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Supporting information for article:

A simple vapor-diffusion method enables protein crystallization inside the HARE serial crystallography chip

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A simple vapor diffusion method enables protein crystallization inside the HARE serial crystallography chip

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Supplementary Material

Supplementary Figures

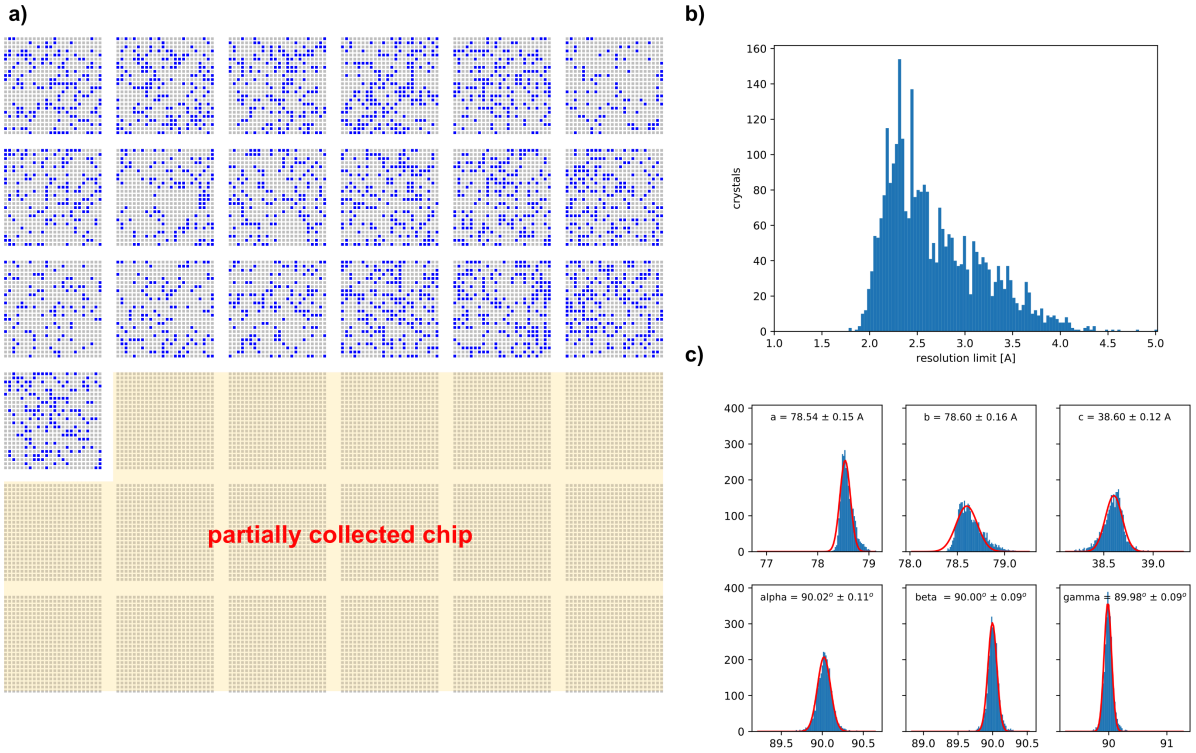
a) Hit-map: a blue dot on the grey outline of the chip compartments indicates a feature for which one or more protein diffraction pattern(s) could be obtained. For partially collected chips, the missing parts are indicated in yellow.

b) Resolution histogram of the diffraction patterns obtained for each chip.

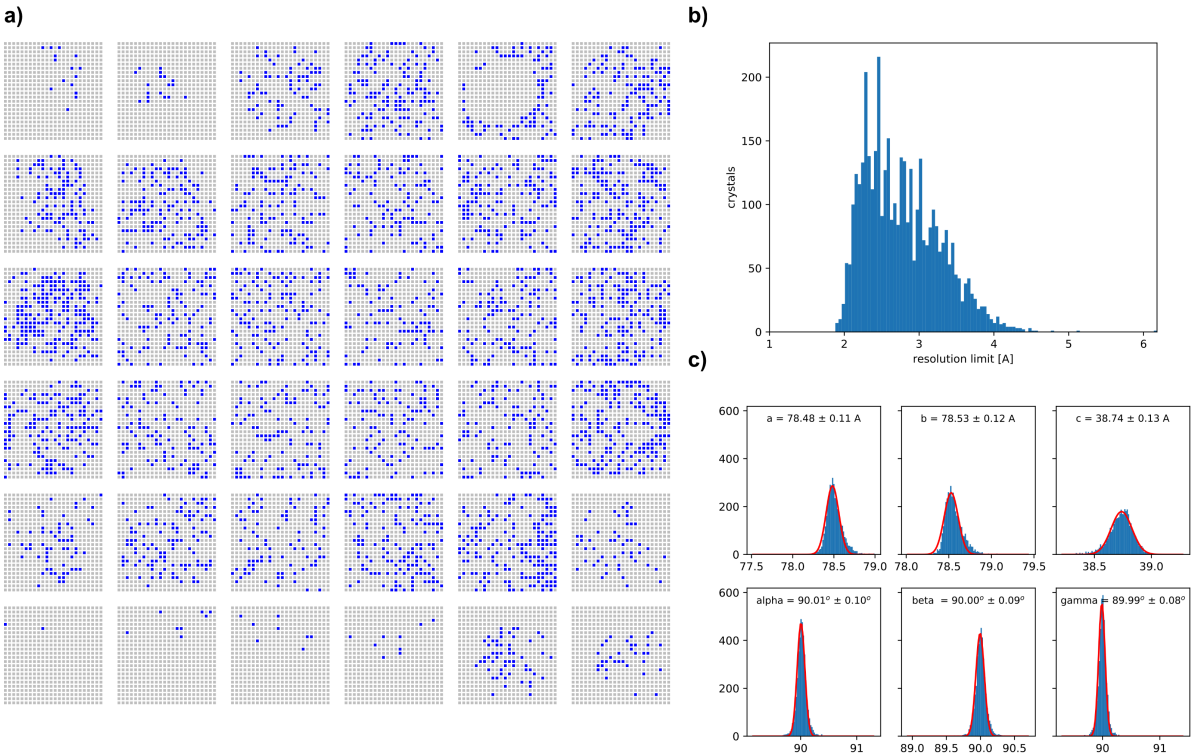
c) Unit cell parameter histogram of the diffraction patterns obtained for each chip.

Lysozyme

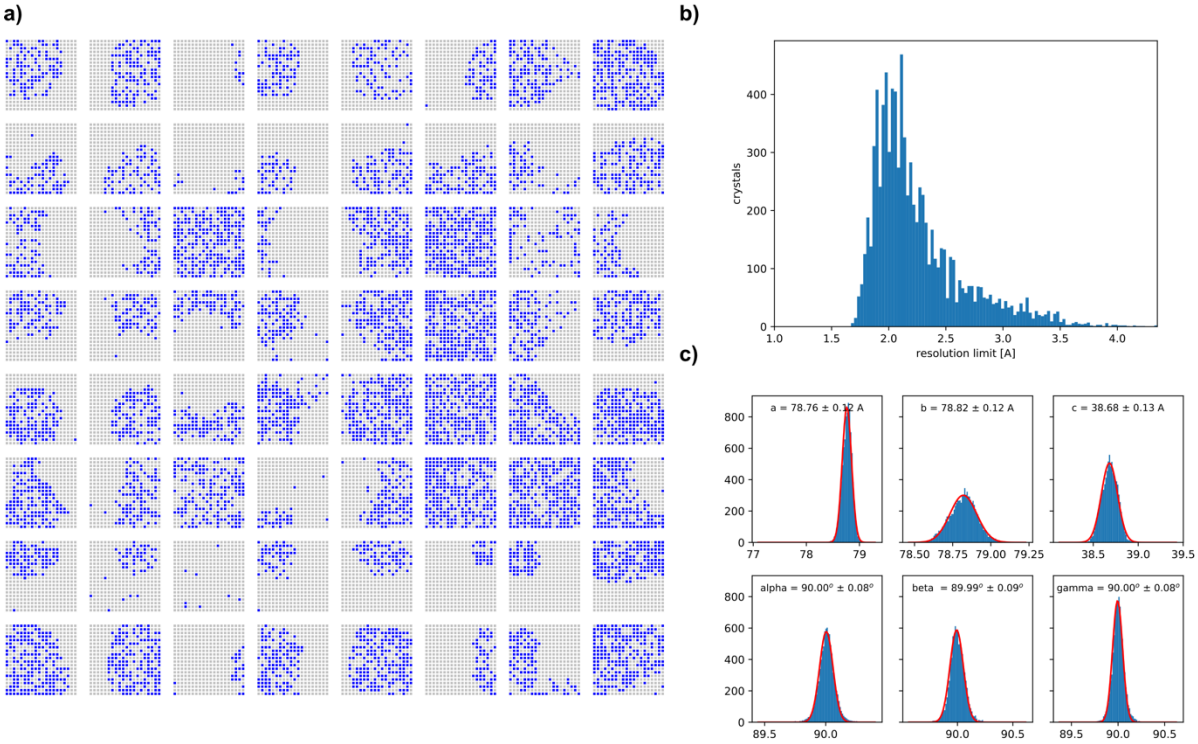
Chip1



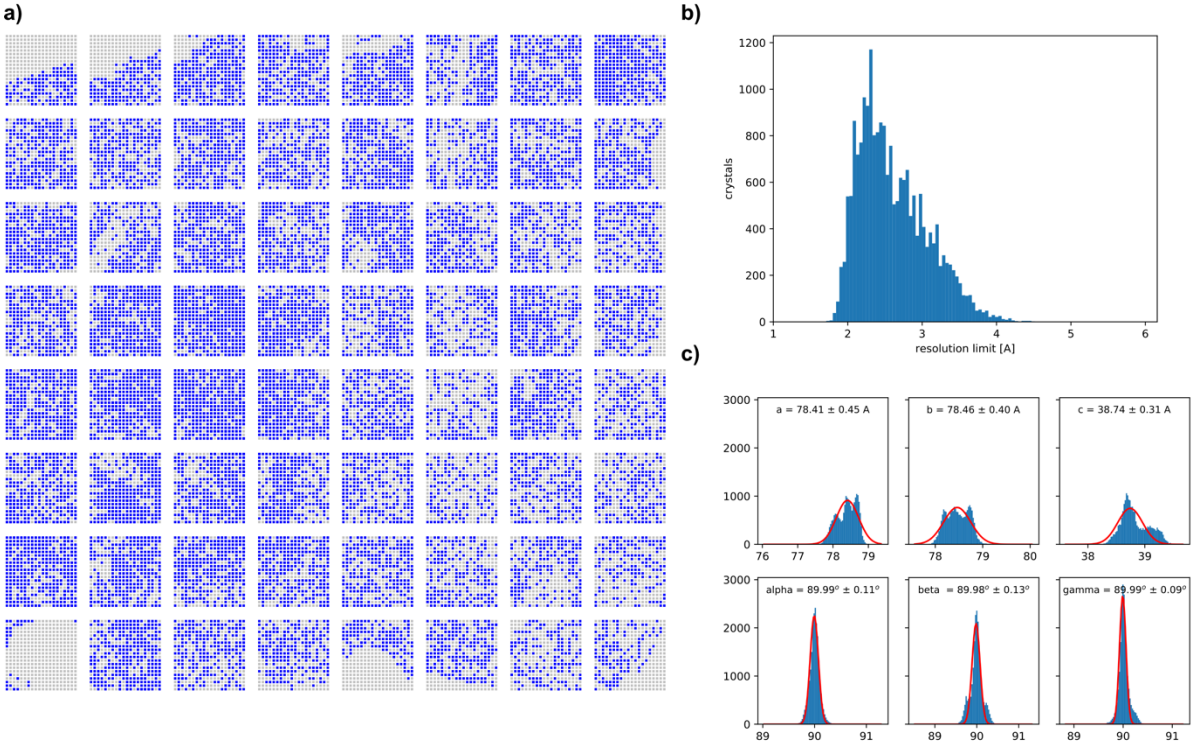
Chip2



Chip3

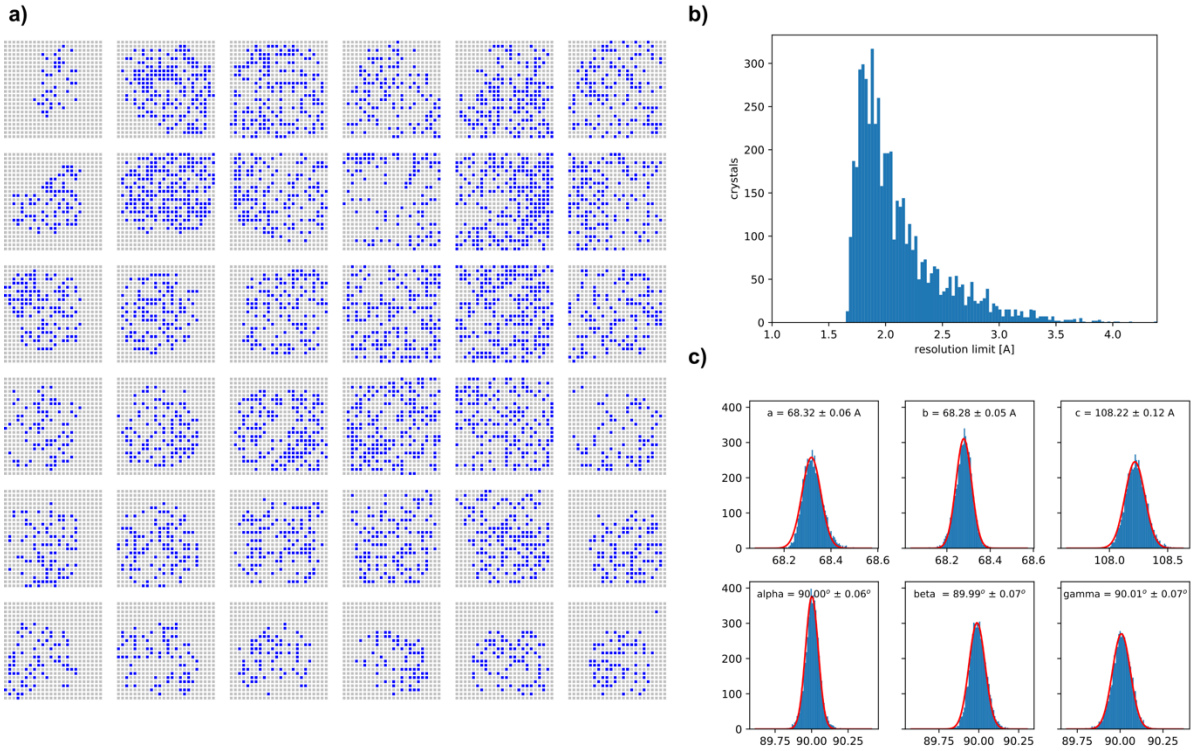

a)
b)
c)
crystals
resolution limit [A]
a = 78.76 ± 0.12 A
b = 78.82 ± 0.12 A
c = 38.68 ± 0.13 A
alpha = 90.00° ± 0.08°
beta = 89.99° ± 0.09°
gamma = 90.00° ± 0.08°

Chip4

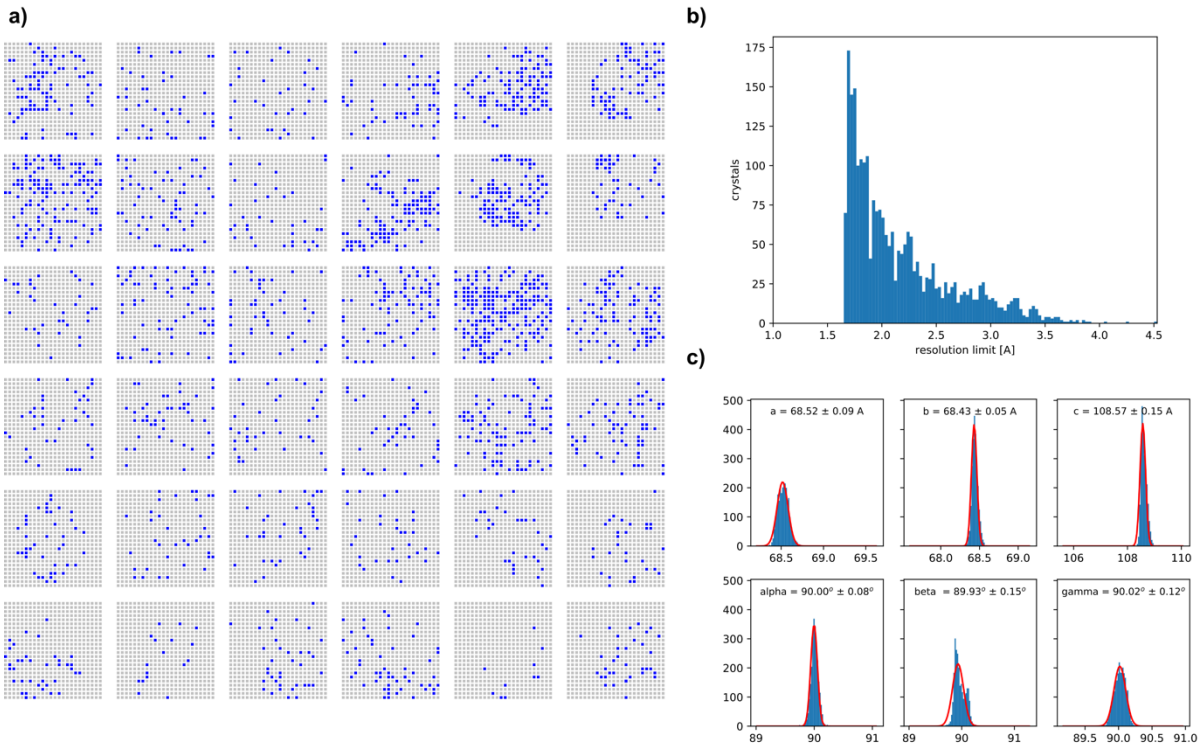

a)
b)
c)
crystals
resolution limit [A]
a = 78.41 ± 0.45 A
b = 78.46 ± 0.40 A
c = 38.74 ± 0.31 A
alpha = 89.99° ± 0.11°
beta = 89.98° ± 0.13°
gamma = 89.99° ± 0.09°

Proteinase K

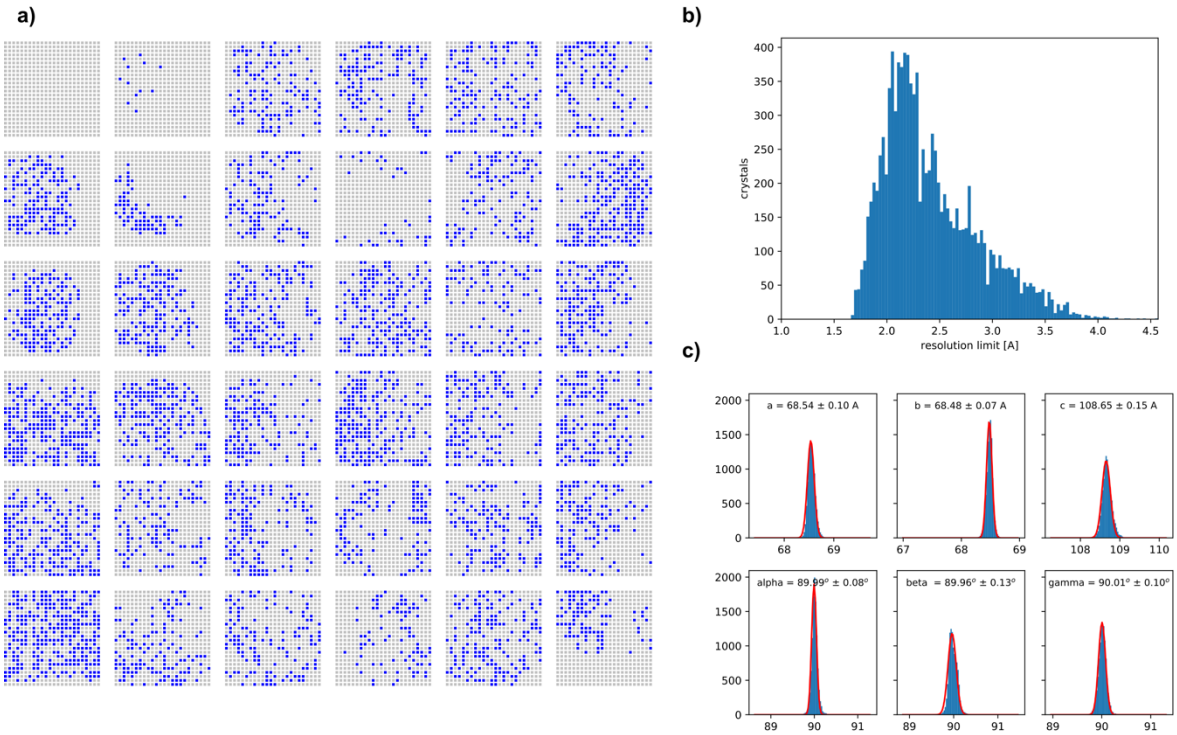
Chip1



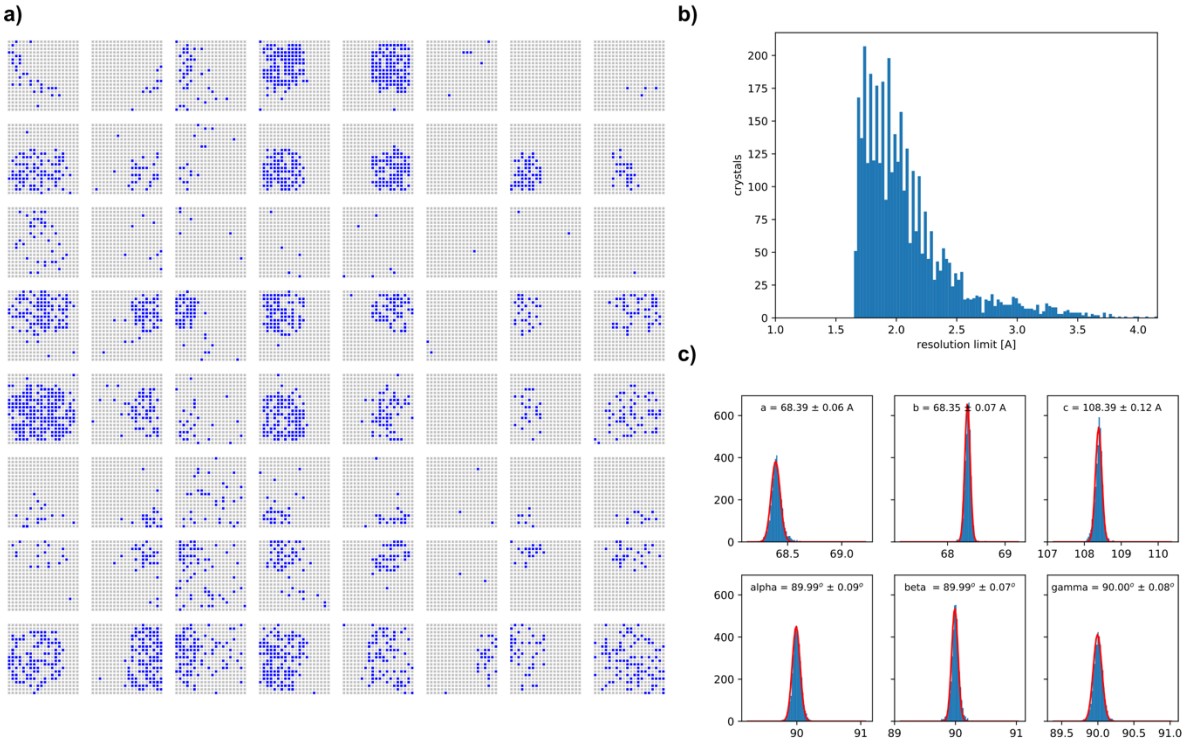
Chip2



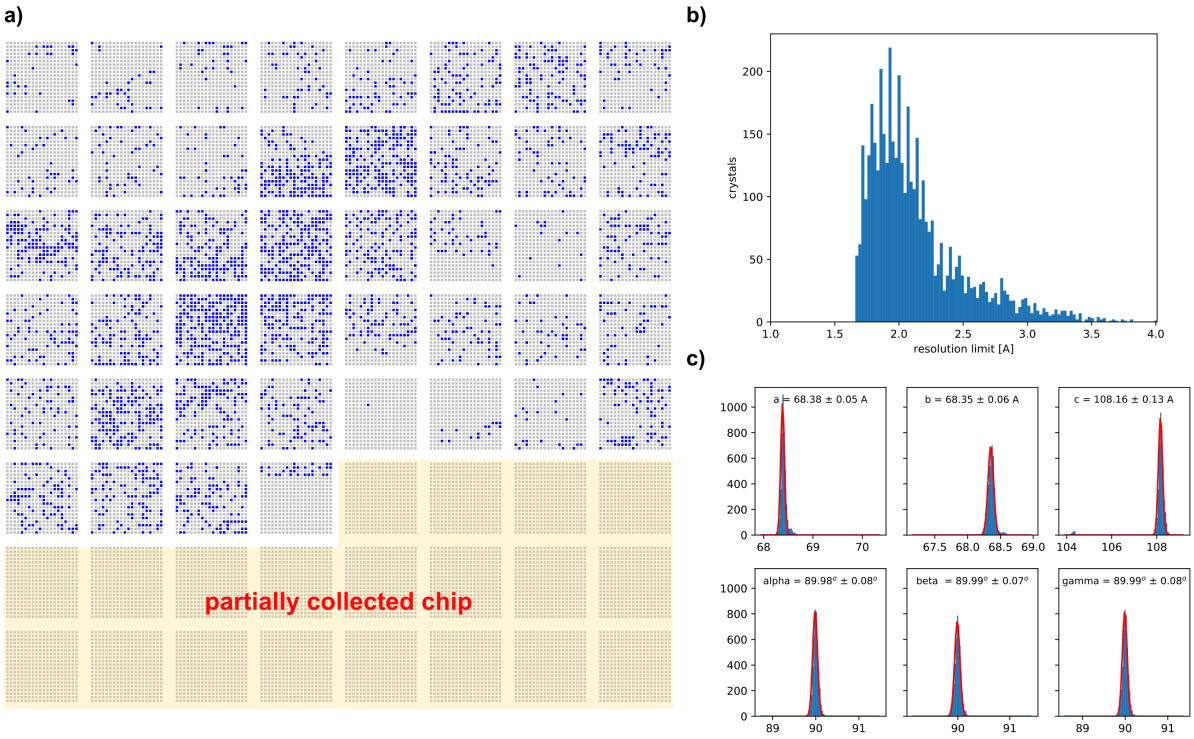
Chip3


a)
b)
crystals
resolution limit [A]
c)
a = 68.54 ± 0.10 A
b = 68.48 ± 0.07 A
c = 108.65 ± 0.15 A
alpha = 89.99° ± 0.08°
beta = 89.96° ± 0.13°
gamma = 90.01° ± 0.10°

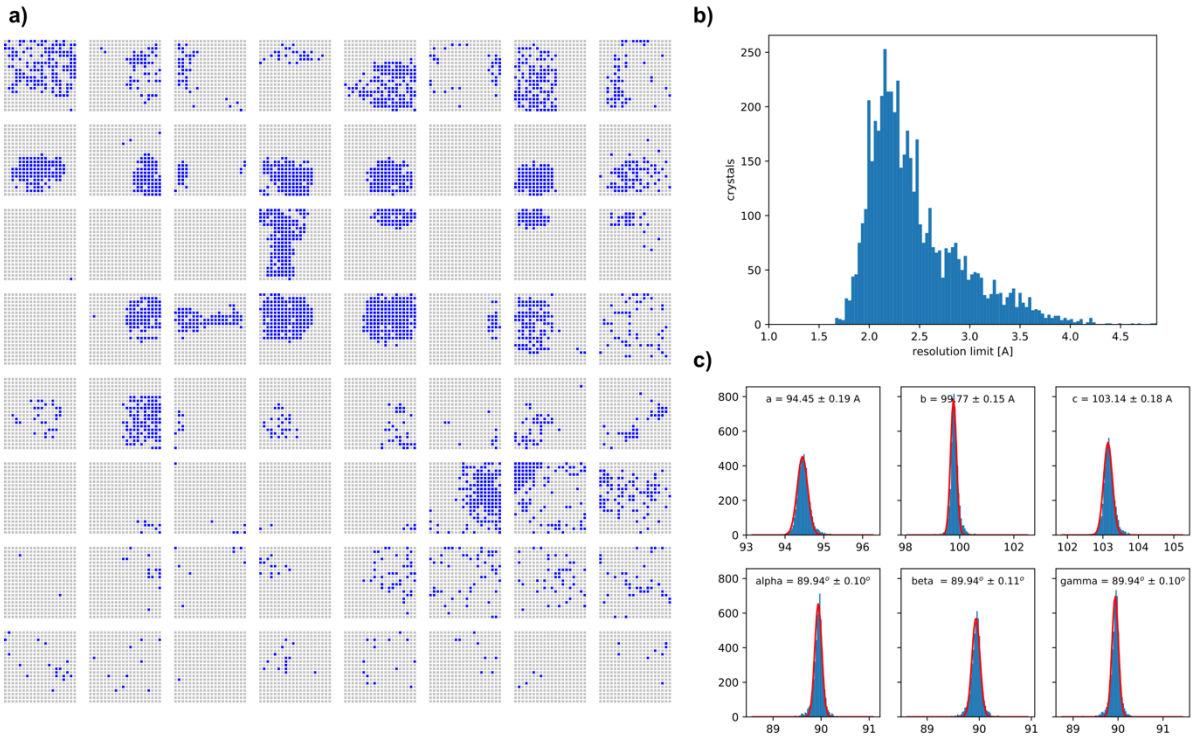
Chip4


a)
b)
crystals
resolution limit [A]
c)
a = 68.39 ± 0.06 A
b = 68.35 ± 0.07 A
c = 108.39 ± 0.12 A
alpha = 89.99° ± 0.09°
beta = 89.99° ± 0.07°
gamma = 90.00° ± 0.08°

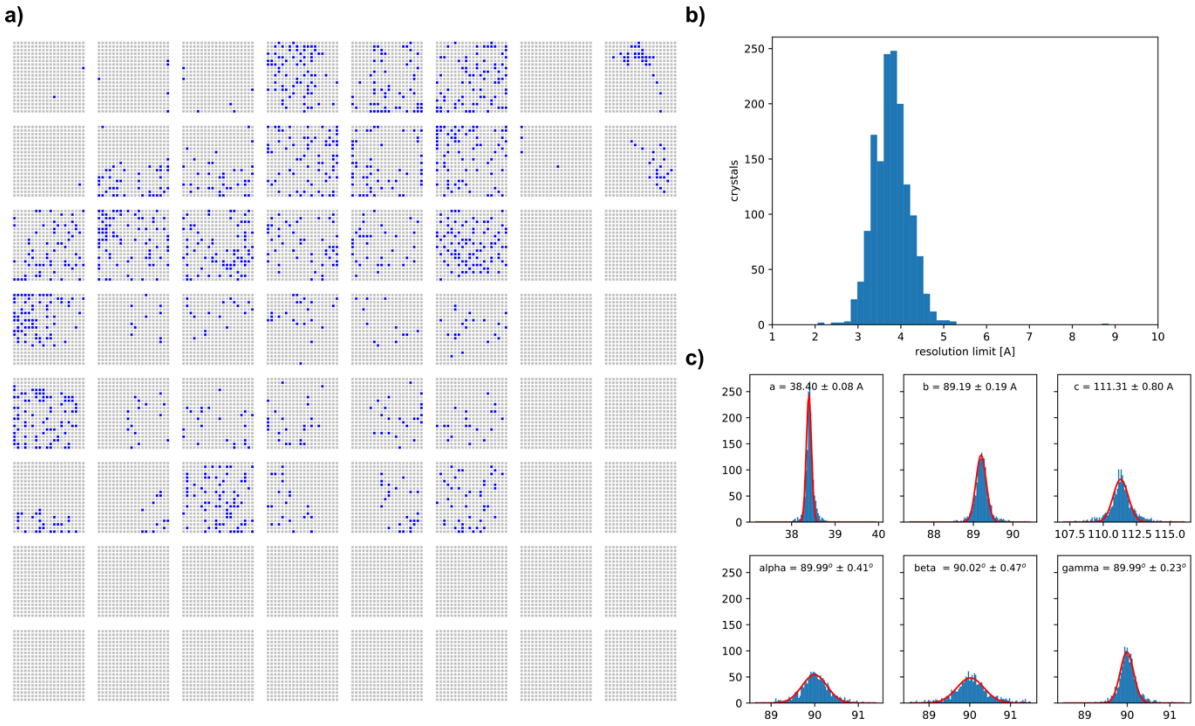
Chip5



Xylose isomerase

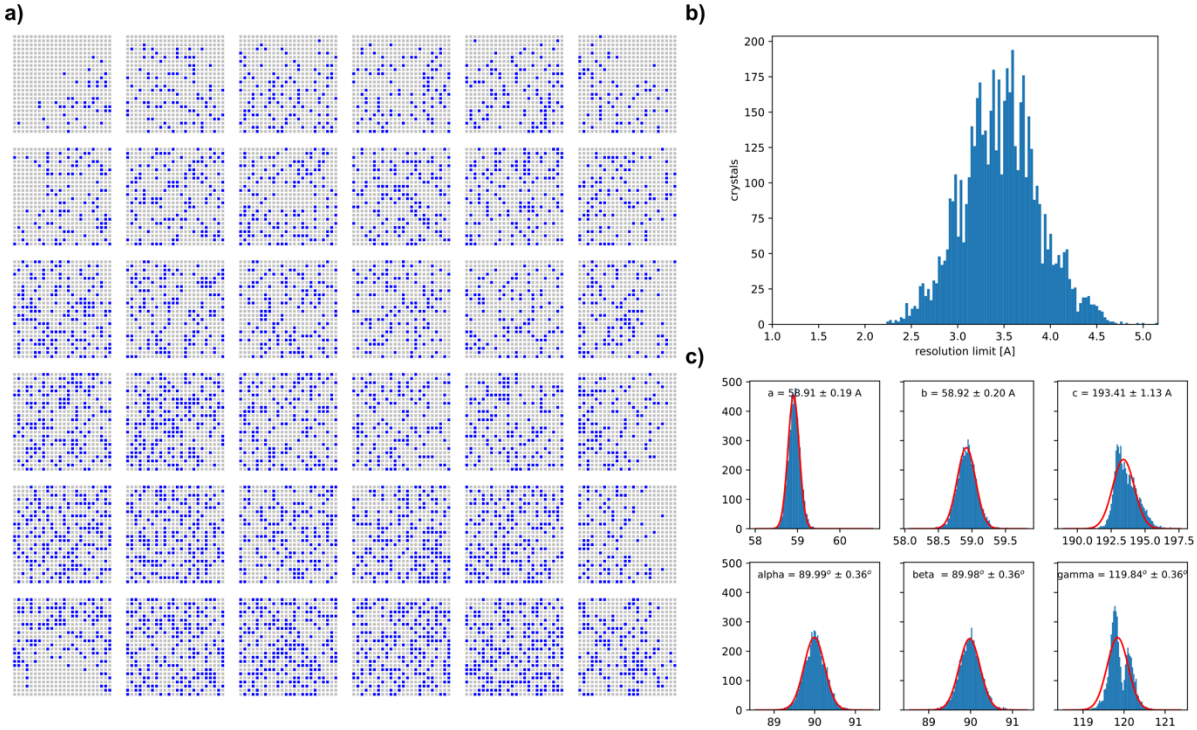


γS-crystallin mutant



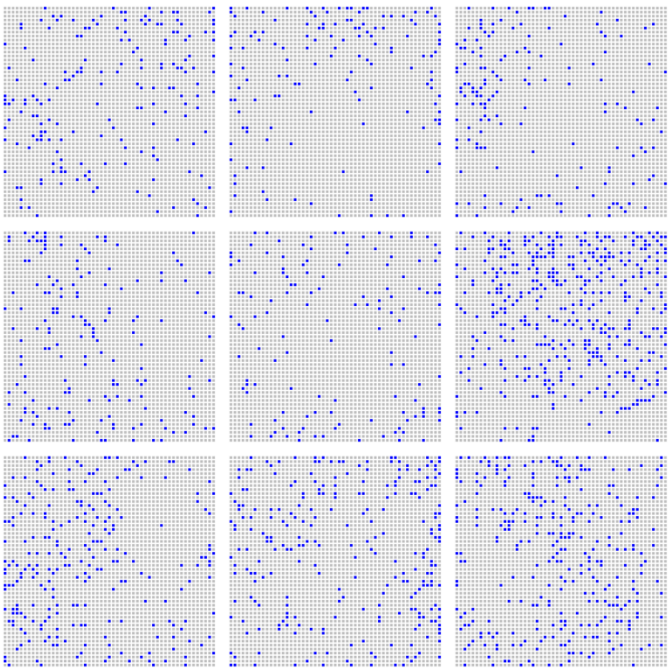
Hex-1

Chip1 (loaded)

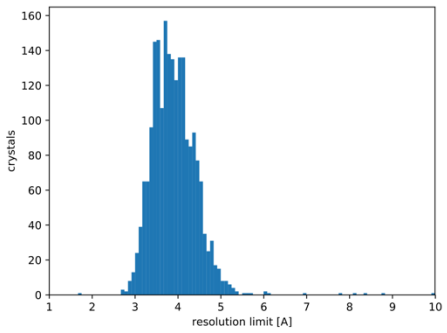


Chip2 (in-situ)

a)



b)



c)