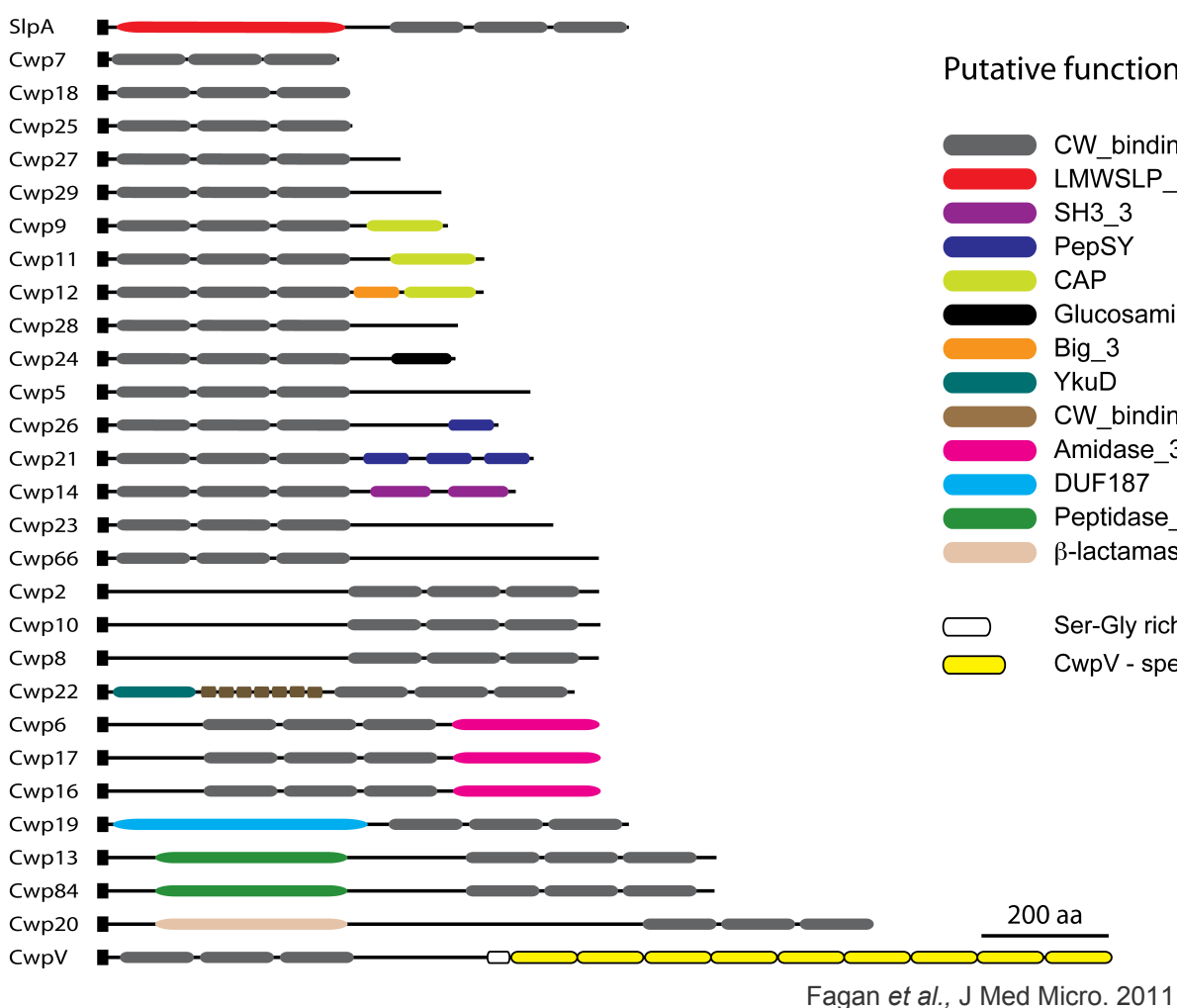


Structural studies of *Clostridium difficile* S-layer

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Putative functions of domains

- CW_binding_2
- LMW_SLP_N
- SH3_3
- PepSY
- CAP
- Glucosaminidase
- Big_3
- YkuD
- CW_binding_1
- Amidase_3
- DUF187
- Peptidase_C1
- β-lactamase

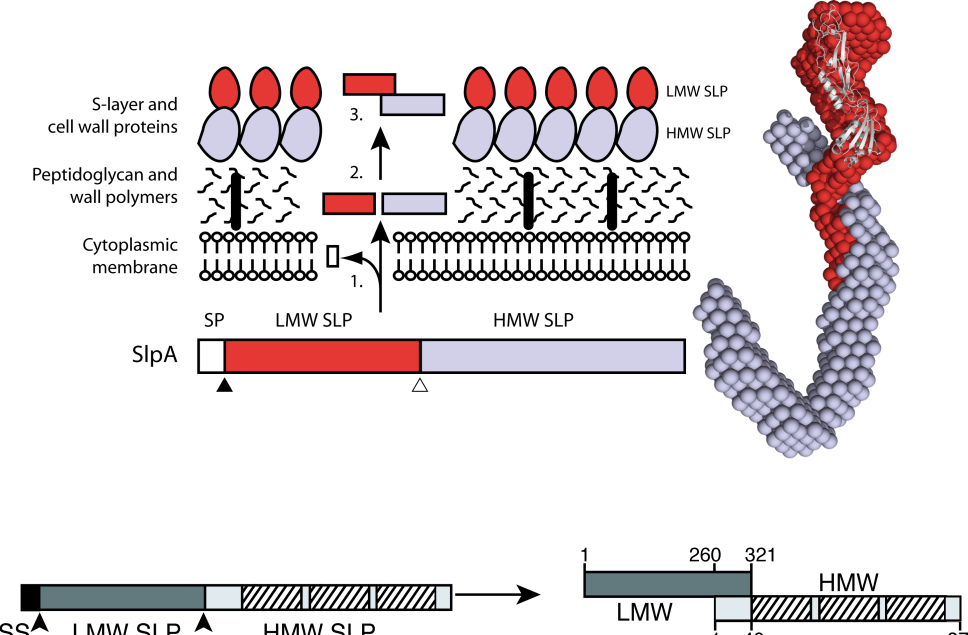
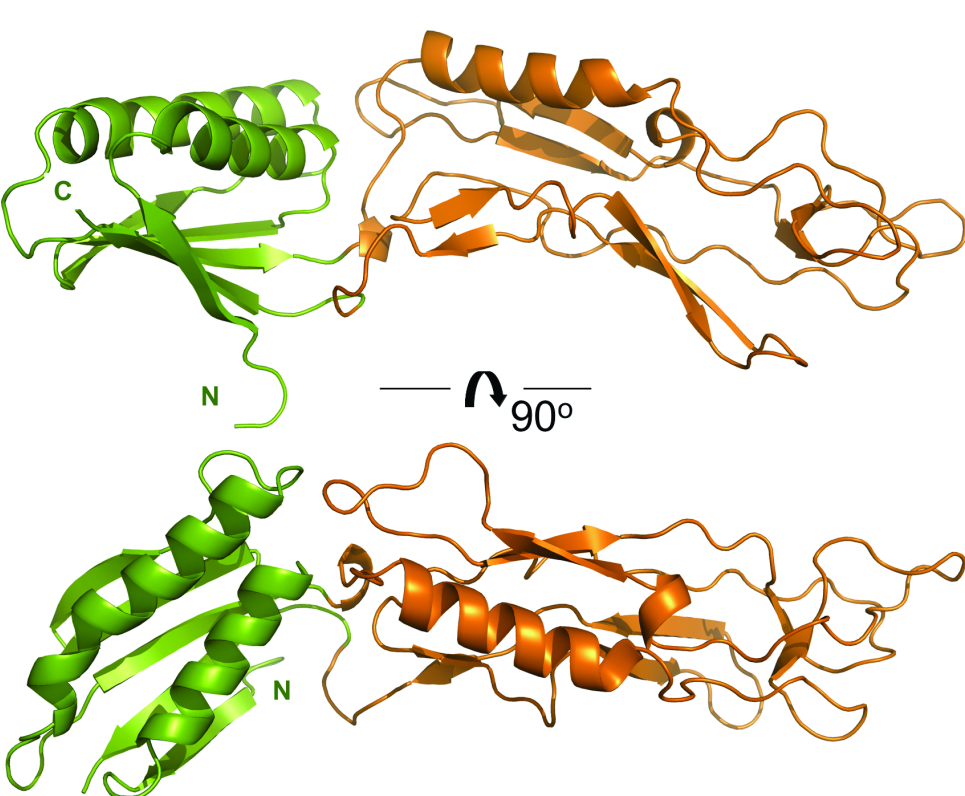
○ Ser-Gly rich region
■ CwpV - specific

Fagan *et al.*, J Med Micro. 2011

***C. difficile* S-layer:**

- SlpA major constituent
- 29 identified CWPs
- Many of unknown or putatively assigned function

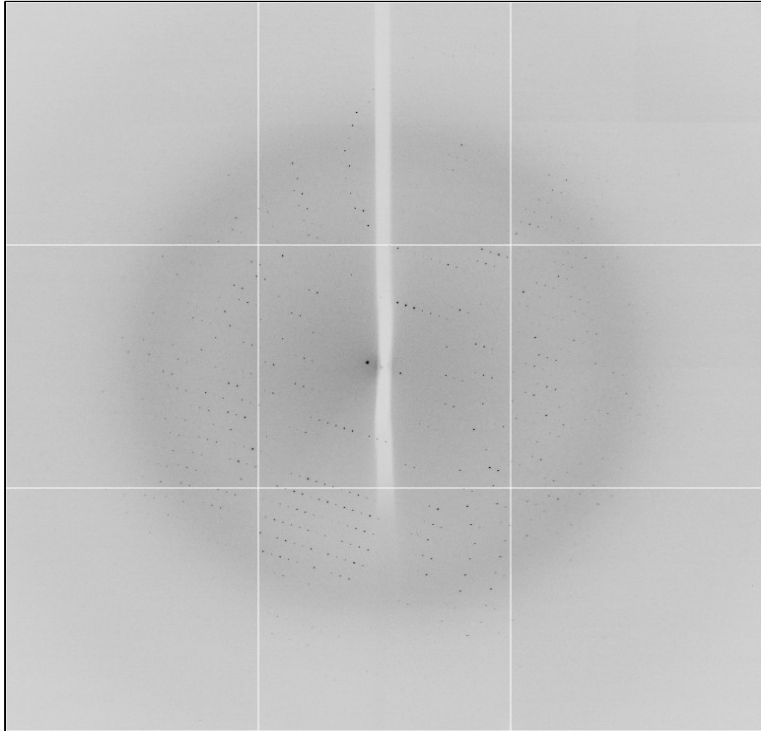
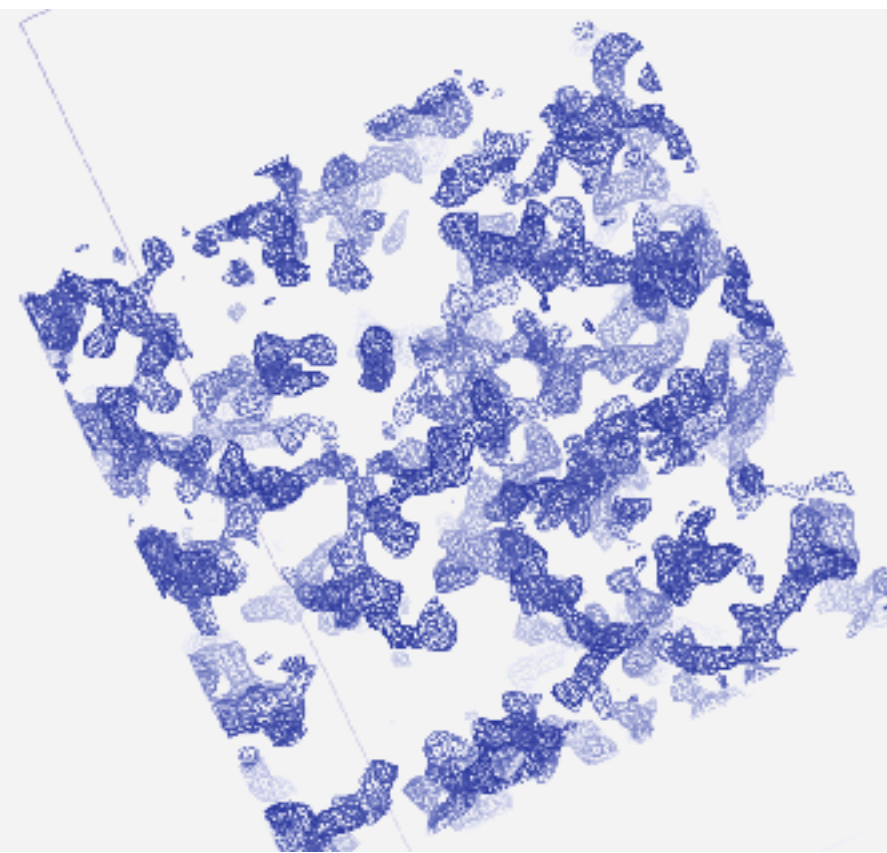
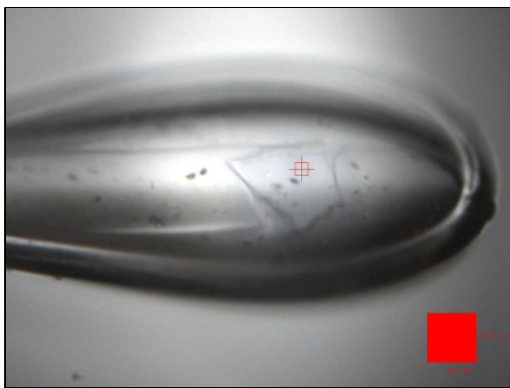
SlpA: Complex of Low (LMW) and High Molecular Weight (HMW)



Fagan *et al.*, Mol Microbiol. 2009

LID-HID complex:

- Interacting domains:
 - Residues 260-321 LMW
 - Residues 1-40 HMW

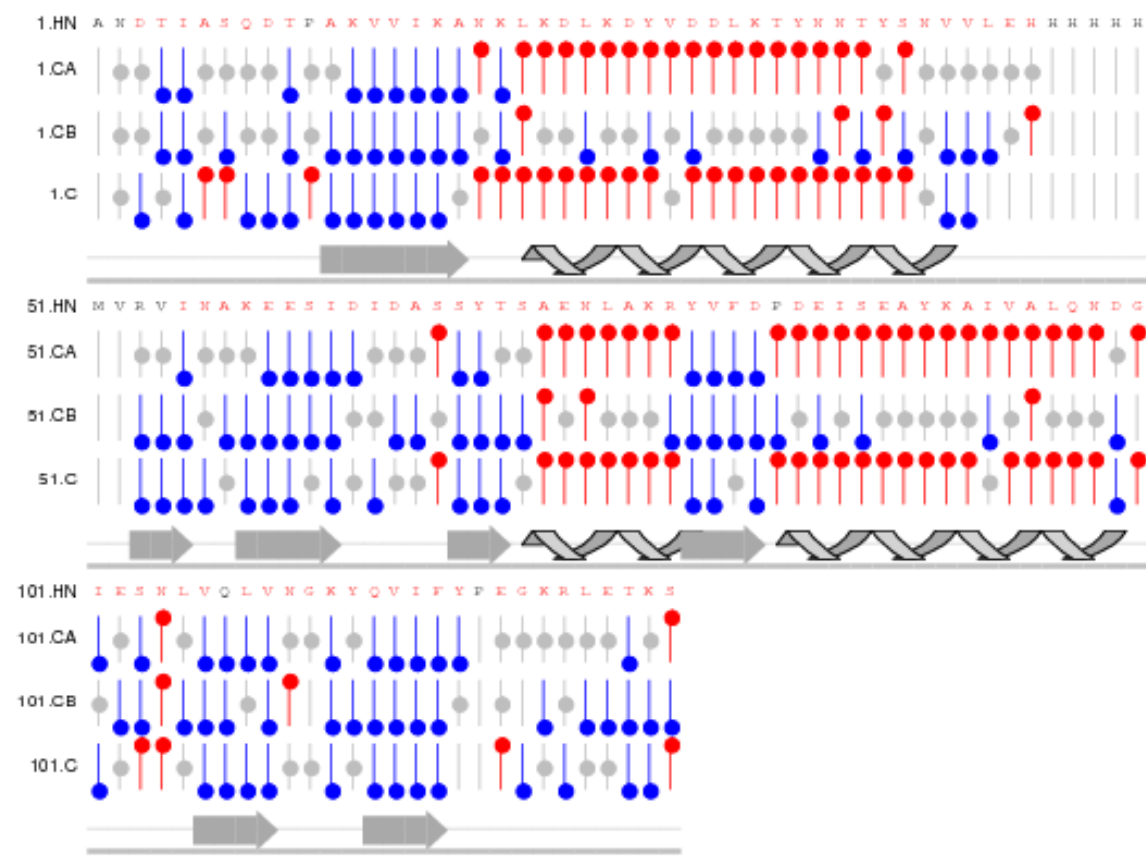


- P2, 8 molecules asymmetric unit
- Phases too weak to build model

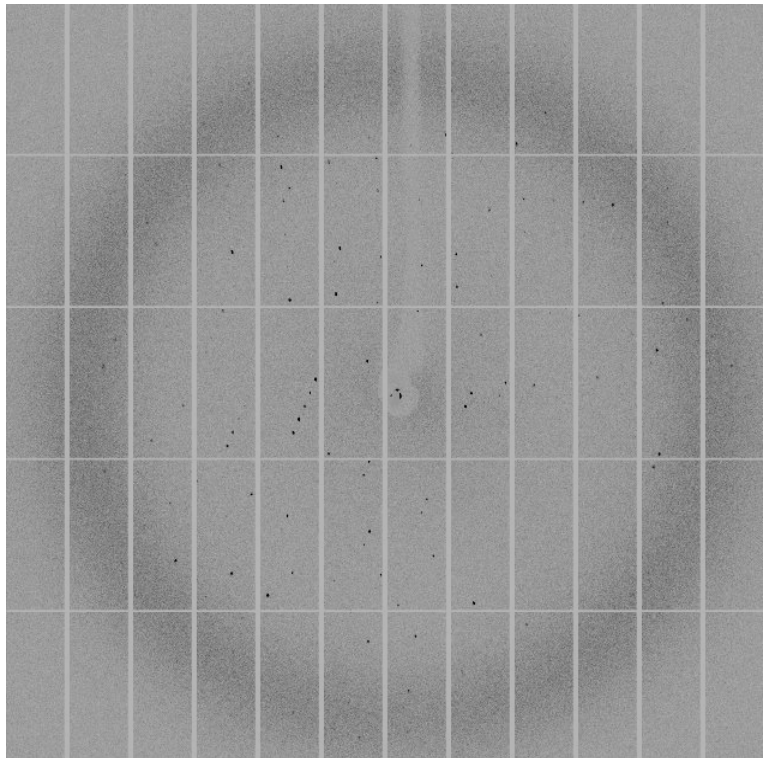
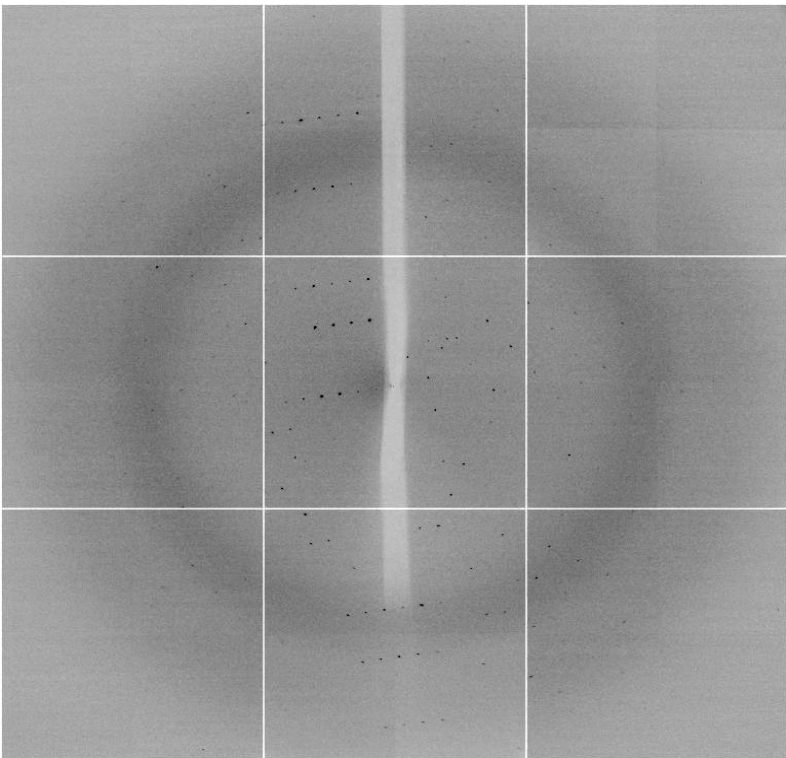
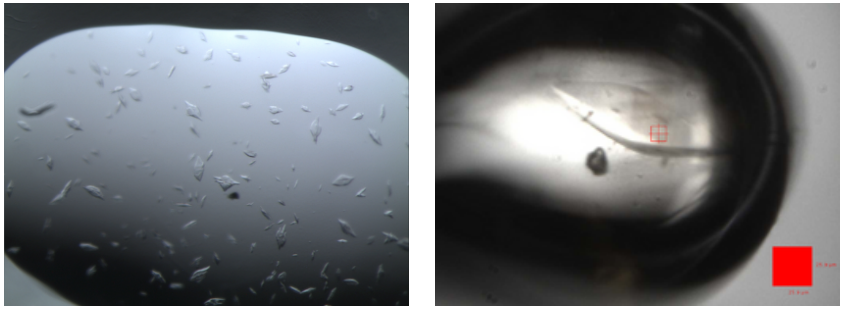
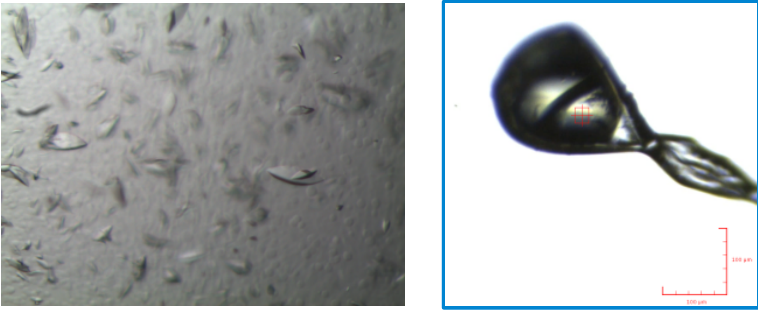
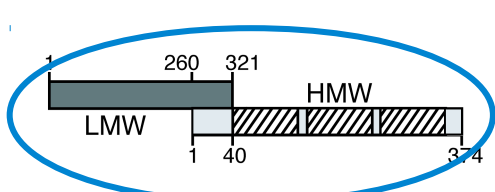
• NMR studies

- Backbone assignment: 91% complete
- Side chains assignment: 75% aliphatic, 100% aromatic

• Structure calculations ongoing



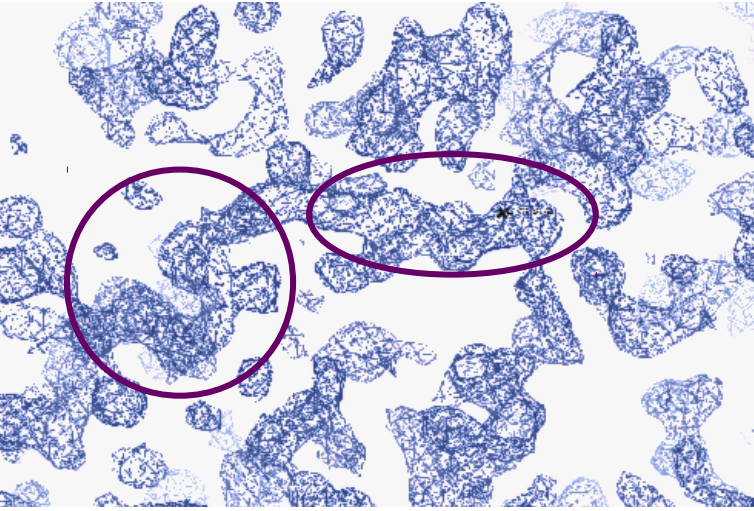
LMW-HMW complex:



Native

SeMet derivative

- P1, 2 molecules asymmetric unit
- Low resolution (~3.0Å)
- Weak anomalous signal for SeMet
- No suitable heavy atom derivative



Compound	Co-xtal	Soak	Processable	Resolutio n	Anomalous signal
K ₂ PtCl ₄	no	yes	3 no, 2 yes	< 4	weak
K ₂ PtBr ₄	no	yes	1 Pt no, 2 Br yes	< 6	weak
NaAuCl ₄	no	yes	no	-	-
(CH ₃) ₃ Pb(CH ₃ COO) (PbTMA)	yes	no	2 yes, 2 no	7 - 8	weak

Future work:

- Finalise LID-HID NMR model
- Determine and refine LID-HID crystal structure
- Study S-layer organisation and assembly by EM

- Optimise crystallisation with PbTMA
- Investigate incorporation of other heavy atoms
- Improve crystal quality using micro-seeding and dehydration
- Introduce Met residues to increase SeMet anomalous phasing power