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OH1 from Orf virus: a new tyrosine phosphatase that displays distinct structural features and triple substrate specificity

Gwenaëlle André-Leroux

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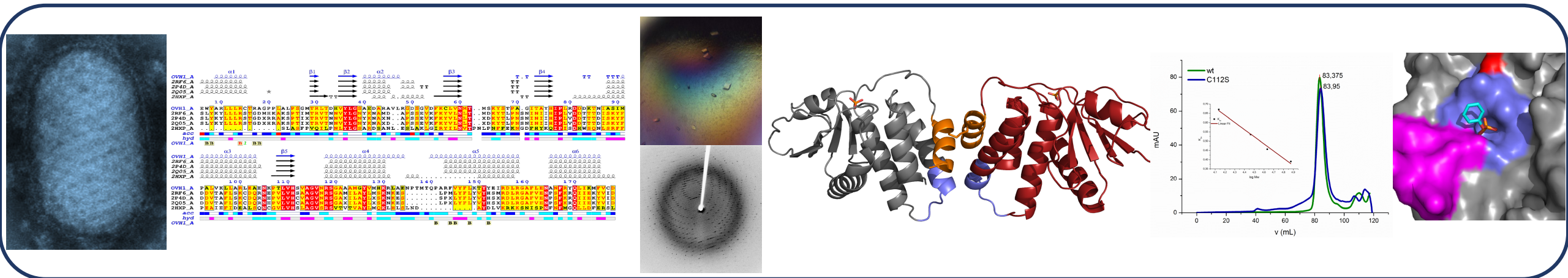
Submitted on 4 Jun 2020

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OH1 from Orf virus: a new tyrosine phosphatase

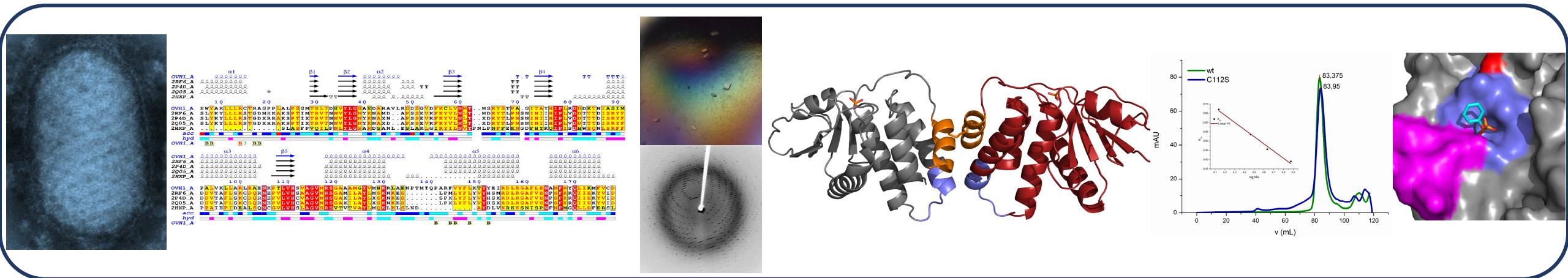
Distinct structural features & triple substrate specificity



Gwenaëlle André-Leroux
 MaIAGE, INRA Jouy-en-Josas
 Mathématique et Informatique Appliqués du Génome à l'Environnement

Workshop: « Modelling bio-molecular interactions: A multi-scale approach joining theory and experiments »

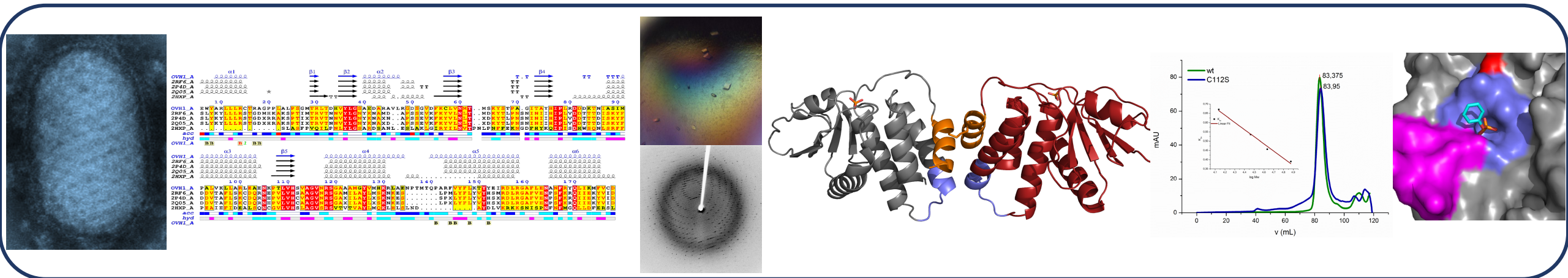
OH1 from Orf virus: a new tyrosine phosphatase



Outline

- Orf virus introduction
- OH1 structural characterization *in silico/in vitro*
- OH1 functional characterization *in silico/in vitro*
- Conclusions & perspectives

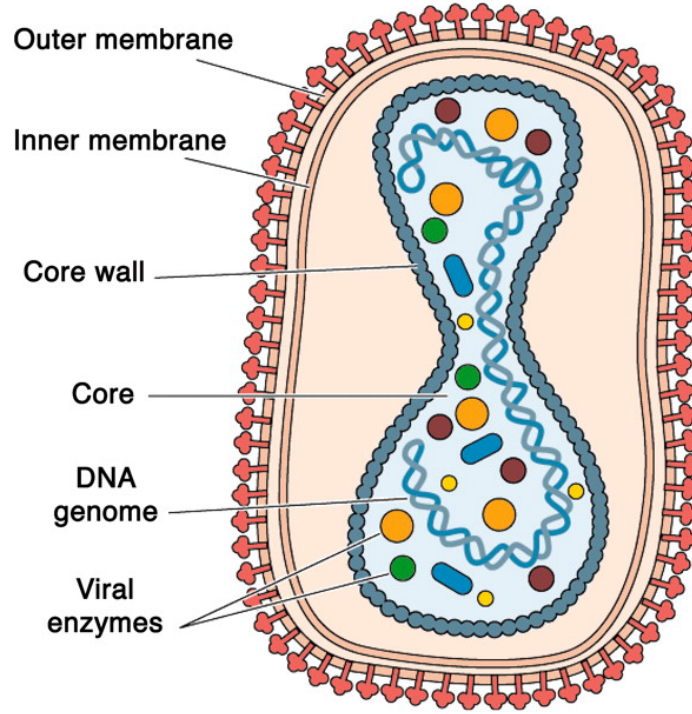
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Orf virus

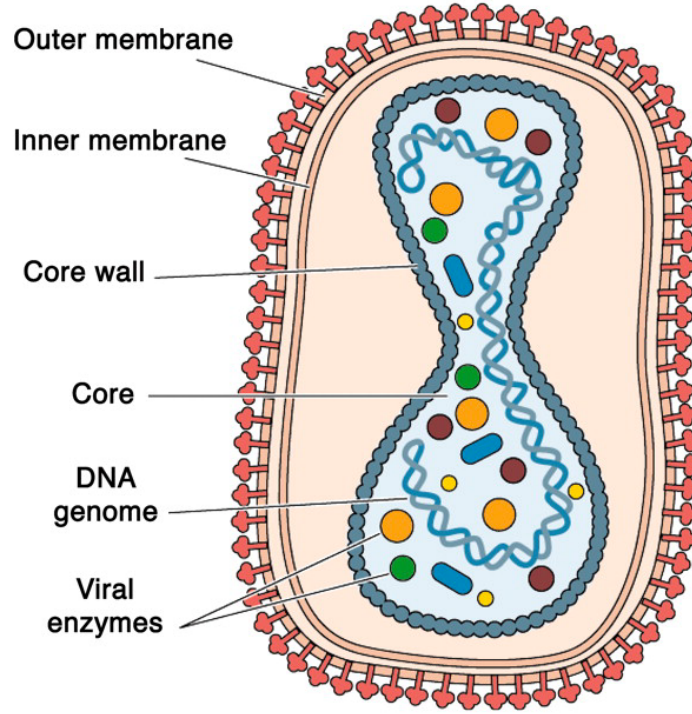


Orf Poxvirus family
Like Vaccinia & Variola virus

dsDNA virus
Large 200-300 nm
Envelope

Orf = old english for « rough »

Orf virus

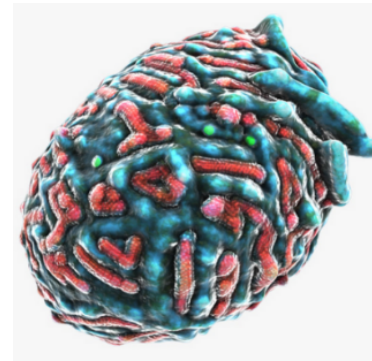
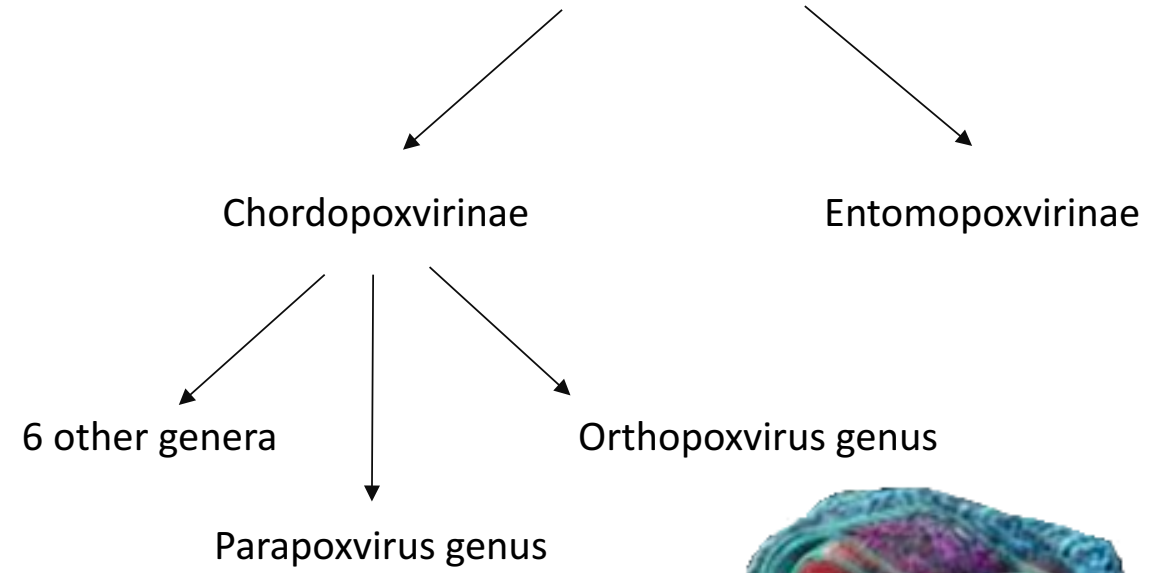


dsDNA virus
Large 200-300 nm
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Orf Poxvirus family
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Poxvirus family



Bovine papular stomatitis virus
Parapoxvirus of red deer in New Zealand
Pseudocowpox virus



Vaccinia virus
Variola virus
Cowpox virus

Orf virus



- Is responsible for Ecthyma disease primarily in sheep and goats
- Is contagious pustular dermatitis
- Replicates in keratinocytes and epithelial cells of the oral mucosa.
- Is reported worldwide
- Is purulent for 7 weeks
- Prevents lambs from sucking and cause weight loss
- Causes mastitis to mother ewes
- In its severe form on immune compromised animals can lead to death

Orf virus



- Is responsible for Ecthyma disease primarily in sheep and goats
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Highly contagious by nature

Zoonotic through direct contact

Live vaccine that can cause reinfection



Vaccine: immunity for 6-8 months

Secondary infections

Economical impact +++

Orf virus : new strain isolated in Uruguay in 2015

Strain UY1107 was fully sequenced : shows 90 essential and conserved genes

➡ Among them, a putative virulence factor was identified, by analogy with Vaccinia and Variola viruses

➡ Codes for a putative tyrosine phosphatase

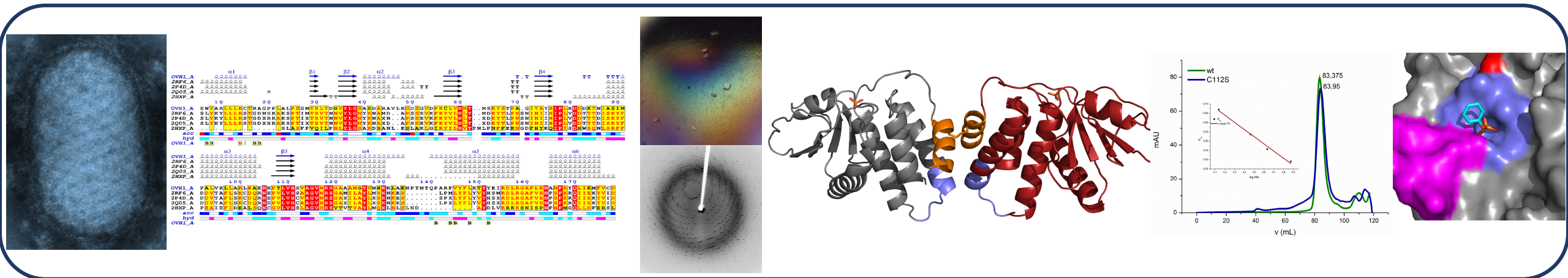
➡ Deposited at genbank ID: KY651216

➡ Hypothesis: KY651216 is a Tyr-phosphatase responsible for dephosphorylation of phosphorylated substrates

Signaling mediators: Tyrosine phosphatase/kinase are molecular switches that turns on/off substrates

OH1 from Orf virus: a new tyrosine phosphatase

Distinct structural features & triple substrate specificity



Outline

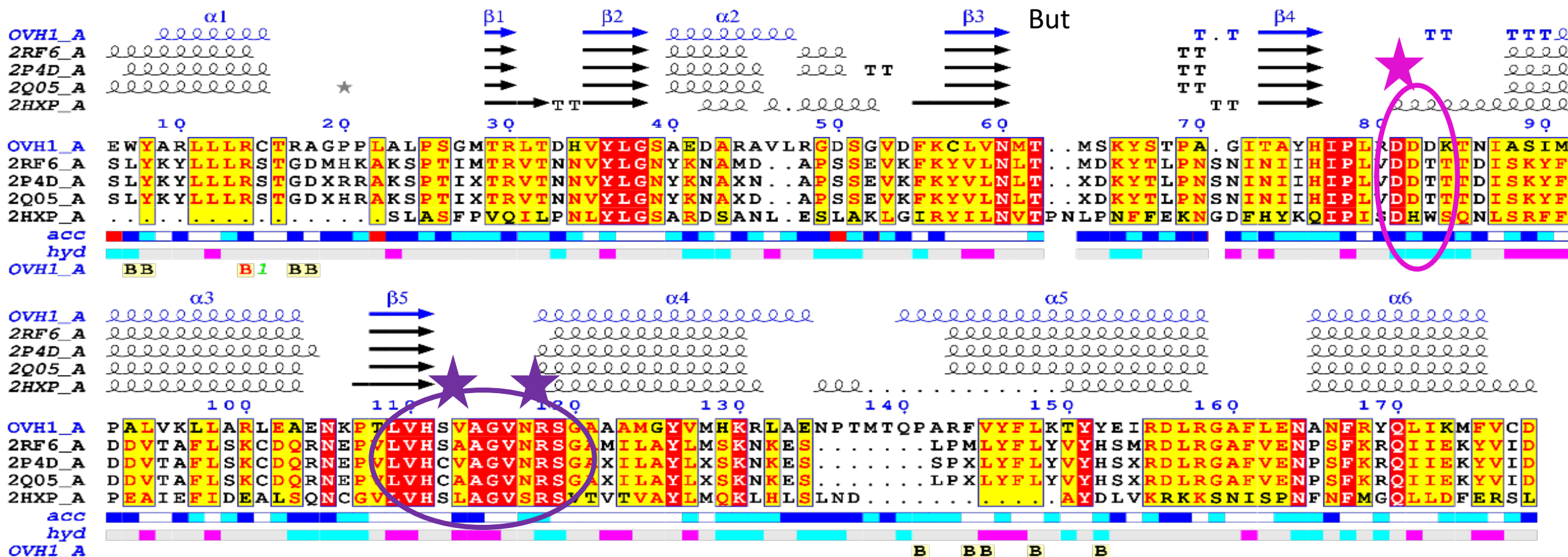
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Putative tyrosine phosphatase

➔ High 40% similarity with Vaccinia and Variola Tyr-phosphatase

➔ Strict conservation of the active site of a Tyr-phosphatase

Active site Aspartate loop

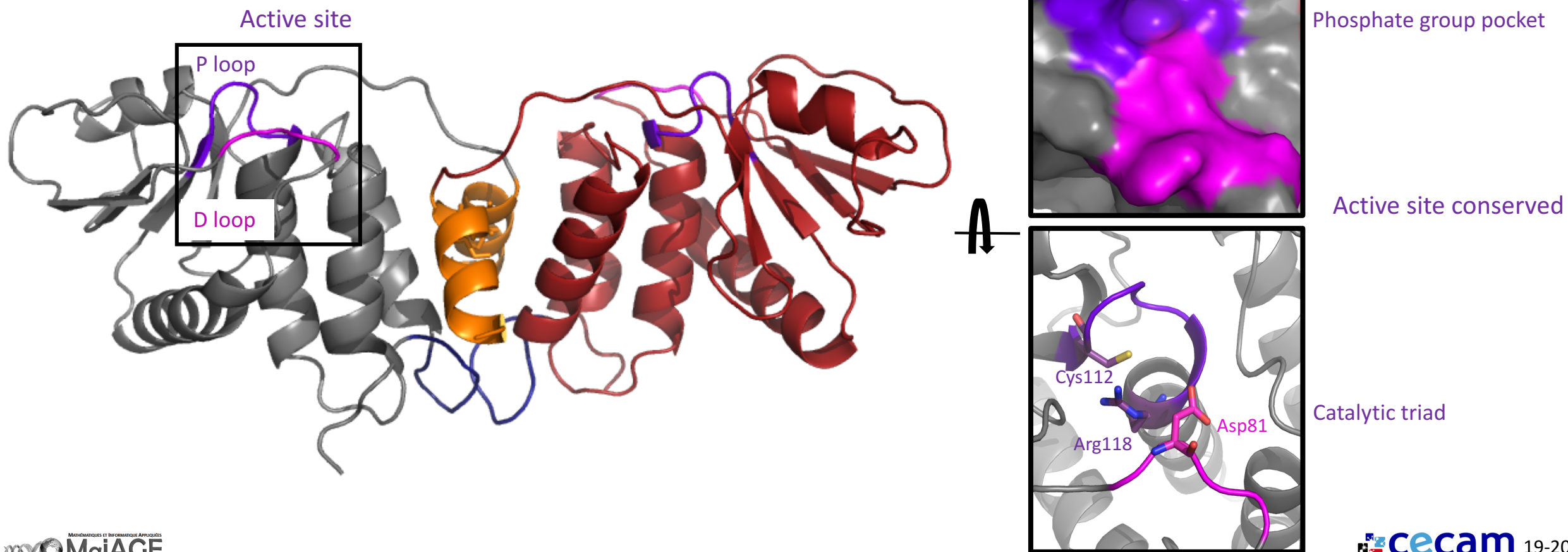


Active site Phosphate loop

7 residue insertion

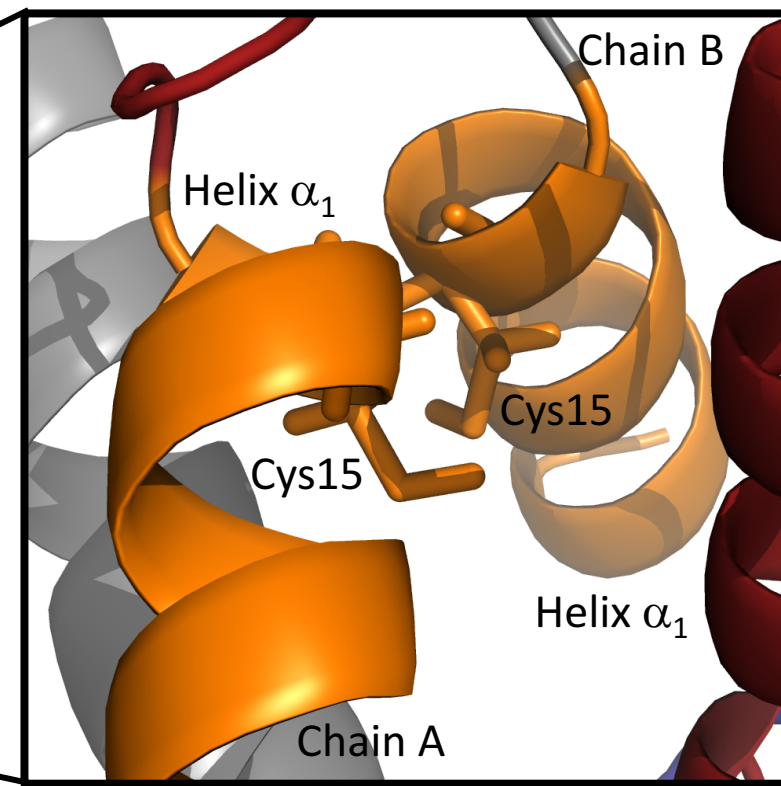
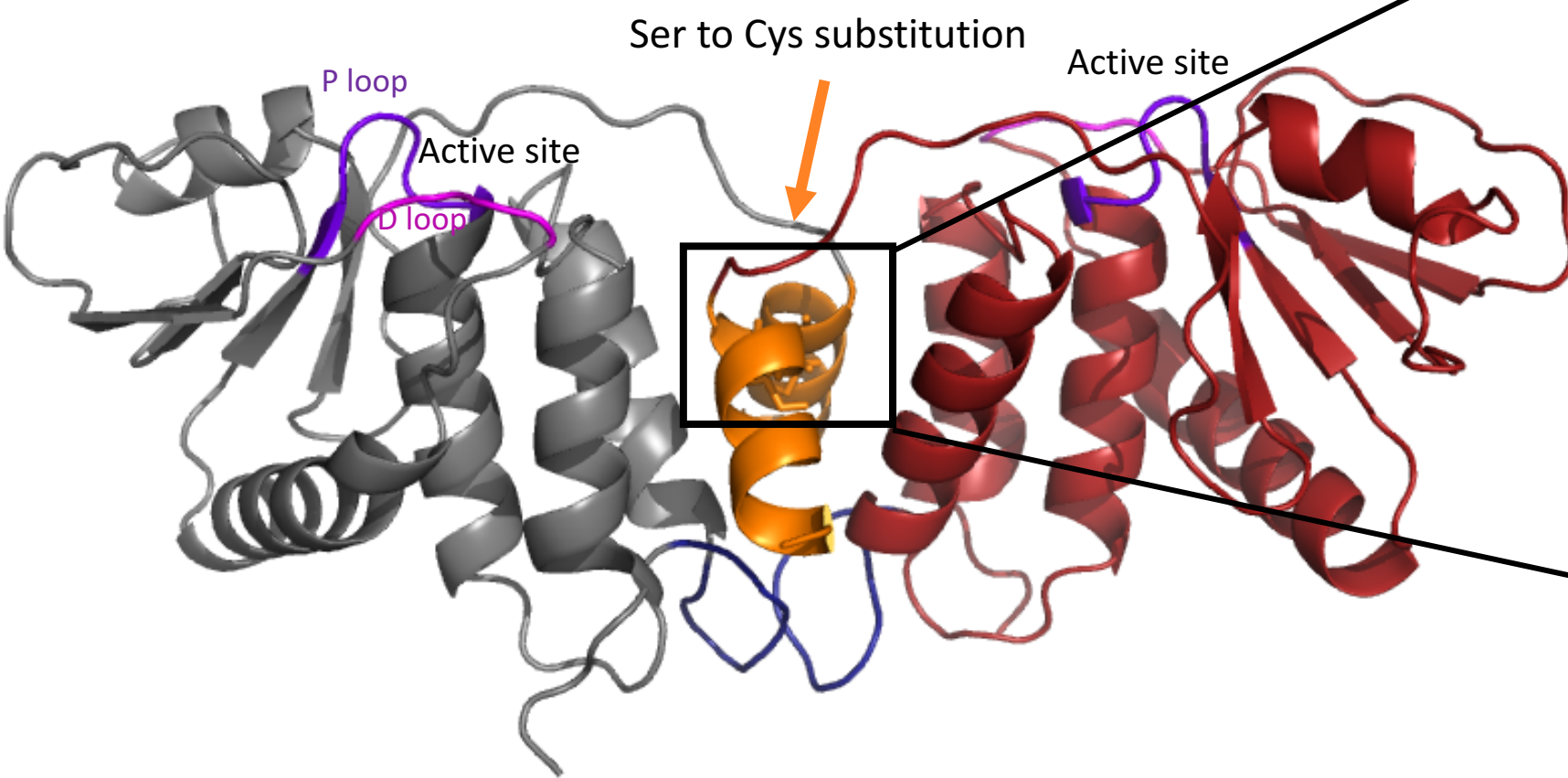
Putative tyrosine phosphatase

- Homology modeling of Tyrosine phosphatase with 3D Vaccinia and Variola VH1 as 3D templates: Chains A then B.
- Reconstruction of the dimer by superposition onto the dimer template.
- Minimisation with Charmm to relax the side chains



Putative tyrosine phosphatase

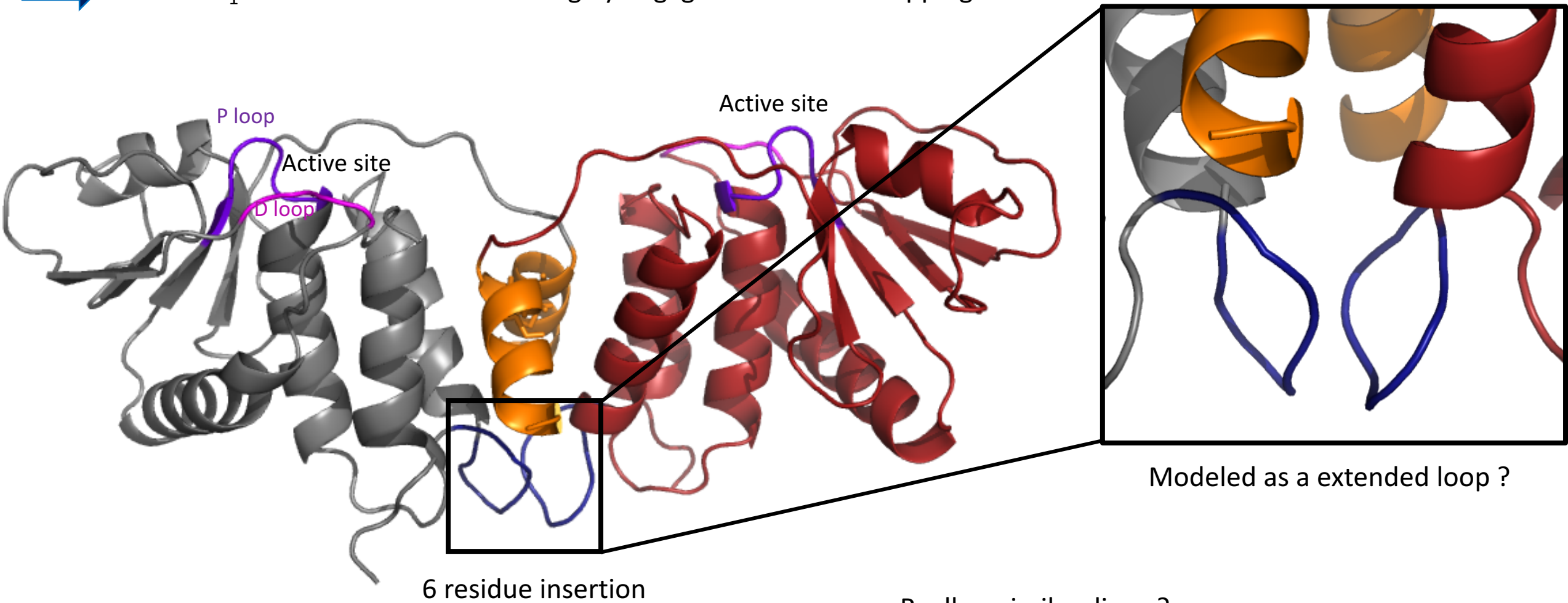
- ➔ The main differences are located at the interface
- ➔ Helix α_1 at the N-terminal end is largely engaged in domain swapping



Cys residues facing each other
Disulfide bridge?

Putative tyrosine phosphatase

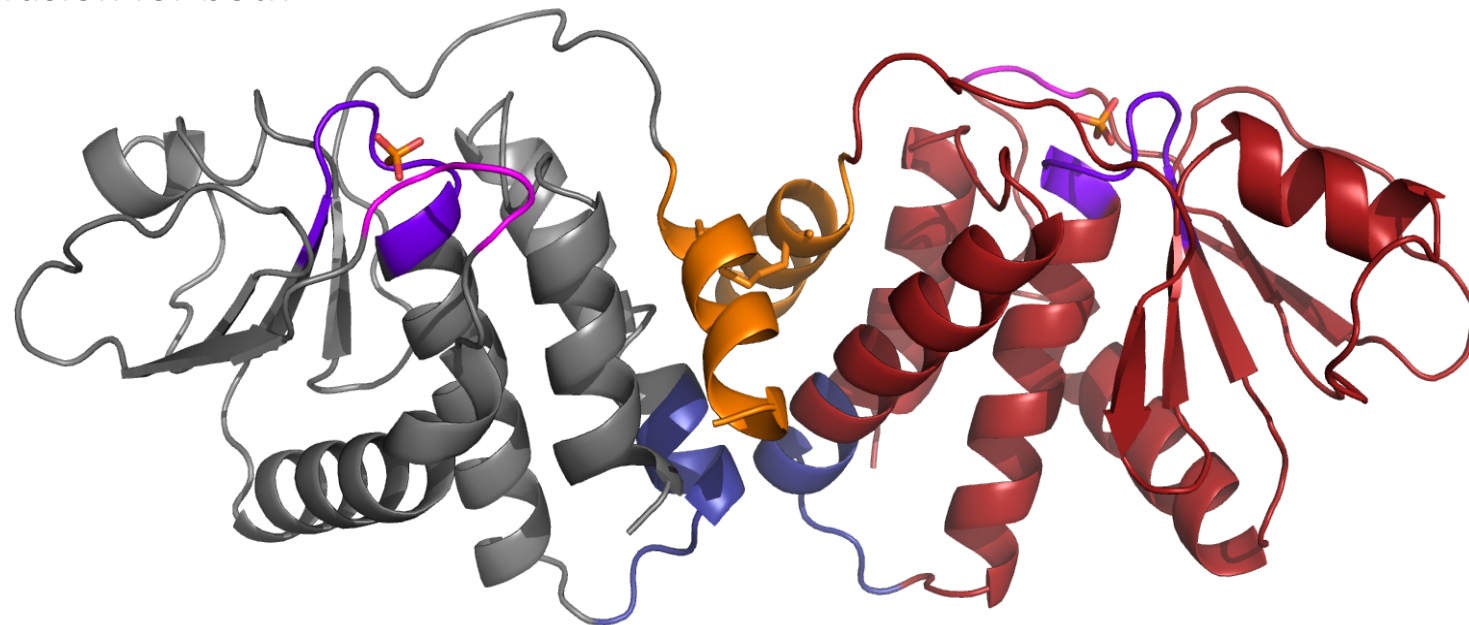
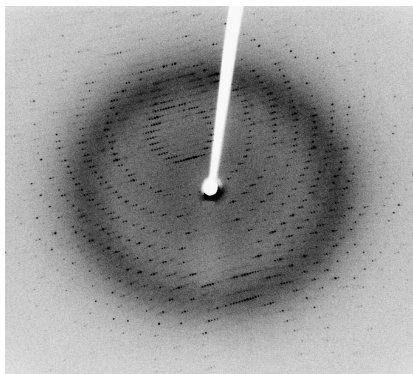
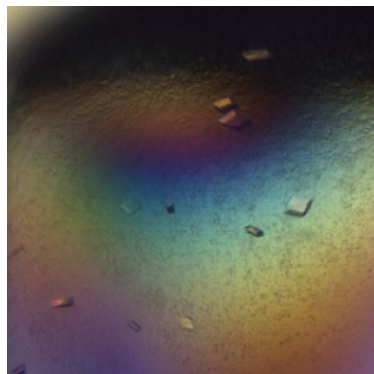
- ➔ The main differences are located at the interface
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Really a similar dimer?

Orf virus : tyrosine phosphatase

- Protein purified to homogeneity Histrap and size-exclusion chromatography wt and C112S
- Crystallisation screening using sitting drop vapor diffusion for both



Cristal conditions
200 mM NH₄SO₄,
100mM NaAc, pH 4,6
PEG MME 2K 30%

Beamline Proxima1
2 sets of data collection



Data statistics 5NCR

P2₁
a, b, c (Å) 49.56 63.55 55.39
 α , β , γ (°) 90.00, 97.07 90.00

Refinement of the best at 1.89 Å resolution

Molecular replacement using Phaser
Model building with Coot
Refinement cycles within Refmac CCP4 package and Buster
Rwork/Rfree 18.72/21.69

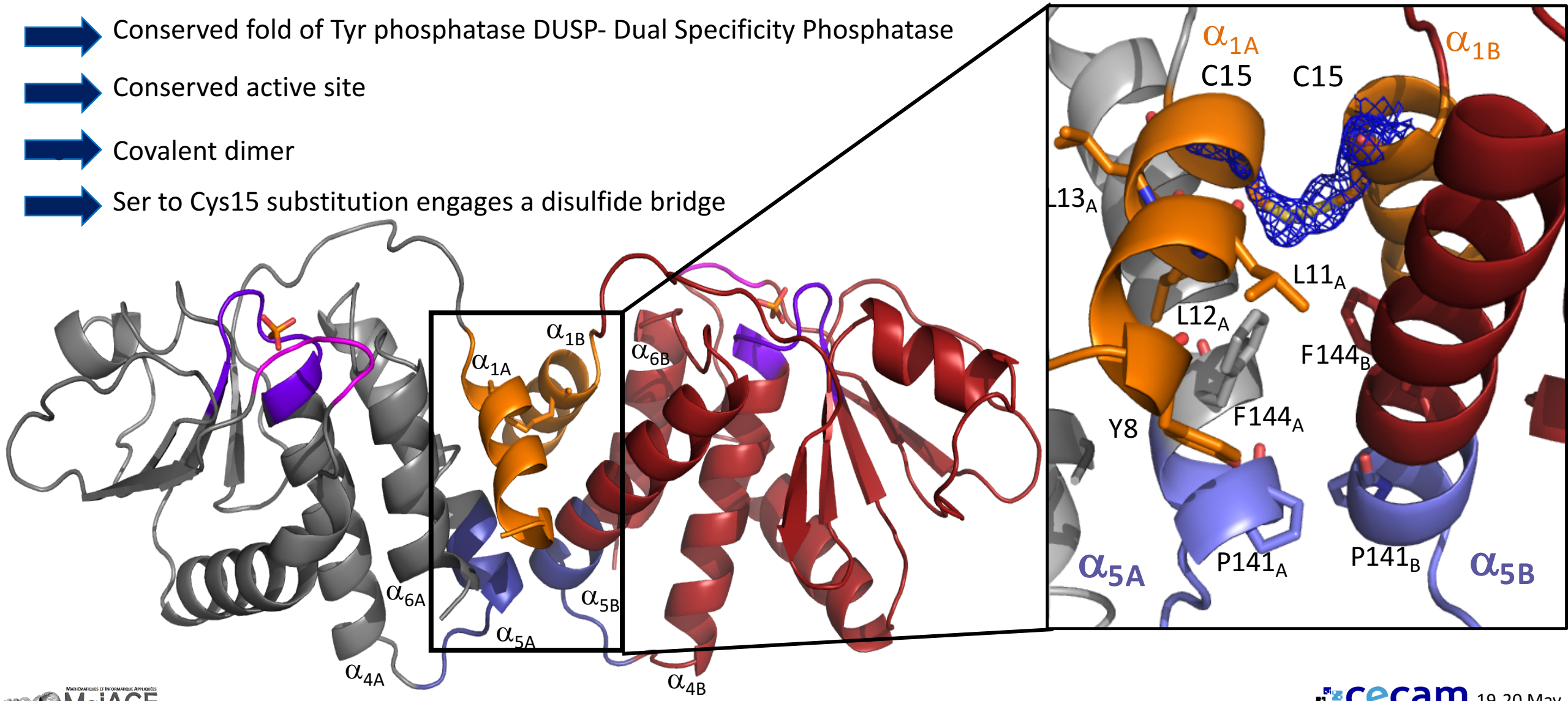
Crystal grew after 3 days for C112S
No crystal after 3 months for wt

Pdb deposition 5NCR

Orf virus : tyrosine phosphatase

Solved structure reveals:

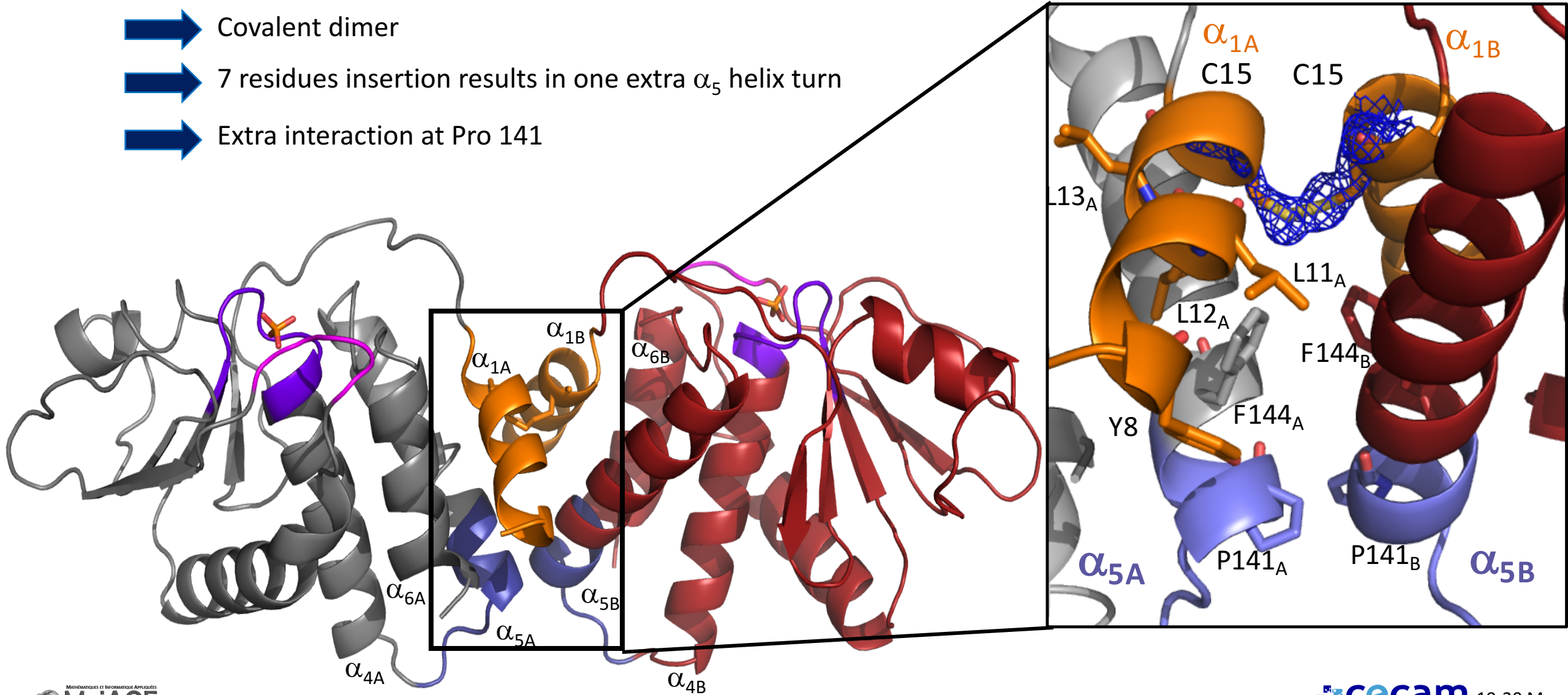
- ➡ Conserved fold of Tyr phosphatase DUSP- Dual Specificity Phosphatase
- ➡ Conserved active site
- ➡ Covalent dimer
- ➡ Ser to Cys15 substitution engages a disulfide bridge



Orf virus : tyrosine phosphatase

Solved structure reveals the conserved fold of DUSP –Dual Specificity Phosphatase

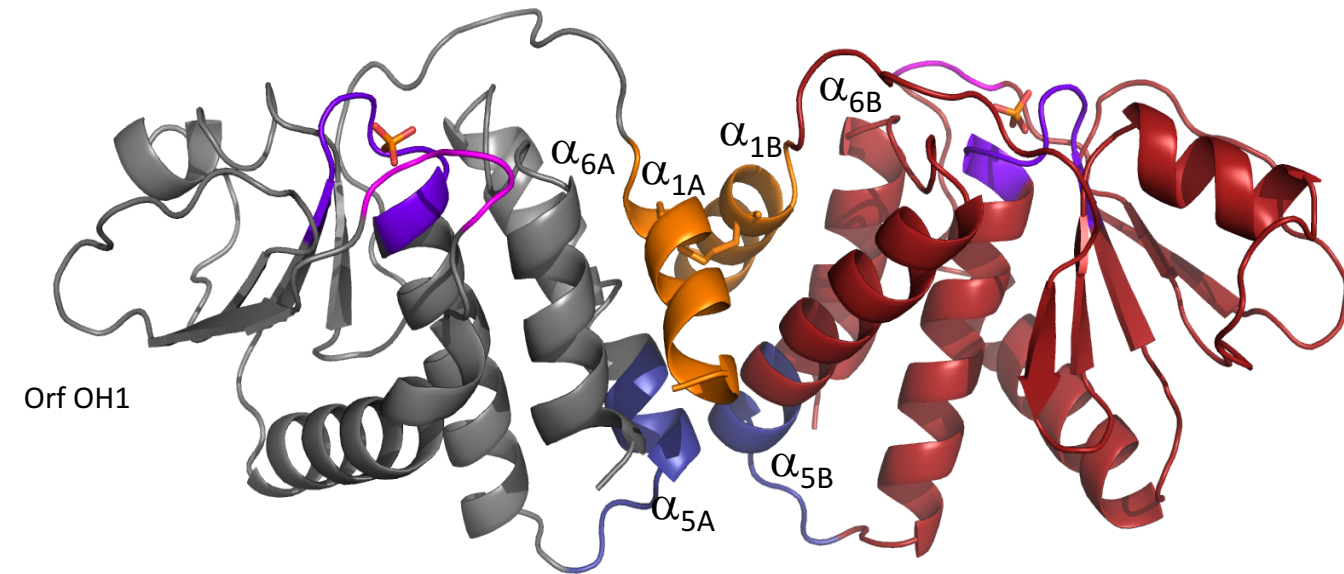
- ➡ Covalent dimer
- ➡ 7 residues insertion results in one extra α_5 helix turn
- ➡ Extra interaction at Pro 141



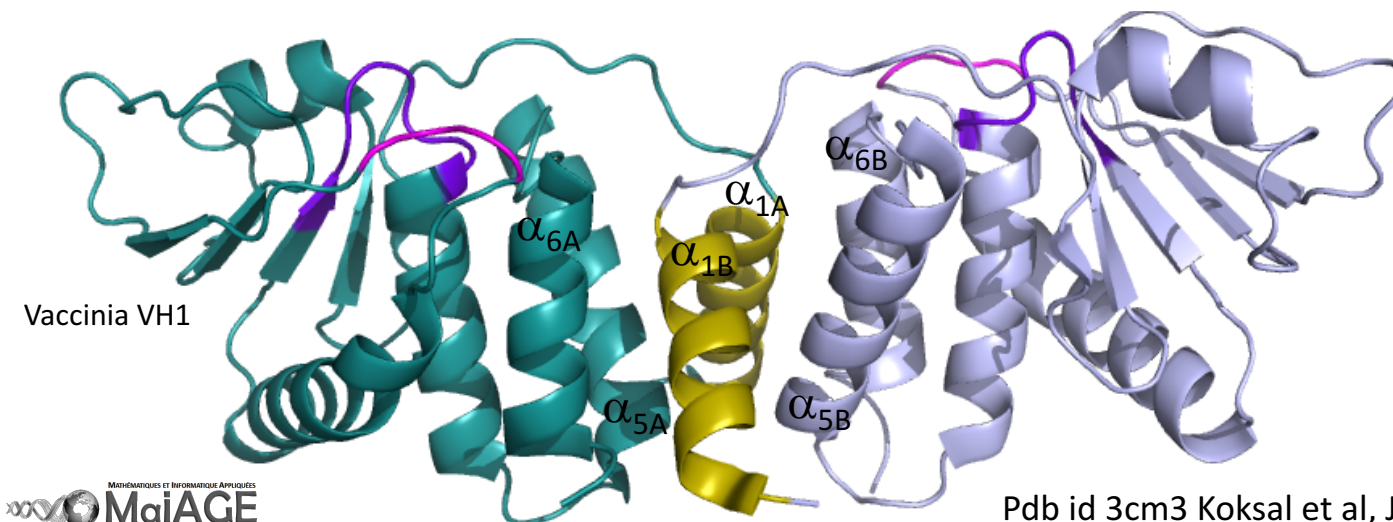
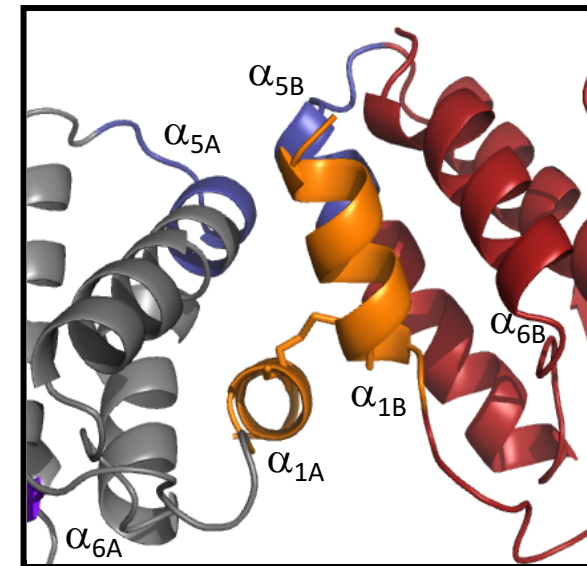
Orf virus : tyrosine phosphatase

Solved structure reveals a dimer organization distinct from Vaccinia phosphatase

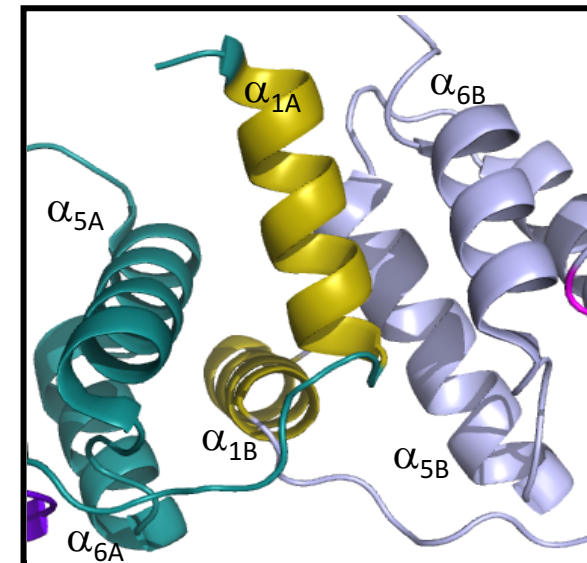
➔ The interface engages the same cluster of helices α_1 , α_5 et α_6



Interface of 678 Å²



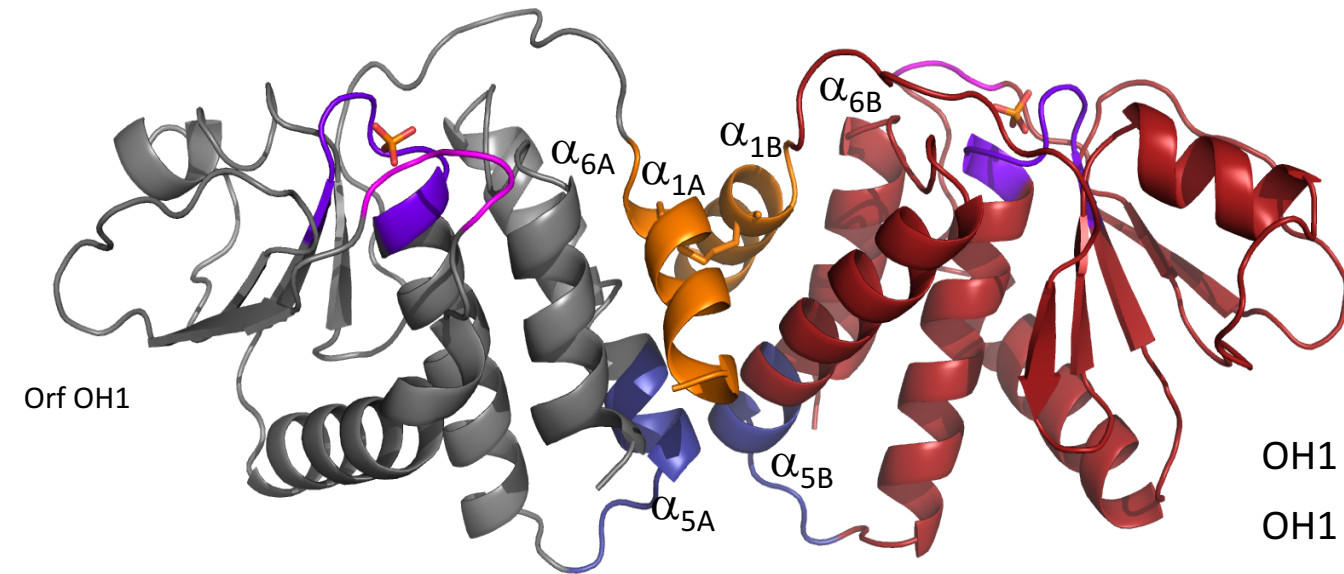
Interface of 978 Å²



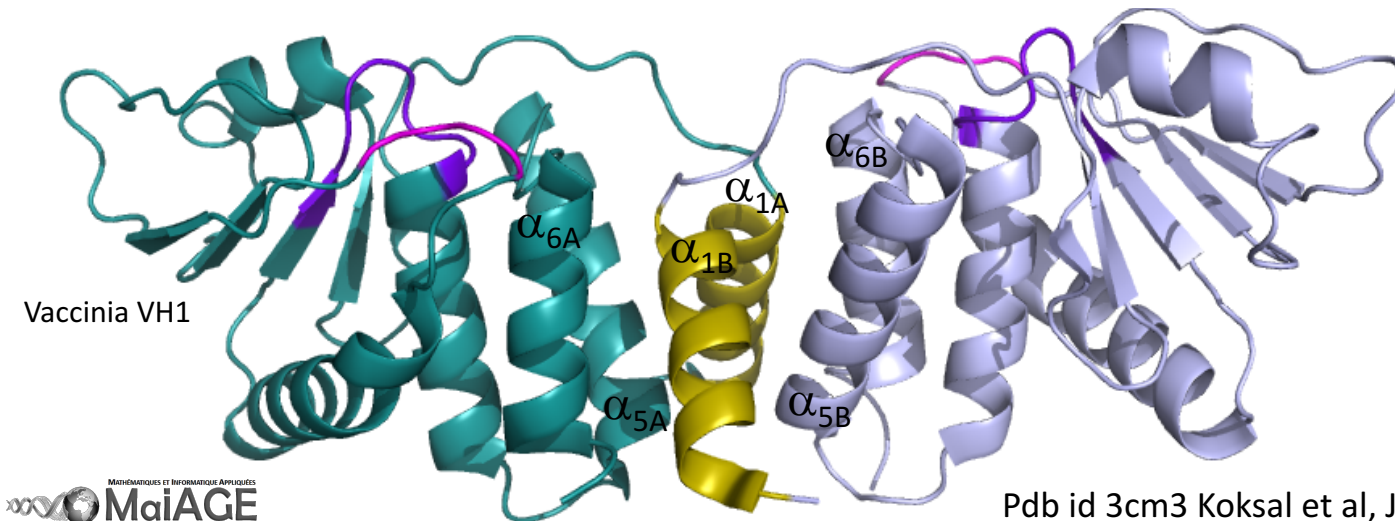
Orf virus : tyrosine phosphatase

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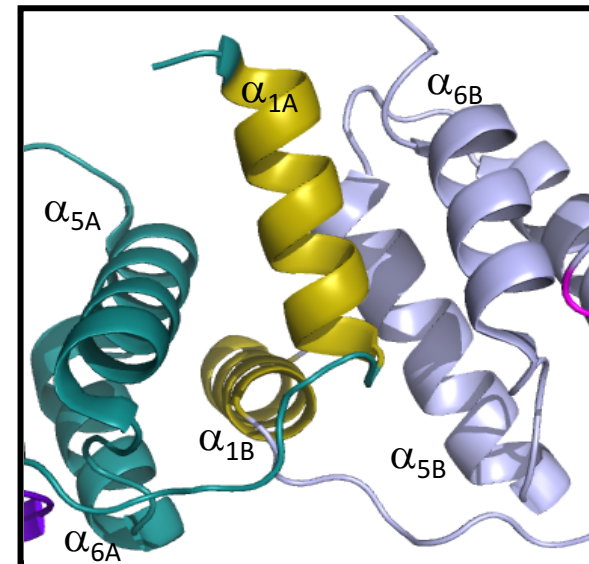
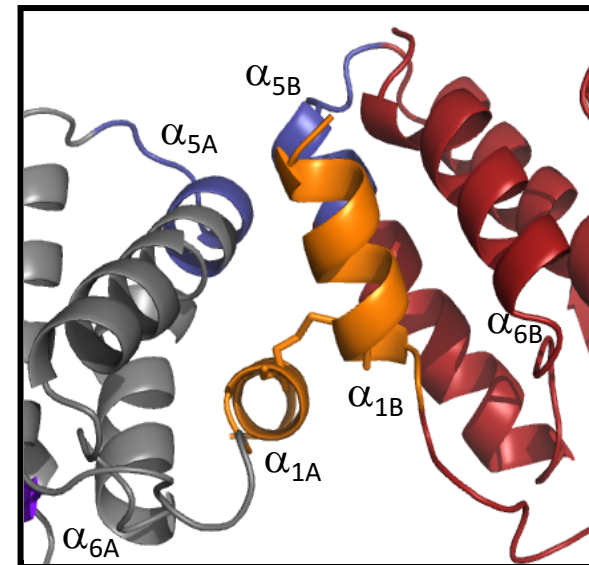
➔ The interface engages the same cluster of helices α_1 , α_5 et α_6



OH1 α_{1A} takes the position of VH1 α_{1B}
 OH1 α_{1B} takes the position of VH1 α_{1A}



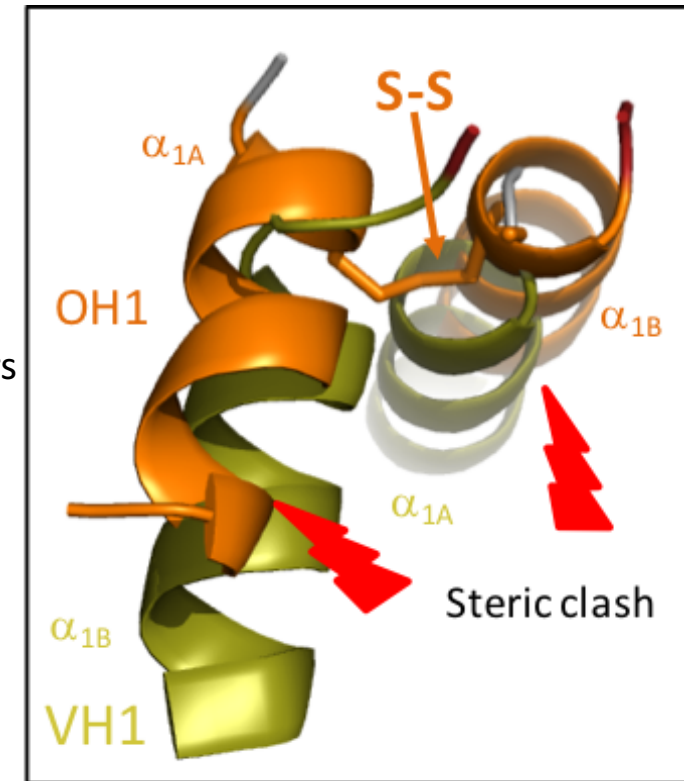
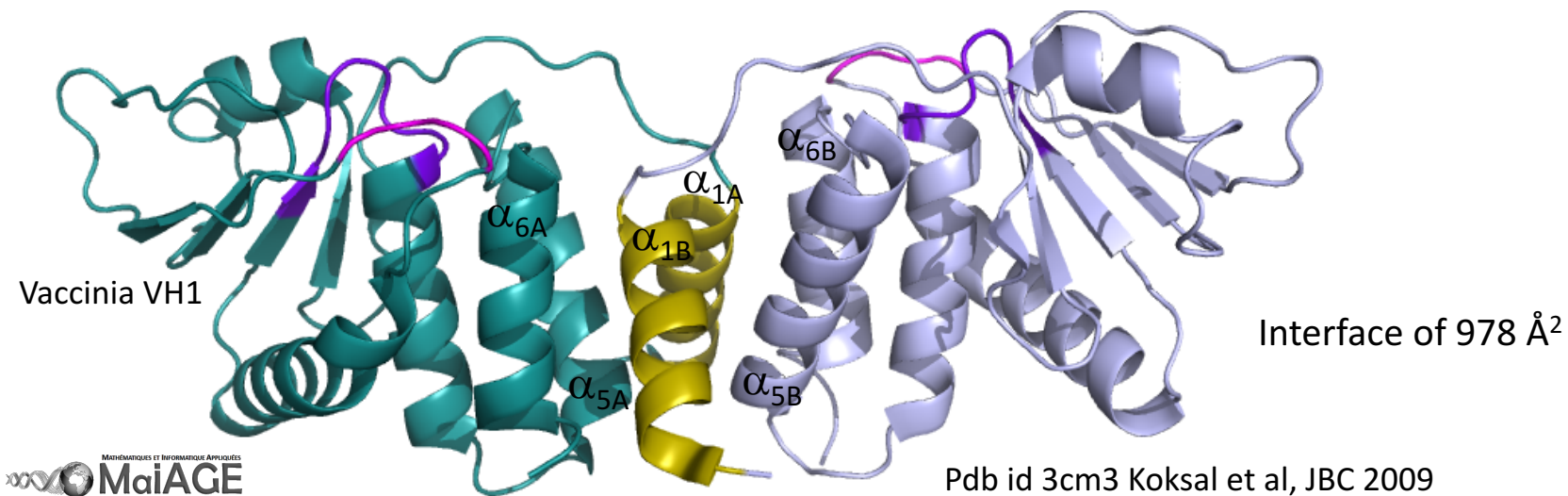
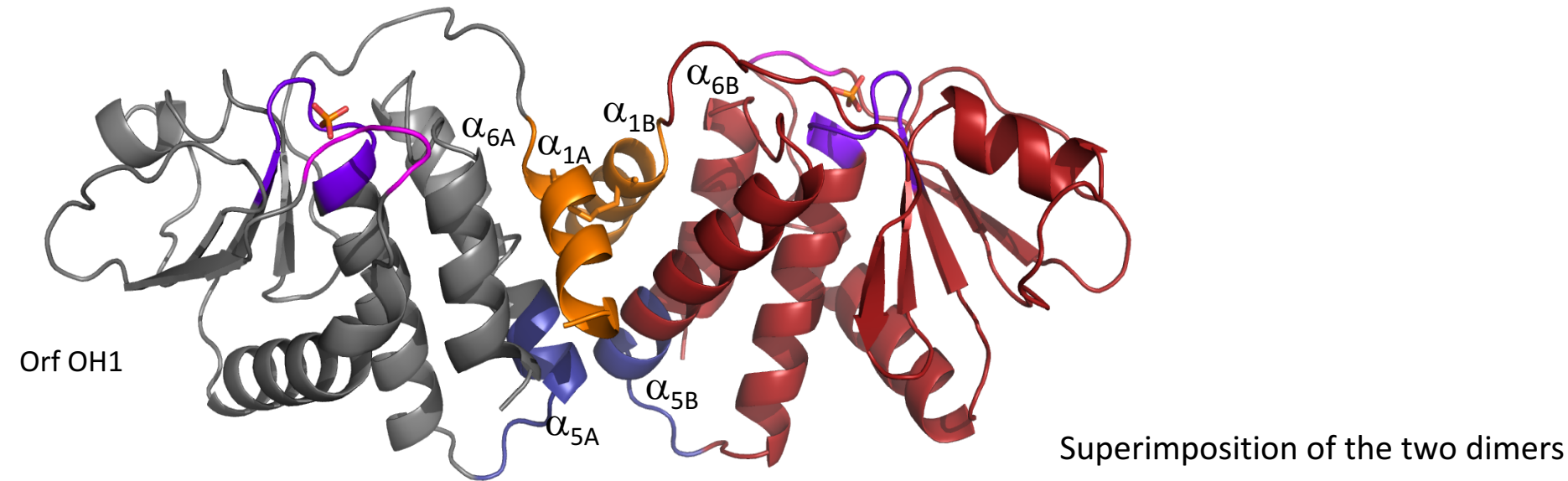
Pdb id 3cm3 Koksal et al, JBC 2009



Orf virus : tyrosine phosphatase

Solved structure reveals a dimer organization distinct from Vaccinia phosphatase

➔ Incompatible with domain swapping

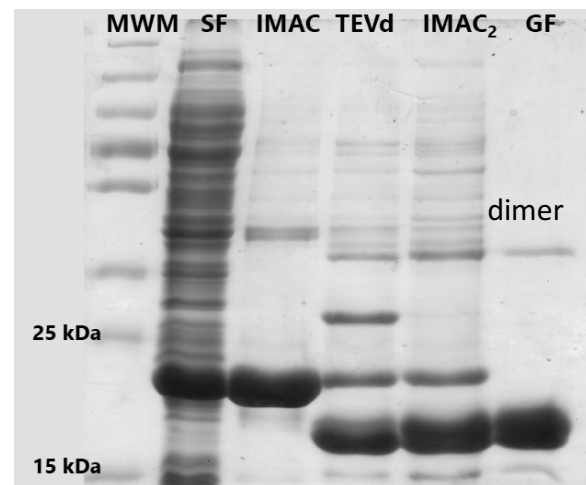


Orf virus : tyrosine phosphatase

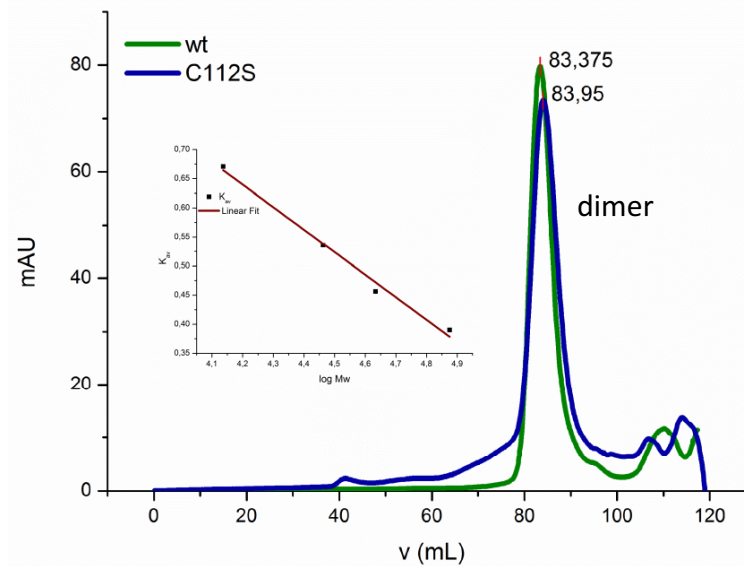
Solved structure reveals a dimer organization distinct from Vaccinia phosphatase

➔ Not a crystallization bias because

- Production of recombinant OH1



- Size exclusion chromatography

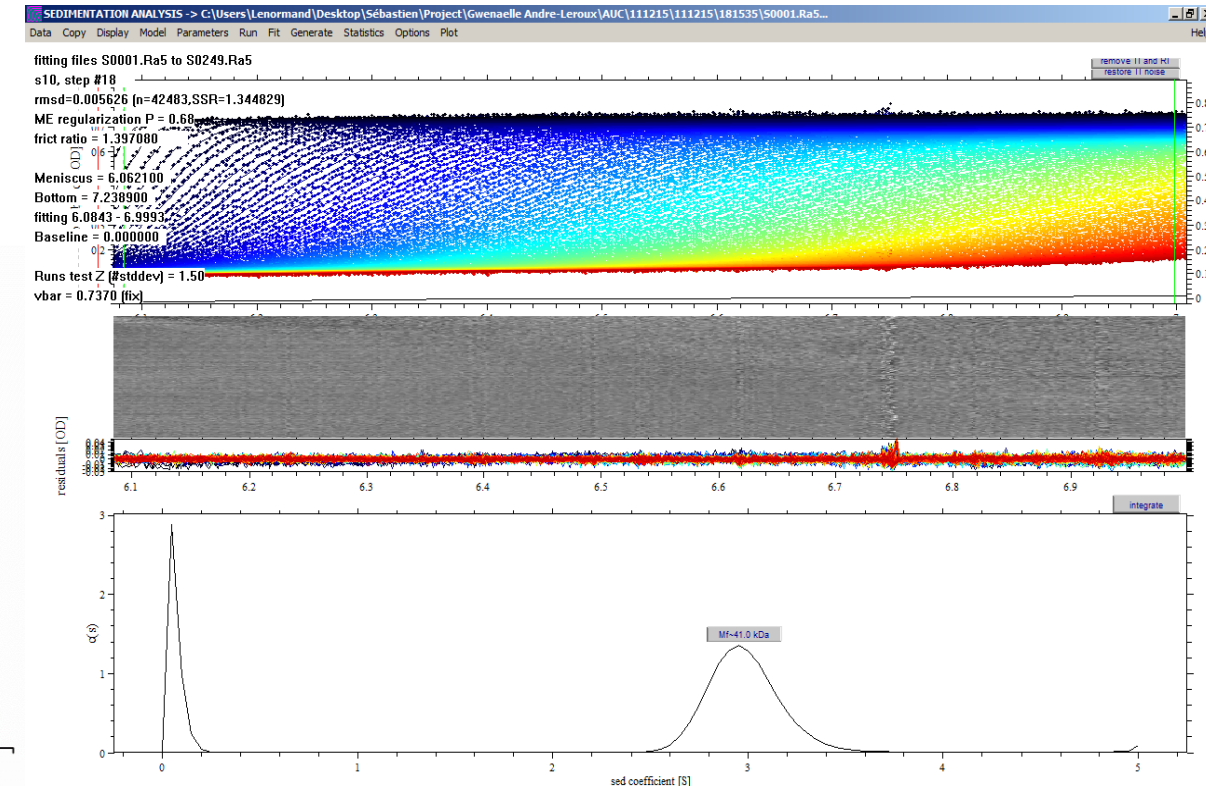


OH1 is a dimer in solution

C15S shows also a dimer (data not shown)

C15S is not mandatory for a dimerization

- Ultra Analytical Centrifugation



40 kDa = 2*20 kDa

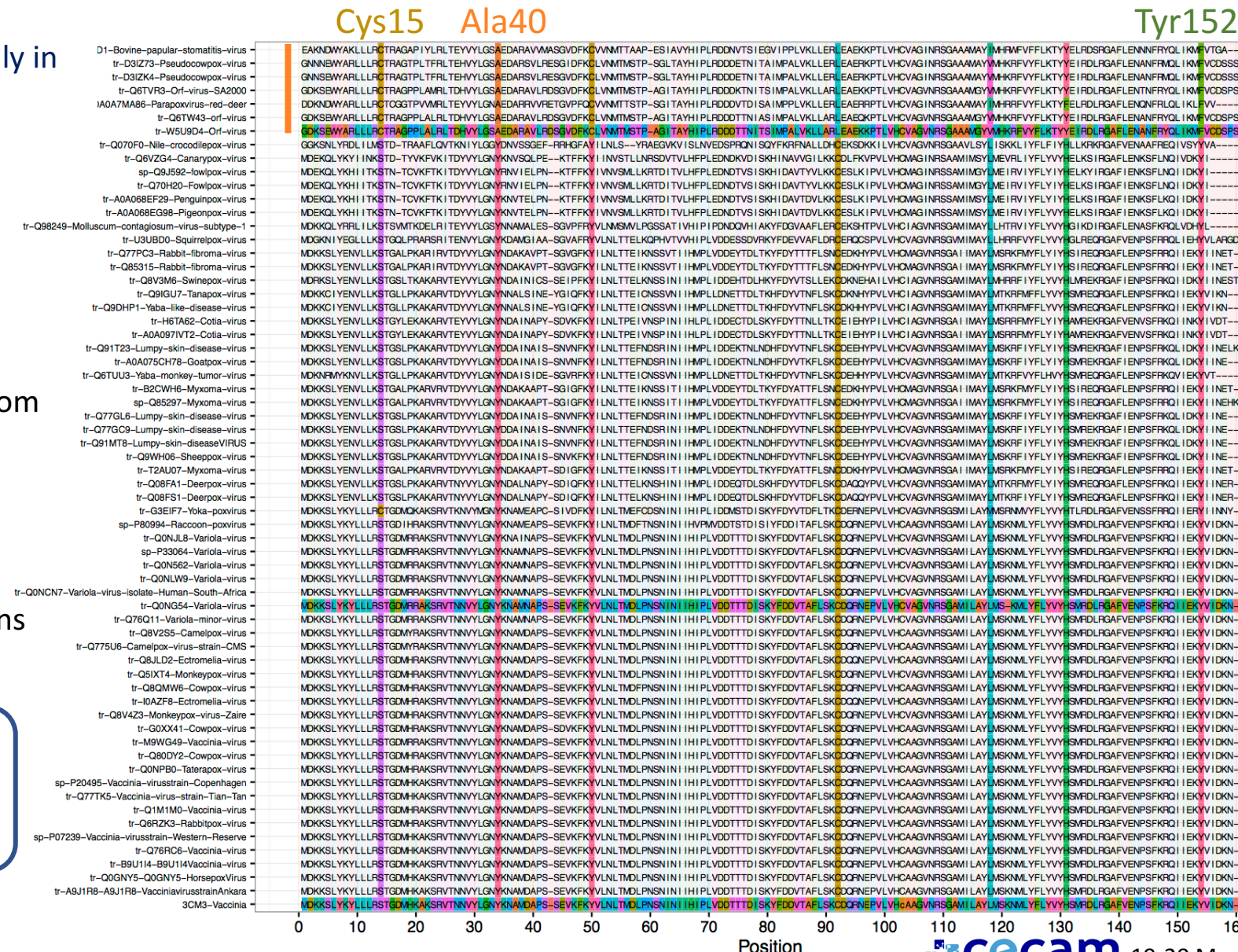
Detection of Parapox specific features of OH1

Cys 15 and 6 residues insertion conserved but only in Parapoxviruses

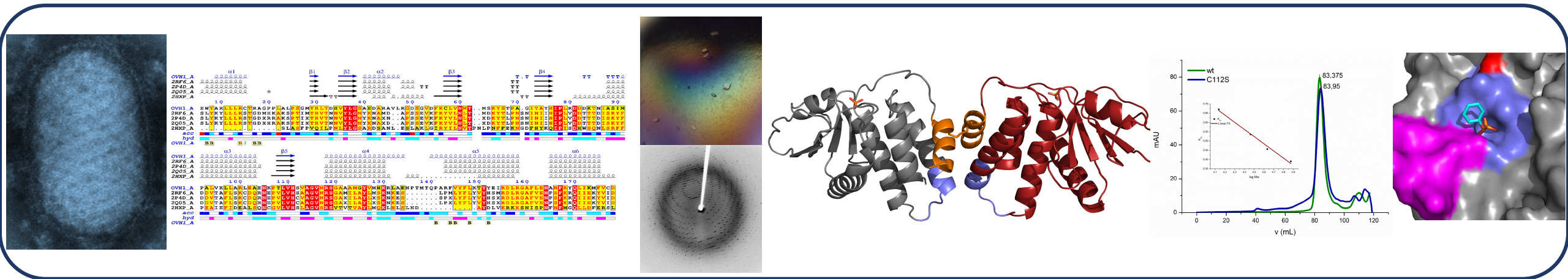
Phylogenetic studies explore how parapoxvirus associates N-terminal Ser15 to Cys substitution

- Multiple sequence alignment of 64 phosphatases from Chordopox family
- Tcoffe
- Position with >50% gaps filtered
- Correlation techniques based on mutual informations

Ala40 locates in the vicinity of the active site
 Tyr152 could stabilize helix α_1



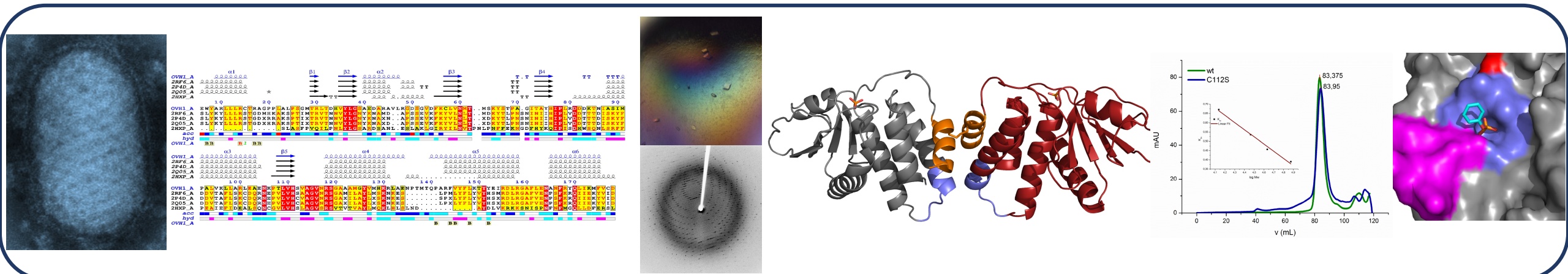
OH1 from Orf virus: a new tyrosine phosphatase



Highlights

- OH1 displays distinct structural features compared to VH1 phosphatases
- Orf virus OH1 is a covalent dimer involving the N-terminal Cys15
- Orf virus OH1 possibly depicts the structure of Parapoxvirus genus phosphatases

OH1 from Orf virus: a new tyrosine phosphatase

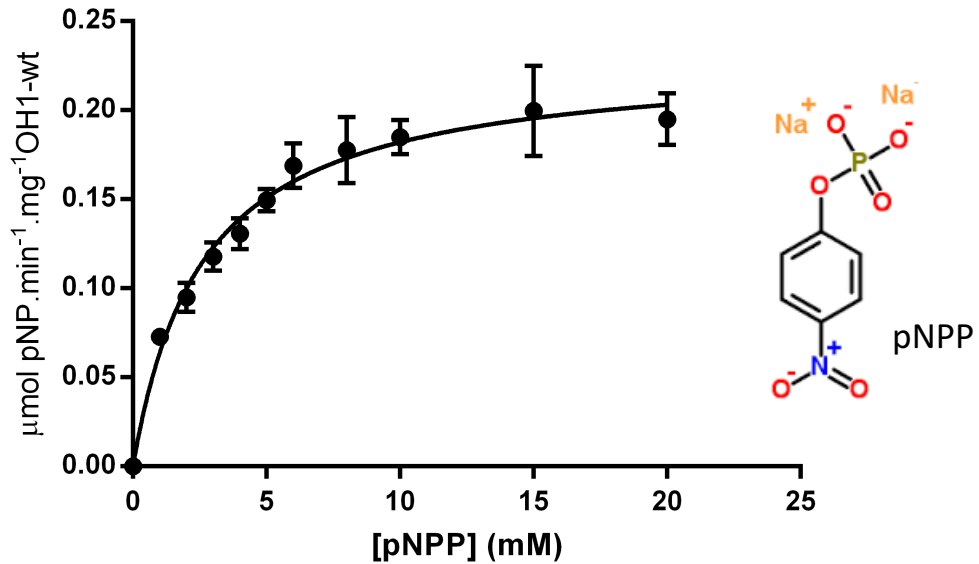


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Tyrosine phosphatase

➔ OH1 shows a phosphatase activity *in vitro*



Monitoring of dephosphorylation by absorbance at 405nm of pNP

Phosphatase activity assayed at 37°C using the artificial substrate pNPP

Michaelis-Menten Kinetics constants

OH1 wt

$$K_m = 2.6 \text{ mM}$$

$$K_{cat} = 0.08 \text{ s}^{-1}$$

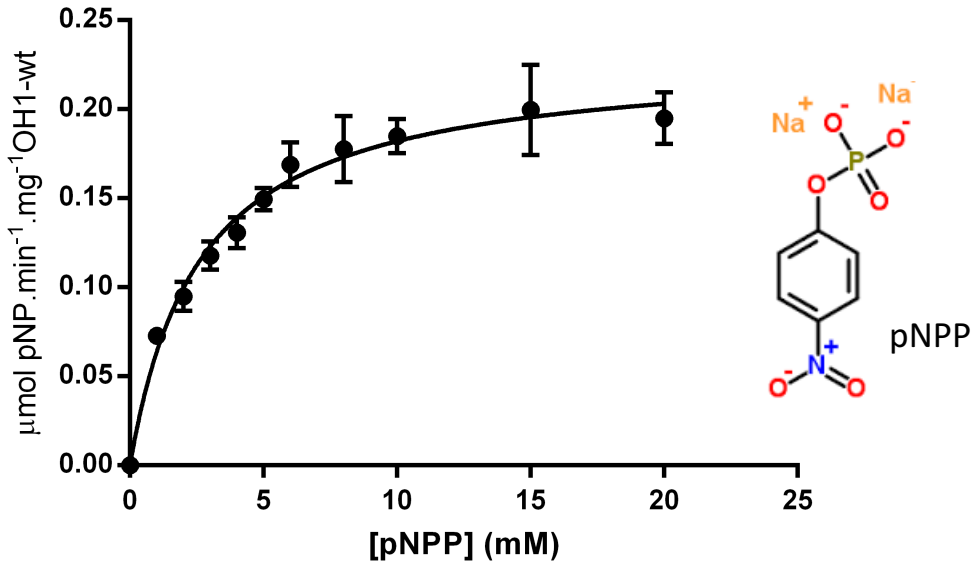
OH1 C15S

$$K_m = 2.0 \text{ mM}$$

$$K_{cat} = 0.08 \text{ s}^{-1}$$

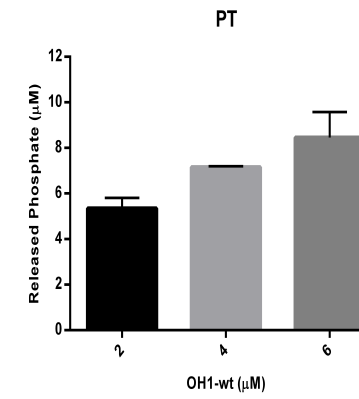
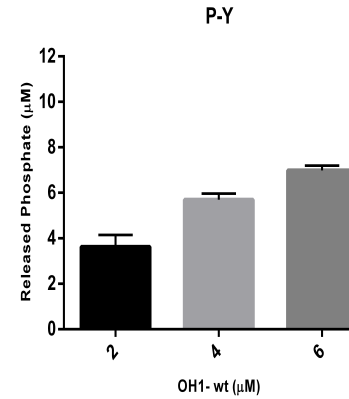
Tyrosine phosphatase

OH1 shows a phosphatase activity *in vitro*



OH1 shows a DUSP –Dual Specificity Phosphatase *in vitro*

Active on p-Tyr containing protein Active on p-Thr 17mer peptide



Dose dependent manner

Phosphatase activity assayed at 37°C using the artificial substrate pNPP

Michaelis-Menten Kinetics constants

OH1 wt

$$K_m = 2.6 \text{ mM}$$

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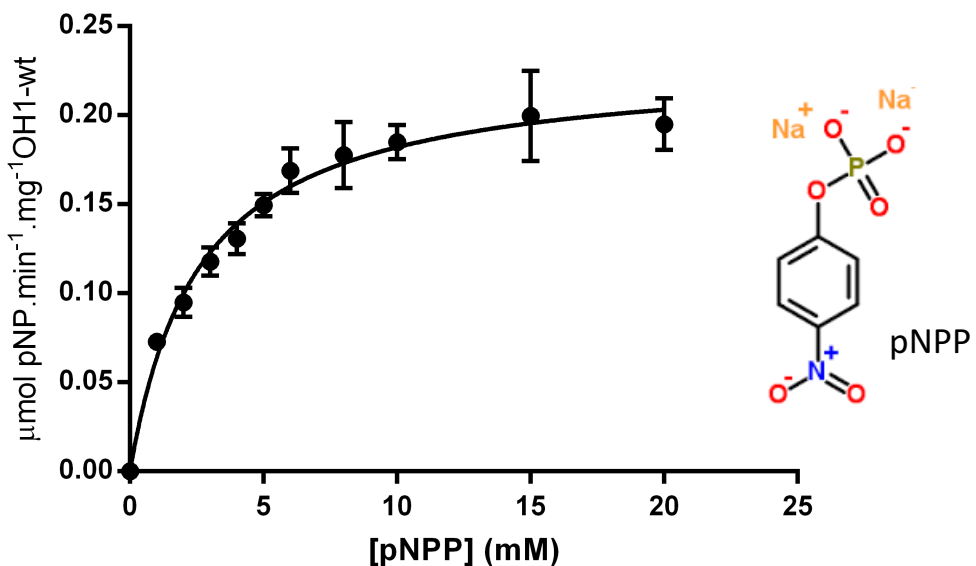
OH1 C15S

$$K_m = 2.0 \text{ mM}$$

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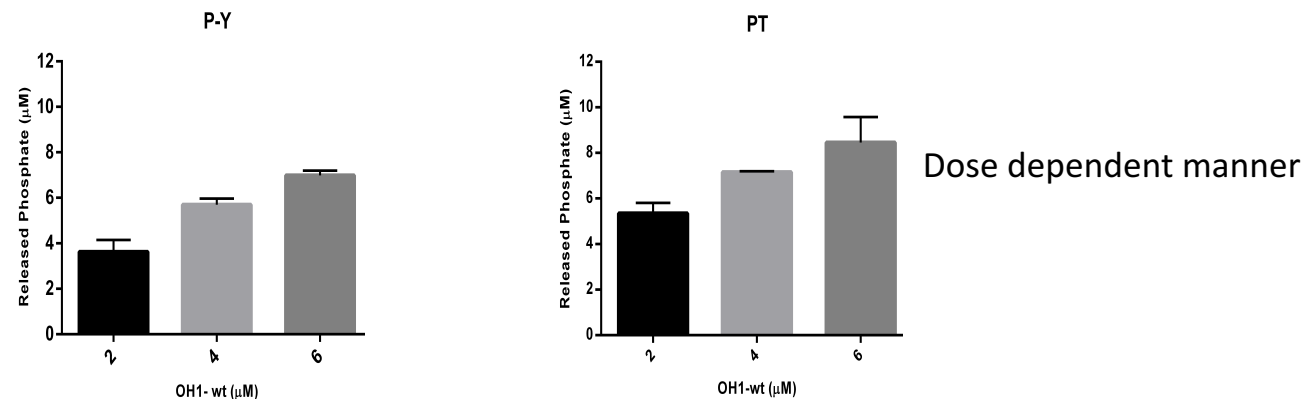
Tyrosine phosphatase

OH1 shows a phosphatase activity *in vitro*

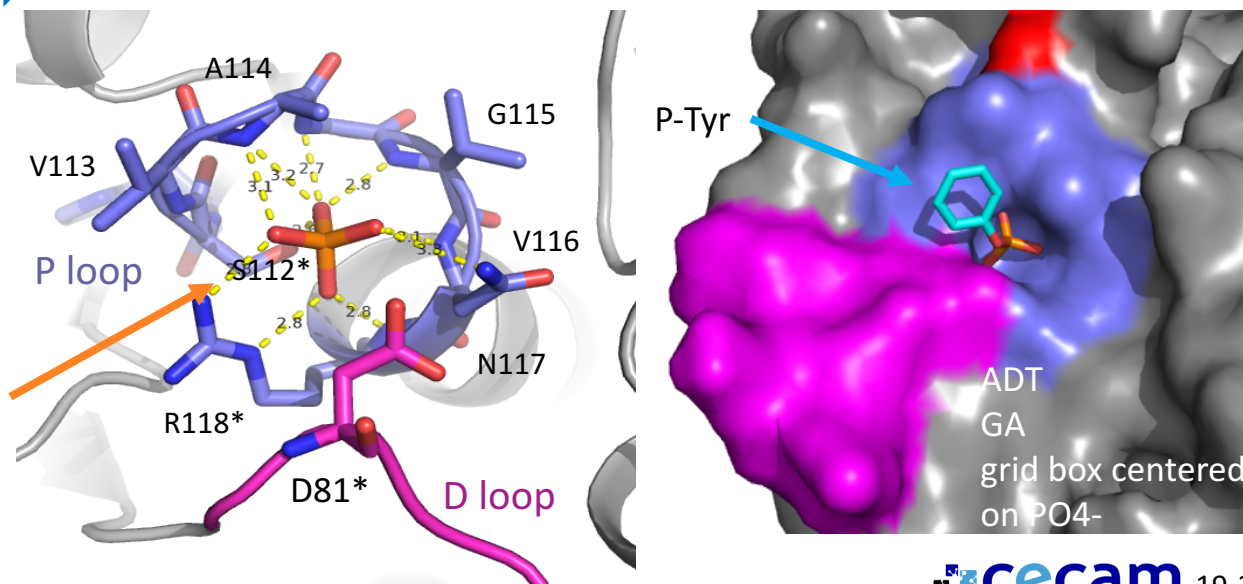


OH1 shows a DUSP –Dual Specificity Phosphatase *in vitro*

Active on p-Tyr containing protein Active on p-Thr 17mer peptide



OH1 accommodates p-Tyr in the active site



Phosphatase activity assayed at 37°C using the artificial substrate pNPP

Michaelis-Menten Kinetics constants

OH1 wt

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$$K_{cat} = 0.08 \text{ s}^{-1}$$

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$$K_m = 2.0 \text{ mM}$$

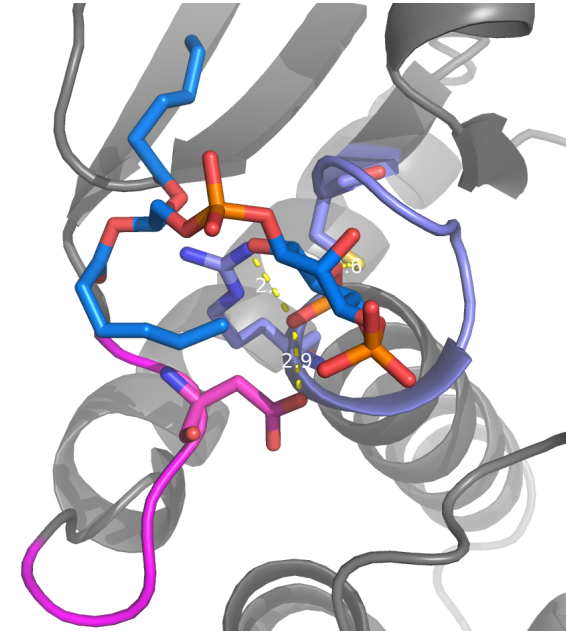
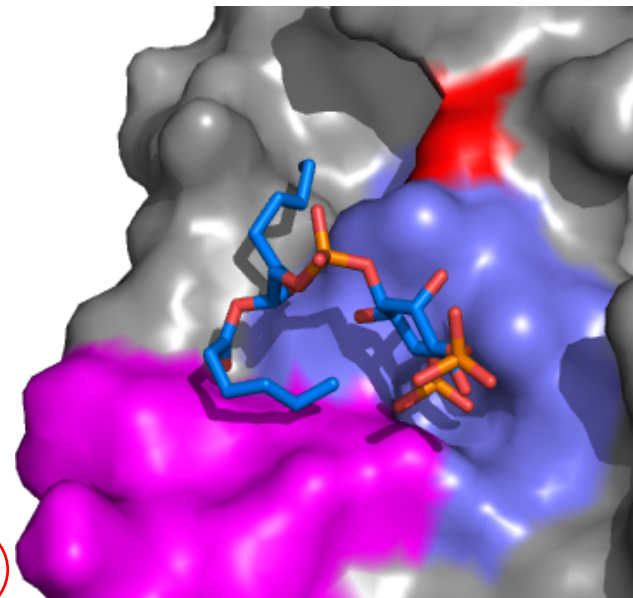
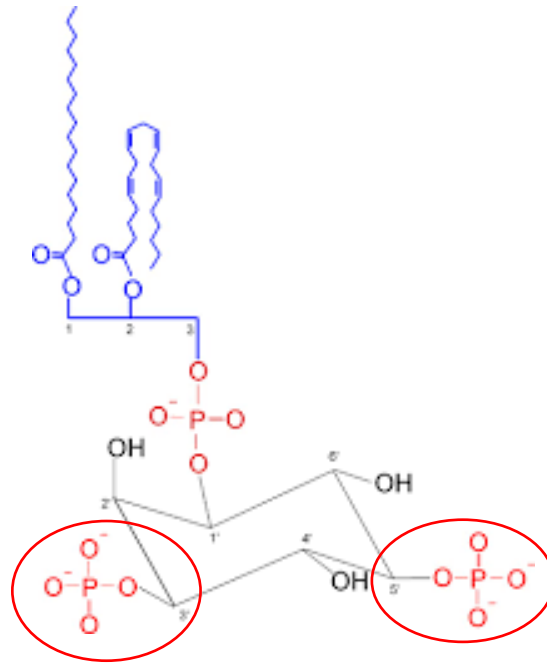
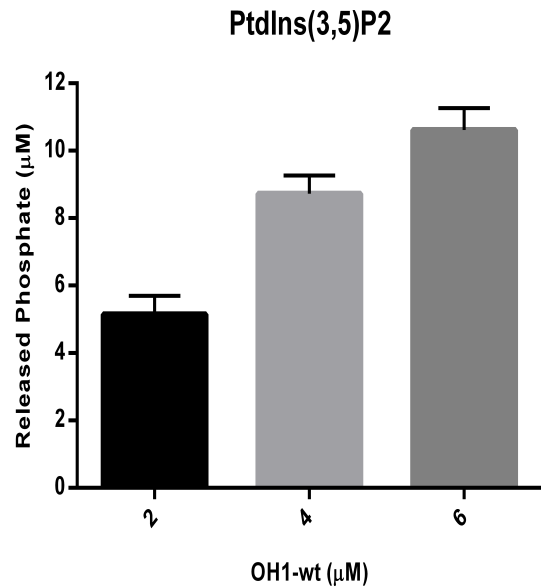
$$K_{cat} = 0.08 \text{ s}^{-1}$$

Crystal phosphate

A new tyrosine phosphatase

➔ OH1 highlights a new activity *in vitro*: a triple specificity

➔ Docking evidences PdtIns bind in the pocket



Phosphoinositides can be dephosphorylated

The phospho-sugar part can be accommodated

PtdIns3P and PtdIns5 (3,5)P2 can be dephosphorylated

The phospho-group in 5' binds into the active pocket

Relevant physiologically?

A new tyrosine phosphatase



Why this phospholipid specificity should be relevant?

PtdIns

- Belong to phosphatidyl glycerides
- Compose the cytosolic side of eukaryotic cell membrane
- Regulate membrane homeostasis
- Are signaling lipids



OH1 could extract and recycle host phospholipids to form viral envelop during virion maturation

- Viral envelop allows to:
- Escape from the cell,
 - Stay stable
 - Get protected from immune system
 - Reinfect cell

Evolution in favor of enveloped virus : Influenza, HIV, Ebola Virus

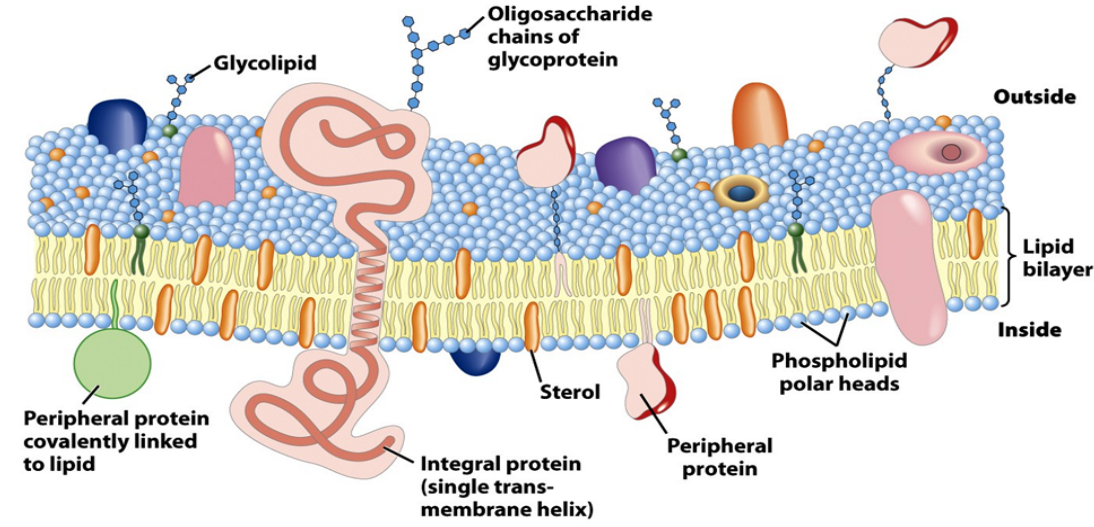
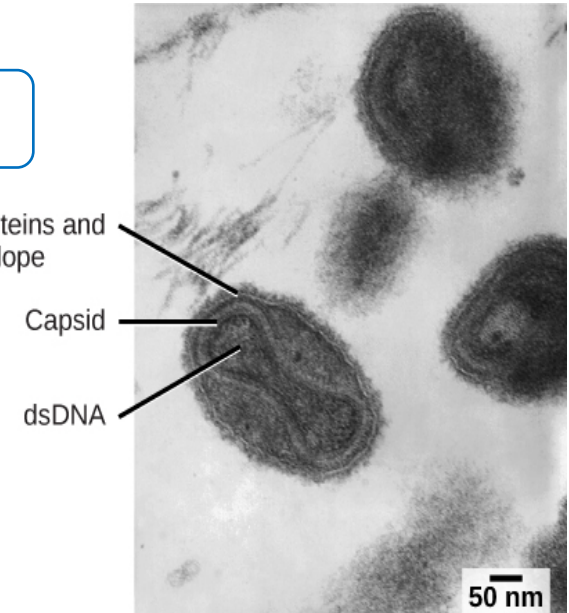
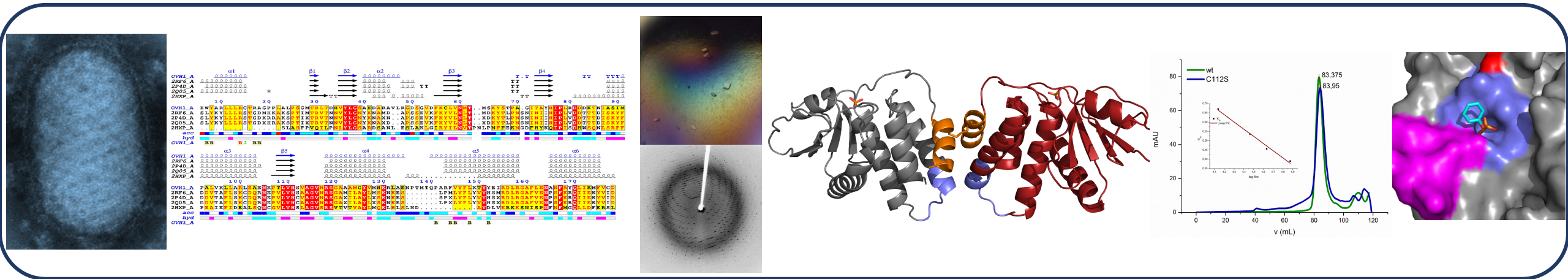


Figure 11-3
Lehninger Principles of Biochemistry, Fifth Edition
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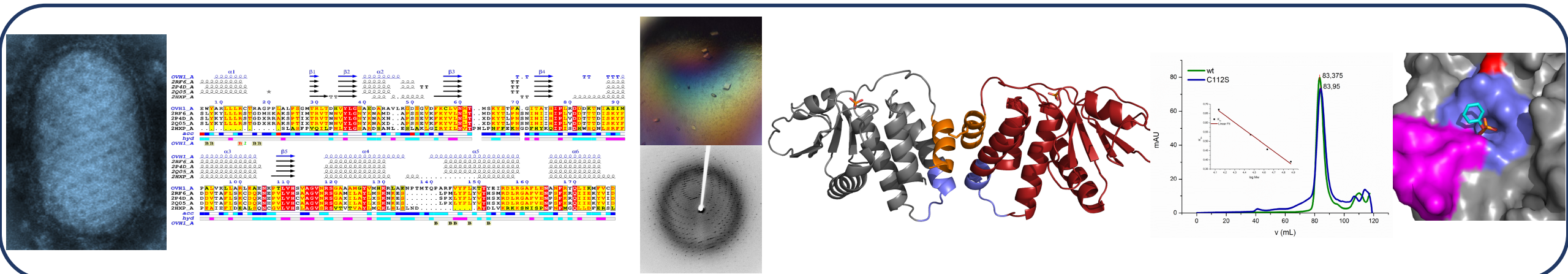
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- Orf virus OH1 is a covalent dimer involving the N-terminal Cys15
- Orf virus OH1 possibly depicts the structure of Parapoxvirus genus phosphatases
- Orf virus OH1 is a dual specificity phosphatase that presents activity towards PInsP *in vitro*

OH1 from Orf virus: a new tyrosine phosphatase

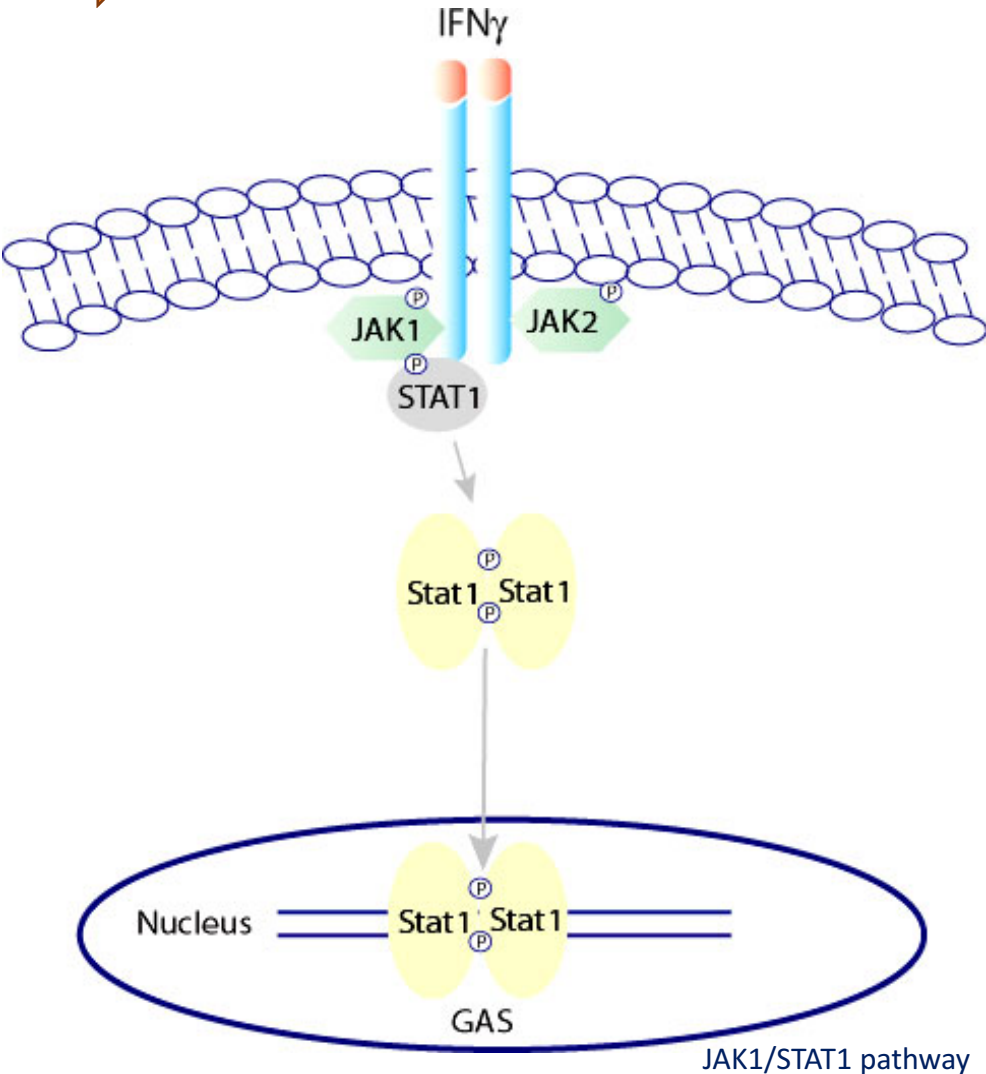


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Interaction with STAT1

➔ Hypothesis: by analogy with Vaccinia and Variola viruses, OH1 could dephosphorylate STAT1



STAT : Signal Transducers and Activators of Transcription

STAT1 is activated upon phosphorylation of its tyrosine Tyr701 -> STAT1 (P)

STAT1 (P) proteins homodimerize

STAT1 (P) homodimer is now capable to translocate to the nucleus

STAT1 (P) transactivates Stat-responsive genes

STAT1 (P) is involved in cardiac hypertrophy, apoptosis, and inflammation.

Interaction with STAT1

➔ OrfV dephosphorylates STAT1

Format: Abstract ▾

Send to ▾

Virus Res. 2015 Oct 2;208:180-8. doi: 10.1016/j.virusres.2015.06.014. Epub 2015 Jun 22.

Orf virus inhibits interferon stimulated gene expression and modulates the JAK/STAT signalling pathway.

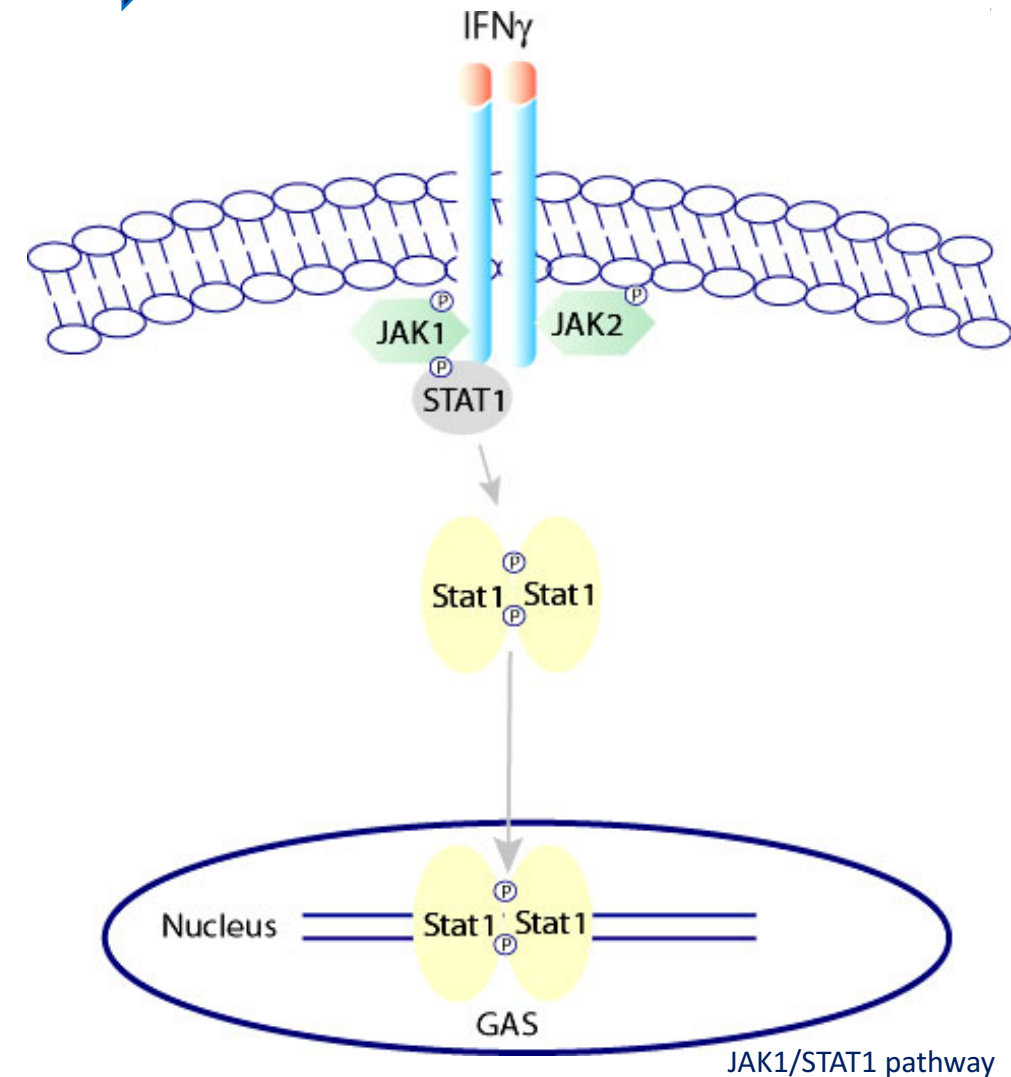
Harvey R¹, McCaughan C², Wise LM³, Mercer AA⁴, Fleming SB⁵.

⊕ Author information

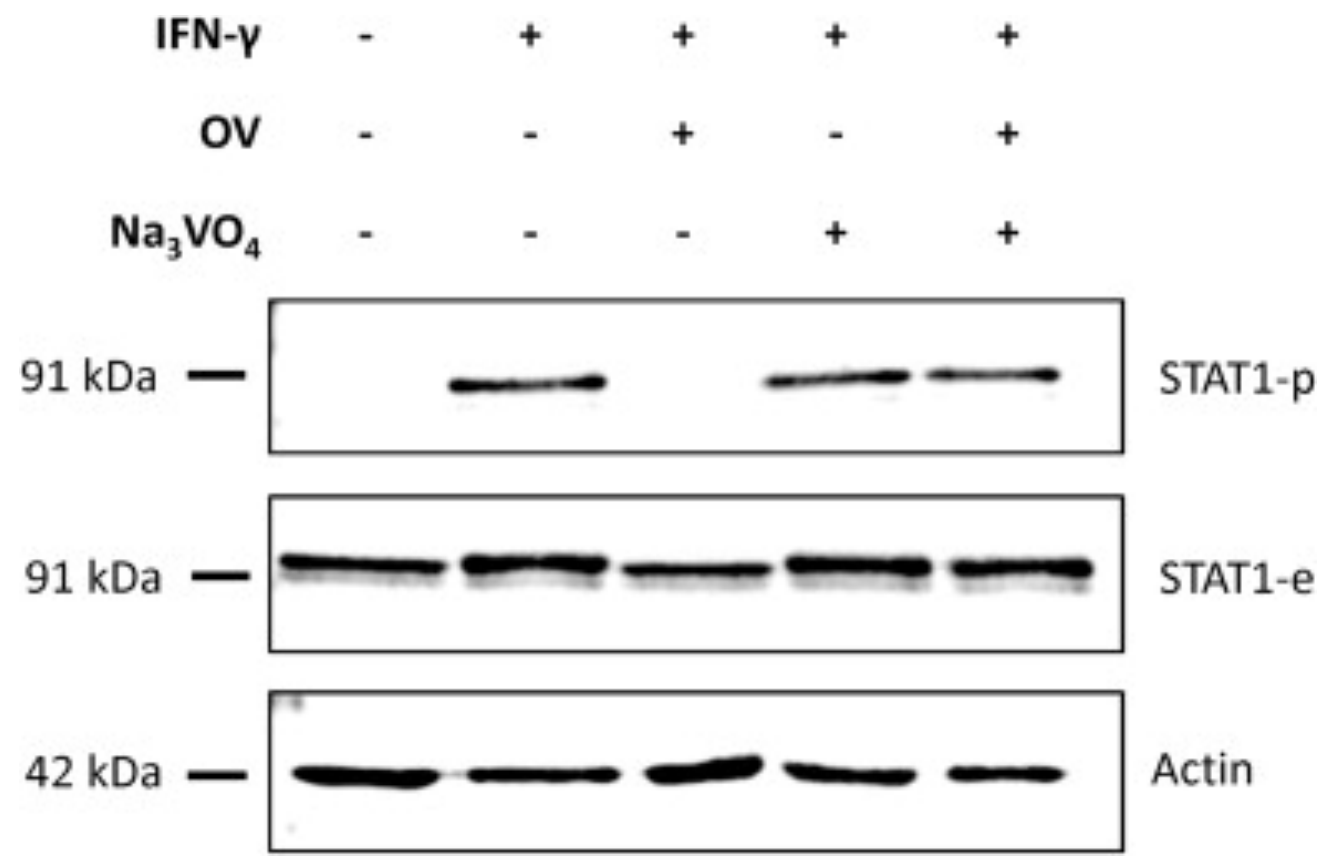
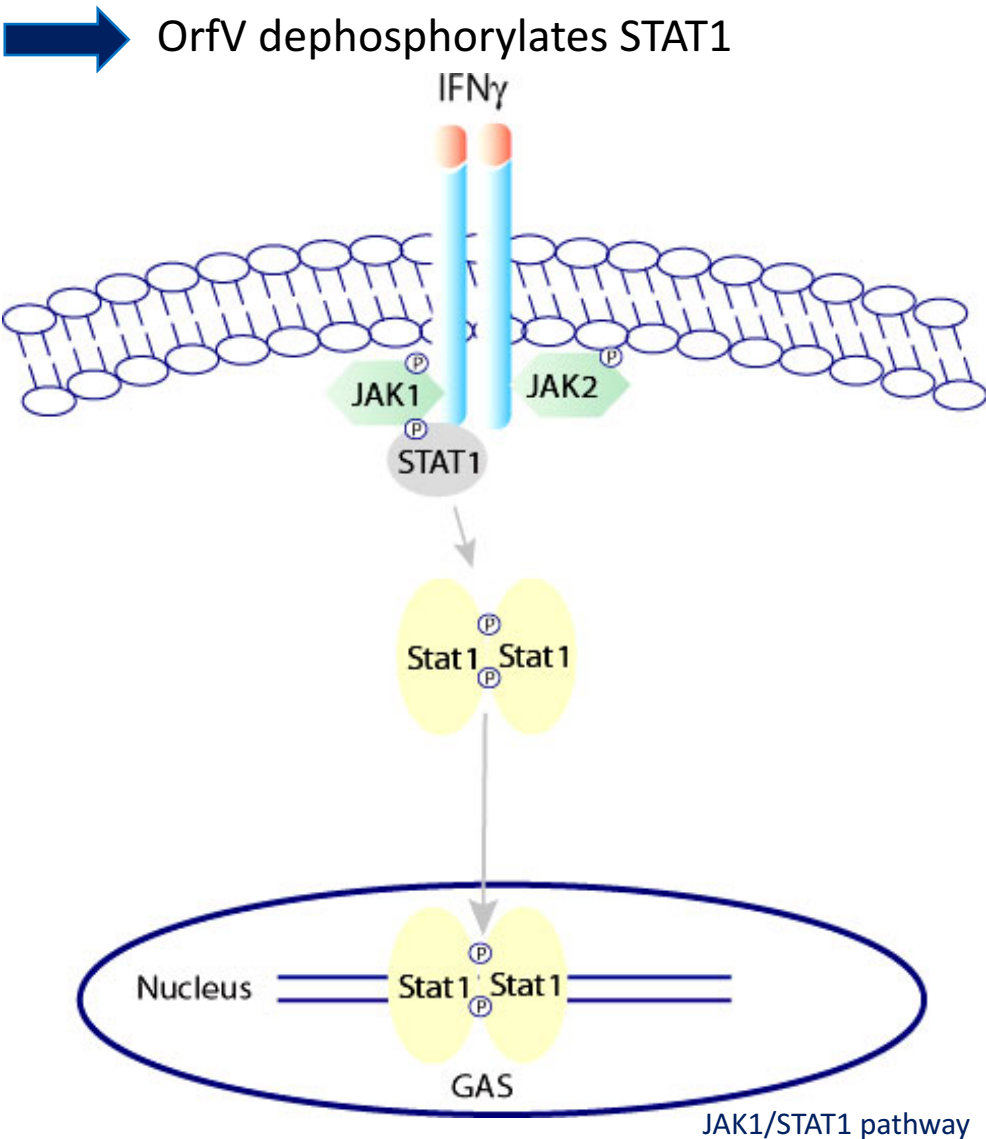
Abstract

Interferons (IFNs) play a critical role as a first line of defence against viral infection. Activation of the Janus kinase/signal transducer and activation of transcription (JAK/STAT) pathway by IFNs leads to the production of IFN stimulated genes (ISGs) that block viral replication. The Parapoxvirus, Orf virus (ORFV) induces acute pustular skin lesions of sheep and goats and is transmissible to man. The virus replicates in keratinocytes that are the immune sentinels of skin. We investigated whether or not ORFV could block the expression of ISGs. The human gene GBP1 is stimulated exclusively by type II IFN while MxA is stimulated exclusively in response to type I IFNs. We found that GBP1 and MxA were strongly inhibited in ORFV infected HeLa cells stimulated with IFN- γ or IFN- α respectively. Furthermore we showed that ORFV inhibition of ISG expression was not affected by cells pretreated with adenosine N1-oxide (ANO), a molecule that inhibits poxvirus mRNA translation. This suggested that new viral gene synthesis was not required and that a virion structural protein was involved. We next investigated whether ORFV infection affected STAT1 phosphorylation in IFN- γ or IFN- α treated HeLa cells. We found that ORFV reduced the levels of phosphorylated STAT1 in a dose-dependent manner and was specific for Tyr701 but not Ser727. Treatment of cells with sodium vanadate suggested that a tyrosine phosphatase was responsible for dephosphorylating STAT1-p. ORFV encodes a factor, ORFV057, with homology to the vaccinia virus structural protein VH1 that impairs the JAK/STAT pathway by dephosphorylating STAT1. Our findings show that ORFV has the capability to block ISG expression and modulate the JAK/STAT signalling pathway.

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Interaction with STAT1



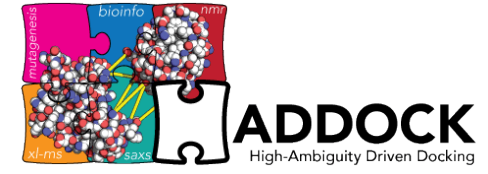
Harvey et al, 2015

➔ Modeling of OH1/STAT1 direct interaction

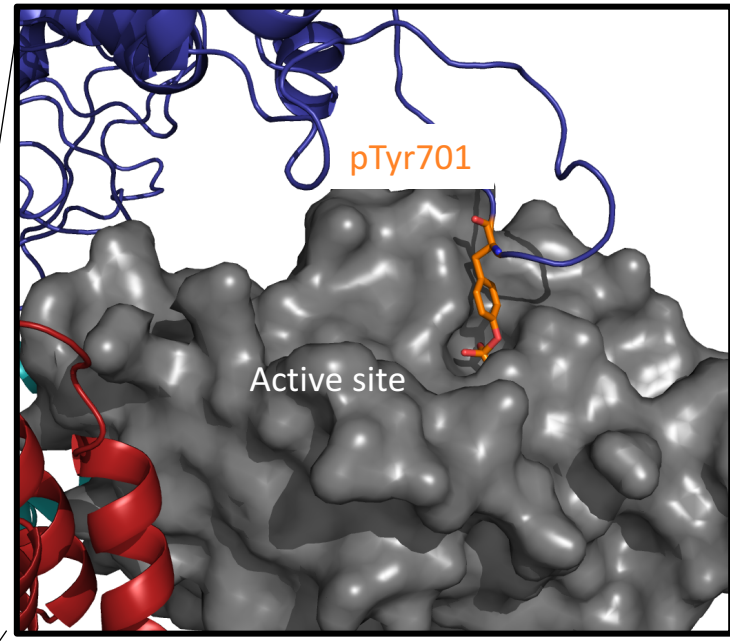
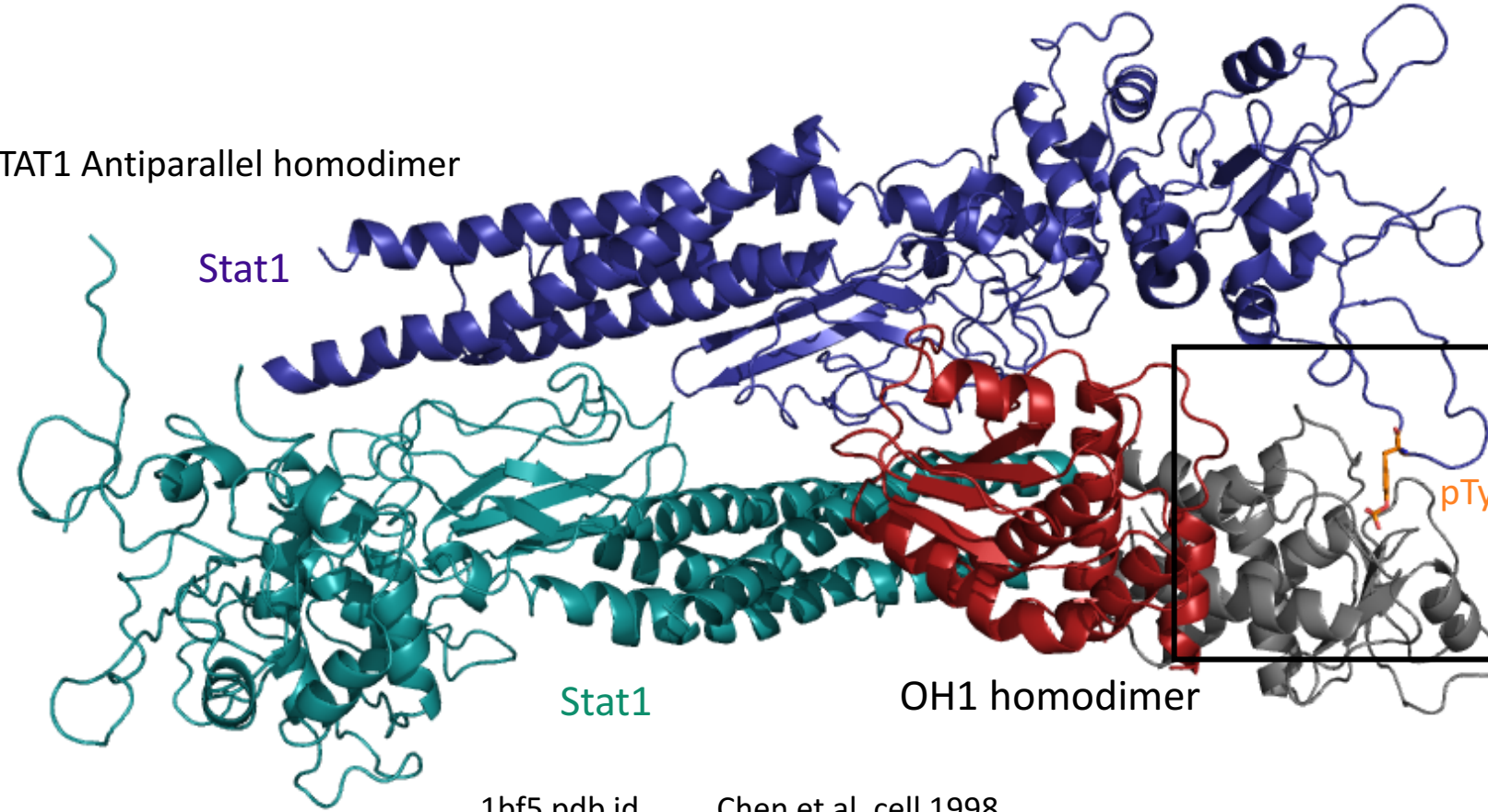
Interaction with STAT1

➔ Running hypothesis: OH1 dephosphorylates STAT1 by a direct interaction

- Modeling of the missing loop and phosphorylation at Tyr 701
- Docking of Protein/Protein interaction using HADDOCK

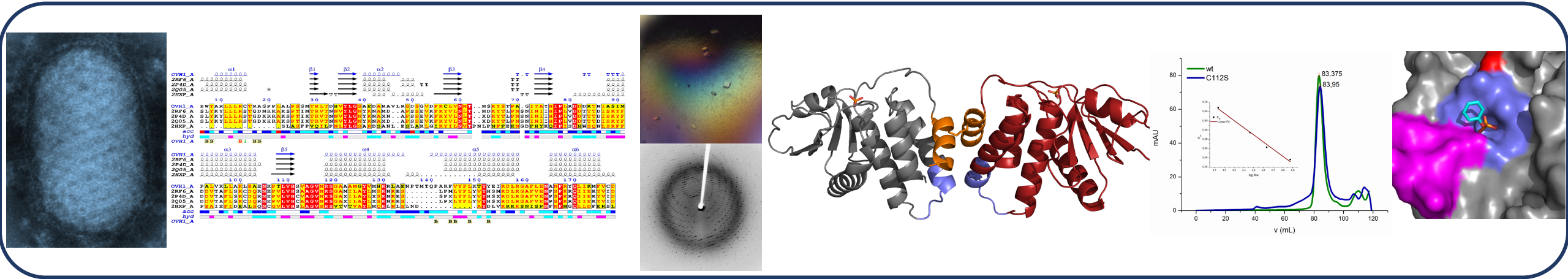


STAT1 Antiparallel homodimer



1bf5 pdb id Chen et al, cell 1998

OH1 from Orf virus: a new tyrosine phosphatase

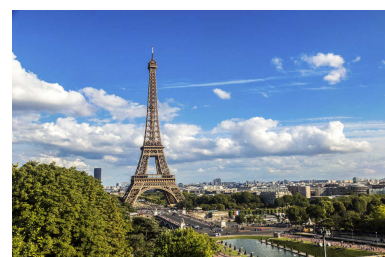


Perspectives

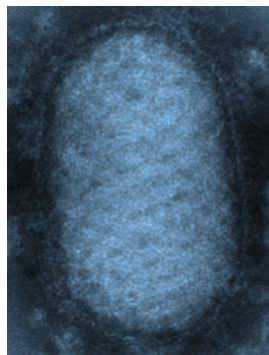
- OH1 /STAT1 needs further investigations *in silico*
- Pull-down *in vitro* experiments show that OH1 interacts directly with STAT1
- Pull-down *in vitro* experiments show that OH1 interacts with GAPDH - Glyceraldehyde-3-phosphate dehydrogenase
- GAPDH is a house-keeping protein involved in glycolysis and modulation of the organization of the cytoskeleton
- GAPDH could not only be a metabolic enzyme but in immunity also



Acknowledgements

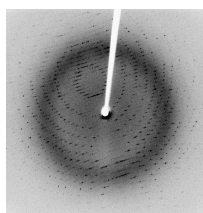
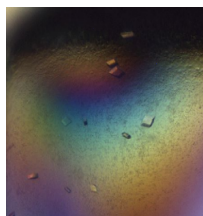


Virology



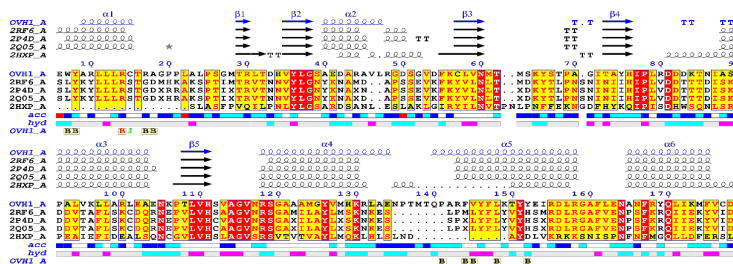
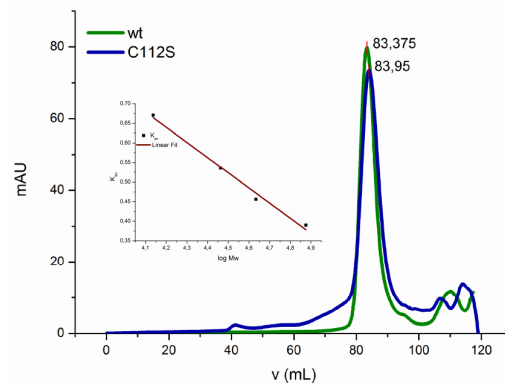
Dario Porley
Mabel Berois

Crystallization



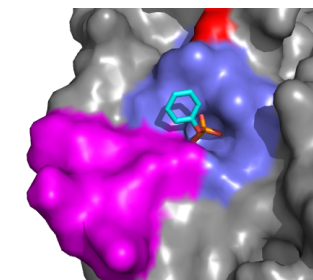
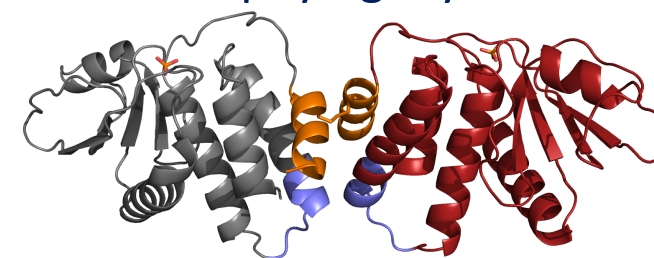
Danilo Segovia
Frederik Saul
Patrick Weber
Ahmed Haouz

Biochemistry



Danilo Segovia
Mariano Martinez
Andrea Villarino

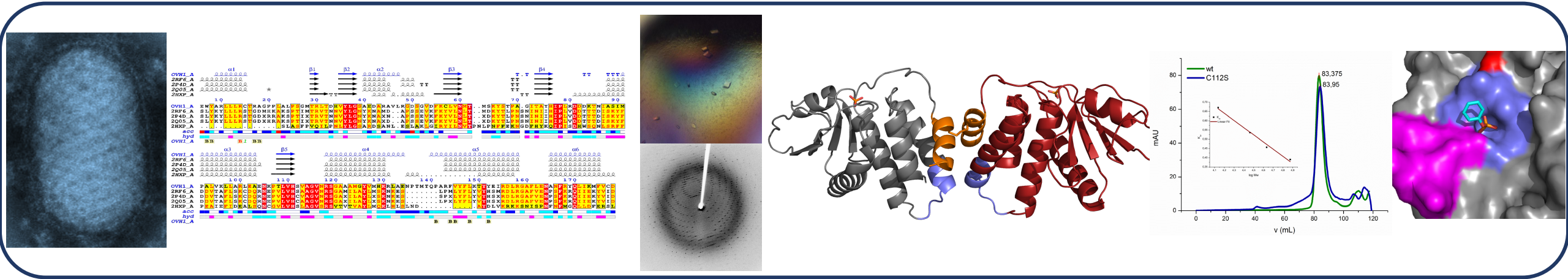
Crystallography, modeling & phylogeny



Danilo Segovia
Dario Porley
Mahendra Mariadassou

OH1 from Orf virus: a new tyrosine phosphatase

Distinct structural features & triple substrate specificity



Thank you very much for your kind attention