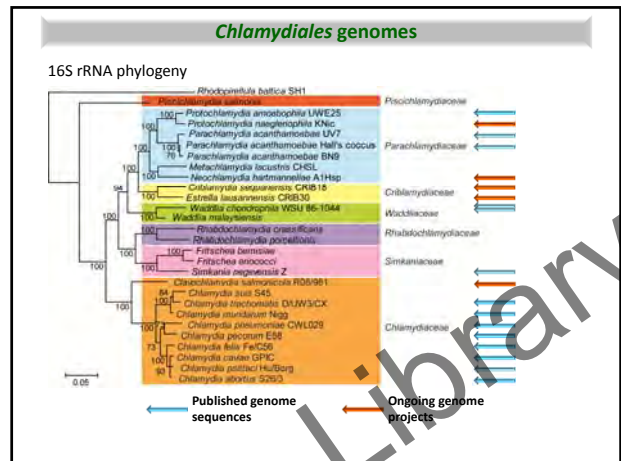


Genomics of *Chlamydia*-related bacteria

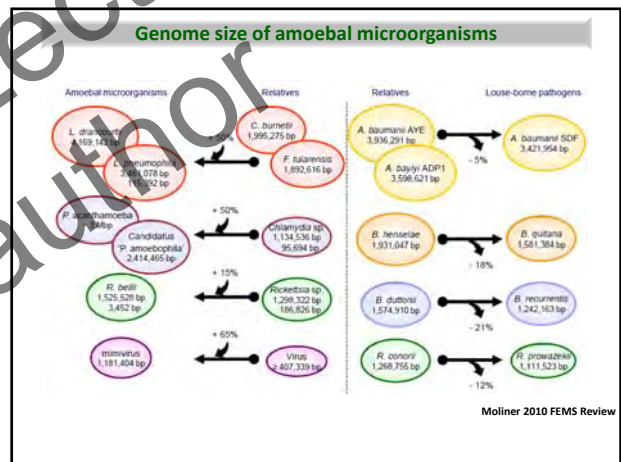
Claire Bertelli

Intracellular Bacteria: From Biology to Clinic
Villars-sur-Ollon, August 2013



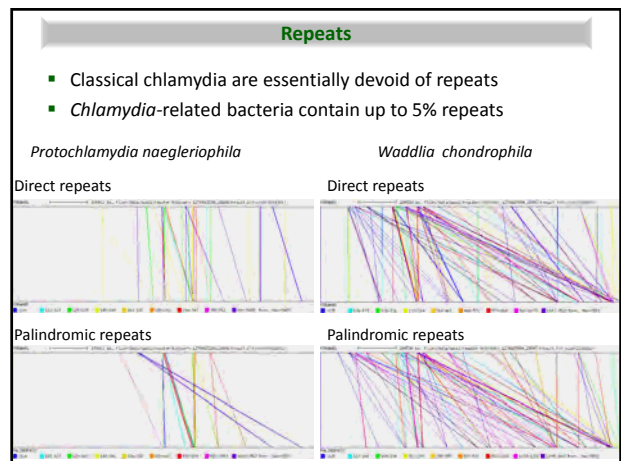
Chlamydiales genomes

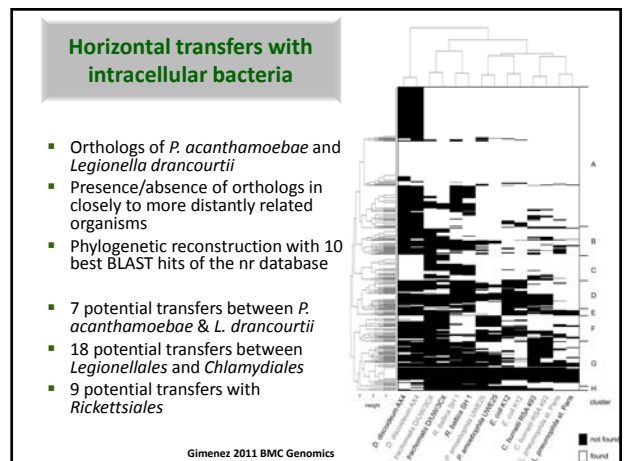
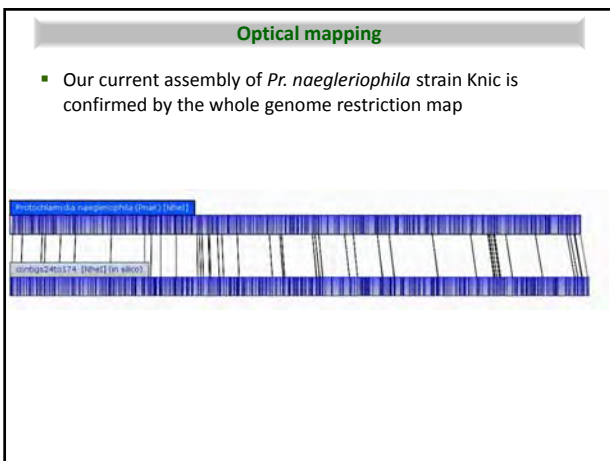
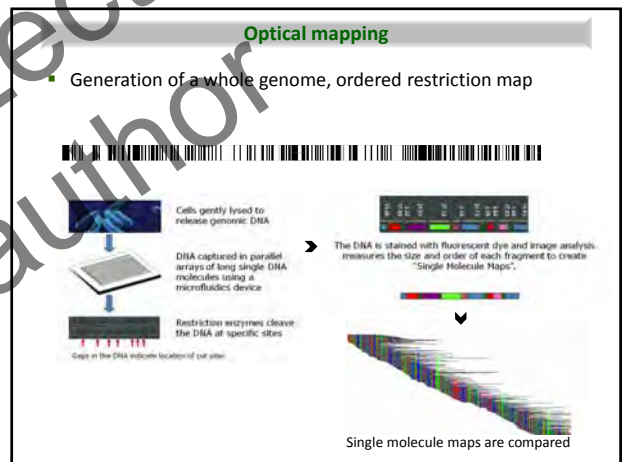
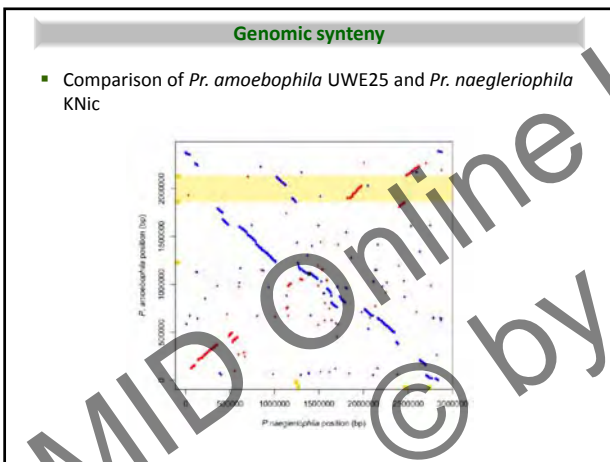
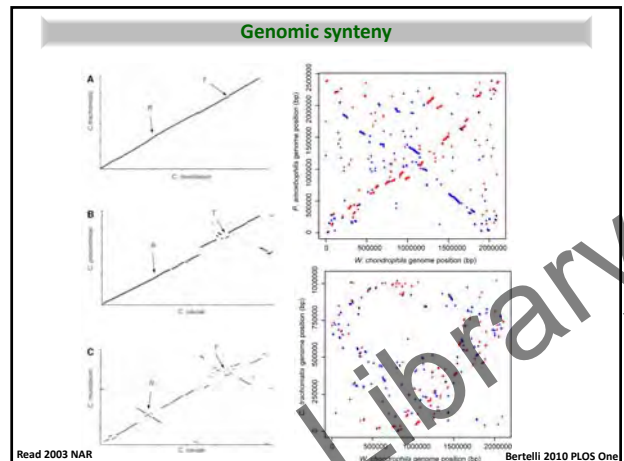
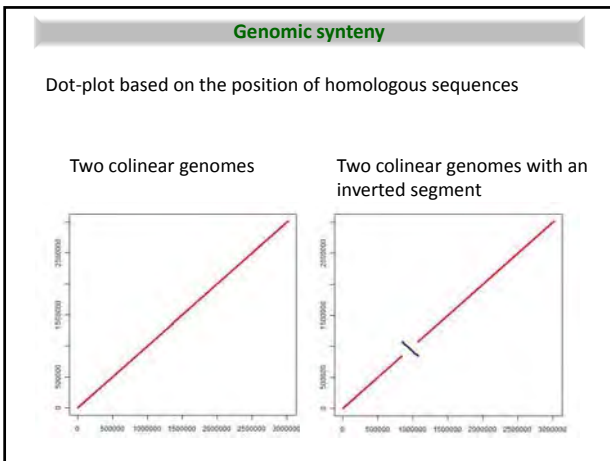
Family	Species	Complete / draft	Representative strain	Genome size (bp)	G+C content	Proteins	tRNA	rRNA	Plasmid size (bp)
Chlamydiaceae	<i>Chlamydia trachomatis</i>	17/6	D/UW-3/CX	1'042'519	41.3%	895	37	6	7'493*
	<i>Chlamydia muridarum</i>	1/2	Nigg	1'072'950	40.3%	903	37	6	7'501
	<i>Chlamydia suis</i>								
	<i>Chlamydia pneumoniae</i>	5	CWL029	1'230'230	40.6%	1'123	38	3	
	<i>Chlamydia pecorum</i>	1	ES8	1'106'197	41.1%	988	38	3	
	<i>Chlamydia felis</i>	1	Fe/C-56	1'166'829	39.4%	1'005	38	3	7'552
	<i>Chlamydia caviae</i>	1	GPIC	1'173'390	39.2%	988	38	3	7'966
	<i>Chlamydia abortus</i>	1/1	S26/3	1'144'377	39.5%	932	38	3	
	<i>Chlamydia psittaci</i>	6/1	68C	1'171'860	39.1%	957	38	3	7'553
	Waddliaceae	<i>Waddlia chondrophila</i>	1/1	WSU86-1044	2'116'312	43.8%	1'934	37	6
Criblamydiaceae	<i>Criblamydia sequanensis</i> *	(1)	CRIB-18	2'368'813	38.2%	2'498	40	12	89'525
	<i>Estrella lausannensis</i> *	(1)	CRIB-30	2'315'214	48.2%	2'416	40	9	9'136
Parachlamydiaceae	<i>Parachlamydia acanthamoebae</i>	1/1	UV-7	3'072'383	39.0%	2'789	40	10	
	<i>Protochlamydia amoebophila</i>	1	UWE25	2'414'465	34.7%	2'031	35	9	
	<i>Protochlamydia naegleriophila</i>	(1)	Knic	2'900'000	42.4%	<3'000	48	12	125'700
	<i>Neochlamydia bartmannellae</i>	(1)		3'078'000	37.9%	2'543	37	6	
	Simkaniaceae	<i>Simkania negevensis</i>	1	Z	2'496'987	41.8%	2'519	35	3

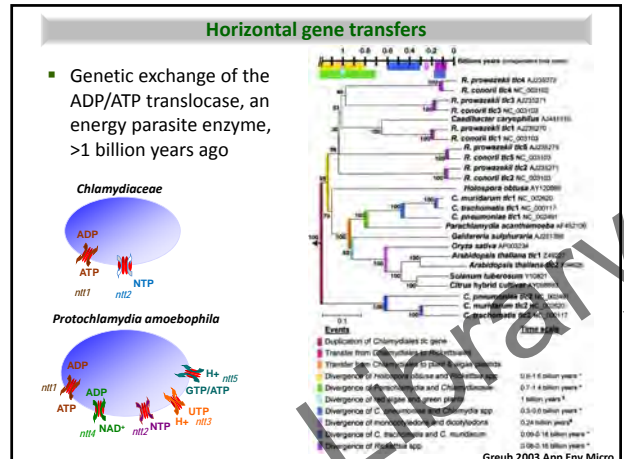
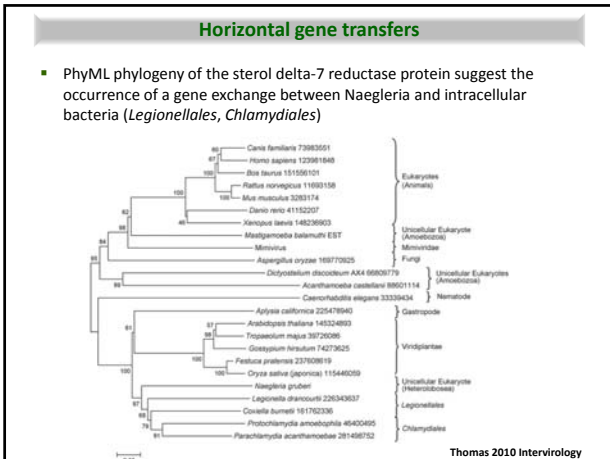


Larger genomes: why?

- Expansion of repetitive elements?
- Host cycling or amoeba as the single natural host?
 - Less specialized pathogens
- Amoeba as a « melting-pot » of evolution?
 - Lateral gene exchanges with
 - other (intracellular) bacteria, viruses,...
 - the host
- In the hypothesis of a free-living ancestor
 - Retain more genes for
 - metabolic capabilities
 - resistance to environmental stresses
 - ...

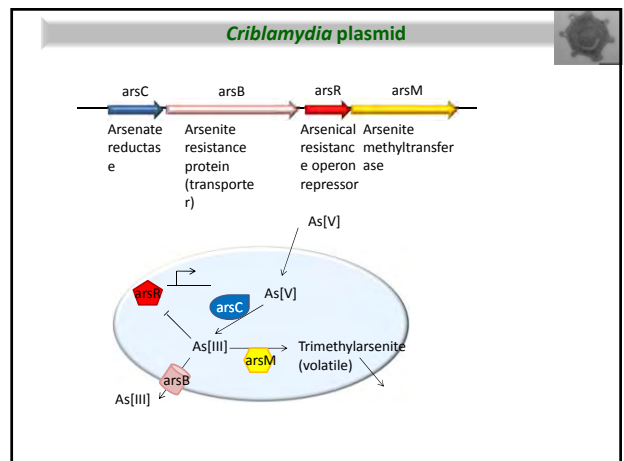
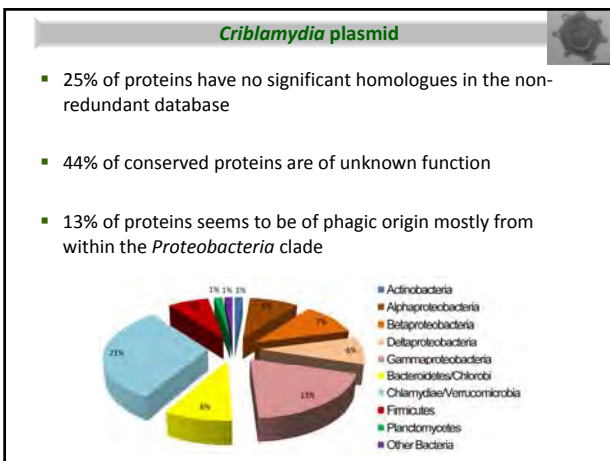
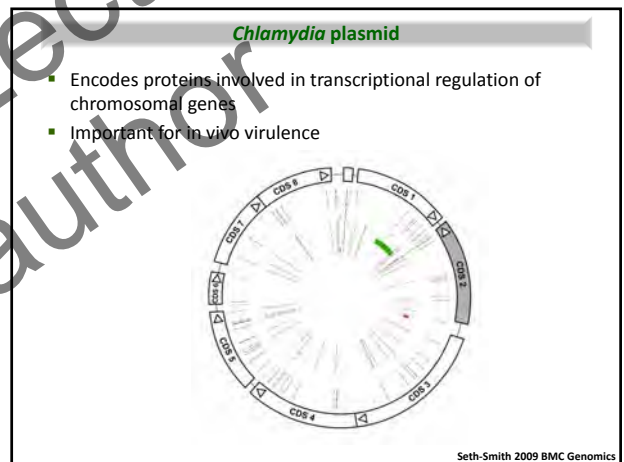






Chlamydial plasmids

Family	Species	Representative strain	Genome size (bp)	G+C content	Plasmid size (bp)
Chlamydiaceae	<i>Chlamydia trachomatis</i>	D/UW-3/CX	1'042'519	41.3%	7'493*
	<i>Chlamydia muridarum</i>	Nigg	1'072'950	40.3%	7'501
	<i>Chlamydia suis</i>				
	<i>Chlamydia pneumoniae</i>	CW/L029	1'230'230	40.6%	
	<i>Chlamydia pecorum</i>	E58	1'106'192	41.1%	
	<i>Chlamydia felis</i>	Fe/C-56	1'166'239	39.4%	7'552
	<i>Chlamydia caviae</i>	GPIC	1'173'890	39.2%	7'966
	<i>Chlamydia abortus</i>	S26/3	1'144'377	39.9%	
	<i>Chlamydia psittaci</i>	68C	1'171'660	39.1%	7'553
	Waddliaceae	<i>Waddlia chondrophila</i>	WSU86-1044	2'116'312	43.8%
Criblamydiaceae	<i>Criblamydia sequaxensis</i> *	CRIB-18	2'968'813	38.2%	89'525
	<i>Estrella lausannensis</i> *	CRIB-30	2'815'214	48.2%	9'136
Parachlamydiaceae	<i>Parachlamydia acanthamoebae</i>	UV-7	3'072'383	39.0%	
	<i>Protochlamydia amoebophila</i>	UWE25	2'414'465	34.7%	-
	<i>Protochlamydia knic</i>	Knic	2'900'000	42.4%	125'700
	<i>Neochlamydia hartmannellae</i> *		3'078'000	37.9%	-
Simkaniaceae	<i>Simkania negevensis</i>	Z	2'486'337	41.8%	132'038



Simkania plasmid

- F-type plasmid that encodes for a type IV secretion system (T4SS)
- F-plasmids carry modules for plasmid stability, replication, adaptation, and propagation
- Genes for protection against heavy metals and metabolic processes like starch and glycerophospholipid metabolism

A type IV secretion system

A

B

Collingro 2011 Mol Biol Evol

Pr. amoebophila T4SS and genomic island

Greub 2004 BMC Microbiology

Pr. naegleriophila T4SS

- A type IV secretion system very similar to that of UWE25 is encoded on the plasmid of *Pr. naegleriophila* KNic, like in *Simkania negevensis*

Evolution of chlamydial plasmids

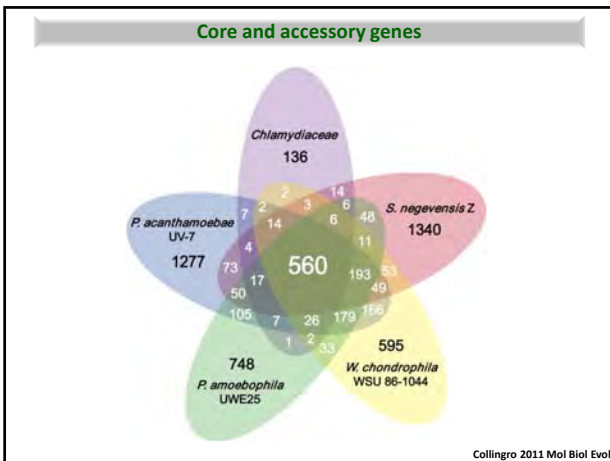
A

B

	chromosome	pGP	pSn	tra
DT	3	12	11	
DB	1	14	3	
W	2	7		
S	1	5		
	5	139	13	
C	1	1		
	8			

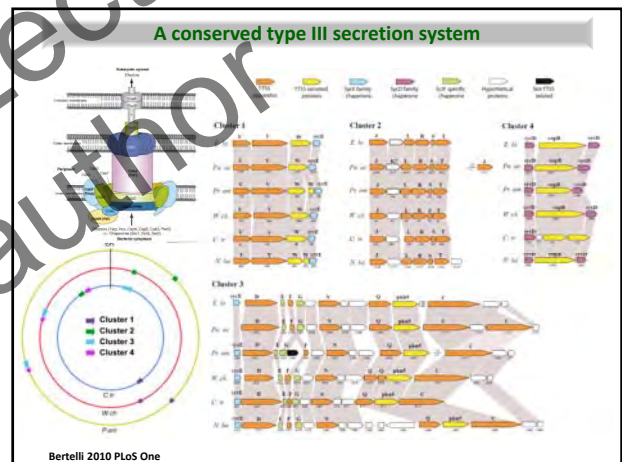
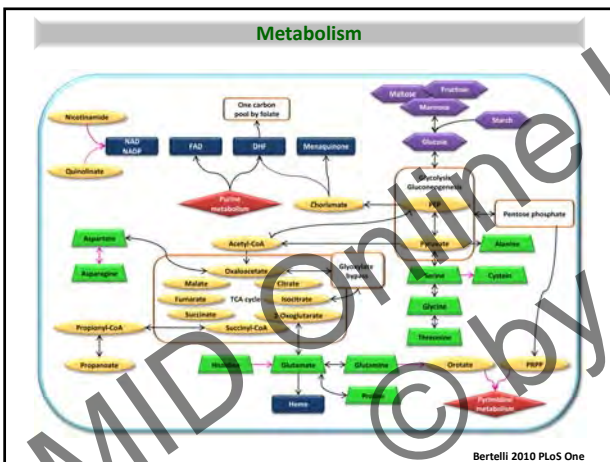
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Gene content, pathogenesis and metabolism

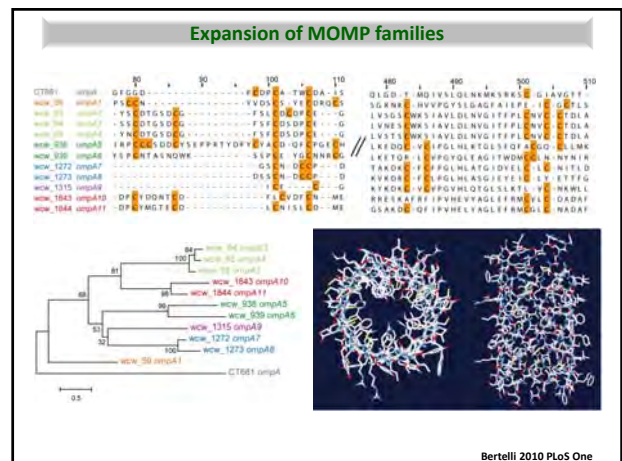


Metabolism

AA	<i>C.trachomatis</i>	<i>P. amoebophila</i>	<i>P. naegleriophila</i>	<i>W. chondrophila</i>
alanine	no	yes	yes	yes
arginine	no	no	no	no
asparagine	no	no	no	yes
aspartate	yes	yes	yes	yes
cysteine	no	no	yes	yes
glutamate	no	yes	yes	yes
glutamine	no	yes	yes	yes
glycine	yes	yes	yes	yes
histidine	no	no	no	no
isoleucine	no	no	no	no
leucine	no	no	no	no
lysine	no	no	no	no
methionine	no	no	no	no
phenylalanine	no	no	no	no
proline	no	yes	yes	yes
serine	no	yes	yes	yes
threonine	no	yes	yes	yes
tryptophan	yes	no	no	no
tyrosine	no	no	no	no
valine	no	no	no	no



- ### The chlamydial outer membrane complex
- Composed of various proteins that play an important role in pathogenicity, adhesion and invasion of the host cell
 - Major outer membrane proteins: MOMP. Functions as large porins and is a major antigen
 - OmcA and OmcB. Cystein-rich proteins that are highly cross-linked on the elementary body thus providing a protective coat. The disulphide bridges are reduced during differentiation to the RB, allowing the cell to swell in size
 - PMPs. Autotransporter proteins that are involved in pathogenesis



Expansion of major outer membrane protein families

- *Simkania* also encodes a high number of MOMP-like proteins ($n = 35$)
- With one exception, they have evolved independently from MOMP-like proteins of *Waddlia*.
- MOMP and MOMP-like proteins are notably absent in *Protochlamydia* and rare in *Parachlamydia*
- Suggests that proliferation and diversification of MOMP-like proteins occurred mainly in *Waddlia* and *Simkania* and may be replaced by structural relatives in *Parachlamydiaceae*

Collingro 2011 Mol Biol Evol

omcA and omcB

- A positional-based search and composition analysis enabled to retrieve small open reading frames with conserved CxxC motives

Rusconi 2013 Antonie van Leeuwenhoek

A structural homolog to chlamydial pmps

Bertelli 2010 PLoS One

Conclusion and perspectives

Conserved genome and gene order
 Few repeated elements
 Shuffled genome
 Few to many repeated elements
 Chlamydia-related bacteria
 Type III secretion system
 Type IV secretion system
 Enhanced metabolic abilities
 Horizontal gene transfer
 Amoebae as melting-pot

Many thanks to:
 Sébastien Aebly
 François Collyn
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 Gilbert Greub
 All our collaborators

IMUL
 Institut de Microbiologie
 UNIL
 Université de Lausanne
 SIB

Intra-arm recombination

- The comparison of *Pr. amoebophila* UWE25 and *Pr. naegleriophila* KNic

