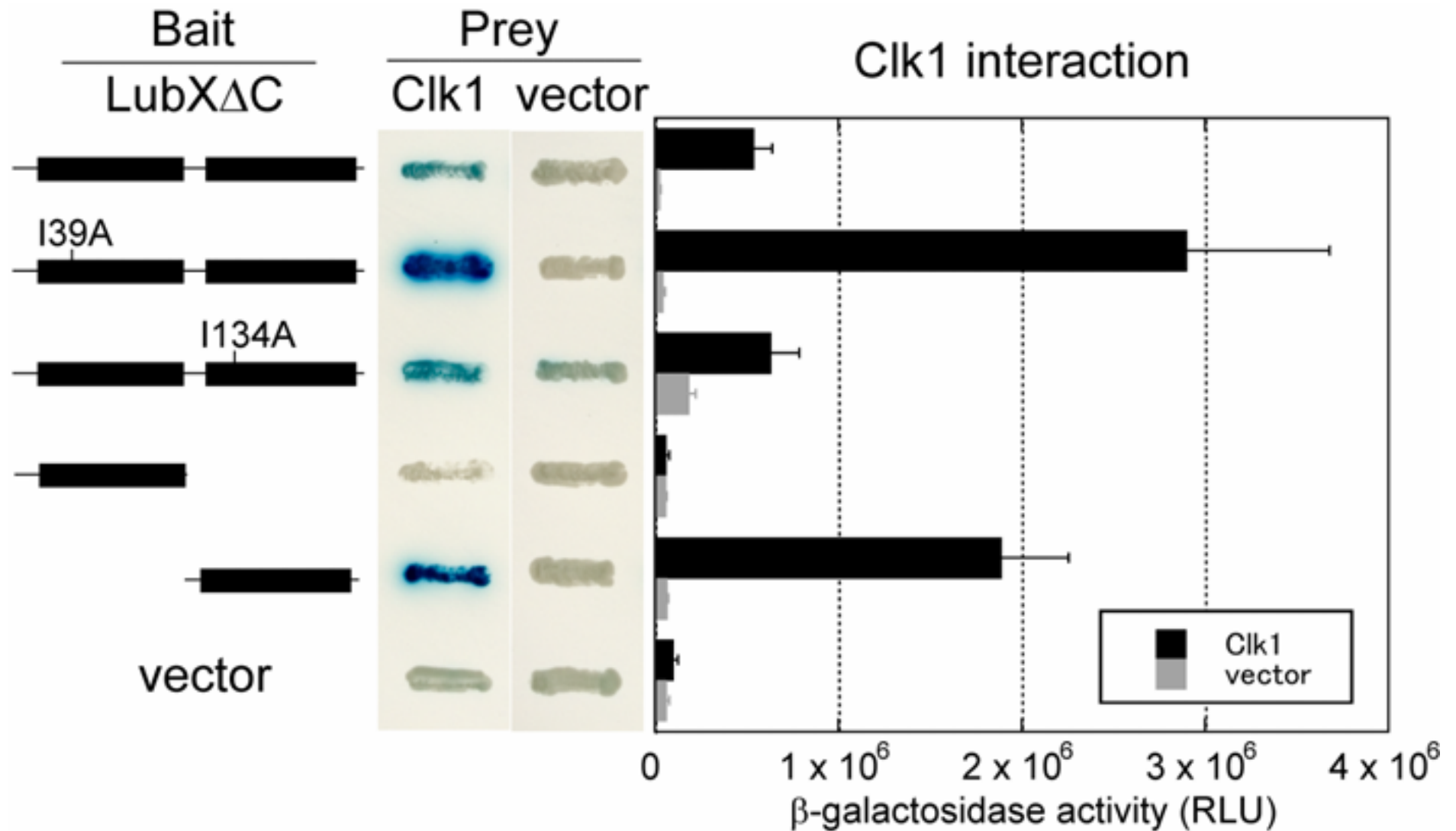
CTD



U-box 1 is essential to E3 Ubiquitin ligase activity.



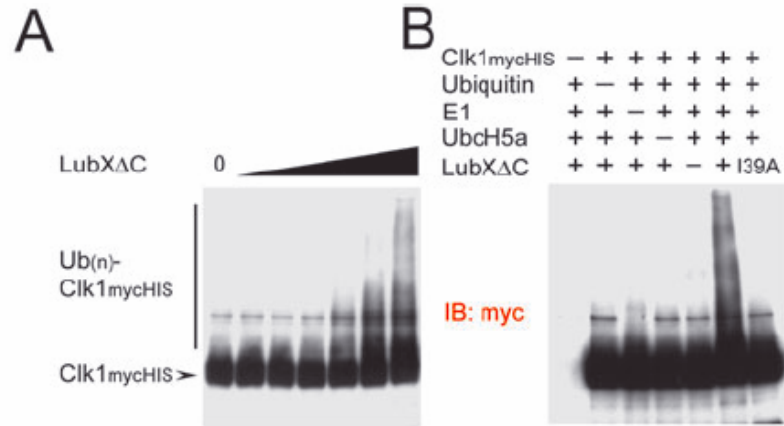
Two hybrid interaction of Clk1 and the LubX U-box 2.



LubX U-box 2 functions as a substrate binding site.



Clk1 is a substrate of LubX



Direct interaction of Ubox2 and Clk1

