



Institut régional de recherche
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UNIVERSITÉ D'ARTOIS

Devenir des protéines dans un système modèle de digestion simulée assisté par spectrométrie de masse

Institut Charles VIOLLETTE:

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2: Equipe QSA, Université d'Artois, Lens.

3: CUMA, Faculté de Pharmacie, Lille.

4: Inserm U1011, « Récepteurs nucléaires, maladies cardiovasculaires et diabète », Lille

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- **Gastrointestinal digestion**



1883

“Shall I refuse my dinner because I do not fully understand the process of digestion?”



Oliver Heaviside (1850-1925)



- Partial hydrolysis by pepsin (*Stomach*)
- proteases (trypsin, chymotrypsin, carboxypeptidases) and microorganisms peptidases (*small intestine lumen*)
- brush border membrane peptidase (*microvilli of epithelial cells*)



Free amino acids

+

Various molecular
weight peptides with
potential bioactivities

Peptidome

● Sources and roles of bioactive peptides

Sources of bioactive peptides

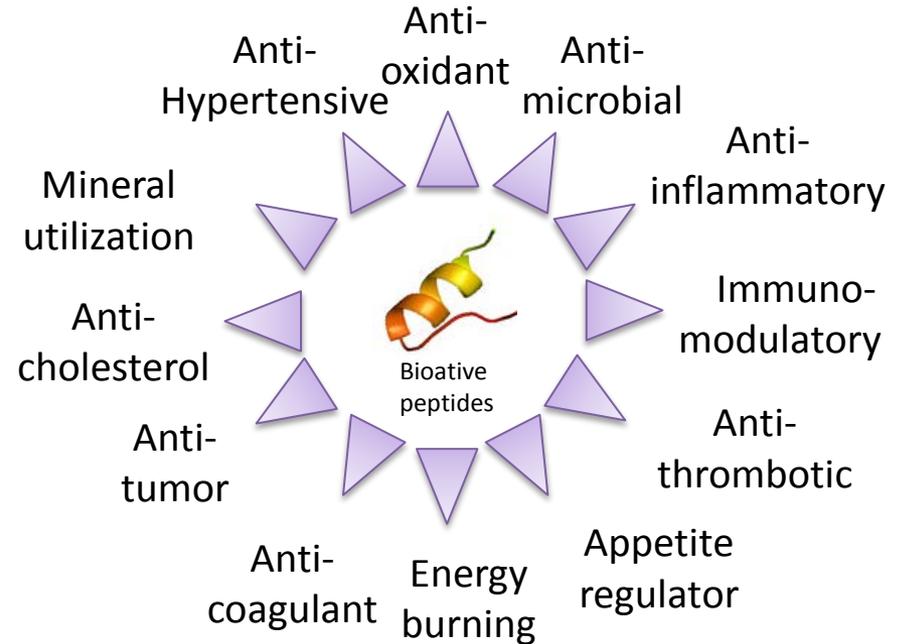
All proteins Animals
 Plants

→ Cow-milk proteins

benefit / harmful

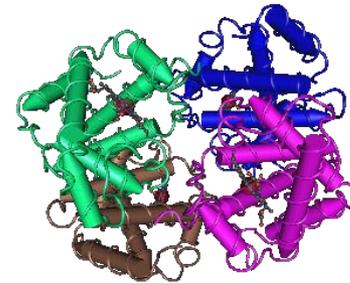


Health –promoting roles of bioactive peptides



- Hemoglobin (Hb) as a potential source of bioactive peptides ?

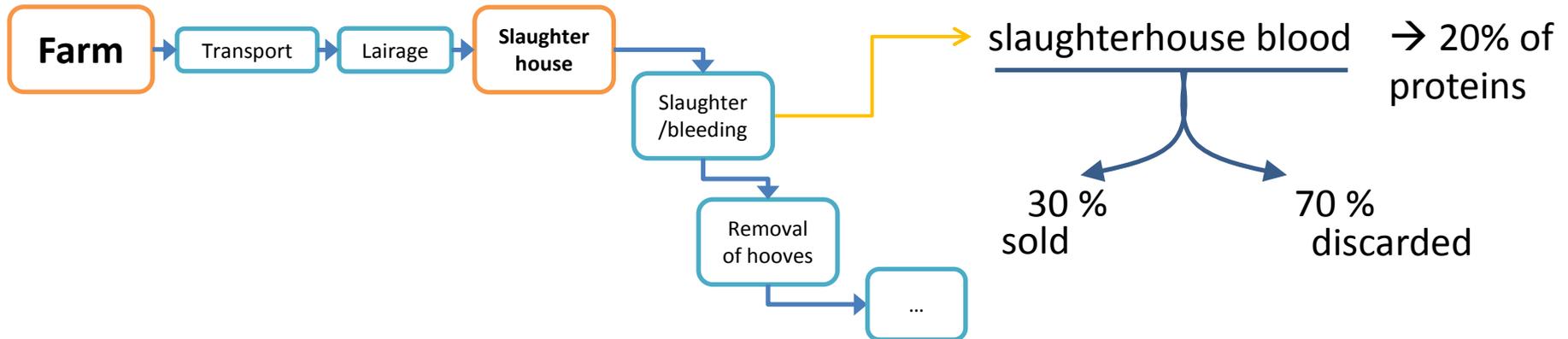
Hb ($\alpha 2/\beta 2$): a model protein



Bovine hemoglobin (Hb)

Source: NCBI

Meat production food chain

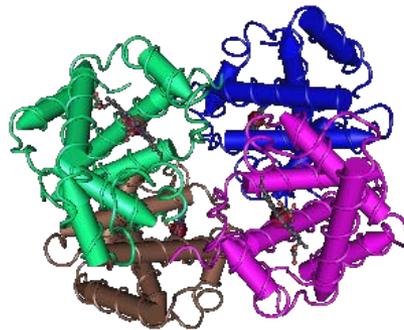


1

- Development of an *in vitro* human digestion model to study protein digestion
- Characterization of peptidomes (GI digestion-derived peptides)

2

- Protein digestion and energy homeostasis: impact of generated peptides on intestinal hormones

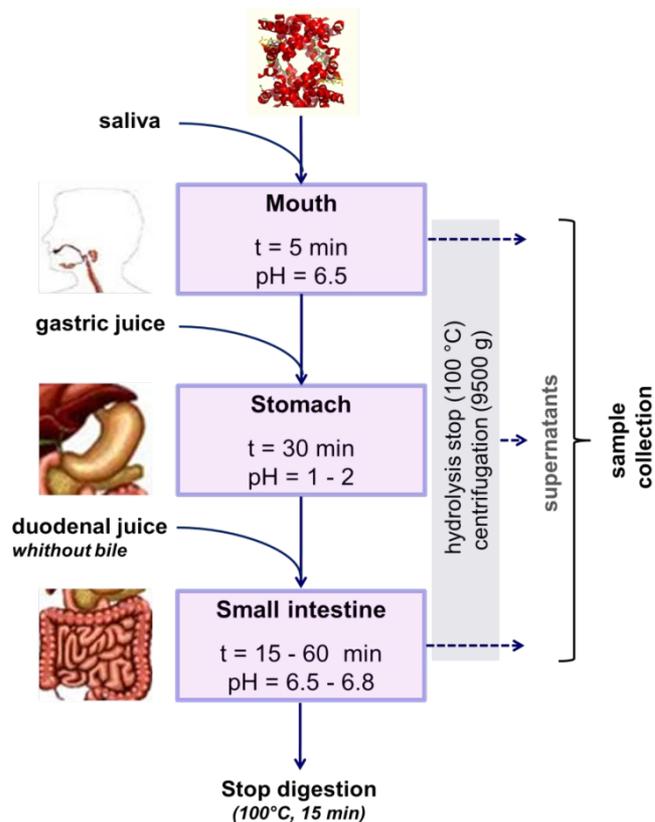


Bovine hemoglobin

Source: NCBI

In vitro GI digestion x 3

No heating
over 37°C



Analytical strategy

Separation
method

C18 RP-HPLC
C18 LiChroCART 250-4,
LiChrospher 100 column
(Merck KGaA,
Darmstadt, Germany)

X 1

Mass
spectrometry/
Bioinformatics

MALDI-MS/MS
AutoFlex speed, Bruker

✓ **Biotoools 3.4**

✓ **Peaks 7**

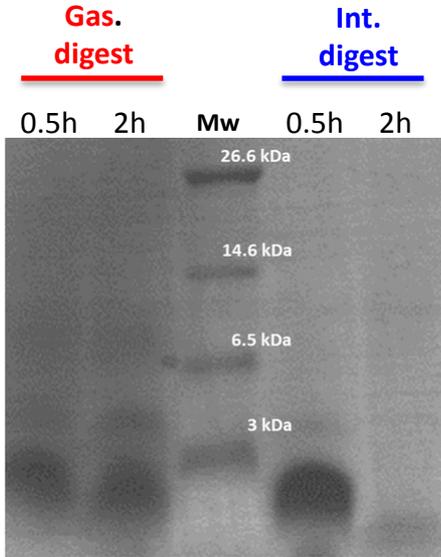
C18 NanoLC
Acclaim Pepmap RSLC,
75 μm ID \times 50 cm,
Thermo Scientific

X 1

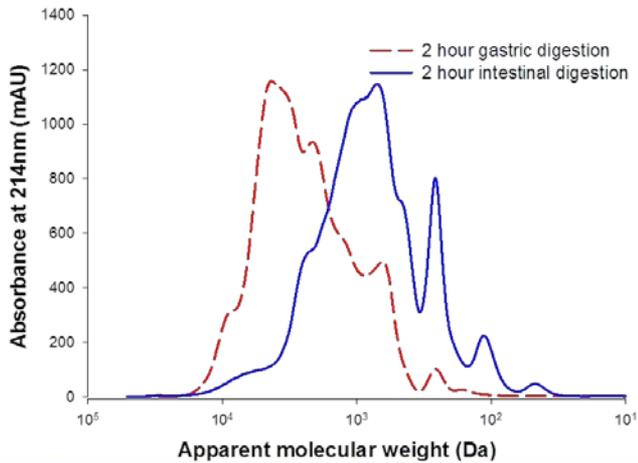
ESI-HR-MS/MS
Thermo Scientific Orbitrap
Elite mass spectrometer

● Hemoglobin (Hb): a highly digestible protein

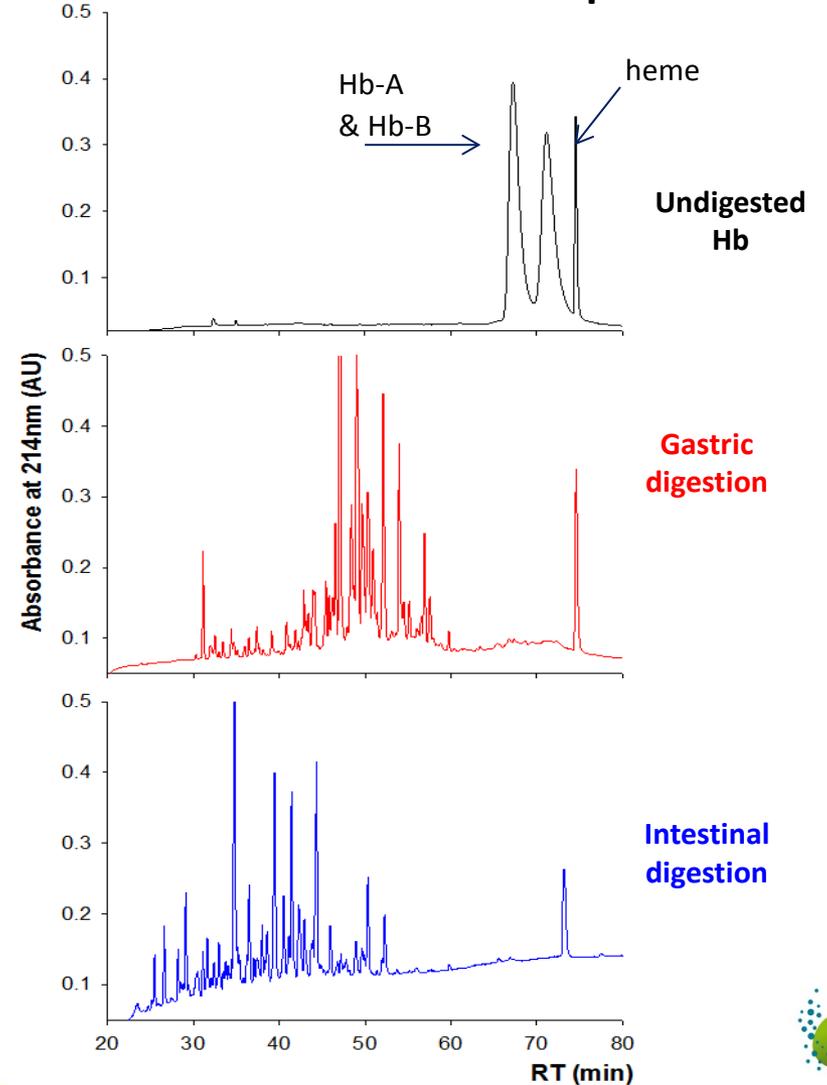
SDS-PAGE: 16.5%



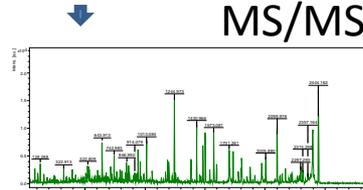
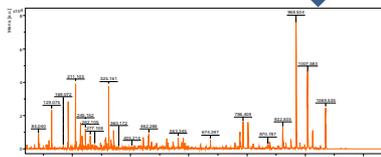
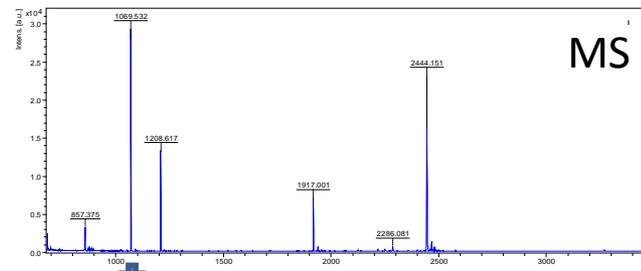
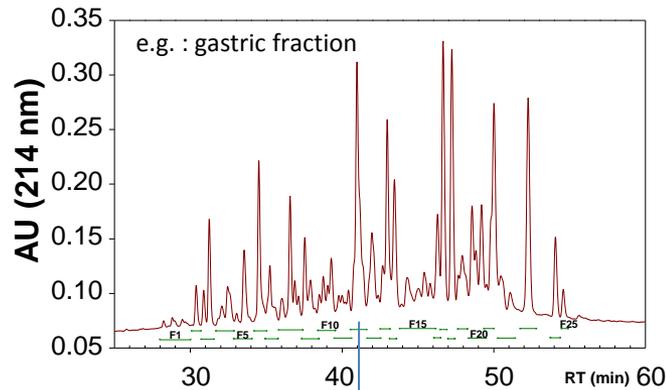
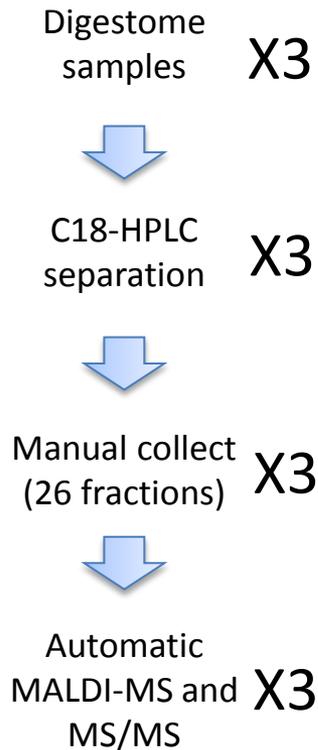
SEC-chromatography



Normal bore C18-HPLC profiles



Normal bore C18 HPLC-MALDI-MS (off-line)



Gathering of all XML files



↓

Combined XML file
+ renumbering of detected peaks



Enzyme : none
Missed cleavage : 36

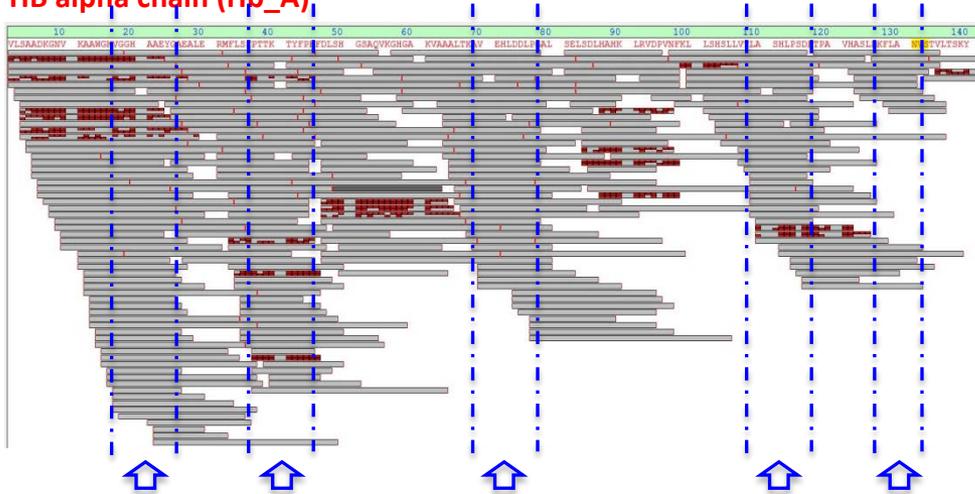
Hb-A and Hb-B
sequences

↓

Peptides
Matching

● Peptide heterogeneity (HPLC-MALDI-MS)

HB alpha chain (Hb_A)



Digestion resistant sequences ?

HB beta chain (Hb_B)



317 matching peptides (based on MS-data)

→ sequence coverage (MS) = 100 %

19 peptides unambiguously identified by MS/MS

→ sequence coverage (MS/MS) = 77 %

339 matching peptides (based on MS-data)

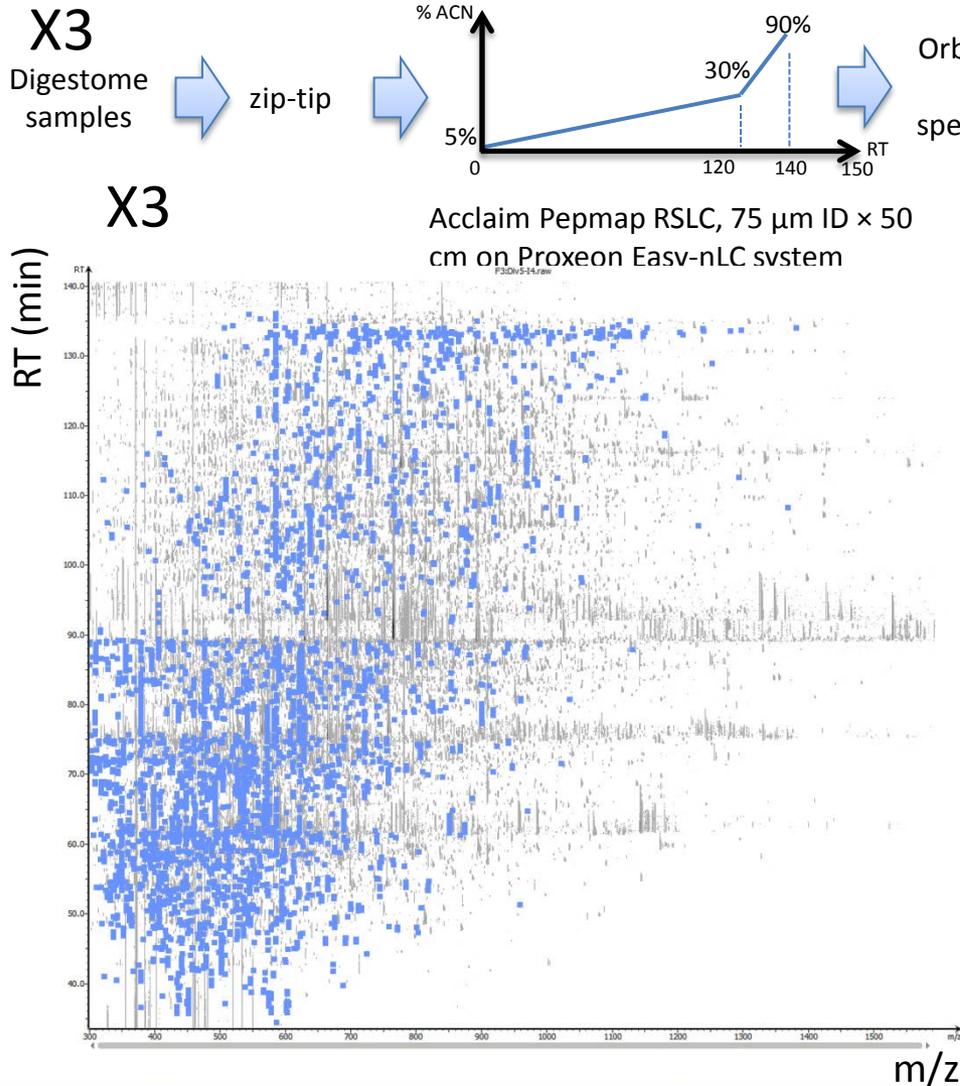
→ sequence coverage (MS) = 100 %

26 peptides unambiguously identified by MS/MS

→ sequence coverage (MS/MS) = 66 %

● nanoLC-ESI-HR-MS/MS

e.g. : intestinal fraction



Peptide identifications

Database :
bovine proteins



Hb_A **306** peptides unambiguously identified by MS/MS
→ sequence coverage (MS/MS) = 100 %

False discovery rate (FDR) = 0%

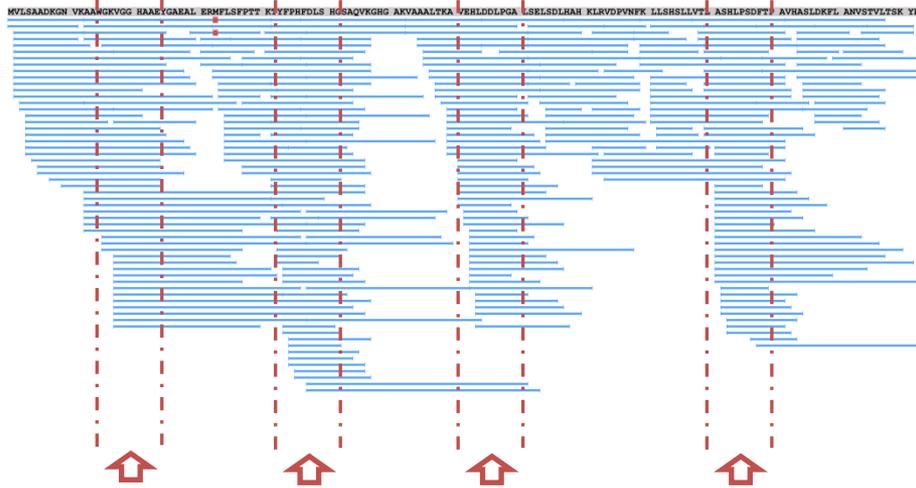
Hb_B **420** peptides unambiguously identified by MS/MS
→ sequence coverage (MS/MS) = 100 %

726
peptides

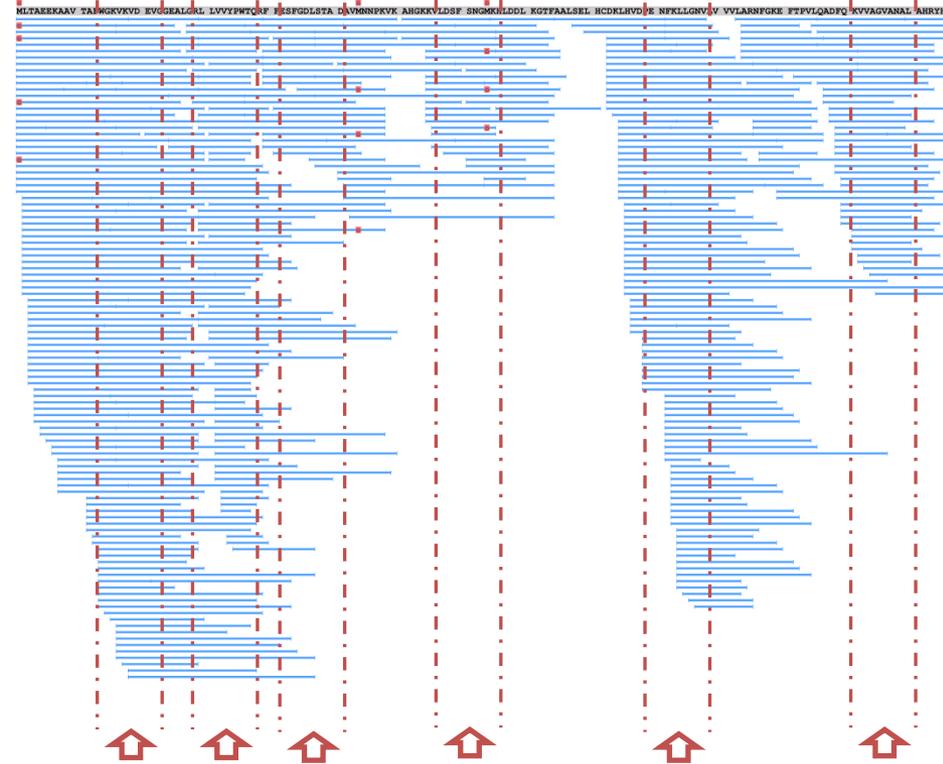
● Peptide heterogeneity(nanoLC-ESI-HR-MS/MS)

e.g. : intestinal fraction

Hb_A



Hb_B



GI digestion-resistant sequences

Ion parent error tolerance **10 ppm** and fragment mass error tolerance **0.2 Da**.

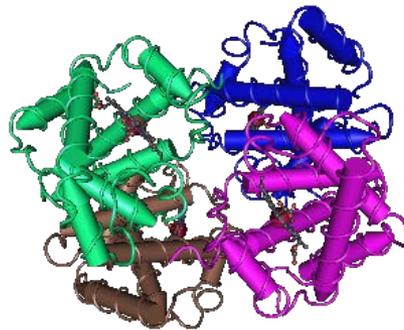


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Bovine hemoglobin

Source: NCBI

- **Energy Homeostasis:**

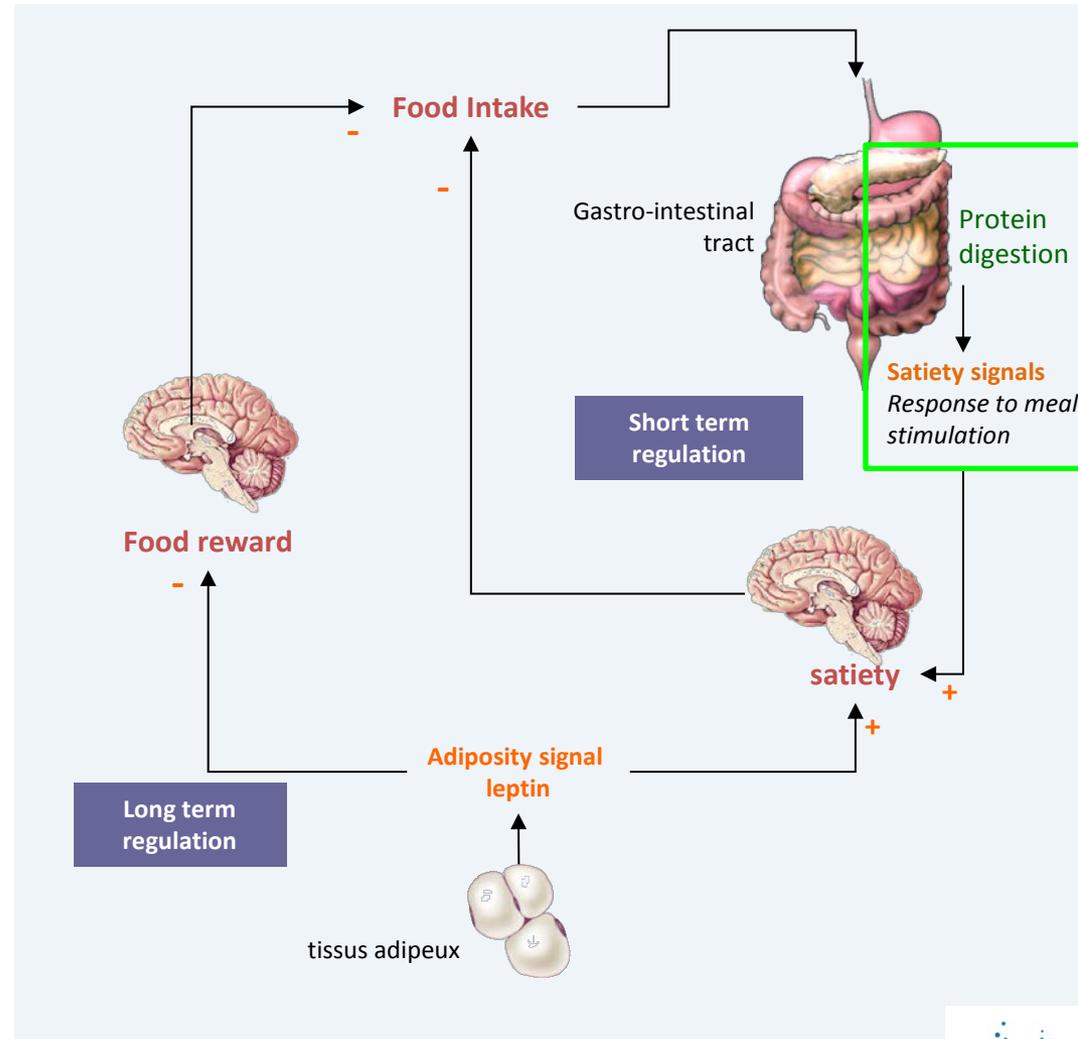
Energy expenditure vs caloric intake:
need to ensure a balance

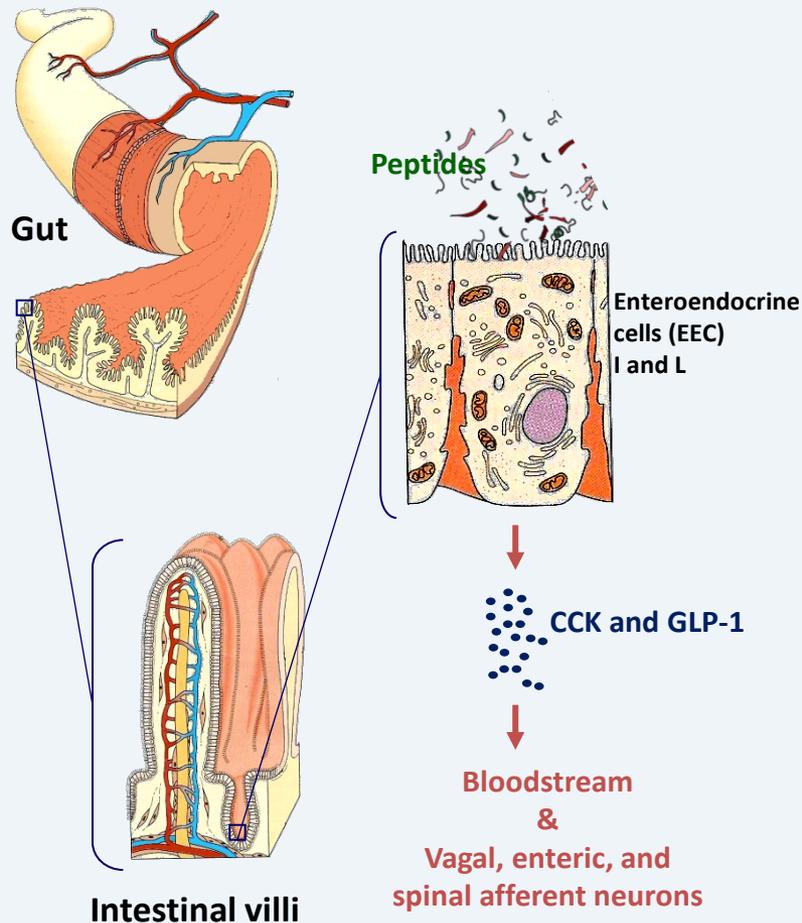


- **Regulation mechanisms**

Long term - adiposity signal:
To maintain body weight
« adiposity negative feedback »
(*Leptin*)

Short term - satiation signal:
(*gut hormones, gastric distension*)





- **Cholecystokinin (CCK)**

Produced by **I cells** (duodenum) in response to lipids and **proteins**.

Promotes **satiety**: increase gastric secretion, decrease gastric emptying, induces satiety feeling by vagal afferents

- **Glucagon-like Peptide 1 (GLP-1)**

Produced by **L cells** (ileum and colon)

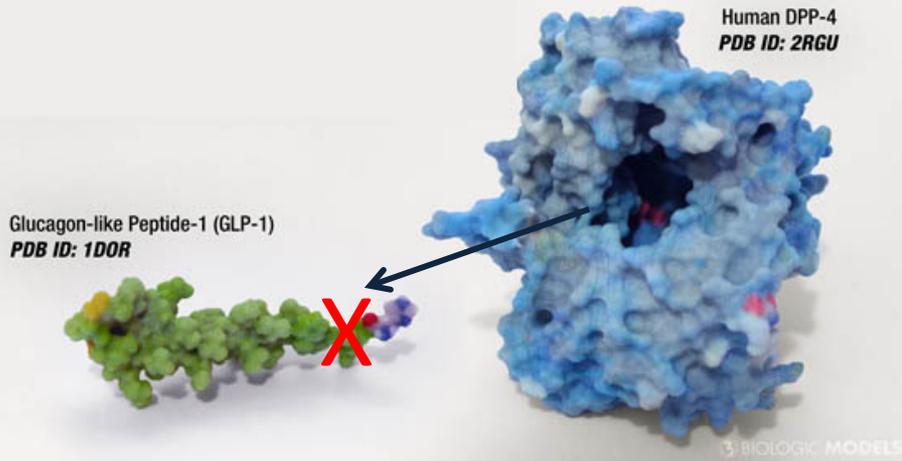
One of the proglucagon products

Promotes satiety by various pathways

Incretin: stimulates glucose-dependant insulin secretion

GLP-1 inactivation by dipeptidyl peptidase IV (**DPP-IV**).

Only 10-20% plasmatic GLP-1 remains



- Dipeptidyl peptidase 4 (**DPP-IV**)

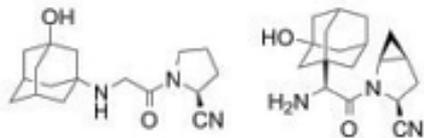
DPP-IV rapidly degrades GLP-1 → decrease in plasma

DPP-IV inhibition → indirect increase of GLP-1 activity
→ indirect impact on food intake

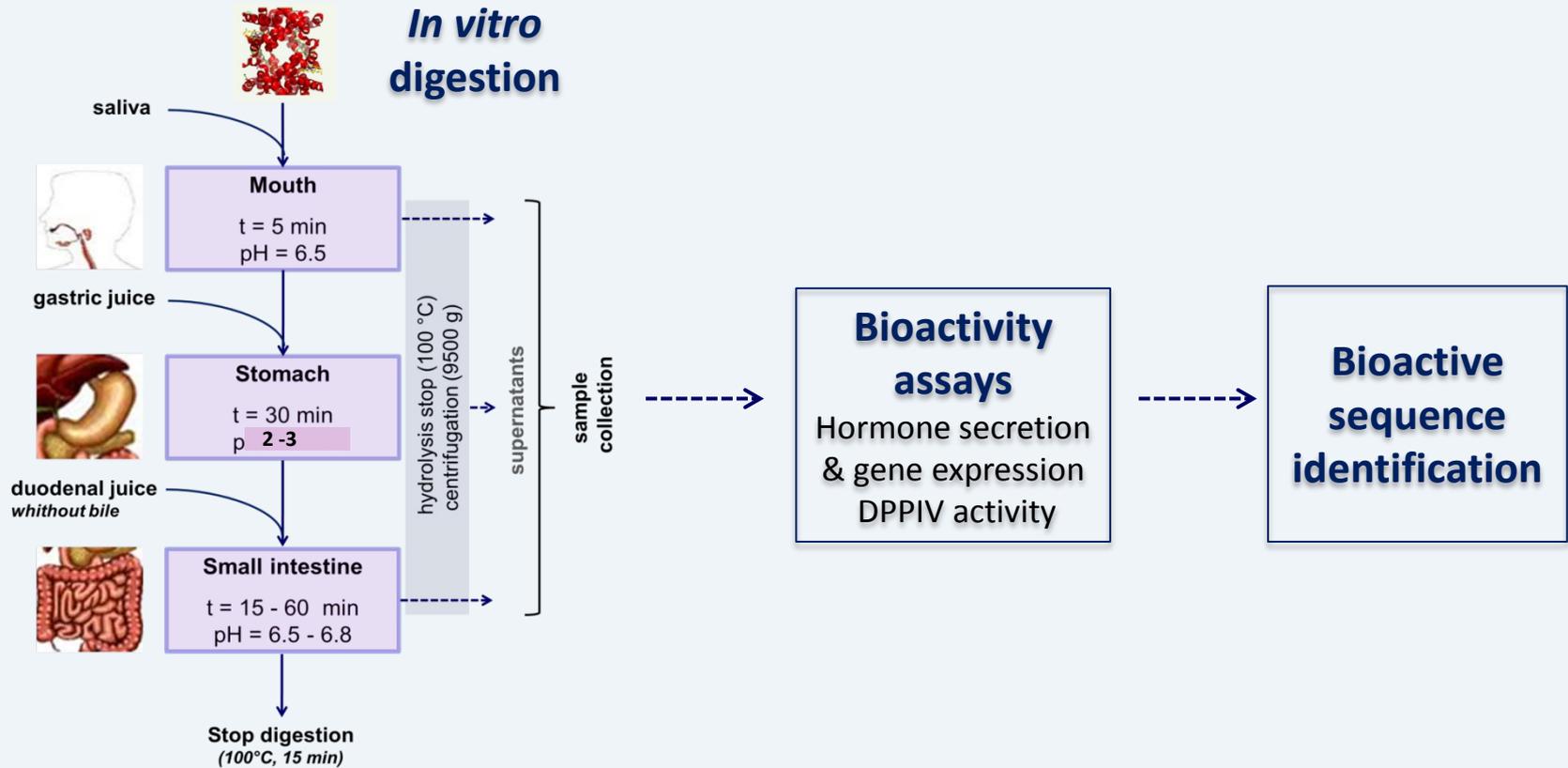
DPP-IV – GLP-1:

Inhibiting DPP-IV extends GLP-1 incretin activity
New target for type-2 diabetes therapy

Ex: Gliptins (e.g. Vildagliptin and saxagliptin)



→ Dietary proteins: promising sources as “natural”
DPP-IV inhibitors



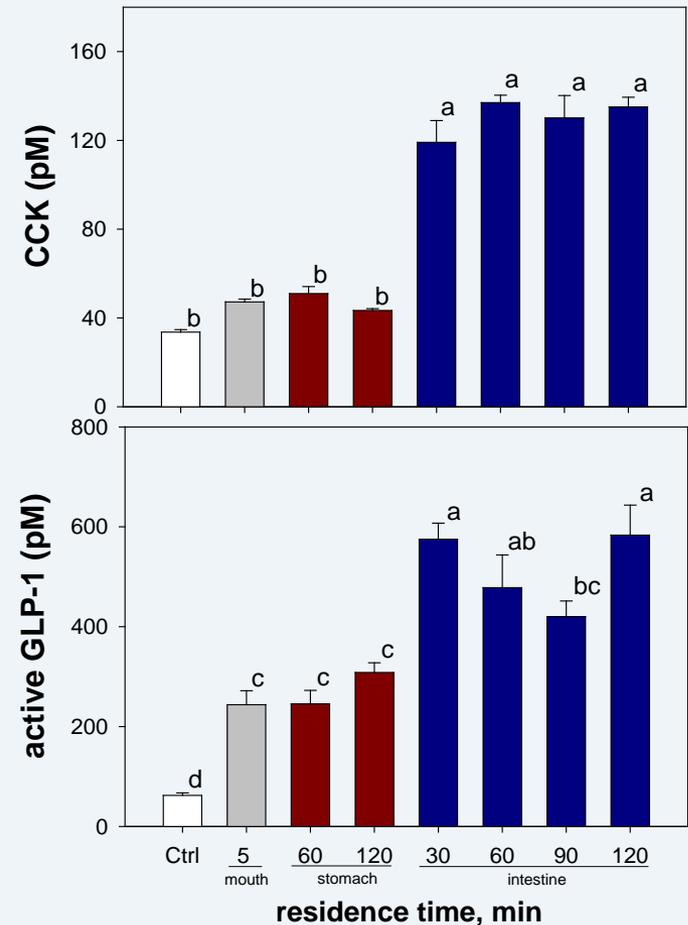
Hormones secretion



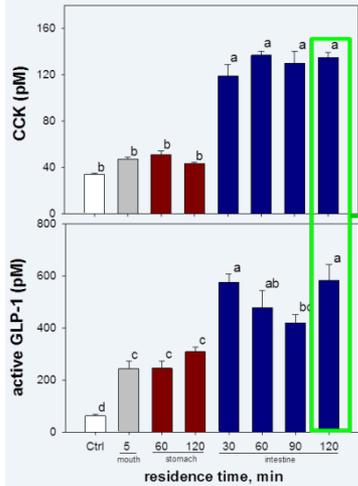
2h → CCK & GLP-1 secretion
RIA detection

Significant increase of both CCK and GLP-1 secretion in presence of intestinal samples

→ Beneficial effect of **intestinal enzymes** on peptide potential bioactivity



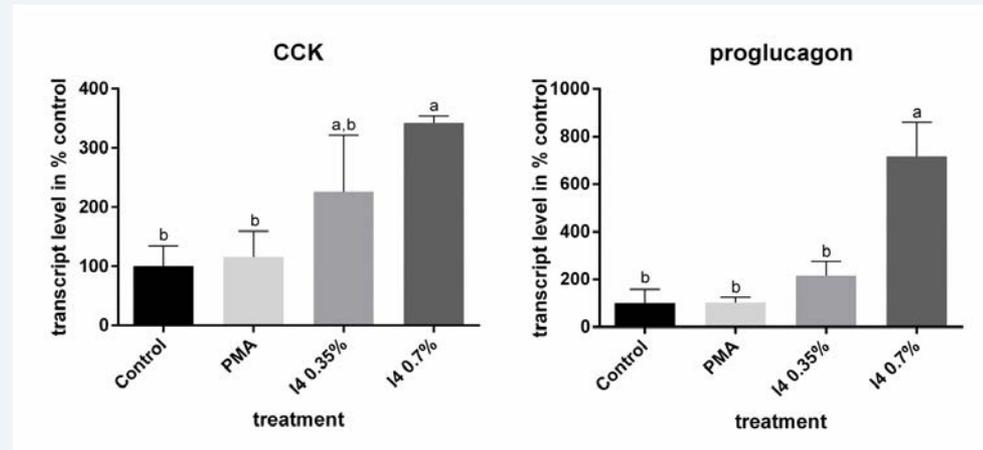
Regulation of hormone gene expression



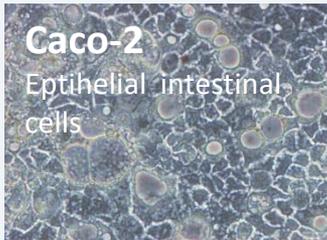
24h

CCK & Proglucagon genes expression qPCR

Intestinal hydrolysate (I4) significantly induces both CCK and proglucagon gene expression



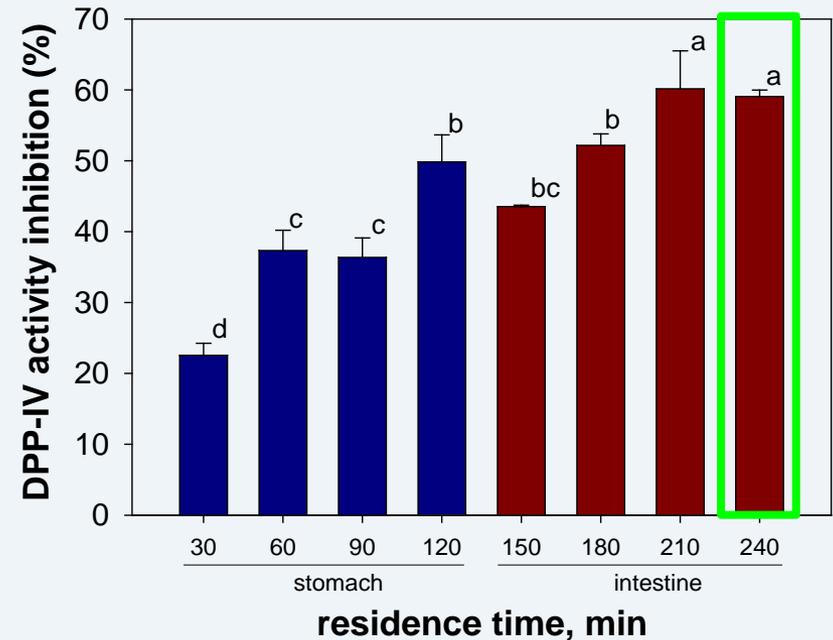
DPP-IV activity assay



Cell extract
DPP-IV → DPP-IV activity inhibition of Hb digests
In vitro colorimetric assays

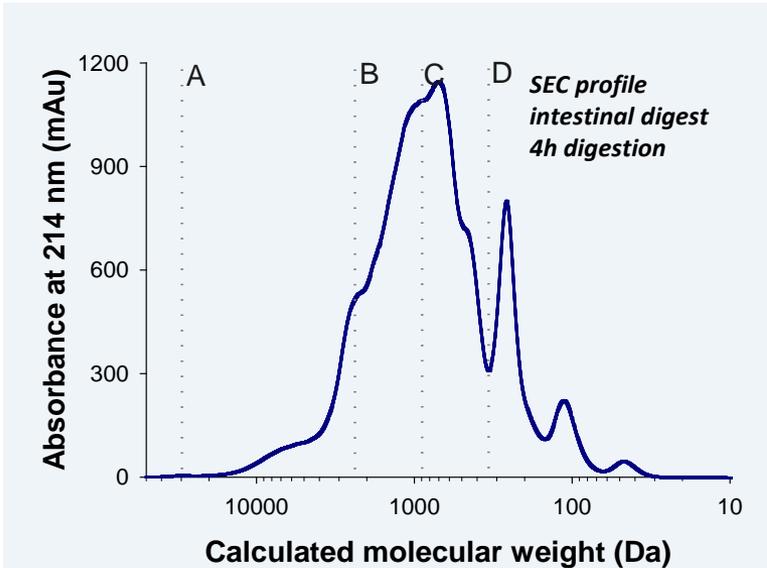
Intestinal DPP-IV inhibition activity is enhanced during GI digestion

Final intestinal hydrolysate: best bioactivity like for intestinal hormone



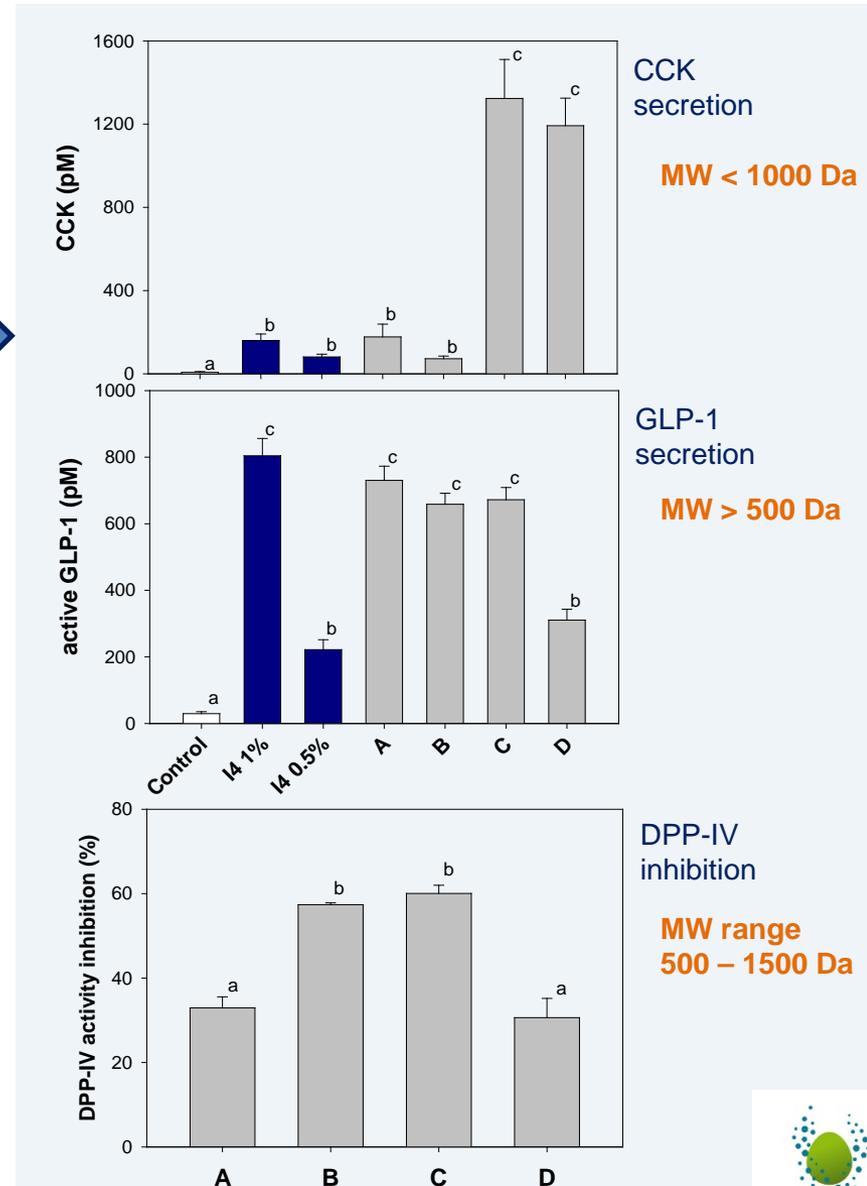
- > **Physiological relevance, same peptides involved?**
- > **Need to identify resistant active sequences**

● Size exclusion chromatography

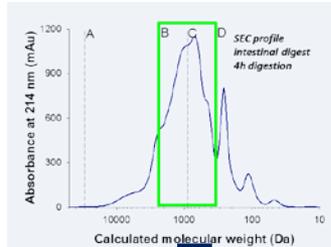


CCK and GLP-1 different peptide groups involved

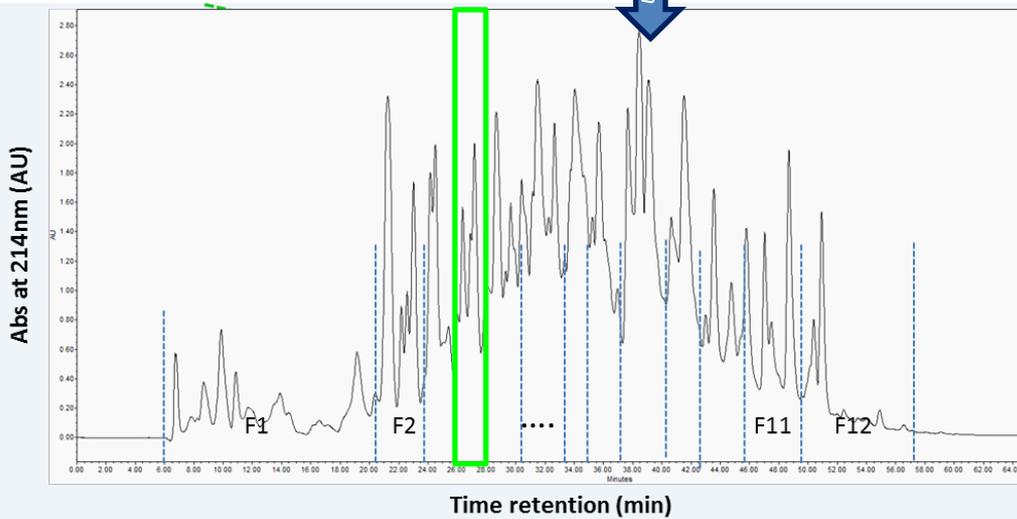
-----> DPP-IV and GLP-1
Same peptides involved?



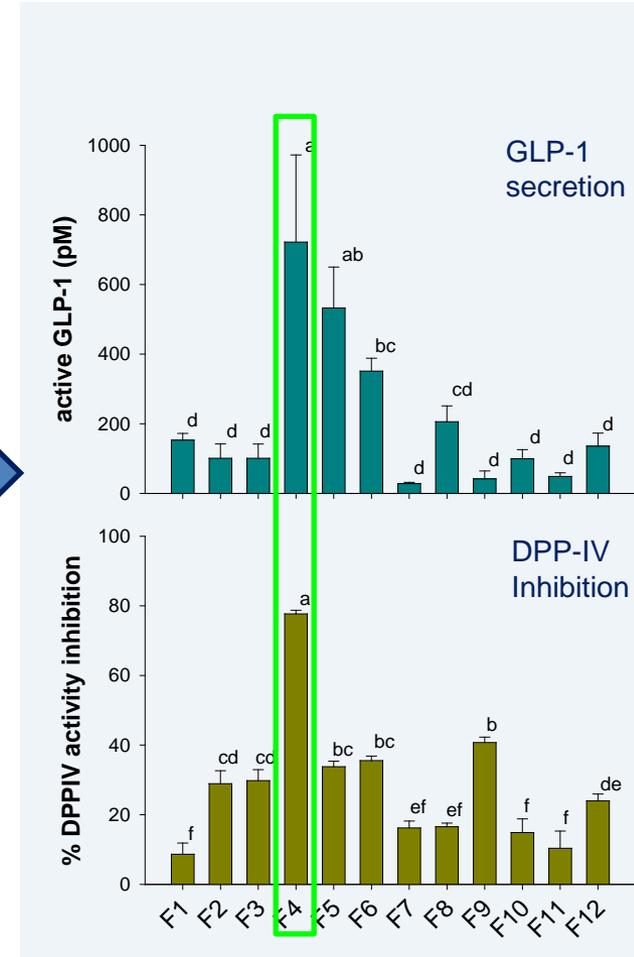
C18 RP-HPLC



Separation



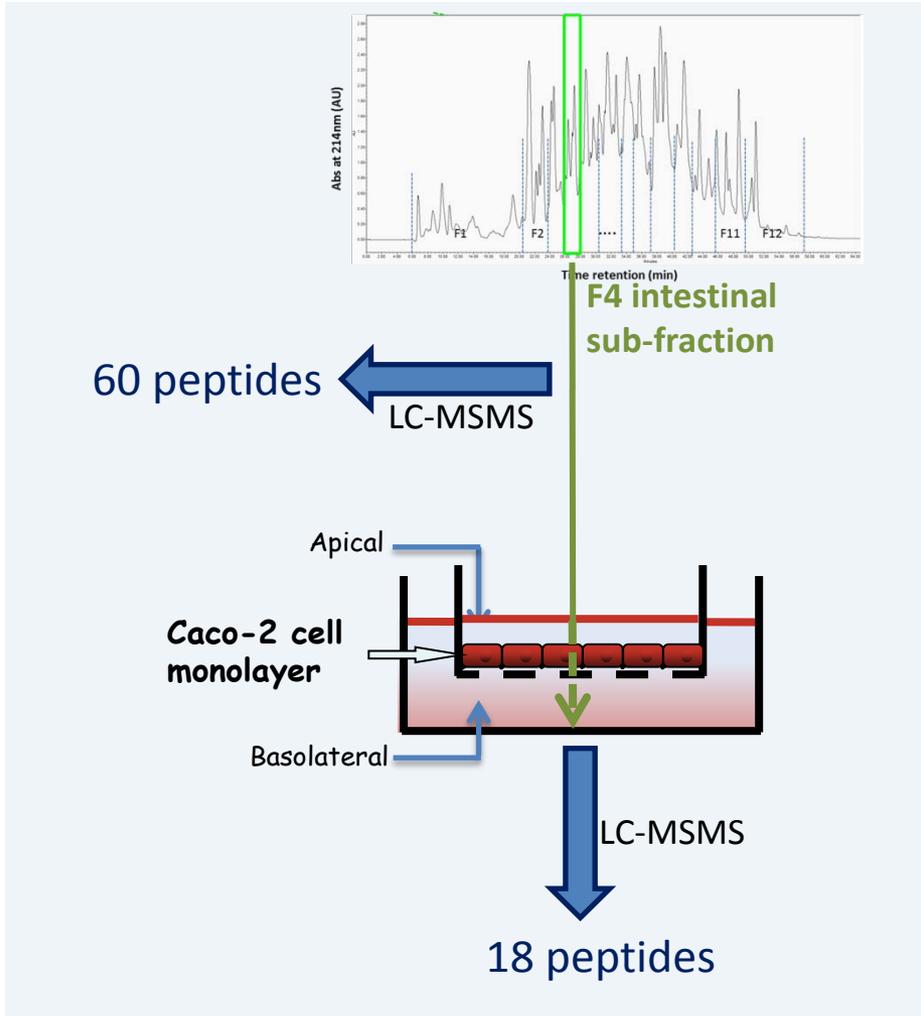
bioactivities



Peptides contained in F4 both stimulate GLP-1 secretion and inhibit DPP-IV activity



Peptide identification and passage across intestinal wall



HB_A: full sequence

VLSAADKGNVKA AWGKVGGHAAEYGAELERMFLSFPTTKTYFPHFDLSHGSAQVKGHGAKV

141 amino acids

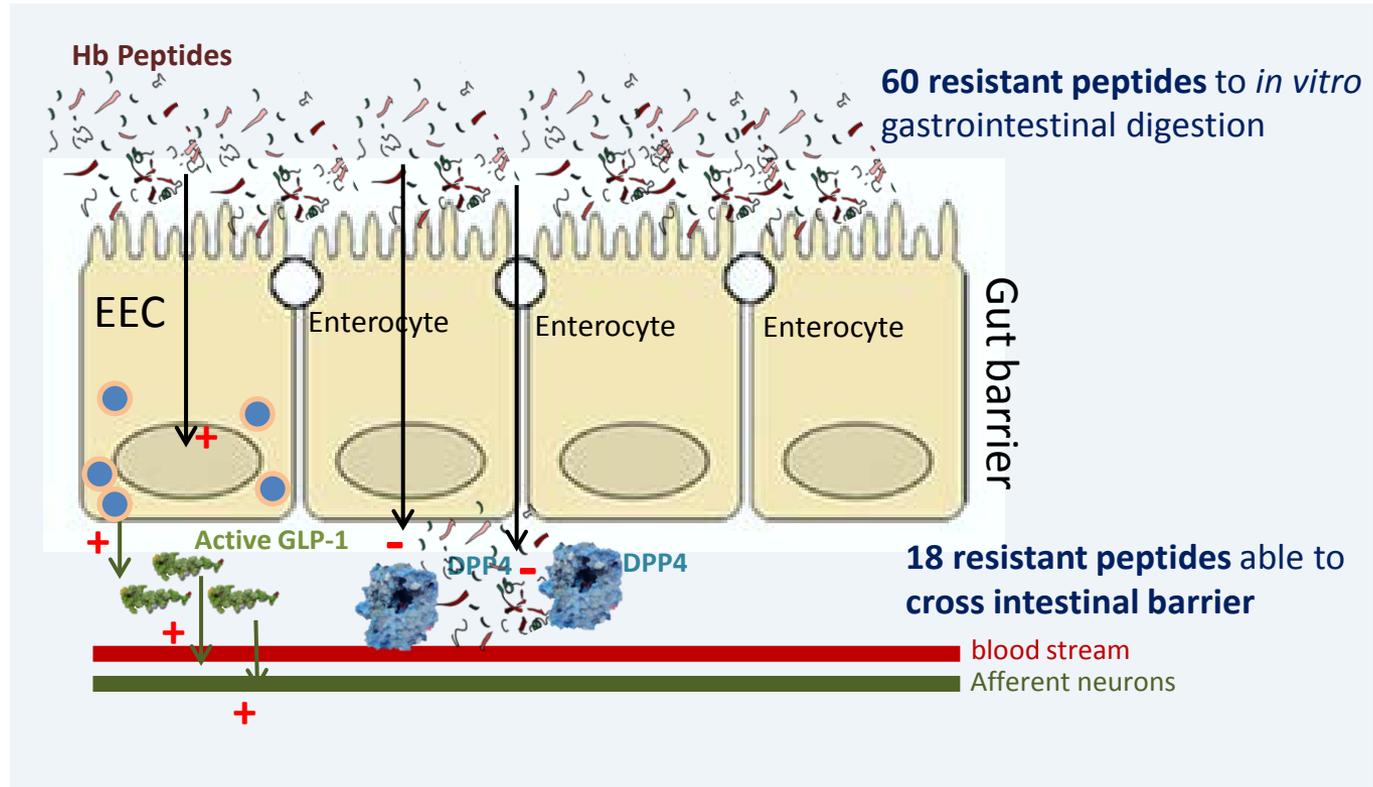
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36
V	L	S	A	A	D	K	G	N	V	K	A	A	W	G	K	V	G	G	H	A	A	E	Y	G	A	E	A	L	E	R	M	F	L	S	F

11 13 20 21 23 23 24 24 25 24 34 33 33 37 36 49 49 49 47 47 47 42 39 39 39 36 34 33 33 33 37 45 43 41



Protein	Sequence	Mass (Da)
HBA_BOVIN	ADKGNV	602.3024
HBA_BOVIN	ADKGNVK	730.3973
HBA_BOVIN	SAADKGNV	760.3715
HBA_BOVIN	SAADKGNVKA	959.5035
HBA_BOVIN	DLHAH	591.28
HBA_BOVIN	SDLHAHK	806.4035
HBB_BOVIN	SDLHAH	678.3085
HBA_BOVIN	DLSHGSAQ	813.3617
HBA_BOVIN	KAAVT	488.2958
HBA_BOVIN	MNNPK	602.2846
HBA_BOVIN	SLDK	461.24
HBA_BOVIN	VAAA	330.19
HBA_BOVIN	VDPVN	542.27
HBA_BOVIN	VGGHAAE	639.2976
HBA_BOVIN	YGAE	438.175
HBA_BOVIN	YGAEA	509.2122
HBB_BOVIN	ANVST	490.2387
HBB_BOVIN	LTAE EK	689.3596

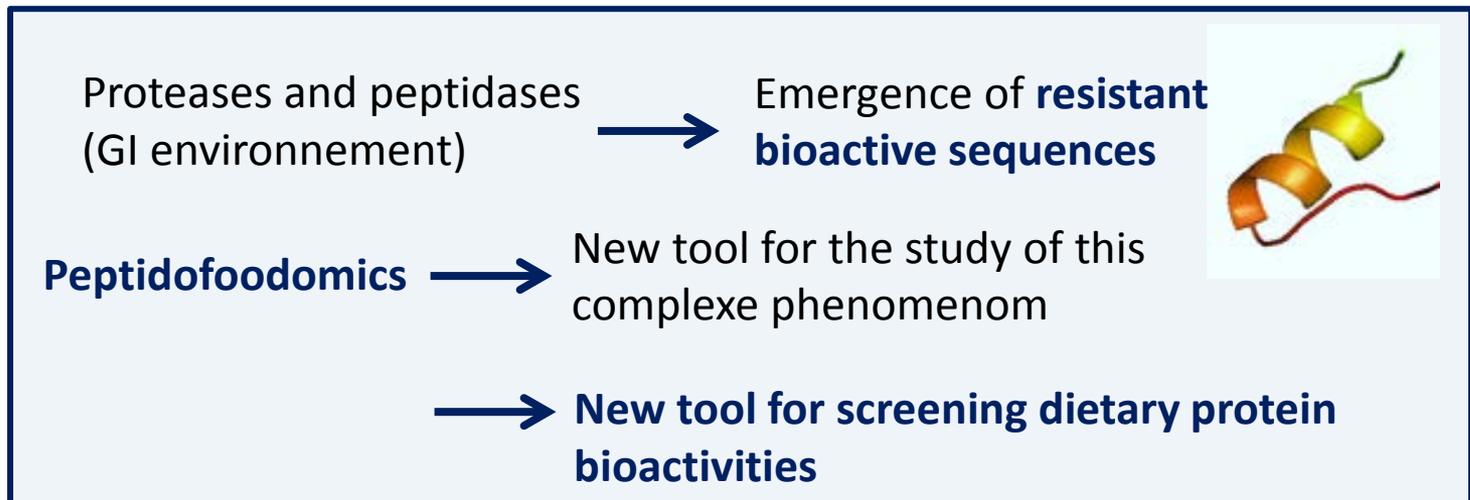
GLP-1 / DPP4



- Significant increase of both GLP-1 secretion and proglucagon gene expression
- Inhibition of DPP-IV activity
- Extending GLP-1 actions (food intake regulation and incretin effect)

● Hemoglobin peptidomes

- More than **700 sequences unambiguously identified** in gastric and intestinal peptidomes
- **Specific cleavages sites** identified
- Resistant sequences identified – **recurent patterns**
- These recurring patterns were made of amino acids that **could be potential preferential cleavage sites** with regard to enzyme specificity.
- **No particular link** between enzyme resistivity and isoelectric point or hydrophobicity index has been found out so far.
- **Peptide conformations** could prevent or slower enzyme activity. **Secondary structure implicated.**



Thank you for your attention !



Charles Violette
research Institute

**Institut Charles
VIOLETTE**



Université
de Lille
1 SCIENCES
ET TECHNOLOGIES



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