

# Characterizing the binding of bovine growth hormone with its induced binding proteins

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### Background

The recombinant bovine growth hormone (rbGH) is administered to cows to enhance milk production. RbGH is a 191 amino acid long protein and although it differs only 1 amino acid from the endogenous form, in 75% of the dairy cows an effect is triggered by the formation of a binding protein.

## **Objective**

RbGH use is pinpointed by, amongst others, detection of the binding proteins formed after rbGH administration. Characterization of these binding proteins by determination of the epitopes they target, and determination if individual cows react on the same epitope, establishes new opportunities in method development.

#### **Experimental**

PHE2 A1	>sp P01246 SOMA_BOVIN Somatotropin OS=Bos taurus GN=GH1 PE=1 SV=1 MMAAGPRTSLLLAFALLCLPWTQVVGAF PAMSLSGLFANAVLRAQHLHQLAADTFK EFERTYIPEGQRYSIQNTQVAFCFSETIPAP TGKNEAQQKSDLELLRISLLLIQSWLGPLQ	KQTYDKFDTNMRSD	<b>CATYDKFDTNMRSDM</b>	<b>XTYDKFDTNMRSDMF</b>	<b>YDKF</b> DTNMRSDMFP	

# Conclusions

- QTYDKFDTNMRSDMF is the most discriminative epitope as determined manually and with multivariate analyses.
- Tyrosine, lysine and phenylalanine are the most important aminoacids needed for binding to the binding protein.

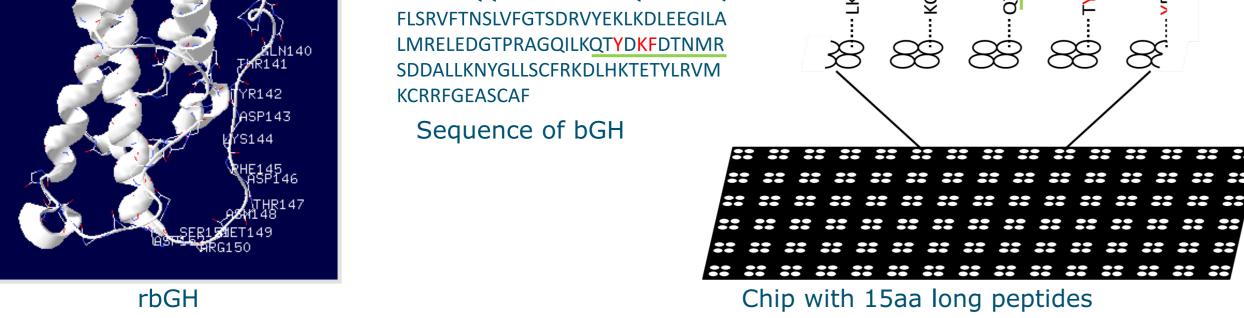
## Outlook

First step was determination of the most discriminative epitope for opportunities in method development; next steps:

- Closer understanding of the interaction of the binding proteins to rbGH and the most discriminative epitope.
- Knowledge on how binding affinities are influenced by the nature of peptide or protein presentation, i.e. in solution or fixed to a platform.

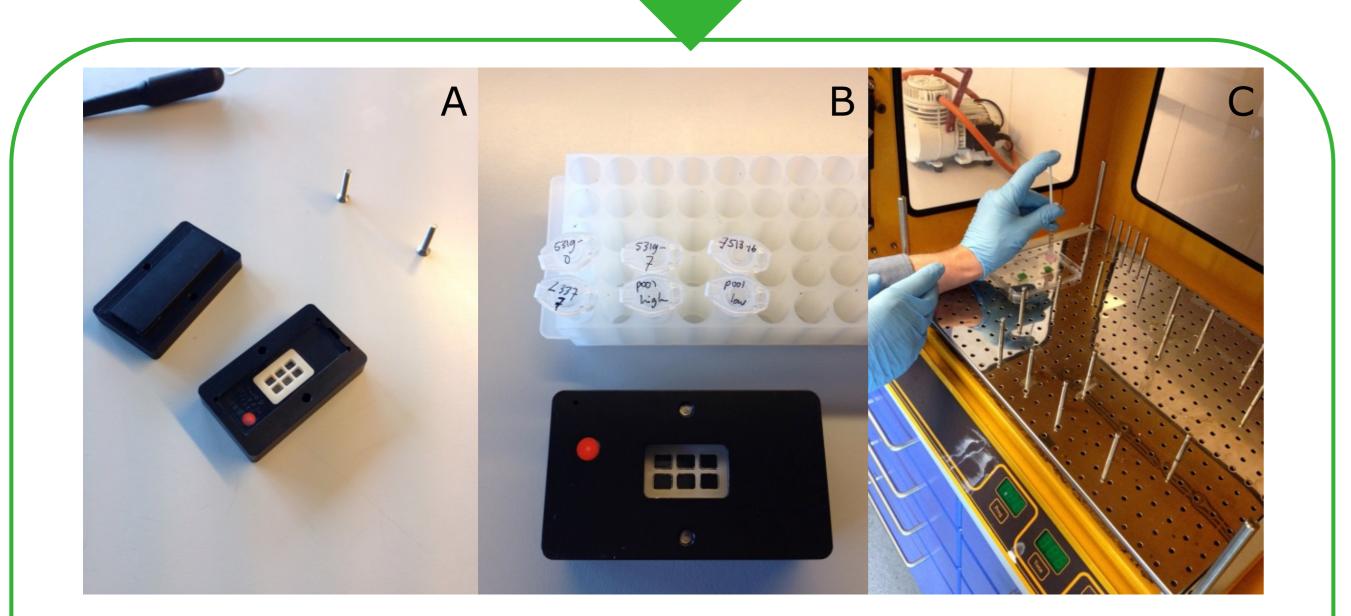
# Results

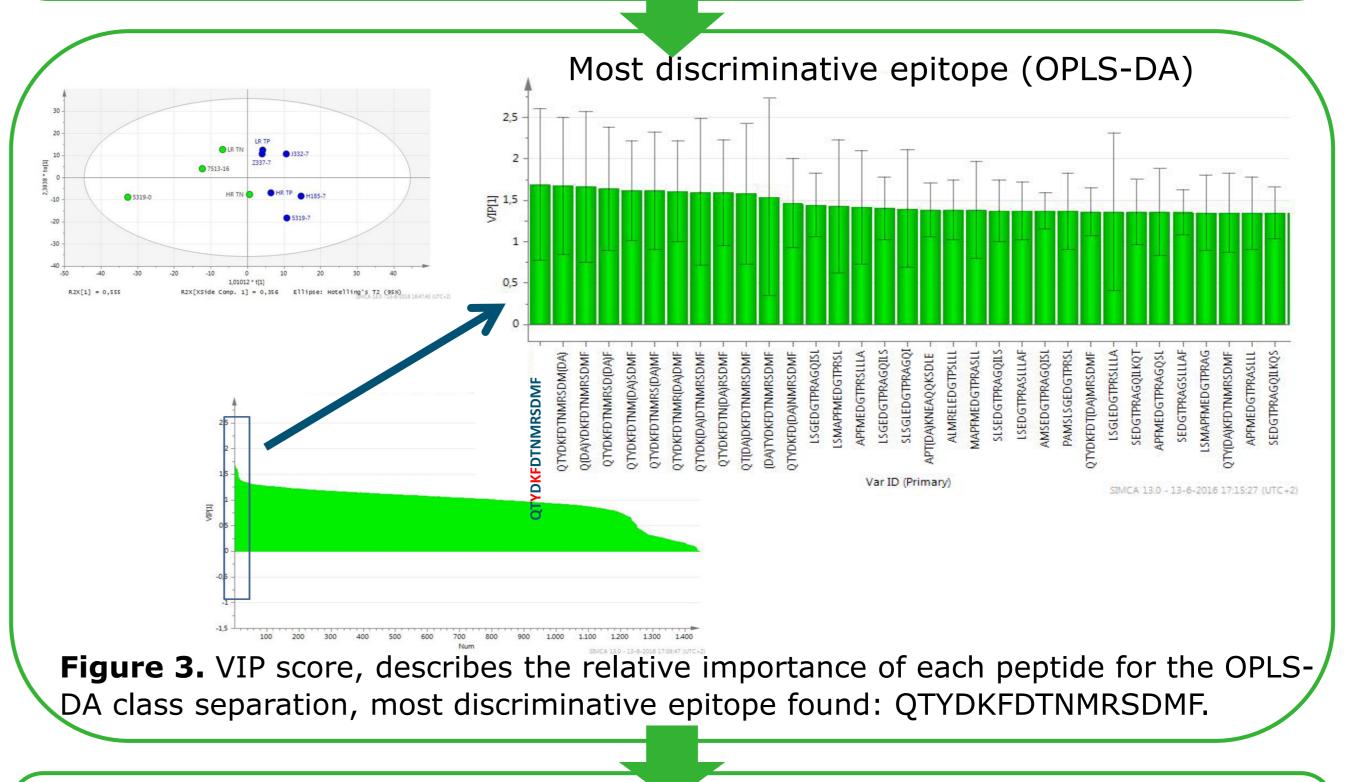
Signals of each sample for 1500 different peptides were obtained and manually judged. To verify the manual judgement Multi Variate analyses was executed (Figure 3) and similar results were found.



**Figure 1.** 15 aminoacid long peptides were synthesized in 2x2 mirrors on a chip. The total bST sequence was used for synthesis; for each new 15 aa long peptide, starting point was the next aa compared to the aa used in the former synthesized peptide, until the total bST protein is synthesized.

<b>Table 1.</b> 10 cow serum samples were	Before rbGH treatment	After rbGH treatment				
selected on prior binding results obtained with a bead based assay where rbST	Cow 1, 2	Cow 1, 3, 4, 5				
coated beads were incubated with the cow	Pool* 1, 2	Pool* 1, 2				
serum samples.	* Each pool contair	* Each pool contains sera of 5 individual				
	COWS					





The importance of every single amino-acid of the most discriminative epitope QTYDKFDTNMRSDMF is explored by single substitution with D-alanine (Table 2).

**Table 2.** Signals obtained after single substitution of each amino-acid with Dalanine as shown in the epitope sequences mentioned in the left column. Signals > highest signal obtained from samples taken before treatment are highlighted in green. When an important amino-acid is replaced, the signal drops (red).

		Delote IDSI	treatment		AIter IDST treatment						
Epitope sequence	Cow 1	Cow 2	Pool 1	Pool 2	Cow 1	Cow 3	Cow 4	Cow 5	Pool 1	Pool 2	

**Figure 2.** 6 sector device to clip the glass slide containing the peptide sectors, enabling incubation with the serum samples (A,B) for one hour, followed by half an hour secondairy antibody (GAB-CY3) incubation (C). Read out was done by a fluorescence microscope equipped with a digital camera.

	QTYDKFDTNMRSDMF	19	29	53	24	98	134	104	113	128	45	
	(DA)TYDKFDTNMRSDMF	43	41	62	34	138	136	150	114	135	62	
	Q(DA)YDKFDTNMRSDMF	18	29	49	23	81	118	95	106	93	50	
	QT <mark>(DA)</mark> DKFDTNMRSDMF	14	17	40	17	71	77	57	77	68	29	
	QTY(DA)KFDTNMRSDMF	23	37	57	28	98	114	87	73	97	39	
	QTYD <mark>(DA)</mark> FDTNMRSDMF	19	28	47	23	65	68	47	69	59	32	
	QTYDK <mark>(DA)</mark> DTNMRSDMF	15	19	41	19	74	77	64	75	80	34	
	QTYDKF(DA)TNMRSDMF	21	34	51	27	105	100	66	42	75	41	
	QTYDKFD(DA)NMRSDMF	24	31	54	26	104	151	78	68	97	45	
	QTYDKFDT(DA)MRSDMF	18	28	45	24	84	118	71	40	80	38	
	QTYDKFDTN(DA)RSDMF	19	26	46	23	82	133	90	56	99	48	
	QTYDKFDTNM(DA)SDMF	16	26	47	20	85	131	80	56	100	46	
	QTYDKFDTNMRS(DA)DMF	19	25	54	23	96	137	102	60	118	45	
	QTYDKFDTNMRS(DA)MF	20	34	54	27	123	145	103	89	113	47	
$\mathbf{X}$	QTYDKFDTNMRSD(DA)F	20	31	54	26	101	139	106	84	120	51	
	QTYDKFDTNMRSDM(DA)	18	29	53	25	103	133	93	102	121	47	



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