ESRF	**Experiment title:** Type IVSSb Efftector Proteins	**Experiment number**: Mx1782
Beamline: ID23-2	**Date of experiment**: from: 5April 2016 to:	**Date of report**:
Shifts:	**Local contact(s)**:	*Received at ESRF:*

Names and affiliations of applicants (* indicates experimentalists):

Dr Marie Prevost
ISMB,
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Report:

We aim to solve the crystal structure of protein effectors from *Legionella pneumophila*, a bacterial intracellular pathogen responsible for Legionnaire's disease.
Those proteins are secreted into the eukaryotic host cell cytoplasm during the infection cycle, and interact with various protein targets to "hijack" the normal cellular processes in order for the bacteria to survive and replicate.
Solving their structure will allow a better understanding of the molecular basis of the infection process.
A native dataset was previously collected from crystals of one of those purified effector, an enzyme that catalyses dephosphorylation reactions. To solve the structure, we are now trying experimental phasing using selenomethionine protein and co-crystalization with heavy atoms.

The beamtime was used to screen selenomethionine protein crystals for structure solving (SAD), and for Mn2+ co-crystallization in the native protein crystal. A total of 6 crystals screened.

Crystals were not good enough for whole data collection, but allowed us to investigate better crystallization conditions.

ESRF	**Experiment title:** Type IVSSb Effector Proteins	**Experiment number**:
Beamline: ID23-1	**Date of experiment**: from: 09May2016 to:	**Date of report**:
Shifts:	**Local contact(s)**:	*Received at ESRF:*

Names and affiliations of applicants (* indicates experimentalists):

Dr Marie Prevost
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Birkbeck College
London, UK

Report:

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The beamtime was used to screen for ion co-crystallization, and for Br-soaked crystals for structure solving (SAD). From the 11 crystals screened, four complete datasets were collected up to 2.8Å, but no heavy atoms were found during processing.