



The Haemolysin System from *E. coli* – a Paradigm for Type I Secretion Systems?

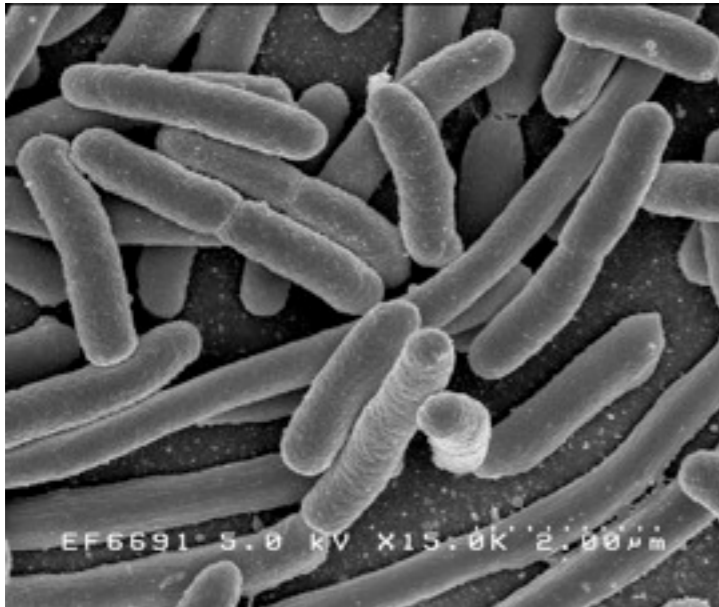
Lutz Schmitt

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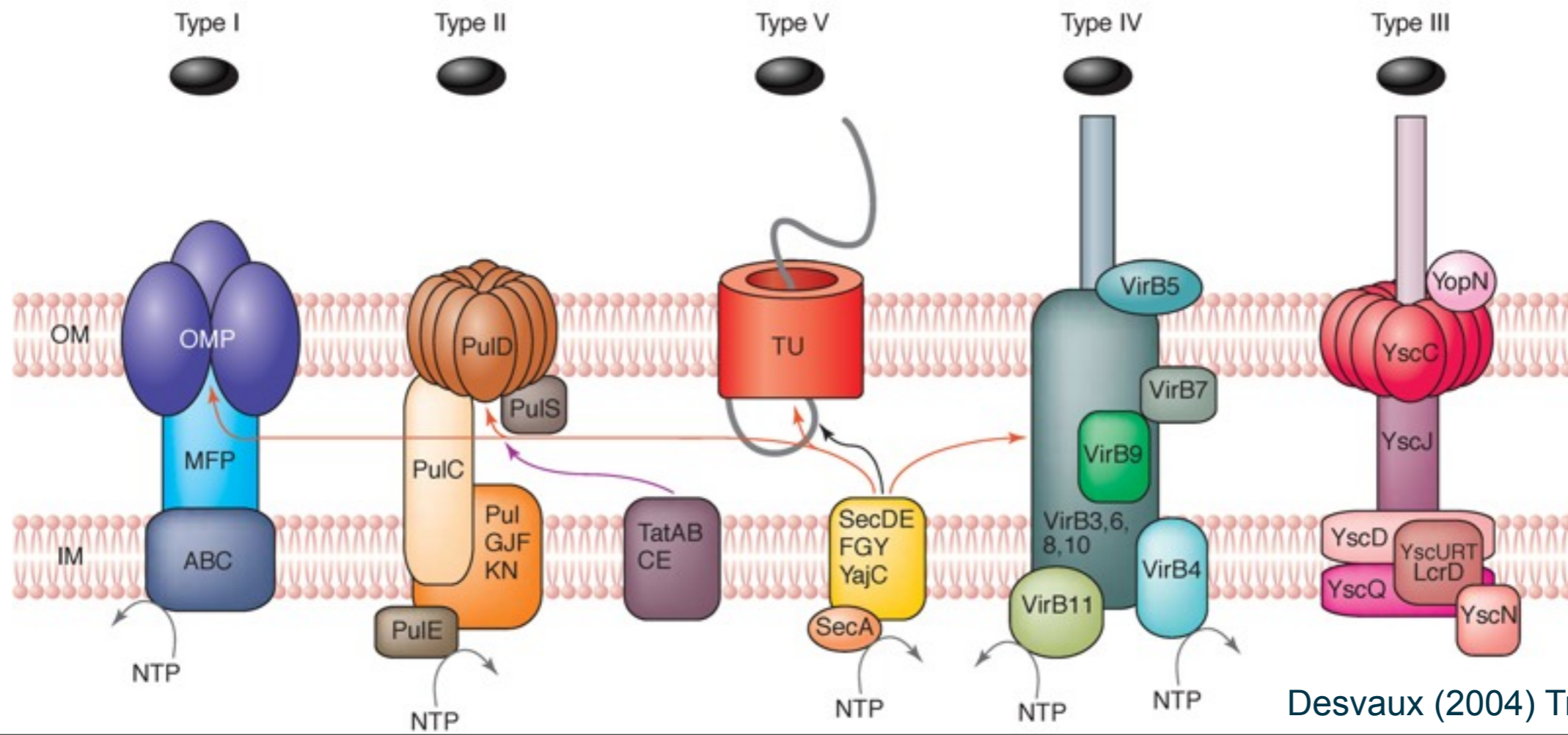
Heinrich Heine

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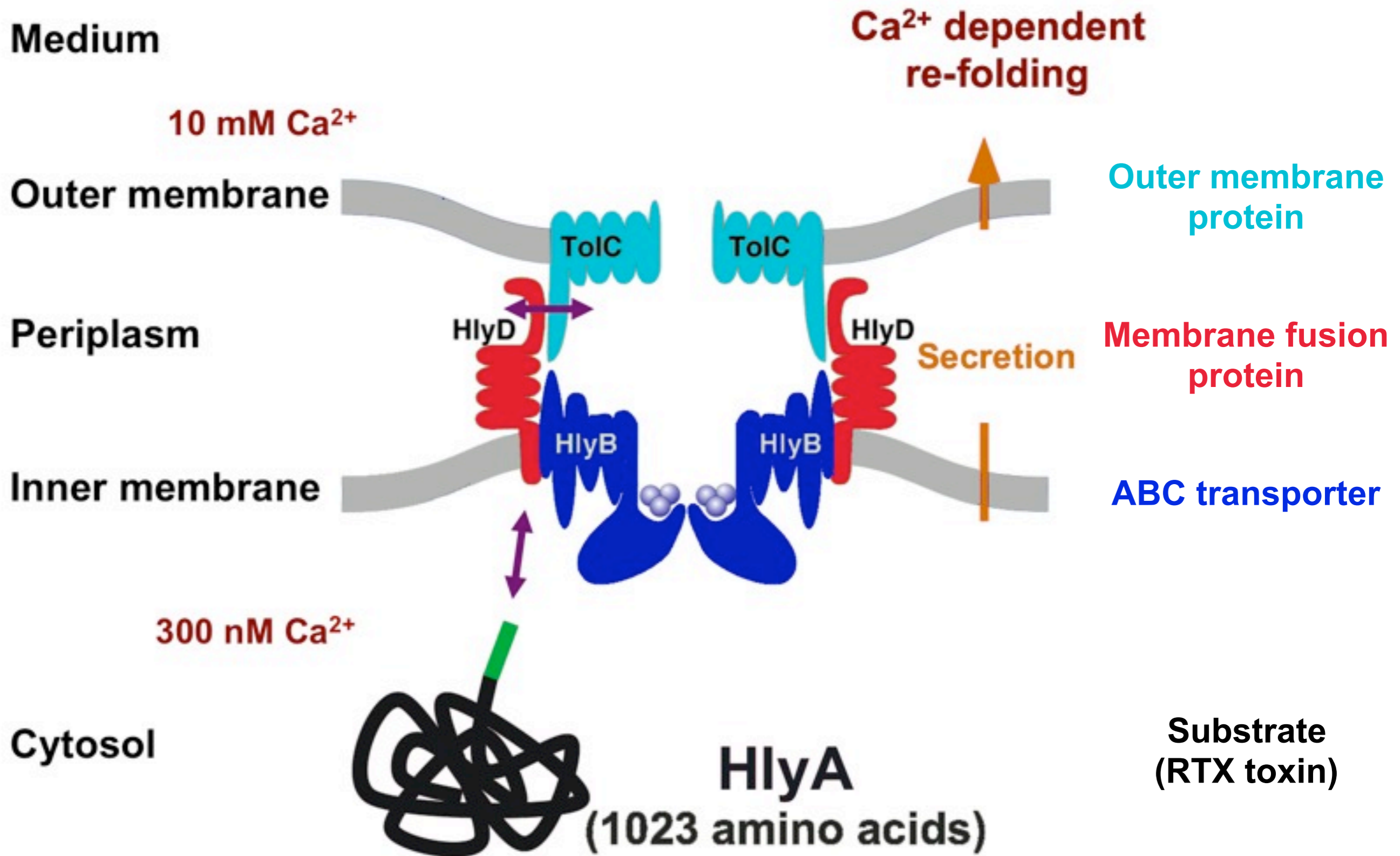
Protein Secretion in Gram-negative Bacteria



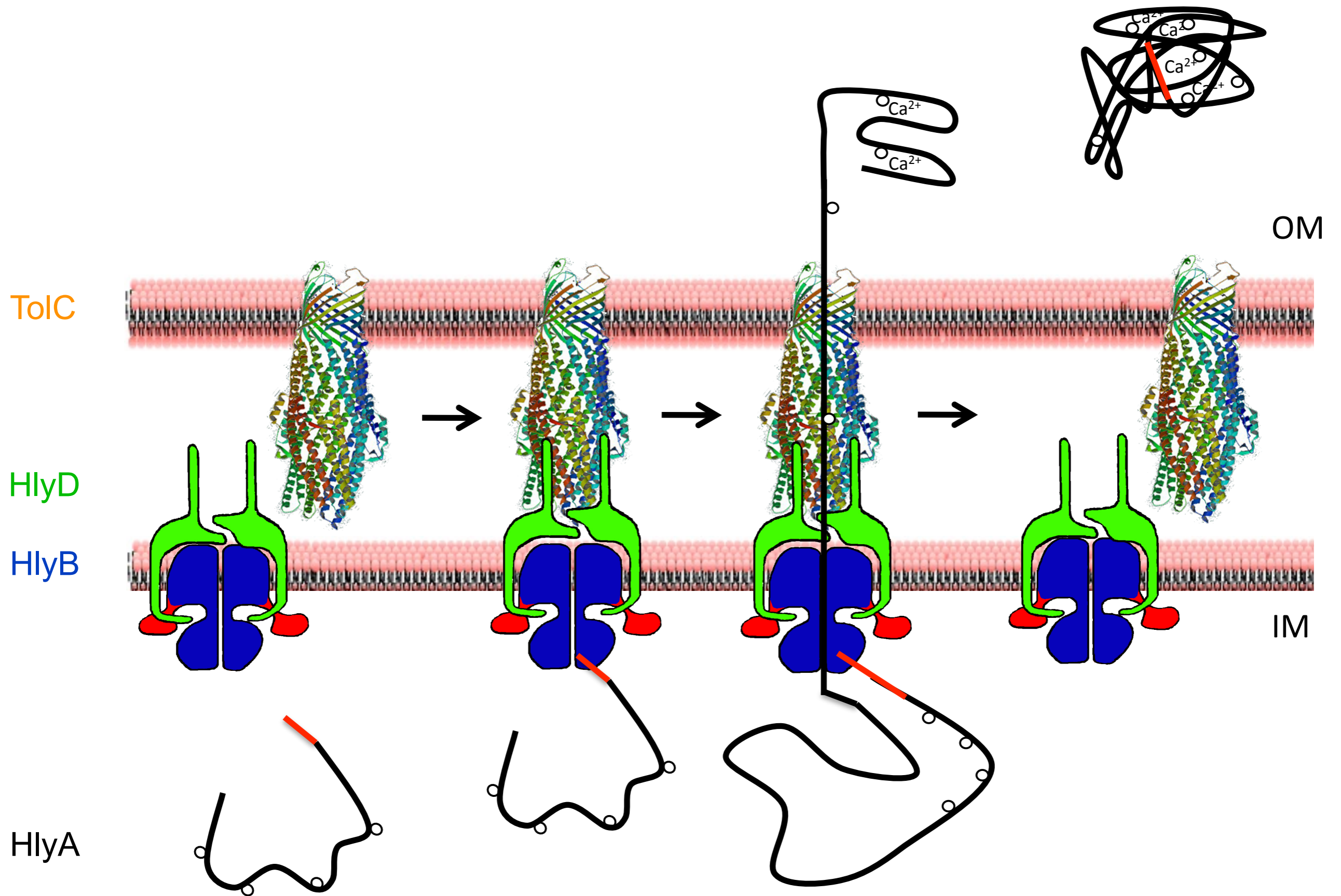
Cytosol
Inner membrane
Periplasmic space
Outer membrane
Extracellular space (**secretion**)



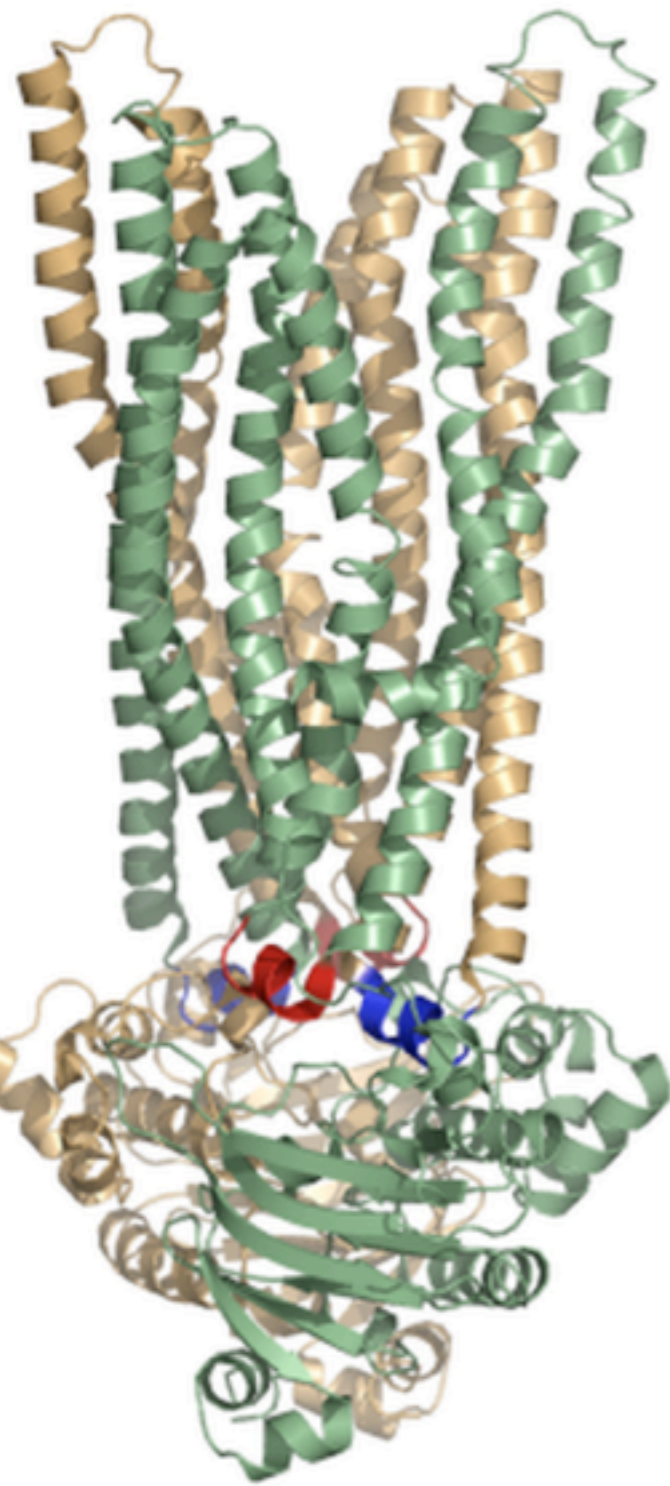
The Haemolysin A Machinery



What we think happens ...



Bacteriocine ABC Transporters



NukT	LQNSDQD	C	L	A	C	S	M	I	L	S	Y	F	G	K	N	V	S	I	N	S	L	Y	K	R	E	M	-	I	P	P	D	G	L	S	I	S	Y	L	K	E	L	N	I	K	Y	E	L	N	M	K	V	Y		
CvaB	HQTETA	C	G	L	A	C	L	A	M	I	C	G	H	F	G	K	N	I	D	L	I	Y	L	R	R	K	F	N	-	L	S	A	R	G	A	T	L	-	-	A	G	I	N	G	I	A	E	Q	L	G	M	A	T	R
ClyB	AQGEHST	C	A	L	A	C	I	T	M	L	L	N	Y	Y	G	N	Q	S	T	L	V	E	L	R	E	K	Y	G	-	V	P	K	G	G	L	T	I	K	N	-	-	I	R	T	V	F	D	E	Y	G	F	D	V	S
LagD	YQQDEKD	C	G	V	A	C	I	A	M	I	L	K	H	Y	G	T	E	I	T	I	Q	R	L	R	E	L	S	G	-	T	D	L	D	G	T	S	A	-	-	F	G	I	K	K	T	F	E	K	L	G	F	D	A	P
LtnT	FQVAQTE	C	G	L	C	C	V	R	T	I	L	D	Y	F	G	Y	E	T	T	V	T	K	L	R	I	L	K	E	-	P	G	R	D	G	S	S	F	-	-	N	D	I	R	K	L	L	E	R	F	G	V	D	S	K
ComA	PQVDQMD	C	G	V	A	S	L	A	M	V	F	G	Y	G	S	Y	F	L	A	H	L	R	E	L	A	K	-	T	T	M	D	G	T	T	A	-	-	L	G	L	V	K	V	A	E	E	I	G	F	E	T	R		
HlyB	-SCHKID	Y	G	L	Y	A	L	E	I	L	A	Q	Y	H	N	S	V	N	P	E	E	I	K	H	R	F	D	-	T	D	G	T	G	L	G	L	-	-	T	S	W	L	L	A	A	K	S	L	E	L	K	V	K	
LktB	-SQKNTN	L	A	L	Q	A	L	E	V	L	A	Q	Y	H	N	I	S	I	N	P	E	E	I	K	H	K	F	D	-	I	D	G	H	G	L	N	Q	-	-	T	K	W	L	L	A	A	K	S	L	G	L	K	V	R
PaxB	SFKQKND	Y	G	L	H	A	L	V	I	L	A	Q	Y	H	N	I	A	V	S	P	E	E	I	K	H	K	F	D	-	P	E	G	K	G	I	D	L	-	-	V	A	W	L	L	A	A	K	S	F	E	L	K	A	K
RtxB	-K--TSQ	P	A	L	S	A	L	I	I	L	A	H	Y	H	G	I	A	A	N	P	A	D	I	S	H	H	F	S	G	S	L	N	N	D	L	S	E	-	-	T	E	W	L	L	A	A	K	K	L	E	L	K	A	K
ApxIIIB	PFNEKID	Y	G	L	H	A	L	V	I	L	A	Q	Y	H	N	V	A	V	N	P	E	E	V	K	H	K	F	D	-	L	D	G	K	G	L	D	L	-	-	V	A	W	L	L	A	A	K	S	L	E	L	K	M	K
AqxB	-FNQKED	Y	G	L	Y	A	L	T	I	L	A	Q	Y	H	N	I	A	V	N	P	E	E	L	K	H	K	F	D	-	L	E	G	K	G	L	D	L	-	-	T	A	W	L	L	A	A	K	S	L	E	L	K	A	K

NukT	RIKDKEK	T	F	R	-	-	V	I	S	K	I	K	P	I	I	V	H	-	-	-	W	-	D	L	N	H	E	V	I	V	K	N	-	-	-	V	K	K	H	I	E	I	N	E	I	-	-	G	K	V	...			
CvaB	ALSL---	E	L	D	-	-	E	L	R	V	L	K	T	P	C	I	L	H	-	-	W	-	D	F	S	H	E	V	V	L	V	S	V	-	-	-	K	R	N	R	Y	V	L	H	D	E	A	R	-	-	G	I	R	...
ClyB	TFKS---	S	F	S	-	-	N	Y	L	D	L	P	T	P	V	I	S	Y	-	-	W	-	N	N	D	H	E	V	V	I	E	K	-	-	-	I	K	K	K	V	L	I	L	D	H	A	S	-	-	N	K	R	...	
LagD	AFKA---	G	D	E	T	W	Q	E	K	D	I	P	L	P	L	I	A	H	I	S	E	Q	K	Y	D	H	Y	V	V	V	Y	K	-	-	-	V	K	G	D	E	I	W	I	A	D	H	A	K	-	-	G	K	I	...
LtnT	LYKV---	K	D	N	R	-	I	F	S	T	L	Q	L	P	I	I	Y	-	-	W	-	K	N	V	H	E	V	C	V	E	R	-	-	-	I	S	K	K	T	V	I	I	M	D	H	S	V	-	-	G	R	T	...	
ComA	AIKA---	D	M	T	L	F	D	L	P	D	L	T	F	P	F	V	A	H	V	L	K	E	G	K	L	L	H	Y	Y	V	V	T	G	-	-	-	Q	D	K	S	I	H	I	A	D	H	D	P	G	V	K	L	T	...
HlyB	QVKK---	T	I	D	-	-	R	L	N	F	I	S	L	P	A	L	W	-	-	-	R	E	D	G	R	H	E	I	L	T	K	V	S	-	-	K	E	A	N	R	Y	L	I	F	D	I	E	Q	-	R	N	P	R	...
LktB	TANK---	T	V	D	-	-	R	L	P	F	L	H	L	P	A	L	W	-	-	-	R	D	D	G	E	H	E	I	L	L	K	I	D	-	-	Q	E	T	D	R	Y	L	I	F	D	I	I	Q	-	K	N	P	I	...
PaxB	KVKK---	S	I	D	-	-	R	L	P	F	I	H	L	P	A	L	W	-	-	-	R	D	D	G	E	H	E	I	L	T	K	I	D	-	-	T	Q	T	N	R	Y	L	I	F	D	I	E	E	-	R	N	P	K	...
RtxB	VVKQ---	P	I	S	-	-	R	L	P	M	A	S	L	P	A	L	W	-	-	-	R	E	D	G	E	H	E	L	L	A	K	I	D	G	T	G	E	A	T	Q	Y	L	I	H	D	I	S	E	-	S	R	P	I	...
ApxIIIB	RVKK---	S	I	E	-	-	R	L	P	F	I	H	L	P	A	L	W	-	-	-	R	D	D	G	E	H	V	I	L	M	K	I	D	-	-	T	Q	T	N	R	Y	L	I	F	D	I	E	E	-	R	N	P	K	...
AqxB	QVKK---	S	I	D	-	-	R	L	E	F	I	A	L	P	A	L	W	-	-	-	R	D	D	G	E	H	E	I	L	T	K	I	D	-	-	S	K	A	Q	K	Y	L	I	F	D	I	E	T	-	R	N	P	R	...

C39 Peptidases

C39 peptidases are cysteine proteases

Specific for ABC transporters

Cleavage occurs after a GG motif

Catalytic dyad/triade (Cys-His-Asp)

Consensus sequence – LSXXELXXIX**GG** (Substrate)

The C39-domain of HlyB:

Consensus sequence – **GGXGXDUX** (RTX)

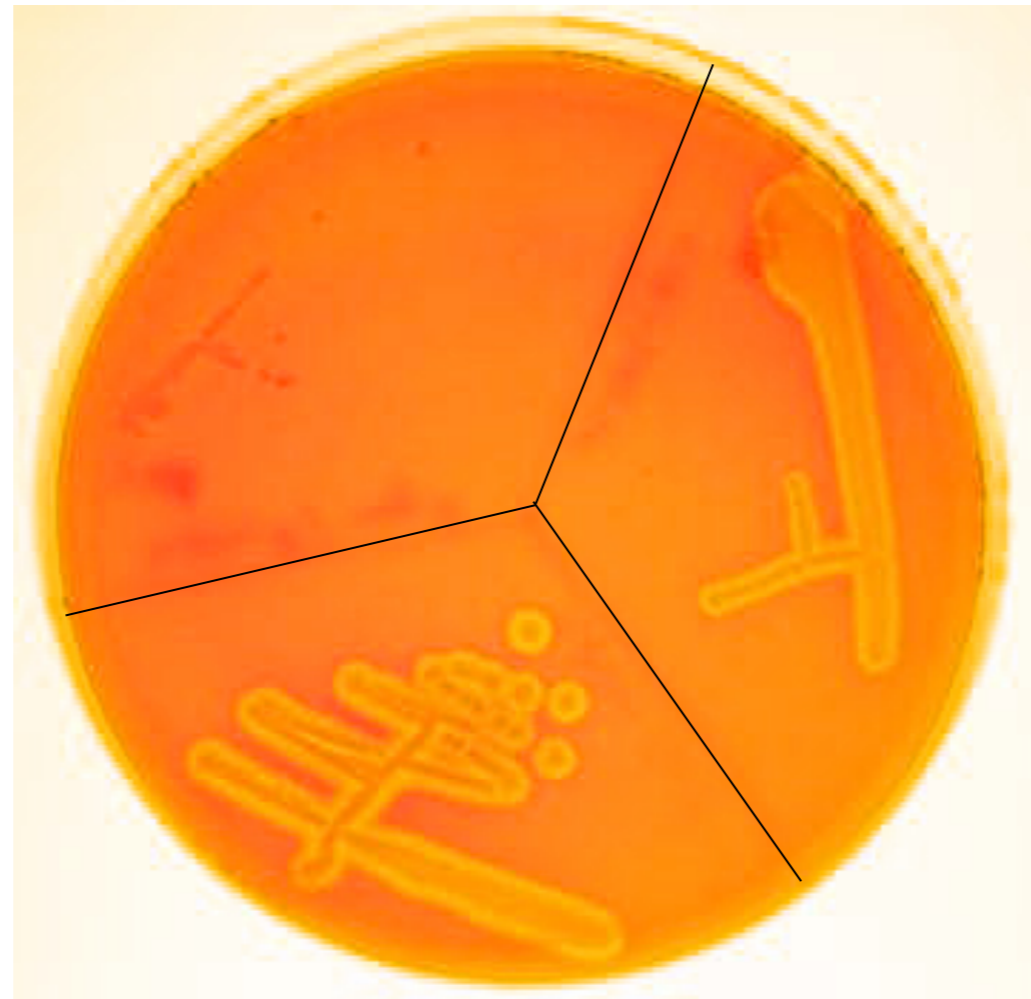
Tyr instead of Cys

C39-like domain (CLD)

A Potential Role of the CLD

E. coli

BL21/HlyB-C39+HlyD



E. coli
SE 5000

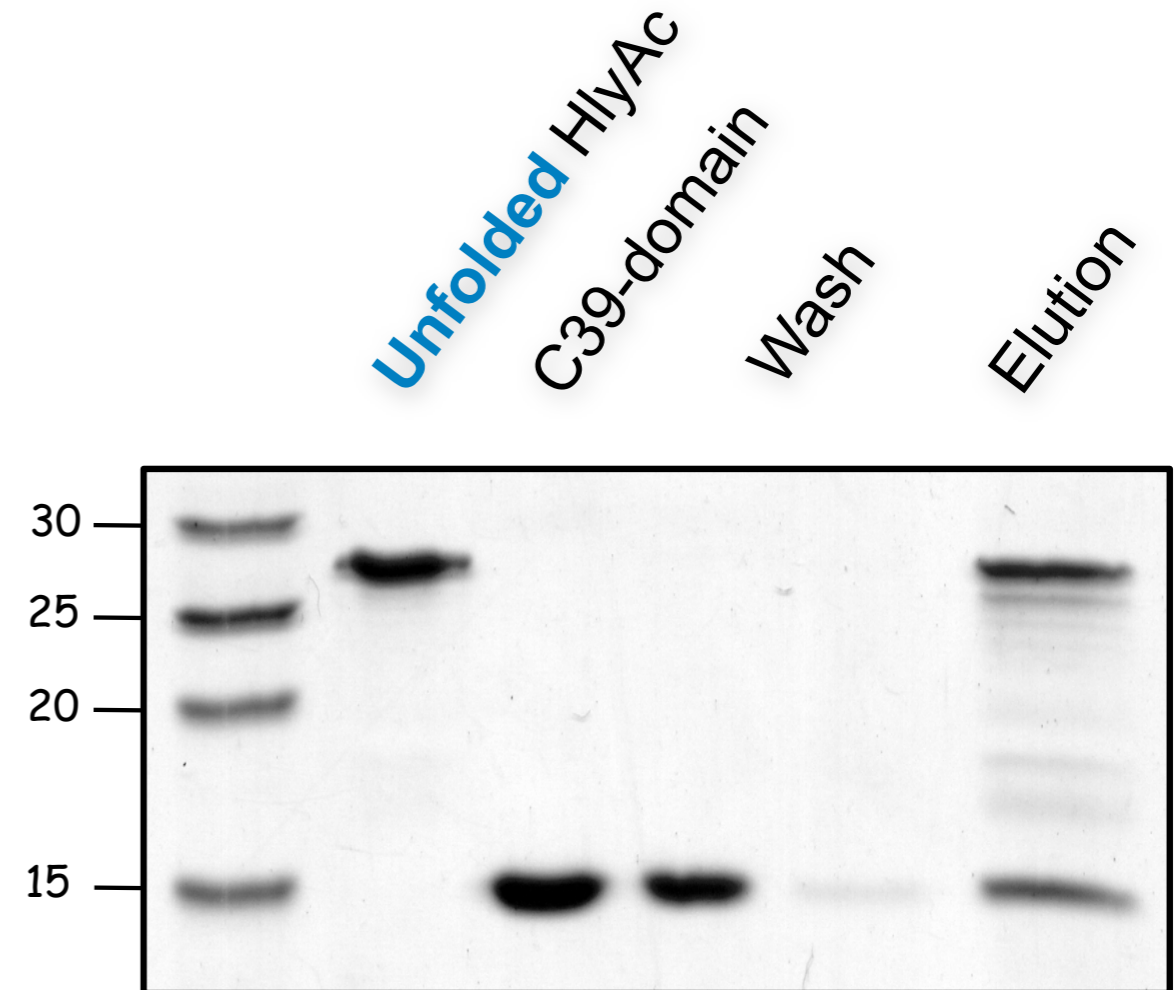
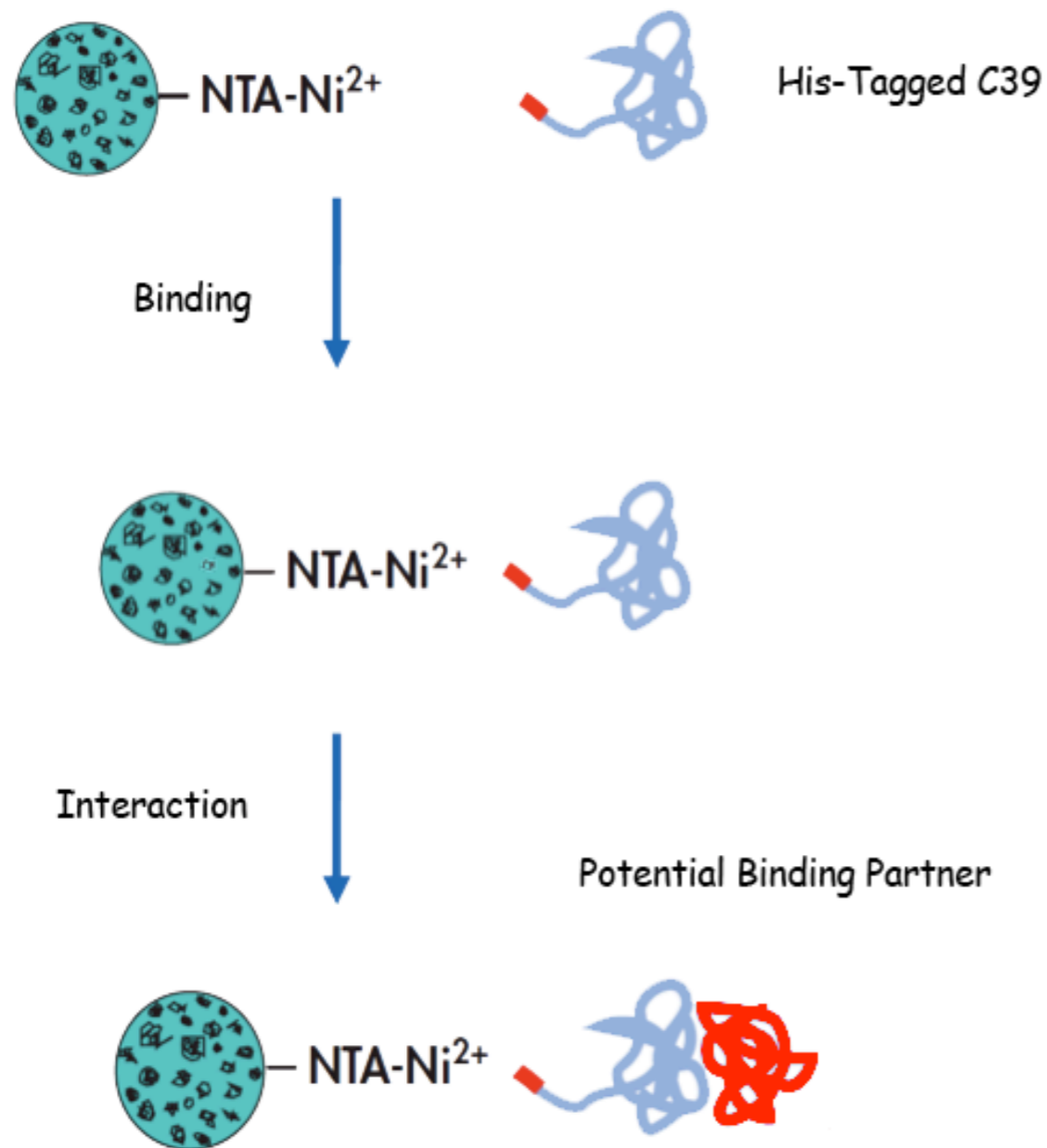
E. coli

BL21/HlyB+HlyD

Interaction Partner(s)

Protein-Protein Interaction

“Interaction Assay Ni-NTA Magnetic Beads”

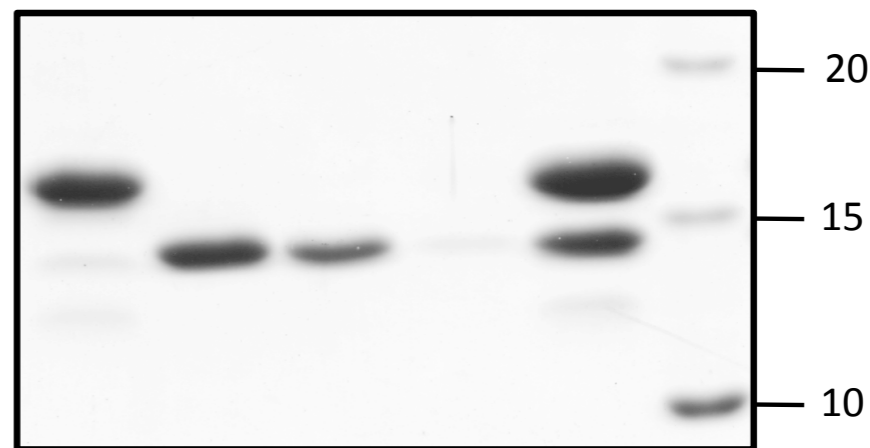


Controls

Folded HlyAC
CLD Wash Elution

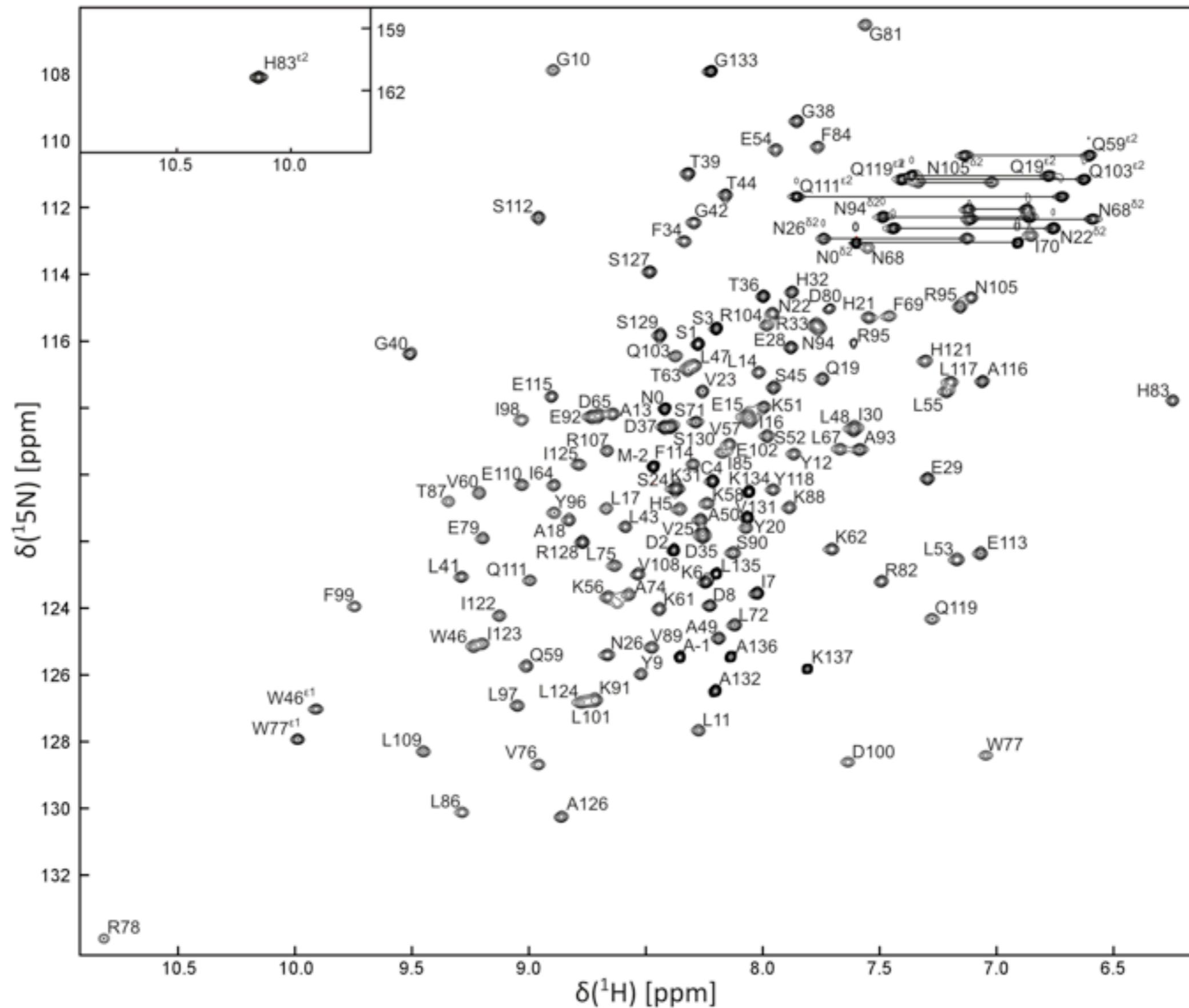


Unfolded HlyAC ~~SecSeq~~
CLD Wash Elution

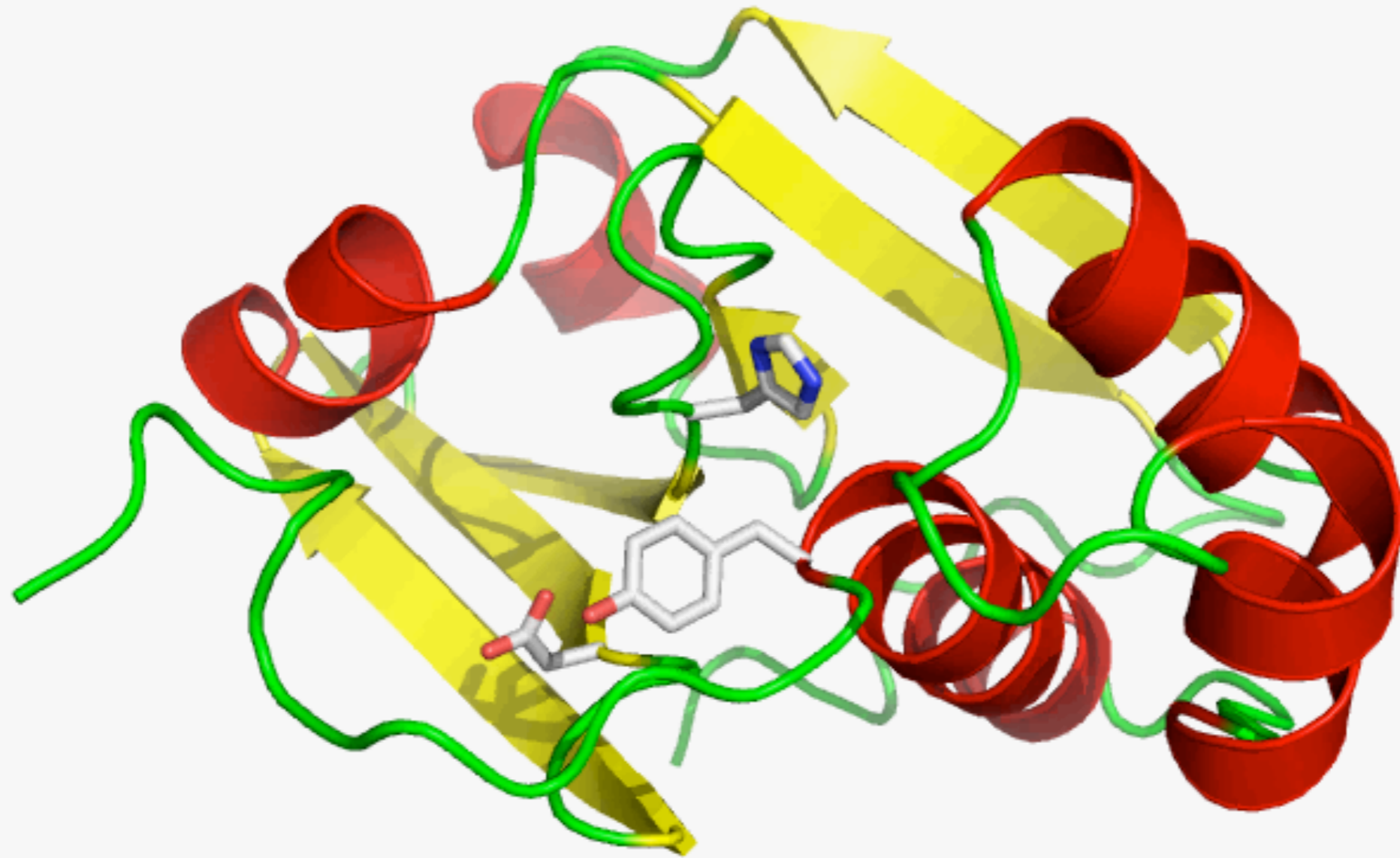


The unfolded state without the SecSeq is recognized

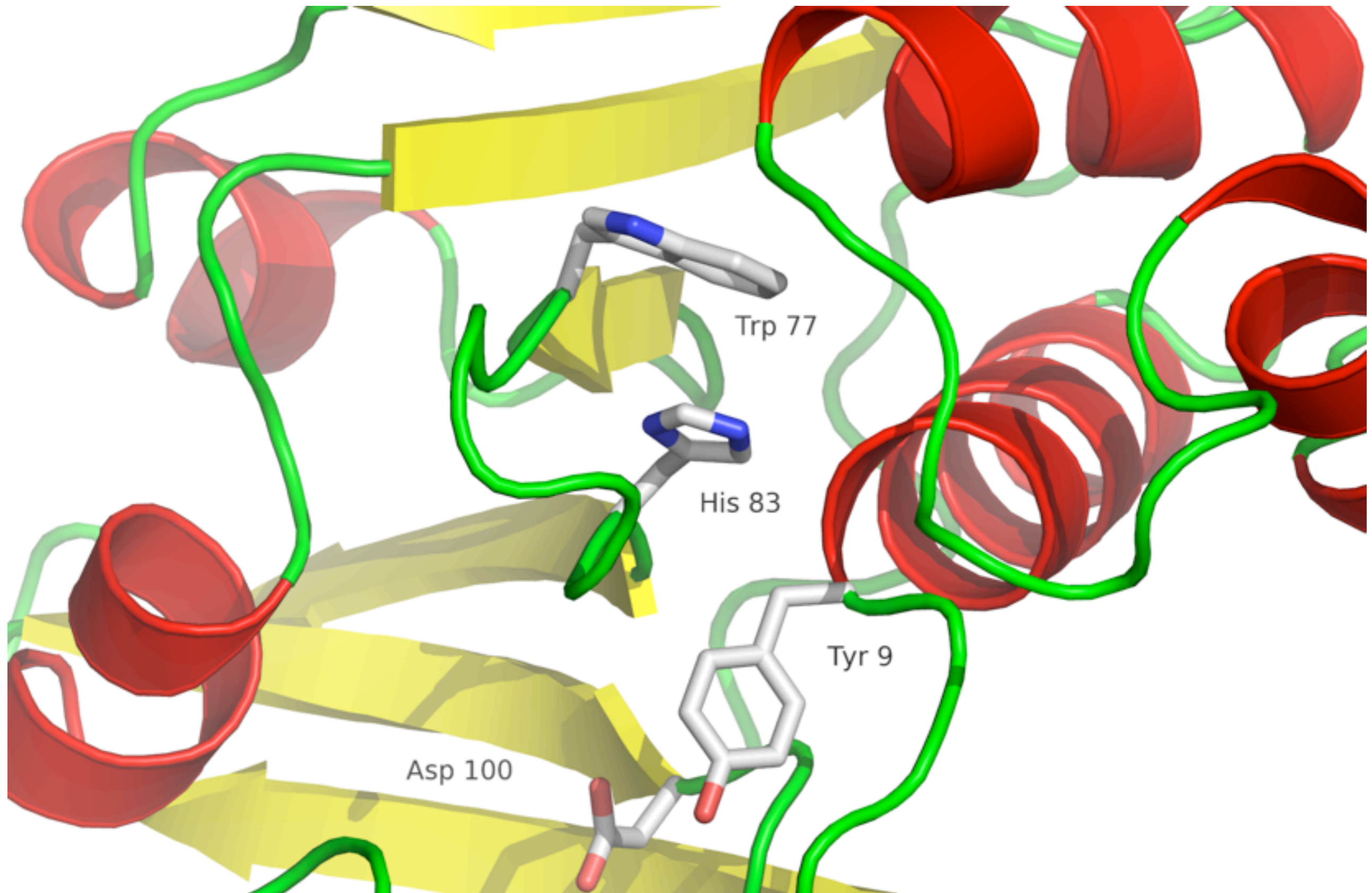
The NMR Structure of the CLD



The Overall Fold

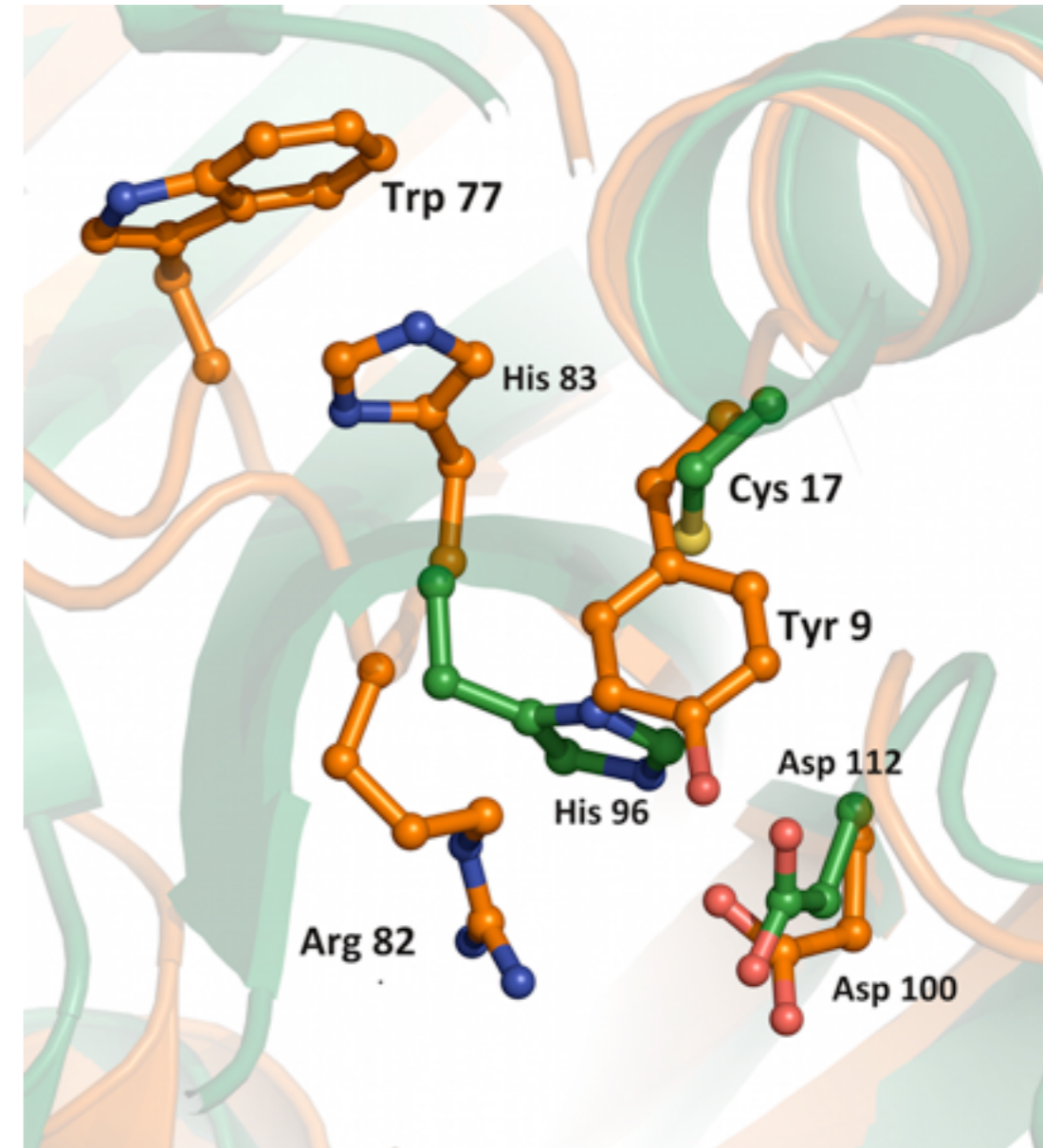
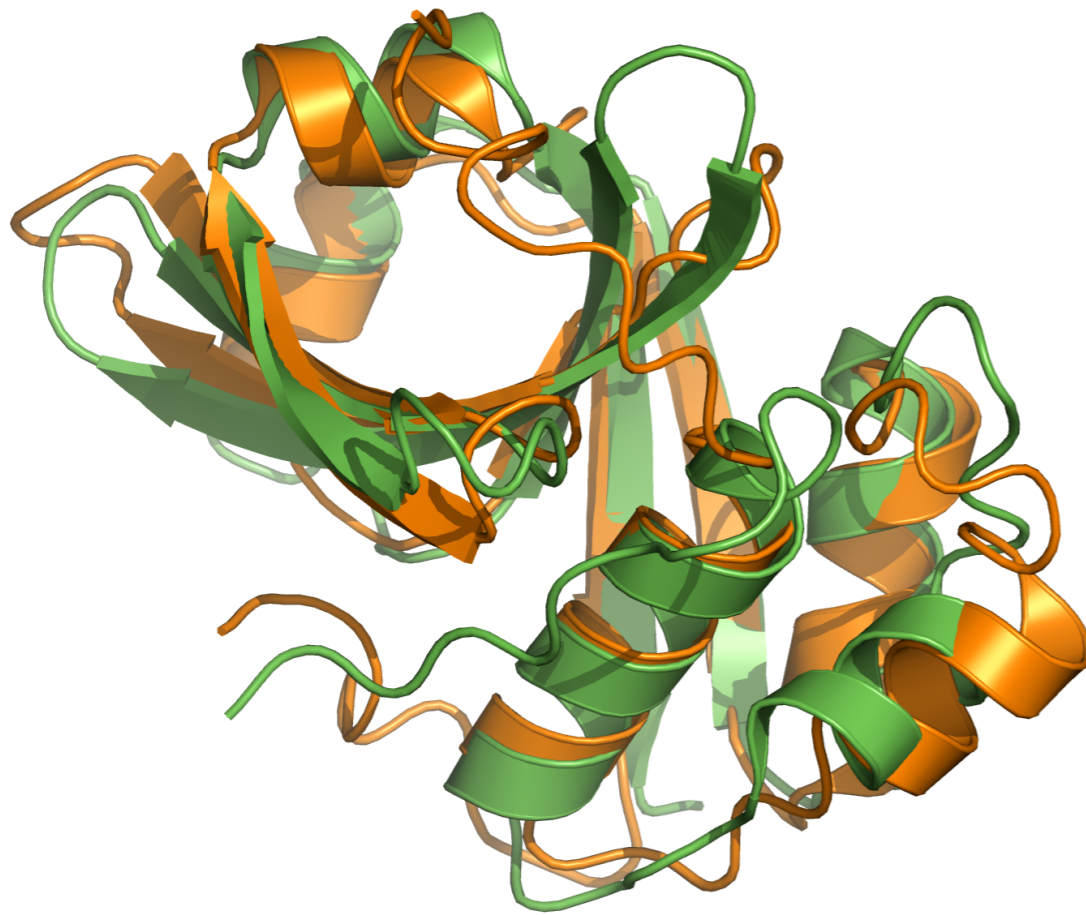


The Active Site

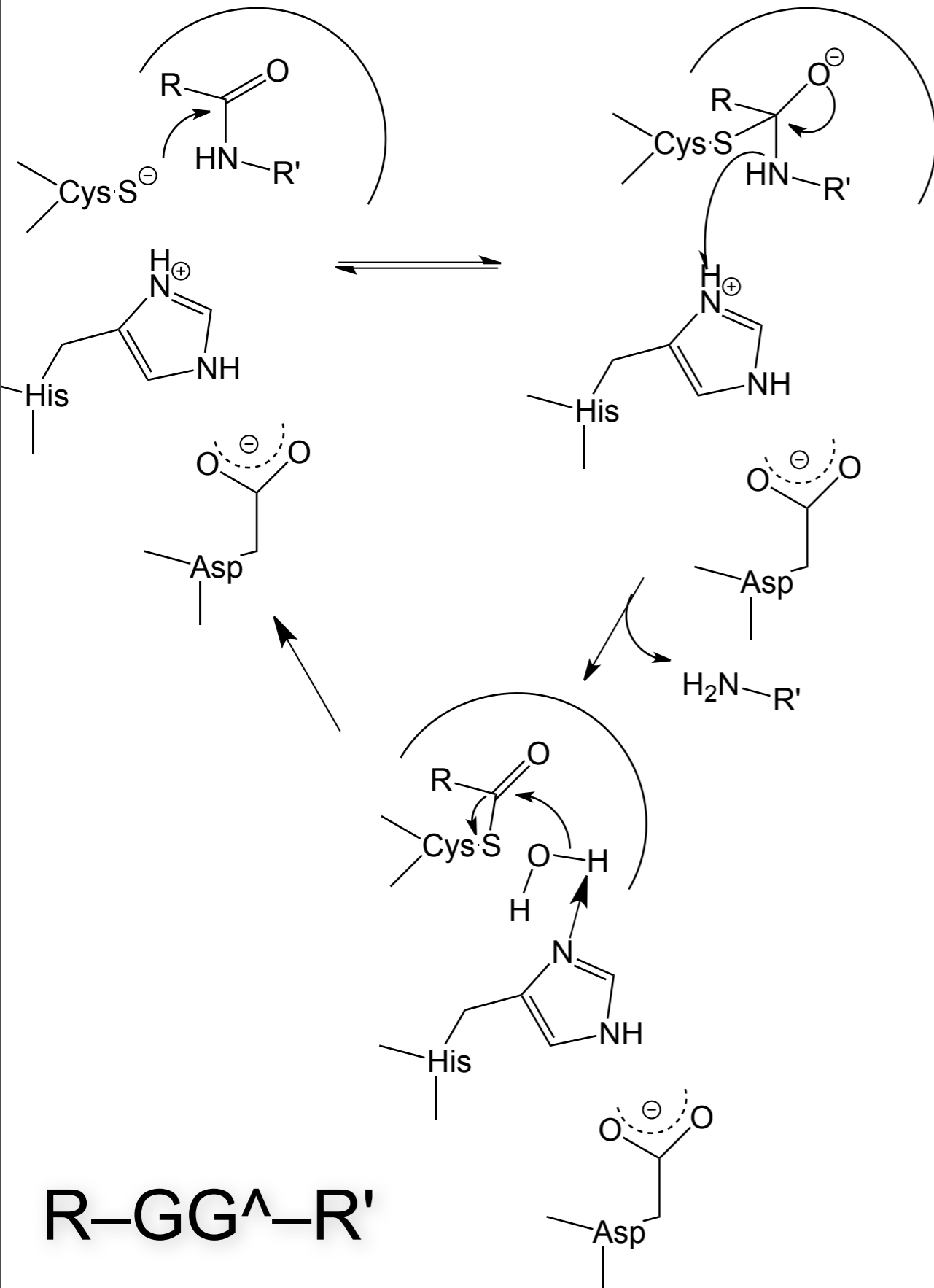


CLD – C39: A Comparison

ComA-PEP* / CLD



Mechanistic Implications



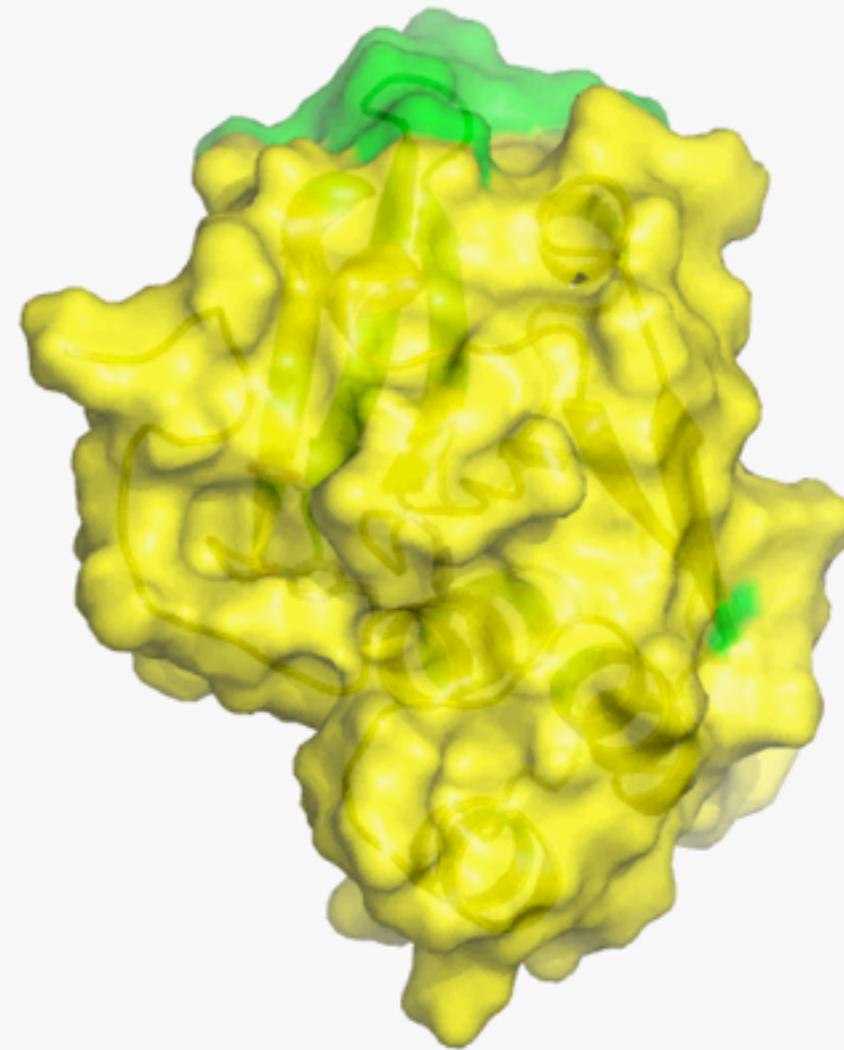
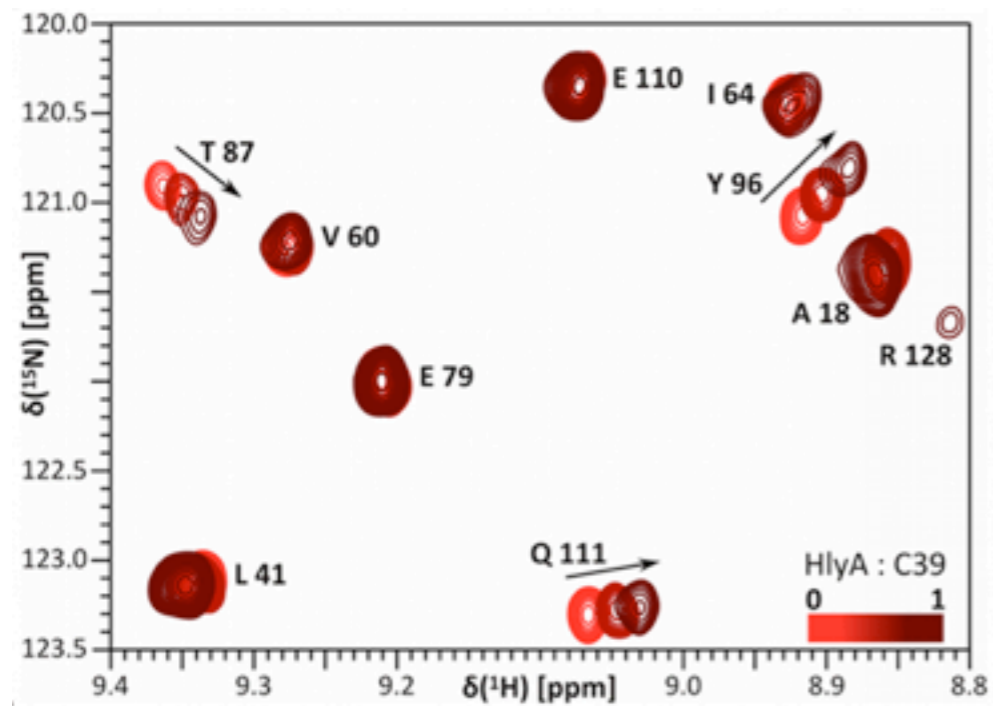
No thiolate (Tyr⁹)

His⁸³ – Trp⁷⁷ interaction

Tyr⁹Cys is still inactive

Interactions by NMR

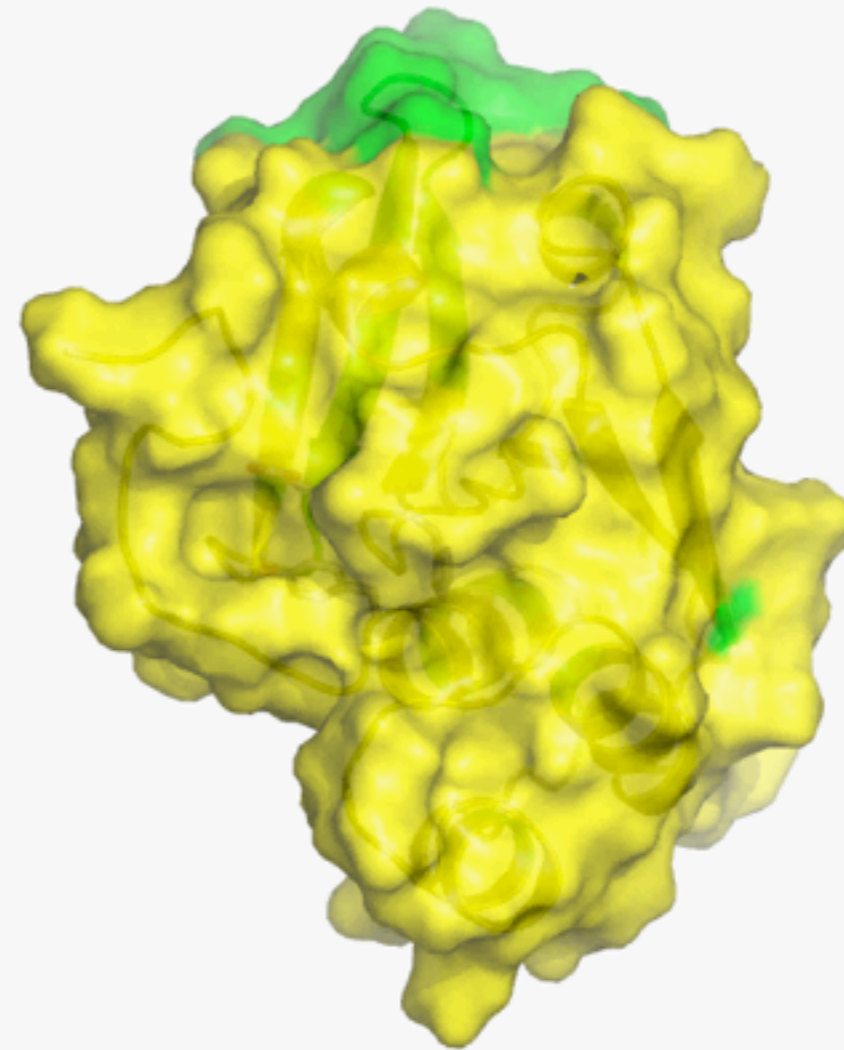
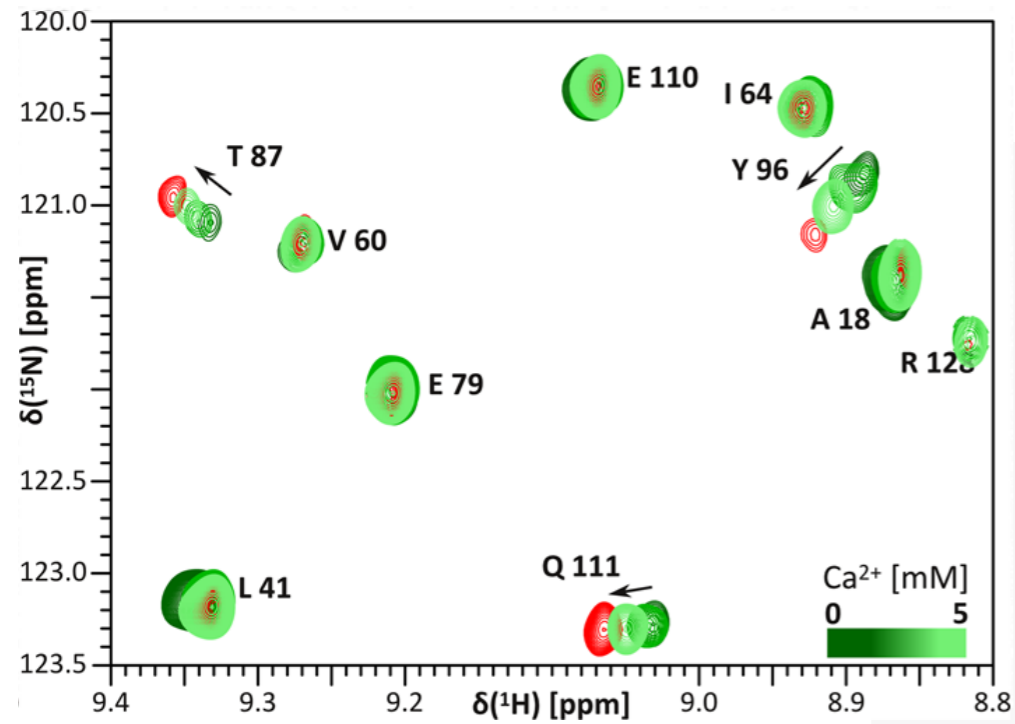
Titration of HlyAc* (no SecSeq) / CLD



CLD harbors a 'continuous' binding site

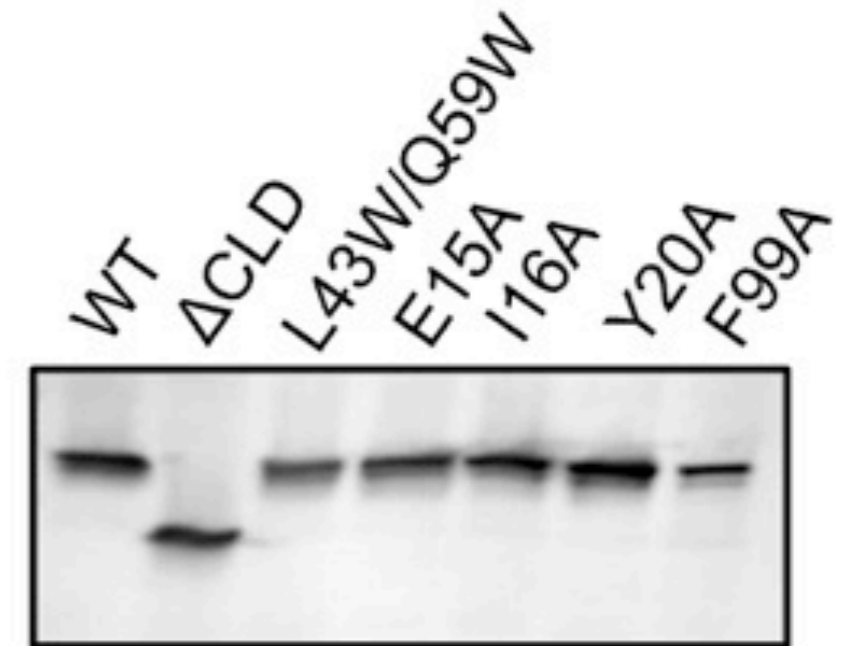
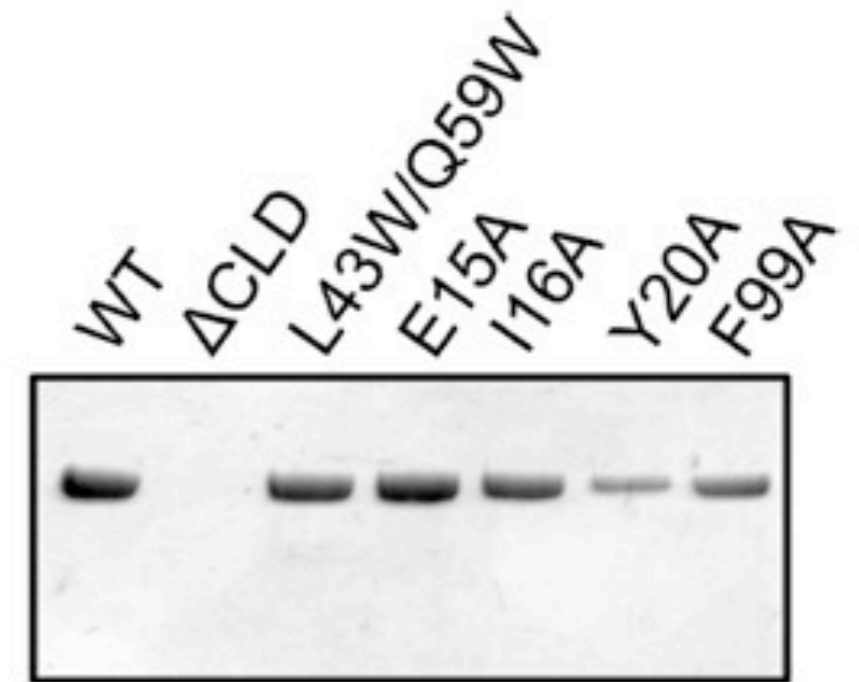
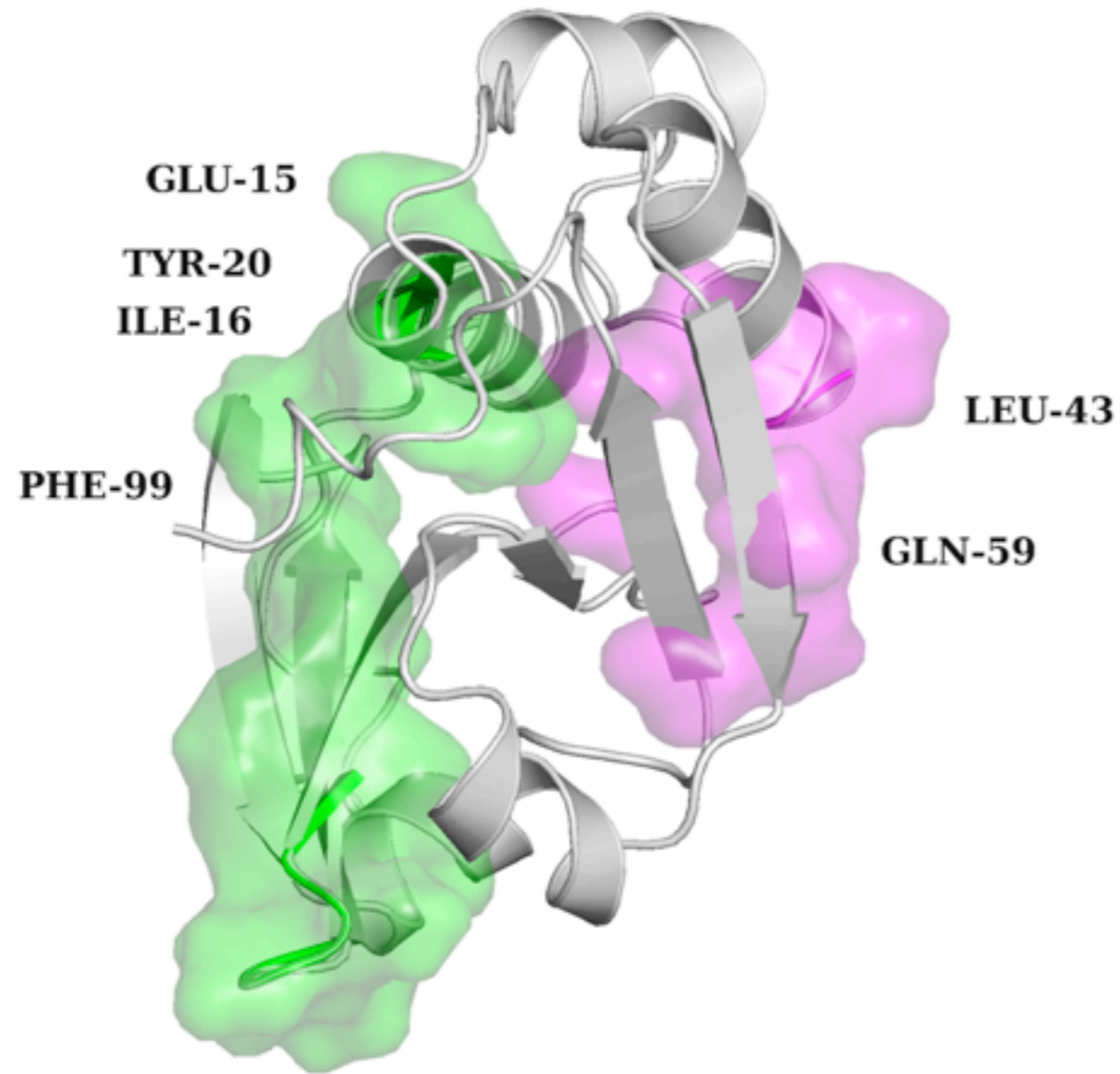
Interactions by NMR

Titration of HlyAc* (no SecSeq) / CLD



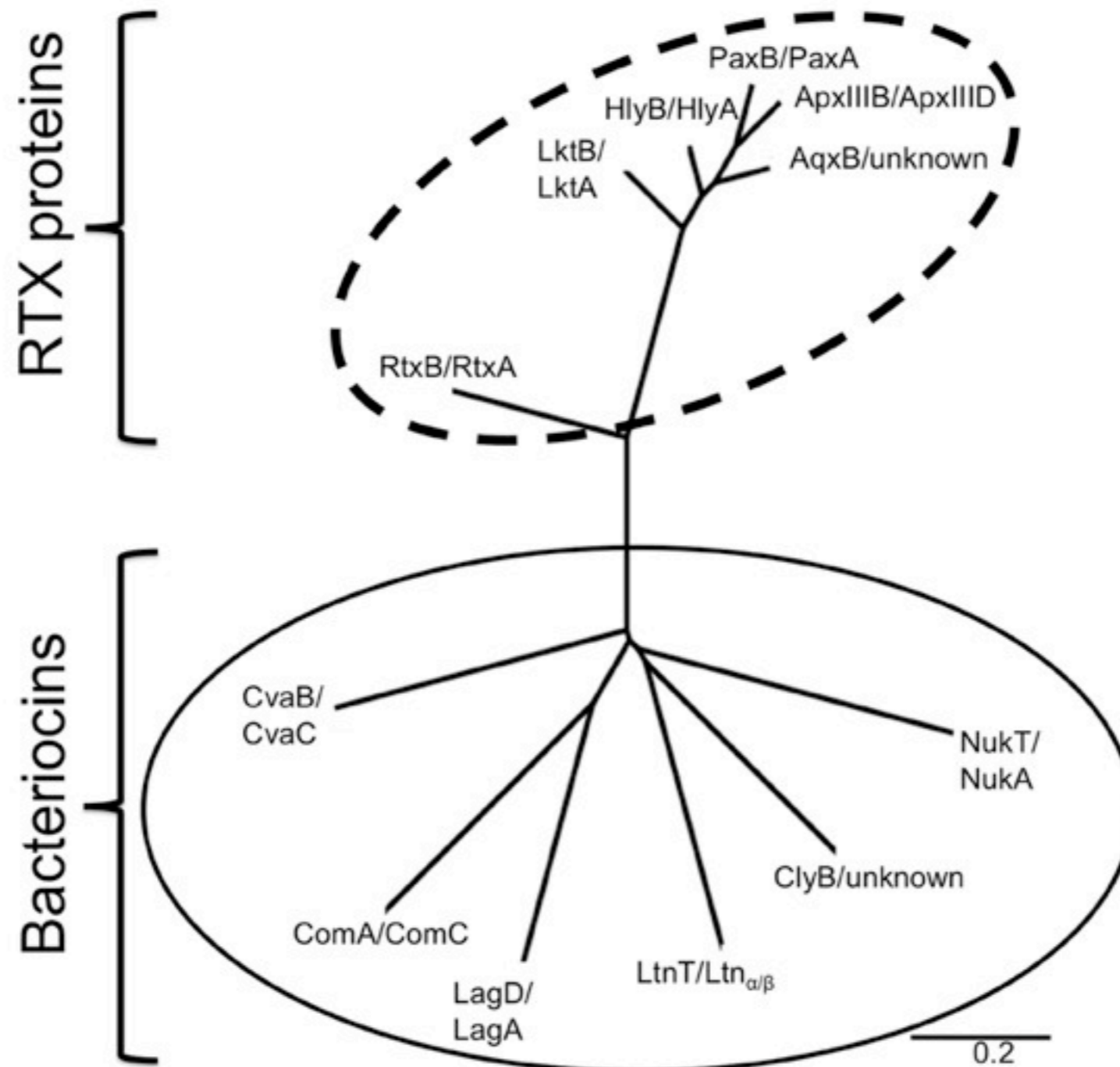
CLD harbors a 'continuous' binding site

Mutations – CLD versus ComA



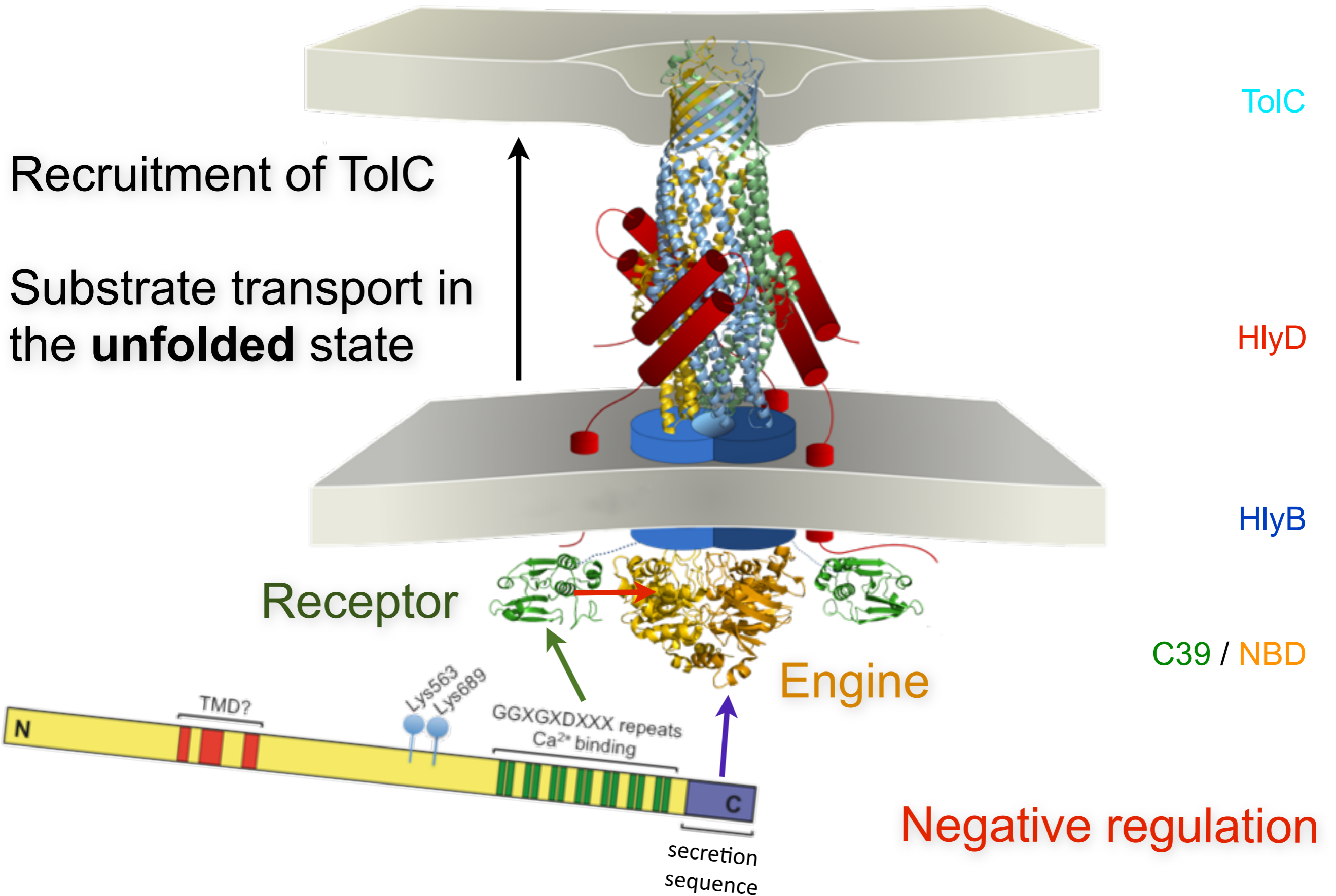
Phylogenetic Consequences

'Trp⁷⁷' – 'His⁸³' as an indicator



HasA/HasD
systems

A Model of the Early Steps



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Text