

Mélanie Forêt Jacquard^{[a]*}, Benoit Gautier^[b], Baptiste Legrand^[c], Nicolas Tricaud^[b], Nicolas Inguibert^[a]

[a] Centre de Recherche Insulaire et Observatoire de l'Environnement (CRIOBE), USR CNRS 3278, CNRS-EPHE-UPVD, Université de Perpignan Via Domitia, Bâtiment T, 58 Avenue P. Alduy, 66860 Perpignan, France. Contact : melanie.foret.jacquard@gmail.com ; nicolas.inguibert@univ-perp.fr

[b] Institut des Neurosciences de Montpellier, INSERM U1051, Université de Montpellier, 80 Rue A. Fliche, 34091 Montpellier, France.

[c] Institut des Biomolécules Max Mousseron, UMR 5247, CNRS, UM, ENSCM, UFR des Sciences Pharmaceutiques et Biologiques, 15 Avenue Charles Flahault, 34093 Montpellier Cedex 5, France.

INTRODUCTION

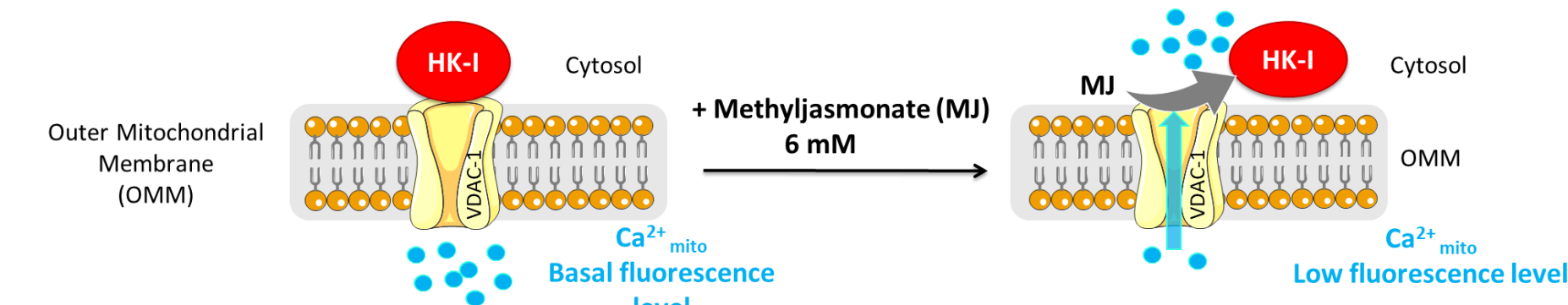
Voltage-Dependent Anion Channel 1 (VDAC1) is a transmembrane β -barrel protein essential for cell metabolism as in the regulation of proteins and metabolites traffic in and out of the mitochondria. VDAC1 displays binding sites for numerous proteins with various functions in cellular activities, such as pro- and anti-apoptotic proteins of the Bcl-2 family proteins and Hexokinases-I and -II (HK-I/II), thus playing a key role in mitochondria-mediated apoptosis. Hexokinase-I (HK-I) is highly expressed in brain and binds to VDAC1 through its N-terminal domain (NHK1) structured in α -helix. Upon apoptotic stimuli, several phenomenon occur : HK dissociates from VDAC1, followed by mitochondrial calcium efflux to the cytosol, VDAC1 oligomerization, and finally release of cytochrome c.^{[1][2]} Therefore, this protein-protein interaction has attracted much attention in the fight against cancer, neurodegenerative and demyelinating diseases such as Alzheimer, Parkinson, or Diabetic Peripheral Neuropathy, among others. Several interaction models of HK-I/II binding to VDAC1 have been proposed, however they show to be very different in terms of binding association. Herein, we aim to develop new biologically active peptides derived from N-terminal region of HK-I (NHK1 peptides) which are able to interact with VDAC1. Then we ensured to structure NHK1 peptides into an α -helix after several modifications, and finally we determined the stability of the NHK1 peptides towards proteases degradation.

1. In-vitro competition assay

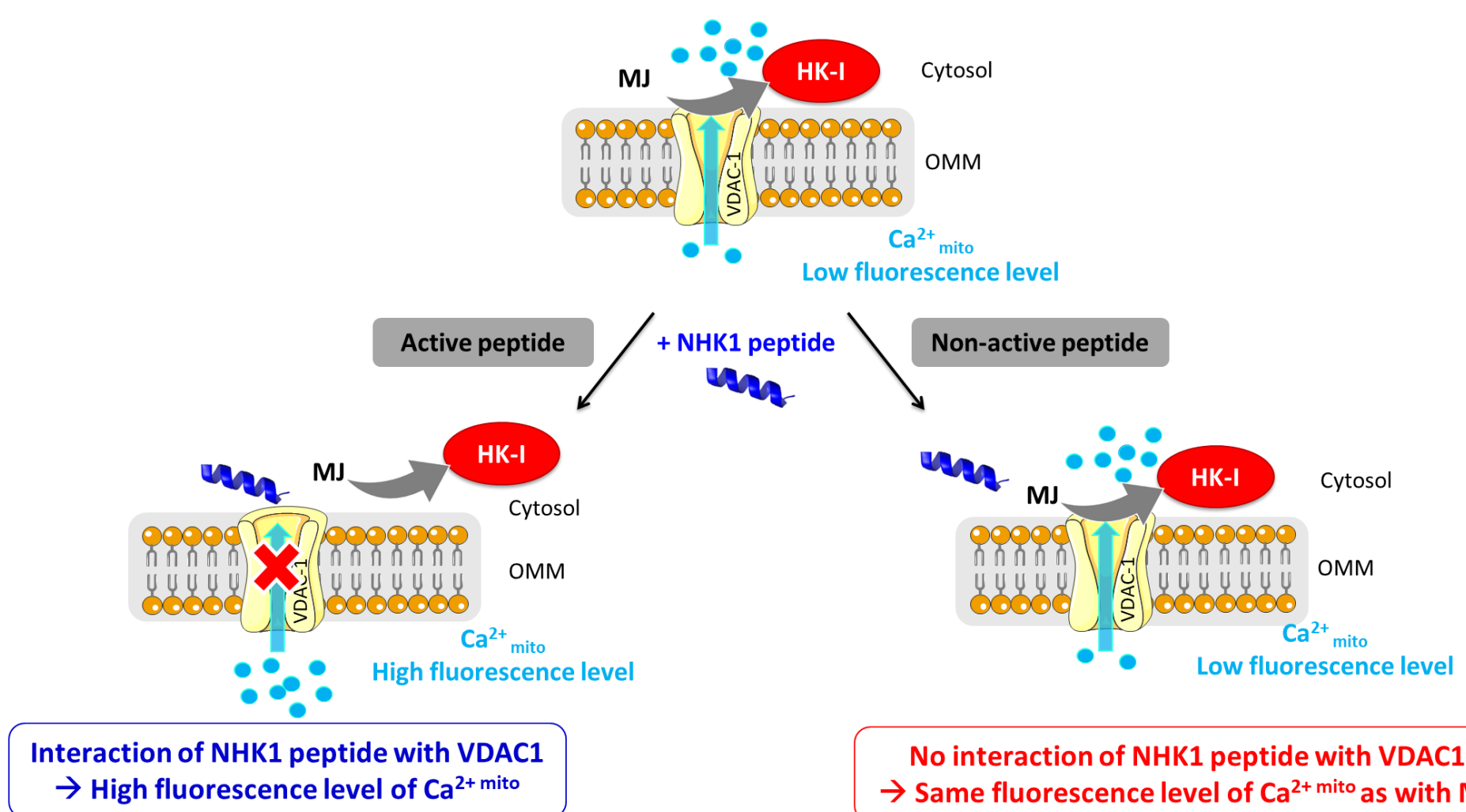
Characteristics

- HEK cells transfected with mito-GCaMP2 probe
- NHK1 sequence coupled to TAT for internalization delivery
 - Methyljasmonate (MJ) induces demyelination at a concentration of 6mM
 - NHK1 peptides ED₅₀ (Ca²⁺_{mito}) = 10 μ M

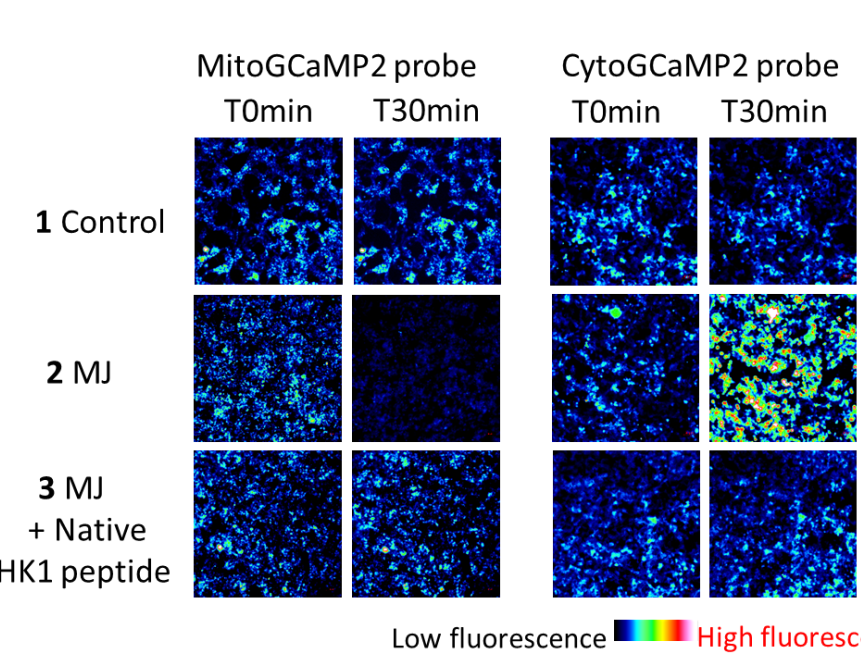
A) Disruption of HK-I : VDAC1 binding using Methyljasmonate (MJ)



B) Competition test between MJ and NHK1 peptides on VDAC1



C) Fluorescence levels of mitoGCaMP2 and cytoGCaMP2 probes with MJ and native NHK1 peptide



Principle of the *in-vitro* assay of NHK1-TAT peptides to VDAC1 in presence of methyljasmonate (MJ). Quantification of the fluorescence levels of the mitoGCaMP2 (Ca²⁺_{mito}) inside the mitochondria, and cytoGCaMP2 within the cytosol and used as control. Active NHK1 peptide would result in fluorescence level of mitochondrial calcium comparable to basal fluorescence level without MJ, while with a non-active peptide, low fluorescence level of mitochondrial calcium would be observed. Experiments were performed by B. Gautier from INM.

2. Structure-Activity relationship studies

Ala-scan and deletion studies of native NHK1 sequence :

- NHK1 minimal active sequence : ¹MIAAQLLAYFTELK¹⁵
 - High activity of compound 1 for VDAC1
 - Identification of key residues involved in the interaction with VDAC1 : ⁴AQLLAYF¹¹

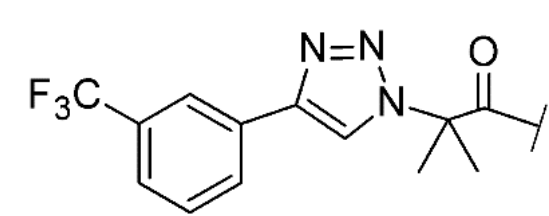
Interaction optimizations of NHK1-TAT peptides :

- Leucine replacement by hydrophobic aminoacids
 - High activity of compound 2 for VDAC1

Reinforcement of helical binding of NHK1-TAT peptides :

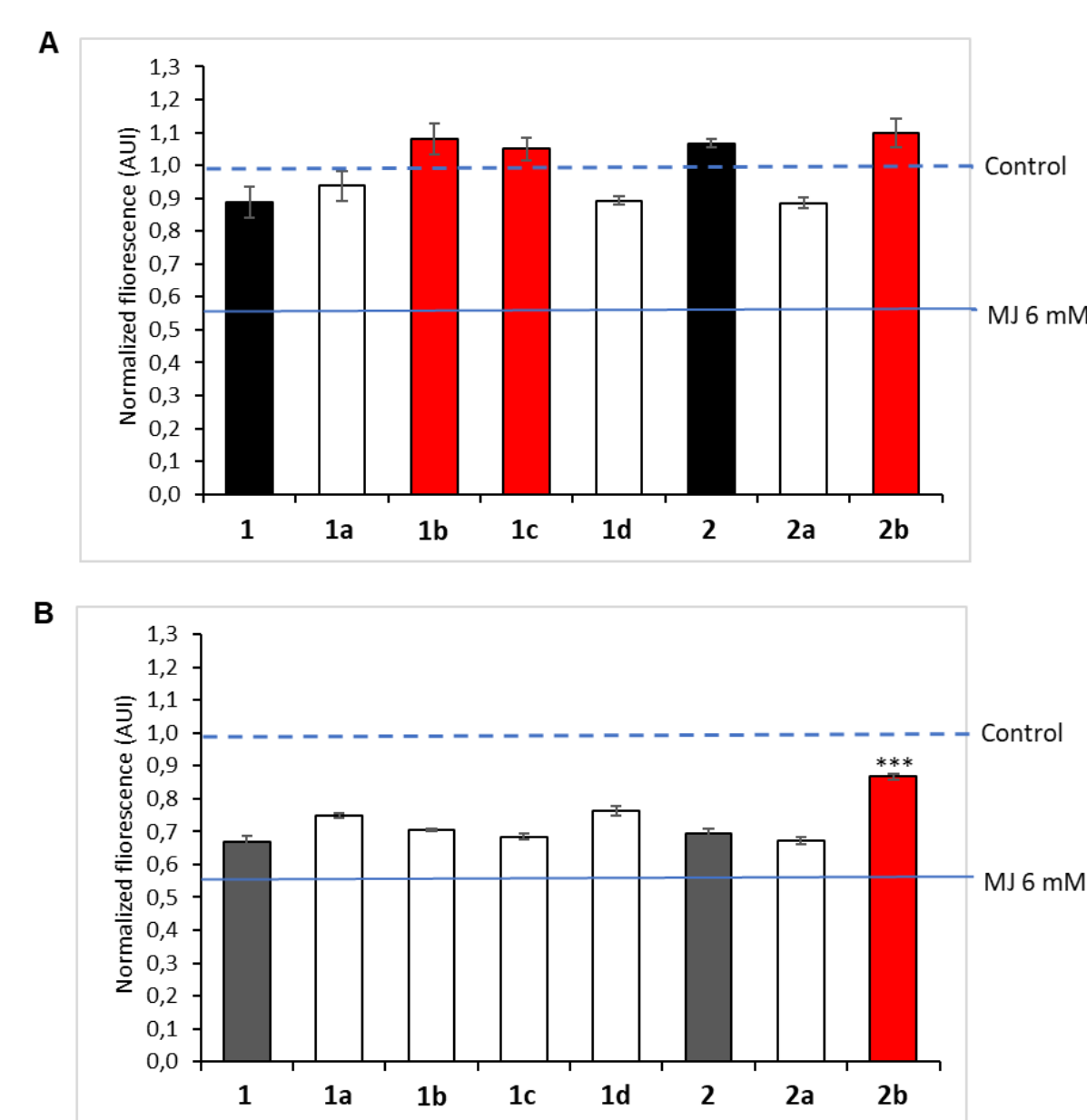
- Introduction of α -aminoisobutyric acid (Aib, U) to NHK1 peptides
 - As AUAU patch at N-terminus
 - By replacing Alanine at 8th position

- Introduction of a hydrophobic tag^[3] : 3-F₃C-Ph[Tz]U



Cpd	NHK1-TAT peptide sequence																			
	(n+1)	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15				
NHK1	Ac-	M	I	A	A	Q	L	L	A	Y	F	T	E	L	K	TAT NH ₂				
1	Ac-					A	Q	L	L	A	Y	F	T	E	L	K TAT NH ₂				
1a	Ac-					A	Q	L	L	U	Y	F	T	E	L	K TAT NH ₂				
1b	Ac-					A	U	A	Q	L	L	U	Y	F	T	E	L	K TAT NH ₂		
1c	Ac-					A	U	A	U	A	Q	L	L	U	Y	F	T	E	L	K TAT NH ₂
1d	Ac-					A	U	A	U	A	Q	L	L	U	Y	F	T	E	L	K TAT NH ₂
2	Ac-					A	Q	W	W	A	Y	F	T	E	W	K TAT NH ₂				
2a	Ac-					A	U	A	U	A	Q	W	W	A	Y	F	T	E	W	K TAT NH ₂
2b						3-CF ₃ Ph[Tz]	U	A	Q	W	W	A	Y	F	T	E	W	K TAT NH ₂		

Mean of fluorescence level of mitochondrial calcium. (N=4-6 tests, triplicate/test). Methyljasmonate (MJ) at 6mM has a mean of fluorescence of 0,55. A) NHK1 peptides tested at a 10 μ M concentration. B) NHK1 peptides tested at a 3 μ M concentration. Experiments were performed by B. Gautier from INM.



CONCLUSION

- Synthesis of NHK1 peptides biologically active for VDAC1 blocking Ca²⁺_{mito} efflux
- Optimization of helical folding of NHK1 peptides
- Optimized degradation kinetic of NHK1 peptides in rat serum
- The binding nature of NHK1 to VDAC1 occurs more preferentially via model no. 2

PERSPECTIVES

- Introduction of peptide bond surrogates in NHK1 peptides to increase peptide's half-life
- CD and NMR studies of NHK1 peptides in trifluoroethanol
- CD experiments on new NHK1 peptides with KUKU or KUAU patch at N-terminus
- Determination of the binding affinity of NHK1 peptides for VDAC1 by Microscale Thermophoresis technology
- Using NHK1 peptides as a tool for crosslinking studies with VDAC1

3. Circular dichroism studies

NHK1-TAT & NHK1 peptides in phosphate buffer :

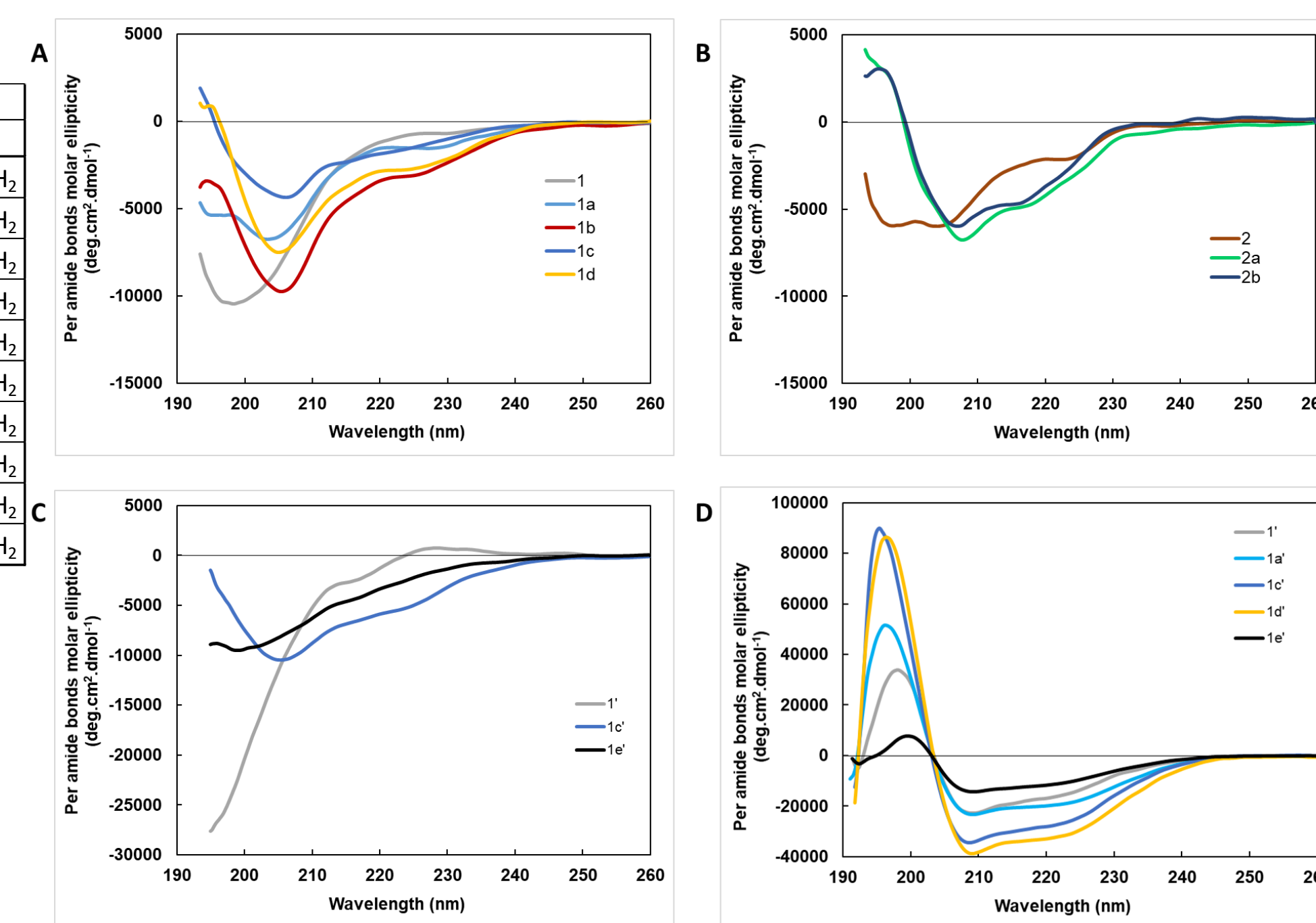
- Compound 1d : tendency to fold into α -helix
- Compounds 2a, 2b : the most folded into α -helix

NHK1 peptides in methanol :

- Compound 1d' is the most structured into α -helix

Cpd	NHK1 peptide sequence																		
	(n+1)	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15			
1'	Ac-	A	Q	L	L	A	Y	F	T	E	L	K	NH ₂						
1a'	Ac-	A	Q	L	L	U	Y	F	T	E	L	K	NH ₂						
1b'	Ac-	A	U	A	Q	L	L	U	Y	F	T	E	L	K	NH ₂				
1c'	Ac-	A	U	A	U	A	Q	L	L	A	Y	F	T	E	L	K	NH ₂		
1d'	Ac-	A	U	A	U	A	Q	L	L	A	Y	F	T	E	L	K	NH ₂		
1e'	Ac-	A	U	A	Q	L	L	A	Y	F	T	E	L	K	NH ₂				
2'	Ac-	A	Q	W	W	A	Y	F	T	E	W	K	NH ₂						
2a'	Ac-	A	U	A	U	A	Q	W	W	A	Y	F	T	E	W	K	NH ₂		
2b'						3-CF ₃ Ph[Tz]	U	A	Q	W	W	A	Y	F	T	E	W	K	NH ₂
2c'						3-CF ₃ Ph[Tz]	U	A	Q	W	U	Y	F	T	E	W	K	NH ₂	

Circular dichroism studies. Conditions A, B, D in DPBS solution pH=7, E in methanol solution. All peptides were dissolved at a 100 μ M concentration. Compounds 1-2b refer to NHK1-TAT peptides, whereas compounds 1'-2c' refer to NHK1 peptides. Experiments were performed by B. Legrand from IBMM.



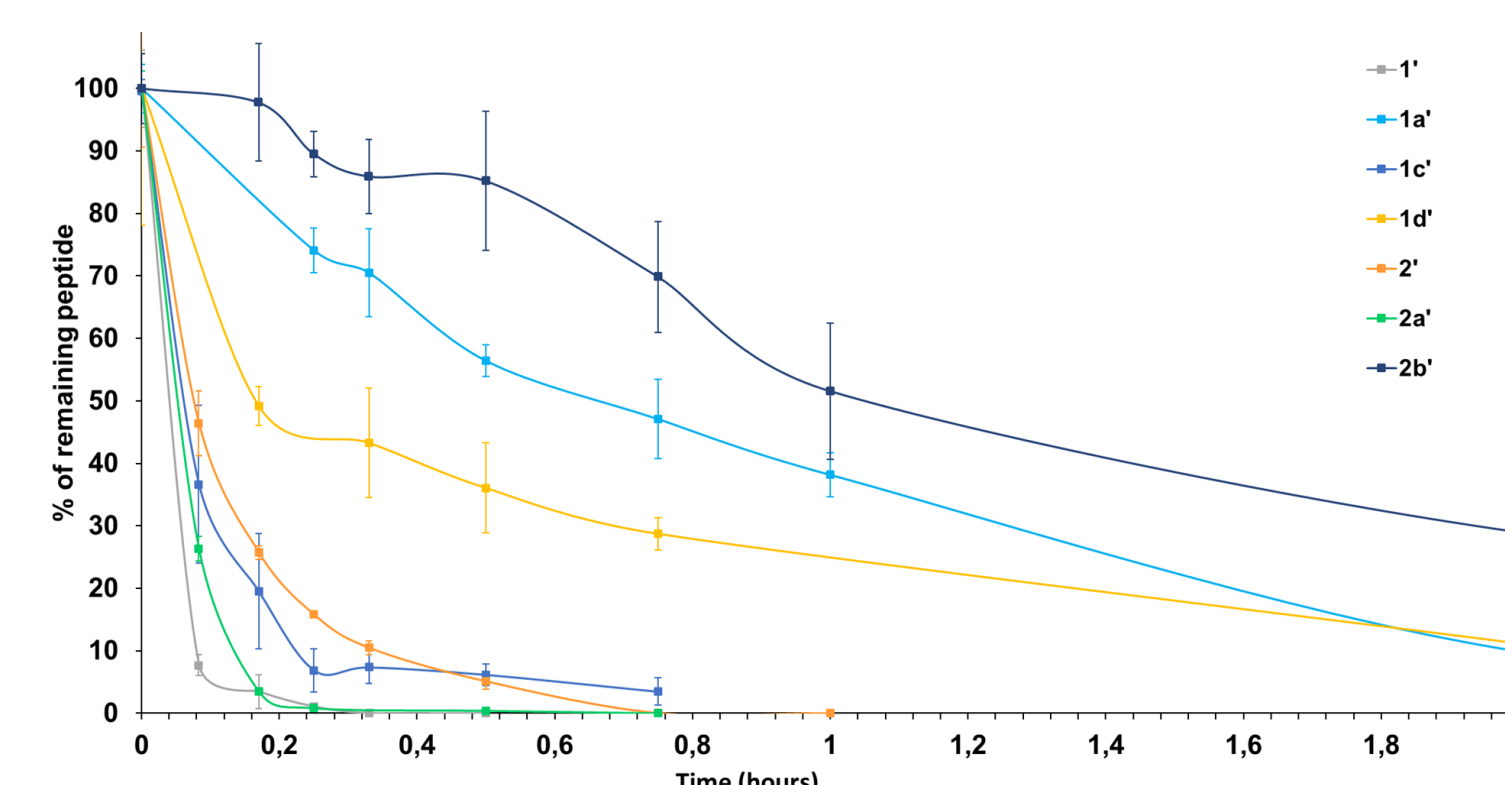
4. Proteolytic stability assays by HPLC-MS

NHK1 peptides stability towards Elastase

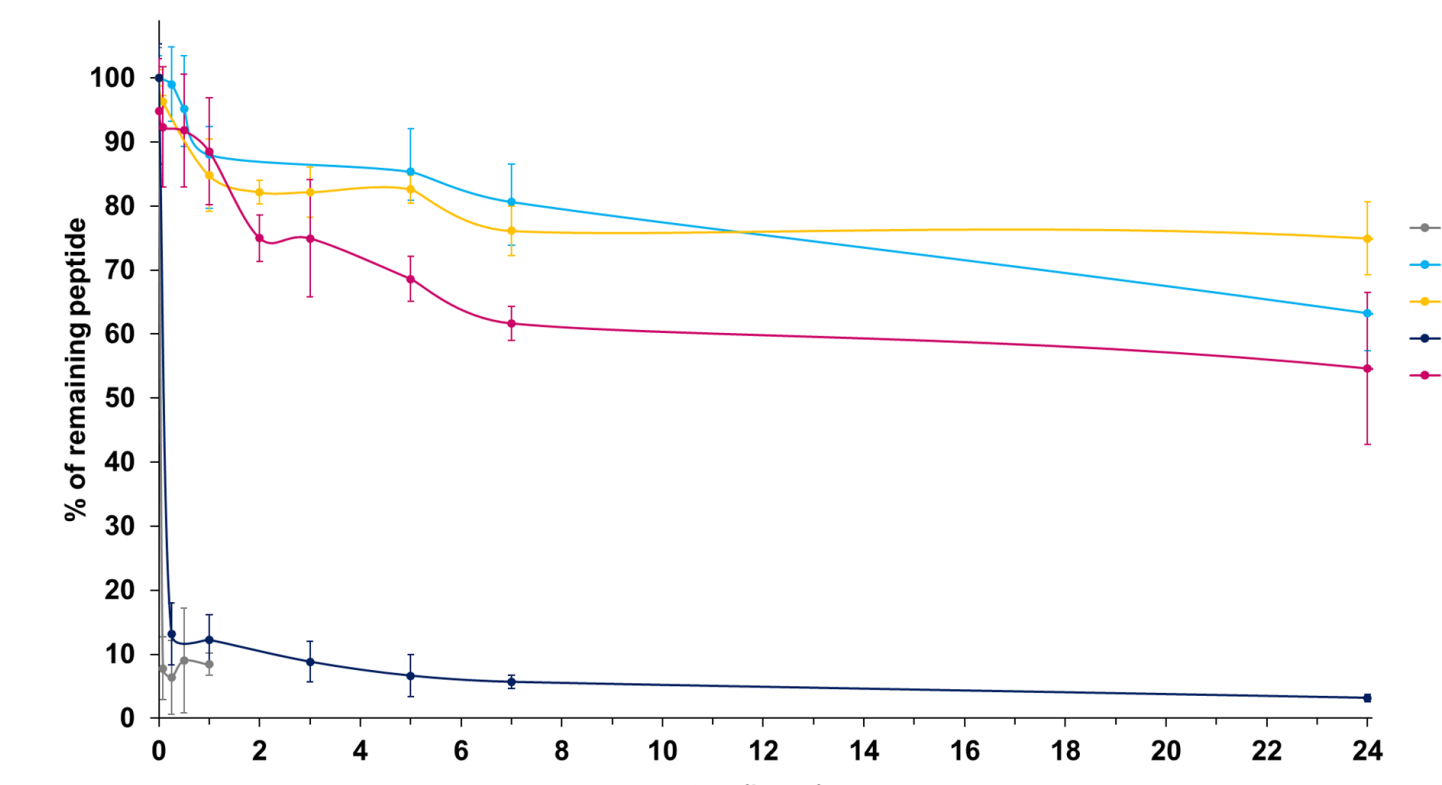
- Compounds 2b' > 1a' > 1d' are the most stable against Elastase

NHK1 peptides stability towards rat serum

- Compounds 1d' > 1a' > 2c' are the most stable against serum proteases



Stability profiles of NHK1 peptides towards Elastase. All peptides were tested at a concentration of 66.6 μ mol/L in presence of 9.4 μ g/mL of Elastase in Tris.HCl buffer pH 8 after incubation at 37°C for 2h. Assays were performed in triplicate.



Stability profiles of NHK1 peptides towards rat serum. All peptides were tested at a concentration of 66.6 μ mol/L in presence of 25% (v/v) of rat serum and MilliQ water after incubation at 37°C for 24h. Assays were performed in triplicate.

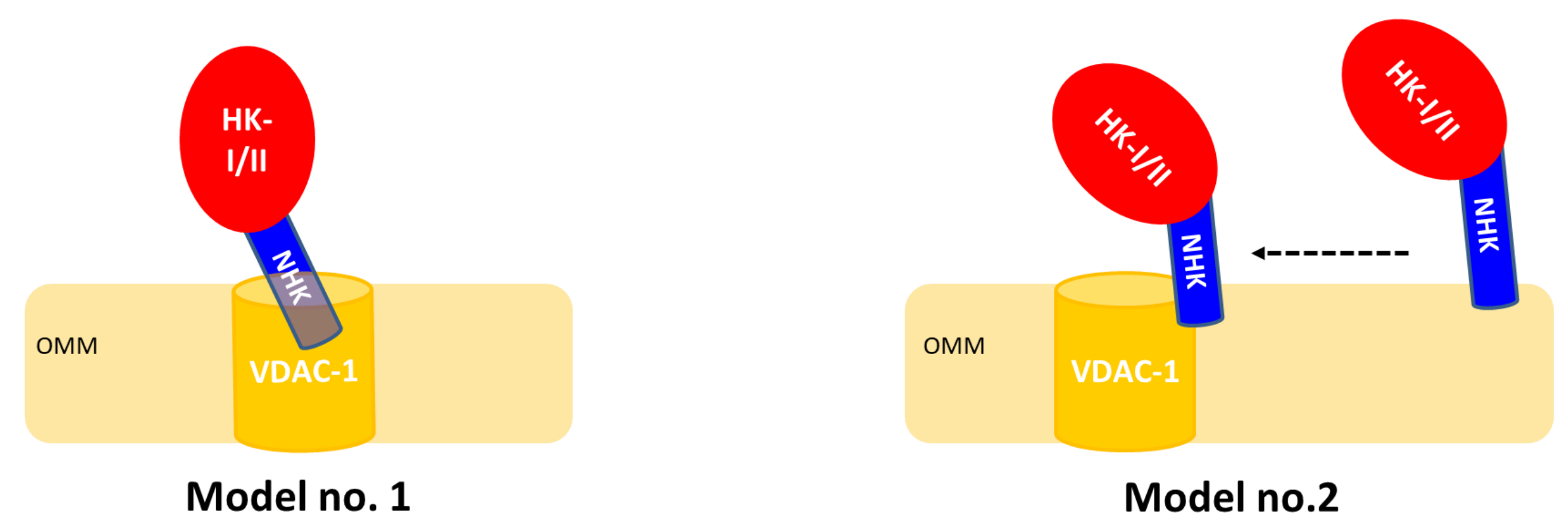
5. Proposed interaction models of HK-I/II and VDAC1

Suggested model no.1 : NHK is inserted into the core of VDAC1^[4]

- NHK is hydrophobic while VDAC's core is hydrophilic

Suggested model no.2 : NHK interacts on the side of VDAC1^[5]

- Step 1: NHK binds to the Outer Mitochondrial Membrane
- Step 2: NHK interacts with VDAC1 through hydrophobic residues



REFERENCES

- NB: NHK1 coupled to TAT sequence : GRKKRRQRRRPQ
- Shoshan-Barmatz, V. *et al.*, *Cell Calcium* 2018, 69, 81-100.
 - Tricaud, N. *et al.*, *bioRxiv* 2019, 581157.
 - Das, S. *et al.*, *Chem. Eur. J.* 2017, 23(71), 17964-17972.
 - Rosano, C., *Mitochondrion* 2011, 11, 513-519
 - Haloi, N. *et al.*, *bioRxiv* 2020, 2020.11.18.365965.

ACKNOWLEDGEMENTS

We thank the Region Occitanie for financial support. All analyses were performed using the facilities of the "Biodiversité et Biotechnologies Marines" platform at the University of Perpignan.